

Gene	Length	M48 TotalReads	M48 GeneReads	M48 RPKM	M48 log2RPKM	P TotalReads	P GeneReads	P RPKM	P log2RPKM	P/ M48 RPKM	G TotalReads	G GeneReads	G RPKM	G log2RPKM	G/ 48 RPKM	COG class defination	Color	Function class defination	Function code(first letter)
gene_111 GeneMark.hmm 105_nt - 79573 79677	105	3992207	21	50.1	5.65	11741144	10	8.11	3.02	-2.63	9397981	0	0	0	-5.65	Aspartate carbamoyltransferase, catalytic chain	METABOLISM	Nucleotide transport and metabolism	F
gene_1001 GeneMark.hmm 1152_nt - 94173 95324	1152	3992207	3327	723.41	9.5	11741144	6142	454.1	8.83	-0.67	9397981	3229	298.25	8.22	-1.28	Predicted Zn peptidase	METABOLISM	Amino acid transport and metabolism	E
gene_1002 GeneMark.hmm 732_nt - 95339 96070	732	3992207	2074	709.72	9.47	11741144	4199	488.57	8.93	-0.54	9397981	2425	352.51	8.46	-1.01	---	---	---	---
gene_1003 GeneMark.hmm 777_nt - 96372 97148	777	3992207	51	16.44	4.04	11741144	523	57.33	5.84	1.8	9397981	379	51.9	5.7	1.66	Tryptophan synthase alpha chain	METABOLISM	Amino acid transport and metabolism	E
gene_1004 GeneMark.hmm 1224_nt - 97141 98364	1224	3992207	46	9.41	3.23	11741144	454	31.59	4.98	1.75	9397981	424	36.86	5.2	1.97	Tryptophan synthase beta chain	METABOLISM	Amino acid transport and metabolism	E
gene_1005 GeneMark.hmm 531_nt - 98494 99024	531	3992207	16	7.55	2.92	11741144	152	24.38	4.61	1.69	9397981	153	30.66	4.94	2.02	Phosphoribosylanthranilate isomerase	METABOLISM	Amino acid transport and metabolism	E
gene_2779 GeneMark.hmm 282_nt + 1 282	282	3992207	11204	9952.01	13.28	11741144	556	167.92	7.39	-5.89	9397981	1226	462.6	8.85	-4.43	---	---	---	---
gene_2188 GeneMark.hmm 876_nt + 2865 3740	876	3992207	7530	2153.17	11.07	11741144	704	68.45	6.1	-4.97	9397981	837	101.67	6.67	-4.4	ABC-type phosphate transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_2813 GeneMark.hmm 402_nt - 2 403	402	3992207	4832	3010.84	11.56	11741144	2777	588.35	9.2	-2.36	9397981	843	223.13	7.8	-3.76	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	METABOLISM	Energy production and conversion	C
gene_1009 GeneMark.hmm 567_nt - 100830 101396	567	3992207	24	10.6	3.41	11741144	183	27.49	4.78	1.37	9397981	123	23.08	4.53	1.12	Anthranilate/para-aminobenzoate synthases component II	METABOLISM	Amino acid transport and metabolism	E
gene_100 GeneMark.hmm 942_nt + 69926 70867	942	3992207	369	98.12	6.62	11741144	3392	306.69	8.26	1.64	9397981	2525	285.22	8.16	1.54	Membrane protein involved in the export of O-antigen and teichoic acid	POORLY CHARACTERIZED	General function prediction only	R
gene_1010 GeneMark.hmm 717_nt - 101393 102109	717	3992207	51	17.82	4.16	11741144	279	33.14	5.05	0.89	9397981	161	23.89	4.58	0.42	Anthranilate/para-aminobenzoate synthases component I	METABOLISM	Amino acid transport and metabolism	E
gene_2154 GeneMark.hmm 747_nt - 85847 86593	747	3992207	5760	1931.47	10.92	11741144	3580	408.18	8.67	-2.25	9397981	1040	148.14	7.21	-3.71	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	METABOLISM	Energy production and conversion	C

gene_1012 GeneM ark.hmm 132_nt 103178 103309	13 2	399 220 7	4	7.5 9	2.92	117 411 44	27	17. 42	4.12	1. 2	939 798 1	17	13. 7	3.78	0. 86	NA			
gene_1013 GeneM ark.hmm 1002_nt 104158 105159	10 02	399 220 7	194	48. 5	5.6	117 411 44	194 8	16 5.5 8	7.37	1. 77	939 798 1	884	93. 88	6.55	0. 95	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1014 GeneM ark.hmm 711_nt 105731 106441	71 1	399 220 7	23	8.1	3.02	117 411 44	318	38. 09	5.25	2. 23	939 798 1	154	23. 05	4.53	1. 51	Uncharacterized membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1783 GeneM ark.hmm 411_nt 49934 50344	41 1	399 220 7	540	32 9.1 1	8.36	117 411 44	387	80. 2	6.33	- 2. 03	939 798 1	97	25. 11	4.65	- 3. 71	Predicted hydrolase (HAD superfamily)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1016 GeneM ark.hmm 1011_nt 108147 109157	10 11	399 220 7	57	14. 12	3.82	117 411 44	647	54. 51	5.77	1. 95	939 798 1	247	26	4.7	0. 88	ABC-type spermidine/putrescine transport systems, ATPase components	METABOLISM	Amino acid transport and metabolism	E
gene_1017 GeneM ark.hmm 852_nt 109260 110111	85 2	399 220 7	39	11. 47	3.52	117 411 44	596	59. 58	5.9	2. 38	939 798 1	214	26. 73	4.74	1. 22	ABC-type Fe3+ transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1018 GeneM ark.hmm 180_nt 110147 110326	18 0	399 220 7	7	9.7 4	3.28	117 411 44	62	29. 34	4.87	1. 59	939 798 1	21	12. 41	3.63	0. 35	ABC-type Fe3+ transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1019 GeneM ark.hmm 660_nt 110351 111010	66 0	399 220 7	35	13. 28	3.73	117 411 44	199	25. 68	4.68	0. 95	939 798 1	84	13. 54	3.76	0. 03	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1578 GeneM ark.hmm 852_nt + 57643 58494	85 2	399 220 7	553 2	16 26. 41	10.6 7	117 411 44	460	45. 98	5.52	- 5. 15	939 798 1	100 7	12 5.7 6	6.97	- 3. 7	---	---	---	---
gene_1020 GeneM ark.hmm 2127_nt 112031 114157	21 27	399 220 7	88	10. 36	3.37	117 411 44	119 1	47. 69	5.58	2. 21	939 798 1	556	27. 81	4.8	1. 43	Endopolygalacturonase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1021 GeneM ark.hmm 1227_nt 115294 116520	12 27	399 220 7	280 4	57 2.4 3	9.16	117 411 44	127 44	88 4.6 1	9.79	0. 63	939 798 1	147 36	12 77. 91	10.3 2	1. 16	Predicted pyridoxal phosphate- dependent enzyme apparently involved in regulation of cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1022 GeneM ark.hmm 693_nt 116563 117255	69 3	399 220 7	874	31 5.9 1	8.3	117 411 44	754 3	92 7.0 4	9.86	1. 56	939 798 1	559 9	85 9.6 9	9.75	1. 45	Sugar transferases involved in lipopolysaccharide synthesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1023 GeneM ark.hmm 615_nt 117428 118042	61 5	399 220 7	431	17 5.5 5	7.46	117 411 44	181 0	25 0.6 6	7.97	0. 51	939 798 1	224 5	38 8.4 2	8.6	1. 14	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1024 GeneM ark.hmm 1131_nt 118097 119227	11 31	399 220 7	515	11 4.0 6	6.83	117 411 44	270 7	20 3.8 5	7.67	0. 84	939 798 1	270 8	25 4.7 7	7.99	1. 16	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V

gene_1025 GeneM ark.hmm 1746_nt - 119217 120962	17 46	399 220 7	485	69. 58	6.12	117 411 44	342 6	16 7.1 2	7.38	1. 26	939 798 1	336 2	20 4.8 9	7.68	1. 56	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1026 GeneM ark.hmm 531_nt - 121090 121620	53 1	399 220 7	61	28. 78	4.85	117 411 44	795	12 7.5 2	6.99	2. 14	939 798 1	350	70. 14	6.13	1. 28	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1027 GeneM ark.hmm 180_nt - 121617 121796	18 0	399 220 7	22	30. 62	4.94	117 411 44	225	10 6.4 6	6.73	1. 79	939 798 1	88	52. 02	5.7	0. 76	---	---	---	---
gene_1028 GeneM ark.hmm 228_nt - 121846 122073	22 8	399 220 7	50	54. 93	5.78	117 411 44	375	14 0.0 8	7.13	1. 35	939 798 1	148	69. 07	6.11	0. 33	---	---	---	---
gene_1029 GeneM ark.hmm 828_nt + 122206 123033	82 8	399 220 7	233 1	70 5.1 8	9.46	117 411 44	883 0	90 8.2 8	9.83	0. 37	939 798 1	439 6	56 4.9 3	9.14	- 0. 32	Exonuclease III	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_102 GeneMa rk.hmm 804_nt + 7 1498 72301	80 4	399 220 7	105 3	32 8.0 6	8.36	117 411 44	449 9	47 6.6	8.9	0. 54	939 798 1	368 6	48 7.8 3	8.93	0. 57	LPS biosynthesis protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1030 GeneM ark.hmm 144_nt + 123045 123188	14 4	399 220 7	40	69. 58	6.12	117 411 44	181	10 7.0 5	6.74	0. 62	939 798 1	85	62. 81	5.97	- 0. 15	Lactoylglutathione lyase and related lyases	METABOLISM	Amino acid transport and metabolism	E
gene_1031 GeneM ark.hmm 240_nt + 123188 123427	24 0	399 220 7	67	69. 93	6.13	117 411 44	500	17 7.4 4	7.47	1. 34	939 798 1	303	13 4.3 4	7.07	0. 94	Lactoylglutathione lyase and related lyases	METABOLISM	Amino acid transport and metabolism	E
gene_862 GeneMa rk.hmm 447_nt - 18288 18734	44 7	399 220 7	101 77	57 02. 95	12.4 8	117 411 44	608 1	11 58. 66	10.1 8	- 2. 3	939 798 1	188 0	44 7.5 2	8.81	- 3. 67	---	---	---	---
gene_1752 GeneM ark.hmm 771_nt + 23717 24487	77 1	399 220 7	313 2	10 17. 55	9.99	117 411 44	173 4	19 1.5 5	7.58	- 2. 41	939 798 1	589	81. 29	6.34	- 3. 65	---	---	---	---
gene_1034 GeneM ark.hmm 462_nt - 126150 126611	46 2	399 220 7	57	30. 9	4.95	117 411 44	623	11 4.8 5	6.84	1. 89	939 798 1	274	63. 11	5.98	1. 03	---	---	---	---
gene_1035 GeneM ark.hmm 765_nt - 126608 127372	76 5	399 220 7	136	44. 53	5.48	117 411 44	103 0	11 4.6 7	6.84	1. 36	939 798 1	655	91. 11	6.51	1. 03	---	---	---	---
gene_1036 GeneM ark.hmm 405_nt - 127553 127957	40 5	399 220 7	80	49. 48	5.63	117 411 44	150 8	31 7.1 3	8.31	2. 68	939 798 1	342	89. 85	6.49	0. 86	Uncharacterized protein, possibly involved in aromatic compounds catabolism	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_1037 GeneM ark.hmm 1482_nt - 128027 129508	14 82	399 220 7	291	49. 18	5.62	117 411 44	236 6	13 5.9 7	7.09	1. 47	939 798 1	494	35. 47	5.15	- 0. 47	Galactose-1-phosphate uridylyltransferase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1038 GeneM ark.hmm 1179_nt - 129527 130705	11 79	399 220 7	136	28. 89	4.85	117 411 44	139 1	10 0.4 9	6.65	1. 8	939 798 1	361	32. 58	5.03	0. 18	Galactokinase	METABOLISM	Carbohydrate transport and metabolism	G

gene_1039 GeneM ark.hmm 1008_nt + 130870 131877	10 08	399 220 7	678	16 8.4 8	7.4	117 411 44	425 8	35 9.7 8	8.49	1. 09	939 798 1	136 7	14 4.3	7.17	- 0. 23	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_103 GeneMa rk.hmm 810_nt + 7 2303 73112	81 0	399 220 7	902	27 8.9 4	8.12	117 411 44	367 3	38 6.2 1	8.59	0. 47	939 798 1	245 0	32 1.8 4	8.33	0. 21	LPS biosynthesis protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1040 GeneM ark.hmm 1038_nt 131923 132960	10 38	399 220 7	718	17 3.2 7	7.44	117 411 44	942	77. 29	6.27	- 1. 17	939 798 1	405	41. 52	5.38	- 2. 06	Threonine dehydrogenase and related Zn-dependent dehydrogenases	METABOLISM	Amino acid transport and metabolism	E
gene_1041 GeneM ark.hmm 354_nt 132961 133314	35 4	399 220 7	53	37. 5	5.23	117 411 44	255	61. 35	5.94	0. 71	939 798 1	106	31. 86	4.99	- 0. 24	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1042 GeneM ark.hmm 891_nt 133558 134448	89 1	399 220 7	127	35. 7	5.16	117 411 44	447	42. 73	5.42	0. 26	939 798 1	254	30. 33	4.92	- 0. 24	Co/Zn/Cd efflux system component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1043 GeneM ark.hmm 537_nt + 134581 135117	53 7	399 220 7	260	12 1.2 8	6.92	117 411 44	752	11 9.2 7	6.9	- 0. 02	939 798 1	346	68. 56	6.1	- 0. 82	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1044 GeneM ark.hmm 807_nt 135283 136089	80 7	399 220 7	71	22. 04	4.46	117 411 44	539	56. 89	5.83	1. 37	939 798 1	478	63. 03	5.98	1. 52	Nicotinamide mononucleotide transporter	METABOLISM	Coenzyme transport and metabolism	H
gene_1045 GeneM ark.hmm 1521_nt 136434 137954	15 21	399 220 7	510 0	83 9.9	9.71	117 411 44	820 1	45 9.2 3	8.84	- 0. 87	939 798 1	231 4	16 1.8 8	7.34	- 2. 37	Periplasmic glycine betaine/choline- binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1046 GeneM ark.hmm 729_nt 137947 138675	72 9	399 220 7	844	29 0	8.18	117 411 44	148 8	17 3.8 5	7.44	- 0. 74	939 798 1	725	10 5.8 2	6.73	- 1. 45	ABC-type proline/glycine betaine transport systems, ATPase components	METABOLISM	Amino acid transport and metabolism	E
gene_1047 GeneM ark.hmm 765_nt 138690 139454	76 5	399 220 7	756	24 7.5 4	7.95	117 411 44	161 3	17 9.5 8	7.49	- 0. 46	939 798 1	113 8	15 8.2 9	7.31	- 0. 64	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1048 GeneM ark.hmm 444_nt 139458 139901	44 4	399 220 7	759	42 8.2	8.74	117 411 44	145 3	27 8.7 2	8.12	- 0. 62	939 798 1	121 8	29 1.9	8.19	- 0. 55	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1049 GeneM ark.hmm 297_nt 140583 140879	29 7	399 220 7	405 5	34 19. 96	11.7 4	117 411 44	735 9	21 10. 34	11.0 4	- 0. 7	939 798 1	424 0	15 19. 06	10.5 7	- 1. 17	---	---	---	---
gene_104 GeneMa rk.hmm 1719_nt 73387 75105	17 19	399 220 7	289 0	42 1.1 2	8.72	117 411 44	542 3	26 8.6 9	8.07	- 0. 65	939 798 1	542 5	33 5.8 1	8.39	- 0. 33	Carbamoylphosphate synthase large subunit (split gene in MJ)	METABOLISM	Amino acid transport and metabolism	E
gene_1050 GeneM ark.hmm 1065_nt 140901 141965	10 65	399 220 7	407 5	95 8.4 4	9.9	117 411 44	200 24	16 01. 37	10.6 5	0. 75	939 798 1	894 1	89 3.3 1	9.8	- 0. 1	Cellulase M and related proteins	METABOLISM	Carbohydrate transport and metabolism	G
gene_1051 GeneM ark.hmm 702_nt + 142364 143065	70 2	399 220 7	122	43. 53	5.44	117 411 44	795	96. 45	6.59	1. 15	939 798 1	556	84. 28	6.4	0. 96	UDP-glucose 4-epimerase	CELLULAR PROCESSES AND	Cell wall/membrane/envelope biogenesis	M

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gene_1052 GeneM ark.hmm 960_nt + 143488 144447	96 0	399 220 7	337	87. 93	6.46	117 411 44	257 2	22 8.1 9	7.83	1. 37	939 798 1	136 8	15 1.6 3	7.24	0. 78	ABC-type enterochelin transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1053 GeneM ark.hmm 957_nt + 144437 145393	95 7	399 220 7	474	12 4.0 7	6.95	117 411 44	369 4	32 8.7 6	8.36	1. 41	939 798 1	934	10 3.8 5	6.7	- 0. 25	ABC-type enterochelin transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1054 GeneM ark.hmm 555_nt + 145390 145944	55 5	399 220 7	559	25 2.2 9	7.98	117 411 44	373 7	57 3.4 8	9.16	1. 18	939 798 1	575	11 0.2 4	6.78	- 1. 2	ABC-type enterochelin transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1055 GeneM ark.hmm 234_nt + 145944 146177	23 4	399 220 7	86	92. 06	6.52	117 411 44	599	21 8.0 2	7.77	1. 25	939 798 1	126	57. 3	5.84	- 0. 68	ABC-type enterochelin transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1056 GeneM ark.hmm 966_nt + 146273 147238	96 6	399 220 7	205 7	53 3.3 9	9.06	117 411 44	120 43	10 61. 81	10.0 5	0. 99	939 798 1	835	91. 98	6.52	- 2. 54	ABC-type enterochelin transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1057 GeneM ark.hmm 243_nt - 147510 147752	24 3	399 220 7	128	13 1.9 4	7.04	117 411 44	241	84. 47	6.4	- 0. 64	939 798 1	338	14 8	7.21	0. 17	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1058 GeneM ark.hmm 87_nt - 147752 147838	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1059 GeneM ark.hmm 630_nt - 147900 148529	63 0	399 220 7	694	27 5.9 3	8.11	117 411 44	159 0	21 4.9 5	7.75	- 0. 36	939 798 1	279 3	47 1.7 3	8.88	0. 77	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_105 GeneMa rk.hmm 147_nt - 75222 75368	14 7	399 220 7	18	30. 67	4.94	117 411 44	81	46. 93	5.55	0. 61	939 798 1	71	51. 39	5.68	0. 74	Carbamoylphosphate synthase large subunit (split gene in MJ)	METABOLISM	Amino acid transport and metabolism	E
gene_1060 GeneM ark.hmm 570_nt - 148516 149085	57 0	399 220 7	470	20 6.5 4	7.69	117 411 44	134 0	20 0.2 3	7.65	- 0. 04	939 798 1	245 1	45 7.5 5	8.84	1. 15	Predicted transcriptional regulator containing the HTH domain	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1061 GeneM ark.hmm 729_nt - 149104 149832	72 9	399 220 7	142 9	49 1.0 1	8.94	117 411 44	268 4	31 3.5 8	8.29	- 0. 65	939 798 1	464 3	67 7.7	9.4	0. 46	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1062 GeneM ark.hmm 741_nt - 149832 150572	74 1	399 220 7	666	22 5.1 3	7.81	117 411 44	215 4	24 7.5 8	7.95	0. 14	939 798 1	339 0	48 6.8	8.93	1. 12	Integrase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1063 GeneM ark.hmm 462_nt - 150563 151024	46 2	399 220 7	537	29 1.1 5	8.19	117 411 44	865	15 9.4 6	7.32	- 0. 87	939 798 1	114 3	26 3.2 5	8.04	- 0. 15	FOG: CBS domain	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1064 GeneM ark.hmm 522_nt - 151021 151542	52 2	399 220 7	529	25 3.8 5	7.99	117 411 44	118 2	19 2.8 6	7.59	- 0. 4	939 798 1	151 5	30 8.8 2	8.27	0. 28	Predicted phosphoesterase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1065 GeneM ark.hmm 972_nt - 151518 152489	97 2	399 220 7	275 0	70 8.6 9	9.47	117 411 44	549 0	48 1.0 6	8.91	- 0. 56	939 798 1	652 0	71 3.7 5	9.48	0. 01	Xanthosine triphosphate pyrophosphatase	METABOLISM	Nucleotide transport and metabolism	F

gene_1066 GeneM ark.hmm 837_nt - 152486 153322	83 7	399 220 7	666	19 9.3 1	7.64	117 411 44	168 0	17 0.9 5	7.42	- 0. 22	939 798 1	155 2	19 7.3	7.62	- 0. 02	Glutamate racemase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1067 GeneM ark.hmm 249_nt - 153529 153777	24 9	399 220 7	469	47 1.8	8.88	117 411 44	396 7	13 56. 91	10.4 1	1. 53	939 798 1	184 2	78 7.1 5	9.62	0. 74	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1068 GeneM ark.hmm 1626_nt - 154033 155658	16 26	399 220 7	70	10. 78	3.43	117 411 44	735	38. 5	5.27	1. 84	939 798 1	363	23. 75	4.57	1. 14	Glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_1069 GeneM ark.hmm 1863_nt - 155836 157698	18 63	399 220 7	62	8.3 4	3.06	117 411 44	810	37. 03	5.21	2. 15	939 798 1	331	18. 91	4.24	1. 18	Phosphotransferase system IIC components, glucose/maltose/N- acetylglucosamine-specific	METABOLISM	Carbohydrate transport and metabolism	G
gene_106 GeneMa rk.hmm 141_nt - 75681 75821	14 1	399 220 7	10	17. 77	4.15	117 411 44	54	32. 62	5.03	0. 88	939 798 1	46	34. 71	5.12	0. 97	Carbamoylphosphate synthase large subunit (split gene in MJ)	METABOLISM	Amino acid transport and metabolism	E
gene_1070 GeneM ark.hmm 102_nt - 157757 157858	10 2	399 220 7	0	0	0	117 411 44	1	0.8 4	- 0.26	- 0. 26	939 798 1	1	1.0 4	0.06	0. 06	Phosphotransferase system IIB components	METABOLISM	Carbohydrate transport and metabolism	G
gene_1071 GeneM ark.hmm 711_nt + 158043 158753	71 1	399 220 7	165	58. 13	5.86	117 411 44	275 3	32 9.7 8	8.37	2. 51	939 798 1	988	14 7.8 6	7.21	1. 35	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1072 GeneM ark.hmm 330_nt + 158908 159237	33 0	399 220 7	43	32. 64	5.03	117 411 44	379	97. 82	6.61	1. 58	939 798 1	660	21 2.8 1	7.73	2. 7	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1073 GeneM ark.hmm 465_nt + 376 840	46 5	399 220 7	284	15 2.9 9	7.26	117 411 44	125 2	22 9.3 2	7.84	0. 58	939 798 1	643	14 7.1 4	7.2	- 0. 06	GAF domain-containing protein	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1074 GeneM ark.hmm 1656_nt + 840 2495	16 56	399 220 7	306 6	46 3.7 7	8.86	117 411 44	937 0	48 1.9 1	8.91	0. 05	939 798 1	584 1	37 5.3 1	8.55	- 0. 31	DNA polymerase III, gamma/tau subunits	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1075 GeneM ark.hmm 195_nt + 2523 2717	19 5	399 220 7	53	68. 08	6.09	117 411 44	112 7	49 2.2 4	8.94	2. 85	939 798 1	251	13 6.9 6	7.1	1. 01	---	---	---	---
gene_1076 GeneM ark.hmm 771_nt + 2867 3637	77 1	399 220 7	530	17 2.1 9	7.43	117 411 44	238 0	26 2.9 1	8.04	0. 61	939 798 1	145 9	20 1.3 6	7.65	0. 22	ABC-type transport system involved in Fe-S cluster assembly, ATPase component	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1077 GeneM ark.hmm 1263_nt + 3665 4927	12 63	399 220 7	201 3	39 9.2 3	8.64	117 411 44	451 3	30 4.3 3	8.25	- 0. 39	939 798 1	277 2	23 3.5 4	7.87	- 0. 77	ABC-type transport system involved in Fe-S cluster assembly, permease component	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1078 GeneM ark.hmm 1227_nt + 4938 6164	12 27	399 220 7	143 3	29 2.5 4	8.19	117 411 44	508 5	35 2.9 7	8.46	0. 27	939 798 1	316 6	27 4.5 6	8.1	- 0. 09	Selenocysteine lyase	METABOLISM	Amino acid transport and metabolism	E
gene_1079 GeneM ark.hmm 441_nt +	44	399 220	582	33 0.5	8.37	117 411	131	25 4.7	7.99	- 0.	939 798	923	22	7.8	- 0.	NifU homolog involved in Fe-S	METABOLISM	Energy production and conversion	C

6151 6591	1	7		8		44	9	4		38	1		2.7		57	cluster formation			
gene_107 GeneMa rk.hmm 1107_nt 76052 77158	11 07	399 220 7	475	10 7.4 8	6.75	117 411 44	152 0	11 6.9 5	6.87	0. 12	939 798 1	149 5	14 3.7	7.17	0. 42	Carbamoylphosphate synthase large subunit (split gene in MJ)	METABOLISM	Amino acid transport and metabolism	E
gene_1080 GeneM ark.hmm 678_nt + 6645 7322	67 8	399 220 7	200 3	74 0.0 1	9.53	117 411 44	288 9	36 2.9 2	8.5	- 1. 03	939 798 1	217 4	34 1.1 9	8.41	- 1. 12	ABC-type transport system involved in Fe-S cluster assembly, permease component	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1081 GeneM ark.hmm 753_nt + 7340 8092	75 3	399 220 7	140 8	46 8.3 8	8.87	117 411 44	344 7	38 9.8 8	8.61	- 0. 26	939 798 1	211 2	29 8.4 5	8.22	- 0. 65	ABC-type transport system involved in Fe-S cluster assembly, permease component	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1082 GeneM ark.hmm 1242_nt 8323 9564	12 42	399 220 7	353 3	71 2.5 4	9.48	117 411 44	149 93	10 28. 15	10.0 1	0. 53	939 798 1	484 2	41 4.8 3	8.7	- 0. 78	D-alanyl-D-alanine carboxypeptidase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1083 GeneM ark.hmm 1110_nt + 9667 10776	11 10	399 220 7	128 6	29 0.2 1	8.18	117 411 44	315 2	24 1.8 5	7.92	- 0. 26	939 798 1	287 2	27 5.3 1	8.1	- 0. 08	Predicted permease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1084 GeneM ark.hmm 57_nt 11782 11838	57	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1085 GeneM ark.hmm 741_nt + 12246 12986	74 1	399 220 7	315 5	10 66. 52	10.0 6	117 411 44	169 24	19 45. 25	10.9 3	0. 87	939 798 1	750 8	10 78. 13	10.0 7	0. 01	Transcriptional regulators of sugar metabolism	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1086 GeneM ark.hmm 555_nt + 12983 13537	55 5	399 220 7	382 7	17 27. 24	10.7 5	117 411 44	153 96	23 62. 68	11.2 1	0. 46	939 798 1	764 6	14 65. 91	10.5 2	- 0. 23	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	METABOLISM	Carbohydrate transport and metabolism	G
gene_1087 GeneM ark.hmm 351_nt + 13596 13946	35 1	399 220 7	412	29 4.0 2	8.2	117 411 44	371 8	90 2.1 8	9.82	1. 62	939 798 1	150 2	45 5.3 3	8.83	0. 63	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	METABOLISM	Carbohydrate transport and metabolism	G
gene_1088 GeneM ark.hmm 1089_nt + 13943 15031	10 89	399 220 7	390 3	89 7.7 5	9.81	117 411 44	343 24	26 84. 48	11.3 9	1. 58	939 798 1	167 95	16 41. 03	10.6 8	0. 87	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_1089 GeneM ark.hmm 855_nt + 15115 15969	85 5	399 220 7	203 5	59 6.1 9	9.22	117 411 44	198 69	19 79. 24	10.9 5	1. 73	939 798 1	931 5	11 59. 26	10.1 8	0. 96	Phosphotransferase system, fructose-specific IIC component	METABOLISM	Carbohydrate transport and metabolism	G
gene_108 GeneMa rk.hmm 552_nt 77501 78052	55 2	399 220 7	171 6	77 8.6 9	9.6	117 411 44	188 0	29 0.0 7	8.18	- 1. 42	939 798 1	232 7	44 8.5 6	8.81	- 0. 79	Carbamoylphosphate synthase small subunit	METABOLISM	Amino acid transport and metabolism	E
gene_1090 GeneM ark.hmm 2214_nt + 16203 18416	22 14	399 220 7	334 7	37 8.6 7	8.56	117 411 44	111 24	42 7.9 3	8.74	0. 18	939 798 1	927 8	44 5.9	8.8	0. 24	DNA segregation ATPase FtsK/SpoIIIE and related proteins	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1091 GeneM ark.hmm 429_nt 18567 18995	42 9	399 220 7	775 1	45 25. 72	12.1 4	117 411 44	109 06	21 65. 2	11.0 8	- 1. 06	939 798 1	118 22	29 32. 24	11.5 2	- 0. 62	---	---	---	---

gene_1092 GeneM ark.hmm 195_nt + 19133 19327	19 5	399 220 7	68	87. 35	6.45	117 411 44	380	16 5.9 7	7.37	0. 92	939 798 1	353	19 2.6 2	7.59	1. 14	Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes	METABOLISM	Amino acid transport and metabolism	E
gene_1093 GeneM ark.hmm 945_nt + 19392 20336	94 5	399 220 7	585	15 5.0 6	7.28	117 411 44	261 8	23 5.9 5	7.88	0. 6	939 798 1	268 6	30 2.4 4	8.24	0. 96	Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes	METABOLISM	Amino acid transport and metabolism	E
gene_1094 GeneM ark.hmm 1215_nt + 20345 21559	12 15	399 220 7	221 9	45 7.4 8	8.84	117 411 44	552 5	38 7.3	8.6	- 0. 24	939 798 1	517 3	45 3.0 3	8.82	- 0. 02	Thiamine biosynthesis ATP pyrophosphatase	METABOLISM	Coenzyme transport and metabolism	H
gene_1095 GeneM ark.hmm 825_nt + 21696 22520	82 5	399 220 7	222	67. 4	6.07	117 411 44	222 3	22 9.5	7.84	1. 77	939 798 1	222 2	28 6.5 9	8.16	2. 09	Predicted hydrolase of the alpha/beta superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1096 GeneM ark.hmm 696_nt + 22542 23237	69 6	399 220 7	185	66. 58	6.06	117 411 44	163 1	19 9.5 9	7.64	1. 58	939 798 1	147 6	22 5.6 5	7.82	1. 76	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1097 GeneM ark.hmm 408_nt + 23295 23702	40 8	399 220 7	114	69. 99	6.13	117 411 44	765	15 9.6 9	7.32	1. 19	939 798 1	876	22 8.4 6	7.84	1. 71	---	---	---	---
gene_1098 GeneM ark.hmm 741_nt + 23699 24439	74 1	399 220 7	156	52. 73	5.72	117 411 44	121 7	13 9.8 8	7.13	1. 41	939 798 1	165 8	23 8.0 8	7.9	2. 18	---	---	---	---
gene_1099 GeneM ark.hmm 1494_nt + 24947 26440	14 94	399 220 7	695	11 6.5 3	6.86	117 411 44	265 5	15 1.3 6	7.24	0. 38	939 798 1	179 2	12 7.6 3	7	0. 14	Type I restriction-modification system methyltransferase subunit	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_109 GeneMa rk.hmm 525_nt - 78130 78654	52 5	399 220 7	925	44 1.3 4	8.79	117 411 44	160 7	26 0.7	8.03	- 0. 76	939 798 1	159 7	32 3.6 8	8.34	- 0. 45	Carbamoylphosphate synthase small subunit	METABOLISM	Amino acid transport and metabolism	E
gene_10 GeneMar k.hmm 1014_nt - 5305 6318	10 14	399 220 7	551	13 6.1 1	7.09	117 411 44	134 9	11 3.3 1	6.82	- 0. 27	939 798 1	172 6	18 1.1 2	7.5	0. 41	ATPase involved in DNA repair	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1100 GeneM ark.hmm 402_nt + 26453 26854	40 2	399 220 7	179	11 1.5 4	6.8	117 411 44	673	14 2.5 9	7.16	0. 36	939 798 1	417	11 0.3 8	6.79	- 0. 01	Restriction endonuclease S subunits	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1101 GeneM ark.hmm 237_nt + 26914 27150	23 7	399 220 7	395	41 7.4 8	8.71	117 411 44	112 7	40 5.0 1	8.66	- 0. 05	939 798 1	137 3	61 6.4 4	9.27	0. 56	---	---	---	---
gene_1102 GeneM ark.hmm 414_nt + 27147 27560	41 4	399 220 7	221	13 3.7 1	7.06	117 411 44	630	12 9.6 1	7.02	- 0. 04	939 798 1	501	12 8.7 7	7.01	- 0. 05	Prophage maintenance system killer protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1103 GeneM ark.hmm 966_nt + 27678 28643	96 6	399 220 7	280	72. 61	6.18	117 411 44	178 5	15 7.3 8	7.3	1. 12	939 798 1	165 7	18 2.5 2	7.51	1. 33	Integrase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1104 GeneM ark.hmm 2202_nt + 29888 32089	22 02	399 220 7	212 7	24 1.9 6	7.92	117 411 44	799 4	30 9.2	8.27	0. 35	939 798 1	680 7	32 8.9 3	8.36	0. 44	Type I site-specific restriction- modification system, R (restriction) subunit and related helicases	CELLULAR PROCESSES AND	Defense mechanisms	V

																	SIGNALING		
gene_1105 GeneM ark.hmm 1095_nt + 32070 33164	10 95	399 220 7	140 7	32 1.8 6	8.33	117 411 44	774 1	60 2.1 1	9.23	0. 9	939 798 1	585 3	56 8.7 6	9.15	0. 82	Type I site-specific restriction- modification system, R (restriction) subunit and related helicases	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1106 GeneM ark.hmm 111_nt + 33435 33545	11 1	399 220 7	12	27. 08	4.76	117 411 44	20	15. 35	3.94	- 0. 82	939 798 1	6	5.7 5	2.52	- 2. 24	NA			
gene_1107 GeneM ark.hmm 471_nt - 33816 34286	47 1	399 220 7	231 3	12 30. 1	10.2 6	117 411 44	748 1	13 52. 78	10.4	0. 14	939 798 1	519 6	11 73. 85	10.2	- 0. 06	Arginine repressor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1108 GeneM ark.hmm 990_nt - 34303 35292	99 0	399 220 7	260 3	65 8.6 1	9.36	117 411 44	877 8	75 5.1 8	9.56	0. 2	939 798 1	602 7	64 7.7 9	9.34	- 0. 02	---	---	---	---
gene_1109 GeneM ark.hmm 1236_nt - 35364 36599	12 36	399 220 7	205 7	41 6.8 7	8.7	117 411 44	618 6	42 6.2 7	8.74	0. 04	939 798 1	299 7	25 8.0 1	8.01	- 0. 69	---	---	---	---
gene_1110 GeneMa rk.hmm 813_nt - 78704 79516	81 3	399 220 7	666	20 5.2	7.68	117 411 44	174 1	18 2.3 9	7.51	- 0. 17	939 798 1	190 9	24 9.8 5	7.96	0. 28	Aspartate carbamoyltransferase, catalytic chain	METABOLISM	Nucleotide transport and metabolism	F
gene_1110 GeneM ark.hmm 801_nt + 36946 37746	80 1	399 220 7	775	24 2.3 6	7.92	117 411 44	125 3	13 3.2 3	7.06	- 0. 86	939 798 1	990	13 1.5 1	7.04	- 0. 88	DNA polymerase III, alpha subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1111 GeneM ark.hmm 801_nt + 37811 38611	80 1	399 220 7	787	24 6.1 1	7.94	117 411 44	126 6	13 4.6 1	7.07	- 0. 87	939 798 1	109 6	14 5.5 9	7.19	- 0. 75	DNA polymerase III, alpha subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1112 GeneM ark.hmm 1494_nt + 38664 40157	14 94	399 220 7	128 4	21 5.2 8	7.75	117 411 44	242 4	13 8.1 9	7.11	- 0. 64	939 798 1	205 5	14 6.3 6	7.19	- 0. 56	DNA polymerase III, alpha subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1113 GeneM ark.hmm 1008_nt + 40240 41247	10 08	399 220 7	358 5	89 0.8 7	9.8	117 411 44	242 64	20 50. 18	11	1. 2	939 798 1	723 4	76 3.6 3	9.58	- 0. 22	6-phosphofructokinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1114 GeneM ark.hmm 1506_nt + 41306 42811	15 06	399 220 7	113 48	18 87. 48	10.8 8	117 411 44	297 94	16 84. 97	10.7 2	- 0. 16	939 798 1	168 19	11 88. 34	10.2 1	- 0. 67	Pyruvate kinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1115 GeneM ark.hmm 129_nt + 43557 43685	12 9	399 220 7	2	3.8 8	1.96	117 411 44	22	14. 53	3.86	1. 9	939 798 1	17	14. 02	3.81	1. 85	NA			
gene_1116 GeneM ark.hmm 873_nt + 44563 45435	87 3	399 220 7	404	11 5.9 2	6.86	117 411 44	836	81. 56	6.35	- 0. 51	939 798 1	781	95. 19	6.57	- 0. 29	---	---	---	---
gene_1117 GeneM ark.hmm 63_nt - 45851 45913	63	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1118 GeneM ark.hmm 1335_nt	13 35	399 220	845	15 8.5	7.31	117 411	154 9	98. 82	6.63	- 0.	939 798	111 8	89. 11	6.48	- 0.	NAD(FAD)-utilizing enzyme possibly involved in translation	INFORMATION STORAGE AND	Translation, ribosomal structure and biogenesis	J

+ 46640 47974		7		5		44				68	1				83		PROCESSING		
gene_1119 GeneM ark.hmm 498_nt + 48058 48555	49 8	399 220 7	627	31 5.3 7	8.3	117 411 44	287 6	49 1.8 7	8.94	0. 64	939 798 1	178 8	38 2.0 4	8.58	0. 28	Uridylate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_1745 GeneM ark.hmm 285_nt + 19441 19725	28 5	399 220 7	443	38 9.3 6	8.6	117 411 44	182	54. 39	5.77	- 2. 83	939 798 1	97	36. 22	5.18	- 3. 42	NA			
gene_1120 GeneM ark.hmm 261_nt + 48578 48838	26 1	399 220 7	101 1	97 0.2 8	9.92	117 411 44	265 4	86 6.0 6	9.76	- 0. 16	939 798 1	207 5	84 5.9 5	9.72	- 0. 2	Uridylate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_1121 GeneM ark.hmm 558_nt + 48847 49404	55 8	399 220 7	311 1	13 96. 54	10.4 5	117 411 44	399 0	60 9.0 2	9.25	- 1. 2	939 798 1	261 0	49 7.7	8.96	- 1. 49	Ribosome recycling factor	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1122 GeneM ark.hmm 855_nt + 49464 50318	85 5	399 220 7	116 8	34 2.1 9	8.42	117 411 44	419 0	41 7.3 9	8.71	0. 29	939 798 1	497 0	61 8.5 2	9.27	0. 85	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1123 GeneM ark.hmm 72_nt + 5 0354 50425	72	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1124 GeneM ark.hmm 135_nt - 50993 51127	13 5	399 220 7	43	79. 79	6.32	117 411 44	346	21 8.2 9	7.77	1. 45	939 798 1	200	15 7.6 4	7.3	0. 98	NA			
gene_1125 GeneM ark.hmm 246_nt + 51310 51555	24 6	399 220 7	109	11 0.9 9	6.79	117 411 44	621	21 5	7.75	0. 96	939 798 1	770	33 3.0 6	8.38	1. 59	Phosphate starvation-inducible protein PhoH, predicted ATPase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1126 GeneM ark.hmm 273_nt + 51641 51913	27 3	399 220 7	235	21 5.6 2	7.75	117 411 44	920	28 7.0 2	8.17	0. 42	939 798 1	110 1	42 9.1 3	8.75	1	Phosphate starvation-inducible protein PhoH, predicted ATPase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1127 GeneM ark.hmm 186_nt + 52016 52201	18 6	399 220 7	137	18 4.5	7.53	117 411 44	827	37 8.6 9	8.56	1. 03	939 798 1	115 8	66 2.4 6	9.37	1. 84	Phosphate starvation-inducible protein PhoH, predicted ATPase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1128 GeneM ark.hmm 357_nt + 52538 52894	35 7	399 220 7	543	38 0.9 9	8.57	117 411 44	174 1	41 5.3 6	8.7	0. 13	939 798 1	176 6	52 6.3 7	9.04	0. 47	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1129 GeneM ark.hmm 144_nt + 52897 53040	14 4	399 220 7	91	15 8.2 9	7.31	117 411 44	778	46 0.1 6	8.85	1. 54	939 798 1	115 7	85 4.9 4	9.74	2. 43	Regulator of competence-specific genes	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_112 GeneMa rk.hmm 522_nt - 79696 80217	52 2	399 220 7	185	88. 77	6.47	117 411 44	354	57. 76	5.85	- 0. 62	939 798 1	372	75. 83	6.24	- 0. 23	Pyrimidine operon attenuation protein/uracil phosphoribosyltransferase	METABOLISM	Nucleotide transport and metabolism	F
gene_1130 GeneM ark.hmm 273_nt - 53523 53795	27 3	399 220 7	67	61. 48	5.94	117 411 44	403	12 5.7 3	6.97	1. 03	939 798 1	589	22 9.5 7	7.84	1. 9	Alanine dehydrogenase	METABOLISM	Amino acid transport and metabolism	E

gene_1131 GeneM ark.hmm 255_nt - 53921 54175	25 5	399 220 7	185	18 1.7 3	7.51	117 411 44	586	19 5.7 3	7.61	0. 1	939 798 1	865	36 0.9 5	8.5	0. 99	Alanine dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1132 GeneM ark.hmm 111_nt - 54326 54436	11 1	399 220 7	2	4.5 1	2.17	117 411 44	15	11. 51	3.52	1. 35	939 798 1	11	10. 54	3.4	1. 23	Alanine dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1133 GeneM ark.hmm 270_nt - 54500 54769	27 0	399 220 7	83	77	6.27	117 411 44	689	21 7.3 4	7.76	1. 49	939 798 1	892	35 1.5 3	8.46	2. 19	Alanine dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1134 GeneM ark.hmm 570_nt + 55028 55597	57 0	399 220 7	140	61. 52	5.94	117 411 44	115 3	17 2.2 8	7.43	1. 49	939 798 1	164 1	30 6.3 4	8.26	2. 32	Acetyltransferases, including N- acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1135 GeneM ark.hmm 651_nt + 55665 56315	65 1	399 220 7	36	13. 85	3.79	117 411 44	308	40. 3	5.33	1. 54	939 798 1	212	34. 65	5.11	1. 32	DNA uptake protein and related DNA-binding proteins	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2474 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	135 9	28 36. 78	11.4 7	117 411 44	114	80. 91	6.34	5. 13	939 798 1	342	30 3.2 6	8.24	- 3. 23	---	---	---	---
gene_1137 GeneM ark.hmm 189_nt + 58718 58906	18 9	399 220 7	21	27. 83	4.8	117 411 44	285	12 8.4 3	7	2. 2	939 798 1	181	10 1.9	6.67	1. 87	---	---	---	---
gene_1138 GeneM ark.hmm 588_nt + 58938 59525	58 8	399 220 7	90	38. 34	5.26	117 411 44	641	92. 85	6.54	1. 28	939 798 1	525	95. 01	6.57	1. 31	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1139 GeneM ark.hmm 1176_nt + 59529 60704	11 76	399 220 7	210	44. 73	5.48	117 411 44	136 1	98. 57	6.62	1. 14	939 798 1	912	82. 52	6.37	0. 89	---	---	---	---
gene_113 GeneMa rk.hmm 630_nt - 80428 81057	63 0	399 220 7	278 6	11 07. 71	10.1 1	117 411 44	696 4	94 1.4 7	9.88	- 0. 23	939 798 1	754 5	12 74. 34	10.3 2	0. 21	Predicted EndoIII-related endonuclease	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1140 GeneM ark.hmm 528_nt + 61025 61552	52 8	399 220 7	633 0	30 03. 01	11.5 5	117 411 44	213 50	34 43. 92	11.7 5	0. 2	939 798 1	101 66	20 48. 72	11	- 0. 55	Translation initiation factor 3 (IF-3)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1141 GeneM ark.hmm 201_nt + 61585 61785	20 1	399 220 7	510	63 5.5 7	9.31	117 411 44	291 5	12 35. 19	10.2 7	0. 96	939 798 1	219 0	11 59. 35	10.1 8	0. 87	Ribosomal protein L35	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1142 GeneM ark.hmm 360_nt + 61837 62196	36 0	399 220 7	793	55 1.7 7	9.11	117 411 44	727 2	17 20. 45	10.7 5	1. 64	939 798 1	566 0	16 72. 94	10.7 1	1. 6	Ribosomal protein L20	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1143 GeneM ark.hmm 168_nt + 62254 62421	16 8	399 220 7	138	20 5.7 6	7.68	117 411 44	137 9	69 9.1 1	9.45	1. 77	939 798 1	162 8	10 31. 12	10.0 1	2. 33	Lactoylglutathione lyase and related lyases	METABOLISM	Amino acid transport and metabolism	E
gene_2006 GeneM ark.hmm 492_nt + 34047 34538	49 2	399 220 7	360 8	18 36. 91	10.8 4	117 411 44	255 0	44 1.4 3	8.79	- 2. 05	939 798 1	913	19 7.4 6	7.63	- 3. 21	Peroxioredoxin	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O

gene_1145 GeneM ark.hmm 801_nt + 62938 63738	80 1	399 220 7	233	72. 86	6.19	117 411 44	126 4	13 4.4	7.07	0. 88	939 798 1	134 3	17 8.4 1	7.48	1. 29	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	METABOLISM	Coenzyme transport and metabolism	H
gene_1146 GeneM ark.hmm 939_nt + 63749 64687	93 9	399 220 7	190	50. 68	5.66	117 411 44	111 6	10 1.2 3	6.66	1	939 798 1	114 1	12 9.3	7.01	1. 35	Dihydroorotate dehydrogenase	METABOLISM	Nucleotide transport and metabolism	F
gene_1147 GeneM ark.hmm 1977_nt + 64786 66762	19 77	399 220 7	856 7	10 85. 45	10.0 8	117 411 44	629 1	27 1.0 2	8.08	-2	939 798 1	551 2	29 6.6 7	8.21	- 1. 87	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1148 GeneM ark.hmm 1656_nt - 66823 68478	16 56	399 220 7	199 8	30 2.2 2	8.24	117 411 44	147 31	75 7.6 4	9.57	1. 33	939 798 1	473 3	30 4.1 2	8.25	0. 01	Predicted RNA-binding protein homologous to eukaryotic snRNP	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1149 GeneM ark.hmm 498_nt + 68583 69080	49 8	399 220 7	114 9	57 7.9 3	9.17	117 411 44	313 7	53 6.5 1	9.07	- 0. 1	939 798 1	269 0	57 4.7 6	9.17	0	Predicted metal-dependent hydrolase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_114 GeneMa rk.hmm 543_nt - 81057 81599	54 3	399 220 7	130 5	60 2	9.23	117 411 44	471 2	73 9.0 9	9.53	0. 3	939 798 1	384 5	75 3.4 6	9.56	0. 33	Predicted metal-binding, possibly nucleic acid-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1150 GeneM ark.hmm 396_nt + 69061 69456	39 6	399 220 7	93	58. 83	5.88	117 411 44	398	85. 6	6.42	0. 54	939 798 1	268	72. 01	6.17	0. 29	Diacylglycerol kinase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1151 GeneM ark.hmm 900_nt + 69473 70372	90 0	399 220 7	152 7	42 4.9 9	8.73	117 411 44	322 4	30 5.1	8.25	- 0. 48	939 798 1	232 2	27 4.5 3	8.1	- 0. 63	GTPase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1152 GeneM ark.hmm 729_nt + 70603 71331	72 9	399 220 7	832	28 5.8 8	8.16	117 411 44	351 6	41 0.7 8	8.68	0. 52	939 798 1	471 6	68 8.3 5	9.43	1. 27	Formamidopyrimidine-DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1153 GeneM ark.hmm 606_nt + 71331 71936	60 6	399 220 7	387	15 9.9 7	7.32	117 411 44	204 3	28 7.1 3	8.17	0. 85	939 798 1	249 3	43 7.7 4	8.77	1. 45	Dephospho-CoA kinase	METABOLISM	Coenzyme transport and metabolism	H
gene_1154 GeneM ark.hmm 1200_nt + 71923 73122	12 00	399 220 7	323	67. 42	6.08	117 411 44	221 3	15 7.0 7	7.3	1. 22	939 798 1	308 1	27 3.2	8.09	2. 01	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_1155 GeneM ark.hmm 132_nt + 73311 73442	13 2	399 220 7	40	75. 91	6.25	117 411 44	336	21 6.8	7.76	1. 51	939 798 1	133	10 7.2 1	6.74	0. 49	Preprotein translocase subunit SecE	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_1156 GeneM ark.hmm 1782_nt + 73717 75498	17 82	399 220 7	180 0	25 3.0 2	7.98	117 411 44	104 49	49 9.4 1	8.96	0. 98	939 798 1	121 79	72 7.2 3	9.51	1. 53	Exoribonuclease R	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1157 GeneM ark.hmm 570_nt + 75564 76133	57 0	399 220 7	371	16 3.0 4	7.35	117 411 44	340 2	50 8.3 3	8.99	1. 64	939 798 1	501 4	93 6	9.87	2. 52	Exoribonuclease R	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1158 GeneM ark.hmm 468_nt + 76096 76563	46 8	399 220 7	277	14 8.2 6	7.21	117 411 44	237 9	43 2.9 5	8.76	1. 55	939 798 1	304 9	69 3.2 3	9.44	2. 23	tmRNA-binding protein	CELLULAR PROCESSES AND	Posttranslational modification, protein turnover, chaperones	O

																	SIGNALING		
gene_1159 GeneM ark.hmm 861_nt + 76579 77439	86 1	399 220 7	141 6	41 1.9 5	8.69	117 411 44	819 2	81 0.3 6	9.66	0. 97	939 798 1	124 34	15 36. 64	10.5 9	1. 9	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_115 GeneMa rk.hmm 318_nt + 8 1769 82086	31 8	399 220 7	216	17 0.1 4	7.41	117 411 44	817	21 8.8 2	7.77	0. 36	939 798 1	541	18 1.0 2	7.5	0. 09	---	---	---	---
gene_2522 GeneM ark.hmm 135_nt + 3 137	13 5	399 220 7	245 7	45 58. 88	12.1 5	117 411 44	274	17 2.8 6	7.43	- 4. 72	939 798 1	627	49 4.2	8.95	- 3. 2	---	---	---	---
gene_1161 GeneM ark.hmm 1833_nt + 78484 80316	18 33	399 220 7	389 3	53 2	9.06	117 411 44	175 96	81 7.6	9.68	0. 62	939 798 1	136 17	79 0.4 7	9.63	0. 57	Oligoendopeptidase F	METABOLISM	Amino acid transport and metabolism	E
gene_1162 GeneM ark.hmm 714_nt + 80318 81031	71 4	399 220 7	753	26 4.1 7	8.05	117 411 44	406 4	48 4.7 8	8.92	0. 87	939 798 1	382 2	56 9.5 8	9.15	1. 1	Predicted O-methyltransferase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1163 GeneM ark.hmm 942_nt + 81098 82039	94 2	399 220 7	206 74	54 97. 44	12.4 2	117 411 44	418 51	37 83. 94	11.8 9	- 0. 53	939 798 1	243 61	27 51. 75	11.4 3	- 0. 99	Parvulin-like peptidyl-prolyl isomerase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_861 GeneMa rk.hmm 648_nt - 17644 18291	64 8	399 220 7	600 2	23 20. 11	11.1 8	117 411 44	408 7	53 7.1 8	9.07	- 2. 11	939 798 1	169 9	27 8.9 9	8.12	- 3. 06	Predicted membrane protein, hemolysin III homolog	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1165 GeneM ark.hmm 621_nt - 83300 83920	62 1	399 220 7	979	39 4.8 9	8.63	117 411 44	672 9	92 2.8 9	9.85	1. 22	939 798 1	495 7	84 9.3 6	9.73	1. 1	Fructose-2,6-bisphosphatase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1166 GeneM ark.hmm 483_nt - 83920 84402	48 3	399 220 7	580	30 0.7 9	8.23	117 411 44	752 9	13 27. 64	10.3 7	2. 14	939 798 1	476 5	10 49. 74	10.0 4	1. 81	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1167 GeneM ark.hmm 843_nt - 84402 85244	84 3	399 220 7	114 2	33 9.3 3	8.41	117 411 44	953 5	96 3.3 5	9.91	1. 5	939 798 1	485 0	61 2.1 8	9.26	0. 85	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1168 GeneM ark.hmm 750_nt - 85339 86088	75 0	399 220 7	861	28 7.5 6	8.17	117 411 44	529 9	60 1.7 6	9.23	1. 06	939 798 1	160 1	22 7.1 4	7.83	- 0. 34	Lysozyme M1 (1,4-beta-N- acetylmuramidase)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1169 GeneM ark.hmm 1380_nt + 86283 87662	13 80	399 220 7	254 4	46 1.7 7	8.85	117 411 44	801 3	49 4.5 4	8.95	0. 1	939 798 1	451 7	34 8.2 9	8.44	- 0. 41	N-acetylglucosamine-1-phosphate uridylyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1116 GeneMa rk.hmm 1527_nt + 82358 83884	15 27	399 220 7	179 5	29 4.4 5	8.2	117 411 44	743 4	41 4.6 4	8.7	0. 5	939 798 1	670 0	46 6.8 8	8.87	0. 67	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1170 GeneM ark.hmm 546_nt + 87672 88217	54 6	399 220 7	656	30 0.9 5	8.23	117 411 44	185 6	28 9.5 2	8.18	- 0. 05	939 798 1	148 1	28 8.6 2	8.17	- 0. 06	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_1171 GeneM ark.hmm 315_nt + 88229 88543	31 5	399 220 7	259	20 5.9 6	7.69	117 411 44	884	23 9.0 2	7.9	0. 21	939 798 1	928	31 3.4 7	8.29	0. 6	---	---	---	---
gene_1172 GeneM ark.hmm 693_nt + 88560 89252	69 3	399 220 7	188 8	68 2.4 3	9.41	117 411 44	371 4	45 6.4 6	8.83	- 0. 58	939 798 1	320 5	49 2.1 1	8.94	- 0. 47	Nucleoside phosphorylase	METABOLISM	Nucleotide transport and metabolism	F
gene_1173 GeneM ark.hmm 492_nt + 89329 89820	49 2	399 220 7	170 5	86 8.0 5	9.76	117 411 44	652 9	11 30. 24	10.1 4	0. 38	939 798 1	415 8	89 9.2 6	9.81	0. 05	---	---	---	---
gene_1174 GeneM ark.hmm 591_nt + 89918 90508	59 1	399 220 7	255	10 8.0 8	6.76	117 411 44	147 9	21 3.1 4	7.74	0. 98	939 798 1	123 0	22 1.4 5	7.79	1. 03	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1175 GeneM ark.hmm 1764_nt + 90517 92280	17 64	399 220 7	665	94. 43	6.56	117 411 44	496 5	23 9.7 2	7.91	1. 35	939 798 1	410 8	24 7.8	7.95	1. 39	Membrane domain of membrane-anchored glycerophosphoryl diester phosphodiesterase	METABOLISM	Energy production and conversion	C
gene_816 GeneMa rk.hmm 393_nt + 3 395	39 3	399 220 7	112 3	71 5.7 7	9.48	117 411 44	136	29. 47	4.88	4. 6	939 798 1	318	86. 1	6.43	- 3. 05	---	---	---	---
gene_1177 GeneM ark.hmm 66_nt + 5 39 604	66	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1178 GeneM ark.hmm 210_nt + 2691 2900	21 0	399 220 7	22	26. 24	4.71	117 411 44	142	57. 59	5.85	1. 14	939 798 1	73	36. 99	5.21	0. 5	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1179 GeneM ark.hmm 273_nt + 2890 3162	27 3	399 220 7	42	38. 54	5.27	117 411 44	311	97. 03	6.6	1. 33	939 798 1	154	60. 02	5.91	0. 64	---	---	---	---
gene_117 GeneMa rk.hmm 900_nt - 84033 84932	90 0	399 220 7	390 6	10 87. 12	10.0 9	117 411 44	119 36	11 29. 55	10.1 4	0. 05	939 798 1	661 4	78 1.9 6	9.61	- 0. 48	Zn-dependent protease with chaperone function	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1180 GeneM ark.hmm 210_nt + 3230 3439	21 0	399 220 7	15	17. 89	4.16	117 411 44	85	34. 47	5.11	0. 95	939 798 1	58	29. 39	4.88	0. 72	---	---	---	---
gene_1181 GeneM ark.hmm 975_nt + 3555 4529	97 5	399 220 7	308	79. 13	6.31	117 411 44	142 5	12 4.4 8	6.96	0. 65	939 798 1	100 0	10 9.1 3	6.77	0. 46	Nicotinic acid phosphoribosyltransferase	METABOLISM	Coenzyme transport and metabolism	H
gene_1182 GeneM ark.hmm 444_nt + 4644 5087	44 4	399 220 7	238	13 4.2 7	7.07	117 411 44	732	14 0.4 2	7.13	0. 06	939 798 1	631	15 1.2 2	7.24	0. 17	Nicotinic acid phosphoribosyltransferase	METABOLISM	Coenzyme transport and metabolism	H
gene_1183 GeneM ark.hmm 330_nt + 5084 5413	33 0	399 220 7	262	19 8.8 7	7.64	117 411 44	729	18 8.1 5	7.56	- 0. 08	939 798 1	652	21 0.2 3	7.72	0. 08	NAD synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_1184 GeneM ark.hmm 222_nt + 5526 5747	22 2	399 220 7	285	32 1.5 7	8.33	117 411 44	494	18 9.5 2	7.57	- 0. 76	939 798 1	490	23 4.8 6	7.88	- 0. 45	NAD synthase	METABOLISM	Coenzyme transport and metabolism	H

gene_1185 GeneM ark.hmm 237_nt + 5830 6066	23 7	399 220 7	601	63 5.2	9.31	117 411 44	708	25 4.4 3	7.99	- 1. 32	939 798 1	113 9	51 1.3 8	9	- 0. 31	NAD synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_1186 GeneM ark.hmm 552_nt + 6416 6967	55 2	399 220 7	184	83. 5	6.38	117 411 44	103 1	15 9.0 8	7.31	0. 93	939 798 1	948	18 2.7 4	7.51	1. 13	Acetyltransferases, including N- acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1187 GeneM ark.hmm 390_nt + 8420 8809	39 0	399 220 7	255	16 3.7 8	7.36	117 411 44	112 6	24 5.9	7.94	0. 58	939 798 1	100 0	27 2.8 4	8.09	0. 73	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1188 GeneM ark.hmm 1068_nt - 9470 10537	10 68	399 220 7	990	23 2.1 9	7.86	117 411 44	403 2	32 1.5 4	8.33	0. 47	939 798 1	327 2	32 5.9 9	8.35	0. 49	S-adenosylmethionine:tRNA- ribosyltransferase-isomerase (queuine synthetase)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1189 GeneM ark.hmm 708_nt + 10688 11395	70 8	399 220 7	170 4	60 2.8 7	9.24	117 411 44	581 4	69 9.4 1	9.45	0. 21	939 798 1	735 2	11 04. 94	10.1 1	0. 87	6- phosphogluconolactonase/Glucosa mine-6-phosphate isomerase/deaminase	METABOLISM	Carbohydrate transport and metabolism	G
gene_118 GeneMa rk.hmm 561_nt - 84934 85494	56 1	399 220 7	446 6	19 94. 08	10.9 6	117 411 44	101 15	15 35. 65	10.5 8	- 0. 38	939 798 1	262 8	49 8.4 6	8.96	-2	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1190 GeneM ark.hmm 177_nt + 11535 11711	17 7	399 220 7	138	19 5.3	7.61	117 411 44	150 0	72 1.7 8	9.5	1. 89	939 798 1	105 7	63 5.4 3	9.31	1. 7	Ribosomal protein S21	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1191 GeneM ark.hmm 810_nt + 11841 12650	81 0	399 220 7	103 7	32 0.6 9	8.33	117 411 44	229 7	24 1.5 3	7.92	- 0. 41	939 798 1	182 0	23 9.0 8	7.9	- 0. 43	Serine kinase of the HPr protein, regulates carbohydrate metabolism	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1192 GeneM ark.hmm 99_nt + 1 2719 12817	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Serine kinase of the HPr protein, regulates carbohydrate metabolism	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1193 GeneM ark.hmm 789_nt + 12810 13598	78 9	399 220 7	204 2	64 8.2 8	9.34	117 411 44	541 1	58 4.1	9.19	- 0. 15	939 798 1	473 6	63 8.7	9.32	- 0. 02	Prolipoprotein diacylglyceryltransferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1194 GeneM ark.hmm 384_nt + 13599 13982	38 4	399 220 7	313	20 4.1 7	7.67	117 411 44	834	18 4.9 8	7.53	0. 14	939 798 1	839	23 2.4 9	7.86	0. 19	Uncharacterized protein containing a divergent version of the methyl- accepting chemotaxis-like domain	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1195 GeneM ark.hmm 390_nt + 13998 14387	39 0	399 220 7	241 2	15 49. 17	10.6	117 411 44	279 9	61 1.2 6	9.26	- 1. 34	939 798 1	293 9	80 1.8 6	9.65	- 0. 95	---	---	---	---
gene_1196 GeneM ark.hmm 1032_nt + 14471 15502	10 32	399 220 7	102 6	24 9.0 3	7.96	117 411 44	283 3	23 3.8 1	7.87	- 0. 09	939 798 1	260 0	26 8.0 8	8.07	0. 11	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases	METABOLISM	Coenzyme transport and metabolism	H
gene_1197 GeneM ark.hmm 87_nt + 1 5600 15686	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases	METABOLISM	Coenzyme transport and metabolism	H
gene_1198 GeneM ark.hmm 738_nt +	73	399 220	695	23 5.8	7.88	117 411	218	25 1.9	7.98	0.	939 798	232	33 5.5	8.39	0.	Acyl-ACP thioesterase	METABOLISM	Lipid transport and metabolism	I

15691 16428	8	7		9		44	3	3		1	1	7	1		51				
gene_119 GeneM ark.hmm 774_nt + 16439 17212	77 4	399 220 7	129 3	41 8.4 5	8.71	117 411 44	336 0	36 9.7 3	8.53	- 0. 18	939 798 1	377 0	51 8.2 8	9.02	0. 31	Predicted sugar phosphatases of the HAD superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_119 GeneMa rk.hmm 714_nt + 8 5588 86301	71 4	399 220 7	182 6	64 0.6	9.32	117 411 44	465 1	55 4.8	9.12	- 0. 2	939 798 1	372 5	55 5.1 3	9.12	- 0. 2	Predicted S-adenosylmethionine- dependent methyltransferase involved in bacterial cell division	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_11 GeneMar k.hmm 432_nt 6325 6756	43 2	399 220 7	114	66. 1	6.05	117 411 44	329	64. 86	6.02	- 0. 03	939 798 1	336	82. 76	6.37	0. 32	Arginine repressor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1200 GeneM ark.hmm 618_nt + 17202 17819	61 8	399 220 7	467	18 9.2 8	7.56	117 411 44	113 0	15 5.7 3	7.28	- 0. 28	939 798 1	122 6	21 1.0 9	7.72	0. 16	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1201 GeneM ark.hmm 402_nt + 18029 18430	40 2	399 220 7	467	29 0.9 9	8.18	117 411 44	319 3	67 6.4 9	9.4	1. 22	939 798 1	259 8	68 7.6 7	9.43	1. 25	Arsenate reductase and related proteins, glutaredoxin family	METABOLISM	Inorganic ion transport and metabolism	P
gene_1202 GeneM ark.hmm 279_nt + 18430 18708	27 9	399 220 7	72	64. 64	6.01	117 411 44	196	59. 83	5.9	- 0. 11	939 798 1	198	75. 51	6.24	0. 23	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1203 GeneM ark.hmm 774_nt + 18698 19471	77 4	399 220 7	210	67. 96	6.09	117 411 44	656	72. 19	6.17	0. 08	939 798 1	581	79. 87	6.32	0. 23	Archaeal fructose-1,6- bisphosphatase and related enzymes of inositol monophosphatase family	METABOLISM	Carbohydrate transport and metabolism	G
gene_1204 GeneM ark.hmm 1305_nt + 19472 20776	13 05	399 220 7	106	20. 35	4.35	117 411 44	565	36. 87	5.2	0. 85	939 798 1	544	44. 36	5.47	1. 12	tRNA and rRNA cytosine-C5- methylases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1205 GeneM ark.hmm 843_nt + 21350 22192	84 3	399 220 7	648	19 2.5 5	7.59	117 411 44	393 6	39 7.6 6	8.64	1. 05	939 798 1	418 1	52 7.7 4	9.04	1. 45	ABC-type phosphate transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1206 GeneM ark.hmm 81_nt + 2 2189 22269	81	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	ABC-type phosphate transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1207 GeneM ark.hmm 273_nt + 22269 22541	27 3	399 220 7	381	34 9.5 8	8.45	117 411 44	106 7	33 2.8 8	8.38	- 0. 07	939 798 1	167 0	65 0.9 1	9.35	0. 9	ABC-type phosphate transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1208 GeneM ark.hmm 639_nt + 22596 23234	63 9	399 220 7	924	36 2.2 1	8.5	117 411 44	294 9	39 3.0 6	8.62	0. 12	939 798 1	466 2	77 6.3 1	9.6	1. 1	ABC-type phosphate transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1209 GeneM ark.hmm 885_nt + 23224 24108	88 5	399 220 7	141 1	39 9.3 7	8.64	117 411 44	402 0	38 6.8 8	8.6	- 0. 04	939 798 1	654 0	78 6.3 2	9.62	0. 98	ABC-type phosphate transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_120 GeneMa rk.hmm 1320_nt + 86519 87838	13 20	399 220 7	171 6	32 5.6 3	8.35	117 411 44	481 1	31 0.4 2	8.28	- 0. 07	939 798 1	506 6	40 8.3 7	8.67	0. 32	Xanthine/uracil permeases	METABOLISM	Nucleotide transport and metabolism	F
gene_1210 GeneM ark.hmm 804_nt +	80	399 220	195	60	9.25	117 411	886	93 8.8	9.87	0.	939 798	149	19 80.	10.9	1.	ABC-type phosphate transport	METABOLISM	Inorganic ion transport and	P

24119 24922	4	7	6	9.4		44	3	9		62	1	66	68	5	7	system, ATPase component		metabolism	
gene_1211 GeneM ark.hmm 759_nt + 24935 25693	75 9	399 220 7	228 5	75 4.1	9.56	117 411 44	564 1	63 3	9.31	- 0.25	939 798 1	102 94	14 43.14	10.4 9	0.93	ABC-type phosphate transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1212 GeneM ark.hmm 654_nt + 25705 26358	65 4	399 220 7	275 1	10 53.66	10.0 4	117 411 44	120 40	15 67.97	10.6 1	0.57	939 798 1	216 66	35 25.06	11.7 8	1.74	Phosphate uptake regulator	METABOLISM	Inorganic ion transport and metabolism	P
gene_1213 GeneM ark.hmm 816_nt + 26515 27330	81 6	399 220 7	136	41.75	5.38	117 411 44	104 2	10 8.76	6.76	1.38	939 798 1	121 6	15 8.57	7.31	1.93	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_1214 GeneM ark.hmm 1272_nt - 27350 28621	12 72	399 220 7	469	92.36	6.53	117 411 44	283 3	18 9.69	7.57	1.04	939 798 1	157 8	13 2	7.04	0.51	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1215 GeneM ark.hmm 732_nt + 28763 29494	73 2	399 220 7	666	22 7.9	7.83	117 411 44	208 2	24 2.25	7.92	0.09	939 798 1	241 3	35 0.76	8.45	0.62	Alpha-acetolactate decarboxylase	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_1216 GeneM ark.hmm 372_nt + 29603 29974	37 2	399 220 7	180	12 1.2	6.92	117 411 44	430	98.45	6.62	- 0.3	939 798 1	400	11 4.41	6.84	- 0.08	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_1217 GeneM ark.hmm 294_nt + 29968 30261	29 4	399 220 7	81	69.01	6.11	117 411 44	419	12 1.38	6.92	0.81	939 798 1	447	16 1.78	7.34	1.23	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_1218 GeneM ark.hmm 681_nt + 30391 31071	68 1	399 220 7	144	52.97	5.73	117 411 44	903	11 2.94	6.82	1.09	939 798 1	593	92.66	6.53	0.8	UDP-N-acetylmuramate dehydrogenase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1219 GeneM ark.hmm 246_nt + 31145 31390	24 6	399 220 7	55	56	5.81	117 411 44	265	91.75	6.52	0.71	939 798 1	184	79.59	6.31	0.5	UDP-N-acetylmuramate dehydrogenase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_121 GeneMa rk.hmm 1572_nt - 88033 89604	15 72	399 220 7	356 0	56 7.26	9.15	117 411 44	609 7	33 0.33	8.37	- 0.78	939 798 1	547 5	37 0.59	8.53	- 0.62	Signal recognition particle GTPase	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_1220 GeneM ark.hmm 1158_nt + 31449 32606	11 58	399 220 7	567	12 2.65	6.94	117 411 44	310 9	22 8.67	7.84	0.9	939 798 1	362 0	33 2.63	8.38	1.44	ABC-type spermidine/putrescine transport systems, ATPase components	METABOLISM	Amino acid transport and metabolism	E
gene_1221 GeneM ark.hmm 237_nt + 32587 32823	23 7	399 220 7	88	93.01	6.54	117 411 44	387	13 9.08	7.12	0.58	939 798 1	470	21 1.02	7.72	1.18	ABC-type spermidine/putrescine transport system, permease component I	METABOLISM	Amino acid transport and metabolism	E
gene_1222 GeneM ark.hmm 141_nt + 32942 33082	14 1	399 220 7	12	21.32	4.41	117 411 44	42	25.37	4.67	0.26	939 798 1	71	53.58	5.74	1.33	ABC-type spermidine/putrescine transport system, permease component I	METABOLISM	Amino acid transport and metabolism	E
gene_1223 GeneM ark.hmm 105_nt +	10	399 220	1	2.3	1.25	117 411	16	12.	3.7	2.	939 798	4	4.0	2.02	0.	ABC-type spermidine/putrescine transport system, permease	METABOLISM	Amino acid transport and	E

33358 33462	5	7		9		44		98		45	1		5		77	component I		metabolism	
gene_1224 GeneM ark.hmm 210_nt + 33661 33870	21 0	399 220 7	51	60. 83	5.93	117 411 44	163	66. 11	6.05	0. 12	939 798 1	233	11 8.0 6	6.88	0. 95	ABC-type spermidine/putrescine transport system, permease component I	METABOLISM	Amino acid transport and metabolism	E
gene_1225 GeneM ark.hmm 774_nt + 33946 34719	77 4	399 220 7	340	11 0.0 3	6.78	117 411 44	137 2	15 0.9 7	7.24	0. 46	939 798 1	173 8	23 8.9 3	7.9	1. 12	ABC-type spermidine/putrescine transport system, permease component II	METABOLISM	Amino acid transport and metabolism	E
gene_1226 GeneM ark.hmm 549_nt + 34716 35264	54 9	399 220 7	600	27 3.7 6	8.1	117 411 44	201 8	31 3.0 7	8.29	0. 19	939 798 1	285 7	55 3.7 4	9.11	1. 01	Spermidine/putrescine-binding periplasmic protein	METABOLISM	Amino acid transport and metabolism	E
gene_1227 GeneM ark.hmm 516_nt + 35331 35846	51 6	399 220 7	724	35 1.4 6	8.46	117 411 44	244 2	40 3.0 7	8.65	0. 19	939 798 1	400 3	82 5.4 7	9.69	1. 23	Spermidine/putrescine-binding periplasmic protein	METABOLISM	Amino acid transport and metabolism	E
gene_1228 GeneM ark.hmm 486_nt + 36613 37098	48 6	399 220 7	330	17 0.0 8	7.41	117 411 44	112 6	19 7.3 3	7.62	0. 21	939 798 1	793	17 3.6 2	7.44	0. 03	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1229 GeneM ark.hmm 2619_nt + 37120 39738	26 19	399 220 7	286 1	27 3.6 3	8.1	117 411 44	739 0	24 0.3 2	7.91	- 0. 19	939 798 1	848 0	34 4.5 3	8.43	0. 33	Alanyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_122 GeneMa rk.hmm 333_nt - 89616 89948	33 3	399 220 7	421	31 6.6 8	8.31	117 411 44	783	20 0.2 7	7.65	- 0. 66	939 798 1	570	18 2.1 4	7.51	- 0. 8	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1230 GeneM ark.hmm 1455_nt - 39828 41282	14 55	399 220 7	790	13 6	7.09	117 411 44	167 1	97. 81	6.61	- 0. 48	939 798 1	157 5	11 5.1 8	6.85	- 0. 24	Glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_1231 GeneM ark.hmm 792_nt + 41462 42253	79 2	399 220 7	133 2	42 1.2 8	8.72	117 411 44	278 3	29 9.2 8	8.23	- 0. 49	939 798 1	185 7	24 9.4 9	7.96	- 0. 76	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1232 GeneM ark.hmm 141_nt + 42234 42374	14 1	399 220 7	51	90. 6	6.5	117 411 44	226	13 6.5 1	7.09	0. 59	939 798 1	144	10 8.6 7	6.76	0. 26	---	---	---	---
gene_1233 GeneM ark.hmm 858_nt + 42526 43383	85 8	399 220 7	508	14 8.3 1	7.21	117 411 44	243 0	24 1.2 2	7.91	0. 7	939 798 1	206 2	25 5.7 2	8	0. 79	---	---	---	---
gene_1234 GeneM ark.hmm 441_nt + 43500 43940	44 1	399 220 7	185	10 5.0 8	6.72	117 411 44	130 7	25 2.4 2	7.98	1. 26	939 798 1	905	21 8.3 6	7.77	1. 05	---	---	---	---
gene_1235 GeneM ark.hmm 177_nt + 44618 44794	17 7	399 220 7	40	56. 61	5.82	117 411 44	353	16 9.8 6	7.41	1. 59	939 798 1	79	47. 49	5.57	- 0. 25	Predicted SAM-dependent methyltransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1236 GeneM ark.hmm 927_nt + 44949 45875	92 7	399 220 7	103 6	27 9.9 4	8.13	117 411 44	219 0	20 1.2 1	7.65	- 0. 48	939 798 1	149 9	17 2.0 6	7.43	- 0. 7	Predicted SAM-dependent methyltransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1237 GeneM ark.hmm 597_nt +	59 7	399 220	744	31 2.1	8.29	117 411	145 7	20 7.8	7.7	- 0.	939 798	118 1	21 0.4	7.72	- 0.	3-dehydroquinate dehydratase	METABOLISM	Amino acid transport and metabolism	E

45872 46468			7		7		44		6		59	1		9		57			
gene_1238 GeneM ark.hmm 855_nt + 46782 47636	85 5	399 220 7	384	11 2.5	6.81	117 411 44	124 9	12 4.4 2	6.96	0. 15	939 798 1	151 6	18 8.6 7	7.56	0. 75	Shikimate 5-dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1239 GeneM ark.hmm 1068_nt + 47655 48722	10 68	399 220 7	536	12 5.7 1	6.97	117 411 44	142 9	11 3.9 6	6.83	- 0. 14	939 798 1	207 4	20 6.6 3	7.69	0. 72	3-dehydroquinase synthetase	METABOLISM	Amino acid transport and metabolism	E
gene_123 GeneMa rk.hmm 105_nt - 90038 90142	10 5	399 220 7	2	4.7 7	2.25	117 411 44	23	18. 66	4.22	1. 97	939 798 1	15	15. 2	3.93	1. 68	---	---	---	---
gene_1240 GeneM ark.hmm 330_nt + 48732 49061	33 0	399 220 7	470	35 6.7 6	8.48	117 411 44	832	21 4.7 3	7.75	- 0. 73	939 798 1	831	26 7.9 5	8.07	- 0. 41	Chorismate synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1241 GeneM ark.hmm 831_nt + 49135 49965	83 1	399 220 7	593	17 8.7 5	7.48	117 411 44	187 9	19 2.5 8	7.59	0. 11	939 798 1	267 1	34 2.0 1	8.42	0. 94	Chorismate synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1242 GeneM ark.hmm 780_nt + 49975 50754	78 0	399 220 7	727	23 3.4 7	7.87	117 411 44	206 6	22 5.5 9	7.82	- 0. 05	939 798 1	244 9	33 4.0 9	8.38	0. 51	Prephenate dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1243 GeneM ark.hmm 318_nt + 50813 51130	31 8	399 220 7	307	24 1.8 2	7.92	117 411 44	870	23 3.0 1	7.86	- 0. 06	939 798 1	900	30 1.1 5	8.23	0. 31	Prephenate dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1244 GeneM ark.hmm 339_nt + 51141 51479	33 9	399 220 7	333	24 6.0 5	7.94	117 411 44	119 6	30 0.4 8	8.23	0. 29	939 798 1	142 0	44 5.7 1	8.8	0. 86	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1245 GeneM ark.hmm 309_nt + 51571 51879	30 9	399 220 7	114	92. 41	6.53	117 411 44	478	13 1.7 5	7.04	0. 51	939 798 1	312	10 7.4 4	6.75	0. 22	5-enolpyruvylshikimate-3-phosphate synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1246 GeneM ark.hmm 972_nt + 51945 52916	97 2	399 220 7	676	17 4.2 1	7.44	117 411 44	233 2	20 4.3 4	7.67	0. 23	939 798 1	277 3	30 3.5 6	8.25	0. 81	5-enolpyruvylshikimate-3-phosphate synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1247 GeneM ark.hmm 477_nt + 52909 53385	47 7	399 220 7	312	16 3.8 4	7.36	117 411 44	113 6	20 2.8 4	7.66	0. 3	939 798 1	112 0	24 9.8 4	7.96	0. 6	Shikimate kinase	METABOLISM	Amino acid transport and metabolism	E
gene_1248 GeneM ark.hmm 849_nt + 53382 54230	84 9	399 220 7	100 3	29 5.9 2	8.21	117 411 44	260 8	26 1.6 3	8.03	- 0. 18	939 798 1	322 3	40 3.9 4	8.66	0. 45	Prephenate dehydratase	METABOLISM	Amino acid transport and metabolism	E
gene_1249 GeneM ark.hmm 1275_nt + 54227 55501	12 75	399 220 7	308 2	60 5.4 9	9.24	117 411 44	711 0	47 4.9 5	8.89	- 0. 35	939 798 1	784 4	65 4.6 3	9.35	0. 11	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_124 GeneMa rk.hmm 270_nt - 90202 90471	27 0	399 220 7	44	40. 82	5.35	117 411 44	313	98. 73	6.63	1. 28	939 798 1	173	68. 18	6.09	0. 74	---	---	---	---
gene_1250 GeneM ark.hmm 846_nt + 55780 56625	84 6	399 220 7	352	10 4.2 2	6.7	117 411 44	240 3	24 1.9 2	7.92	1. 22	939 798 1	134 5	16 9.1 7	7.4	0. 7	LPS biosynthesis protein	CELLULAR PROCESSES AND	Cell wall/membrane/envelope biogenesis	M

																	SIGNALING		
gene_1251 GeneM ark.hmm 1074_nt + 56645 57718	10 74	399 220 7	391	91. 19	6.51	117 411 44	207 9	16 4.8 7	7.37	0. 86	939 798 1	152 3	15 0.8 9	7.24	0. 73	Glycosyltransferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1252 GeneM ark.hmm 177_nt + 57720 57896	17 7	399 220 7	50	70. 76	6.14	117 411 44	365	17 5.6 3	7.46	1. 32	939 798 1	282	16 9.5 3	7.41	1. 27	Glycosyltransferases involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1253 GeneM ark.hmm 801_nt + 57962 58762	80 1	399 220 7	157	49. 1	5.62	117 411 44	149 9	15 9.3 9	7.32	1. 7	939 798 1	108 7	14 4.4	7.17	1. 55	Glycosyltransferases involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1254 GeneM ark.hmm 1434_nt + 58778 60211	14 34	399 220 7	775	13 5.3 8	7.08	117 411 44	383 7	22 7.8 9	7.83	0. 75	939 798 1	322 2	23 9.0 8	7.9	0. 82	---	---	---	---
gene_1255 GeneM ark.hmm 1035_nt + 60240 61274	10 35	399 220 7	220 6	53 3.8 9	9.06	117 411 44	548 8	45 1.6 1	8.82	- 0. 24	939 798 1	471 5	48 4.7 4	8.92	- 0. 14	---	---	---	---
gene_1256 GeneM ark.hmm 678_nt + 61534 62211	67 8	399 220 7	362 2	13 38. 15	10.3 9	117 411 44	962 5	12 09. 1	10.2 4	- 0. 15	939 798 1	512 9	80 4.9 5	9.65	- 0. 74	Negative regulator of genetic competence, sporulation and motility	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1257 GeneM ark.hmm 1287_nt + 62362 63648	12 87	399 220 7	221 3	43 0.7 1	8.75	117 411 44	667 5	44 1.7 4	8.79	0. 04	939 798 1	769 2	63 5.9 5	9.31	0. 56	Homoserine dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1258 GeneM ark.hmm 129_nt + 63650 63778	12 9	399 220 7	86	16 6.9 9	7.38	117 411 44	194	12 8.0 9	7	- 0. 38	939 798 1	153	12 6.2	6.98	- 0. 4	Homoserine kinase	METABOLISM	Amino acid transport and metabolism	E
gene_1259 GeneM ark.hmm 210_nt + 63965 64174	21 0	399 220 7	166	19 8	7.63	117 411 44	311	12 6.1 3	6.98	- 0. 65	939 798 1	308	15 6.0 6	7.29	- 0. 34	Homoserine kinase	METABOLISM	Amino acid transport and metabolism	E
gene_125 GeneMa rk.hmm 591_nt + 9 0642 91232	59 1	399 220 7	617	26 1.5 1	8.03	117 411 44	325 9	46 9.6 6	8.88	0. 85	939 798 1	126 2	22 7.2 2	7.83	- 0. 2	HD superfamily phosphohydrolases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1260 GeneM ark.hmm 267_nt + 64274 64540	26 7	399 220 7	100	93. 82	6.55	117 411 44	457	14 5.7 8	7.19	0. 64	939 798 1	414	16 4.9 9	7.37	0. 82	Homoserine kinase	METABOLISM	Amino acid transport and metabolism	E
gene_1261 GeneM ark.hmm 246_nt + 64604 64849	24 6	399 220 7	89	90. 62	6.5	117 411 44	329	11 3.9 1	6.83	0. 33	939 798 1	390	16 8.6 9	7.4	0. 9	Homoserine kinase	METABOLISM	Amino acid transport and metabolism	E
gene_1262 GeneM ark.hmm 939_nt + 65099 66037	93 9	399 220 7	149 9	39 9.8 7	8.64	117 411 44	409 1	37 1.0 7	8.54	- 0. 1	939 798 1	392 2	44 4.4 3	8.8	0. 16	Peptide methionine sulfoxide reductase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1263 GeneM ark.hmm 1725_nt	17 25	399 220	121 1	17 5.8	7.46	117 411	484 0	23 8.9	7.9	0. 44	939 798	611 3	37 7.0	8.56	1. 1	ABC-type multidrug transport system, ATPase and permease	CELLULAR PROCESSES AND	Defense mechanisms	V

+ 66095 67819		7		5		44		7			1		8			components	SIGNALING		
gene_1264 GeneM ark.hmm 1749_nt + 67821 69569	17 49	399 220 7	168 1	24 0.7 5	7.91	117 411 44	685 0	33 3.5 7	8.38	0. 47	939 798 1	835 5	50 8.3	8.99	1. 08	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1265 GeneM ark.hmm 1260_nt + 69826 71085	12 60	399 220 7	135 2	26 8.7 8	8.07	117 411 44	473 8	32 0.2 7	8.32	0. 25	939 798 1	315 3	26 6.2 7	8.06	- 0. 01	Cytosine deaminase and related metal-dependent hydrolases	METABOLISM	Nucleotide transport and metabolism	F
gene_1266 GeneM ark.hmm 501_nt + 71335 71835	50 1	399 220 7	369 6	18 47. 91	10.8 5	117 411 44	170 77	29 03. 11	11.5	0. 65	939 798 1	162 20	34 44. 92	11.7 5	0. 9	Ribosomal protein L10	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1267 GeneM ark.hmm 369_nt + 71911 72279	36 9	399 220 7	324 5	22 02. 8	11.1 1	117 411 44	164 41	37 94. 82	11.8 9	0. 78	939 798 1	159 33	45 94. 48	12.1 7	1. 06	Ribosomal protein L7/L12	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2191 GeneM ark.hmm 753_nt + 5531 6283	75 3	399 220 7	269 5	89 6.5	9.81	117 411 44	706	79. 85	6.32	- 3. 49	939 798 1	861	12 1.6 7	6.93	- 2. 88	ABC-type phosphate transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_2091 GeneM ark.hmm 321_nt + 31710 32030	32 1	399 220 7	110 62	86 32. 08	13.0 8	117 411 44	408 7	10 84. 4	10.0 8	-3	939 798 1	453 8	15 04. 27	10.5 5	- 2. 53	---	---	---	---
gene_126 GeneMa rk.hmm 681_nt + 9 1357 92037	68 1	399 220 7	142 0	52 2.3 1	9.03	117 411 44	417 0	52 1.5 3	9.03	0	939 798 1	241 7	37 7.6 5	8.56	- 0. 47	HD superfamily phosphohydrolases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2107 GeneM ark.hmm 270_nt - 41935 42204	27 0	399 220 7	143 73	13 33 4.3 1	13.7	117 411 44	927 5	29 25. 77	11.5 1	- 2. 19	939 798 1	608 3	23 97. 28	11.2 3	- 2. 47	Superoxide dismutase	METABOLISM	Inorganic ion transport and metabolism	P
gene_349 GeneMa rk.hmm 567_nt - 43992 44558	56 7	399 220 7	553	24 4.3	7.93	117 411 44	320	48. 07	5.59	- 2. 34	939 798 1	254	47. 67	5.57	- 2. 36	Thiol-disulfide isomerase and thioredoxins	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1272 GeneM ark.hmm 1224_nt + 75276 76499	12 24	399 220 7	188	38. 47	5.27	117 411 44	898	62. 49	5.97	0. 7	939 798 1	342	29. 73	4.89	- 0. 38	Serine/threonine protein kinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1273 GeneM ark.hmm 345_nt + 77714 78058	34 5	399 220 7	76	55. 18	5.79	117 411 44	244	60. 24	5.91	0. 12	939 798 1	111	34. 23	5.1	- 0. 69	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1274 GeneM ark.hmm 84_nt + 7 9513 79596	84	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	---	---	---	---
gene_1275 GeneM ark.hmm 288_nt + 80528 80815	28 8	399 220 7	86	74. 8	6.22	117 411 44	350	10 3.5 1	6.69	0. 47	939 798 1	250	92. 37	6.53	0. 31	NA			
gene_1276 GeneM ark.hmm 144_nt + 80817 80960	14 4	399 220 7	17	29. 57	4.89	117 411 44	107	63. 29	5.98	1. 09	939 798 1	63	46. 55	5.54	0. 65	NA			

gene_1277 GeneM ark.hmm 297_nt + 80973 81269	29 7	399 220 7	19	16. 02	4	117 411 44	113	32. 4	5.02	1. 02	939 798 1	93	33. 32	5.06	1. 06	NA			
gene_1278 GeneM ark.hmm 117_nt + 81864 81980	11 7	399 220 7	1	2.1 4	1.1	117 411 44	14	10. 19	3.35	2. 25	939 798 1	6	5.4 6	2.45	1. 35	NA			
gene_1652 GeneM ark.hmm 423_nt - 65847 66269	42 3	399 220 7	943 9	55 89. 49	12.4 5	117 411 44	422	84. 97	6.41	- 6. 04	939 798 1	438 9	11 04. 05	10.1 1	- 2. 34	Predicted rRNA methylase (SpoU class)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_127 GeneMa rk.hmm 807_nt + 9 2050 92856	80 7	399 220 7	566 6	17 58. 69	10.7 8	117 411 44	102 10	10 77. 56	10.0 7	- 0. 71	939 798 1	449 8	59 3.0 8	9.21	- 1. 57	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1280 GeneM ark.hmm 975_nt - 482 1456	97 5	399 220 7	548	14 0.7 9	7.14	117 411 44	283 1	24 7.3	7.95	0. 81	939 798 1	197 7	21 5.7 6	7.75	0. 61	Phosphotransacetylase	METABOLISM	Energy production and conversion	C
gene_1281 GeneM ark.hmm 897_nt - 1500 2396	89 7	399 220 7	289	80. 7	6.33	117 411 44	216 1	20 5.1 9	7.68	1. 35	939 798 1	136 2	16 1.5 7	7.34	1. 01	Pseudouridylate synthases, 23S RNA-specific	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1282 GeneM ark.hmm 705_nt - 2393 3097	70 5	399 220 7	300	10 6.5 9	6.74	117 411 44	195 3	23 5.9 4	7.88	1. 14	939 798 1	931	14 0.5 2	7.13	0. 39	Predicted sugar kinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1283 GeneM ark.hmm 672_nt - 3269 3940	67 2	399 220 7	528	19 6.8 1	7.62	117 411 44	225 5	28 5.8	8.16	0. 54	939 798 1	926	14 6.6 2	7.2	- 0. 42	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1284 GeneM ark.hmm 459_nt + 4068 4526	45 9	399 220 7	54	29. 47	4.88	117 411 44	366	67. 91	6.09	1. 21	939 798 1	108	25. 04	4.65	- 0. 23	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1285 GeneM ark.hmm 960_nt + 4832 5791	96 0	399 220 7	173 4	45 2.4 4	8.82	117 411 44	839 7	74 4.9 8	9.54	0. 72	939 798 1	256 4	28 4.1 9	8.15	- 0. 67	Phosphoribosylpyrophosphate synthetase	METABOLISM	Nucleotide transport and metabolism	F
gene_1286 GeneM ark.hmm 1116_nt + 5801 6916	11 16	399 220 7	467 0	10 48. 19	10.0 3	117 411 44	166 95	12 74. 12	10.3 2	0. 29	939 798 1	796 3	75 9.2 4	9.57	- 0. 46	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes	METABOLISM	Amino acid transport and metabolism	E
gene_1287 GeneM ark.hmm 348_nt + 6921 7268	34 8	399 220 7	670	48 2.2 6	8.91	117 411 44	222 3	54 4.0 6	9.09	0. 18	939 798 1	957	29 2.6 2	8.19	- 0. 72	---	---	---	---
gene_1288 GeneM ark.hmm 216_nt + 7276 7491	21 6	399 220 7	912	10 57. 62	10.0 5	117 411 44	305 3	12 03. 82	10.2 3	0. 18	939 798 1	976	48 0.8	8.91	- 1. 14	---	---	---	---
gene_1289 GeneM ark.hmm 417_nt + 7574 7990	41 7	399 220 7	267	16 0.3 8	7.33	117 411 44	124 3	25 3.8 8	7.99	0. 66	939 798 1	607	15 4.8 9	7.28	- 0. 05	AT-rich DNA-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_128 GeneMa rk.hmm 348_nt - 93024 93371	34 8	399 220 7	526 0	37 86. 11	11.8 9	117 411 44	268 47	65 70. 62	12.6 8	0. 79	939 798 1	217 44	66 48. 53	12.7	0. 81	Ribosomal protein L19	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1290 GeneM ark.hmm 222_nt +	22	399 220	96	10 8.3	6.76	117 411	545	20 9.0	7.71	0.	939 798	200	95.	6.58	- 0.	AT-rich DNA-binding protein	POORLY CHARACTERIZ	General function prediction only	R

8049 8270	2	7		2		44		9		95	1		86		18		ED		
gene_1291 GeneM ark.hmm 690_nt + 8288 8977	69 0	399 220 7	873	31 6.9 2	8.31	117 411 44	631 6	77 9.6 2	9.61	1. 3	939 798 1	327 6	50 5.2	8.98	0. 67	Predicted glutamine amidotransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1292 GeneM ark.hmm 681_nt - 8974 9654	68 1	399 220 7	144	52. 97	5.73	117 411 44	108 4	13 5.5 7	7.08	1. 35	939 798 1	647	10 1.0 9	6.66	0. 93	DNA repair proteins	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1293 GeneM ark.hmm 603_nt - 9697 10299	60 3	399 220 7	696	28 9.1 2	8.18	117 411 44	177 5	25 0.7 1	7.97	- 0. 21	939 798 1	147 9	26 0.9 9	8.03	- 0. 15	Superfamily I DNA and RNA helicases	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1294 GeneM ark.hmm 1683_nt - 10359 12041	16 83	399 220 7	373 9	55 6.4 9	9.12	117 411 44	637 3	32 2.5 1	8.33	- 0. 79	939 798 1	459 0	29 0.2	8.18	- 0. 94	Superfamily I DNA and RNA helicases	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1295 GeneM ark.hmm 390_nt - 12232 12621	39 0	399 220 7	265	17 0.2	7.41	117 411 44	855	18 6.7 2	7.54	0. 13	939 798 1	111 2	30 3.3 9	8.25	0. 84	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1296 GeneM ark.hmm 135_nt - 12638 12772	13 5	399 220 7	15	27. 83	4.8	117 411 44	26	16. 4	4.04	- 0. 76	939 798 1	31	24. 43	4.61	- 0. 19	---	---	---	---
gene_1297 GeneM ark.hmm 66_nt - 13020 13085	66	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1298 GeneM ark.hmm 255_nt - 13667 13921	25 5	399 220 7	306	30 0.5 9	8.23	117 411 44	114 8	38 3.4 3	8.58	0. 35	939 798 1	881	36 7.6 2	8.52	0. 29	Methionine aminopeptidase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1299 GeneM ark.hmm 603_nt - 13979 14581	60 3	399 220 7	577	23 9.6 9	7.91	117 411 44	225 4	31 8.3 7	8.31	0. 4	939 798 1	192 0	33 8.8	8.4	0. 49	Methionine aminopeptidase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_814 GeneMa rk.hmm 1608_nt + 192106 193713	16 08	399 220 7	456 2	71 0.6 5	9.47	117 411 44	252 4	13 3.6 9	7.06	- 2. 41	939 798 1	227 3	15 0.4 1	7.23	- 2. 24	Glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_12 GeneMar k.hmm 816_nt - 6749 7564	81 6	399 220 7	344	10 5.6	6.72	117 411 44	110 8	11 5.6 5	6.85	0. 13	939 798 1	135 5	17 6.6 9	7.47	0. 75	Predicted rRNA methylase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1300 GeneM ark.hmm 1278_nt - 14597 15874	12 78	399 220 7	224 4	43 9.8 2	8.78	117 411 44	991 3	66 0.6 4	9.37	0. 59	939 798 1	966 3	80 4.5 4	9.65	0. 87	Predicted transcriptional regulator containing CBS domains	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1301 GeneM ark.hmm 552_nt - 15867 16418	55 2	399 220 7	468	21 2.3 7	7.73	117 411 44	310 9	47 9.7	8.91	1. 18	939 798 1	312 7	60 2.7 7	9.24	1. 51	Acetyltransferases, including N- acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1302 GeneM ark.hmm 1260_nt - 16434 17693	12 60	399 220 7	417 4	82 9.7 9	9.7	117 411 44	198 28	13 40. 29	10.3 9	0. 69	939 798 1	152 68	12 89. 37	10.3 3	0. 63	UDP-N-acetylglucosamine enolpyruvyl transferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1303 GeneM ark.hmm 159_nt -	15 9	399 220	14	22. 06	4.46	117 411	105	56. 24	5.81	1. 35	939 798	77	51. 53	5.69	1. 23	---	---	---	---

[18836]18994		7				44					1								
gene_1304[GeneM ark.hmm]1311_nt[- 19004]20314	13 11	399 220 7	258 9	49 4.6 7	8.95	117 411 44	519 4	33 7.4 3	8.4	- 0. 55	939 798 1	647 3	52 5.3 7	9.04	0. 09	Predicted GTPase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1305[GeneM ark.hmm]135_nt[- 20378]20512	13 5	399 220 7	23	42. 68	5.42	117 411 44	131	82. 65	6.37	0. 95	939 798 1	123	96. 95	6.6	1. 18	---	---	---	---
gene_1306[GeneM ark.hmm]177_nt[- 20571]20747	17 7	399 220 7	72	10 1.8 9	6.67	117 411 44	178	85. 65	6.42	- 0. 25	939 798 1	202	12 1.4 3	6.92	0. 25	Putative stress-responsive transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1307[GeneM ark.hmm]1326_nt[- 20778]22103	13 26	399 220 7	158 5	29 9.4 1	8.23	117 411 44	404 3	25 9.6 9	8.02	- 0. 21	939 798 1	387 4	31 0.8 7	8.28	0. 05	Glycosyltransferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1308[GeneM ark.hmm]678_nt[- 22119]22796	67 8	399 220 7	663	24 4.9 5	7.94	117 411 44	293 1	36 8.1 9	8.52	0. 58	939 798 1	206 4	32 3.9 3	8.34	0. 4	Glycosyltransferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1309[GeneM ark.hmm]336_nt[- 22852]23187	33 6	399 220 7	219	16 3.2 6	7.35	117 411 44	132 7	33 6.3 7	8.39	1. 04	939 798 1	637	20 1.7 3	7.66	0. 31	Glycosyltransferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_130[GeneMa rk.hmm]330_nt[- 93858]94187	33 0	399 220 7	56	42. 51	5.41	117 411 44	456	11 7.6 9	6.88	1. 47	939 798 1	447	14 4.1 3	7.17	1. 76	Integral membrane protein possibly involved in chromosome condensation	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1310[GeneM ark.hmm]330_nt[- 23329]23658	33 0	399 220 7	339 7	25 78. 51	11.3 3	117 411 44	287 1	74 0.9 8	9.53	- 1. 8	939 798 1	402 0	12 96. 22	10.3 4	- 0. 99	Predicted metal-sulfur cluster biosynthetic enzyme	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1311[GeneM ark.hmm]1110_nt[- 23672]24781	11 10	399 220 7	395 6	89 2.7 3	9.8	117 411 44	515 4	39 5.4 7	8.63	- 1. 17	939 798 1	737 6	70 7.0 7	9.47	- 0. 33	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1312[GeneM ark.hmm]1761_nt[- 24784]26544	17 61	399 220 7	397 6	56 5.5 5	9.14	117 411 44	698 8	33 7.9 7	8.4	- 0. 74	939 798 1	788 0	47 6.1 4	8.9	- 0. 24	DNA primase (bacterial type)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1313[GeneM ark.hmm]759_nt[- 26634]27392	75 9	399 220 7	62	20. 46	4.35	117 411 44	310	34. 79	5.12	0. 77	939 798 1	616	86. 36	6.43	2. 08	ABC-type uncharacterized transport system, ATPase component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1314[GeneM ark.hmm]867_nt[- 27389]28255	86 7	399 220 7	39	11. 27	3.49	117 411 44	348	34. 19	5.1	1. 61	939 798 1	616	75. 6	6.24	2. 75	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1315[GeneM ark.hmm]348_nt[- 28324]28671	34 8	399 220 7	62	44. 63	5.48	117 411 44	189	46. 26	5.53	0. 05	939 798 1	343	10 4.8 8	6.71	1. 23	ABC-type uncharacterized transport system, periplasmic component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1316[GeneM ark.hmm]651_nt[- 28742]29392	65 1	399 220 7	58	22. 32	4.48	117 411 44	425	55. 6	5.8	1. 32	939 798 1	786	12 8.4 7	7.01	2. 53	ABC-type uncharacterized transport system, periplasmic component	POORLY CHARACTERIZ ED	General function prediction only	R

gene_1317 GeneM ark.hmm 1050_nt - 29805 30854	10 50	399 220 7	237 4	56 6.3 4	9.15	117 411 44	555 1	45 0.2 7	8.81	- 0. 34	939 798 1	555 0	56 2.4 3	9.14	- 0. 01	Phosphoenolpyruvate carboxylase	METABOLISM	Energy production and conversion	C
gene_1318 GeneM ark.hmm 189_nt - 30952 31140	18 9	399 220 7	71	94. 1	6.56	117 411 44	383	17 2.5 9	7.43	0. 87	939 798 1	358	20 1.5 5	7.66	1. 1	Phosphoenolpyruvate carboxylase	METABOLISM	Energy production and conversion	C
gene_1319 GeneM ark.hmm 1479_nt - 31258 32736	14 79	399 220 7	148 4	25 1.3 3	7.97	117 411 44	101 60	58 5.0 8	9.19	1. 22	939 798 1	803 3	57 7.9 3	9.17	1. 2	Phosphoenolpyruvate carboxylase	METABOLISM	Energy production and conversion	C
gene_131 GeneMa rk.hmm 267_nt - 94229 94495	26 7	399 220 7	62	58. 17	5.86	117 411 44	499	15 9.1 8	7.31	1. 45	939 798 1	293	11 6.7 7	6.87	1. 01	Chorismate mutase	METABOLISM	Amino acid transport and metabolism	E
gene_1320 GeneM ark.hmm 252_nt - 32756 33007	25 2	399 220 7	72	71. 57	6.16	117 411 44	542	18 3.1 8	7.52	1. 36	939 798 1	321	13 5.5 4	7.08	0. 92	Bacterial cell division membrane protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1321 GeneM ark.hmm 126_nt - 33135 33260	12 6	399 220 7	5	9.9 4	3.31	117 411 44	99	66. 92	6.06	2. 75	939 798 1	46	38. 85	5.28	1. 97	Bacterial cell division membrane protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1322 GeneM ark.hmm 837_nt - 33327 34163	83 7	399 220 7	342	10 2.3 5	6.68	117 411 44	307 0	31 2.3 9	8.29	1. 61	939 798 1	143 9	18 2.9 4	7.52	0. 84	Bacterial cell division membrane protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1323 GeneM ark.hmm 114_nt + 34480 34593	11 4	399 220 7	4	8.7 9	3.14	117 411 44	29	21. 67	4.44	1. 3	939 798 1	7	6.5 3	2.71	- 0. 43	NA			
gene_1324 GeneM ark.hmm 423_nt - 34722 35144	42 3	399 220 7	61	36. 12	5.17	117 411 44	313	63. 02	5.98	0. 81	939 798 1	119	29. 93	4.9	- 0. 27	Predicted aminoglycoside phosphotransferase	POORLY CHARACTERIZED	General function prediction only	R
gene_1325 GeneM ark.hmm 474_nt - 35251 35724	47 4	399 220 7	133	70. 28	6.14	117 411 44	512	92	6.52	0. 38	939 798 1	75	16. 84	4.07	- 2. 07	NA			
gene_369 GeneMa rk.hmm 6420_nt - 62617 69036	64 20	399 220 7	541 3	21 1.2	7.72	117 411 44	367 2	48. 71	5.61	- 2. 11	939 798 1	271 8	45. 05	5.49	- 2. 23	Subtilisin-like serine proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2192 GeneM ark.hmm 651_nt + 6298 6948	65 1	399 220 7	130 3	50 1.3 6	8.97	117 411 44	620	81. 11	6.34	- 2. 63	939 798 1	677	11 0.6 6	6.79	- 2. 18	Phosphate uptake regulator	METABOLISM	Inorganic ion transport and metabolism	P
gene_1328 GeneM ark.hmm 162_nt - 37824 37985	16 2	399 220 7	0	0	0	117 411 44	6	3.1 5	1.66	1. 66	939 798 1	2	1.3 1	0.39	0. 39	NA			
gene_348 GeneMa rk.hmm 327_nt - 43655 43981	32 7	399 220 7	141	10 8.0 1	6.76	117 411 44	89	23. 18	4.53	- 2. 23	939 798 1	74	24. 08	4.59	- 2. 17	Peptide methionine sulfoxide reductase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O

gene_132 GeneMa rk.hmm 444_nt - 94611 95054	44 4	399 220 7	539	30 4.0 8	8.25	117 411 44	205 9	39 4.9 7	8.63	0. 38	939 798 1	126 5	30 3.1 6	8.24	- 0. 01	Flavodoxins	METABOLISM	Energy production and conversion	C
gene_1330 GeneM ark.hmm 147_nt - 39740 39886	14 7	399 220 7	3	5.1 1	2.35	117 411 44	17	9.8 5	3.3	0. 95	939 798 1	13	9.4 1	3.23	0. 88	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_748 GeneMa rk.hmm 1845_nt + 121296 123140	18 45	399 220 7	947 3	12 86. 11	10.3 3	117 411 44	458 9	21 1.8 4	7.73	- 2. 6	939 798 1	511 8	29 5.1 7	8.21	- 2. 12	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1332 GeneM ark.hmm 420_nt - 40685 41104	42 0	399 220 7	21	12. 52	3.65	117 411 44	184	37. 31	5.22	1. 57	939 798 1	100	25. 33	4.66	1. 01	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1333 GeneM ark.hmm 105_nt - 41365 41469	10 5	399 220 7	0	0	0	117 411 44	5	4.0 6	2.02	2. 02	939 798 1	2	2.0 3	1.02	1. 02	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1334 GeneM ark.hmm 819_nt - 41471 42289	81 9	399 220 7	57	17. 43	4.12	117 411 44	306	31. 82	4.99	0. 87	939 798 1	161	20. 92	4.39	0. 27	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1335 GeneM ark.hmm 993_nt - 42291 43283	99 3	399 220 7	117	29. 51	4.88	117 411 44	647	55. 49	5.79	0. 91	939 798 1	361	38. 68	5.27	0. 39	ABC-type uncharacterized transport system, ATPase component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1336 GeneM ark.hmm 792_nt - 46713 47504	79 2	399 220 7	64	20. 24	4.34	117 411 44	384	41. 29	5.37	1. 03	939 798 1	156	20. 96	4.39	0. 05	Seryl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1337 GeneM ark.hmm 1098_nt - 47506 48603	10 98	399 220 7	106	24. 18	4.6	117 411 44	721	55. 93	5.81	1. 21	939 798 1	350	33. 92	5.08	0. 48	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolicase, phosphonopyruvate decarboxylase]	METABOLISM	Amino acid transport and metabolism	E
gene_1338 GeneM ark.hmm 846_nt - 48593 49438	84 6	399 220 7	181	53. 59	5.74	117 411 44	806	81. 14	6.34	0. 6	939 798 1	354	44. 52	5.48	- 0. 26	PEP phosphonomutase and related enzymes	METABOLISM	Carbohydrate transport and metabolism	G
gene_1339 GeneM ark.hmm 1098_nt - 52819 53916	10 98	399 220 7	64	14. 6	3.87	117 411 44	360	27. 92	4.8	0. 93	939 798 1	251	24. 32	4.6	0. 73	Adenosylmethionine-8-amino-7- oxononoate aminotransferase	METABOLISM	Coenzyme transport and metabolism	H
gene_133 GeneMa rk.hmm 102_nt + 9 5158 95259	10 2	399 220 7	0	0	0	117 411 44	5	4.1 8	2.06	2. 06	939 798 1	1	1.0 4	0.06	0. 06	Exopolysphatase-related proteins	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1340 GeneM ark.hmm 750_nt - 54907 55656	75 0	399 220 7	303	10 1.2	6.66	117 411 44	826	93. 8	6.55	- 0. 11	939 798 1	515	73. 07	6.19	- 0. 47	Transketolase, N-terminal subunit	METABOLISM	Carbohydrate transport and metabolism	G
gene_1341 GeneM ark.hmm 1209_nt - 56602 57810	12 09	399 220 7	358	74. 17	6.21	117 411 44	884	62. 28	5.96	- 0. 25	939 798 1	497	43. 74	5.45	- 0. 76	Enolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1342 GeneM ark.hmm 966_nt -	96	399 220	186	48.	5.59	117 411	871	76.	6.26	0.	939 798	533	58.	5.88	0.	D-alanine-D-alanine ligase and	CELLULAR PROCESSES	Cell wall/membrane/envelope	M

[57876 58841	6	7		23		44		79		67	1		71		29	related ATP-grasp enzymes	AND SIGNALING	biogenesis	
gene_1343 GeneM ark.hmm 690_nt 59121 59810	690	3992207	35	12.71	3.67	11741144	332	40.98	5.36	1.69	9397981	158	24.37	4.61	0.94	---	---	---	---
gene_1344 GeneM ark.hmm 1140_nt 59832 60971	1140	3992207	67	14.72	3.88	11741144	796	59.47	5.89	2.01	9397981	579	54.04	5.76	1.88	Type IV secretory pathway, VirD2 components (relaxase)	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_1345 GeneM ark.hmm 366_nt 60958 61323	366	3992207	12	8.21	3.04	11741144	138	32.11	5.01	1.97	9397981	63	18.32	4.2	1.16	---	---	---	---
gene_1346 GeneM ark.hmm 360_nt 61333 61692	360	3992207	23	16	4	11741144	186	44	5.46	1.46	9397981	114	33.7	5.07	1.07	---	---	---	---
gene_1347 GeneM ark.hmm 873_nt 62524 63396	873	3992207	157	45.05	5.49	11741144	291	28.39	4.83	0.66	9397981	177	21.57	4.43	1.06	---	---	---	---
gene_1348 GeneM ark.hmm 600_nt 63709 64308	600	3992207	562	234.62	7.87	11741144	561	79.63	6.32	1.55	9397981	204	36.18	5.18	2.69	---	---	---	---
gene_1349 GeneM ark.hmm 282_nt 64308 64589	282	3992207	103	91.49	6.52	11741144	163	49.23	5.62	0.9	9397981	52	19.62	4.29	2.23	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_134 GeneMa rk.hmm 828_nt + 9 5325 96152	828	3992207	573	173.34	7.44	11741144	2574	264.77	8.05	0.61	9397981	1460	187.62	7.55	0.11	Exopolyphosphatase-related proteins	POORLY CHARACTERIZED	General function prediction only	R
gene_1350 GeneM ark.hmm 456_nt 65310 65765	456	3992207	49	26.92	4.75	11741144	335	62.57	5.97	1.22	9397981	166	38.74	5.28	0.53	---	---	---	---
gene_1351 GeneM ark.hmm 1509_nt 66040 67548	1509	3992207	76	12.62	3.66	11741144	686	38.72	5.27	1.61	9397981	247	17.42	4.12	0.46	Glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_347 GeneMa rk.hmm 891_nt 42823 43713	891	3992207	910	255.83	8	11741144	512	48.94	5.61	2.39	9397981	502	59.95	5.91	2.09	Conserved domain frequently associated with peptide methionine sulfoxide reductase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1353 GeneM ark.hmm 885_nt 68017 68901	885	3992207	473	133.88	7.06	11741144	1177	113.27	6.82	0.24	9397981	659	79.23	6.31	0.75	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	METABOLISM	Lipid transport and metabolism	I
gene_1354 GeneM ark.hmm 660_nt 69013 69672	660	3992207	46	17.46	4.13	11741144	225	29.04	4.86	0.73	9397981	239	38.53	5.27	1.14	ADP-ribosylglycohydrolase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1355 GeneM ark.hmm 159_nt 69759 69917	159	3992207	21	33.08	5.05	11741144	87	46.6	5.54	0.49	9397981	138	92.35	6.53	1.48	ADP-ribosylglycohydrolase	CELLULAR PROCESSES AND	Posttranslational modification, protein turnover, chaperones	O

																	SIGNALING		
gene_1356 GeneM ark.hmm 816_nt - 69917 70732	81 6	399 220 7	28	8.6	3.1	117 411 44	385	40. 18	5.33	2. 23	939 798 1	259	33. 77	5.08	1. 98	---	---	---	---
gene_1357 GeneM ark.hmm 567_nt - 71304 71870	56 7	399 220 7	55	24. 3	4.6	117 411 44	280	42. 06	5.39	0. 79	939 798 1	187	35. 09	5.13	0. 53	---	---	---	---
gene_1358 GeneM ark.hmm 582_nt - 72138 72719	58 2	399 220 7	142	61. 12	5.93	117 411 44	383	56. 05	5.81	- 0. 12	939 798 1	324	59. 24	5.89	- 0. 04	Site-specific recombinases, DNA invertase Pin homologs	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1359 GeneM ark.hmm 216_nt - 73289 73504	21 6	399 220 7	133	15 4.2 4	7.27	117 411 44	192	75. 71	6.24	- 1. 03	939 798 1	184	90. 64	6.5	- 0. 77	Site-specific recombinases, DNA invertase Pin homologs	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_135 GeneMa rk.hmm 243_nt + 9 6248 96490	24 3	399 220 7	387 37	39 93 0.6 8	15.2 9	117 411 44	117 706	41 25 5.5 1	15.3 3	0. 04	939 798 1	201 52	88 24. 24	13.1 1	- 2. 18	Ribosomal protein L31	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1360 GeneM ark.hmm 216_nt - 73560 73775	21 6	399 220 7	19	22. 03	4.46	117 411 44	68	26. 81	4.74	0. 28	939 798 1	41	20. 2	4.34	- 0. 12	Site-specific recombinases, DNA invertase Pin homologs	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_815 GeneMa rk.hmm 174_nt + 1 93872 194045	17 4	399 220 7	118	16 9.8 7	7.41	117 411 44	83	40. 63	5.34	- 2. 07	939 798 1	68	41. 58	5.38	- 2. 03	NA			
gene_1362 GeneM ark.hmm 795_nt - 75907 76701	79 5	399 220 7	836	26 3.4 1	8.04	117 411 44	407 1	43 6.1 4	8.77	0. 73	939 798 1	336 8	45 0.7 9	8.82	0. 78	ABC-type cobalamin/Fe3+- siderophores transport systems, ATPase components	METABOLISM	Inorganic ion transport and metabolism	P
gene_1363 GeneM ark.hmm 414_nt + 76813 77226	41 4	399 220 7	73	44. 17	5.46	117 411 44	550	11 3.1 5	6.82	1. 36	939 798 1	472	12 1.3 1	6.92	1. 46	NA			
gene_1364 GeneM ark.hmm 1026_nt - 78705 79730	10 26	399 220 7	363 6	88 7.6 9	9.79	117 411 44	903 9	75 0.3 5	9.55	- 0. 24	939 798 1	281 7	29 2.1 5	8.19	- 1. 6	ABC-type Fe3+-hydroxamate transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1365 GeneM ark.hmm 219_nt - 80123 80341	21 9	399 220 7	175	20 0.1 6	7.65	117 411 44	327	12 7.1 7	6.99	- 0. 66	939 798 1	98	47. 62	5.57	- 2. 08	Predicted transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1366 GeneM ark.hmm 1632_nt - 81079 82710	16 32	399 220 7	332 1	50 9.7 2	8.99	117 411 44	125 45	65 4.7	9.35	0. 36	939 798 1	986 5	64 3.1 9	9.33	0. 34	SAM-dependent methyltransferases related to tRNA (uracil-5-)- methyltransferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1367 GeneM ark.hmm 975_nt - 82784 83758	97 5	399 220 7	668 20	17 16 6.7 8	14.0 7	117 411 44	135 648	11 84 9.4 5	13.5 3	- 0. 54	939 798 1	111 987	12 22 1.6 1	13.5 8	- 0. 49	Predicted secreted protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1368 GeneM ark.hmm 573_nt - 83832 84404	57 3	399 220 7	496	21 6.8 3	7.76	117 411 44	532 5	79 1.5 1	9.63	1. 87	939 798 1	693 4	12 87. 64	10.3 3	2. 57	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M

gene_1369 GeneM ark.hmm 975_nt - 84505 85479	97 5	399 220 7	853	21 9.1 4	7.78	117 411 44	819 6	5.9 6	9.48	1. 7	939 798 1	770 4	84 0.7 7	9.72	1. 94	---	---	---	---
gene_136 GeneMa rk.hmm 219_nt - 96547 96765	21 9	399 220 7	16	18. 3	4.19	117 411 44	172	66. 89	6.06	1. 87	939 798 1	74	35. 95	5.17	0. 98	---	---	---	---
gene_1370 GeneM ark.hmm 447_nt - 85487 85933	44 7	399 220 7	193 7	10 85. 45	10.0 8	117 411 44	507 1	96 6.2 2	9.92	- 0. 16	939 798 1	453 9	10 80. 48	10.0 8	0	Glycine/serine hydroxymethyltransferase	METABOLISM	Amino acid transport and metabolism	E
gene_1371 GeneM ark.hmm 753_nt - 86052 86804	75 3	399 220 7	146 6	48 7.6 7	8.93	117 411 44	103 88	11 74. 97	10.2	1. 27	939 798 1	848 3	11 98. 73	10.2 3	1. 3	Glycine/serine hydroxymethyltransferase	METABOLISM	Amino acid transport and metabolism	E
gene_1372 GeneM ark.hmm 432_nt - 86866 87297	43 2	399 220 7	493	28 5.8 6	8.16	117 411 44	298 4	58 8.3 1	9.2	1. 04	939 798 1	230 9	56 8.7 3	9.15	0. 99	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1373 GeneM ark.hmm 603_nt - 87299 87901	60 3	399 220 7	116 6	48 4.3 6	8.92	117 411 44	702 8	99 2.6 7	9.96	1. 04	939 798 1	598 2	10 55. 59	10.0 4	1. 12	Putative translation factor (SUA5)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1374 GeneM ark.hmm 840_nt - 87885 88724	84 0	399 220 7	493	14 7.0 1	7.2	117 411 44	296 0	30 0.1 2	8.23	1. 03	939 798 1	284 2	36 0.0 1	8.49	1. 29	Methylase of polypeptide chain release factors	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1375 GeneM ark.hmm 1080_nt - 88724 89803	10 80	399 220 7	117 4	27 2.2 9	8.09	117 411 44	386 1	30 4.4 8	8.25	0. 16	939 798 1	446 0	43 9.4 2	8.78	0. 69	Protein chain release factor A	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1376 GeneM ark.hmm 591_nt - 89800 90390	59 1	399 220 7	113 9	48 2.7 5	8.92	117 411 44	328 6	47 3.5 5	8.89	- 0. 03	939 798 1	263 9	47 5.1 4	8.89	- 0. 03	Thymidine kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_1377 GeneM ark.hmm 183_nt + 90513 90695	18 3	399 220 7	212	29 0.1 8	8.18	117 411 44	301	14 0.0 9	7.13	- 1. 05	939 798 1	118	68. 61	6.1	- 2. 08	Uncharacterized protein, 4- oxalocrotonate tautomerase homolog	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1378 GeneM ark.hmm 1374_nt + 90899 92272	13 74	399 220 7	199 7	36 4.0 6	8.51	117 411 44	479 2	29 7.0 4	8.21	- 0. 3	939 798 1	264 2	20 4.6	7.68	- 0. 83	Predicted GTPase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1379 GeneM ark.hmm 936_nt - 92319 93254	93 6	399 220 7	284	76	6.25	117 411 44	255 6	23 2.5 8	7.86	1. 61	939 798 1	399 3	45 3.9 3	8.83	2. 58	Dihydrodipicolinate synthase/N- acetylneuraminate lyase	METABOLISM	Amino acid transport and metabolism	E
gene_137 GeneMa rk.hmm 153_nt - 97073 97225	15 3	399 220 7	24	39. 29	5.3	117 411 44	155	86. 28	6.43	1. 13	939 798 1	97	67. 46	6.08	0. 78	---	---	---	---
gene_323 GeneMa rk.hmm 228_nt - 21338 21565	22 8	399 220 7	9	9.8 9	3.31	117 411 44	189	70. 6	6.14	2. 83	939 798 1	85	39. 67	5.31	2	---	---	---	---
gene_1548 GeneM ark.hmm 1350_nt + 21286 22635	13 50	399 220 7	79	14. 66	3.87	117 411 44	958	60. 44	5.92	2. 05	939 798 1	742	58. 48	5.87	2	---	---	---	---
gene_1841 GeneM ark.hmm 702_nt -	70	399 220	11	3.9	1.97	117 411	169	20.	4.36	2.	939 798	104	15.	3.98	2.	Uncharacterized membrane protein	POORLY CHARACTERIZ	Function unknown	S

[2863 3564	2	7		3		44		5		39	1		76		01		ED		
gene_1383 GeneM ark.hmm 510_nt - 95022 95531	51 0	399 220 7	157	77. 11	6.27	117 411 44	142 3	23 7.6 4	7.89	1. 62	939 798 1	663	13 8.3 3	7.11	0. 84	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1384 GeneM ark.hmm 432_nt + 95654 96085	43 2	399 220 7	24	13. 92	3.8	117 411 44	290	57. 17	5.84	2. 04	939 798 1	84	20. 69	4.37	0. 57	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1385 GeneM ark.hmm 378_nt + 96167 96544	37 8	399 220 7	148 5	98 4.0 6	9.94	117 411 44	658 3	14 83. 27	10.5 3	0. 59	939 798 1	149 6	42 1.1 2	8.72	- 1. 22	Large-conductance mechanosensitive channel	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1386 GeneM ark.hmm 273_nt - 96586 96858	27 3	399 220 7	38	34. 87	5.12	117 411 44	308	96. 09	6.59	1. 47	939 798 1	163	63. 53	5.99	0. 87	Protoheme ferro-lyase (ferrochelataze)	METABOLISM	Coenzyme transport and metabolism	H
gene_1796 GeneM ark.hmm 114_nt + 5314 5427	11 4	399 220 7	2	4.3 9	2.14	117 411 44	26	19. 42	4.28	2. 14	939 798 1	19	17. 73	4.15	2. 01	NA			
gene_1388 GeneM ark.hmm 1224_nt + 97680 98903	12 24	399 220 7	359 2	73 5.0 9	9.52	117 411 44	817 5	56 8.8 5	9.15	- 0. 37	939 798 1	480 2	41 7.4 5	8.71	- 0. 81	Di- and tripeptidases	METABOLISM	Amino acid transport and metabolism	E
gene_524 GeneMa rk.hmm 873_nt - 30697 31569	87 3	399 220 7	20	5.7 4	2.52	117 411 44	430	41. 95	5.39	2. 87	939 798 1	191	23. 28	4.54	2. 02	Type II secretory pathway, component PulF	CELLULAR PROCESSES AND SIGNALING	Cell motility	N
gene_138 GeneMa rk.hmm 1347_nt + 98011 99357	13 47	399 220 7	421 8	78 4.3 8	9.62	117 411 44	251 79	15 92. 06	10.6 4	1. 02	939 798 1	159 38	12 59. 02	10.3	0. 68	Glutamate dehydrogenase/leucine dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_301 GeneMa rk.hmm 681_nt + 2 702 3382	68 1	399 220 7	29	10. 67	3.42	117 411 44	378	47. 28	5.56	2. 14	939 798 1	277	43. 28	5.44	2. 02	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_302 GeneMa rk.hmm 678_nt + 3 342 4019	67 8	399 220 7	25	9.2 4	3.21	117 411 44	436	54. 77	5.78	2. 57	939 798 1	239	37. 51	5.23	2. 02	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_1392 GeneM ark.hmm 3120_nt - 101368 104487	31 20	399 220 7	837	67. 2	6.07	117 411 44	102 37	27 9.4 5	8.13	2. 06	939 798 1	754 2	25 7.2 2	8.01	1. 94	---	---	---	---
gene_1393 GeneM ark.hmm 480_nt - 104697 105176	48 0	399 220 7	104 0	54 2.7 2	9.08	117 411 44	355 5	63 0.7 9	9.3	0. 22	939 798 1	237 7	52 6.9 3	9.04	- 0. 04	---	---	---	---
gene_2426 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	3	6.2 6	2.65	117 411 44	48	34. 07	5.09	2. 44	939 798 1	29	25. 71	4.68	2. 03	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_730 GeneMa rk.hmm 1299_nt + 102034 103332	12 99	399 220 7	118	22. 75	4.51	117 411 44	194 4	12 7.4 6	6.99	2. 48	939 798 1	113 8	93. 22	6.54	2. 03	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_957 GeneMa rk.hmm 960_nt + 5	96	399 220	200	52.	5.71	117 411	297	26 4.1	8.05	2.	939 798	196	21	7.77	2.	Na+/serine symporter	METABOLISM	Amino acid transport and	E

6560 57519	0	7		19		44	7	2		34	1	5	7.8		06			metabolism	
gene_1397 GeneM ark.hmm 159_nt + 502 660	15 9	399 220 7	0	0	0	117 411 44	1	0.5 4	-0.9	- 0. 9	939 798 1	7	4.6 8	2.23	2. 23	NA			
gene_1398 GeneM ark.hmm 102_nt + 756 857	10 2	399 220 7	0	0	0	117 411 44	4	3.3 4	1.74	1. 74	939 798 1	28	29. 21	4.87	4. 87	NA			
gene_1399 GeneM ark.hmm 1197_nt 456 1652	11 97	399 220 7	190 121	39 78 5.3 2	15.2 8	117 411 44	401 386	28 55 9.9 6	14.8	- 0. 48	939 798 1	142 486	12 66 6.1 2	13.6 3	- 1. 65	GTPases - translation elongation factors	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_139 GeneMa rk.hmm 348_nt 100036 100383	34 8	399 220 7	183	13 1.7 2	7.04	117 411 44	781	19 1.1 4	7.58	0. 54	939 798 1	332	10 1.5 1	6.67	- 0. 37	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_13 GeneMar k.hmm 876_nt 7557 8432	87 6	399 220 7	286	81. 78	6.35	117 411 44	615	59. 79	5.9	- 0. 45	939 798 1	775	94. 14	6.56	0. 21	Geranylgeranyl pyrophosphate synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_1400 GeneM ark.hmm 870_nt 2573 3442	87 0	399 220 7	109 81	31 61. 62	11.6 3	117 411 44	115 53	11 31. 01	10.1 4	- 1. 49	939 798 1	809 2	98 9.7	9.95	- 1. 68	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	METABOLISM	Carbohydrate transport and metabolism	G
gene_517 GeneMa rk.hmm 381_nt 28161 28541	38 1	399 220 7	4	2.6 3	1.39	117 411 44	87	19. 45	4.28	2. 89	939 798 1	39	10. 89	3.45	2. 06	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_1402 GeneM ark.hmm 168_nt 4084 4251	16 8	399 220 7	0	0	0	117 411 44	8	4.0 6	2.02	2. 02	939 798 1	4	2.5 3	1.34	1. 34	---	---	---	---
gene_194 GeneMa rk.hmm 621_nt + 5 1395 52015	62 1	399 220 7	25	10. 08	3.33	117 411 44	392	53. 76	5.75	2. 42	939 798 1	246	42. 15	5.4	2. 07	---	---	---	---
gene_322 GeneMa rk.hmm 726_nt + 2 0573 21298	72 6	399 220 7	37	12. 77	3.67	117 411 44	803	94. 2	6.56	2. 89	939 798 1	366	53. 64	5.75	2. 08	16S rRNA uridine-516 pseudouridylylase synthase and related pseudouridylylase synthases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2258 GeneM ark.hmm 3018_nt 78763 81780	30 18	399 220 7	78	6.4 7	2.69	117 411 44	147 3	41. 57	5.38	2. 69	939 798 1	785	27. 68	4.79	2. 1	---	---	---	---
gene_1406 GeneM ark.hmm 321_nt + 7170 7490	32 1	399 220 7	660	51 5.0 2	9.01	117 411 44	138 4	36 7.2 2	8.52	- 0. 49	939 798 1	662	21 9.4 4	7.78	- 1. 23	Phosphomannomutase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1407 GeneM ark.hmm 1392_nt + 7560 8951	13 92	399 220 7	628 6	11 31. 15	10.1 4	117 411 44	129 02	78 9.4 2	9.62	- 0. 52	939 798 1	786 3	60 1.0 6	9.23	- 0. 91	Phosphomannomutase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1408 GeneM ark.hmm 348_nt + 9062 9409	34 8	399 220 7	183 53	13 21 0.3 6	13.6 9	117 411 44	460 64	11 27 3.8 4	13.4 6	- 0. 23	939 798 1	515 8	15 77. 13	10.6 2	- 3. 07	Thiol-disulfide isomerase and thioredoxins	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O

gene_1409 GeneM ark.hmm 837_nt - 9688 10524	83 7	399 220 7	940	28 1.3 1	8.14	117 411 44	621 5	63 2.4 2	9.3	1. 16	939 798 1	415 7	52 8.4 7	9.05	0. 91	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_140 GeneMa rk.hmm 390_nt - 100631 101020	39 0	399 220 7	105 1	67 5.0 3	9.4	117 411 44	234 2	51 1.4 6	9	- 0. 4	939 798 1	199 9	54 5.4	9.09	- 0. 31	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1410 GeneM ark.hmm 630_nt - 10537 11166	63 0	399 220 7	275	10 9.3 4	6.77	117 411 44	262 2	35 4.4 7	8.47	1. 7	939 798 1	167 5	28 2.9	8.14	1. 37	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_1411 GeneM ark.hmm 642_nt - 11176 11817	64 2	399 220 7	375	14 6.3 1	7.19	117 411 44	345 7	45 8.6 2	8.84	1. 65	939 798 1	178 9	29 6.5 1	8.21	1. 02	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_1412 GeneM ark.hmm 1230_nt - 11963 13192	12 30	399 220 7	350 6	71 3.9 9	9.48	117 411 44	100 05	69 2.7 9	9.44	- 0. 04	939 798 1	804 7	69 6.1 4	9.44	- 0. 04	FOG: TPR repeat	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1413 GeneM ark.hmm 1167_nt - 13182 14348	11 67	399 220 7	201 9	43 3.3 6	8.76	117 411 44	612 4	44 6.9 4	8.8	0. 04	939 798 1	385 1	35 1.1 3	8.46	- 0. 3	Predicted permease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1414 GeneM ark.hmm 1014_nt + 14492 15505	10 14	399 220 7	119 42	29 50. 03	11.5 3	117 411 44	136 84	11 49. 38	10.1 7	- 1. 36	939 798 1	693 8	72 8.0 5	9.51	- 2. 02	3-carboxymuconate cyclase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1415 GeneM ark.hmm 420_nt - 15550 15969	42 0	399 220 7	132 2	78 8.4 4	9.62	117 411 44	850 6	17 24. 91	10.7 5	1. 13	939 798 1	842 8	21 35. 21	11.0 6	1. 44	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)	METABOLISM	Energy production and conversion	C
gene_1416 GeneM ark.hmm 585_nt - 15980 16564	58 5	399 220 7	291 3	12 47. 3	10.2 8	117 411 44	216 67	31 54. 51	11.6 2	1. 34	939 798 1	235 58	42 84. 97	12.0 7	1. 79	F0F1-type ATP synthase, beta subunit	METABOLISM	Energy production and conversion	C
gene_1417 GeneM ark.hmm 804_nt - 16695 17498	80 4	399 220 7	233 8	72 8.4 1	9.51	117 411 44	210 45	22 29. 37	11.1 2	1. 61	939 798 1	201 69	26 69. 28	11.3 8	1. 87	F0F1-type ATP synthase, beta subunit	METABOLISM	Energy production and conversion	C
gene_1418 GeneM ark.hmm 879_nt - 17584 18462	87 9	399 220 7	558 6	15 91. 84	10.6 4	117 411 44	345 59	33 48. 59	11.7 1	1. 07	939 798 1	346 58	41 95. 46	12.0 3	1. 39	F0F1-type ATP synthase, gamma subunit	METABOLISM	Energy production and conversion	C
gene_1419 GeneM ark.hmm 351_nt - 18478 18828	35 1	399 220 7	690	49 2.4 1	8.94	117 411 44	514 6	12 48. 68	10.2 9	1. 35	939 798 1	472 4	14 32. 08	10.4 8	1. 54	F0F1-type ATP synthase, alpha subunit	METABOLISM	Energy production and conversion	C
gene_141 GeneMa rk.hmm 159_nt - 101116 101274	15 9	399 220 7	54	85. 07	6.41	117 411 44	79	42. 32	5.4	- 1. 01	939 798 1	44	29. 45	4.88	- 1. 53	---	---	---	---
gene_1420 GeneM ark.hmm 849_nt - 18942 19790	84 9	399 220 7	234 2	69 0.9 8	9.43	117 411 44	224 85	22 55. 67	11.1 4	1. 71	939 798 1	174 05	21 81. 38	11.0 9	1. 66	F0F1-type ATP synthase, alpha subunit	METABOLISM	Energy production and conversion	C
gene_795 GeneMa rk.hmm 435_nt + 1 73726 174160	43 5	399 220 7	10	5.7 6	2.53	117 411 44	173	33. 87	5.08	2. 55	939 798 1	101	24. 71	4.63	2. 1	Phosphotransferase system, mannose/fructose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G

gene_1422 GeneM ark.hmm 537_nt - 20231 20767	53 7	399 220 7	732	34 1.4 5	8.42	117 411 44	852 9	13 52. 74	10.4	1. 98	939 798 1	511 9	10 14. 32	9.99	1. 57	F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein)	METABOLISM	Energy production and conversion	C
gene_1423 GeneM ark.hmm 495_nt - 20767 21261	49 5	399 220 7	644 4	32 60. 9	11.6 7	117 411 44	365 29	62 85. 24	12.6 2	0. 95	939 798 1	176 44	37 92. 78	11.8 9	0. 22	F0F1-type ATP synthase, subunit b	METABOLISM	Energy production and conversion	C
gene_1424 GeneM ark.hmm 717_nt - 21275 21991	71 7	399 220 7	210 5	73 5.3 9	9.52	117 411 44	150 76	17 90. 84	10.8 1	1. 29	939 798 1	938 3	13 92. 48	10.4 4	0. 92	F0F1-type ATP synthase, subunit a	METABOLISM	Energy production and conversion	C
gene_1425 GeneM ark.hmm 201_nt - 22026 22226	20 1	399 220 7	132 3	16 48. 73	10.6 9	117 411 44	266 5	11 29. 25	10.1 4	- 0. 55	939 798 1	126 2	66 8.0 8	9.38	- 1. 31	F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+- ATPase, subunit K	METABOLISM	Energy production and conversion	C
gene_1011 GeneM ark.hmm 642_nt - 102165 102806	64 2	399 220 7	13	5.0 7	2.34	117 411 44	164	21. 76	4.44	2. 1	939 798 1	131	21. 71	4.44	2. 1	Anthranilate/para-aminobenzoate synthases component I	METABOLISM	Amino acid transport and metabolism	E
gene_1427 GeneM ark.hmm 399_nt - 22988 23386	39 9	399 220 7	110	69. 06	6.11	117 411 44	117 2	25 0.1 8	7.97	1. 86	939 798 1	144 4	38 5.0 9	8.59	2. 48	Transposase and inactivated derivatives, IS30 family	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_55 GeneMar k.hmm 543_nt - 35630 36172	54 3	399 220 7	143	65. 97	6.04	117 411 44	202 8	31 8.1	8.31	2. 27	939 798 1	144 9	28 3.9 4	8.15	2. 11	Helicase subunit of the DNA excision repair complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1429 GeneM ark.hmm 483_nt - 24714 25196	48 3	399 220 7	110 0	57 0.4 7	9.16	117 411 44	794 5	14 00. 99	10.4 5	1. 29	939 798 1	586 0	12 90. 97	10.3 3	1. 17	Transcription elongation factor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1743 GeneM ark.hmm 2412_nt + 14689 17100	24 12	399 220 7	30	3.1 2	1.64	117 411 44	727	25. 67	4.68	3. 04	939 798 1	308	13. 59	3.76	2. 12	DNA methylase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1430 GeneM ark.hmm 1656_nt - 25267 26922	16 56	399 220 7	820 9	12 41. 7	10.2 8	117 411 44	401 16	20 63. 23	11.0 1	0. 73	939 798 1	244 56	15 71. 41	10.6 2	0. 34	Predicted periplasmic solute-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1431 GeneM ark.hmm 495_nt - 27003 27497	49 5	399 220 7	237	11 9.9 3	6.91	117 411 44	203 7	35 0.4 9	8.45	1. 54	939 798 1	241 8	51 9.7 8	9.02	2. 11	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1432 GeneM ark.hmm 429_nt - 27579 28007	42 9	399 220 7	510	29 7.7 8	8.22	117 411 44	219 2	43 5.1 8	8.77	0. 55	939 798 1	288 6	71 5.8 2	9.48	1. 26	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1433 GeneM ark.hmm 1380_nt - 28017 29396	13 80	399 220 7	482 1	87 5.0 7	9.77	117 411 44	175 17	10 81. 11	10.0 8	0. 31	939 798 1	151 81	11 70. 54	10.1 9	0. 42	UDP-N-acetylmuramate-alanine ligase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1434 GeneM ark.hmm 153_nt - 29407 29559	15 3	399 220 7	191	31 2.7	8.29	117 411 44	799	44 4.7 8	8.8	0. 51	939 798 1	807	56 1.2 4	9.13	0. 84	---	---	---	---
gene_1435 GeneM ark.hmm 462_nt - 29617 30078	46 2	399 220 7	622	33 7.2 4	8.4	117 411 44	329 0	60 6.5 2	9.24	0. 84	939 798 1	246 7	56 8.1 9	9.15	0. 75	---	---	---	---

gene_1436 GeneM ark.hmm 3105_nt - 30126 33230	31 05	399 220 7	223 2	18 0.0 6	7.49	117 411 44	451 3	12 3.7 9	6.95	- 0. 54	939 798 1	577 2	19 7.8	7.63	0. 14	Superfamily II DNA/RNA helicases, SNF2 family	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1437 GeneM ark.hmm 885_nt - 33323 34207	88 5	399 220 7	82	23. 21	4.54	117 411 44	412	39. 65	5.31	0. 77	939 798 1	557	66. 97	6.07	1. 53	Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities	METABOLISM	Amino acid transport and metabolism	E
gene_1438 GeneM ark.hmm 279_nt - 34278 34556	27 9	399 220 7	22	19. 75	4.3	117 411 44	83	25. 34	4.66	0. 36	939 798 1	117	44. 62	5.48	1. 18	Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities	METABOLISM	Amino acid transport and metabolism	E
gene_1439 GeneM ark.hmm 1095_nt - 34564 35658	10 95	399 220 7	126	28. 82	4.85	117 411 44	583	45. 35	5.5	0. 65	939 798 1	548	53. 25	5.73	0. 88	Cystathionine beta- lyases/cystathionine gamma- synthases	METABOLISM	Amino acid transport and metabolism	E
gene_143 GeneMa rk.hmm 195_nt + 8 48 1042	19 5	399 220 7	14	17. 98	4.17	117 411 44	108	47. 17	5.56	1. 39	939 798 1	387	21 1.1 7	7.72	3. 55	---	---	---	---
gene_1440 GeneM ark.hmm 723_nt - 35886 36608	72 3	399 220 7	28	9.7	3.28	117 411 44	238	28. 04	4.81	1. 53	939 798 1	228	33. 56	5.07	1. 79	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1441 GeneM ark.hmm 624_nt - 36681 37304	62 4	399 220 7	25	10. 04	3.33	117 411 44	281	38. 35	5.26	1. 93	939 798 1	249	42. 46	5.41	2. 08	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1442 GeneM ark.hmm 1959_nt - 37740 39698	19 59	399 220 7	317	40. 53	5.34	117 411 44	180 5	78. 48	6.29	0. 95	939 798 1	122 2	66. 37	6.05	0. 71	ABC-type oligopeptide transport system, periplasmic component	METABOLISM	Amino acid transport and metabolism	E
gene_1443 GeneM ark.hmm 1623_nt - 39901 41523	16 23	399 220 7	317 4	48 9.8 6	8.94	117 411 44	626 9	32 8.9 8	8.36	- 0. 58	939 798 1	493 9	32 3.8 1	8.34	- 0. 6	Membrane protein involved in the export of O-antigen and teichoic acid	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1444 GeneM ark.hmm 1446_nt + 41629 43074	14 46	399 220 7	282 0	48 8.5	8.93	117 411 44	723 3	42 6.0 3	8.73	- 0. 2	939 798 1	376 2	27 6.8 3	8.11	- 0. 82	UDP-N-acetylmuramyl tripeptide synthase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1445 GeneM ark.hmm 195_nt - 43120 43314	19 5	399 220 7	933	11 98. 49	10.2 3	117 411 44	194 6	84 9.9 6	9.73	- 0. 5	939 798 1	144 1	78 6.3 1	9.62	- 0. 61	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1446 GeneM ark.hmm 597_nt - 43415 44011	59 7	399 220 7	768	32 2.2 4	8.33	117 411 44	312 6	44 5.9 7	8.8	0. 47	939 798 1	440 7	78 5.4 8	9.62	1. 29	---	---	---	---
gene_1447 GeneM ark.hmm 513_nt - 44048 44560	51 3	399 220 7	740	36 1.3 3	8.5	117 411 44	228 0	37 8.5 4	8.56	0. 06	939 798 1	337 7	70 0.4 5	9.45	0. 95	---	---	---	---
gene_1448 GeneM ark.hmm 936_nt - 44646 45581	93 6	399 220 7	104 26	27 90. 16	11.4 5	117 411 44	141 74	12 89. 75	10.3 3	- 1. 12	939 798 1	126 96	14 43. 3	10.5	- 0. 95	Inorganic pyrophosphatase/exopolyphosphata se	METABOLISM	Energy production and conversion	C
gene_1449 GeneM ark.hmm 300_nt -	30 0	399 220	595	49 6.8	8.96	117 411	238 5	67 7.1	9.4	0. 44	939 798	333 6	11 83.	10.2 1	1. 25	Predicted endonuclease containing a URI domain	INFORMATION STORAGE AND	Replication, recombination and repair	L

[45652 45951		7				44		1			1		23				PROCESSING		
gene_1606 GeneM ark.hmm 690_nt - 19990 20679	69 0	399 220 7	81	29. 41	4.88	117 411 44	151 8	18 7.3 8	7.55	2. 67	939 798 1	839	12 9.3 8	7.02	2. 14	Predicted metal-dependent membrane protease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1450 GeneM ark.hmm 597_nt - 45941 46537	59 7	399 220 7	277 8	11 65. 59	10.1 9	117 411 44	842 7	12 02. 23	10.2 3	0. 04	939 798 1	130 00	23 17. 04	11.1 8	0. 99	Predicted O-methyltransferase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1451 GeneM ark.hmm 213_nt - 46791 47003	21 3	399 220 7	163 6	19 23. 94	10.9 1	117 411 44	244 2	97 6.4 6	9.93	- 0. 98	939 798 1	418 0	20 88. 15	11.0 3	0. 12	Predicted RNA binding protein (contains ribosomal protein S1 domain)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1452 GeneM ark.hmm 144_nt - 47078 47221	14 4	399 220 7	41	71. 32	6.16	117 411 44	199	11 7.7	6.88	0. 72	939 798 1	367	27 1.1 9	8.08	1. 92	Predicted RNA binding protein (contains ribosomal protein S1 domain)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1453 GeneM ark.hmm 1401_nt - 47223 48623	14 01	399 220 7	195 7	34 9.9	8.45	117 411 44	792 3	48 1.6 6	8.91	0. 46	939 798 1	953 3	72 4.0 3	9.5	1. 05	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1454 GeneM ark.hmm 240_nt - 48918 49157	24 0	399 220 7	783	81 7.2 2	9.67	117 411 44	439 3	15 58. 98	10.6 1	0. 94	939 798 1	363 9	16 13. 38	10.6 6	0. 99	Ribosomal protein S18	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1455 GeneM ark.hmm 471_nt - 49189 49659	47 1	399 220 7	165 95	88 25. 58	13.1 1	117 411 44	355 23	64 23. 6	12.6 5	- 0. 46	939 798 1	210 15	47 47. 6	12.2 1	- 0. 9	Single-stranded DNA-binding protein	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1456 GeneM ark.hmm 291_nt - 49671 49961	29 1	399 220 7	185 9	16 00. 2	10.6 4	117 411 44	605 8	17 73. 07	10.7 9	0. 15	939 798 1	435 8	15 93. 53	10.6 4	0	Ribosomal protein S6	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1457 GeneM ark.hmm 1344_nt - 50114 51457	13 44	399 220 7	416 4	77 6.0 7	9.6	117 411 44	130 15	82 4.7 7	9.69	0. 09	939 798 1	158 78	12 57. 08	10.3	0. 7	Aspartyl/asparaginyl-tRNA synthetases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1458 GeneM ark.hmm 366_nt - 51476 51841	36 6	399 220 7	248	16 9.7 3	7.41	117 411 44	186 8	43 4.7	8.76	1. 35	939 798 1	203 5	59 1.6 3	9.21	1. 8	Lactoylglutathione lyase and related lyases	METABOLISM	Amino acid transport and metabolism	E
gene_1459 GeneM ark.hmm 654_nt - 51834 52487	65 4	399 220 7	714	27 3.4 7	8.1	117 411 44	276 7	36 0.3 5	8.49	0. 39	939 798 1	366 9	59 6.9 5	9.22	1. 12	Aspartate/tyrosine/aromatic aminotransferase	METABOLISM	Amino acid transport and metabolism	E
gene_681 GeneMa rk.hmm 141_nt + 7 4249 74389	14 1	399 220 7	20	35. 53	5.15	117 411 44	264	15 9.4 7	7.32	2. 17	939 798 1	207	15 6.2 1	7.29	2. 14	---	---	---	---
gene_1460 GeneM ark.hmm 567_nt - 52498 53064	56 7	399 220 7	242	10 6.9 1	6.74	117 411 44	104 6	15 7.1 2	7.3	0. 56	939 798 1	113 4	21 2.8 1	7.73	0. 99	Aspartate/tyrosine/aromatic aminotransferase	METABOLISM	Amino acid transport and metabolism	E
gene_1461 GeneM ark.hmm 432_nt - 53061 53492	43 2	399 220 7	415	24 0.6 3	7.91	117 411 44	251 5	49 5.8 4	8.95	1. 04	939 798 1	203 5	50 1.2 4	8.97	1. 06	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1462 GeneM ark.hmm 591_nt + 53870 54460	59 1	399 220 7	810 7	34 36. 05	11.7 5	117 411 44	913 8	13 16. 9	10.3 6	- 1. 39	939 798 1	311 1	56 0.1 2	9.13	- 2. 62	Predicted flavoprotein	POORLY CHARACTERIZ ED	General function prediction only	R

gene_1463 GeneM ark.hmm 699_nt 54898 55596	69 9	399 220 7	111 9	40 1	8.65	117 411 44	322 3	39 2.7 1	8.62	- 0.03	939 798 1	269 1	40 9.6 4	8.68	0.03	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1464 GeneM ark.hmm 165_nt 55705 55869	16 5	399 220 7	132	20 0.3 9	7.65	117 411 44	104 9	54 1.4 8	9.08	1.43	939 798 1	189 2	12 20.12	10.2 5	2.6	NA			
gene_1465 GeneM ark.hmm 1596_nt 56036 57631	15 96	399 220 7	161 2	25 3	7.98	117 411 44	573 9	30 6.2 6	8.26	0.28	939 798 1	514 2	34 2.8 2	8.42	0.44	---	---	---	---
gene_1466 GeneM ark.hmm 411_nt 57643 58053	41 1	399 220 7	228	13 8.9 6	7.12	117 411 44	767	15 8.9 4	7.31	0.19	939 798 1	824	21 3.3 3	7.74	0.62	N-formylmethionyl-tRNA deformylase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1467 GeneM ark.hmm 792_nt 58169 58960	79 2	399 220 7	646	20 4.3 1	7.67	117 411 44	276 9	29 7.7 7	8.22	0.55	939 798 1	297 2	39 9.2 9	8.64	0.97	Glutathione S-transferase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1468 GeneM ark.hmm 1449_nt 58973 60421	14 49	399 220 7	144 5	24 9.8	7.96	117 411 44	468 5	27 5.3 8	8.11	0.15	939 798 1	557 4	40 9.3 2	8.68	0.72	Cation transport ATPase	METABOLISM	Inorganic ion transport and metabolism	P
gene_1469 GeneM ark.hmm 1209_nt 60285 61493	12 09	399 220 7	124 3	25 7.5 3	8.01	117 411 44	501 8	35 3.5	8.47	0.46	939 798 1	542 1	47 7.1 1	8.9	0.89	Cation transport ATPase	METABOLISM	Inorganic ion transport and metabolism	P
gene_522 GeneMa rk.hmm 405_nt 29972 30376	40 5	399 220 7	5	3.0 9	1.63	117 411 44	124	26. 08	4.7	3.07	939 798 1	52	13. 66	3.77	2.14	Type II secretory pathway, pseudopilin PulG	CELLULAR PROCESSES AND SIGNALING	Cell motility	N
gene_1470 GeneM ark.hmm 195_nt 61553 61747	19 5	399 220 7	59	75. 79	6.24	117 411 44	625	27 2.9 8	8.09	1.85	939 798 1	492	26 8.4 7	8.07	1.83	Cation transport ATPase	METABOLISM	Inorganic ion transport and metabolism	P
gene_1471 GeneM ark.hmm 1185_nt + 62051 63235	11 85	399 220 7	897	18 9.6 1	7.57	117 411 44	480 6	34 5.4 3	8.43	0.86	939 798 1	342 2	30 7.2 7	8.26	0.69	Predicted Co/Zn/Cd cation transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_1472 GeneM ark.hmm 1872_nt 63378 65249	18 72	399 220 7	439 4	58 7.9 5	9.2	117 411 44	188 59	85 8.0 3	9.74	0.54	939 798 1	257 60	14 64. 22	10.5 2	1.32	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1473 GeneM ark.hmm 969_nt 65246 66214	96 9	399 220 7	125 5	32 4.4 2	8.34	117 411 44	440 5	38 7.1 8	8.6	0.26	939 798 1	614 7	67 5	9.4	1.06	tRNA nucleotidyltransferase/poly(A) polymerase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1474 GeneM ark.hmm 207_nt 66272 66478	20 7	399 220 7	39	47. 19	5.56	117 411 44	294	12 0.9 7	6.92	1.36	939 798 1	408	20 9.7 3	7.71	2.15	tRNA nucleotidyltransferase/poly(A) polymerase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1475 GeneM ark.hmm 768_nt 66490 67257	76 8	399 220 7	198 3	64 6.7 7	9.34	117 411 44	712 1	78 9.7 1	9.63	0.29	939 798 1	704 6	97 6.2 2	9.93	0.59	Dihydrodipicolinate reductase	METABOLISM	Amino acid transport and metabolism	E
gene_1476 GeneM ark.hmm 849_nt 67534 68382	84 9	399 220 7	794 5	23 44. 08	11.1 9	117 411 44	156 67	15 71. 69	10.6 2	- 0.57	939 798 1	124 36	15 58. 61	10.6 1	- 0.58	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S

gene_1477 GeneM ark.hmm 375_nt - 68384 68758	37 5	399 220 7	242	16 1.6 5	7.34	117 411 44	132 3	30 0.4 8	8.23	0. 89	939 798 1	931	26 4.1 7	8.05	0. 71	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1478 GeneM ark.hmm 1353_nt - 68832 70184	13 53	399 220 7	406 6	75 2.7 6	9.56	117 411 44	850 0	53 5.0 7	9.06	- 0. 5	939 798 1	864 0	67 9.4 9	9.41	- 0. 15	Phosphomannomutase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1479 GeneM ark.hmm 780_nt - 70208 70987	78 0	399 220 7	115 8	37 1.8 8	8.54	117 411 44	213 0	23 2.5 8	7.86	- 0. 68	939 798 1	203 5	27 7.6 1	8.12	- 0. 42	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_507 GeneMa rk.hmm 666_nt - 19772 20437	66 6	399 220 7	16	6.0 2	2.59	117 411 44	407	52. 05	5.7	3. 11	939 798 1	166	26. 52	4.73	2. 14	3-hexulose-6-phosphate synthase and related proteins	METABOLISM	Carbohydrate transport and metabolism	G
gene_1480 GeneM ark.hmm 858_nt - 70974 71831	85 8	399 220 7	110 4	32 2.3 1	8.33	117 411 44	207 7	20 6.1 8	7.69	- 0. 64	939 798 1	177 3	21 9.8 8	7.78	- 0. 55	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1481 GeneM ark.hmm 420_nt + 71967 72386	42 0	399 220 7	394	23 4.9 8	7.88	117 411 44	411	83. 35	6.38	- 1. 5	939 798 1	209	52. 95	5.73	- 2. 15	Thioredoxin reductase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1482 GeneM ark.hmm 546_nt + 72447 72992	54 6	399 220 7	649	29 7.7 4	8.22	117 411 44	892	13 9.1 4	7.12	- 1. 1	939 798 1	757	14 7.5 3	7.2	- 1. 02	Thioredoxin reductase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1483 GeneM ark.hmm 912_nt - 73026 73937	91 2	399 220 7	449 0	12 33. 21	10.2 7	117 411 44	839 3	78 3.8 1	9.61	- 0. 66	939 798 1	972 5	11 34. 65	10.1 5	- 0. 12	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1484 GeneM ark.hmm 786_nt - 73934 74719	78 6	399 220 7	236 4	75 3.3 8	9.56	117 411 44	343 5	37 2.2 1	8.54	- 1. 02	939 798 1	378 3	51 2.1 3	9	- 0. 56	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1485 GeneM ark.hmm 891_nt - 74943 75833	89 1	399 220 7	150 1	42 1.9 8	8.72	117 411 44	297 8	28 4.6 7	8.15	- 0. 57	939 798 1	374 0	44 6.6 4	8.8	0. 08	Predicted P-loop-containing kinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1486 GeneM ark.hmm 381_nt - 75885 76265	38 1	399 220 7	145 1	95 3.9 6	9.9	117 411 44	228 7	51 1.2 5	9	- 0. 9	939 798 1	210 5	58 7.8 9	9.2	- 0. 7	Putative translation initiation inhibitor, yjgF family	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1487 GeneM ark.hmm 588_nt - 76276 76863	58 8	399 220 7	252 1	10 73. 95	10.0 7	117 411 44	467 9	67 7.7 4	9.4	- 0. 67	939 798 1	486 7	88 0.7 4	9.78	- 0. 29	Predicted GTPase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1488 GeneM ark.hmm 1023_nt - 76872 77894	10 23	399 220 7	262 9	64 3.7 3	9.33	117 411 44	400 9	33 3.7 7	8.38	- 0. 95	939 798 1	383 3	39 8.6 8	8.64	- 0. 69	ATP-dependent protease Clp, ATPase subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1489 GeneM ark.hmm 252_nt - 77891 78142	25 2	399 220 7	102	10 1.3 9	6.66	117 411 44	320	10 8.1 5	6.76	0. 1	939 798 1	267	11 2.7 4	6.82	0. 16	ATP-dependent protease Clp, ATPase subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_148 GeneMa rk.hmm 600_nt + 3	60	399 220	155	64.	6.02	117 411	977	13 8.6	7.12	1.	939 798	201	35 7.5	8.48	2.	Response regulator containing a CheY-like receiver domain and an	CELLULAR PROCESSES	Signal transduction mechanisms	T

786 4385	0	7		71		44		9		1	1	6	2		46	HTH DNA-binding domain	AND SIGNALING		
gene_1490 GeneM ark.hmm 171_nt - 78174 78344	17 1	399 220 7	59	86. 43	6.43	117 411 44	149	74. 21	6.21	- 0. 22	939 798 1	127	79. 03	6.3	- 0. 13	---	---	---	---
gene_1491 GeneM ark.hmm 507_nt - 78344 78850	50 7	399 220 7	145 4	71 8.3 6	9.49	117 411 44	296 9	49 8.7 6	8.96	- 0. 53	939 798 1	284 7	59 7.5 1	9.22	- 0. 27	Dihydrofolate reductase	METABOLISM	Coenzyme transport and metabolism	H
gene_1492 GeneM ark.hmm 519_nt - 78980 79498	51 9	399 220 7	313 64	15 13 7.3 9	13.8 9	117 411 44	830 98	13 63 6.8 1	13.7 4	- 0. 15	939 798 1	342 56	70 23. 2	12.7 8	- 1. 11	DNA-binding ferritin-like protein (oxidative damage protectant)	METABOLISM	Inorganic ion transport and metabolism	P
gene_1493 GeneM ark.hmm 813_nt - 79994 80806	81 3	399 220 7	471 7	14 53. 32	10.5 1	117 411 44	226 30	23 70. 74	11.2 1	0. 7	939 798 1	264 10	34 56. 55	11.7 6	1. 25	NA			
gene_1494 GeneM ark.hmm 363_nt - 80921 81283	36 3	399 220 7	114 8	79 2.1 8	9.63	117 411 44	535 6	12 56. 68	10.3	0. 67	939 798 1	496 3	14 54. 8	10.5 1	0. 88	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZED	General function prediction only	R
gene_1495 GeneM ark.hmm 789_nt - 81354 82142	78 9	399 220 7	113 22	35 94. 46	11.8 1	117 411 44	345 18	37 26. 13	11.8 6	0. 05	939 798 1	213 27	28 76. 19	11.4 9	- 0. 32	Triosephosphate isomerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1496 GeneM ark.hmm 678_nt - 82239 82916	67 8	399 220 7	598	22 0.9 3	7.79	117 411 44	260 7	32 7.4 9	8.36	0. 57	939 798 1	353 6	55 4.9 4	9.12	1. 33	Putative primosome component and related proteins	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1497 GeneM ark.hmm 945_nt - 82925 83869	94 5	399 220 7	216 2	57 3.0 7	9.16	117 411 44	701 8	63 2.5 2	9.3	0. 14	939 798 1	714 5	80 4.5 2	9.65	0. 49	Homoserine trans-succinylase	METABOLISM	Amino acid transport and metabolism	E
gene_1498 GeneM ark.hmm 513_nt - 84051 84563	51 3	399 220 7	182 2	88 9.6 5	9.8	117 411 44	492 9	81 8.3 3	9.68	- 0. 12	939 798 1	266 0	55 1.7 3	9.11	- 0. 69	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	METABOLISM	Nucleotide transport and metabolism	F
gene_1499 GeneM ark.hmm 759_nt - 84650 85408	75 9	399 220 7	204	67. 32	6.07	117 411 44	937	10 5.1 4	6.72	0. 65	939 798 1	161 1	22 5.8 5	7.82	1. 75	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_149 GeneMa rk.hmm 1011_nt + 4810 5820	10 11	399 220 7	261 1	64 6.9 1	9.34	117 411 44	142 67	12 01. 91	10.2 3	0. 89	939 798 1	835 2	87 9.0 3	9.78	0. 44	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_14 GeneMar k.hmm 213_nt - 8429 8641	21 3	399 220 7	160	18 8.1 6	7.56	117 411 44	223	89. 17	6.48	- 1. 08	939 798 1	221	11 0.4	6.79	- 0. 77	Exonuclease VII small subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1500 GeneM ark.hmm 1131_nt - 85909 87039	11 31	399 220 7	132 61	29 36. 98	11.5 2	117 411 44	866 6	65 2.6	9.35	- 2. 17	939 798 1	963 3	90 6.2 8	9.82	- 1. 7	ABC-type sugar transport systems, ATPase components	METABOLISM	Carbohydrate transport and metabolism	G
gene_1501 GeneM ark.hmm 576_nt - 87490 88065	57 6	399 220 7	768	33 3.9 8	8.38	117 411 44	154 2	22 8.0 1	7.83	- 0. 55	939 798 1	135 8	25 0.8 7	7.97	- 0. 41	Amidases related to nicotinamidase	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_1502 GeneM ark.hmm 789_nt -	78	399 220	541	17 1.7	7.42	117 411	131	14 1.7	7.15	- 0.	939 798	140	18 9.4	7.57	0.	Pleiotropic transcriptional repressor	INFORMATION STORAGE AND	Transcription	K

[88065 88853	9	7		5		44	3	4		27	1	5	8		15		PROCESSING		
gene_1503 GeneM ark.hmm 1575_nt - 89117 90691	15 75	399 220 7	383 2	60 9.4 4	9.25	117 411 44	256 30	13 85. 98	10.4 4	1. 19	939 798 1	417 36	28 19. 65	11.4 6	2. 21	Superfamily II DNA and RNA helicases	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1504 GeneM ark.hmm 1227_nt - 90890 92116	12 27	399 220 7	328	66. 96	6.07	117 411 44	111 5	77. 4	6.27	0. 2	939 798 1	841	72. 93	6.19	0. 12	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_1505 GeneM ark.hmm 1317_nt + 92310 93626	13 17	399 220 7	147 90	28 13	11.4 6	117 411 44	268 63	17 37. 23	10.7 6	- 0. 7	939 798 1	123 30	99 6.1 9	9.96	- 1. 5	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1506 GeneM ark.hmm 1377_nt + 93725 95101	13 77	399 220 7	424 3	77 1.8 4	9.59	117 411 44	851 2	52 6.4 9	9.04	- 0. 55	939 798 1	692 8	53 5.3 5	9.06	- 0. 53	UDP-N-acetylmuramyl tripeptide synthase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1507 GeneM ark.hmm 666_nt + 95101 95766	66 6	399 220 7	208 7	78 4.9 4	9.62	117 411 44	332 7	42 5.4 7	8.73	- 0. 89	939 798 1	286 5	45 7.7 4	8.84	- 0. 78	Predicted glutamine amidotransferase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1508 GeneM ark.hmm 108_nt + 95829 95936	10 8	399 220 7	2	4.6 4	2.21	117 411 44	6	4.7 3	2.24	0. 03	939 798 1	4	3.9 4	1.98	0. 23	Predicted glutamine amidotransferase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1509 GeneM ark.hmm 1083_nt + 96062 97144	10 83	399 220 7	365 6	84 5.6	9.72	117 411 44	866 7	68 1.6	9.41	- 0. 31	939 798 1	493 0	48 4.3 8	8.92	- 0. 8	Xaa-Pro aminopeptidase	METABOLISM	Amino acid transport and metabolism	E
gene_150 GeneMa rk.hmm 147_nt + 5 884 6030	14 7	399 220 7	45	76. 68	6.26	117 411 44	121	70. 11	6.13	- 0. 13	939 798 1	95	68. 77	6.1	- 0. 16	NA			
gene_1510 GeneM ark.hmm 312_nt - 97467 97778	31 2	399 220 7	24	19. 27	4.27	117 411 44	159	43. 4	5.44	1. 17	939 798 1	94	32. 06	5	0. 73	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1511 GeneM ark.hmm 138_nt + 3 140	13 8	399 220 7	17	30. 86	4.95	117 411 44	130	80. 23	6.33	1. 38	939 798 1	130	10 0.2 4	6.65	1. 7	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1512 GeneM ark.hmm 1692_nt - 530 2221	16 92	399 220 7	269 7	39 9.2 7	8.64	117 411 44	973 9	49 0.2 3	8.94	0. 3	939 798 1	753 7	47 3.9 8	8.89	0. 25	Arginyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1513 GeneM ark.hmm 447_nt + 2357 2803	44 7	399 220 7	196	10 9.8 3	6.78	117 411 44	182 4	34 7.5 4	8.44	1. 66	939 798 1	656	15 6.1 6	7.29	0. 51	Arginine repressor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1514 GeneM ark.hmm 2535_nt + 2854 5388	25 35	399 220 7	114 8	11 3.4 4	6.83	117 411 44	614 4	20 6.4 3	7.69	0. 86	939 798 1	708 0	29 7.1 8	8.22	1. 39	Mismatch repair ATPase (MutS family)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1515 GeneM ark.hmm 1695_nt + 5535 7229	16 95	399 220 7	104 6	15 4.5 8	7.27	117 411 44	484 4	24 3.4	7.93	0. 66	939 798 1	453 4	28 4.6 3	8.15	0. 88	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V

gene_1516 GeneM ark.hmm 1767_nt + 8144 9910	17 67	399 220 7	323 9	45 9.1 6	8.84	117 411 44	140 08	67 5.1 9	9.4	0. 56	939 798 1	106 72	64 2.6 5	9.33	0. 49	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1517 GeneM ark.hmm 690_nt + 10049 10738	69 0	399 220 7	278	10 0.9 2	6.66	117 411 44	167 5	20 6.7 5	7.69	1. 03	939 798 1	139 1	21 4.5 1	7.74	1. 08	Predicted glutamine amidotransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1518 GeneM ark.hmm 1350_nt + 10908 12257	13 50	399 220 7	852 3	15 81. 41	10.6 3	117 411 44	277 46	17 50. 48	10.7 7	0. 14	939 798 1	124 65	98 2.4 8	9.94	- 0. 69	Glucose-6-phosphate isomerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1519 GeneM ark.hmm 1461_nt + 12381 13841	14 61	399 220 7	472 4	80 9.9 3	9.66	117 411 44	159 85	93 1.8 6	9.86	0. 2	939 798 1	108 30	78 8.7 6	9.62	- 0. 04	Glutamyl- and glutaminyl-tRNA synthetases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_151 GeneMa rk.hmm 963_nt - 6027 6989	96 3	399 220 7	103 1	26 8.1 8	8.07	117 411 44	229 4	20 2.8 9	7.66	- 0. 41	939 798 1	147 2	16 2.6 5	7.35	- 0. 72	L-asparaginase/archaeal Glu- tRNA ^{Gln} amidotransferase subunit D	METABOLISM	Amino acid transport and metabolism	E
gene_1520 GeneM ark.hmm 435_nt + 13855 14289	43 5	399 220 7	135 4	77 9.6 8	9.61	117 411 44	551 0	10 78. 83	10.0 8	0. 47	939 798 1	359 8	88 0.1 1	9.78	0. 17	Cytidine deaminase	METABOLISM	Nucleotide transport and metabolism	F
gene_1521 GeneM ark.hmm 96_nt + 4 91 586	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1522 GeneM ark.hmm 144_nt - 3 146	14 4	399 220 7	9	15. 66	3.97	117 411 44	65	38. 45	5.26	1. 29	939 798 1	253	18 6.9 5	7.55	3. 58	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1604 GeneM ark.hmm 612_nt - 19059 19670	61 2	399 220 7	54	22. 1	4.47	117 411 44	108 4	15 0.8 6	7.24	2. 77	939 798 1	565	98. 23	6.62	2. 15	Predicted metal-dependent membrane protease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1524 GeneM ark.hmm 1329_nt + 887 2215	13 29	399 220 7	159 5	30 0.6 2	8.23	117 411 44	870 9	55 8.1 3	9.12	0. 89	939 798 1	654 4	52 3.9 4	9.03	0. 8	Adenylosuccinate synthase	METABOLISM	Nucleotide transport and metabolism	F
gene_1525 GeneM ark.hmm 468_nt + 2416 2883	46 8	399 220 7	56	29. 97	4.91	117 411 44	604	10 9.9 2	6.78	1. 87	939 798 1	576	13 0.9 6	7.03	2. 12	Cytosine/adenosine deaminases	METABOLISM	Nucleotide transport and metabolism	F
gene_1526 GeneM ark.hmm 444_nt + 3070 3513	44 4	399 220 7	96	54. 16	5.76	117 411 44	480	92. 08	6.52	0. 76	939 798 1	105 2	25 2.1 1	7.98	2. 22	dUTPase	METABOLISM	Nucleotide transport and metabolism	F
gene_1527 GeneM ark.hmm 516_nt + 3515 4030	51 6	399 220 7	89	43. 2	5.43	117 411 44	397	65. 53	6.03	0. 6	939 798 1	643	13 2.5 9	7.05	1. 62	Fructose-2,6-bisphosphatase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1528 GeneM ark.hmm 1263_nt + 4143 5405	12 63	399 220 7	293	58. 11	5.86	117 411 44	140 6	94. 81	6.57	0. 71	939 798 1	284 8	23 9.9 4	7.91	2. 05	Predicted ATP-dependent serine protease	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1529 GeneM ark.hmm 477_nt + 5499 5975	47 7	399 220 7	288	15 1.2 4	7.24	117 411 44	745	13 3.0 2	7.06	- 0. 18	939 798 1	958	21 3.7	7.74	0. 5	Carbonic anhydrase	METABOLISM	Inorganic ion transport and metabolism	P

gene_152 GeneMa rk.hmm 1389_nt[+] 7055 8443	13 89	399 220 7	111 1	20 0.3 5	7.65	117 411 44	340 0	20 8.4 8	7.7	0. 05	939 798 1	240 3	18 4.0 8	7.52	- 0. 13	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1530 GeneM ark.hmm 285_nt[+] 6000 6284	28 5	399 220 7	23	20. 21	4.34	117 411 44	242	72. 32	6.18	1. 84	939 798 1	282	10 5.2 9	6.72	2. 38	---	---	---	---
gene_1531 GeneM ark.hmm 477_nt[+] 6354 6830	47 7	399 220 7	290	15 2.2 9	7.25	117 411 44	785	14 0.1 7	7.13	- 0. 12	939 798 1	913	20 3.6 7	7.67	0. 42	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1532 GeneM ark.hmm 969_nt[+] 6975 7943	96 9	399 220 7	136 4	35 2.6	8.46	117 411 44	378 4	33 2.6	8.38	- 0. 08	939 798 1	180 1	19 7.7 7	7.63	- 0. 83	Phosphoribosylpyrophosphate synthetase	METABOLISM	Nucleotide transport and metabolism	F
gene_1533 GeneM ark.hmm 252_nt[-] 8402 8653	25 2	399 220 7	127	12 6.2 4	6.98	117 411 44	435	14 7.0 2	7.2	0. 22	939 798 1	399	16 8.4 8	7.4	0. 42	---	---	---	---
gene_1534 GeneM ark.hmm 117_nt[-] 8646 8762	11 7	399 220 7	16	34. 25	5.1	117 411 44	25	18. 2	4.19	- 0. 91	939 798 1	26	23. 65	4.56	- 0. 54	NA			
gene_1535 GeneM ark.hmm 192_nt[-] 8977 9168	19 2	399 220 7	67	87. 41	6.45	117 411 44	211	93. 6	6.55	0. 1	939 798 1	266	14 7.4 2	7.2	0. 75	---	---	---	---
gene_1536 GeneM ark.hmm 177_nt[+] 9181 9357	17 7	399 220 7	28	39. 63	5.31	117 411 44	91	43. 79	5.45	0. 14	939 798 1	98	58. 91	5.88	0. 57	NA			
gene_1537 GeneM ark.hmm 2613_nt[-] + 9604 12216	26 13	399 220 7	364 2	34 9.1 3	8.45	117 411 44	117 79	38 3.9 4	8.58	0. 13	939 798 1	114 13	46 4.7 6	8.86	0. 41	DNA polymerase I - 3'-5' exonuclease and polymerase domains	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1538 GeneM ark.hmm 438_nt[+] 12301 12738	43 8	399 220 7	844	48 2.6 8	8.91	117 411 44	184 6	35 8.9 6	8.49	- 0. 42	939 798 1	216 5	52 5.9 6	9.04	0. 13	Predicted CoA-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1539 GeneM ark.hmm 171_nt[+] 12779 12949	17 1	399 220 7	534	78 2.2 3	9.61	117 411 44	469 4	23 37. 96	11.1 9	1. 58	939 798 1	338 8	21 08. 2	11.0 4	1. 43	NA			
gene_153 GeneMa rk.hmm 453_nt[-] 8478 8930	45 3	399 220 7	581	32 1.2 7	8.33	117 411 44	177 9	33 4.4 8	8.39	0. 06	939 798 1	412	96. 78	6.6	- 1. 73	Universal stress protein UspA and related nucleotide-binding proteins	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1540 GeneM ark.hmm 1011_nt[-] 13140 14150	10 11	399 220 7	263 9	65 3.8 5	9.35	117 411 44	213 77	18 00. 88	10.8 1	1. 46	939 798 1	131 56	13 84. 64	10.4 4	1. 09	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1541 GeneM ark.hmm 1170_nt[-] + 14299 15468	11 70	399 220 7	116 6	24 9.6 3	7.96	117 411 44	229 8	16 7.2 8	7.39	- 0. 57	939 798 1	320 8	29 1.7 5	8.19	0. 23	Aspartate/tyrosine/aromatic aminotransferase	METABOLISM	Amino acid transport and metabolism	E
gene_1542 GeneM ark.hmm 771_nt[+] 15465 16235	77 1	399 220 7	417	13 5.4 8	7.08	117 411 44	849	93. 79	6.55	- 0. 53	939 798 1	111 9	15 4.4 3	7.27	0. 19	Recombinational DNA repair protein (RecF pathway)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_1543 GeneM ark.hmm 993_nt + 16232 17224	99 3	399 220 7	111 1	28 0.2 5	8.13	117 411 44	148 2	12 7.1 1	6.99	- 1. 14	939 798 1	257 3	27 5.7 1	8.11	- 0. 02	Fatty acid/phospholipid biosynthesis enzyme	METABOLISM	Lipid transport and metabolism	I
gene_1544 GeneM ark.hmm 234_nt + 17230 17463	23 4	399 220 7	40	42. 82	5.42	117 411 44	247	89. 9	6.49	1. 07	939 798 1	206	93. 67	6.55	1. 13	Acyl carrier protein	METABOLISM	Lipid transport and metabolism	I
gene_1545 GeneM ark.hmm 63_nt + 1 7506 17568	63	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2274 GeneM ark.hmm 1245_nt - 99054 100298	12 45	399 220 7	46	9.2 5	3.21	117 411 44	839 3	57 4.1 7	9.17	5. 96	939 798 1	479	40. 94	5.36	2. 15	Predicted membrane protein involved in D-alanine export	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1576 GeneM ark.hmm 450_nt + 56344 56793	45 0	399 220 7	85	47. 31	5.56	117 411 44	102 1	19 3.2 4	7.59	2. 03	939 798 1	894	21 1.3 9	7.72	2. 16	Glycosyltransferases involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1687 GeneM ark.hmm 357_nt + 14556 14912	35 7	399 220 7	15	10. 52	3.4	117 411 44	178	42. 47	5.41	2. 01	939 798 1	161	47. 99	5.58	2. 18	---	---	---	---
gene_392 GeneMa rk.hmm 375_nt + 7 876 8250	37 5	399 220 7	20	13. 36	3.74	117 411 44	182 2	41 3.8 2	8.69	4. 95	939 798 1	217	61. 57	5.94	2. 2	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_154 GeneMa rk.hmm 294_nt + 9 092 9385	29 4	399 220 7	69	58. 79	5.88	117 411 44	495	14 3.4	7.16	1. 28	939 798 1	216	78. 18	6.29	0. 41	---	---	---	---
gene_202 GeneMa rk.hmm 207_nt + 6 0185 60391	20 7	399 220 7	8	9.6 8	3.28	117 411 44	116	47. 73	5.58	2. 3	939 798 1	87	44. 72	5.48	2. 2	NA			
gene_830 GeneMa rk.hmm 594_nt - 14890 15483	59 4	399 220 7	546	23 0.2 5	7.85	117 411 44	663 9	95 1.9 3	9.89	2. 04	939 798 1	590 9	10 58. 51	10.0 5	2. 2	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_293 GeneMa rk.hmm 693_nt - 65706 66398	69 3	399 220 7	13	4.7	2.23	117 411 44	254	31. 22	4.96	2. 73	939 798 1	141	21. 65	4.44	2. 21	Capsular polysaccharide biosynthesis protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_129 GeneMa rk.hmm 141_nt - 93724 93864	14 1	399 220 7	2	3.5 5	1.83	117 411 44	33	19. 93	4.32	2. 49	939 798 1	22	16. 6	4.05	2. 22	Integral membrane protein possibly involved in chromosome condensation	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1554 GeneM ark.hmm 1548_nt + 31193 32740	15 48	399 220 7	83	13. 43	3.75	117 411 44	535	29. 44	4.88	1. 13	939 798 1	289	19. 87	4.31	0. 56	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in AfuI)	METABOLISM	Nucleotide transport and metabolism	F
gene_1555 GeneM ark.hmm 1263_nt + 32862 34124	12 63	399 220 7	46	9.1 2	3.19	117 411 44	528	35. 61	5.15	1. 96	939 798 1	255	21. 48	4.43	1. 24	Phosphoribosylamine-glycine ligase	METABOLISM	Nucleotide transport and metabolism	F
gene_1556 GeneM ark.hmm 489_nt +	48	399 220	23	11.	3.56	117 411	354	61.	5.95	2.	939 798	174	37.	5.24	1.	Phosphoribosylcarboxyaminoimidaz	METABOLISM	Nucleotide transport and	F

34527 35015	9	7		78		44		66		39	1		86		68	ole (NCAIR) mutase		metabolism	
gene_1557 GeneM ark.hmm 1092_nt + 35002 36093	10 92	399 220 7	106	24. 31	4.6	117 411 44	746	58. 18	5.86	1. 26	939 798 1	449	43. 75	5.45	0. 85	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)	METABOLISM	Nucleotide transport and metabolism	F
gene_1558 GeneM ark.hmm 228_nt + 36103 36330	22 8	399 220 7	269	29 5.5 3	8.21	117 411 44	213 3	79 6.7 9	9.64	1. 43	939 798 1	141 4	65 9.9	9.37	1. 16	---	---	---	---
gene_1559 GeneM ark.hmm 1299_nt + 36393 37691	12 99	399 220 7	122 2	23 5.6 4	7.88	117 411 44	602 8	39 5.2 3	8.63	0. 75	939 798 1	587 2	48 1	8.91	1. 03	Adenylosuccinate lyase	METABOLISM	Nucleotide transport and metabolism	F
gene_155 GeneMa rk.hmm 1215_nt + 9541 10755	12 15	399 220 7	757 4	15 61. 48	10.6 1	117 411 44	876 6	61 4.4 9	9.26	- 1. 35	939 798 1	924 3	80 9.4 7	9.66	- 0. 95	Aspartate/tyrosine/aromatic aminotransferase	METABOLISM	Amino acid transport and metabolism	E
gene_1560 GeneM ark.hmm 3939_nt - 37746 41684	39 39	399 220 7	491	31. 22	4.96	117 411 44	343 0	74. 16	6.21	1. 25	939 798 1	186 1	50. 27	5.65	0. 69	N-acetyl-beta-hexosaminidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1561 GeneM ark.hmm 717_nt - 41999 42715	71 7	399 220 7	172 08	60 11. 71	12.5 5	117 411 44	882 76	10 48 6.0 8	13.3 6	0. 81	939 798 1	512 31	76 02. 9	12.8 9	0. 34	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1562 GeneM ark.hmm 1788_nt + 43063 44850	17 88	399 220 7	179	25. 08	4.65	117 411 44	159 1	75. 79	6.24	1. 59	939 798 1	272 3	16 2.0 5	7.34	2. 69	Beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_316 GeneMa rk.hmm 2022_nt - 15345 17366	20 22	399 220 7	43	5.3 3	2.41	117 411 44	845	35. 59	5.15	2. 74	939 798 1	470	24. 73	4.63	2. 22	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1564 GeneM ark.hmm 906_nt + 45351 46256	90 6	399 220 7	81	22. 39	4.49	117 411 44	472	44. 37	5.47	0. 98	939 798 1	464	54. 49	5.77	1. 28	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_1565 GeneM ark.hmm 816_nt + 46243 47058	81 6	399 220 7	51	15. 66	3.97	117 411 44	511	53. 34	5.74	1. 77	939 798 1	357	46. 55	5.54	1. 57	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IID	METABOLISM	Carbohydrate transport and metabolism	G
gene_1566 GeneM ark.hmm 405_nt + 47065 47469	40 5	399 220 7	51	31. 54	4.98	117 411 44	312	65. 61	6.04	1. 06	939 798 1	259	68. 05	6.09	1. 11	Phosphotransferase system, mannose/fructose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G
gene_1567 GeneM ark.hmm 1167_nt + 47722 48888	11 67	399 220 7	142	30. 48	4.93	117 411 44	834	60. 87	5.93	1	939 798 1	440	40. 12	5.33	0. 4	Predicted phosphosugar isomerases	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1568 GeneM ark.hmm 1038_nt + 49004 50041	10 38	399 220 7	201	48. 5	5.6	117 411 44	844	69. 25	6.11	0. 51	939 798 1	444	45. 51	5.51	- 0. 09	Galactose mutarotase and related enzymes	METABOLISM	Carbohydrate transport and metabolism	G
gene_1569 GeneM ark.hmm 855_nt + 50248 51102	85 5	399 220 7	373	10 9.2 8	6.77	117 411 44	105 0	10 4.6	6.71	- 0. 06	939 798 1	310	38. 58	5.27	- 1. 5	Predicted ring-cleavage extradiol dioxygenase	POORLY CHARACTERIZ ED	General function prediction only	R

gene_156 GeneMa rk.hmm 135_nt + 1 0900 11034	13 5	399 220 7	280	51 9.5 3	9.02	117 411 44	699	44 0.9 9	8.78	- 0. 24	939 798 1	330	26 0.1	8.02	-1	Ribosomal protein L34	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1570 GeneM ark.hmm 258_nt + 51252 51509	25 8	399 220 7	153	14 8.5 5	7.21	117 411 44	770	25 4.1 9	7.99	0. 78	939 798 1	255	10 5.1 7	6.72	- 0. 49	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1571 GeneM ark.hmm 117_nt - 52220 52336	11 7	399 220 7	1	2.1 4	1.1	117 411 44	11	8.0 1	3	1. 9	939 798 1	7	6.3 7	2.67	1. 57	NA			
gene_1572 GeneM ark.hmm 153_nt - 52340 52492	15 3	399 220 7	5	8.1 9	3.03	117 411 44	19	10. 58	3.4	0. 37	939 798 1	13	9.0 4	3.18	0. 15	NA			
gene_1573 GeneM ark.hmm 765_nt + 52557 53321	76 5	399 220 7	162	53. 04	5.73	117 411 44	141 0	15 6.9 8	7.29	1. 56	939 798 1	142 8	19 8.6 2	7.63	1. 9	---	---	---	---
gene_1574 GeneM ark.hmm 1380_nt + 53931 55310	13 80	399 220 7	466 0	84 5.8 5	9.72	117 411 44	274 39	16 93. 47	10.7 3	1. 01	939 798 1	204 07	15 73. 5	10.6 2	0. 9	Trk-type K+ transport systems, membrane components	METABOLISM	Inorganic ion transport and metabolism	P
gene_1575 GeneM ark.hmm 666_nt + 55324 55989	66 6	399 220 7	299 7	11 27. 2	10.1 4	117 411 44	138 27	17 68. 25	10.7 9	0. 65	939 798 1	172 09	27 49. 46	11.4 2	1. 28	K+ transport systems, NAD-binding component	METABOLISM	Inorganic ion transport and metabolism	P
gene_436 GeneMa rk.hmm 234_nt - 24148 24381	23 4	399 220 7	2	2.1 4	1.1	117 411 44	35	12. 74	3.67	2. 57	939 798 1	22	10	3.32	2. 22	---	---	---	---
gene_1577 GeneM ark.hmm 411_nt + 56950 57360	41 1	399 220 7	115	70. 09	6.13	117 411 44	112 1	23 2.3	7.86	1. 73	939 798 1	142 8	36 9.7	8.53	2. 4	Glycosyltransferases involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2381 GeneM ark.hmm 114_nt - 3 116	11 4	399 220 7	2	4.3 9	2.14	117 411 44	62	46. 32	5.53	3. 39	939 798 1	22	20. 53	4.36	2. 22	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1579 GeneM ark.hmm 162_nt + 2 163	16 2	399 220 7	15	23. 19	4.54	117 411 44	116	60. 99	5.93	1. 39	939 798 1	94	61. 74	5.95	1. 41	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_157 GeneMa rk.hmm 900_nt + 1 1318 12217	90 0	399 220 7	385	10 7.1 5	6.74	117 411 44	433 5	41 0.2 4	8.68	1. 94	939 798 1	831 9	98 3.5 4	9.94	3. 2	---	---	---	---
gene_1580 GeneM ark.hmm 90_nt + 6 18 707	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1581 GeneM ark.hmm 804_nt - 1025 1828	80 4	399 220 7	179	55. 77	5.8	117 411 44	638	67. 59	6.08	0. 28	939 798 1	295	39. 04	5.29	- 0. 51	Protein involved in cell division	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1582 GeneM ark.hmm 756_nt - 2105 2860	75 6	399 220 7	39	12. 92	3.69	117 411 44	408	45. 97	5.52	1. 83	939 798 1	186	26. 18	4.71	1. 02	FOG: Zn-finger	POORLY CHARACTERIZ ED	General function prediction only	R

gene_1583 GeneM ark.hmm 2043_nt - 2930 4972	20 43	399 220 7	172 8	21 1.8 7	7.73	117 411 44	558 5	23 2.8 3	7.86	0. 13	939 798 1	654 4	34 0.8 3	8.41	0. 68	Valyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1584 GeneM ark.hmm 606_nt - 5037 5642	60 6	399 220 7	127	52. 5	5.71	117 411 44	112 3	15 7.8 3	7.3	1. 59	939 798 1	124 5	21 8.6 1	7.77	2. 06	Valyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1935 GeneM ark.hmm 1278_nt + 61351 62628	12 78	399 220 7	422	82. 71	6.37	117 411 44	561 9	37 4.4 7	8.55	2. 18	939 798 1	466 9	38 8.7 4	8.6	2. 23	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1586 GeneM ark.hmm 561_nt - 6213 6773	56 1	399 220 7	67	29. 92	4.9	117 411 44	460	69. 84	6.13	1. 23	939 798 1	464	88. 01	6.46	1. 56	Acetyltransferases, including N- acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1587 GeneM ark.hmm 450_nt - 6760 7209	45 0	399 220 7	75	41. 75	5.38	117 411 44	639	12 0.9 4	6.92	1. 54	939 798 1	500	11 8.2 3	6.89	1. 51	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1588 GeneM ark.hmm 396_nt - 7622 8017	39 6	399 220 7	254	16 0.6 7	7.33	117 411 44	181 3	38 9.9 3	8.61	1. 28	939 798 1	982	26 3.8 6	8.04	0. 71	---	---	---	---
gene_1589 GeneM ark.hmm 255_nt - 8113 8367	25 5	399 220 7	100	98. 23	6.62	117 411 44	294	98. 2	6.62	0	939 798 1	313	13 0.6 1	7.03	0. 41	---	---	---	---
gene_158 GeneMa rk.hmm 774_nt + 1 2522 13295	77 4	399 220 7	777	25 1.4 6	7.97	117 411 44	922	10 1.4 6	6.66	- 1. 31	939 798 1	107 8	14 8.2	7.21	- 0. 76	Mg-dependent DNase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1590 GeneM ark.hmm 435_nt - 8377 8811	43 5	399 220 7	590	33 9.7 4	8.41	117 411 44	906	17 7.3 9	7.47	- 0. 94	939 798 1	100 3	24 5.3 4	7.94	- 0. 47	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1591 GeneM ark.hmm 882_nt - 8865 9746	88 2	399 220 7	447	12 6.9 5	6.99	117 411 44	125 2	12 0.9	6.92	- 0. 07	939 798 1	915	11 0.3 9	6.79	- 0. 2	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1592 GeneM ark.hmm 234_nt - 9746 9979	23 4	399 220 7	141	15 0.9 4	7.24	117 411 44	289	10 5.1 9	6.72	- 0. 52	939 798 1	215	97. 77	6.61	- 0. 63	---	---	---	---
gene_2257 GeneM ark.hmm 729_nt - 78020 78748	72 9	399 220 7	10	3.4 4	1.78	117 411 44	183	21. 38	4.42	2. 64	939 798 1	110	16. 06	4.01	2. 23	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	METABOLISM	Carbohydrate transport and metabolism	G
gene_49 GeneMar k.hmm 564_nt - 33084 33647	56 4	399 220 7	110	48. 85	5.61	117 411 44	153 1	23 1.2	7.85	2. 24	939 798 1	122 0	23 0.1 7	7.85	2. 24	Acetyltransferases, including N- acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1595 GeneM ark.hmm 351_nt - 11625 11975	35 1	399 220 7	113	80. 64	6.33	117 411 44	763	18 5.1 4	7.53	1. 2	939 798 1	853	25 8.5 9	8.01	1. 68	Ribosome-binding factor A	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1596 GeneM ark.hmm 2778_nt - 12226 15003	27 78	399 220 7	828 0	74 6.5 9	9.54	117 411 44	359 85	11 03. 26	10.1 1	0. 57	939 798 1	550 67	21 09. 23	11.0 4	1. 5	Translation initiation factor 2 (IF-2; GTPase)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J

gene_1015 GeneM ark.hmm 1692_nt - 106444 108135	16 92	399 220 7	29	4.2 9	2.1	117 411 44	619	31. 16	4.96	2. 86	939 798 1	329	20. 69	4.37	2. 27	ABC-type Fe3+ transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1598 GeneM ark.hmm 294_nt - 15327 15620	29 4	399 220 7	99	84. 35	6.4	117 411 44	114 5	33 1.7	8.37	1. 97	939 798 1	164 7	59 6.0 9	9.22	2. 82	Predicted nucleic-acid-binding protein implicated in transcription termination	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1599 GeneM ark.hmm 114_nt - 15642 15755	11 4	399 220 7	4	8.7 9	3.14	117 411 44	6	4.4 8	2.16	- 0. 98	939 798 1	14	13. 07	3.71	0. 57	Transcription elongation factor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_159 GeneMa rk.hmm 561_nt + 1 3295 13855	56 1	399 220 7	100 3	44 7.8 4	8.81	117 411 44	869	13 1.9 3	7.04	- 1. 77	939 798 1	943	17 8.8 6	7.48	- 1. 33	Small primase-like proteins (Toprim domain)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_15 GeneMar k.hmm 498_nt - 8619 9116	49 8	399 220 7	58	29. 17	4.87	117 411 44	160	27. 36	4.77	- 0. 1	939 798 1	147	31. 41	4.97	0. 1	Exonuclease VII, large subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1600 GeneM ark.hmm 1017_nt - 15807 16823	10 17	399 220 7	198 0	48 7.6 8	8.93	117 411 44	625 4	52 3.7 5	9.03	0. 1	939 798 1	731 9	76 5.7 7	9.58	0. 65	Transcription elongation factor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1601 GeneM ark.hmm 480_nt - 16867 17346	48 0	399 220 7	101 0	52 7.0 7	9.04	117 411 44	391 2	69 4.1 4	9.44	0. 4	939 798 1	351 0	77 8.0 9	9.6	0. 56	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1602 GeneM ark.hmm 636_nt - 17472 18107	63 6	399 220 7	500	19 6.9 2	7.62	117 411 44	337 7	45 2.2 3	8.82	1. 2	939 798 1	354 9	59 3.7 6	9.21	1. 59	Predicted S-adenosylmethionine- dependent methyltransferase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1603 GeneM ark.hmm 795_nt - 18104 18898	79 5	399 220 7	118 5	37 3.3 7	8.54	117 411 44	681 6	73 0.2 2	9.51	0. 97	939 798 1	520 8	69 7.0 6	9.45	0. 91	Predicted choline kinase involved in LPS biosynthesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1000 GeneM ark.hmm 660_nt + 93462 94121	66 0	399 220 7	15	5.6 9	2.51	117 411 44	233	30. 07	4.91	2. 4	939 798 1	170	27. 41	4.78	2. 27	Type II secretory pathway, prepilin signal peptidase PulO and related peptidases	CELLULAR PROCESSES AND SIGNALING	Cell motility	N
gene_1605 GeneM ark.hmm 249_nt - 19700 19948	24 9	399 220 7	21	21. 13	4.4	117 411 44	262	89. 62	6.49	2. 09	939 798 1	129	55. 13	5.78	1. 38	---	---	---	---
gene_2251 GeneM ark.hmm 216_nt - 72928 73143	21 6	399 220 7	3	3.4 8	1.8	117 411 44	102	40. 22	5.33	3. 53	939 798 1	34	16. 75	4.07	2. 27	---	---	---	---
gene_1551 GeneM ark.hmm 1443_nt + 27532 28974	14 43	399 220 7	25	4.3 4	2.12	117 411 44	412	24. 32	4.6	2. 48	939 798 1	287	21. 16	4.4	2. 28	Glutamine phosphoribosylpyrophosphate amidotransferase	METABOLISM	Nucleotide transport and metabolism	F
gene_2235 GeneM ark.hmm 2031_nt - 50032 52062	20 31	399 220 7	63	7.7 7	2.96	117 411 44	117 5	49. 27	5.62	2. 66	939 798 1	721	37. 77	5.24	2. 28	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_976 GeneMa rk.hmm 228_nt - 69930 70157	22 8	399 220 7	2	2.2	1.14	117 411 44	47	17. 56	4.13	2. 99	939 798 1	23	10. 73	3.42	2. 28	---	---	---	---

gene_160 GeneMark.hmm 900_nt + 13927 14826	900	3992207	335	93.24	6.54	11741144	679	64.26	6.01	-0.53	9397981	647	76.49	6.26	-0.28	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1610 GeneMark.hmm 588_nt + 23218 23805	588	3992207	81	34.51	5.11	11741144	665	96.32	6.59	1.48	9397981	723	130.84	7.03	1.92	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1799 GeneMark.hmm 552_nt - 8232 8783	552	3992207	13	5.9	2.56	11741144	284	43.82	5.45	2.89	9397981	150	28.91	4.85	2.29	Uncharacterized membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_1612 GeneMark.hmm 441_nt + 24465 24905	441	3992207	333	189.14	7.56	11741144	1526	294.72	8.2	0.64	9397981	1925	464.47	8.86	1.3	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1613 GeneMark.hmm 504_nt + 24874 25377	504	3992207	270	134.19	7.07	11741144	1509	255	7.99	0.92	9397981	1702	359.33	8.49	1.42	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1614 GeneMark.hmm 1362_nt + 25388 26749	1362	3992207	361	66.39	6.05	11741144	3437	214.93	7.75	1.7	9397981	2352	183.75	7.52	1.47	---	---	---	---
gene_1615 GeneMark.hmm 156_nt + 26806 26961	156	3992207	2	3.21	1.68	11741144	39	21.29	4.41	2.73	9397981	15	10.23	3.35	1.67	---	---	---	---
gene_1616 GeneMark.hmm 1341_nt - 27003 28343	1341	3992207	390	72.85	6.19	11741144	2197	139.54	7.12	0.93	9397981	2579	204.64	7.68	1.49	Predicted signal transduction protein with a C-terminal ATPase domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1617 GeneMark.hmm 738_nt - 28357 29094	738	3992207	747	253.54	7.99	11741144	2297	265.09	8.05	0.06	9397981	2465	355.41	8.47	0.48	Response regulator of the LytR/AlgR family	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1618 GeneMark.hmm 339_nt - 29099 29437	339	3992207	102	75.37	6.24	11741144	512	128.64	7.01	0.77	9397981	411	129.01	7.01	0.77	Response regulator of the LytR/AlgR family	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1619 GeneMark.hmm 330_nt + 29713 30042	330	3992207	82	62.24	5.96	11741144	303	78.2	6.29	0.33	9397981	183	59.01	5.88	-0.08	---	---	---	---
gene_161 GeneMark.hmm 1800_nt + 15095 16894	1800	3992207	305	42.44	5.41	11741144	1014	47.98	5.58	0.17	9397981	674	39.84	5.32	-0.09	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_1620 GeneMark.hmm 1050_nt - 30210 31259	1050	3992207	1574	375.49	8.55	11741144	5014	406.71	8.67	0.12	9397981	3629	367.76	8.52	-0.03	Predicted ABC-type exoprotein transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_1621 GeneMark.hmm 732_nt - 31256 31987	732	3992207	598	204.63	7.68	11741144	2090	243.18	7.93	0.25	9397981	880	127.92	7	-0.68	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V

gene_1622 GeneM ark.hmm 411_nt + 32055 32465	41 1	399 220 7	140 8	85 8.1 2	9.75	117 411 44	398 7	82 6.2 2	9.69	- 0.06	939 798 1	938	24 2.8 4	7.92	- 1.83	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	METABOLISM	Nucleotide transport and metabolism	F
gene_1623 GeneM ark.hmm 288_nt + 32475 32762	28 8	399 220 7	956	83 1.4 8	9.7	117 411 44	207 9	61 4.8 3	9.26	- 0.44	939 798 1	540	19 9.5 1	7.64	- 2.06	---	---	---	---
gene_1624 GeneM ark.hmm 1137_nt 33440 34576	11 37	399 220 7	646	14 2.3 2	7.15	117 411 44	307 1	23 0.0 4	7.85	0. 7	939 798 1	240 7	22 5.2 6	7.82	0. 67	DnaJ-class molecular chaperone with C-terminal Zn finger domain	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1625 GeneM ark.hmm 354_nt 34781 35134	35 4	399 220 7	190 0	13 44. 43	10.3 9	117 411 44	956 0	23 00. 09	11.1 7	0. 78	939 798 1	330 9	99 4.6 2	9.96	- 0.43	NA			
gene_1626 GeneM ark.hmm 576_nt 35147 35722	57 6	399 220 7	142 66	62 03. 93	12.6	117 411 44	189 52	28 02. 35	11.4 5	- 1.15	939 798 1	686 9	12 68. 93	10.3 1	- 2.29	Molecular chaperone	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1627 GeneM ark.hmm 1320_nt 35683 37002	13 20	399 220 7	105 93	20 10. 17	10.9 7	117 411 44	290 62	18 75. 17	10.8 7	- 0.1	939 798 1	102 41	82 5.5 3	9.69	- 1.28	Molecular chaperone	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1628 GeneM ark.hmm 525_nt 37482 38006	52 5	399 220 7	118 86	56 71. 05	12.4 7	117 411 44	113 04	18 33. 84	10.8 4	- 1.63	939 798 1	481 2	97 5.2 9	9.93	- 2.54	Molecular chaperone GrpE (heat shock protein)	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1629 GeneM ark.hmm 1035_nt 38033 39067	10 35	399 220 7	634 7	15 36. 08	10.5 9	117 411 44	938 4	77 2.2 1	9.59	-1	939 798 1	363 3	37 3.5	8.54	- 2.05	Transcriptional regulator of heat shock gene	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_162 GeneMa rk.hmm 228_nt + 1 6938 17165	22 8	399 220 7	51	56. 03	5.81	117 411 44	59	22. 04	4.46	- 1.35	939 798 1	83	38. 74	5.28	- 0.53	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1279 GeneM ark.hmm 165_nt + 2 166	16 5	399 220 7	2	3.0 4	1.6	117 411 44	29	14. 97	3.9	2. 3	939 798 1	23	14. 83	3.89	2. 29	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1631 GeneM ark.hmm 2334_nt + 40348 42681	23 34	399 220 7	198 2	21 2.7 1	7.73	117 411 44	438 3	15 9.9 4	7.32	- 0.41	939 798 1	320 2	14 5.9 8	7.19	- 0.54	Type I site-specific restriction- modification system, R (restriction) subunit and related helicases	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1632 GeneM ark.hmm 1464_nt + 42694 44157	14 64	399 220 7	499	85. 38	6.42	117 411 44	206 5	12 0.1 3	6.91	0. 49	939 798 1	164 5	11 9.5 6	6.9	0. 48	Type I restriction-modification system methyltransferase subunit	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1633 GeneM ark.hmm 1551_nt + 44157 45707	15 51	399 220 7	584	94. 32	6.56	117 411 44	252 1	13 8.4 4	7.11	0. 55	939 798 1	173 4	11 8.9 6	6.89	0. 33	Restriction endonuclease S subunits	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1786 GeneM ark.hmm 237_nt -	23 7	399 220	2	2.1 1	1.08	117 411	48	17. 25	4.11	3. 03	939 798	23	10. 33	3.37	2. 29	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ	Function unknown	S

[51457 51693		7				44					1						ED		
gene_1635 GeneM ark.hmm 1083_nt - 47121 48203	10 83	399 220 7	160	37. 01	5.21	117 411 44	156 6	12 3.1 6	6.94	1. 73	939 798 1	123 8	12 1.6 3	6.93	1. 72	Restriction endonuclease S subunits	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1636 GeneM ark.hmm 1347_nt - 49194 50540	13 47	399 220 7	622 3	11 57. 23	10.1 8	117 411 44	205 25	12 97. 79	10.3 4	0. 16	939 798 1	279 01	22 04. 03	11.1 1	0. 93	Glutamine synthetase	METABOLISM	Amino acid transport and metabolism	E
gene_1637 GeneM ark.hmm 357_nt - 50577 50933	35 7	399 220 7	114 0	79 9.8 8	9.64	117 411 44	272 1	64 9.1 6	9.34	- 0. 3	939 798 1	447 1	13 32. 61	10.3 8	0. 74	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1638 GeneM ark.hmm 528_nt - 51010 51537	52 8	399 220 7	203	96. 31	6.59	117 411 44	118 9	19 1.8	7.58	0. 99	939 798 1	433	87. 26	6.45	- 0. 14	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1639 GeneM ark.hmm 1197_nt - 51673 52869	11 97	399 220 7	930 2	19 46. 57	10.9 3	117 411 44	398 50	28 35. 46	11.4 7	0. 54	939 798 1	951 3	84 5.6 5	9.72	- 1. 21	3-phosphoglycerate kinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_163 GeneMa rk.hmm 642_nt + 1 7167 17808	64 2	399 220 7	182	71. 01	6.15	117 411 44	452	59. 96	5.91	- 0. 24	939 798 1	423	70. 11	6.13	- 0. 02	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1640 GeneM ark.hmm 1374_nt - 52959 54428	14 70	399 220 7	169	28. 8	4.85	117 411 44	617	35. 75	5.16	0. 31	939 798 1	440	31. 85	4.99	0. 14	---	---	---	---
gene_1641 GeneM ark.hmm 1347_nt - 54446 55792	13 47	399 220 7	62	11. 53	3.53	117 411 44	519	32. 82	5.04	1. 51	939 798 1	262	20. 7	4.37	0. 84	---	---	---	---
gene_1642 GeneM ark.hmm 681_nt - 55852 56532	68 1	399 220 7	36	13. 24	3.73	117 411 44	227	28. 39	4.83	1. 1	939 798 1	128	20	4.32	0. 59	Endo-beta-N-acetylglucosaminidase D	METABOLISM	Carbohydrate transport and metabolism	G
gene_1643 GeneM ark.hmm 1374_nt - 56583 57956	13 74	399 220 7	60	10. 94	3.45	117 411 44	556	34. 46	5.11	1. 66	939 798 1	322	24. 94	4.64	1. 19	Endo-beta-N-acetylglucosaminidase D	METABOLISM	Carbohydrate transport and metabolism	G
gene_1644 GeneM ark.hmm 1632_nt + 58249 59880	16 32	399 220 7	447 5	68 6.8 5	9.42	117 411 44	191 89	10 01. 43	9.97	0. 55	939 798 1	157 44	10 26. 5	10	0. 58	Na+/phosphate symporter	METABOLISM	Inorganic ion transport and metabolism	P
gene_1645 GeneM ark.hmm 1608_nt - 60439 62046	16 08	399 220 7	123 6	19 2.5 4	7.59	117 411 44	517 9	27 4.3 1	8.1	0. 51	939 798 1	660 0	43 6.7 4	8.77	1. 18	CTP synthase (UTP-ammonia lyase)	METABOLISM	Nucleotide transport and metabolism	F
gene_1646 GeneM ark.hmm 588_nt - 62436 63023	58 8	399 220 7	714 2	30 42. 49	11.5 7	117 411 44	161 95	23 45. 81	11.2	- 0. 37	939 798 1	101 74	18 41. 11	10.8 5	- 0. 72	DNA-directed RNA polymerase, delta subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1647 GeneM ark.hmm 450_nt - 63151 63600	45 0	399 220 7	521	29 0.0 1	8.18	117 411 44	286 1	54 1.5	9.08	0. 9	939 798 1	173 6	41 0.4 9	8.68	0. 5	Sortase and related acyltransferases	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M

gene_1648 GeneM ark.hmm 420_nt - 63605 64024	42 0	399 220 7	211	12 5.8 4	6.98	117 411 44	732	14 8.4 4	7.21	0. 23	939 798 1	628	15 9.1	7.31	0. 33	---	---	---	---
gene_1649 GeneM ark.hmm 627_nt - 64052 64678	62 7	399 220 7	392	15 6.6	7.29	117 411 44	269 2	36 5.6 8	8.51	1. 22	939 798 1	207 7	35 2.4 8	8.46	1. 17	Membrane-associated phospholipid phosphatase	METABOLISM	Lipid transport and metabolism	I
gene_164 GeneMa rk.hmm 309_nt + 1 7801 18109	30 9	399 220 7	123	99. 71	6.64	117 411 44	97	26. 74	4.74	- 1. 9	939 798 1	129	44. 42	5.47	- 1. 17	---	---	---	---
gene_1650 GeneM ark.hmm 564_nt - 64692 65255	56 4	399 220 7	125 6	55 7.8 2	9.12	117 411 44	310 2	46 8.4 4	8.87	- 0. 25	939 798 1	122 1	23 0.3 6	7.85	- 1. 27	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1651 GeneM ark.hmm 78_nt - 65708 65785	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Predicted rRNA methylase (SpoU class)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1868 GeneM ark.hmm 774_nt + 22821 23594	77 4	399 220 7	18	5.8 3	2.54	117 411 44	372	40. 93	5.36	2. 82	939 798 1	207	28. 46	4.83	2. 29	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_1653 GeneM ark.hmm 222_nt - 66462 66683	22 2	399 220 7	14	15. 8	3.98	117 411 44	110	42. 2	5.4	1. 42	939 798 1	67	32. 11	5.01	1. 03	ABC-type cobalt transport system, permease component CbiQ and related transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_1654 GeneM ark.hmm 606_nt - 66758 67363	60 6	399 220 7	275	11 3.6 7	6.83	117 411 44	755	10 6.1 1	6.73	- 0. 1	939 798 1	456	80. 07	6.32	- 0. 51	ABC-type cobalt transport system, permease component CbiQ and related transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_1655 GeneM ark.hmm 399_nt - 67348 67746	39 9	399 220 7	322	20 2.1 5	7.66	117 411 44	506	10 8.0 1	6.76	- 0. 9	939 798 1	389	10 3.7 4	6.7	- 0. 96	ABC-type cobalt transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1656 GeneM ark.hmm 1278_nt - 67807 69084	12 78	399 220 7	484	94. 86	6.57	117 411 44	211 2	14 0.7 5	7.14	0. 57	939 798 1	165 2	13 7.5 4	7.1	0. 53	ABC-type cobalt transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1657 GeneM ark.hmm 213_nt - 69186 69398	21 3	399 220 7	21	24. 7	4.63	117 411 44	85	33. 99	5.09	0. 46	939 798 1	109	54. 45	5.77	1. 14	NA			
gene_1658 GeneM ark.hmm 549_nt - 69405 69953	54 9	399 220 7	77	35. 13	5.13	117 411 44	385	59. 73	5.9	0. 77	939 798 1	467	90. 51	6.5	1. 37	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1659 GeneM ark.hmm 849_nt - 69968 70816	84 9	399 220 7	206	60. 78	5.93	117 411 44	815	81. 76	6.35	0. 42	939 798 1	765	95. 88	6.58	0. 65	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_165 GeneMa rk.hmm 873_nt + 1 8240 19112	87 3	399 220 7	146 7	42 0.9 2	8.72	117 411 44	266 2	25 9.7 1	8.02	- 0. 7	939 798 1	221 1	26 9.4 9	8.07	- 0. 65	Dimethyladenosine transferase (rRNA methylation)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1660 GeneM ark.hmm 1350_nt + 71004 72353	13 50	399 220 7	101 0	18 7.4	7.55	117 411 44	779 2	49 1.5 9	8.94	1. 39	939 798 1	406 6	32 0.4 8	8.32	0. 77	K+ transport systems, NAD-binding component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1661 GeneM ark.hmm 1428_nt	14	399 220	104	18 2.7	7.51	117 411	869	51 8.3	9.02	1.	939 798	806	60 0.8	9.23	1.	Trk-type K+ transport systems,	METABOLISM	Inorganic ion transport and	P

+ 72369 73796	28	7	2	8		44	1	6		51	1	3	1		72	membrane components		metabolism	
gene_435 GeneMa rk.hmm 447_nt - 23558 24004	44 7	399 220 7	2	1.1 2	0.16	117 411 44	47	8.9 6	3.16	3	939 798 1	23	5.4 8	2.45	2. 29	Predicted metal-dependent membrane protease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1663 GeneM ark.hmm 285_nt + 75353 75637	28 5	399 220 7	152	13 3.5 9	7.06	117 411 44	361	10 7.8 8	6.75	- 0. 31	939 798 1	173	64. 59	6.01	- 1. 05	---	---	---	---
gene_1664 GeneM ark.hmm 87_nt + 7 5630 75716	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1665 GeneM ark.hmm 219_nt + 75964 76182	21 9	399 220 7	8	9.1 5	3.19	117 411 44	110	42. 78	5.42	2. 23	939 798 1	52	25. 27	4.66	1. 47	NA			
gene_1164 GeneM ark.hmm 342_nt - 82158 82499	34 2	399 220 7	3	2.2	1.14	117 411 44	80	19. 92	4.32	3. 18	939 798 1	35	10. 89	3.44	2. 3	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2827 GeneM ark.hmm 144_nt - 2 145	14 4	399 220 7	5	8.7	3.12	117 411 44	159	94. 04	6.56	3. 44	939 798 1	58	42. 86	5.42	2. 3	---	---	---	---
gene_1668 GeneM ark.hmm 198_nt + 1 198	19 8	399 220 7	25	31. 63	4.98	117 411 44	196	84. 31	6.4	1. 42	939 798 1	301	16 1.7 6	7.34	2. 36	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1669 GeneM ark.hmm 423_nt - 523 945	42 3	399 220 7	472 0	27 95. 04	11.4 5	117 411 44	141 22	28 43. 45	11.4 7	0. 02	939 798 1	745 5	18 75. 31	10.8 7	- 0. 58	Transcription termination factor	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_166 GeneMa rk.hmm 879_nt + 1 9114 19992	87 9	399 220 7	100 6	28 6.6 8	8.16	117 411 44	222 9	21 5.9 8	7.75	- 0. 41	939 798 1	266 7	32 2.8 5	8.33	0. 17	Predicted GTPases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1670 GeneM ark.hmm 390_nt - 938 1327	39 0	399 220 7	666 3	42 79. 49	12.0 6	117 411 44	135 57	29 60. 66	11.5 3	- 0. 53	939 798 1	721 7	19 69. 05	10.9 4	- 1. 12	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1671 GeneM ark.hmm 561_nt - 1349 1909	56 1	399 220 7	101 54	45 33. 79	12.1 5	117 411 44	256 01	38 86. 72	11.9 2	- 0. 23	939 798 1	723 4	13 72. 09	10.4 2	- 1. 73	Translation elongation factor P (EF- P)/translation initiation factor 5A (eIF-5A)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1672 GeneM ark.hmm 798_nt - 2038 2835	79 8	399 220 7	244 8	76 8.4 1	9.59	117 411 44	586 2	62 5.6 5	9.29	- 0. 3	939 798 1	438 0	58 4.0 3	9.19	- 0. 4	Asp-tRNAAsn/Glu-tRNA ^{Gln} amidotransferase B subunit (PET112 homolog)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1673 GeneM ark.hmm 330_nt - 2887 3216	33 0	399 220 7	309	23 4.5 5	7.87	117 411 44	874	22 5.5 7	7.82	- 0. 05	939 798 1	630	20 3.1 4	7.67	- 0. 2	Asp-tRNAAsn/Glu-tRNA ^{Gln} amidotransferase B subunit (PET112 homolog)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1674 GeneM ark.hmm 141_nt - 3564 3704	14 1	399 220 7	27	47. 97	5.58	117 411 44	209	12 6.2 5	6.98	1. 4	939 798 1	67	50. 56	5.66	0. 08	Asp-tRNAAsn/Glu-tRNA ^{Gln} amidotransferase B subunit (PET112 homolog)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1675 GeneM ark.hmm 852_nt - 3704 4555	85 2	399 220 7	187 1	55 0.0 7	9.1	117 411 44	547 4	54 7.2 1	9.1	0	939 798 1	295 1	36 8.5 5	8.53	- 0. 57	Asp-tRNAAsn/Glu-tRNA ^{Gln} amidotransferase A subunit and related amidases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J

gene_1676 GeneM ark.hmm 612_nt - 4612 5223	61 2	399 220 7	630	25 7.8 6	8.01	117 411 44	219 0	30 4.7 8	8.25	0. 24	939 798 1	917	15 9.4 3	7.32	- 0. 69	Asp-tRNAAsn/Glu-tRNA Gln amidotransferase A subunit and related amidases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1677 GeneM ark.hmm 303_nt - 5223 5525	30 3	399 220 7	655	54 1.4 8	9.08	117 411 44	414 9	11 66. 25	10.1 9	1. 11	939 798 1	984	34 5.5 6	8.43	- 0. 65	Asp-tRNAAsn/Glu-tRNA Gln amidotransferase C subunit	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1678 GeneM ark.hmm 1545_nt + 5738 7282	15 45	399 220 7	164 7	26 7.0 3	8.06	117 411 44	400 8	22 0.9 5	7.79	- 0. 27	939 798 1	434 2	29 9.0 4	8.22	0. 16	Peptide chain release factor RF-3	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1679 GeneM ark.hmm 198_nt + 7537 7734	19 8	399 220 7	31	39. 22	5.29	117 411 44	218	93. 77	6.55	1. 26	939 798 1	341	18 3.2 5	7.52	2. 23	Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_167 GeneMa rk.hmm 657_nt + 2 0003 20659	65 7	399 220 7	106 6	40 6.4 2	8.67	117 411 44	183 7	23 8.1 4	7.9	- 0. 77	939 798 1	216 4	35 0.4 8	8.45	- 0. 22	Pentose-5-phosphate-3-epimerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1680 GeneM ark.hmm 189_nt + 8137 8325	18 9	399 220 7	635	84 1.5 9	9.72	117 411 44	160 3	72 2.3 7	9.5	- 0. 22	939 798 1	176 2	99 2	9.95	0. 23	Ribosomal protein L28	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1681 GeneM ark.hmm 366_nt + 8482 8847	36 6	399 220 7	622	42 5.6 9	8.73	117 411 44	284 6	66 2.2 8	9.37	0. 64	939 798 1	162 8	47 3.3	8.89	0. 16	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1682 GeneM ark.hmm 1668_nt + 8850 10517	16 68	399 220 7	123 18	18 49. 83	10.8 5	117 411 44	285 67	14 58. 67	10.5 1	- 0. 34	939 798 1	227 96	14 54. 21	10.5 1	- 0. 34	Predicted kinase related to dihydroxyacetone kinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_424 GeneMa rk.hmm 237_nt - 17097 17333	23 7	399 220 7	0	0	0	117 411 44	29	10. 42	3.38	3. 38	939 798 1	11	4.9 4	2.3	2. 3	NA			
gene_1684 GeneM ark.hmm 477_nt + 12411 12887	47 7	399 220 7	70	36. 76	5.2	117 411 44	575	10 2.6 7	6.68	1. 48	939 798 1	773	17 2.4 4	7.43	2. 23	Acetolactate synthase, small (regulatory) subunit	METABOLISM	Amino acid transport and metabolism	E
gene_1685 GeneM ark.hmm 1023_nt + 12953 13975	10 23	399 220 7	369	90. 35	6.5	117 411 44	320 0	26 6.4 2	8.06	1. 56	939 798 1	338 3	35 1.8 8	8.46	1. 96	Ketol-acid reductoisomerase	METABOLISM	Amino acid transport and metabolism	E
gene_1421 GeneM ark.hmm 267_nt - 19950 20216	26 7	399 220 7	358	33 5.8 6	8.39	117 411 44	801 8	25 57. 67	11.3 2	2. 93	939 798 1	420 8	16 76. 99	10.7 1	2. 32	F0F1-type ATP synthase, alpha subunit	METABOLISM	Energy production and conversion	C
gene_1915 GeneM ark.hmm 2553_nt + 40493 43045	25 53	399 220 7	310	30. 42	4.93	117 411 44	375 0	12 5.1	6.97	2. 04	939 798 1	364 7	15 2	7.25	2. 32	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1688 GeneM ark.hmm 1251_nt + 14962 16212	12 51	399 220 7	176	35. 24	5.14	117 411 44	192 5	13 1.0 6	7.03	1. 89	939 798 1	243 0	20 6.6 9	7.69	2. 55	Threonine dehydratase	METABOLISM	Amino acid transport and metabolism	E
gene_1689 GeneM ark.hmm 216_nt + 17084 17299	21 6	399 220 7	340 4	39 47. 51	11.9 5	117 411 44	597 4	23 55. 6	11.2	- 0. 75	939 798 1	239 5	11 79. 82	10.2	- 1. 75	---	---	---	---

gene_168 GeneMa rk.hmm 663_nt + 2 0622 21284	66 3	399 220 7	788	29 7.7 1	8.22	117 411 44	149 7	19 2.3 1	7.59	- 0. 63	939 798 1	192 3	30 8.6 3	8.27	0. 05	Thiamine pyrophosphokinase	METABOLISM	Coenzyme transport and metabolism	H
gene_1690 GeneM ark.hmm 741_nt 17408 18148	74 1	399 220 7	392	13 2.5 1	7.05	117 411 44	122 6	14 0.9 2	7.14	0. 09	939 798 1	102 0	14 6.4 7	7.19	0. 14	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_1691 GeneM ark.hmm 1566_nt 18148 19713	15 66	399 220 7	492	78. 7	6.3	117 411 44	301 2	16 3.8 1	7.36	1. 06	939 798 1	317 3	21 5.6	7.75	1. 45	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_1692 GeneM ark.hmm 1890_nt + 19851 21740	18 90	399 220 7	370	49. 04	5.62	117 411 44	280 9	12 6.5 8	6.98	1. 36	939 798 1	337 4	18 9.9 5	7.57	1. 95	---	---	---	---
gene_1693 GeneM ark.hmm 291_nt 22415 22705	29 1	399 220 7	775	66 7.1 1	9.38	117 411 44	281 9	82 5.0 7	9.69	0. 31	939 798 1	253 4	92 6.5 7	9.86	0. 48	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1694 GeneM ark.hmm 66_nt 22990 23055	66	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1695 GeneM ark.hmm 846_nt + 23357 24202	84 6	399 220 7	221 0	65 4.3 5	9.35	117 411 44	100 39	10 10. 67	9.98	0. 63	939 798 1	753 0	94 7.0 9	9.89	0. 54	Uncharacterized bacitracin resistance protein	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1696 GeneM ark.hmm 1062_nt 24349 25410	10 62	399 220 7	299	70. 52	6.14	117 411 44	112 4	90. 14	6.49	0. 35	939 798 1	991	99. 29	6.63	0. 49	Nucleotidyltransferase/DNA polymerase involved in DNA repair	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1697 GeneM ark.hmm 2325_nt + 25758 28082	23 25	399 220 7	767 19	82 65. 46	13.0 1	117 411 44	214 858	78 70. 79	12.9 4	- 0. 07	939 798 1	711 52	32 56. 34	11.6 7	- 1. 34	Pyruvate-formate lyase	METABOLISM	Energy production and conversion	C
gene_1698 GeneM ark.hmm 177_nt 28220 28396	17 7	399 220 7	24	33. 96	5.09	117 411 44	238	11 4.5 2	6.84	1. 75	939 798 1	212	12 7.4 5	6.99	1. 9	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1887 GeneM ark.hmm 267_nt 12408 12674	26 7	399 220 7	22	20. 64	4.37	117 411 44	319	10 1.7 6	6.67	2. 3	939 798 1	260	10 3.6 2	6.7	2. 33	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_169 GeneMa rk.hmm 1257_nt + 21286 22542	12 57	399 220 7	330 3	65 8.2	9.36	117 411 44	487 5	33 0.3 2	8.37	- 0. 99	939 798 1	707 0	59 8.4 8	9.23	- 0. 13	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_16 GeneMar k.hmm 837_nt 9202 10038	83 7	399 220 7	237	70. 93	6.15	117 411 44	888	90. 36	6.5	0. 35	939 798 1	540	68. 65	6.1	- 0. 05	Exonuclease VII, large subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2788 GeneM ark.hmm 105_nt + 2 106	10 5	399 220 7	0	0	0	117 411 44	5	4.0 6	2.02	2. 02	939 798 1	5	5.0 7	2.34	2. 34	NA			
gene_1701 GeneM ark.hmm 957_nt 590 1546	95 7	399 220 7	542	14 1.8 6	7.15	117 411 44	205 8	18 3.1 6	7.52	0. 37	939 798 1	241 7	26 8.7 4	8.07	0. 92	Uncharacterized ABC-type transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R

gene_1702 GeneM ark.hmm 1059_nt - 1549 2607	10 59	399 220 7	217	51. 33	5.68	117 411 44	114 9	92. 41	6.53	0. 85	939 798 1	128 0	12 8.6 1	7.01	1. 33	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1703 GeneM ark.hmm 105_nt - 2600 2704	10 5	399 220 7	0	0	0	117 411 44	3	2.4 3	1.28	1. 28	939 798 1	4	4.0 5	2.02	2. 02	ABC-type uncharacterized transport systems, ATPase components	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1704 GeneM ark.hmm 1428_nt - 2804 4231	14 28	399 220 7	124 2	21 7.8 6	7.77	117 411 44	439 0	26 1.8 3	8.03	0. 26	939 798 1	257 1	19 1.5 8	7.58	- 0. 19	ABC-type uncharacterized transport systems, ATPase components	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1705 GeneM ark.hmm 1053_nt - 4375 5427	10 53	399 220 7	115 57	27 49. 18	11.4 2	117 411 44	107 52	86 9.6 6	9.76	- 1. 66	939 798 1	131 11	13 24. 87	10.3 7	- 1. 05	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1706 GeneM ark.hmm 390_nt - 5518 5907	39 0	399 220 7	236	15 1.5 8	7.24	117 411 44	643	14 0.4 2	7.13	- 0. 11	939 798 1	556	15 1.7	7.25	0. 01	Cytidine deaminase	METABOLISM	Nucleotide transport and metabolism	F
gene_1707 GeneM ark.hmm 663_nt - 5894 6556	66 3	399 220 7	665	25 1.2 4	7.97	117 411 44	326 0	41 8.7 9	8.71	0. 74	939 798 1	241 4	38 7.4 3	8.6	0. 63	Deoxyribose-phosphate aldolase	METABOLISM	Nucleotide transport and metabolism	F
gene_1708 GeneM ark.hmm 675_nt - 6574 7248	67 5	399 220 7	168	62. 34	5.96	117 411 44	440	55. 52	5.79	- 0. 17	939 798 1	389	61. 32	5.94	- 0. 02	Thymidine phosphorylase	METABOLISM	Nucleotide transport and metabolism	F
gene_1709 GeneM ark.hmm 372_nt - 7329 7700	37 2	399 220 7	162	10 9.0 8	6.77	117 411 44	260	59. 53	5.9	- 0. 87	939 798 1	236	67. 5	6.08	- 0. 69	Thymidine phosphorylase	METABOLISM	Nucleotide transport and metabolism	F
gene_170 GeneMa rk.hmm 942_nt + 2 2532 23473	94 2	399 220 7	190 0	50 5.2 3	8.98	117 411 44	335 7	30 3.5 2	8.25	- 0. 73	939 798 1	478 5	54 0.5	9.08	0. 1	Predicted HD-superfamily hydrolase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1710 GeneM ark.hmm 219_nt - 7760 7978	21 9	399 220 7	27	30. 88	4.95	117 411 44	113	43. 95	5.46	0. 51	939 798 1	82	39. 84	5.32	0. 37	Thymidine phosphorylase	METABOLISM	Nucleotide transport and metabolism	F
gene_1711 GeneM ark.hmm 582_nt - 7975 8556	58 2	399 220 7	406	17 4.7 4	7.45	117 411 44	748	10 9.4 6	6.77	- 0. 68	939 798 1	497	90. 87	6.51	- 0. 94	16S RNA G1207 methylase RsmC	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_889 GeneMa rk.hmm 585_nt - 38159 38743	58 5	399 220 7	17	7.2 8	2.86	117 411 44	396	57. 65	5.85	2. 99	939 798 1	202	36. 74	5.2	2. 34	---	---	---	---
gene_1713 GeneM ark.hmm 921_nt + 9366 10286	92 1	399 220 7	231	62. 83	5.97	117 411 44	136 8	12 6.5 1	6.98	1. 01	939 798 1	874	10 0.9 8	6.66	0. 69	Panthothenate kinase	METABOLISM	Coenzyme transport and metabolism	H
gene_1714 GeneM ark.hmm 237_nt + 10354 10590	23 7	399 220 7	291 0	30 75. 61	11.5 9	117 411 44	200 75	72 14. 34	12.8 2	1. 23	939 798 1	517 3	23 22. 52	11.1 8	- 0. 41	Ribosomal protein S20	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1715 GeneM ark.hmm 525_nt + 10643 11167	52 5	399 220 7	141	67. 27	6.07	117 411 44	889	14 4.2 2	7.17	1. 1	939 798 1	690	13 9.8 5	7.13	1. 06	Adenylate kinase and related kinases	METABOLISM	Nucleotide transport and metabolism	F
gene_1716 GeneM ark.hmm 705_nt -	70	399 220	484	17 1.9	7.43	117 411	137	16 6.1	7.38	- 0.	939 798	183	27 6.3	8.11	0.	Purine-nucleoside phosphorylase	METABOLISM	Nucleotide transport and	F

[11190 11894	5	7		7		44	5	1		05	1	1	5		68			metabolism	
gene_1717 GeneM ark.hmm 513_nt - 12640 13152	51 3	399 220 7	136 9	66 8.4 6	9.38	117 411 44	173 0	28 7.2 2	8.17	- 1. 21	939 798 1	243 8	50 5.6 9	8.98	- 0. 4	---	---	---	---
gene_1718 GeneM ark.hmm 576_nt - 13177 13752	57 6	399 220 7	486	21 1.3 5	7.72	117 411 44	120 3	17 7.8 8	7.47	- 0. 25	939 798 1	161 3	29 7.9 7	8.22	0. 5	---	---	---	---
gene_1719 GeneM ark.hmm 1023_nt - 13762 14784	10 23	399 220 7	506	12 3.9	6.95	117 411 44	181 7	15 1.2 8	7.24	0. 29	939 798 1	198 7	20 6.6 7	7.69	0. 74	---	---	---	---
gene_171 GeneMa rk.hmm 828_nt + 2 3740 24567	82 8	399 220 7	250 9	75 9.0 3	9.57	117 411 44	690 5	71 0.2 7	9.47	- 0. 1	939 798 1	606 2	77 9.0 2	9.61	0. 04	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	METABOLISM	Nucleotide transport and metabolism	F
gene_1720 GeneM ark.hmm 810_nt - 15281 16090	81 0	399 220 7	577	17 8.4 3	7.48	117 411 44	919	96. 63	6.59	- 0. 89	939 798 1	114 2	15 0.0 2	7.23	- 0. 25	Purine nucleoside phosphorylase	METABOLISM	Nucleotide transport and metabolism	F
gene_1721 GeneM ark.hmm 543_nt - 16106 16648	54 3	399 220 7	914	42 1.6 3	8.72	117 411 44	156 4	24 5.3 2	7.94	- 0. 78	939 798 1	209 3	41 0.1 4	8.68	- 0. 04	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1722 GeneM ark.hmm 1212_nt - 16650 17861	12 12	399 220 7	136 8	28 2.7 3	8.14	117 411 44	250 7	17 6.1 7	7.46	- 0. 68	939 798 1	266 9	23 4.3 2	7.87	- 0. 27	Phosphopentomutase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1723 GeneM ark.hmm 666_nt - 17875 18540	66 6	399 220 7	372	13 9.9 1	7.13	117 411 44	106 5	13 6.2	7.09	- 0. 04	939 798 1	810	12 9.4 1	7.02	- 0. 11	Ribose 5-phosphate isomerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1724 GeneM ark.hmm 873_nt - 18840 19712	87 3	399 220 7	170 5	48 9.2 1	8.93	117 411 44	227 6	22 2.0 5	7.79	- 1. 14	939 798 1	183 5	22 3.6 6	7.81	- 1. 12	Predicted sugar kinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1725 GeneM ark.hmm 858_nt - 19854 20711	85 8	399 220 7	241	70. 36	6.14	117 411 44	142 7	14 1.6 5	7.15	1. 01	939 798 1	138 5	17 1.7 6	7.42	1. 28	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	METABOLISM	Coenzyme transport and metabolism	H
gene_1726 GeneM ark.hmm 735_nt - 20865 21599	73 5	399 220 7	91	31. 01	4.95	117 411 44	670	77. 64	6.28	1. 33	939 798 1	402	58. 2	5.86	0. 91	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_1727 GeneM ark.hmm 492_nt - 21599 22090	49 2	399 220 7	129	65. 68	6.04	117 411 44	901	15 5.9 7	7.29	1. 25	939 798 1	497	10 7.4 9	6.75	0. 71	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_1728 GeneM ark.hmm 231_nt + 22497 22727	23 1	399 220 7	703	76 2.3 1	9.57	117 411 44	905 9	33 40. 09	11.7 1	2. 14	939 798 1	175 1	80 6.5 7	9.66	0. 09	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1729 GeneM ark.hmm 1452_nt + 22956 24407	14 52	399 220 7	791 9	13 66. 13	10.4 2	117 411 44	222 89	13 07. 42	10.3 5	- 0. 07	939 798 1	116 93	85 6.8 9	9.74	- 0. 68	ATPases with chaperone activity, ATP-binding subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_172 GeneMa rk.hmm 1251_nt +	12 51	399 220	134 3	26 8.9	8.07	117 411	552 9	37 6.4	8.56	0. 49	939 798	598 3	50 8.8	8.99	0. 92	Diaminopimelate decarboxylase	METABOLISM	Amino acid transport and metabolism	E

24634 25884		7		1		44		3			1		9						
gene_1730 GeneM ark.hmm 801_nt + 24459 25259	80 1	399 220 7	710 0	22 20. 31	11.1 2	117 411 44	165 93	17 64. 34	10.7 8	- 0. 34	939 798 1	834 5	11 08. 56	10.1 1	- 1. 01	ATPases with chaperone activity, ATP-binding subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1987 GeneM ark.hmm 177_nt + 15141 15317	17 7	399 220 7	39	55. 19	5.79	117 411 44	472	22 7.1 2	7.83	2. 04	939 798 1	466	28 0.1 4	8.13	2. 34	---	---	---	---
gene_1269 GeneM ark.hmm 255_nt + 72636 72890	25 5	399 220 7	2	1.9 6	0.97	117 411 44	39	13. 03	3.7	2. 73	939 798 1	24	10. 01	3.32	2. 35	---	---	---	---
gene_1271 GeneM ark.hmm 234_nt + 73644 73877	23 4	399 220 7	2	2.1 4	1.1	117 411 44	43	15. 65	3.97	2. 87	939 798 1	24	10. 91	3.45	2. 35	---	---	---	---
gene_1734 GeneM ark.hmm 1920_nt + 3312 5231	19 20	399 220 7	127 2	16 5.9 5	7.37	117 411 44	275 1	12 2.0 3	6.93	- 0. 44	939 798 1	220 7	12 2.3 1	6.93	- 0. 44	Translation elongation factors (GTPases)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2514 GeneM ark.hmm 129_nt + 2 130	12 9	399 220 7	1	1.9 4	0.96	117 411 44	23	15. 19	3.92	2. 96	939 798 1	12	9.9	3.31	2. 35	NA			
gene_796 GeneMa rk.hmm 1191_nt + 174172 175362	11 91	399 220 7	26	5.4 7	2.45	117 411 44	772	55. 21	5.79	3. 34	939 798 1	315	28. 14	4.81	2. 36	---	---	---	---
gene_418 GeneMa rk.hmm 228_nt - 10371 10598	22 8	399 220 7	0	0	0	117 411 44	34	12. 7	3.67	3. 67	939 798 1	11	5.1 3	2.36	2. 36	NA			
gene_769 GeneMa rk.hmm 708_nt + 1 48332 149039	70 8	399 220 7	37	13. 09	3.71	117 411 44	497	59. 79	5.9	2. 19	939 798 1	447	67. 18	6.07	2. 36	Predicted metal-dependent membrane protease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1739 GeneM ark.hmm 1218_nt + 7830 9047	12 18	399 220 7	204	41. 95	5.39	117 411 44	897	62. 72	5.97	0. 58	939 798 1	629	54. 95	5.78	0. 39	Integrase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_173 GeneMa rk.hmm 795_nt + 2 6010 26804	79 5	399 220 7	468 9	14 77. 41	10.5 3	117 411 44	770 4	82 5.3 5	9.69	- 0. 84	939 798 1	591 2	79 1.2 8	9.63	- 0. 9	Pyruvate-formate lyase-activating enzyme	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1740 GeneM ark.hmm 732_nt + 9973 10704	73 2	399 220 7	72	24. 64	4.62	117 411 44	584	67. 95	6.09	1. 47	939 798 1	178	25. 87	4.69	0. 07	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1547 GeneM ark.hmm 2154_nt + 19120 21273	21 54	399 220 7	67	7.7 9	2.96	117 411 44	113 3	44. 8	5.49	2. 53	939 798 1	820	40. 51	5.34	2. 38	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1738 GeneM ark.hmm 204_nt + 7545 7748	20 4	399 220 7	0	0	0	117 411 44	16	6.6 8	2.74	2. 74	939 798 1	10	5.2 2	2.38	2. 38	NA			

gene_406 GeneMa rk.hmm 306_nt - 812 1117	30 6	399 220 7	0	0	0	117 411 44	45	12. 53	3.65	3. 65	939 798 1	15	5.2 2	2.38	2. 38	---	---	---	---
gene_1744 GeneM ark.hmm 2148_nt + 17219 19366	21 48	399 220 7	34	3.9 6	1.99	117 411 44	462	18. 32	4.2	2. 21	939 798 1	193	9.5 6	3.26	1. 27	DNA methylase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2259 GeneM ark.hmm 2217_nt - 81791 84007	22 17	399 220 7	44	4.9 7	2.31	117 411 44	919	35. 31	5.14	2. 83	939 798 1	537	25. 77	4.69	2. 38	Alpha-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1746 GeneM ark.hmm 297_nt + 19739 20035	29 7	399 220 7	51	43. 01	5.43	117 411 44	81	23. 23	4.54	- 0. 89	939 798 1	46	16. 48	4.04	- 1. 39	NA			
gene_1136 GeneM ark.hmm 2070_nt + 56470 58539	20 70	399 220 7	68	8.2 3	3.04	117 411 44	114 9	47. 28	5.56	2. 52	939 798 1	839	43. 13	5.43	2. 39	Predicted membrane metal-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2262 GeneM ark.hmm 711_nt - 87222 87932	71 1	399 220 7	14	4.9 3	2.3	117 411 44	239	28. 63	4.84	2. 54	939 798 1	175	26. 19	4.71	2. 41	ABC-type sugar transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_1749 GeneM ark.hmm 234_nt + 22169 22402	23 4	399 220 7	3	3.2 1	1.68	117 411 44	38	13. 83	3.79	2. 11	939 798 1	27	12. 28	3.62	1. 94	NA			
gene_174 GeneMa rk.hmm 927_nt - 26879 27805	92 7	399 220 7	606 7	16 39. 39	10.6 8	117 411 44	151 94	13 95. 99	10.4 5	- 0. 23	939 798 1	155 22	17 81. 7	10.8	0. 12	Preprotein translocase subunit YidC	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_1750 GeneM ark.hmm 384_nt + 22399 22782	38 4	399 220 7	4	2.6 1	1.38	117 411 44	57	12. 64	3.66	2. 28	939 798 1	33	9.1 4	3.19	1. 81	NA			
gene_1751 GeneM ark.hmm 255_nt + 23463 23717	25 5	399 220 7	111	10 9.0 4	6.77	117 411 44	188	62. 79	5.97	- 0. 8	939 798 1	57	23. 78	4.57	- 2. 2	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_504 GeneMa rk.hmm 1674_nt - 16349 18022	16 74	399 220 7	23	3.4 4	1.78	117 411 44	493	25. 08	4.65	2. 87	939 798 1	287	18. 24	4.19	2. 41	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1753 GeneM ark.hmm 684_nt + 24743 25426	68 4	399 220 7	843	30 8.7 2	8.27	117 411 44	124 3	15 4.7 8	7.27	-1	939 798 1	171	26. 6	4.73	- 3. 54	Predicted transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1754 GeneM ark.hmm 1416_nt + 25429 26844	14 16	399 220 7	125 2	22 1.4 8	7.79	117 411 44	267 3	16 0.7 8	7.33	- 0. 46	939 798 1	678	50. 95	5.67	- 2. 12	Nucleotidyltransferase/DNA polymerase involved in DNA repair	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1755 GeneM ark.hmm 363_nt + 26844 27206	36 3	399 220 7	544	37 5.3 9	8.55	117 411 44	112 1	26 3.0 2	8.04	- 0. 51	939 798 1	181	53. 06	5.73	- 2. 82	NA			
gene_1756 GeneM ark.hmm 291_nt + 27196 27486	29 1	399 220 7	13	11. 19	3.48	117 411 44	123	36	5.17	1. 69	939 798 1	33	12. 07	3.59	0. 11	NA			

gene_1699 GeneMark.hmm 498_nt -[28460 28957	498	3992207	12	6.04	2.59	11741144	144	24.63	4.62	2.03	9397981	151	32.26	5.01	2.42	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_732 GeneMark.hmm 669_nt +[05940 106608	669	3992207	92	34.45	5.11	11741144	1430	182.05	7.51	2.4	9397981	1159	184.34	7.53	2.42	Transaldolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_768 GeneMark.hmm 1419_nt +[146860 148278	1419	3992207	125	22.07	4.46	11741144	1676	100.6	6.65	2.19	9397981	1571	117.8	6.88	2.42	Permeases	POORLY CHARACTERIZED	General function prediction only	R
gene_175 GeneMark.hmm 279_nt -[27883 28161	279	3992207	32	28.73	4.84	11741144	169	51.59	5.69	0.85	9397981	116	44.24	5.47	0.63	Acylphosphatases	METABOLISM	Energy production and conversion	C
gene_1760 GeneMark.hmm 852_nt +[32829 33680	852	3992207	855	251.37	7.97	11741144	5867	586.5	9.2	1.23	9397981	3952	493.56	8.95	0.98	Predicted GTPases	POORLY CHARACTERIZED	General function prediction only	R
gene_1761 GeneMark.hmm 357_nt +[33667 34023	357	3992207	286	200.67	7.65	11741144	1308	312.05	8.29	0.64	9397981	808	240.83	7.91	0.26	Ribonuclease HII	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1762 GeneMark.hmm 420_nt +[34077 34496	420	3992207	1138	678.7	9.41	11741144	6965	1412.41	10.46	1.05	9397981	5783	1465.11	10.52	1.11	Ribonuclease HII	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1763 GeneMark.hmm 198_nt +[34512 34709	198	3992207	235	297.3	8.22	11741144	754	324.34	8.34	0.12	9397981	755	405.74	8.66	0.44	Chloride channel protein EriC	METABOLISM	Inorganic ion transport and metabolism	P
gene_1764 GeneMark.hmm 1347_nt +[34783 36129	1347	3992207	5353	995.44	9.96	11741144	28914	1828.23	10.84	0.88	9397981	24917	1968.31	10.94	0.98	Chloride channel protein EriC	METABOLISM	Inorganic ion transport and metabolism	P
gene_1765 GeneMark.hmm 1071_nt +[36713 37783	1071	3992207	2619	612.54	9.26	11741144	2492	198.17	7.63	-1.63	9397981	5121	508.78	8.99	-0.27	Integrase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1766 GeneMark.hmm 903_nt -[37848 38750	903	3992207	1003	278.23	8.12	11741144	2149	202.69	7.66	-0.46	9397981	2266	267.02	8.06	-0.06	Lipoate-protein ligase A	METABOLISM	Coenzyme transport and metabolism	H
gene_1767 GeneMark.hmm 147_nt -[39170 39316	147	3992207	180	306.72	8.26	11741144	264	152.96	7.26	-1	9397981	265	191.82	7.58	-0.68	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1768 GeneMark.hmm 618_nt -[39458 40075	618	3992207	543	220.09	7.78	11741144	1012	139.47	7.12	-0.66	9397981	1320	227.27	7.83	0.05	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1769 GeneMark.hmm 480_nt -[40333 40812	480	3992207	56	29.22	4.87	11741144	354	62.81	5.97	1.1	9397981	390	86.45	6.43	1.56	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	METABOLISM	Energy production and conversion	C

gene_176 GeneMa rk.hmm 711_nt + 2 8225 28935	71 1	399 220 7	971	34 2.0 9	8.42	117 411 44	354 0	42 4.0 6	8.73	0. 31	939 798 1	219 7	32 8.8	8.36	- 0. 06	rRNA methylases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1770 GeneM ark.hmm 393_nt 40865 41257	39 3	399 220 7	191	12 1.7 4	6.93	117 411 44	771	16 7.0 9	7.38	0. 45	939 798 1	854	23 1.2 2	7.85	0. 92	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1771 GeneM ark.hmm 609_nt 41303 41911	60 9	399 220 7	482	19 8.2 5	7.63	117 411 44	839	11 7.3 4	6.87	- 0. 76	939 798 1	932	16 2.8 4	7.35	- 0. 28	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1772 GeneM ark.hmm 141_nt 42063 42203	14 1	399 220 7	24	42. 64	5.41	117 411 44	168	10 1.4 8	6.67	1. 26	939 798 1	190	14 3.3 8	7.16	1. 75	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1773 GeneM ark.hmm 210_nt 42256 42465	21 0	399 220 7	83	99	6.63	117 411 44	198	80. 3	6.33	- 0. 3	939 798 1	243	12 3.1 3	6.94	0. 31	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_1774 GeneM ark.hmm 1035_nt 42684 43718	10 35	399 220 7	635	15 3.6 8	7.26	117 411 44	127 2	10 4.6 7	6.71	- 0. 55	939 798 1	134 5	13 8.2 8	7.11	- 0. 15	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit	METABOLISM	Energy production and conversion	C
gene_1775 GeneM ark.hmm 477_nt 43734 44210	47 7	399 220 7	253	13 2.8 6	7.05	117 411 44	736	13 1.4 2	7.04	- 0. 01	939 798 1	102 2	22 7.9 8	7.83	0. 78	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit	METABOLISM	Energy production and conversion	C
gene_1776 GeneM ark.hmm 483_nt 44346 44828	48 3	399 220 7	580	30 0.7 9	8.23	117 411 44	186 2	32 8.3 4	8.36	0. 13	939 798 1	130 6	28 7.7 1	8.17	- 0. 06	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit	METABOLISM	Energy production and conversion	C
gene_1777 GeneM ark.hmm 585_nt 44982 45566	58 5	399 220 7	116 4	49 8.4 1	8.96	117 411 44	147 8	21 5.1 8	7.75	- 1. 21	939 798 1	189 0	34 3.7 7	8.43	- 0. 53	Na+-driven multidrug efflux pump	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1778 GeneM ark.hmm 771_nt 45627 46397	77 1	399 220 7	279	90. 64	6.5	117 411 44	116 4	12 8.5 8	7.01	0. 51	939 798 1	112 1	15 4.7 1	7.27	0. 77	Na+-driven multidrug efflux pump	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1779 GeneM ark.hmm 261_nt 46408 46668	26 1	399 220 7	69	66. 22	6.05	117 411 44	212	69. 18	6.11	0. 06	939 798 1	167	68. 08	6.09	0. 04	NA			
gene_177 GeneMa rk.hmm 513_nt + 2 8991 29503	51 3	399 220 7	615 8	30 06. 83	11.5 5	117 411 44	113 35	18 81. 89	10.8 8	- 0. 67	939 798 1	920 3	19 08. 88	10.9	- 0. 65	Integral membrane protein, interacts with FtsH	POORLY CHARACTERIZ ED	General function prediction only	R

gene_1780 GeneM ark.hmm 1269_nt - 46682 47950	12 69	399 220 7	236 0	46 5.8 4	8.86	117 411 44	322 8	21 6.6 5	7.76	- 1	939 798 1	339 1	28 4.3 4	8.15	- 0.71	Dihydroorotase and related cyclic amidohydrolases	METABOLISM	Nucleotide transport and metabolism	F
gene_1781 GeneM ark.hmm 246_nt - 48229 48474	24 6	399 220 7	180	18 3.2 8	7.52	117 411 44	530	18 3.5	7.52	0	939 798 1	370	16 0.0 4	7.32	- 0.2	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1782 GeneM ark.hmm 669_nt - 48484 49152	66 9	399 220 7	233 4	87 3.9	9.77	117 411 44	357 3	45 4.8 8	8.83	- 0.94	939 798 1	132 8	21 1.2 2	7.72	- 2.05	Uracil DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_80 GeneMar k.hmm 360_nt - 55286 55645	36 0	399 220 7	20	13. 92	3.8	117 411 44	267	63. 17	5.98	2. 18	939 798 1	253	74. 78	6.22	2. 42	3-isopropylmalate dehydratase small subunit	METABOLISM	Amino acid transport and metabolism	E
gene_1784 GeneM ark.hmm 219_nt - 50423 50641	21 9	399 220 7	184	21 0.4 6	7.72	117 411 44	383	14 8.9 5	7.22	- 0.5	939 798 1	71	34. 5	5.11	- 2.61	Predicted hydrolase (HAD superfamily)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1785 GeneM ark.hmm 138_nt - 51260 51397	13 8	399 220 7	2	3.6 3	1.86	117 411 44	12	7.4 1	2.89	1. 03	939 798 1	7	5.4	2.43	0. 57	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1007 GeneM ark.hmm 831_nt - 99775 100605	83 1	399 220 7	23	6.9 3	2.79	117 411 44	336	34. 44	5.11	2. 32	939 798 1	292	37. 39	5.22	2. 43	Anthranilate phosphoribosyltransferase	METABOLISM	Amino acid transport and metabolism	E
gene_1787 GeneM ark.hmm 150_nt - 52115 52264	15 0	399 220 7	26	43. 42	5.44	117 411 44	121	68. 7	6.1	0. 66	939 798 1	58	41. 14	5.36	- 0.08	---	---	---	---
gene_1788 GeneM ark.hmm 270_nt - 52336 52605	27 0	399 220 7	186	17 2.5 6	7.43	117 411 44	492	15 5.2	7.28	- 0.15	939 798 1	185	72. 91	6.19	- 1.24	---	---	---	---
gene_1789 GeneM ark.hmm 102_nt - 1 102	10 2	399 220 7	28	68. 76	6.1	117 411 44	22	18. 37	4.2	- 1.9	939 798 1	11	11. 48	3.52	- 2.58	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_178 GeneMa rk.hmm 168_nt + 2 9556 29723	16 8	399 220 7	40	59. 64	5.9	117 411 44	133	67. 43	6.08	0. 18	939 798 1	94	59. 54	5.9	0	Integral membrane protein, interacts with FtsH	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1790 GeneM ark.hmm 906_nt - 99 1004	90 6	399 220 7	574 3	15 87. 81	10.6 3	117 411 44	171 11	16 08. 56	10.6 5	0. 02	939 798 1	101 75	11 95. 01	10.2 2	- 0.41	Predicted permeases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1791 GeneM ark.hmm 132_nt - 1005 1136	13 2	399 220 7	291	55 2.2 1	9.11	117 411 44	285	18 3.8 9	7.52	- 1.59	939 798 1	259	20 8.7 8	7.71	- 1.4	NA			
gene_1792 GeneM ark.hmm 2130_nt + 1571 3700	21 30	399 220 7	158 6	18 6.5 1	7.54	117 411 44	423 0	16 9.1 4	7.4	- 0.14	939 798 1	494 8	24 7.1 8	7.95	0. 41	Transcriptional accessory protein	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1793 GeneM ark.hmm 450_nt + 3687 4136	45 0	399 220 7	112 4	62 5.6 6	9.29	117 411 44	156 9	29 6.9 6	8.21	- 1.08	939 798 1	161 4	38 1.6 4	8.58	- 0.71	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1794 GeneM ark.hmm 273_nt +	27	399 220	302	27 71	14.7	117 411	417	13 02	13.6	- 1.	939 798	504	19 66	14.2	- 0.	Putative stress-responsive	INFORMATION STORAGE AND	Transcription	K

4195 4467	3	7	04	3.3 3	6	44	44	3.3	7	09	1	51	4.0 3	6	5	transcriptional regulator	PROCESSING		
gene_1795 GeneM ark.hmm 192_nt - 4821 5012	19 2	399 220 7	56	73. 06	6.19	117 411 44	101	44. 8	5.49	- 0. 7	939 798 1	66	36. 58	5.19	-1	---	---	---	---
gene_405 GeneMa rk.hmm 807_nt - 3 809	80 7	399 220 7	7	2.1 7	1.12	117 411 44	174	18. 36	4.2	3. 08	939 798 1	89	11. 73	3.55	2. 43	NA			
gene_1797 GeneM ark.hmm 759_nt + 5442 6200	75 9	399 220 7	210	69. 3	6.11	117 411 44	969	10 8.7 4	6.76	0. 65	939 798 1	646	90. 56	6.5	0. 39	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1798 GeneM ark.hmm 1989_nt + 6202 8190	19 89	399 220 7	469	59. 06	5.88	117 411 44	249 2	10 6.7 1	6.74	0. 86	939 798 1	126 0	67. 41	6.07	0. 19	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1630 GeneM ark.hmm 510_nt - 39231 39740	51 0	399 220 7	8	3.9 3	1.97	117 411 44	248	41. 42	5.37	3. 4	939 798 1	102	21. 28	4.41	2. 44	---	---	---	---
gene_179 GeneMa rk.hmm 993_nt + 2 9835 30827	99 3	399 220 7	343 2	86 5.7 4	9.76	117 411 44	111 32	95 4.8	9.9	0. 14	939 798 1	691 9	74 1.4 1	9.53	- 0. 23	Asparagine synthetase A	METABOLISM	Amino acid transport and metabolism	E
gene_17 GeneMar k.hmm 639_nt - 10166 10804	63 9	399 220 7	598	23 4.4 2	7.87	117 411 44	185 6	24 7.3 8	7.95	0. 08	939 798 1	126 5	21 0.6 5	7.72	- 0. 15	Uridine kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_207 GeneMa rk.hmm 552_nt + 6 2742 63293	55 2	399 220 7	45	20. 42	4.35	117 411 44	868	13 3.9 3	7.07	2. 72	939 798 1	579	11 1.6 1	6.8	2. 45	---	---	---	---
gene_1801 GeneM ark.hmm 660_nt + 10809 11468	66 0	399 220 7	103 7	39 3.5 7	8.62	117 411 44	663	85. 56	6.42	- 2. 2	939 798 1	132 8	21 4.1	7.74	- 0. 88	Arginine/lysine/ornithine decarboxylases	METABOLISM	Amino acid transport and metabolism	E
gene_1802 GeneM ark.hmm 117_nt + 11631 11747	11 7	399 220 7	16	34. 25	5.1	117 411 44	14	10. 19	3.35	- 1. 75	939 798 1	10	9.0 9	3.18	- 1. 92	Arginine/lysine/ornithine decarboxylases	METABOLISM	Amino acid transport and metabolism	E
gene_1803 GeneM ark.hmm 522_nt + 11991 12512	52 2	399 220 7	467	22 4.1	7.81	117 411 44	451	73. 59	6.2	- 1. 61	939 798 1	108 5	22 1.1 7	7.79	- 0. 02	Arginine/lysine/ornithine decarboxylases	METABOLISM	Amino acid transport and metabolism	E
gene_1804 GeneM ark.hmm 207_nt - 13025 13231	20 7	399 220 7	65	78. 66	6.3	117 411 44	90	37. 03	5.21	- 1. 09	939 798 1	159	81. 73	6.35	0. 05	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1805 GeneM ark.hmm 63_nt - 13380 13442	63	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1806 GeneM ark.hmm 138_nt + 13528 13665	13 8	399 220 7	21	38. 12	5.25	117 411 44	196	12 0.9 7	6.92	1. 67	939 798 1	167	12 8.7 7	7.01	1. 76	NA			

gene_1807 GeneM ark.hmm 291_nt + 13696 13986	29 1	399 220 7	138	11 8.7 9	6.89	117 411 44	225	65. 85	6.04	- 0. 85	939 798 1	473	17 2.9 6	7.43	0. 54	Spermidine synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1808 GeneM ark.hmm 534_nt + 14106 14639	53 4	399 220 7	105 6	49 5.3 5	8.95	117 411 44	842	13 4.3	7.07	- 1. 88	939 798 1	214 0	42 6.4 2	8.74	- 0. 21	Spermidine synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1809 GeneM ark.hmm 294_nt + 14636 14929	29 4	399 220 7	347	29 5.6 4	8.21	117 411 44	458	13 2.6 8	7.05	- 1. 16	939 798 1	105 8	38 2.9 2	8.58	0. 37	Saccharopine dehydrogenase and related proteins	METABOLISM	Amino acid transport and metabolism	E
gene_180 GeneMa rk.hmm 540_nt + 3 0892 31431	54 0	399 220 7	245	11 3.6 5	6.83	117 411 44	760	11 9.8 7	6.91	0. 08	939 798 1	637	12 5.5 2	6.97	0. 14	N6-adenine-specific methylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1810 GeneM ark.hmm 957_nt + 15009 15965	95 7	399 220 7	108 0	28 2.6 8	8.14	117 411 44	133 6	11 8.9	6.89	- 1. 25	939 798 1	303 5	33 7.4 5	8.4	0. 26	Saccharopine dehydrogenase and related proteins	METABOLISM	Amino acid transport and metabolism	E
gene_1811 GeneM ark.hmm 1128_nt + 15965 17092	11 28	399 220 7	155 2	34 4.6 4	8.43	117 411 44	182 3	13 7.6 5	7.1	- 1. 33	939 798 1	432 8	40 8.2 7	8.67	0. 24	Diaminopimelate decarboxylase	METABOLISM	Amino acid transport and metabolism	E
gene_1812 GeneM ark.hmm 1086_nt + 17089 18174	10 86	399 220 7	311 7	71 8.9 4	9.49	117 411 44	324 2	25 4.2 6	7.99	- 1. 5	939 798 1	845 4	82 8.3 2	9.69	0. 2	Peptidylarginine deiminase and related enzymes	METABOLISM	Amino acid transport and metabolism	E
gene_1813 GeneM ark.hmm 876_nt + 18184 19059	87 6	399 220 7	235 2	67 2.5 4	9.39	117 411 44	245 4	23 8.5 9	7.9	- 1. 49	939 798 1	673 3	81 7.8 4	9.68	0. 29	Predicted amidohydrolase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1814 GeneM ark.hmm 897_nt - 19191 20087	89 7	399 220 7	566	15 8.0 6	7.3	117 411 44	182 7	17 3.4 7	7.44	0. 14	939 798 1	595	70. 58	6.14	- 1. 16	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1815 GeneM ark.hmm 306_nt + 21000 21305	30 6	399 220 7	6	4.9 1	2.3	117 411 44	72	20. 04	4.32	2. 02	939 798 1	44	15. 3	3.94	1. 64	Predicted metal-dependent membrane protease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1816 GeneM ark.hmm 909_nt + 21547 22455	90 9	399 220 7	450	12 4	6.95	117 411 44	165 4	15 4.9 7	7.28	0. 33	939 798 1	144 2	16 8.8	7.4	0. 45	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1817 GeneM ark.hmm 462_nt + 22452 22913	46 2	399 220 7	71	38. 49	5.27	117 411 44	422	77. 8	6.28	1. 01	939 798 1	322	74. 16	6.21	0. 94	Lipoprotein signal peptidase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1818 GeneM ark.hmm 111_nt + 22903 23013	11 1	399 220 7	7	15. 8	3.98	117 411 44	26	19. 95	4.32	0. 34	939 798 1	43	41. 22	5.37	1. 39	Pseudouridylate synthases, 23S RNA-specific	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1819 GeneM ark.hmm 774_nt + 23068 23841	77 4	399 220 7	153	49. 52	5.63	117 411 44	115 6	12 7.2 1	6.99	1. 36	939 798 1	133 2	18 3.1 2	7.52	1. 89	Pseudouridylate synthases, 23S RNA-specific	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_181 GeneMa rk.hmm 489_nt + 3 1421 31909	48 9	399 220 7	185	94. 77	6.57	117 411 44	509	88. 65	6.47	- 0. 1	939 798 1	597	12 9.9 1	7.02	0. 45	Phosphopantetheine adenylyltransferase	METABOLISM	Coenzyme transport and metabolism	H

gene_1820 GeneM ark.hmm 1896_nt + 23844 25739	18 96	399 220 7	107 0	14 1.3 6	7.14	117 411 44	548 8	24 6.5 3	7.95	0. 81	939 798 1	604 9	33 9.4 8	8.41	1. 27	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1821 GeneM ark.hmm 1110_nt + 25840 26949	11 10	399 220 7	176	39. 72	5.31	117 411 44	964	73. 97	6.21	0. 9	939 798 1	642	61. 54	5.94	0. 63	Glutamate 5-kinase	METABOLISM	Amino acid transport and metabolism	E
gene_1822 GeneM ark.hmm 1263_nt + 26959 28221	12 63	399 220 7	345	68. 42	6.1	117 411 44	130 1	87. 73	6.46	0. 36	939 798 1	124 1	10 4.5 5	6.71	0. 61	Gamma-glutamyl phosphate reductase	METABOLISM	Amino acid transport and metabolism	E
gene_1823 GeneM ark.hmm 798_nt + 28225 29022	79 8	399 220 7	389	12 2.1 1	6.93	117 411 44	119 0	12 7.0 1	6.99	0. 06	939 798 1	108 6	14 4.8 1	7.18	0. 25	Pyrroline-5-carboxylate reductase	METABOLISM	Amino acid transport and metabolism	E
gene_1824 GeneM ark.hmm 639_nt + 29242 29880	63 9	399 220 7	172	67. 42	6.08	117 411 44	576	76. 77	6.26	0. 18	939 798 1	470	78. 26	6.29	0. 21	Thymidylate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_1825 GeneM ark.hmm 1225_nt + 29877 30101	22 5	399 220 7	62	69. 02	6.11	117 411 44	111	42. 02	5.39	0. 72	939 798 1	124	58. 64	5.87	- 0. 24	ATPase involved in DNA replication	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1826 GeneM ark.hmm 660_nt + 30157 30816	66 0	399 220 7	341	12 9.4 2	7.02	117 411 44	984	12 6.9 8	6.99	- 0. 03	939 798 1	104 0	16 7.6 7	7.39	0. 37	ATPase involved in DNA replication	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1827 GeneM ark.hmm 318_nt + 30856 31173	31 8	399 220 7	282	22 2.1 3	7.8	117 411 44	376	10 0.7	6.65	- 1. 15	939 798 1	359	12 0.1 2	6.91	- 0. 89	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1828 GeneM ark.hmm 870_nt + 31176 32045	87 0	399 220 7	735	21 1.6 2	7.73	117 411 44	116 4	11 3.9 5	6.83	- 0. 9	939 798 1	102 9	12 5.8 5	6.98	- 0. 75	Predicted methyltransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1829 GeneM ark.hmm 519_nt + 32272 32790	51 9	399 220 7	900	43 4.3 7	8.76	117 411 44	151 8	24 9.1 1	7.96	- 0. 8	939 798 1	133 1	27 2.8 8	8.09	- 0. 67	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_182 GeneMa rk.hmm 1038_nt + 31893 32930	10 38	399 220 7	610	14 7.2	7.2	117 411 44	117 2	96. 17	6.59	- 0. 61	939 798 1	157 5	16 1.4 5	7.33	0. 13	Predicted secreted protein containing a PDZ domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_781 GeneMa rk.hmm 1974_nt + 157609 159582	19 74	399 220 7	20	2.5 4	1.34	117 411 44	587	25. 33	4.66	3. 32	939 798 1	257	13. 85	3.79	2. 45	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1831 GeneM ark.hmm 138_nt - 33835 33972	13 8	399 220 7	32	58. 08	5.86	117 411 44	137	84. 55	6.4	0. 54	939 798 1	76	58. 6	5.87	0. 01	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1832 GeneM ark.hmm 153_nt - 3 155	15 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	---	---	---	---
gene_1833 GeneM ark.hmm 537_nt - 277 813	53 7	399 220 7	109 4	51 0.3 1	9	117 411 44	793 4	12 58. 37	10.3	1. 3	939 798 1	907 9	17 98. 99	10.8 1	1. 81	Transcription antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K

gene_1834 GeneM ark.hmm 177_nt - 868 1044	17 7	399 220 7	94	13 3.0 3	7.06	117 411 44	264	12 7.0 3	6.99	- 0. 07	939 798 1	209	12 5.6 4	6.97	- 0. 09	Preprotein translocase subunit SecE	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_1835 GeneM ark.hmm 2196_nt - 1259 3454	21 96	399 220 7	228 2	26 0.3	8.02	117 411 44	119 59	46 3.8 2	8.86	0. 84	939 798 1	140 74	68 1.9 5	9.41	1. 39	Membrane carboxypeptidase (penicillin-binding protein)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1836 GeneM ark.hmm 756_nt + 3661 4416	75 6	399 220 7	160 8	53 2.7 8	9.06	117 411 44	443 5	49 9.6 4	8.96	- 0. 1	939 798 1	251 8	35 4.4	8.47	- 0. 59	Pseudouridylate synthases, 23S RNA-specific	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1837 GeneM ark.hmm 1008_nt - 4484 5491	10 08	399 220 7	859 13	21 34 9.3 8	14.3 8	117 411 44	204 983	17 31 9.9 6	14.0 8	- 0. 3	939 798 1	127 104	13 41 7.2 7	13.7 1	- 0. 67	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4- phosphate dehydrogenase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1838 GeneM ark.hmm 426_nt - 5668 6093	42 6	399 220 7	257	15 1.1 2	7.24	117 411 44	126 6	25 3.1 1	7.98	0. 74	939 798 1	624	15 5.8 6	7.28	0. 04	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1839 GeneM ark.hmm 507_nt - 6112 6618	50 7	399 220 7	474	23 4.1 8	7.87	117 411 44	250 8	42 1.3 2	8.72	0. 85	939 798 1	135 8	28 5.0 1	8.15	0. 28	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_183 GeneMa rk.hmm 858_nt + 3 3242 34099	85 8	399 220 7	567	16 5.5 3	7.37	117 411 44	152 3	15 1.1 8	7.24	- 0. 13	939 798 1	170 6	21 1.5 7	7.73	0. 36	UDP-N-acetylglucosamine enolpyruvyl transferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1840 GeneM ark.hmm 345_nt - 6704 7048	34 5	399 220 7	607	44 0.7 1	8.78	117 411 44	331 2	81 7.6 4	9.68	0. 9	939 798 1	148 1	45 6.7 7	8.84	0. 06	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_956 GeneMa rk.hmm 189_nt + 5 6375 56563	18 9	399 220 7	28	37. 11	5.21	117 411 44	122 1	55 0.2 3	9.1	3. 89	939 798 1	362	20 3.8	7.67	2. 46	Na+/serine symporter	METABOLISM	Amino acid transport and metabolism	E
gene_1842 GeneM ark.hmm 1488_nt - 3566 5053	14 88	399 220 7	58	9.7 6	3.29	117 411 44	590	33. 77	5.08	1. 79	939 798 1	383	27. 39	4.78	1. 49	ABC-type Fe3+ transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1843 GeneM ark.hmm 1005_nt - 5272 6276	10 05	399 220 7	60	14. 95	3.9	117 411 44	521	44. 15	5.46	1. 56	939 798 1	357	37. 8	5.24	1. 34	ABC-type spermidine/putrescine transport systems, ATPase components	METABOLISM	Amino acid transport and metabolism	E
gene_1844 GeneM ark.hmm 1062_nt - 6293 7354	10 62	399 220 7	51	12. 03	3.59	117 411 44	585	46. 92	5.55	1. 96	939 798 1	396	39. 68	5.31	1. 72	ABC-type Fe3+ transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1845 GeneM ark.hmm 894_nt - 7312 8205	89 4	399 220 7	26	7.2 8	2.86	117 411 44	282	26. 87	4.75	1. 89	939 798 1	213	25. 35	4.66	1. 8	NA			
gene_1846 GeneM ark.hmm 312_nt - 8644 8955	31 2	399 220 7	34	27. 3	4.77	117 411 44	248	67. 7	6.08	1. 31	939 798 1	170	57. 98	5.86	1. 09	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_1847 GeneM ark.hmm 459_nt + 9216 9674	45 9	399 220 7	104 3	56 9.1 9	9.15	117 411 44	180 3	33 4.5 6	8.39	- 0. 76	939 798 1	330	76. 5	6.26	- 2. 89	---	---	---	---
gene_1848 GeneM ark.hmm 609_nt + 9687 10295	60 9	399 220 7	202 1	83 1.2 6	9.7	117 411 44	238 1	33 2.9 9	8.38	- 1. 32	939 798 1	872	15 2.3 6	7.25	- 2. 45	---	---	---	---
gene_1849 GeneM ark.hmm 411_nt + 10288 10698	41 1	399 220 7	166 7	10 15. 97	9.99	117 411 44	157 3	32 5.9 7	8.35	- 1. 64	939 798 1	786	20 3.4 9	7.67	- 2. 32	---	---	---	---
gene_184 GeneMa rk.hmm 573_nt + 3 3996 34568	57 3	399 220 7	102 1	44 6.3 3	8.8	117 411 44	248 9	36 9.9 6	8.53	- 0. 27	939 798 1	277 3	51 4.9 4	9.01	0. 21	UDP-N-acetylglucosamine enolpyruvyl transferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1850 GeneM ark.hmm 1416_nt + 10709 12124	14 16	399 220 7	465 1	82 2.7 5	9.68	117 411 44	619 6	37 2.6 8	8.54	- 1. 14	939 798 1	321 3	24 1.4 4	7.92	- 1. 76	---	---	---	---
gene_1851 GeneM ark.hmm 717_nt + 13005 13721	71 7	399 220 7	445 4	15 56. 03	10.6	117 411 44	986 8	11 72. 19	10.1 9	- 0. 41	939 798 1	390 3	57 9.2 2	9.18	- 1. 42	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2261 GeneM ark.hmm 1320_nt - 85906 87225	13 20	399 220 7	23	4.3 6	2.13	117 411 44	659	42. 52	5.41	3. 28	939 798 1	300	24. 18	4.6	2. 47	Alpha-L-fucosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1853 GeneM ark.hmm 363_nt + 14030 14392	36 3	399 220 7	40	27. 6	4.79	117 411 44	296	69. 45	6.12	1. 33	939 798 1	282	82. 66	6.37	1. 58	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1854 GeneM ark.hmm 504_nt + 14389 14892	50 4	399 220 7	30	14. 91	3.9	117 411 44	289	48. 84	5.61	1. 71	939 798 1	280	59. 11	5.89	1. 99	Membrane-associated phospholipid phosphatase	METABOLISM	Lipid transport and metabolism	I
gene_1855 GeneM ark.hmm 447_nt + 15006 15452	44 7	399 220 7	717	40 1.7 9	8.65	117 411 44	154 4	29 4.1 9	8.2	- 0. 45	939 798 1	314 5	74 8.6 5	9.55	0. 9	Response regulator of the LytR/AlgR family	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1856 GeneM ark.hmm 675_nt + 15458 16132	67 5	399 220 7	745	27 6.4 6	8.11	117 411 44	181 5	22 9.0 1	7.84	- 0. 27	939 798 1	276 6	43 6.0 3	8.77	0. 66	---	---	---	---
gene_1857 GeneM ark.hmm 102_nt + 16383 16484	10 2	399 220 7	2	4.9 1	2.3	117 411 44	12	10. 02	3.32	1. 02	939 798 1	19	19. 82	4.31	2. 01	NA			
gene_1858 GeneM ark.hmm 276_nt + 16793 17068	27 6	399 220 7	182	16 5.1 8	7.37	117 411 44	934	28 8.2 2	8.17	0. 8	939 798 1	551	21 2.4 3	7.73	0. 36	---	---	---	---
gene_1859 GeneM ark.hmm 318_nt + 17065 17382	31 8	399 220 7	526	41 4.3 3	8.69	117 411 44	107 2	28 7.1 2	8.17	- 0. 52	939 798 1	576	19 2.7 4	7.59	- 1. 1	Thiol-disulfide isomerase and thioredoxins	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_185 GeneMa rk.hmm 195_nt + 3 4555 34749	19 5	399 220 7	131	16 8.2 8	7.39	117 411 44	410	17 9.0 8	7.48	0. 09	939 798 1	542	29 5.7 5	8.21	0. 82	---	---	---	---

gene_1860 GeneM ark.hmm 627_nt + 17398 18024	62 7	399 220 7	701	28 0.0 5	8.13	117 411 44	232 8	31 6.2 3	8.3	0. 17	939 798 1	178 6	30 3.1	8.24	0. 11	EMAP domain	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1861 GeneM ark.hmm 762_nt + 18057 18818	76 2	399 220 7	682	22 4.1 9	7.81	117 411 44	143 7	16 0.6 2	7.33	- 0. 48	939 798 1	145 3	20 2.9	7.66	- 0. 15	Short-chain alcohol dehydrogenase of unknown specificity	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1862 GeneM ark.hmm 396_nt + 18895 19290	39 6	399 220 7	46	29. 1	4.86	117 411 44	368	79. 15	6.31	1. 45	939 798 1	519	13 9.4 6	7.12	2. 26	Single-stranded DNA-binding protein	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1863 GeneM ark.hmm 285_nt + 19560 19844	28 5	399 220 7	405 9	35 67. 48	11.8	117 411 44	608 5	18 18. 47	10.8 3	- 0. 97	939 798 1	158 4	59 1.3 9	9.21	- 2. 59	Co-chaperonin GroES (HSP10)	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1864 GeneM ark.hmm 1623_nt + 19860 21482	16 23	399 220 7	152 66	23 56. 1	11.2	117 411 44	261 25	13 70. 97	10.4 2	- 0. 78	939 798 1	100 13	65 6.4 6	9.36	- 1. 84	Chaperonin GroEL (HSP60 family)	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1865 GeneM ark.hmm 105_nt + 21620 21724	10 5	399 220 7	13	31. 01	4.95	117 411 44	22	17. 85	4.16	- 0. 79	939 798 1	14	14. 19	3.83	- 1. 12	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1866 GeneM ark.hmm 210_nt + 21740 21949	21 0	399 220 7	120	14 3.1 4	7.16	117 411 44	474	19 2.2 4	7.59	0. 43	939 798 1	308	15 6.0 6	7.29	0. 13	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1867 GeneM ark.hmm 246_nt + 22049 22294	24 6	399 220 7	345	35 1.2 9	8.46	117 411 44	587	20 3.2 3	7.67	- 0. 79	939 798 1	473	20 4.5 9	7.68	- 0. 78	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_731 GeneMa rk.hmm 2439_nt + 103483 105921	24 39	399 220 7	230	23. 62	4.56	117 411 44	456 8	15 9.5 2	7.32	2. 76	939 798 1	299 8	13 0.7 9	7.03	2. 47	Pyruvate-formate lyase	METABOLISM	Energy production and conversion	C
gene_1869 GeneM ark.hmm 534_nt - 24821 25354	53 4	399 220 7	274 9	12 89. 5	10.3 3	117 411 44	154 71	24 67. 55	11.2 7	0. 94	939 798 1	527 8	10 51. 7	10.0 4	- 0. 29	Uncharacterized domain/protein associated with RNAses G and E	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_186 GeneMa rk.hmm 825_nt + 3 4788 35612	82 5	399 220 7	705	21 4.0 5	7.74	117 411 44	219 6	22 6.7 1	7.82	0. 08	939 798 1	278 7	35 9.4 6	8.49	0. 75	---	---	---	---
gene_1870 GeneM ark.hmm 735_nt - 25443 26177	73 5	399 220 7	346	11 7.9 2	6.88	117 411 44	113 2	13 1.1 7	7.04	0. 16	939 798 1	374	54. 14	5.76	- 1. 12	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1871 GeneM ark.hmm 804_nt + 26302 27105	80 4	399 220 7	482	15 0.1 7	7.23	117 411 44	168 7	17 8.7 1	7.48	0. 25	939 798 1	614	81. 26	6.34	- 0. 89	SAM-dependent methyltransferases related to tRNA (uracil-5-)- methyltransferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1872 GeneM ark.hmm 435_nt + 27178 27612	43 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	SAM-dependent methyltransferases related to tRNA (uracil-5-)- methyltransferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1873 GeneM ark.hmm 1779_nt - 1 1779	17 79	399 220 7	611 5	86 1.0 1	9.75	117 411 44	280 20	13 41. 47	10.3 9	0. 64	939 798 1	166 05	99 3.1 8	9.96	0. 21	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R

gene_1874 GeneM ark.hmm 528_nt - 1858 2385	52 8	399 220 7	67	31. 79	4.99	117 411 44	477	76. 94	6.27	1. 28	939 798 1	348	70. 13	6.13	1. 14	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1875 GeneM ark.hmm 1179_nt - 2480 3658	11 79	399 220 7	380	80. 73	6.34	117 411 44	420 5	30 3.7 7	8.25	1. 91	939 798 1	317 0	28 6.1	8.16	1. 82	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1876 GeneM ark.hmm 654_nt - 3808 4461	65 4	399 220 7	269	10 3.0 3	6.69	117 411 44	215 4	28 0.5 2	8.13	1. 44	939 798 1	157 7	25 6.5 8	8	1. 31	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1877 GeneM ark.hmm 1911_nt - 4782 6692	19 11	399 220 7	190 5	24 9.7	7.96	117 411 44	736 9	32 8.4 3	8.36	0. 4	939 798 1	569 9	31 7.3 2	8.31	0. 35	ATPases with chaperone activity, ATP-binding subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1878 GeneM ark.hmm 579_nt - 6658 7236	57 9	399 220 7	283	12 2.4 3	6.94	117 411 44	117 0	17 2.1 1	7.43	0. 49	939 798 1	762	14 0.0 4	7.13	0. 19	ATPases with chaperone activity, ATP-binding subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1879 GeneM ark.hmm 459_nt - 7238 7696	45 9	399 220 7	108	58. 94	5.88	117 411 44	622	11 5.4 2	6.85	0. 97	939 798 1	286	66. 3	6.05	0. 17	Transcriptional repressor of class III stress genes	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_187 GeneMa rk.hmm 1332_nt + 35903 37234	13 32	399 220 7	134 6	25 3.1 2	7.98	117 411 44	580 4	37 1.1 2	8.54	0. 56	939 798 1	672 8	53 7.4 6	9.07	1. 09	Hemolysins and related proteins containing CBS domains	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1880 GeneM ark.hmm 729_nt - 7815 8543	72 9	399 220 7	988	33 9.4 8	8.41	117 411 44	315 0	36 8.0 2	8.52	0. 11	939 798 1	170 3	24 8.5 7	7.96	- 0. 45	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1881 GeneM ark.hmm 1008_nt - 8543 9550	10 08	399 220 7	867	21 5.4 5	7.75	117 411 44	271 6	22 9.4 9	7.84	0. 09	939 798 1	137 2	14 4.8 3	7.18	- 0. 57	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	METABOLISM	Inorganic ion transport and metabolism	P
gene_1882 GeneM ark.hmm 759_nt - 9589 10347	75 9	399 220 7	274	90. 43	6.5	117 411 44	698	78. 33	6.29	- 0. 21	939 798 1	376	52. 71	5.72	- 0. 78	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1883 GeneM ark.hmm 291_nt - 10310 10600	29 1	399 220 7	143	12 3.0 9	6.94	117 411 44	437	12 7.9	7	0. 06	939 798 1	233	85. 2	6.41	- 0. 53	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_84 GeneMar k.hmm 633_nt - 57426 58058	63 3	399 220 7	28	11. 08	3.47	117 411 44	597	80. 33	6.33	2. 86	939 798 1	368	61. 86	5.95	2. 48	Isopropylmalate/homocitrate/citrama late synthases	METABOLISM	Amino acid transport and metabolism	E
gene_1585 GeneM ark.hmm 579_nt - 5635 6213	57 9	399 220 7	81	35. 04	5.13	117 411 44	100 2	14 7.3 9	7.2	2. 07	939 798 1	106 3	19 5.3 5	7.61	2. 48	---	---	---	---
gene_2378 GeneM ark.hmm 114_nt +	11 4	399 220	0	0	0	117 411	15	11. 21	3.49	3. 49	939 798	6	5.6	2.49	2. 49	NA			

2 115		7				44					1								
gene_1917 GeneM ark.hmm 768_nt - 43911 44678	76 8	399 220 7	43	14. 02	3.81	117 411 44	747	82. 84	6.37	2. 56	939 798 1	572	79. 25	6.31	2. 5	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1888 GeneM ark.hmm 1353_nt - 12676 14028	13 53	399 220 7	141 1	26 1.2 3	8.03	117 411 44	766 9	48 2.7 6	8.92	0. 89	939 798 1	559 0	43 9.6 2	8.78	0. 75	Replicative DNA helicase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1889 GeneM ark.hmm 453_nt - 14072 14524	45 3	399 220 7	297	16 4.2 3	7.36	117 411 44	194 1	36 4.9 4	8.51	1. 15	939 798 1	130 7	30 7	8.26	0. 9	Ribosomal protein L9	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_188 GeneMa rk.hmm 3612_nt + 37918 41529	36 12	399 220 7	202 45	14 03. 97	10.4 6	117 411 44	199 67	47 0.8 2	8.88	- 1. 58	939 798 1	352 60	10 38. 72	10.0 2	- 0. 44	DNA-directed RNA polymerase, beta subunit/140 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1890 GeneM ark.hmm 1812_nt - 14521 16332	18 12	399 220 7	179 7	24 8.4 1	7.96	117 411 44	143 37	67 3.8 9	9.4	1. 44	939 798 1	885 4	51 9.9 3	9.02	1. 06	Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1891 GeneM ark.hmm 549_nt - 16631 17179	54 9	399 220 7	627 6	28 63. 5	11.4 8	117 411 44	127 09	19 71. 64	10.9 5	- 0. 53	939 798 1	201 5	39 0.5 4	8.61	- 2. 87	Ribosome-associated protein Y (PSrp-1)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1387 GeneM ark.hmm 651_nt - 96876 97526	65 1	399 220 7	73	28. 09	4.81	117 411 44	135 4	17 7.1 4	7.47	2. 66	939 798 1	970	15 8.5 5	7.31	2. 5	Protoheme ferro-lyase (ferrochelataase)	METABOLISM	Coenzyme transport and metabolism	H
gene_1976 GeneM ark.hmm 1086_nt - 3949 5034	10 86	399 220 7	37	8.5 3	3.09	117 411 44	663	52	5.7	2. 61	939 798 1	501	49. 09	5.62	2. 53	Phosphotransferase system, fructose-specific IIC component	METABOLISM	Carbohydrate transport and metabolism	G
gene_1894 GeneM ark.hmm 636_nt + 19272 19907	63 6	399 220 7	534	21 0.3 2	7.72	117 411 44	154 5	20 6.9	7.69	- 0. 03	939 798 1	474	79. 3	6.31	- 1. 41	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1895 GeneM ark.hmm 921_nt + 20192 21112	92 1	399 220 7	847	23 0.3 6	7.85	117 411 44	290 9	26 9.0 1	8.07	0. 22	939 798 1	137 5	15 8.8 6	7.31	- 0. 54	Cysteine synthase	METABOLISM	Amino acid transport and metabolism	E
gene_1896 GeneM ark.hmm 399_nt - 21309 21707	39 9	399 220 7	20	12. 56	3.65	117 411 44	159	33. 94	5.08	1. 43	939 798 1	112	29. 87	4.9	1. 25	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1897 GeneM ark.hmm 120_nt - 22416 22535	12 0	399 220 7	6	12. 52	3.65	117 411 44	20	14. 2	3.83	0. 18	939 798 1	8	7.0 9	2.83	- 0. 82	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1898 GeneM ark.hmm 114_nt - 22762 22875	11 4	399 220 7	7	15. 38	3.94	117 411 44	26	19. 42	4.28	0. 34	939 798 1	16	14. 93	3.9	- 0. 04	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1899 GeneM ark.hmm 1041_nt - 23121 24161	10 41	399 220 7	134 11	32 26. 99	11.6 6	117 411 44	403 98	33 05. 21	11.6 9	0. 03	939 798 1	386 55	39 51. 12	11.9 5	0. 29	Translation elongation factor Ts	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_189 GeneMa rk.hmm 3678_nt +	36 78	399 220	185 65	12 64.	10.3	117 411	191 29	44 2.9	8.79	- 1.	939 798	365 24	10 56.	10.0 5	- 0.	DNA-directed RNA polymerase, beta' subunit/160 kD subunit	INFORMATION STORAGE AND	Transcription	K

41562 45239		7		36		44		7		51	1		65		25		PROCESSING		
gene_18 GeneMar k.hmm 303_nt - 10912 11214	30 3	399 220 7	126 2	10 43. 29	10.0 3	117 411 44	346 9	97 5.1	9.93	- 0. 1	939 798 1	249 6	87 6.5 3	9.78	- 0. 25	---	---	---	---
gene_1900 GeneM ark.hmm 780_nt - 24240 25019	78 0	399 220 7	144 32	46 34. 67	12.1 8	117 411 44	492 95	53 82. 67	12.3 9	0. 21	939 798 1	579 05	78 99. 27	12.9 5	0. 77	Ribosomal protein S2	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1901 GeneM ark.hmm 1179_nt - 25243 26421	11 79	399 220 7	322 77	68 57. 51	12.7 4	117 411 44	525 86	37 98. 8	11.8 9	- 0. 85	939 798 1	118 22	10 66. 95	10.0 6	- 2. 68	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1902 GeneM ark.hmm 819_nt - 27009 27827	81 9	399 220 7	110 8	33 8.8 8	8.4	117 411 44	445 5	46 3.2 9	8.86	0. 46	939 798 1	548 8	71 3.0 1	9.48	1. 08	Cell shape-determining protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1903 GeneM ark.hmm 795_nt - 27886 28680	79 5	399 220 7	243	76. 56	6.26	117 411 44	100 0	10 7.1 3	6.74	0. 48	939 798 1	107 6	14 4.0 2	7.17	0. 91	ABC-type cobalt transport system, permease component CbiQ and related transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_1904 GeneM ark.hmm 840_nt - 28673 29512	84 0	399 220 7	101 5	30 2.6 7	8.24	117 411 44	382 2	38 7.5 3	8.6	0. 36	939 798 1	386 7	48 9.8 5	8.94	0. 7	ABC-type cobalt transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1905 GeneM ark.hmm 828_nt - 29497 30324	82 8	399 220 7	682	20 6.3 2	7.69	117 411 44	288 7	29 6.9 7	8.21	0. 52	939 798 1	243 4	31 2.7 9	8.29	0. 6	ABC-type cobalt transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1906 GeneM ark.hmm 546_nt - 30321 30866	54 6	399 220 7	208	95. 42	6.58	117 411 44	820	12 7.9 1	7	0. 42	939 798 1	534	10 4.0 7	6.7	0. 12	Phosphatidylglycerophosphate synthase	METABOLISM	Lipid transport and metabolism	I
gene_1907 GeneM ark.hmm 822_nt - 30877 31698	82 2	399 220 7	644	19 6.2 5	7.62	117 411 44	320 0	33 1.5 6	8.37	0. 75	939 798 1	212 6	27 5.2 1	8.1	0. 48	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1908 GeneM ark.hmm 1284_nt - 31740 33023	12 84	399 220 7	135 5	26 4.3 4	8.05	117 411 44	787 0	52 2.0 3	9.03	0. 98	939 798 1	651 0	53 9.4 9	9.08	1. 03	Predicted Zn-dependent peptidases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1909 GeneM ark.hmm 1251_nt - 33020 34270	12 51	399 220 7	115 7	23 1.6 7	7.86	117 411 44	124 52	84 7.7 6	9.73	1. 87	939 798 1	868 3	73 8.5 5	9.53	1. 67	Predicted Zn-dependent peptidases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_190 GeneMa rk.hmm 414_nt + 4 5350 45763	41 4	399 220 7	466	28 1.9 5	8.14	117 411 44	627	12 8.9 9	7.01	- 1. 13	939 798 1	858	22 0.5 2	7.78	- 0. 36	Nucleoside diphosphate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_1910 GeneM ark.hmm 369_nt + 34429 34797	36 9	399 220 7	291	19 7.5 4	7.63	117 411 44	233 2	53 8.2 6	9.07	1. 44	939 798 1	109 3	31 5.1 8	8.3	0. 67	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1911 GeneM ark.hmm 984_nt + 34914 35897	98 4	399 220 7	710	18 0.7 4	7.5	117 411 44	395 6	34 2.4 1	8.42	0. 92	939 798 1	215 0	23 2.4 9	7.86	0. 36	Recombinational DNA repair ATPase (RecF pathway)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1912 GeneM ark.hmm 1479_nt -	14 79	399 220	229 3	38 8.3	8.6	117 411	117 35	67 5.7	9.4	0. 8	939 798	497 9	35 8.2	8.48	- 0.	IMP dehydrogenase/GMP reductase	METABOLISM	Nucleotide transport and metabolism	F

[35948 37426		7		5		44		8			1		1		12				
gene_1913 GeneMark.hmm 1026_nt - 37578 38603	1026	3992207	1276	311.52	8.28	11741144	3487	289.46	8.18	-0.1	9397981	1902	197.26	7.62	-0.66	Tryptophanyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1914 GeneMark.hmm 1623_nt + 38809 40431	1623	3992207	3952	609.94	9.25	11741144	14129	741.45	9.53	0.28	9397981	6444	422.48	8.72	-0.53	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZED	General function prediction only	R
gene_390 GeneMark.hmm 294_nt + 6106 6399	294	3992207	7	5.96	2.58	11741144	552	159.91	7.32	4.74	9397981	96	34.74	5.12	2.54	Phosphotransferase system cellobiose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G
gene_636 GeneMark.hmm 666_nt + 31851 32516	666	3992207	38	14.29	3.84	11741144	623	79.67	6.32	2.48	9397981	521	83.24	6.38	2.54	Predicted metal-dependent membrane protease	POORLY CHARACTERIZED	General function prediction only	R
gene_907 GeneMark.hmm 576_nt - 11060 11635	576	3992207	11	4.78	2.26	11741144	354	52.34	5.71	3.45	9397981	151	27.89	4.8	2.54	---	---	---	---
gene_1918 GeneMark.hmm 543_nt + 44857 45399	543	3992207	144	66.43	6.05	11741144	739	115.91	6.86	0.81	9397981	464	90.93	6.51	0.46	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1919 GeneMark.hmm 753_nt - 45642 46394	753	3992207	333	110.77	6.79	11741144	1086	122.84	6.94	0.15	9397981	846	119.55	6.9	0.11	Response regulator of the LytR/AlgR family	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_191 GeneMark.hmm 633_nt - 46691 47323	633	3992207	484	191.53	7.58	11741144	2173	292.38	8.19	0.61	9397981	1302	218.86	7.77	0.19	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1920 GeneMark.hmm 756_nt - 46391 47146	756	3992207	245	81.18	6.34	11741144	1258	141.73	7.15	0.81	9397981	1297	182.55	7.51	1.17	Predicted signal transduction protein with a C-terminal ATPase domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1921 GeneMark.hmm 126_nt - 47737 47862	126	3992207	10	19.88	4.31	11741144	45	30.42	4.93	0.62	9397981	54	45.6	5.51	1.2	NA			
gene_1922 GeneMark.hmm 480_nt - 48145 48624	480	3992207	108	56.36	5.82	11741144	767	136.1	7.09	1.27	9397981	329	72.93	6.19	0.37	Uncharacterized conserved protein	POORLY CHARACTERIZED	Function unknown	S
gene_1923 GeneMark.hmm 1182_nt + 48807 49988	1182	3992207	58476	12392.16	13.6	11741144	112326	8093.8	12.98	-0.62	9397981	60772	5470.81	12.42	-1.18	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1924 GeneMark.hmm 759_nt + 50046 50804	759	3992207	76037	25094.01	14.62	11741144	87284	9794.5	13.26	-1.36	9397981	39722	5568.71	12.44	-2.18	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1925 GeneMark.hmm 1362_nt + 51017 52378	1362	3992207	3489	641.67	9.33	11741144	16120	1008.04	9.98	0.65	9397981	18596	1452.81	10.5	1.17	ATPase involved in DNA replication initiation	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_1926 GeneM ark.hmm 1137_nt + 52537 53673	11 37	399 220 7	247 1	54 4.3 8	9.09	117 411 44	156 38	11 71 41	10.1 9	1. 1	939 798 1	160 50	15 02. 03	10.5 5	1. 46	DNA polymerase sliding clamp subunit (PCNA homolog)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1886 GeneM ark.hmm 558_nt - 11762 12319	55 8	399 220 7	22	9.8 8	3.3	117 411 44	327	49. 91	5.64	2. 34	939 798 1	302	57. 59	5.85	2. 55	Surface antigen	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1928 GeneM ark.hmm 1116_nt + 54016 55131	11 16	399 220 7	876	19 6.6 2	7.62	117 411 44	481 9	36 7.7 8	8.52	0. 9	939 798 1	319 2	30 4.3 4	8.25	0. 63	Predicted GTPase, probable translation factor	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1929 GeneM ark.hmm 570_nt + 55202 55771	57 0	399 220 7	123	54. 05	5.76	117 411 44	882	13 1.7 9	7.04	1. 28	939 798 1	598	11 1.6 3	6.8	1. 04	Peptidyl-tRNA hydrolase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_192 GeneMa rk.hmm 2016_nt - 47325 49340	20 16	399 220 7	148 0	18 3.8 9	7.52	117 411 44	645 0	27 2.5	8.09	0. 57	939 798 1	412 3	21 7.6 1	7.77	0. 25	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1930 GeneM ark.hmm 3510_nt + 55772 59281	35 10	399 220 7	941	67. 15	6.07	117 411 44	661 4	16 0.4 9	7.33	1. 26	939 798 1	467 1	14 1.6	7.15	1. 08	Transcription-repair coupling factor (superfamily II helicase)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1931 GeneM ark.hmm 267_nt + 59339 59605	26 7	399 220 7	554	51 9.7 4	9.02	117 411 44	467 4	14 90. 96	10.5 4	1. 52	939 798 1	161 9	64 5.2 1	9.33	0. 31	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1932 GeneM ark.hmm 369_nt + 59598 59966	36 9	399 220 7	424	28 7.8 2	8.17	117 411 44	331 6	76 5.3 8	9.58	1. 41	939 798 1	169 1	48 7.6 2	8.93	0. 76	Septum formation initiator	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_1933 GeneM ark.hmm 123_nt + 59971 60093	12 3	399 220 7	21	42. 77	5.42	117 411 44	140	96. 94	6.6	1. 18	939 798 1	65	56. 23	5.81	0. 39	NA			
gene_1934 GeneM ark.hmm 1269_nt + 60086 61354	12 69	399 220 7	139 5	27 5.3 6	8.11	117 411 44	119 95	80 5.0 6	9.65	1. 54	939 798 1	759 1	63 6.5 1	9.31	1. 2	Beta-lactamase class A	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_733 GeneMa rk.hmm 1089_nt + 106626 107714	10 89	399 220 7	183	42. 09	5.4	117 411 44	299 1	23 3.9 3	7.87	2. 47	939 798 1	254 1	24 8.2 8	7.96	2. 56	Glycerol dehydrogenase and related enzymes	METABOLISM	Energy production and conversion	C
gene_1936 GeneM ark.hmm 543_nt + 62632 63174	54 3	399 220 7	136 2	62 8.3	9.3	117 411 44	807 5	12 66. 58	10.3 1	1. 01	939 798 1	376 4	73 7.5 9	9.53	0. 23	Hypoxanthine-guanine phosphoribosyltransferase	METABOLISM	Nucleotide transport and metabolism	F
gene_1937 GeneM ark.hmm 1959_nt + 63190 65148	19 59	399 220 7	120 08	15 35. 41	10.5 8	117 411 44	487 31	21 18. 66	11.0 5	0. 47	939 798 1	218 82	11 88. 55	10.2 1	- 0. 37	ATP-dependent Zn proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1938 GeneM ark.hmm 87_nt + 9 6 182	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1939 GeneM ark.hmm 201_nt +	20 1	399 220	5	6.2 3	2.64	117 411	44	18. 64	4.22	1. 58	939 798	20	10. 59	3.4	0. 76	---	---	---	---

488 688		7				44					1								
gene_984 GeneMa rk.hmm 1482_nt - 78619 80100	14 82	399 220 7	28	4.7 3	2.24	117 411 44	972	55. 86	5.8	3. 56	939 798 1	388	27. 86	4.8	2. 56	---	---	---	
gene_1940 GeneM ark.hmm 417_nt + 713 1129	41 7	399 220 7	8	4.8 1	2.26	117 411 44	115	23. 49	4.55	2. 29	939 798 1	53	13. 52	3.76	1. 5	---	---	---	
gene_1941 GeneM ark.hmm 708_nt + 1360 2067	70 8	399 220 7	889	31 4.5 3	8.3	117 411 44	307 4	36 9.7 9	8.53	0. 23	939 798 1	499	75	6.23	- 2. 07	Cytochrome c biogenesis protein	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1942 GeneM ark.hmm 558_nt + 2078 2635	55 8	399 220 7	430 6	19 32. 98	10.9 2	117 411 44	675 5	10 31. 05	10.0 1	- 0. 91	939 798 1	146 9	28 0.1 3	8.13	- 2. 79	Thiol-disulfide isomerase and thioredoxins	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1943 GeneM ark.hmm 1392_nt + 3008 4399	13 92	399 220 7	385	69. 28	6.11	117 411 44	301 4	18 4.4 1	7.53	1. 42	939 798 1	146 5	11 1.9 9	6.81	0. 7	Amino acid transporters	METABOLISM	Amino acid transport and metabolism	E
gene_1944 GeneM ark.hmm 918_nt + 4542 5459	91 8	399 220 7	484	13 2.0 7	7.05	117 411 44	367 8	34 1.2 4	8.41	1. 36	939 798 1	338 7	39 2.5 9	8.62	1. 57	ABC-type metal ion transport system, periplasmic component/surface adhesin	METABOLISM	Inorganic ion transport and metabolism	P
gene_1945 GeneM ark.hmm 567_nt + 5467 6033	56 7	399 220 7	316	13 9.6	7.13	117 411 44	334 9	50 3.0 6	8.97	1. 84	939 798 1	250 9	47 0.8 5	8.88	1. 75	---	---	---	---
gene_1946 GeneM ark.hmm 180_nt + 3 182	18 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Uncharacterized protein with a von Willebrand factor type A (vWA) domain	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1947 GeneM ark.hmm 141_nt - 441 581	14 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1948 GeneM ark.hmm 186_nt - 2 187	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 7	- 0.81	- 0. 81	NA			
gene_1949 GeneM ark.hmm 156_nt - 426 581	15 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.3 6	0.45	0. 45	NA			
gene_2349 GeneM ark.hmm 108_nt - 2 109	10 8	399 220 7	0	0	0	117 411 44	8	6.3 1	2.66	2. 66	939 798 1	6	5.9 1	2.56	2. 56	NA			
gene_1950 GeneM ark.hmm 192_nt + 3 194	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 5	- 0.85	- 0. 85	NA			
gene_1951 GeneM ark.hmm 132_nt + 458 589	13 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2170 GeneM ark.hmm 444_nt +	44	399 220	16	9.0	3.17	117 411	240	46.	5.52	2.	939 798	222	53.	5.73	2.	Transposase and inactivated	INFORMATION STORAGE AND	Replication, recombination and	L

3 446	4	7		3		44		04		35	1		2		56	derivatives	PROCESSING	repair	
gene_1953 GeneM ark.hmm 87_nt + 1 87	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_519 GeneMa rk.hmm 414_nt 28892 29305	41 4	399 220 7	5	3.0 3	1.6	117 411 44	131	26. 95	4.75	3. 15	939 798 1	70	17. 99	4.17	2. 57	---	---	---	---
gene_1955 GeneM ark.hmm 156_nt 894 1049	15 6	399 220 7	3	4.8 2	2.27	117 411 44	16	8.7 4	3.13	0. 86	939 798 1	37	25. 24	4.66	2. 39	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1956 GeneM ark.hmm 936_nt 1256 2191	93 6	399 220 7	610	16 3.2 5	7.35	117 411 44	144 0	13 1.0 3	7.03	- 0. 32	939 798 1	101 6	11 5.5	6.85	- 0. 5	Biotin-(acetyl-CoA carboxylase) ligase	METABOLISM	Coenzyme transport and metabolism	H
gene_1957 GeneM ark.hmm 861_nt 2188 3048	86 1	399 220 7	108 5	31 5.6 6	8.3	117 411 44	194 7	19 2.6	7.59	- 0. 71	939 798 1	128 4	15 8.6 8	7.31	- 0. 99	AraC-type DNA-binding domain- containing proteins	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1958 GeneM ark.hmm 900_nt + 3156 4055	90 0	399 220 7	116	32. 29	5.01	117 411 44	125 3	11 8.5 8	6.89	1. 88	939 798 1	189	22. 35	4.48	- 0. 53	Alpha-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1959 GeneM ark.hmm 1224_nt + 4162 5385	12 24	399 220 7	174	35. 61	5.15	117 411 44	225 9	15 7.1 9	7.3	2. 15	939 798 1	358	31. 12	4.96	- 0. 19	Alpha-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_195 GeneMa rk.hmm 444_nt + 5 2101 52544	44 4	399 220 7	140	78. 98	6.3	117 411 44	877	16 8.2 3	7.39	1. 09	939 798 1	624	14 9.5 4	7.22	0. 92	Predicted ATPase or kinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1960 GeneM ark.hmm 1260_nt + 5420 6679	12 60	399 220 7	235	46. 72	5.55	117 411 44	215 7	14 5.8	7.19	1. 64	939 798 1	331	27. 95	4.8	- 0. 75	ABC-type sugar transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_1961 GeneM ark.hmm 867_nt + 6693 7559	86 7	399 220 7	58	16. 76	4.07	117 411 44	112 3	11 0.3 2	6.79	2. 72	939 798 1	226	27. 74	4.79	0. 72	ABC-type sugar transport systems, permease components	METABOLISM	Carbohydrate transport and metabolism	G
gene_1962 GeneM ark.hmm 837_nt + 7570 8406	83 7	399 220 7	294	87. 99	6.46	117 411 44	295 0	30 0.1 8	8.23	1. 77	939 798 1	330	41. 95	5.39	- 1. 07	ABC-type sugar transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_1963 GeneM ark.hmm 141_nt + 8413 8553	14 1	399 220 7	3	5.3 3	2.41	117 411 44	38	22. 95	4.52	2. 11	939 798 1	12	9.0 6	3.18	0. 77	NA			
gene_1964 GeneM ark.hmm 1443_nt + 8764 10206	14 43	399 220 7	322	55. 9	5.8	117 411 44	551 2	32 5.3 4	8.35	2. 55	939 798 1	725	53. 46	5.74	- 0. 06	Glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_1965 GeneM ark.hmm 1023_nt + 10515 11537	10 23	399 220 7	782	19 1.4 8	7.58	117 411 44	498 7	41 5.2	8.7	1. 12	939 798 1	299 5	31 1.5 2	8.28	0. 7	Lipid A core - O-antigen ligase and related enzymes	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1966 GeneM ark.hmm 1980_nt	19 80	399 220	860 7	10 88.	10.0 9	117 411	301 29	12 96.	10.3 4	0. 25	939 798	541 76	29 11.	11.5 1	1. 42	ABC-type oligopeptide transport system, periplasmic component	METABOLISM	Amino acid transport and metabolism	E

+ 12224 14203		7		86		44		01		1		44							
gene_1967 GeneM ark.hmm 1479_nt + 14288 15766	14 79	399 220 7	211 0	35 7.3 6	8.48	117 411 44	126 87	73 0.6	9.51	1. 03	939 798 1	186 23	13 39. 82	10.3 9	1. 91	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	METABOLISM	Amino acid transport and metabolism	E
gene_1968 GeneM ark.hmm 927_nt + 15766 16692	92 7	399 220 7	218 5	59 0.4 2	9.21	117 411 44	880 1	80 8.6 2	9.66	0. 45	939 798 1	115 44	13 25. 08	10.3 7	1. 16	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	METABOLISM	Amino acid transport and metabolism	E
gene_1969 GeneM ark.hmm 1068_nt + 16701 17768	10 68	399 220 7	565 1	13 25. 38	10.3 7	117 411 44	179 79	14 33. 78	10.4 9	0. 12	939 798 1	247 14	24 62. 28	11.2 7	0. 9	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_196 GeneMa rk.hmm 519_nt + 5 2534 53052	51 9	399 220 7	697	33 6.4	8.39	117 411 44	226 7	37 2.0 3	8.54	0. 15	939 798 1	191 1	39 1.7 9	8.61	0. 22	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1970 GeneM ark.hmm 234_nt + 17779 18012	23 4	399 220 7	256	27 4.0 4	8.1	117 411 44	170 4	62 0.2 2	9.28	1. 18	939 798 1	221 5	10 07. 22	9.98	1. 88	ABC-type oligopeptide transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_1971 GeneM ark.hmm 687_nt + 18070 18756	68 7	399 220 7	228 3	83 2.4 1	9.7	117 411 44	958 7	11 88. 54	10.2 1	0. 51	939 798 1	115 11	17 82. 88	10.8	1. 1	ABC-type oligopeptide transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_1972 GeneM ark.hmm 204_nt - 3 206	20 4	399 220 7	15	18. 42	4.2	117 411 44	117	48. 85	5.61	1. 41	939 798 1	109	56. 85	5.83	1. 63	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1973 GeneM ark.hmm 1626_nt - 1188 2813	16 26	399 220 7	151	23. 26	4.54	117 411 44	146 9	76. 95	6.27	1. 73	939 798 1	128 4	84. 03	6.39	1. 85	Transketolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1382 GeneM ark.hmm 417_nt - 94092 94508	41 7	399 220 7	215	12 9.1 5	7.01	117 411 44	257 7	52 6.3 4	9.04	2. 03	939 798 1	305 3	77 9.0 3	9.61	2. 6	Aspartate-semialdehyde dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_1975 GeneM ark.hmm 696_nt - 3243 3938	69 6	399 220 7	39	14. 04	3.81	117 411 44	369	45. 16	5.5	1. 69	939 798 1	268	40. 97	5.36	1. 55	Pentose-5-phosphate-3-epimerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1686 GeneM ark.hmm 267_nt + 14052 14318	26 7	399 220 7	24	22. 52	4.49	117 411 44	342	10 9.0 9	6.77	2. 28	939 798 1	341	13 5.9	7.09	2. 6	---	---	---	---
gene_1712 GeneM ark.hmm 405_nt - 8772 9176	40 5	399 220 7	0	0	0	117 411 44	54	11. 36	3.51	3. 51	939 798 1	23	6.0 4	2.6	2. 6	---	---	---	---
gene_2444 GeneM ark.hmm 123_nt - 1 123	12 3	399 220 7	0	0	0	117 411 44	7	4.8 5	2.28	2. 28	939 798 1	7	6.0 6	2.6	2. 6	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1979 GeneM ark.hmm 429_nt - 5826 6254	42 9	399 220 7	28	16. 35	4.03	117 411 44	291	57. 77	5.85	1. 82	939 798 1	270	66. 97	6.07	2. 04	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G

gene_197 GeneMark.hmm 1017_nt[+ 53060 54076	10 17	399 220 7	194 7	47 9.5 5	8.91	117 411 44	412 7	34 5.6 2	8.43	- 0.48	939 798 1	331 1	34 6.4 2	8.44	- 0.47	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_571 GeneMark.hmm 1113_nt[+ 22580 23692	11 13	399 220 7	326	73. 37	6.2	117 411 44	952 6	72 8.9 6	9.51	3. 31	939 798 1	466 7	44 6.1 8	8.8	2. 6	Predicted ferric reductase	METABOLISM	Inorganic ion transport and metabolism	P
gene_1981 GeneMark.hmm 2337_nt[- 8239 10575	23 37	399 220 7	163 1	17 4.8 2	7.45	117 411 44	649 1	23 6.5 6	7.89	0. 44	939 798 1	795 5	36 2.2	8.5	1. 05	Cation transport ATPase	METABOLISM	Inorganic ion transport and metabolism	P
gene_1982 GeneMark.hmm 750_nt[+ 10708 11457	75 0	399 220 7	477	15 9.3 1	7.32	117 411 44	145 0	16 4.6 6	7.36	0. 04	939 798 1	145 0	20 5.7 2	7.68	0. 36	1-acyl-sn-glycerol-3-phosphate acyltransferase	METABOLISM	Lipid transport and metabolism	I
gene_1983 GeneMark.hmm 615_nt[- 11750 12364	61 5	399 220 7	282 9	11 52. 24	10.1 7	117 411 44	106 74	14 78. 23	10.5 3	0. 36	939 798 1	791 9	13 70. 13	10.4 2	0. 25	Predicted permease, cadmium resistance protein	METABOLISM	Inorganic ion transport and metabolism	P
gene_1984 GeneMark.hmm 270_nt[- 13099 13368	27 0	399 220 7	881 2	81 75. 19	13	117 411 44	611 53	19 29 0.5	14.2 4	1. 24	939 798 1	248 48	97 92. 49	13.2 6	0. 26	Ribosomal protein S15P/S13E	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1985 GeneMark.hmm 630_nt[- 13509 14138	63 0	399 220 7	176	69. 98	6.13	117 411 44	172 4	23 3.0 7	7.86	1. 73	939 798 1	454	76. 68	6.26	0. 13	Putative NADH-flavin reductase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1986 GeneMark.hmm 141_nt[+ 14994 15134	14 1	399 220 7	28	49. 74	5.64	117 411 44	219	13 2.2 9	7.05	1. 41	939 798 1	225	16 9.8	7.41	1. 77	---	---	---	---
gene_624 GeneMark.hmm 153_nt[- 18681 18833	15 3	399 220 7	3	4.9 1	2.3	117 411 44	53	29. 5	4.88	2. 58	939 798 1	43	29. 9	4.9	2. 6	---	---	---	---
gene_1988 GeneMark.hmm 1410_nt[+ 15375 16784	14 10	399 220 7	129 8	23 0.5 9	7.85	117 411 44	112 44	67 9.1 9	9.41	1. 56	939 798 1	112 80	85 1.2 5	9.73	1. 88	Threonyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1989 GeneMark.hmm 528_nt[+ 16839 17366	52 8	399 220 7	705	33 4.4 6	8.39	117 411 44	484 8	78 2.0 2	9.61	1. 22	939 798 1	523 5	10 54. 99	10.0 4	1. 65	Threonyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_198 GeneMark.hmm 1257_nt[+ 54160 55416	12 57	399 220 7	494	98. 44	6.62	117 411 44	223 7	15 1.5 7	7.24	0. 62	939 798 1	353 2	29 8.9 9	8.22	1. 6	Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1990 GeneMark.hmm 975_nt[- 17415 18389	97 5	399 220 7	339	87. 09	6.44	117 411 44	101 4	88. 58	6.47	0. 03	939 798 1	812	88. 62	6.47	0. 03	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1991 GeneMark.hmm 678_nt[- 18382 19059	67 8	399 220 7	123	45. 44	5.51	117 411 44	637	80. 02	6.32	0. 81	939 798 1	433	67. 96	6.09	0. 58	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1992 GeneMark.hmm 1074_nt[+ 19215 20288	10 74	399 220 7	372	86. 76	6.44	117 411 44	118 1	93. 66	6.55	0. 11	939 798 1	722	71. 53	6.16	- 0.28	---	---	---	---

gene_1993 GeneM ark.hmm 438_nt - 20750 21187	43 8	399 220 7	426	24 3.6 3	7.93	117 411 44	184 1	35 7.9 9	8.48	0. 55	939 798 1	112 8	27 4.0 3	8.1	0. 17	Predicted transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1994 GeneM ark.hmm 843_nt - 21263 22105	84 3	399 220 7	164	48. 73	5.61	117 411 44	966	97. 6	6.61	1	939 798 1	685	86. 46	6.43	0. 82	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1995 GeneM ark.hmm 651_nt + 22217 22867	65 1	399 220 7	928	35 7.0 7	8.48	117 411 44	527 8	69 0.5 2	9.43	0. 95	939 798 1	270 3	44 1.8	8.79	0. 31	Mn-dependent transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1996 GeneM ark.hmm 678_nt + 23044 23721	67 8	399 220 7	199	73. 52	6.2	117 411 44	892	11 2.0 5	6.81	0. 61	939 798 1	793	12 4.4 5	6.96	0. 76	---	---	---	---
gene_1997 GeneM ark.hmm 414_nt + 23823 24236	41 4	399 220 7	65	39. 33	5.3	117 411 44	490	10 0.8 1	6.66	1. 36	939 798 1	323	83. 02	6.38	1. 08	---	---	---	---
gene_1998 GeneM ark.hmm 444_nt - 24710 25153	44 4	399 220 7	331	18 6.7 4	7.54	117 411 44	778	14 9.2 4	7.22	- 0. 32	939 798 1	843	20 2.0 3	7.66	0. 12	D-Tyr-tRNA ^{tyr} deacylase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1999 GeneM ark.hmm 447_nt - 25183 25629	44 7	399 220 7	379	21 2.3 8	7.73	117 411 44	102 9	19 6.0 6	7.62	- 0. 11	939 798 1	775	18 4.4 8	7.53	- 0. 2	Guanosine polyphosphate pyrophosphohydrolases/synthetases	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_199 GeneMa rk.hmm 1167_nt + 55471 56637	11 67	399 220 7	507 3	10 88. 88	10.0 9	117 411 44	815 7	59 5.3 2	9.22	- 0. 87	939 798 1	976 1	89 0	9.8	- 0. 29	RecA/RadA recombinase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_19 GeneMar k.hmm 96_nt - 11211 11306	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	---	---	---	---
gene_1 GeneMark. hmm 345_nt + 1 3 45	34 5	399 220 7	121	87. 85	6.46	117 411 44	954	23 5.5 2	7.88	1. 42	939 798 1	876	27 0.1 8	8.08	1. 62	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2000 GeneM ark.hmm 1770_nt - 25698 27467	17 70	399 220 7	929	13 1.4 7	7.04	117 411 44	237 3	11 4.1 9	6.84	- 0. 2	939 798 1	216 4	13 0.0 9	7.02	- 0. 02	Guanosine polyphosphate pyrophosphohydrolases/synthetases	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2001 GeneM ark.hmm 630_nt + 28461 29090	63 0	399 220 7	262 4	10 43. 3	10.0 3	117 411 44	440 8	59 5.9 2	9.22	- 0. 81	939 798 1	265 8	44 8.9 3	8.81	- 1. 22	Zn-dependent hydrolases, including glyoxylases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2002 GeneM ark.hmm 1893_nt - 29213 31105	18 93	399 220 7	618 1	81 7.8 9	9.68	117 411 44	426 31	19 18. 07	10.9 1	1. 23	939 798 1	204 84	11 51. 41	10.1 7	0. 49	Predicted metalloendopeptidase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2003 GeneM ark.hmm 723_nt + 31396 32118	72 3	399 220 7	230 9	79 9.9 7	9.64	117 411 44	477 9	56 2.9 7	9.14	- 0. 5	939 798 1	678 8	99 9.0 1	9.96	0. 32	ABC-type Mn/Zn transport systems, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_2004 GeneM ark.hmm 849_nt +	84	399 220	213	63 1.0	9.3	117 411	458	45 9.9	8.85	- 0.	939 798	659	82 6.6	9.69	0.	ABC-type Mn ²⁺ /Zn ²⁺ transport	METABOLISM	Inorganic ion transport and	P

32115 32963	9	7	9	9		44	5	6		45	1	6	8		39	systems, permease components		metabolism	
gene_2005 GeneM ark.hmm 930_nt + 32995 33924	93 0	399 220 7	116 99	31 51. 03	11.6 2	117 411 44	110 42	10 11. 24	9.98	- 1. 64	939 798 1	125 27	14 33. 28	10.4 9	- 1. 13	ABC-type metal ion transport system, periplasmic component/surface adhesin	METABOLISM	Inorganic ion transport and metabolism	P
gene_821 GeneMa rk.hmm 930_nt + 4 523 5452	93 0	399 220 7	10	2.6 9	1.43	117 411 44	419	38. 37	5.26	3. 83	939 798 1	144	16. 48	4.04	2. 61	ABC-type polysaccharide transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2007 GeneM ark.hmm 2709_nt 34634 37342	27 09	399 220 7	107 0	98. 94	6.63	117 411 44	251 5	79. 07	6.31	- 0. 32	939 798 1	272 1	10 6.8 8	6.74	0. 11	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2008 GeneM ark.hmm 702_nt 37344 38045	70 2	399 220 7	210	74. 93	6.23	117 411 44	649	78. 74	6.3	0. 07	939 798 1	395	59. 87	5.9	- 0. 33	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2009 GeneM ark.hmm 1620_nt 38295 39914	16 20	399 220 7	391	60. 46	5.92	117 411 44	141 3	74. 29	6.22	0. 3	939 798 1	112 7	74. 02	6.21	0. 29	---	---	---	---
gene_200 GeneMa rk.hmm 1371_nt + 56944 58314	13 71	399 220 7	349 4	63 8.3 7	9.32	117 411 44	113 51	70 5.1 6	9.46	0. 14	939 798 1	108 78	84 4.2 6	9.72	0. 4	Na+-driven multidrug efflux pump	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2010 GeneM ark.hmm 759_nt 39992 40750	75 9	399 220 7	107	35. 31	5.14	117 411 44	518	58. 13	5.86	0. 72	939 798 1	315	44. 16	5.46	0. 32	---	---	---	---
gene_2011 GeneM ark.hmm 693_nt 40803 41495	69 3	399 220 7	761 4	27 52. 12	11.4 3	117 411 44	130 60	16 05. 09	10.6 5	- 0. 78	939 798 1	315 4	48 4.2 8	8.92	- 2. 51	Phosphoglycerate mutase 1	METABOLISM	Carbohydrate transport and metabolism	G
gene_2227 GeneM ark.hmm 1248_nt 41694 42941	12 48	399 220 7	29	5.8 2	2.54	117 411 44	436	29. 76	4.9	2. 36	939 798 1	418	35. 64	5.16	2. 62	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_2013 GeneM ark.hmm 2793_nt 42823 45615	27 93	399 220 7	244 0	21 8.8 3	7.77	117 411 44	116 89	35 6.4 5	8.48	0. 71	939 798 1	179 17	68 2.5 9	9.41	1. 64	Isoleucyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2014 GeneM ark.hmm 117_nt 45868 45984	11 7	399 220 7	67	14 3.4 4	7.16	117 411 44	185	13 4.6 7	7.07	- 0. 09	939 798 1	203	18 4.6 2	7.53	0. 37	NA			
gene_2015 GeneM ark.hmm 735_nt 46015 46749	73 5	399 220 7	513 5	17 50. 01	10.7 7	117 411 44	191 98	22 24. 63	11.1 2	0. 35	939 798 1	183 55	26 57. 25	11.3 8	0. 61	Cell division initiation protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2016 GeneM ark.hmm 786_nt 46758 47543	78 6	399 220 7	466 6	14 86. 99	10.5 4	117 411 44	200 33	21 70. 77	11.0 8	0. 54	939 798 1	187 75	25 41. 69	11.3 1	0. 77	Uncharacterized conserved protein, contains S4-like domain	POORLY CHARACTERIZ ED	Function unknown	S
gene_2017 GeneM ark.hmm 264_nt 47540 47803	26 4	399 220 7	156	14 8.0 2	7.21	117 411 44	152 9	49 3.2 8	8.95	1. 74	939 798 1	195 5	78 7.9 7	9.62	2. 41	Predicted integral membrane protein	POORLY CHARACTERIZ ED	Function unknown	S

gene_2018 GeneM ark.hmm 540_nt - 47803 48342	54 0	399 220 7	279 7	12 97. 44	10.3 4	117 411 44	112 01	17 66. 66	10.7 9	0. 45	939 798 1	132 78	26 16. 4	11.3 5	1. 01	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2019 GeneM ark.hmm 672_nt - 48352 49023	67 2	399 220 7	765 6	28 53. 77	11.4 8	117 411 44	189 64	24 03. 53	11.2 3	- 0. 25	939 798 1	264 63	41 90. 2	12.0 3	0. 55	Predicted enzyme with a TIM-barrel fold	POORLY CHARACTERIZ ED	General function prediction only	R
gene_201 GeneMa rk.hmm 957_nt + 5 8690 59646	95 7	399 220 7	802 5	21 00. 49	11.0 4	117 411 44	162 77	14 48. 61	10.5	- 0. 54	939 798 1	161 86	17 99. 67	10.8 1	- 0. 23	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2020 GeneM ark.hmm 1092_nt - 49028 50119	10 92	399 220 7	717 3	16 45. 38	10.6 8	117 411 44	139 76	10 90. 06	10.0 9	- 0. 59	939 798 1	158 91	15 48. 44	10.6	- 0. 08	Cell division GTPase	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2021 GeneM ark.hmm 162_nt - 50172 50333	16 2	399 220 7	362	55 9.7 3	9.13	117 411 44	139 2	73 1.8 4	9.52	0. 39	939 798 1	138 8	91 1.6 7	9.83	0. 7	Cell division GTPase	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2022 GeneM ark.hmm 1374_nt - 50350 51723	13 74	399 220 7	640 5	11 67. 67	10.1 9	117 411 44	166 68	10 33. 2	10.0 1	- 0. 18	939 798 1	133 54	10 34. 17	10.0 1	- 0. 18	Actin-like ATPase involved in cell division	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2023 GeneM ark.hmm 705_nt - 51942 52646	70 5	399 220 7	139 4	49 5.2 9	8.95	117 411 44	678 8	82 0.0 5	9.68	0. 73	939 798 1	481 7	72 7.0 3	9.51	0. 56	---	---	---	---
gene_2024 GeneM ark.hmm 612_nt - 52737 53348	61 2	399 220 7	252	10 3.1 4	6.69	117 411 44	110 2	15 3.3 6	7.26	0. 57	939 798 1	124 9	21 7.1 6	7.76	1. 07	ADP-ribose pyrophosphatase	METABOLISM	Nucleotide transport and metabolism	F
gene_2025 GeneM ark.hmm 1374_nt - 53335 54708	13 74	399 220 7	726	13 2.3 5	7.05	117 411 44	319 6	19 8.1 1	7.63	0. 58	939 798 1	403 2	31 2.2 5	8.29	1. 24	UDP-N-acetylmuramyl pentapeptide synthase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2026 GeneM ark.hmm 1044_nt - 54792 55835	10 44	399 220 7	211 0	50 6.2 5	8.98	117 411 44	103 15	84 1.5 1	9.72	0. 74	939 798 1	680 4	69 3.4 7	9.44	0. 46	D-alanine-D-alanine ligase and related ATP-grasp enzymes	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2027 GeneM ark.hmm 549_nt - 56097 56645	54 9	399 220 7	108 1	49 3.2 2	8.95	117 411 44	195 2	30 2.8 3	8.24	- 0. 71	939 798 1	197 7	38 3.1 8	8.58	- 0. 37	Recombinational DNA repair protein (RecF pathway)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2028 GeneM ark.hmm 2043_nt - 56656 58698	20 43	399 220 7	207 3	25 4.1 7	7.99	117 411 44	660 7	27 5.4 4	8.11	0. 12	939 798 1	576 2	30 0.1	8.23	0. 24	Cell division protein FtsI/penicillin- binding protein 2	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2029 GeneM ark.hmm 336_nt + 58913 59248	33 6	399 220 7	133 6	99 5.9 9	9.96	117 411 44	360 6	91 4.0 6	9.84	- 0. 12	939 798 1	228 0	72 2.0 4	9.5	- 0. 46	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2802 GeneM ark.hmm 348_nt - 3 350	34 8	399 220 7	32	23. 03	4.53	117 411 44	378	92. 51	6.53	2	939 798 1	472	14 4.3 2	7.17	2. 64	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_2030 GeneM ark.hmm 552_nt + 59253 59804	55 2	399 220 7	248 0	11 25.38	10.1 4	117 411 44	752 4	11 60.91	10.1 8	0.04	939 798 1	493 0	95 0.33	9.89	- 0.25	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2031 GeneM ark.hmm 171_nt - 59820 59990	17 1	399 220 7	27	39.55	5.31	117 411 44	133	66.24	6.05	0.74	939 798 1	91	56.63	5.82	0.51	Transcriptional regulator/sugar kinase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2032 GeneM ark.hmm 708_nt - 60056 60763	70 8	399 220 7	534	18 8.93	7.56	117 411 44	191 9	23 0.85	7.85	0.29	939 798 1	142 5	21 4.16	7.74	0.18	Transcriptional regulator/sugar kinase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2033 GeneM ark.hmm 918_nt - 60781 61698	91 8	399 220 7	936	25 5.4	8	117 411 44	184 4	17 1.08	7.42	- 0.58	939 798 1	145 8	16 9	7.4	- 0.6	Dihydrodipicolinate synthase/N- acetylneuraminate lyase	METABOLISM	Amino acid transport and metabolism	E
gene_2034 GeneM ark.hmm 645_nt - 61867 62511	64 5	399 220 7	160	62.14	5.96	117 411 44	893	11 7.92	6.88	0.92	939 798 1	698	11 5.15	6.85	0.89	---	---	---	---
gene_2035 GeneM ark.hmm 345_nt - 62796 63140	34 5	399 220 7	253	18 3.69	7.52	117 411 44	120 0	29 6.25	8.21	0.69	939 798 1	851	26 2.47	8.04	0.52	---	---	---	---
gene_2036 GeneM ark.hmm 453_nt - 63237 63689	45 3	399 220 7	293	16 2.02	7.34	117 411 44	602	11 3.18	6.82	- 0.52	939 798 1	418	98.18	6.62	- 0.72	Beta-galactosidase, beta subunit	METABOLISM	Carbohydrate transport and metabolism	G
gene_2037 GeneM ark.hmm 840_nt - 63962 64801	84 0	399 220 7	572	17 0.57	7.41	117 411 44	126 5	12 8.26	7	- 0.41	939 798 1	742	93.99	6.55	- 0.86	ABC-type sugar transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2038 GeneM ark.hmm 570_nt - 64817 65386	57 0	399 220 7	351	15 4.25	7.27	117 411 44	792	11 8.34	6.89	- 0.38	939 798 1	514	95.95	6.58	- 0.69	ABC-type sugar transport systems, permease components	METABOLISM	Carbohydrate transport and metabolism	G
gene_2039 GeneM ark.hmm 432_nt - 65316 65747	43 2	399 220 7	226	13 1.04	7.03	117 411 44	529	10 4.29	6.7	- 0.33	939 798 1	266	65.52	6.03	-1	ABC-type sugar transport systems, permease components	METABOLISM	Carbohydrate transport and metabolism	G
gene_203 GeneMa rk.hmm 186_nt + 6 0610 60795	18 6	399 220 7	8	10.77	3.43	117 411 44	47	21.52	4.43	1	939 798 1	32	18.31	4.19	0.76	---	---	---	---
gene_2040 GeneM ark.hmm 1245_nt - 65969 67213	12 45	399 220 7	389 8	78 4.26	9.62	117 411 44	340 4	23 2.87	7.86	- 1.76	939 798 1	171 9	14 6.92	7.2	- 2.42	ABC-type sugar transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2041 GeneM ark.hmm 81_nt - 67278 67358	81	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2042 GeneM ark.hmm 1518_nt - 67483 69000	15 18	399 220 7	111 5	18 3.99	7.52	117 411 44	211 9	11 8.89	6.89	- 0.63	939 798 1	948	66.45	6.05	- 1.47	Phosphotransferase system IIC components, glucose/maltose/N- acetylglucosamine-specific	METABOLISM	Carbohydrate transport and metabolism	G
gene_2043 GeneM ark.hmm 699_nt - 69019 69717	69 9	399 220 7	122 4	43 8.62	8.78	117 411 44	131 0	15 9.62	7.32	- 1.46	939 798 1	600	91.34	6.51	- 2.27	Putative N-acetylmannosamine-6- phosphate epimerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2044 GeneM ark.hmm 1104_nt -	11	399 220	45	10.	3.35	117 411	469	36.	5.18	1.	939 798	196	18.	4.24	0.	Predicted dehydrogenases and	POORLY CHARACTERIZ	General function prediction only	R

[69891 70994	04	7		21		44		18		83	1		89		89	related proteins	ED		
gene_2045 GeneM ark.hmm 2094_nt - 71007 73100	20 94	399 220 7	34	4.0 7	2.02	117 411 44	708	28. 8	4.85	2. 83	939 798 1	311	15. 8	3.98	1. 96	Neuraminidase (sialidase)	METABOLISM	Carbohydrate transport and metabolism	G
gene_726 GeneMa rk.hmm 747_nt + 9 9409 100155	74 7	399 220 7	92	30. 85	4.95	117 411 44	414 0	47 2.0 3	8.88	3. 93	939 798 1	135 7	19 3.3	7.59	2. 64	Transcriptional regulators of sugar metabolism	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2047 GeneM ark.hmm 885_nt - 73952 74836	88 5	399 220 7	15	4.2 5	2.09	117 411 44	274	26. 37	4.72	2. 63	939 798 1	131	15. 75	3.98	1. 89	ABC-type sugar transport systems, permease components	METABOLISM	Carbohydrate transport and metabolism	G
gene_2048 GeneM ark.hmm 1338_nt - 74915 76252	13 38	399 220 7	80	14. 98	3.9	117 411 44	326	20. 75	4.38	0. 48	939 798 1	154	12. 25	3.61	- 0. 29	ABC-type sugar transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2049 GeneM ark.hmm 453_nt - 76271 76723	45 3	399 220 7	18	9.9 5	3.32	117 411 44	211	39. 67	5.31	1. 99	939 798 1	90	21. 14	4.4	1. 08	Beta-galactosidase, beta subunit	METABOLISM	Carbohydrate transport and metabolism	G
gene_204 GeneMa rk.hmm 426_nt + 6 0924 61349	42 6	399 220 7	56	32. 93	5.04	117 411 44	437	87. 37	6.45	1. 41	939 798 1	253	63. 19	5.98	0. 94	---	---	---	---
gene_2050 GeneM ark.hmm 96_nt - 76862 76957	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2051 GeneM ark.hmm 771_nt - 77738 78508	77 1	399 220 7	513	16 6.6 7	7.38	117 411 44	823	90. 91	6.51	- 0. 87	939 798 1	448	61. 83	5.95	- 1. 43	NA			
gene_2052 GeneM ark.hmm 2208_nt - 78469 80676	22 08	399 220 7	699	79. 3	6.31	117 411 44	135 9	52. 42	5.71	- 0. 6	939 798 1	587	28. 29	4.82	- 1. 49	Neuraminidase (sialidase)	METABOLISM	Carbohydrate transport and metabolism	G
gene_2053 GeneM ark.hmm 207_nt + 2 208	20 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.0 3	0.04	0. 04	ABC-type transport system involved in resistance to organic solvents, permease component	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_2054 GeneM ark.hmm 195_nt - 434 628	19 5	399 220 7	0	0	0	117 411 44	1	0.4 4	-1.2	- 1. 2	939 798 1	0	0	0	0	NA			
gene_2055 GeneM ark.hmm 210_nt + 1 210	21 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 1	- 0.98	- 0. 98	NA			
gene_2056 GeneM ark.hmm 189_nt + 453 641	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 3	0.17	0. 17	NA			
gene_2057 GeneM ark.hmm 714_nt + 458 1171	71 4	399 220 7	175	61. 39	5.94	117 411 44	406	48. 43	5.6	- 0. 34	939 798 1	442	65. 87	6.04	0. 1	Pseudouridylate synthase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2058 GeneM ark.hmm 774_nt + 1161 1934	77 4	399 220 7	106	34. 3	5.1	117 411 44	429	47. 21	5.56	0. 46	939 798 1	375	51. 55	5.69	0. 59	Hydroxymethylpyrimidine/phosphom ethylpyrimidine kinase	METABOLISM	Coenzyme transport and metabolism	H

gene_2059 GeneMark.hmm 462_nt[+] 1912 2373	46 2	399 220 7	47	25. 48	4.67	117 411 44	127	23. 41	4.55	- 0. 12	939 798 1	129	29. 71	4.89	0. 22	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_631 GeneMark.hmm 831_nt[+] 26572 27402	83 1	399 220 7	19	5.7 3	2.52	117 411 44	491	50. 32	5.65	3. 13	939 798 1	280	35. 85	5.16	2. 64	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2060 GeneMark.hmm 456_nt[+] 124 579	45 6	399 220 7	42	23. 07	4.53	117 411 44	300	56. 03	5.81	1. 28	939 798 1	156	36. 4	5.19	0. 66	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2061 GeneMark.hmm 300_nt[+] 744 1043	30 0	399 220 7	264 7	22 10. 14	11.1 1	117 411 44	552 8	15 69. 41	10.6 2	- 0. 49	939 798 1	130 2	46 1.8	8.85	- 2. 26	---	---	---	---
gene_2062 GeneMark.hmm 237_nt[+] 1304 1540	23 7	399 220 7	229	24 2.0 3	7.92	117 411 44	604	21 7.0 6	7.76	- 0. 16	939 798 1	437	19 6.2	7.62	- 0. 3	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2063 GeneMark.hmm 1728_nt[-] 2429 4156	17 28	399 220 7	921 4	13 35. 65	10.3 8	117 411 44	305 05	15 03. 55	10.5 5	0. 17	939 798 1	221 25	13 62. 4	10.4 1	0. 03	Negative regulator of septation ring formation	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2064 GeneMark.hmm 1947_nt[-] 4238 6184	19 47	399 220 7	449 2	57 7.9 1	9.17	117 411 44	127 01	55 5.6	9.12	- 0. 05	939 798 1	110 05	60 1.4 4	9.23	0. 06	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2065 GeneMark.hmm 573_nt[-] 6199 6771	57 3	399 220 7	833	36 4.1 5	8.51	117 411 44	364 0	54 1.0 5	9.08	0. 57	939 798 1	272 9	50 6.7 7	8.99	0. 48	Predicted phosphatases	POORLY CHARACTERIZED	General function prediction only	R
gene_2066 GeneMark.hmm 555_nt[-] 6847 7401	55 5	399 220 7	488	22 0.2 5	7.78	117 411 44	802	12 3.0 8	6.94	- 0. 84	939 798 1	116 5	22 3.3 6	7.8	0. 02	Putative intracellular protease/amidase	POORLY CHARACTERIZED	General function prediction only	R
gene_2067 GeneMark.hmm 1224_nt[-] 7412 8635	12 24	399 220 7	495	10 1.3	6.66	117 411 44	107 3	74. 66	6.22	- 0. 44	939 798 1	102 6	89. 19	6.48	- 0. 18	Bacterial cell division membrane protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2068 GeneMark.hmm 2451_nt[-] 8672 11122	24 51	399 220 7	205 8	21 0.3 2	7.72	117 411 44	487 4	16 9.3 7	7.4	- 0. 32	939 798 1	406 8	17 6.6 1	7.46	- 0. 26	Rad3-related DNA helicases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2069 GeneMark.hmm 930_nt[-] 11322 12251	93 0	399 220 7	143 3	38 5.9 7	8.59	117 411 44	868 9	79 5.7 5	9.64	1. 05	939 798 1	724 4	82 8.8 2	9.69	1. 1	Collagenase and related proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_206 GeneMark.hmm 198_nt[+] 62555 62752	19 8	399 220 7	15	18. 98	4.25	117 411 44	79	33. 98	5.09	0. 84	939 798 1	72	38. 69	5.27	1. 02	---	---	---	---
gene_2070 GeneMark.hmm 288_nt[+] 12391 12678	28 8	399 220 7	941	81 8.4 3	9.68	117 411 44	841 9	24 89. 76	11.2 8	1. 6	939 798 1	272 6	10 07. 16	9.98	0. 3	---	---	---	---
gene_2071 GeneMark.hmm 1335_nt[-]	13	399 220	158	29 75.	11.5	117 411	323	20 66.	11.0	- 0.	939 798	970	77 32.	12.9	1.	Signal transduction histidine kinase	CELLULAR PROCESSES	Signal transduction mechanisms	T

[12712 14046	35	7	57	27	4	44	93	61	1	53	1	13	4	2	38		AND SIGNALING		
gene_2072 GeneM ark.hmm 717_nt - 14036 14752	71 7	399 220 7	703 0	24 55. 97	11.2 6	117 411 44	927 1	11 01. 28	10.1	- 1. 16	939 798 1	283 92	42 13. 49	12.0 4	0. 78	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2073 GeneM ark.hmm 2547_nt - 14861 17407	25 47	399 220 7	136 16	13 39. 08	10.3 9	117 411 44	666 61	22 29. 11	11.1 2	0. 73	939 798 1	579 12	24 19. 39	11.2 4	0. 85	Aminopeptidase N	METABOLISM	Amino acid transport and metabolism	E
gene_2074 GeneM ark.hmm 426_nt - 17530 17955	42 6	399 220 7	179	10 5.2 5	6.72	117 411 44	784	15 6.7 5	7.29	0. 57	939 798 1	107 0	26 7.2 6	8.06	1. 34	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_2075 GeneM ark.hmm 870_nt - 17945 18814	87 0	399 220 7	999	28 7.6 3	8.17	117 411 44	189 4	18 5.4 2	7.53	- 0. 64	939 798 1	217 1	26 5.5 3	8.05	- 0. 12	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2076 GeneM ark.hmm 699_nt - 18856 19554	69 9	399 220 7	162	58. 05	5.86	117 411 44	130 7	15 9.2 5	7.32	1. 46	939 798 1	126 7	19 2.8 7	7.59	1. 73	NA			
gene_2077 GeneM ark.hmm 480_nt - 19592 20071	48 0	399 220 7	82	42. 79	5.42	117 411 44	537	95. 28	6.57	1. 15	939 798 1	487	10 7.9 6	6.75	1. 33	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2078 GeneM ark.hmm 699_nt - 20082 20780	69 9	399 220 7	230	82. 42	6.36	117 411 44	615	74. 94	6.23	- 0. 13	939 798 1	625	95. 14	6.57	0. 21	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	METABOLISM	Lipid transport and metabolism	I
gene_2079 GeneM ark.hmm 237_nt - 20773 21009	23 7	399 220 7	34	35. 93	5.17	117 411 44	197	70. 8	6.15	0. 98	939 798 1	141	63. 3	5.98	0. 81	---	---	---	---
gene_1008 GeneM ark.hmm 306_nt - 100514 100819	30 6	399 220 7	8	6.5 5	2.71	117 411 44	136	37. 85	5.24	2. 53	939 798 1	119	41. 38	5.37	2. 66	Anthranilate phosphoribosyltransferase	METABOLISM	Amino acid transport and metabolism	E
gene_2080 GeneM ark.hmm 927_nt - 21105 22031	92 7	399 220 7	168	45. 4	5.5	117 411 44	685	62. 94	5.98	0. 48	939 798 1	481	55. 21	5.79	0. 29	Predicted oxidoreductase	POORLY CHARACTERIZED	General function prediction only	R
gene_2081 GeneM ark.hmm 816_nt - 22106 22921	81 6	399 220 7	940	28 8.5 5	8.17	117 411 44	118 5	12 3.6 9	6.95	- 1. 22	939 798 1	187 1	24 3.9 8	7.93	- 0. 24	---	---	---	---
gene_2082 GeneM ark.hmm 321_nt - 22925 23245	32 1	399 220 7	243	18 9.6 2	7.57	117 411 44	592	15 7.0 7	7.3	- 0. 27	939 798 1	477	15 8.1 2	7.3	- 0. 27	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2083 GeneM ark.hmm 1998_nt - 23531 25528	19 98	399 220 7	538 4	67 4.9 9	9.4	117 411 44	144 53	61 6.1	9.27	- 0. 13	939 798 1	100 31	53 4.2 1	9.06	- 0. 34	Methionyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2084 GeneM ark.hmm 1260_nt - 25652 26911	12 60	399 220 7	488	97. 01	6.6	117 411 44	177 0	11 9.6 4	6.9	0. 3	939 798 1	324 7	27 4.2 1	8.1	1. 5	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V

gene_2085 GeneM ark.hmm 702_nt - 26913 27614	70 2	399 220 7	119	42. 46	5.41	117 411 44	553	67. 09	6.07	0. 66	939 798 1	108 2	16 4	7.36	1. 95	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2086 GeneM ark.hmm 684_nt - 27598 28281	68 4	399 220 7	285	10 4.3 7	6.71	117 411 44	878	10 9.3 3	6.77	0. 06	939 798 1	156 5	24 3.4 6	7.93	1. 22	Membrane-fusion protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2087 GeneM ark.hmm 591_nt - 28236 28826	59 1	399 220 7	299	12 6.7 3	6.99	117 411 44	873	12 5.8 1	6.98	- 0. 01	939 798 1	127 5	22 9.5 6	7.84	0. 85	Membrane-fusion protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2088 GeneM ark.hmm 1347_nt + 29112 30458	13 47	399 220 7	104 46	19 42. 54	10.9 2	117 411 44	124 63	78 8.0 3	9.62	- 1. 3	939 798 1	252 0	19 9.0 7	7.64	- 3. 28	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	METABOLISM	Energy production and conversion	C
gene_2089 GeneM ark.hmm 537_nt + 30655 31191	53 7	399 220 7	202	94. 22	6.56	117 411 44	104 3	16 5.4 2	7.37	0. 81	939 798 1	232 3	46 0.3	8.85	2. 29	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_208 GeneMa rk.hmm 261_nt + 6 3352 63612	26 1	399 220 7	37	35. 51	5.15	117 411 44	237	77. 34	6.27	1. 12	939 798 1	143	58. 3	5.87	0. 72	---	---	---	---
gene_2090 GeneM ark.hmm 216_nt - 31397 31612	21 6	399 220 7	140	16 2.3 5	7.34	117 411 44	687	27 0.8 9	8.08	0. 74	939 798 1	728	35 8.6 3	8.49	1. 15	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_1893 GeneM ark.hmm 1299_nt - 17918 19216	12 99	399 220 7	17	3.2 8	1.71	117 411 44	541	35. 47	5.15	3. 44	939 798 1	252	20. 64	4.37	2. 66	Superfamily II DNA/RNA helicase required for DNA uptake (late competence protein)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2092 GeneM ark.hmm 339_nt - 32060 32398	33 9	399 220 7	431	31 8.4 7	8.32	117 411 44	177 8	44 6.7 1	8.8	0. 48	939 798 1	150 7	47 3.0 2	8.89	0. 57	---	---	---	---
gene_2093 GeneM ark.hmm 720_nt - 32410 33129	72 0	399 220 7	167 5	58 2.7 3	9.19	117 411 44	522 5	61 8.0 8	9.27	0. 08	939 798 1	476 6	70 4.3 5	9.46	0. 27	tRNA-(guanine-N1)- methyltransferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2094 GeneM ark.hmm 519_nt - 33119 33637	51 9	399 220 7	709	34 2.1 9	8.42	117 411 44	207 2	34 0.0 3	8.41	- 0. 01	939 798 1	160 7	32 9.4 7	8.36	- 0. 06	RimM protein, required for 16S rRNA processing	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2095 GeneM ark.hmm 789_nt - 33668 34456	78 9	399 220 7	874	27 7.4 7	8.12	117 411 44	466 3	50 3.3 6	8.98	0. 86	939 798 1	315 3	42 5.2 2	8.73	0. 61	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2096 GeneM ark.hmm 240_nt - 35033 35272	24 0	399 220 7	224	23 3.7 9	7.87	117 411 44	105 6	37 4.7 5	8.55	0. 68	939 798 1	865	38 3.5	8.58	0. 71	Predicted RNA-binding protein (contains KH domain)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2097 GeneM ark.hmm 273_nt - 35292 35564	27 3	399 220 7	296 7	27 22. 34	11.4 1	117 411 44	809 3	25 24. 86	11.3	- 0. 11	939 798 1	649 8	25 32. 69	11.3 1	- 0. 1	Ribosomal protein S16	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J

gene_2098 GeneM ark.hmm 222_nt[+] 36422 36643	22 2	399 220 7	5	5.6 4	2.5	117 411 44	53	20. 33	4.35	1. 85	939 798 1	64	30. 68	4.94	2. 44	---	---	---	---
gene_2099 GeneM ark.hmm 804_nt[+] 36726 37529	80 4	399 220 7	289 6	90 2.2 6	9.82	117 411 44	962 7	10 19. 82	9.99	0. 17	939 798 1	257 8	34 1.1 9	8.41	- 1. 41	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_209 GeneMa rk.hmm 204_nt - 64350 64553	20 4	399 220 7	48	58. 94	5.88	117 411 44	247	10 3.1 2	6.69	0. 81	939 798 1	170	88. 67	6.47	0. 59	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_20 GeneMar k.hmm 879_nt - 11455 12333	87 9	399 220 7	941	26 8.1 6	8.07	117 411 44	132 5	12 8.3 9	7	- 1. 07	939 798 1	168 1	20 3.4 9	7.67	- 0. 4	Pseudouridine synthase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2100 GeneM ark.hmm 1203_nt - 37585 38787	12 03	399 220 7	251 3	52 3.2 6	9.03	117 411 44	577 8	40 9.0 7	8.68	- 0. 35	939 798 1	912 4	80 7.0 2	9.66	0. 63	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2101 GeneM ark.hmm 345_nt - 38860 39204	34 5	399 220 7	69	50. 1	5.65	117 411 44	285	70. 36	6.14	0. 49	939 798 1	462	14 2.4 9	7.15	1. 5	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2102 GeneM ark.hmm 483_nt - 39206 39688	48 3	399 220 7	102	52. 9	5.73	117 411 44	553	97. 51	6.61	0. 88	939 798 1	601	13 2.4	7.05	1. 32	Glycopeptide antibiotics resistance protein	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2103 GeneM ark.hmm 663_nt - 39688 40350	66 3	399 220 7	485	18 3.2 4	7.52	117 411 44	189 1	24 2.9 2	7.92	0. 4	939 798 1	191 8	30 7.8 2	8.27	0. 75	Predicted Fe-S-cluster redox enzyme	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2104 GeneM ark.hmm 420_nt - 40417 40836	42 0	399 220 7	132	78. 72	6.3	117 411 44	501	10 1.6	6.67	0. 37	939 798 1	417	10 5.6 5	6.72	0. 42	Predicted Fe-S-cluster redox enzyme	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2105 GeneM ark.hmm 531_nt - 40857 41387	53 1	399 220 7	675	31 8.4 2	8.31	117 411 44	223 1	35 7.8 4	8.48	0. 17	939 798 1	135 4	27 1.3 2	8.08	- 0. 23	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2106 GeneM ark.hmm 330_nt - 41544 41873	33 0	399 220 7	189 3	14 36. 89	10.4 9	117 411 44	227 0	58 5.8 7	9.19	- 1. 3	939 798 1	142 1	45 8.1 9	8.84	- 1. 65	Superoxide dismutase	METABOLISM	Inorganic ion transport and metabolism	P
gene_637 GeneMa rk.hmm 1227_nt[+] 32588 33814	12 27	399 220 7	58	11. 84	3.57	117 411 44	775	53. 8	5.75	2. 18	939 798 1	865	75. 01	6.23	2. 66	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_2108 GeneM ark.hmm 1038_nt - 42377 43414	10 38	399 220 7	373 8	90 2.0 5	9.82	117 411 44	118 89	97 5.5 2	9.93	0. 11	939 798 1	140 14	14 36. 58	10.4 9	0. 67	DNA polymerase III, delta subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2109 GeneM ark.hmm 936_nt - 43448 44383	93 6	399 220 7	345 7	92 5.1 5	9.85	117 411 44	690 6	62 8.4 1	9.3	- 0. 55	939 798 1	693 8	78 8.7 2	9.62	- 0. 23	Dihydrooorotate dehydrogenase	METABOLISM	Nucleotide transport and metabolism	F
gene_210 GeneMa rk.hmm 72_nt - 64851 64922	72	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			

gene_2110 GeneM ark.hmm 1191_ntl- 44936 46126	11 91	399 220 7	361 3	75 9.8 8	9.57	117 411 44	190 02	13 58. 87	10.4 1	0. 84	939 798 1	200 31	17 89. 6	10.8 1	1. 24	S-adenosylmethionine synthetase	METABOLISM	Coenzyme transport and metabolism	H
gene_2111 GeneM ark.hmm 1344_ntl- 46341 47684	13 44	399 220 7	245 5	45 7.5 5	8.84	117 411 44	971 9	61 5.9	9.27	0. 43	939 798 1	751 2	59 4.7 3	9.22	0. 38	Superfamily II DNA and RNA helicases	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2112 GeneM ark.hmm 816_ntl- 47824 48639	81 6	399 220 7	134	41. 13	5.36	117 411 44	497	51. 87	5.7	0. 34	939 798 1	742	96. 76	6.6	1. 24	Metal-dependent hydrolase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2113 GeneM ark.hmm 2181_ntl- 48691 50871	21 81	399 220 7	190 0	21 8.2 2	7.77	117 411 44	212 3	82. 91	6.37	- 1. 4	939 798 1	339 1	16 5.4 4	7.37	- 0. 4	Phosphotransferase system IIC components, glucose/maltose/N- acetylglucosamine-specific	METABOLISM	Carbohydrate transport and metabolism	G
gene_2114 GeneM ark.hmm 927_ntl- 51157 52083	92 7	399 220 7	169 3	45 7.4 7	8.84	117 411 44	584 0	53 6.5 7	9.07	0. 23	939 798 1	586 1	67 2.7 6	9.39	0. 55	Cell division protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2115 GeneM ark.hmm 321_ntl- 52076 52396	32 1	399 220 7	298	23 2.5 4	7.86	117 411 44	127 0	33 6.9 7	8.4	0. 54	939 798 1	196 7	65 2.0 3	9.35	1. 49	Predicted ATPase involved in cell division	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2116 GeneM ark.hmm 510_ntl- 52299 52808	51 0	399 220 7	378	18 5.6 6	7.54	117 411 44	125 6	20 9.7 5	7.71	0. 17	939 798 1	104 8	21 8.6 5	7.77	0. 23	Predicted ATPase involved in cell division	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2117 GeneM ark.hmm 978_ntl- 52826 53803	97 8	399 220 7	679	17 3.9 1	7.44	117 411 44	304 3	26 5	8.05	0. 61	939 798 1	231 9	25 2.3 1	7.98	0. 54	Protein chain release factor B	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2118 GeneM ark.hmm 657_ntl- 54029 54685	65 7	399 220 7	335	12 7.7 2	7	117 411 44	671	86. 99	6.44	- 0. 56	939 798 1	644	10 4.3	6.7	- 0. 3	FOG: CBS domain	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2119 GeneM ark.hmm 711_ntl- 54993 55703	71 1	399 220 7	464	16 3.4 7	7.35	117 411 44	208 0	24 9.1 6	7.96	0. 61	939 798 1	445 1	66 6.1 2	9.38	2. 03	ABC-type branched-chain amino acid transport systems, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_85 GeneMar k.hmm 306_ntl- 58077 58382	30 6	399 220 7	11	9	3.17	117 411 44	228	63. 46	5.99	2. 82	939 798 1	165	57. 38	5.84	2. 67	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2120 GeneM ark.hmm 765_ntl- 55703 56467	76 5	399 220 7	322	10 5.4 3	6.72	117 411 44	115 7	12 8.8 1	7.01	0. 29	939 798 1	302 0	42 0.0 6	8.71	1. 99	ABC-type branched-chain amino acid transport systems, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_2121 GeneM ark.hmm 957_ntl- 56467 57423	95 7	399 220 7	106	27. 74	4.79	117 411 44	977	86. 95	6.44	1. 65	939 798 1	202 1	22 4.7 1	7.81	3. 02	ABC-type branched-chain amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_2122 GeneM ark.hmm 870_ntl- 57427 58296	87 0	399 220 7	331	95. 3	6.57	117 411 44	103 4	10 1.2 3	6.66	0. 09	939 798 1	217 9	26 6.5	8.06	1. 49	Branched-chain amino acid ABC- type transport system, permease components	METABOLISM	Amino acid transport and metabolism	E
gene_2123 GeneM ark.hmm 1161_ntl-	11 61	399 220	120 3	25 9.5	8.02	117 411	526 5	38 6.2	8.59	0. 57	939 798	630 1	57 7.4	9.17	1. 15	ABC-type branched-chain amino acid transport systems, periplasmic	METABOLISM	Amino acid transport and metabolism	E

[58564 59724		7		5		44		4			1		9			component			
gene_2124 GeneM ark.hmm 249_nt - 59826 60074	24 9	399 220 7	402	40 4.4	8.66	117 411 44	154 9	52 9.8 4	9.05	0. 39	939 798 1	113 9	48 6.7 3	8.93	0. 27	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2125 GeneM ark.hmm 591_nt - 60153 60743	59 1	399 220 7	687 8	29 15. 15	11.5 1	117 411 44	142 72	20 56. 78	11.0 1	- 0. 5	939 798 1	569 2	10 24. 81	10	- 1. 51	Protease subunit of ATP-dependent Clp proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2126 GeneM ark.hmm 630_nt - 60917 61546	63 0	399 220 7	622 4	24 74. 66	11.2 7	117 411 44	287 12	38 81. 62	11.9 2	0. 65	939 798 1	436 8	73 7.7 5	9.53	- 1. 74	Uracil phosphoribosyltransferase	METABOLISM	Nucleotide transport and metabolism	F
gene_2127 GeneM ark.hmm 468_nt - 61635 62102	46 8	399 220 7	77	41. 21	5.37	117 411 44	462	84. 08	6.39	1. 02	939 798 1	228	51. 84	5.7	0. 33	Deoxycytidylate deaminase	METABOLISM	Nucleotide transport and metabolism	F
gene_2128 GeneM ark.hmm 546_nt - 62195 62740	54 6	399 220 7	59	27. 07	4.76	117 411 44	483	75. 34	6.24	1. 48	939 798 1	236	45. 99	5.52	0. 76	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2129 GeneM ark.hmm 846_nt + 62865 63710	84 6	399 220 7	163 9	48 5.2 8	8.92	117 411 44	355 8	35 8.2	8.48	- 0. 44	939 798 1	211 9	26 6.5 2	8.06	- 0. 86	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_212 GeneMa rk.hmm 234_nt + 1 462 1695	23 4	399 220 7	26	27. 83	4.8	117 411 44	139	50. 59	5.66	0. 86	939 798 1	129	58. 66	5.87	1. 07	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2130 GeneM ark.hmm 1194_nt + 63751 64944	11 94	399 220 7	540	11 3.2 9	6.82	117 411 44	259 4	18 5.0 4	7.53	0. 71	939 798 1	307 1	27 3.6 8	8.1	1. 28	Predicted flavoproteins	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2131 GeneM ark.hmm 417_nt + 65003 65419	41 7	399 220 7	186	11 1.7 3	6.8	117 411 44	901	18 4.0 3	7.52	0. 72	939 798 1	113 1	28 8.6	8.17	1. 37	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2132 GeneM ark.hmm 417_nt - 65439 65855	41 7	399 220 7	110	66. 08	6.05	117 411 44	309	63. 11	5.98	- 0. 07	939 798 1	473	12 0.7	6.92	0. 87	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2133 GeneM ark.hmm 924_nt + 66416 67339	92 4	399 220 7	295	79. 97	6.32	117 411 44	814	75. 03	6.23	- 0. 09	939 798 1	787	90. 63	6.5	0. 18	Na+-dependent transporters of the SNF family	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2134 GeneM ark.hmm 390_nt + 67414 67803	39 0	399 220 7	14	8.9 9	3.17	117 411 44	168	36. 69	5.2	2. 03	939 798 1	101	27. 56	4.78	1. 61	Na+-dependent transporters of the SNF family	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2135 GeneM ark.hmm 945_nt - 67824 68768	94 5	399 220 7	211 1	55 9.5 6	9.13	117 411 44	194 0	17 4.8 5	7.45	- 1. 68	939 798 1	161 4	18 1.7 3	7.51	- 1. 62	Phosphomannose isomerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1006 GeneM ark.hmm 768_nt - 99011 99778	76 8	399 220 7	14	4.5 7	2.19	117 411 44	272	30. 16	4.91	2. 72	939 798 1	212	29. 37	4.88	2. 69	Indole-3-glycerol phosphate synthase	METABOLISM	Amino acid transport and metabolism	E
gene_2137 GeneM ark.hmm 348_nt -	34 8	399 220	137	98. 61	6.62	117 411	995	24 3.5	7.93	1. 31	939 798	639	19 5.3	7.61	0. 99	Lactoylglutathione lyase and related lyases	METABOLISM	Amino acid transport and metabolism	E

[70236 70583		7				44		2			1		8						
gene_2138 GeneM ark.hmm 1527_nt -[70694 72220	15 27	399 220 7	269 62	44 22. 83	12.1 1	117 411 44	108 442	60 48. 51	12.5 6	0. 45	939 798 1	370 22	25 79. 8	11.3 3	- 0. 78	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]	METABOLISM	Amino acid transport and metabolism	E
gene_2139 GeneM ark.hmm 291_nt -[72217 72507	29 1	399 220 7	164 6	14 16. 85	10.4 7	117 411 44	230 75	67 53. 65	12.7 2	2. 25	939 798 1	402 6	14 72. 13	10.5 2	0. 05	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]	METABOLISM	Amino acid transport and metabolism	E
gene_213 GeneMa rk.hmm 444_nt -[2590 3033	44 4	399 220 7	595	33 5.6 8	8.39	117 411 44	119 3	22 8.8 5	7.84	- 0. 55	939 798 1	141 0	33 7.9 1	8.4	0. 01	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2140 GeneM ark.hmm 2244_nt -[72714 74957	22 44	399 220 7	151	16. 86	4.08	117 411 44	964	36. 59	5.19	1. 11	939 798 1	681	32. 29	5.01	0. 93	Cation transport ATPase	METABOLISM	Inorganic ion transport and metabolism	P
gene_2141 GeneM ark.hmm 372_nt -[74967 75338	37 2	399 220 7	42	28. 28	4.82	117 411 44	104	23. 81	4.57	- 0. 25	939 798 1	101	28. 89	4.85	0. 03	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2142 GeneM ark.hmm 396_nt -[75349 75744	39 6	399 220 7	14	8.8 6	3.15	117 411 44	116	24. 95	4.64	1. 49	939 798 1	60	16. 12	4.01	0. 86	Predicted transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2143 GeneM ark.hmm 792_nt +[76110 76901	79 2	399 220 7	446 1	14 10. 89	10.4 6	117 411 44	532 5	57 2.6 4	9.16	- 1. 3	939 798 1	496 0	66 6.3 8	9.38	- 1. 08	Hydroxymethylpyrimidine/phosphom ethylpyrimidine kinase	METABOLISM	Coenzyme transport and metabolism	H
gene_2144 GeneM ark.hmm 633_nt -[77110 77742	63 3	399 220 7	74	29. 28	4.87	117 411 44	332	44. 67	5.48	0. 61	939 798 1	303	50. 93	5.67	0. 8	Thiamine monophosphate synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_2145 GeneM ark.hmm 804_nt -[77735 78538	80 4	399 220 7	119	37. 07	5.21	117 411 44	441	46. 72	5.55	0. 34	939 798 1	367	48. 57	5.6	0. 39	Hydroxyethylthiazole kinase, sugar kinase family	METABOLISM	Coenzyme transport and metabolism	H
gene_2146 GeneM ark.hmm 525_nt -[78538 79062	52 5	399 220 7	71	33. 88	5.08	117 411 44	241	39. 1	5.29	0. 21	939 798 1	231	46. 82	5.55	0. 47	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2147 GeneM ark.hmm 693_nt -[79067 79759	69 3	399 220 7	65	23. 49	4.55	117 411 44	376	46. 21	5.53	0. 98	939 798 1	210	32. 24	5.01	0. 46	Putative transcription activator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2148 GeneM ark.hmm 651_nt -[79770 80420	65 1	399 220 7	29	11. 16	3.48	117 411 44	379	49. 58	5.63	2. 15	939 798 1	221	36. 12	5.17	1. 69	---	---	---	---
gene_2149 GeneM ark.hmm 1386_nt -[80422 81807	13 86	399 220 7	130	23. 49	4.55	117 411 44	105 2	64. 65	6.01	1. 46	939 798 1	519	39. 84	5.32	0. 77	ABC-type cobalt transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_214 GeneMa rk.hmm 1482_nt +	14	399 220	477	80.	6.33	117 411	291	16 7.4	7.39	1.	939 798	214	15 4.0	7.27	0.	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B	INFORMATION STORAGE AND	Replication, recombination and	L

3169 4650	82	7		62		44	3	1		06	1	6	8		94	subunit	PROCESSING	repair	
gene_2150 GeneM ark.hmm 561_nt - 81808 82368	56 1	399 220 7	65	29. 02	4.86	117 411 44	346	52. 53	5.72	0. 86	939 798 1	179	33. 95	5.09	0. 23	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2151 GeneM ark.hmm 630_nt - 82927 83556	63 0	399 220 7	69	27. 43	4.78	117 411 44	428	57. 86	5.85	1. 07	939 798 1	334	56. 41	5.82	1. 04	Thiamine monophosphate synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_2152 GeneM ark.hmm 783_nt - 83558 84340	78 3	399 220 7	241	77. 1	6.27	117 411 44	808	87. 89	6.46	0. 19	939 798 1	920	12 5.0 2	6.97	0. 7	Hydroxyethylthiazole kinase, sugar kinase family	METABOLISM	Coenzyme transport and metabolism	H
gene_2153 GeneM ark.hmm 669_nt - 84622 85290	66 9	399 220 7	97	36. 32	5.18	117 411 44	737	93. 83	6.55	1. 37	939 798 1	869	13 8.2 2	7.11	1. 93	Putative transcription activator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2252 GeneM ark.hmm 252_nt - 73131 73382	25 2	399 220 7	5	4.9 7	2.31	117 411 44	182	61. 51	5.94	3. 63	939 798 1	76	32. 09	5	2. 69	NA			
gene_1546 GeneM ark.hmm 231_nt + 18175 18405	23 1	399 220 7	30	32. 53	5.02	117 411 44	372	13 7.1 6	7.1	2. 08	939 798 1	454	20 9.1 3	7.71	2. 69	---	---	---	---
gene_101 GeneMa rk.hmm 519_nt + 7 0970 71488	51 9	399 220 7	54	26. 06	4.7	117 411 44	840	13 7.8 5	7.11	2. 41	939 798 1	823	16 8.7 3	7.4	2. 7	Membrane protein involved in the export of O-antigen and teichoic acid	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2157 GeneM ark.hmm 678_nt + 1773 2450	67 8	399 220 7	72	26. 6	4.73	117 411 44	366	45. 98	5.52	0. 79	939 798 1	280	43. 94	5.46	0. 73	Predicted SAM-dependent methyltransferase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2158 GeneM ark.hmm 798_nt + 2437 3234	79 8	399 220 7	184	57. 76	5.85	117 411 44	501	53. 47	5.74	- 0. 11	939 798 1	506	67. 47	6.08	0. 23	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2159 GeneM ark.hmm 1149_nt + 3251 4399	11 49	399 220 7	149	32. 48	5.02	117 411 44	657	48. 7	5.61	0. 59	939 798 1	700	64. 83	6.02	1	Glycine/D-amino acid oxidases (deaminating)	METABOLISM	Amino acid transport and metabolism	E
gene_215 GeneMa rk.hmm 510_nt + 4 647 5156	51 0	399 220 7	212	10 4.1 2	6.7	117 411 44	827	13 8.1 1	7.11	0. 41	939 798 1	100 5	20 9.6 8	7.71	1. 01	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2160 GeneM ark.hmm 1020_nt + 4655 5674	10 20	399 220 7	508 6	12 49	10.2 9	117 411 44	234 52	19 58. 26	10.9 4	0. 65	939 798 1	707 7	73 8.2 7	9.53	- 0. 76	UDP-glucose 4-epimerase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2161 GeneM ark.hmm 972_nt + 5658 6629	97 2	399 220 7	286	73. 7	6.2	117 411 44	300 1	26 2.9 6	8.04	1. 84	939 798 1	252 0	27 5.8 7	8.11	1. 91	Glycosyltransferases involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2162 GeneM ark.hmm 117_nt - 6691 6807	11 7	399 220 7	23	49. 24	5.62	117 411 44	66	48. 04	5.59	- 0. 03	939 798 1	39	35. 47	5.15	- 0. 47	Ferredoxin	METABOLISM	Energy production and conversion	C
gene_2163 GeneM ark.hmm 174_nt +	17	399 220	218	31 3.8	8.29	117 411	889	43 5.1	8.77	0.	939 798	144	88 3.6	9.79	1.	---	---	---	---

6949 7122	4	7		3		44		5		48	1	5	6		5				
gene_2164 GeneM ark.hmm 300_nt + 7189 7488	30 0	399 220 7	407	33 9.8 3	8.41	117 411 44	179 8	51 0.4 6	9	0. 59	939 798 1	172 8	61 2.9	9.26	0. 85	---	---	---	
gene_2165 GeneM ark.hmm 432_nt + 7497 7928	43 2	399 220 7	510	29 5.7 2	8.21	117 411 44	239 9	47 2.9 7	8.89	0. 68	939 798 1	301 9	74 3.6 1	9.54	1. 33	Cytidylate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_2166 GeneM ark.hmm 237_nt + 7997 8233	23 7	399 220 7	39	41. 22	5.37	117 411 44	304	10 9.2 5	6.77	1. 4	939 798 1	334	14 9.9 6	7.23	1. 86	Cytidylate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_2167 GeneM ark.hmm 339_nt + 8364 8702	33 9	399 220 7	262 9	19 42. 58	10.9 2	117 411 44	853 3	21 43. 84	11.0 7	0. 15	939 798 1	557 8	17 50. 83	10.7 7	- 0. 15	Uncharacterized Zn-ribbon- containing protein involved in phosphonate metabolism	METABOLISM	Inorganic ion transport and metabolism	P
gene_2168 GeneM ark.hmm 630_nt + 8705 9334	63 0	399 220 7	484	19 2.4 4	7.59	117 411 44	231 3	31 2.7	8.29	0. 7	939 798 1	219 6	37 0.9	8.53	0. 94	---	---	---	
gene_2169 GeneM ark.hmm 1152_nt + 9574 10725	11 52	399 220 7	806	17 5.2 5	7.45	117 411 44	254 4	18 8.0 9	7.56	0. 11	939 798 1	310 1	28 6.4 3	8.16	0. 71	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_216 GeneMa rk.hmm 108_nt + 5 156 5263	10 8	399 220 7	2	4.6 4	2.21	117 411 44	12	9.4 6	3.24	1. 03	939 798 1	10	9.8 5	3.3	1. 09	NA			
gene_778 GeneMa rk.hmm 1437_nt + 155314 156750	14 37	399 220 7	17	2.9 6	1.57	117 411 44	685	40. 6	5.34	3. 77	939 798 1	265	19. 62	4.29	2. 72	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2171 GeneM ark.hmm 420_nt - 735 1154	42 0	399 220 7	29	17. 3	4.11	117 411 44	317	64. 28	6.01	1. 9	939 798 1	169	42. 82	5.42	1. 31	Argininosuccinate synthase	METABOLISM	Amino acid transport and metabolism	E
gene_2172 GeneM ark.hmm 807_nt - 1171 1977	80 7	399 220 7	62	19. 24	4.27	117 411 44	314	33. 14	5.05	0. 78	939 798 1	231	30. 46	4.93	0. 66	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_2173 GeneM ark.hmm 642_nt - 2184 2825	64 2	399 220 7	796	31 0.5 7	8.28	117 411 44	120 1	15 9.3 3	7.32	- 0. 96	939 798 1	111 5	18 4.8	7.53	- 0. 75	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2174 GeneM ark.hmm 2085_nt - 2822 4906	20 85	399 220 7	253 6	30 4.6 7	8.25	117 411 44	391 8	16 0.0 5	7.32	- 0. 93	939 798 1	352 1	17 9.6 9	7.49	- 0. 76	---	---	---	---
gene_2175 GeneM ark.hmm 252_nt - 4982 5233	25 2	399 220 7	546	54 2.7 2	9.08	117 411 44	434	14 6.6 8	7.2	- 1. 88	939 798 1	337	14 2.3	7.15	- 1. 93	---	---	---	---
gene_2176 GeneM ark.hmm 279_nt + 3 281	27 9	399 220 7	549	49 2.9	8.95	117 411 44	402 8	12 29. 63	10.2 6	1. 31	939 798 1	235 8	89 9.3	9.81	0. 86	NA			
gene_2177 GeneM ark.hmm 459_nt -	45	399 220	753	41 0.9	8.68	117 411	299	55 5.9	9.12	0.	939 798	114	26 4.5	8.05	- 0.	tRNA-dihydrouridine synthase	INFORMATION STORAGE AND	Translation, ribosomal structure and	J

[500]958	9	7		3		44	6	3		44	1	1	1		63		PROCESSING	biogenesis	
gene_2178 GeneM ark.hmm 519_nt - 1003 1521	51 9	399 220 7	528	25 4.8 3	7.99	117 411 44	175 7	28 8.3 3	8.17	0. 18	939 798 1	820	16 8.1 2	7.39	- 0. 6	tRNA-dihydrouridine synthase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2179 GeneM ark.hmm 873_nt - 1508 2380	87 3	399 220 7	547	15 6.9 5	7.29	117 411 44	351 4	34 2.8 3	8.42	1. 13	939 798 1	148 8	18 1.3 7	7.5	0. 21	Disulfide bond chaperones of the HSP33 family	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_217 GeneMa rk.hmm 1611_nt + 5612 7222	16 11	399 220 7	858	13 3.4 1	7.06	117 411 44	387 6	20 4.9 2	7.68	0. 62	939 798 1	649 0	42 8.6 6	8.74	1. 68	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2180 GeneM ark.hmm 1410_nt + 2563 3972	14 10	399 220 7	131 6	23 3.7 9	7.87	117 411 44	564 3	34 0.8 6	8.41	0. 54	939 798 1	276 2	20 8.4 3	7.7	- 0. 17	---	---	---	---
gene_2181 GeneM ark.hmm 1509_nt + 4131 5639	15 09	399 220 7	133	22. 08	4.46	117 411 44	821	46. 34	5.53	1. 07	939 798 1	485	34. 2	5.1	0. 64	Glycerol kinase	METABOLISM	Energy production and conversion	C
gene_2182 GeneM ark.hmm 1827_nt + 5786 7612	18 27	399 220 7	135	18. 51	4.21	117 411 44	999	46. 57	5.54	1. 33	939 798 1	508	29. 59	4.89	0. 68	Glycerol-3-phosphate dehydrogenase	METABOLISM	Energy production and conversion	C
gene_2183 GeneM ark.hmm 705_nt + 7682 8386	70 5	399 220 7	65	23. 09	4.53	117 411 44	396	47. 84	5.58	1. 05	939 798 1	224	33. 81	5.08	0. 55	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	METABOLISM	Carbohydrate transport and metabolism	G
gene_2184 GeneM ark.hmm 204_nt + 8577 8780	20 4	399 220 7	36	44. 2	5.47	117 411 44	95	39. 66	5.31	- 0. 16	939 798 1	45	23. 47	4.55	- 0. 92	---	---	---	---
gene_2185 GeneM ark.hmm 510_nt + 66 575	51 0	399 220 7	903	44 3.5 1	8.79	117 411 44	291 8	48 7.3 1	8.93	0. 14	939 798 1	413 3	86 2.3	9.75	0. 96	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2186 GeneM ark.hmm 708_nt + 659 1366	70 8	399 220 7	186 1	65 8.4 2	9.36	117 411 44	637 3	76 6.6 6	9.58	0. 22	939 798 1	565 3	84 9.5 9	9.73	0. 37	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2187 GeneM ark.hmm 1332_nt + 1367 2698	13 32	399 220 7	577 7	10 86. 39	10.0 9	117 411 44	152 42	97 4.6	9.93	- 0. 16	939 798 1	172 59	13 78. 72	10.4 3	0. 34	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_995 GeneMa rk.hmm 204_nt - 88881 89084	20 4	399 220 7	2	2.4 6	1.3	117 411 44	44	18. 37	4.2	2. 9	939 798 1	31	16. 17	4.02	2. 72	Phosphotransferase system cellobiose-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_2189 GeneM ark.hmm 816_nt + 3906 4721	81 6	399 220 7	900	27 6.2 7	8.11	117 411 44	454	47. 39	5.57	- 2. 54	939 798 1	543	70. 81	6.15	- 1. 96	ABC-type phosphate transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_218 GeneMa rk.hmm 819_nt + 7 277 8095	81 9	399 220 7	313	95. 73	6.58	117 411 44	148 0	15 3.9 1	7.27	0. 69	939 798 1	295 9	38 4.4 4	8.59	2. 01	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_2190 GeneM ark.hmm 816_nt + 4714 5529	81 6	399 220 7	534	16 3.9 2	7.36	117 411 44	406	42. 38	5.41	- 1. 95	939 798 1	415	54. 12	5.76	- 1. 6	ABC-type phosphate transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1978 GeneM ark.hmm 450_nt - 5399 5848	45 0	399 220 7	22	12. 25	3.61	117 411 44	321	60. 76	5.92	2. 31	939 798 1	341	80. 63	6.33	2. 72	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_1800 GeneM ark.hmm 822_nt - 9281 10102	82 2	399 220 7	129	39. 31	5.3	117 411 44	178 1	18 4.5 4	7.53	2. 23	939 798 1	203 1	26 2.9 1	8.04	2. 74	Transposase and inactivated derivatives, IS30 family	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2193 GeneM ark.hmm 426_nt + 7016 7441	42 6	399 220 7	17	10	3.32	117 411 44	103	20. 59	4.36	1. 04	939 798 1	78	19. 48	4.28	0. 96	---	---	---	---
gene_2194 GeneM ark.hmm 441_nt - 7555 7995	44 1	399 220 7	15	8.5 2	3.09	117 411 44	145	28	4.81	1. 72	939 798 1	107	25. 82	4.69	1. 6	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2195 GeneM ark.hmm 1017_nt + 8207 9223	10 17	399 220 7	341 59	84 13. 39	13.0 4	117 411 44	432 79	36 24. 48	11.8 2	- 1. 22	939 798 1	290 69	30 41. 41	11.5 7	- 1. 47	Glycerol-3-phosphate dehydrogenase	METABOLISM	Energy production and conversion	C
gene_2196 GeneM ark.hmm 900_nt + 9245 10144	90 0	399 220 7	199 38	55 49. 14	12.4 4	117 411 44	334 26	31 63. 24	11.6 3	- 0. 81	939 798 1	198 77	23 50. 03	11.2	- 1. 24	UDP-glucose pyrophosphorylase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2197 GeneM ark.hmm 678_nt - 10211 10888	67 8	399 220 7	840	31 0.3 4	8.28	117 411 44	183 3	23 0.2 6	7.85	- 0. 43	939 798 1	234 4	36 7.8 7	8.52	0. 24	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2198 GeneM ark.hmm 540_nt - 10872 11411	54 0	399 220 7	378	17 5.3 4	7.45	117 411 44	980	15 4.5 7	7.27	- 0. 18	939 798 1	122 3	24 0.9 9	7.91	0. 46	5-formyltetrahydrofolate cyclo-ligase	METABOLISM	Coenzyme transport and metabolism	H
gene_2199 GeneM ark.hmm 1131_nt - 11423 12553	11 31	399 220 7	884	19 5.7 8	7.61	117 411 44	230 5	17 3.5 8	7.44	- 0. 17	939 798 1	315 1	29 6.4 5	8.21	0. 6	Metal-dependent amidase/aminoacylase/carboxypepti dase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_219 GeneMa rk.hmm 1023_nt + 8225 9247	10 23	399 220 7	598	14 6.4 2	7.19	117 411 44	448 8	37 3.6 5	8.55	1. 36	939 798 1	758 8	78 9.2 5	9.62	2. 43	Branched-chain amino acid aminotransferase/4-amino-4- deoxychorismate lyase	METABOLISM	Amino acid transport and metabolism	E
gene_21 GeneMar k.hmm 1275_nt - 12343 13617	12 75	399 220 7	710	13 9.4 9	7.12	117 411 44	247 1	16 5.0 6	7.37	0. 25	939 798 1	204 9	17 1	7.42	0. 3	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2200 GeneM ark.hmm 699_nt - 12621 13319	69 9	399 220 7	105 7	37 8.7 8	8.57	117 411 44	286 4	34 8.9 7	8.45	- 0. 12	939 798 1	266 3	40 5.3 8	8.66	0. 09	Tetrahydrodipicolinate N- succinyltransferase	METABOLISM	Amino acid transport and metabolism	E
gene_2201 GeneM ark.hmm 801_nt - 13549 14349	80 1	399 220 7	473	14 7.9 2	7.21	117 411 44	196 8	20 9.2 6	7.71	0. 5	939 798 1	224 9	29 8.7 6	8.22	1. 01	Permeases of the drug/metabolite transporter (DMT) superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_2202 GeneM ark.hmm 2466_nt - 14525 16990	24 66	399 220 7	326 9	33 2.0 5	8.38	117 411 44	974 8	33 6.6 8	8.4	0. 02	939 798 1	850 9	36 7.1 6	8.52	0. 14	Membrane carboxypeptidase (penicillin-binding protein)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M

gene_2203 GeneM ark.hmm 1257_nt + 17132 18388	12 57	399 220 7	397 6	79 2.3 2	9.63	117 411 44	175 99	11 92. 46	10.2 2	0. 59	939 798 1	901 9	76 3.4 6	9.58	- 0. 05	Tyrosyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2204 GeneM ark.hmm 2064_nt - 18466 20529	20 64	399 220 7	247 7	30 0.6 1	8.23	117 411 44	123 72	51 0.5 3	9	0. 77	939 798 1	154 54	79 6.7	9.64	1. 41	Cation transport ATPase	METABOLISM	Inorganic ion transport and metabolism	P
gene_2205 GeneM ark.hmm 279_nt - 20531 20809	27 9	399 220 7	293 3	26 33. 27	11.3 6	117 411 44	953 3	29 10. 15	11.5 1	0. 15	939 798 1	917 2	34 98. 04	11.7 7	0. 41	---	---	---	---
gene_2206 GeneM ark.hmm 849_nt + 20961 21809	84 9	399 220 7	585	17 2.6	7.43	117 411 44	301 2	30 2.1 6	8.24	0. 81	939 798 1	139 6	17 4.9 6	7.45	0. 02	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_2207 GeneM ark.hmm 573_nt + 22608 23180	57 3	399 220 7	130 2	56 9.1 7	9.15	117 411 44	479 1	71 2.1 3	9.48	0. 33	939 798 1	128 8	23 9.1 8	7.9	- 1. 25	---	---	---	---
gene_2208 GeneM ark.hmm 2259_nt - 24224 26482	22 59	399 220 7	221 99	24 61. 52	11.2 7	117 411 44	428 43	16 15. 3	10.6 6	0. 61	939 798 1	344 98	16 24. 96	10.6 7	- 0. 6	Glucan phosphorylase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2209 GeneM ark.hmm 528_nt - 26508 27035	52 8	399 220 7	624 6	29 63. 16	11.5 3	117 411 44	900 6	14 52. 74	10.5	- 1. 03	939 798 1	117 89	23 75. 79	11.2 1	- 0. 32	4-alpha-glucanotransferase	METABOLISM	Carbohydrate transport and metabolism	G
gene_220 GeneMa rk.hmm 678_nt + 9 330 10007	67 8	399 220 7	236	87. 19	6.45	117 411 44	232 2	29 1.6 9	8.19	1. 74	939 798 1	407 3	63 9.2 2	9.32	2. 87	ABC-type oligopeptide transport system, periplasmic component	METABOLISM	Amino acid transport and metabolism	E
gene_2210 GeneM ark.hmm 987_nt - 27093 28079	98 7	399 220 7	375 0	95 1.7	9.89	117 411 44	856 2	73 8.8 4	9.53	- 0. 36	939 798 1	145 48	15 68. 38	10.6 2	0. 73	4-alpha-glucanotransferase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2211 GeneM ark.hmm 1272_nt + 28629 29900	12 72	399 220 7	530 0	10 43. 7	10.0 3	117 411 44	778 5	52 1.2 7	9.03	-1	939 798 1	470 9	39 3.9 2	8.62	- 1. 41	Maltose-binding periplasmic proteins/domains	METABOLISM	Carbohydrate transport and metabolism	G
gene_2212 GeneM ark.hmm 1293_nt + 30011 31303	12 93	399 220 7	985	19 0.8 2	7.58	117 411 44	451 6	29 7.4 7	8.22	0. 64	939 798 1	380 9	31 3.4 6	8.29	0. 71	ABC-type sugar transport systems, permease components	METABOLISM	Carbohydrate transport and metabolism	G
gene_2213 GeneM ark.hmm 843_nt + 31305 32147	84 3	399 220 7	258	76. 66	6.26	117 411 44	160 9	16 2.5 6	7.34	1. 08	939 798 1	147 6	18 6.3	7.54	1. 28	ABC-type maltose transport systems, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2214 GeneM ark.hmm 801_nt + 32408 33208	80 1	399 220 7	141 1	44 1.2 5	8.79	117 411 44	722 1	76 7.8 1	9.58	0. 79	939 798 1	326 9	43 4.2 6	8.76	- 0. 03	Predicted integral membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2215 GeneM ark.hmm 987_nt + 33218 34204	98 7	399 220 7	115 5	29 3.1 2	8.2	117 411 44	978 5	84 4.3 7	9.72	1. 52	939 798 1	518 1	55 8.5 5	9.13	0. 93	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2216 GeneM ark.hmm 942_nt - 34540 35481	94 2	399 220 7	141 9	37 7.3 3	8.56	117 411 44	335 5	30 3.3 4	8.24	- 0. 32	939 798 1	183 2	20 6.9 4	7.69	- 0. 87	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2217 GeneM ark.hmm 1764_nt -	17	399 220	209	29 7.0	8.21	117 411	549	26 5.3	8.05	- 0.	939 798	326	19 7.0	7.62	- 0.	Aspartyl-tRNA synthetase	INFORMATION STORAGE AND	Translation, ribosomal structure and	J

[35459 37222	64	7	2	6		44	5	1		16	1	7	7		59		PROCESSING	biogenesis	
gene_2218 GeneMark.hmm 66_nt + 37344 37409	66	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2219 GeneMark.hmm 231_nt - 37582 37812	23 1	399 220 7	369 6	40 07. 81	11.9 7	117 411 44	208 85	77 00. 38	12.9 1	0. 94	939 798 1	131 19	60 43. 02	12.5 6	0. 59	---	---	---	---
gene_221 GeneMark.hmm 690_nt + 10072 10761	69 0	399 220 7	573	20 8.0 1	7.7	117 411 44	459 0	56 6.5 7	9.15	1. 45	939 798 1	759 8	11 71. 7	10.1 9	2. 49	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_2220 GeneMark.hmm 642_nt - 37830 38471	64 2	399 220 7	177	69. 06	6.11	117 411 44	508	67. 39	6.07	- 0. 04	939 798 1	365	60. 5	5.92	- 0. 19	Predicted metal-dependent membrane protease	POORLY CHARACTERIZED	General function prediction only	R
gene_2221 GeneMark.hmm 735_nt - 38483 39217	73 5	399 220 7	60	20. 45	4.35	117 411 44	451	52. 26	5.71	1. 36	939 798 1	291	42. 13	5.4	1. 05	---	---	---	---
gene_2222 GeneMark.hmm 198_nt - 39220 39417	19 8	399 220 7	14	17. 71	4.15	117 411 44	52	22. 37	4.48	0. 33	939 798 1	51	27. 41	4.78	0. 63	---	---	---	---
gene_2223 GeneMark.hmm 216_nt - 39417 39632	21 6	399 220 7	15	17. 4	4.12	117 411 44	178	70. 19	6.13	2. 01	939 798 1	93	45. 81	5.52	1. 4	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2224 GeneMark.hmm 195_nt - 39633 39827	19 5	399 220 7	11	14. 13	3.82	117 411 44	151	65. 95	6.04	2. 22	939 798 1	91	49. 66	5.63	1. 81	---	---	---	---
gene_2225 GeneMark.hmm 102_nt - 40100 40201	10 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2226 GeneMark.hmm 1275_nt - 40342 41616	12 75	399 220 7	250 4	49 1.9 4	8.94	117 411 44	706 5	47 1.9 5	8.88	- 0. 06	939 798 1	457 1	38 1.4 8	8.58	- 0. 36	Histidyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_525 GeneMark.hmm 942_nt - 31661 32602	94 2	399 220 7	22	5.8 5	2.55	117 411 44	804	72. 69	6.18	3. 63	939 798 1	349	39. 42	5.3	2. 75	Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB	CELLULAR PROCESSES AND SIGNALING	Cell motility	N
gene_380 GeneMark.hmm 345_nt + 814 1158	34 5	399 220 7	0	0	0	117 411 44	41	10. 12	3.34	3. 34	939 798 1	22	6.7 9	2.76	2. 76	Galactose mutarotase and related enzymes	METABOLISM	Carbohydrate transport and metabolism	G
gene_2229 GeneMark.hmm 342_nt + 44109 44450	34 2	399 220 7	87	63. 72	5.99	117 411 44	798	19 8.7 3	7.63	1. 64	939 798 1	131 0	40 7.5 8	8.67	2. 68	Predicted metal-sulfur cluster biosynthetic enzyme	POORLY CHARACTERIZED	General function prediction only	R
gene_222 GeneMark.hmm 924_nt + 10758 11681	92 4	399 220 7	282	76. 45	6.26	117 411 44	215 2	19 8.3 6	7.63	1. 37	939 798 1	460 6	53 0.4 2	9.05	2. 79	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_2230 GeneMark.hmm 1704_nt -	17 04	399 220	225 2	33 1.0	8.37	117 411	232 79	11 63.	10.1 8	1. 81	939 798	400 96	25 03.	11.2 9	2. 92	Dihydroxyacid dehydratase/phosphogluconate	METABOLISM	Amino acid transport and metabolism	E

[44659 46362		7		4		44		55			1		78			dehydratase			
gene_2231 GeneM ark.hmm 933_nt - 46595 47527	93 3	399 220 7	65	17. 45	4.13	117 411 44	474	43. 27	5.44	1. 31	939 798 1	396	45. 16	5.5	1. 37	Transketolase, C-terminal subunit	METABOLISM	Carbohydrate transport and metabolism	G
gene_2232 GeneM ark.hmm 858_nt - 47524 48381	85 8	399 220 7	63	18. 39	4.2	117 411 44	403	40	5.32	1. 12	939 798 1	379	47	5.55	1. 35	Transketolase, N-terminal subunit	METABOLISM	Carbohydrate transport and metabolism	G
gene_2233 GeneM ark.hmm 1347_nt - 48385 49731	13 47	399 220 7	80	14. 88	3.89	117 411 44	664	41. 98	5.39	1. 5	939 798 1	593	46. 84	5.55	1. 66	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_485 GeneMa rk.hmm 171_nt + 7 1153 71323	17 1	399 220 7	1	1.4 6	0.55	117 411 44	27	13. 45	3.75	3. 2	939 798 1	16	9.9 6	3.32	2. 77	---	---	---	---
gene_419 GeneMa rk.hmm 387_nt - 10627 11013	38 7	399 220 7	2	1.2 9	0.37	117 411 44	102	22. 45	4.49	4. 12	939 798 1	32	8.8	3.14	2. 77	---	---	---	---
gene_2236 GeneM ark.hmm 1008_nt + 52253 53260	10 08	399 220 7	611	15 1.8 3	7.25	117 411 44	249 7	21 0.9 8	7.72	0. 47	939 798 1	133 6	14 1.0 3	7.14	- 0. 11	Membrane protease subunits, stomatin/prohibitin homologs	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2237 GeneM ark.hmm 201_nt + 53263 53463	20 1	399 220 7	27	33. 65	5.07	117 411 44	205	86. 87	6.44	1. 37	939 798 1	141	74. 64	6.22	1. 15	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2238 GeneM ark.hmm 183_nt + 53615 53797	18 3	399 220 7	288 6	39 50. 32	11.9 5	117 411 44	726 8	33 82. 62	11.7 2	- 0. 23	939 798 1	517 0	30 06. 11	11.5 5	- 0. 4	Ribosomal protein L32	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2239 GeneM ark.hmm 150_nt + 53813 53962	15 0	399 220 7	322	53 7.7 1	9.07	117 411 44	155 8	88 4.6 4	9.79	0. 72	939 798 1	135 3	95 9.7 8	9.91	0. 84	Ribosomal protein L33	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_223 GeneMa rk.hmm 645_nt + 1 1696 12340	64 5	399 220 7	426	16 5.4 4	7.37	117 411 44	268 8	35 4.9 4	8.47	1. 1	939 798 1	634 9	10 47. 4	10.0 3	2. 66	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_591 GeneMa rk.hmm 1881_nt - 40980 42860	18 81	399 220 7	46	6.1 3	2.61	117 411 44	106 9	48. 4	5.6	2. 99	939 798 1	741	41. 92	5.39	2. 78	Methionine synthase II (cobalamin- independent)	METABOLISM	Amino acid transport and metabolism	E
gene_2241 GeneM ark.hmm 870_nt - 56258 57127	87 0	399 220 7	57	16. 41	4.04	117 411 44	379	37. 1	5.21	1. 17	939 798 1	594	72. 65	6.18	2. 14	Transcriptional regulator/sugar kinase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2242 GeneM ark.hmm 2646_nt - 57211 59856	26 46	399 220 7	154	14. 58	3.87	117 411 44	137 3	44. 19	5.47	1. 6	939 798 1	158 6	63. 78	6	2. 13	Alpha-mannosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2243 GeneM ark.hmm 1281_nt - 59947 61227	12 81	399 220 7	53	10. 36	3.37	117 411 44	594	39. 49	5.3	1. 93	939 798 1	553	45. 93	5.52	2. 15	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2244 GeneM ark.hmm 2085_nt	20	399 220	300	36.	5.17	117 411	220	89.	6.49	1.	939 798	196	10 0.3	6.65	1.	Putative alpha-1,2-mannosidase	METABOLISM	Carbohydrate transport and	G

+ 61399 63483	85	7		04		44	2	95		32	1	7	8		48			metabolism	
gene_2245 GeneM ark.hmm 1680_nt - 63523 65202	16 80	399 220 7	147	21. 92	4.45	117 411 44	869	44. 06	5.46	1. 01	939 798 1	491	31. 1	4.96	0. 51	Alpha-L-fucosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2246 GeneM ark.hmm 1230_nt + 65957 67186	12 30	399 220 7	653	13 2.9 8	7.06	117 411 44	100 8	69. 8	6.13	- 0. 93	939 798 1	349	30. 19	4.92	- 2. 14	Arginine deiminase	METABOLISM	Amino acid transport and metabolism	E
gene_2247 GeneM ark.hmm 1017_nt + 67244 68260	10 17	399 220 7	530	13 0.5 4	7.03	117 411 44	945	79. 14	6.31	- 0. 72	939 798 1	392	41. 01	5.36	- 1. 67	Ornithine carbamoyltransferase	METABOLISM	Amino acid transport and metabolism	E
gene_2248 GeneM ark.hmm 948_nt + 68425 69372	94 8	399 220 7	41	10. 83	3.44	117 411 44	484	43. 48	5.44	2	939 798 1	211	23. 68	4.57	1. 13	Carbamate kinase	METABOLISM	Amino acid transport and metabolism	E
gene_2249 GeneM ark.hmm 1512_nt + 69583 71094	15 12	399 220 7	155	25. 68	4.68	117 411 44	120 6	67. 93	6.09	1. 41	939 798 1	586	41. 24	5.37	0. 69	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_224 GeneMa rk.hmm 231_nt + 1 2508 12738	23 1	399 220 7	81	87. 83	6.46	117 411 44	719	26 5.1	8.05	1. 59	939 798 1	251	11 5.6 2	6.85	0. 39	---	---	---	---
gene_2250 GeneM ark.hmm 1332_nt + 71116 72447	13 32	399 220 7	170	31. 97	5	117 411 44	582	37. 21	5.22	0. 22	939 798 1	415	33. 15	5.05	0. 05	Acetylornithine deacetylase/Succinyl- diaminopimelate desuccinylase and related deacylases	METABOLISM	Amino acid transport and metabolism	E
gene_822 GeneMa rk.hmm 924_nt + 5 466 6389	92 4	399 220 7	12	3.2 5	1.7	117 411 44	436	40. 19	5.33	3. 63	939 798 1	194	22. 34	4.48	2. 78	ABC-type sugar transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_1563 GeneM ark.hmm 477_nt + 44847 45323	47 7	399 220 7	28	14. 7	3.88	117 411 44	354	63. 21	5.98	2. 1	939 798 1	456	10 1.7 2	6.67	2. 79	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_2253 GeneM ark.hmm 900_nt - 73905 74804	90 0	399 220 7	171 3	47 6.7 6	8.9	117 411 44	108 77	10 29. 33	10.0 1	1. 11	939 798 1	170 0	20 0.9 9	7.65	- 1. 25	Membrane protease subunits, stomatin/prohibitin homologs	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2254 GeneM ark.hmm 1152_nt - 74934 76085	11 52	399 220 7	104	22. 61	4.5	117 411 44	619	45. 76	5.52	1. 02	939 798 1	194	17. 92	4.16	- 0. 34	Alcohol dehydrogenase, class IV	METABOLISM	Energy production and conversion	C
gene_2255 GeneM ark.hmm 807_nt - 76231 77037	80 7	399 220 7	24	7.4 5	2.9	117 411 44	216	22. 8	4.51	1. 61	939 798 1	97	12. 79	3.68	0. 78	L-fucose isomerase and related proteins	METABOLISM	Carbohydrate transport and metabolism	G
gene_2256 GeneM ark.hmm 1020_nt - 76988 78007	10 20	399 220 7	26	6.3 8	2.67	117 411 44	293	24. 47	4.61	1. 94	939 798 1	155	16. 17	4.02	1. 35	L-fucose isomerase and related proteins	METABOLISM	Carbohydrate transport and metabolism	G
gene_2012 GeneM ark.hmm 381_nt - 42030 42410	38 1	399 220 7	6	3.9 4	1.98	117 411 44	112	25. 04	4.65	2. 67	939 798 1	99	27. 65	4.79	2. 81	---	---	---	---

gene_1389 GeneM ark.hmm 360_nt - 98939 99298	36 0	399 220 7	39	27. 14	4.76	117 411 44	525	12 4.2 1	6.96	2. 2	939 798 1	645	19 0.6 4	7.57	2. 81	---	---	---	---
gene_1553 GeneM ark.hmm 546_nt + 30030 30575	54 6	399 220 7	5	2.2 9	1.2	117 411 44	120	18. 72	4.23	3. 03	939 798 1	83	16. 18	4.02	2. 82	Folate-dependent phosphoribosylglycinamide formyltransferase PurN	METABOLISM	Nucleotide transport and metabolism	F
gene_225 GeneMa rk.hmm 1203_nt + 13111 14313	12 03	399 220 7	116 14	24 18. 26	11.2 4	117 411 44	924 12	65 42. 63	12.6 8	1. 44	939 798 1	779 72	68 96. 65	12.7 5	1. 51	Ribosomal protein S1	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1741 GeneM ark.hmm 411_nt + 12511 12921	41 1	399 220 7	3	1.8 3	0.87	117 411 44	108	22. 38	4.48	3. 61	939 798 1	50	12. 94	3.69	2. 82	NA			
gene_389 GeneMa rk.hmm 216_nt + 5 855 6070	21 6	399 220 7	3	3.4 8	1.8	117 411 44	214	84. 38	6.4	4. 6	939 798 1	50	24. 63	4.62	2. 82	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_409 GeneMa rk.hmm 498_nt - 3891 4388	49 8	399 220 7	5	2.5 1	1.33	117 411 44	119	20. 35	4.35	3. 02	939 798 1	83	17. 73	4.15	2. 82	Antirestriction protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2263 GeneM ark.hmm 930_nt - 88064 88993	93 0	399 220 7	70	18. 85	4.24	117 411 44	462	42. 31	5.4	1. 16	939 798 1	371	42. 45	5.41	1. 17	ABC-type sugar transport systems, permease components	METABOLISM	Carbohydrate transport and metabolism	G
gene_2264 GeneM ark.hmm 1293_nt - 89080 90372	12 93	399 220 7	27	5.2 3	2.39	117 411 44	386	25. 43	4.67	2. 28	939 798 1	226	18. 6	4.22	1. 83	ABC-type sugar transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2265 GeneM ark.hmm 1404_nt - 90401 91804	14 04	399 220 7	29	5.1 7	2.37	117 411 44	501	30. 39	4.93	2. 56	939 798 1	248	18. 8	4.23	1. 86	Sugar (pentulose and hexulose) kinases	METABOLISM	Carbohydrate transport and metabolism	G
gene_2266 GeneM ark.hmm 756_nt + 91980 92735	75 6	399 220 7	731	24 2.2	7.92	117 411 44	325 9	36 7.1 6	8.52	0. 6	939 798 1	114 2	16 0.7 3	7.33	- 0. 59	Transcriptional regulators of sugar metabolism	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2267 GeneM ark.hmm 99_nt + 9 3576 93674	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2268 GeneM ark.hmm 1506_nt - 93927 95432	15 06	399 220 7	408 7	67 9.7 8	9.41	117 411 44	914 4	51 7.1 3	9.01	- 0. 4	939 798 1	159 87	11 29. 56	10.1 4	0. 73	ABC-type metal ion transport system, periplasmic component/surface adhesin	METABOLISM	Inorganic ion transport and metabolism	P
gene_2269 GeneM ark.hmm 807_nt - 95442 96248	80 7	399 220 7	450	13 9.6 8	7.13	117 411 44	704	74. 3	6.22	- 0. 91	939 798 1	128 3	16 9.1 7	7.4	0. 27	ABC-type Mn2+/Zn2+ transport systems, permease components	METABOLISM	Inorganic ion transport and metabolism	P
gene_226 GeneMa rk.hmm 90_nt - 14585 14674	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2270 GeneM ark.hmm 705_nt - 96241 96945	70 5	399 220 7	330	11 7.2 5	6.87	117 411 44	875	10 5.7 1	6.72	- 0. 15	939 798 1	146 8	22 1.5 7	7.79	0. 92	ABC-type Mn/Zn transport systems, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_2271 GeneM ark.hmm 441_nt -	44	399 220	306	17 3.8	7.44	117 411	690	13 3.2	7.06	- 0.	939 798	673	16 2.3	7.34	- 0.	Transcriptional regulators	INFORMATION STORAGE AND	Transcription	K

[96945 97385	1	7		1		44		6		38	1		8		1		PROCESSING		
gene_438 GeneMa rk.hmm 450_nt - 24767 25216	45 0	399 220 7	7	3.9	1.96	117 411 44	303	57. 35	5.84	3. 88	939 798 1	116	27. 43	4.78	2. 82	---	---	---	---
gene_2273 GeneM ark.hmm 240_nt - 98801 99040	24 0	399 220 7	13	13. 57	3.76	117 411 44	280 0	99 3.6 6	9.96	6. 2	939 798 1	107	47. 44	5.57	1. 81	Acyl carrier protein	METABOLISM	Lipid transport and metabolism	I
gene_2415 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	13	9.2 3	3.21	3. 21	939 798 1	8	7.0 9	2.83	2. 83	NA			
gene_73 GeneMar k.hmm 987_nt - 49897 50883	98 7	399 220 7	489	12 4.1	6.96	117 411 44	974 7	84 1.0 9	9.72	2. 76	939 798 1	828 6	89 3.2 9	9.8	2. 84	IMP dehydrogenase/GMP reductase	METABOLISM	Nucleotide transport and metabolism	F
gene_2276 GeneM ark.hmm 99_nt + 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2277 GeneM ark.hmm 99_nt - 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2278 GeneM ark.hmm 99_nt + 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2279 GeneM ark.hmm 96_nt + 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_227 GeneMa rk.hmm 213_nt - 14940 15152	21 3	399 220 7	98	11 5.2 5	6.85	117 411 44	590	23 5.9 2	7.88	1. 03	939 798 1	961	48 0.0 8	8.91	2. 06	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2280 GeneM ark.hmm 99_nt + 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2281 GeneM ark.hmm 96_nt + 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2282 GeneM ark.hmm 99_nt + 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	---	---	---	---
gene_2283 GeneM ark.hmm 99_nt + 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2284 GeneM ark.hmm 99_nt - 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2285 GeneM ark.hmm 96_nt - 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			

gene_2286 GeneM ark.hmm 96_nt - 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2287 GeneM ark.hmm 99_nt - 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2288 GeneM ark.hmm 99_nt - 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2289 GeneM ark.hmm 99_nt - 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_93 GeneMar k.hmm 615_nt - 64654 65268	61 5	399 220 7	39	15. 88	3.99	117 411 44	459	63. 57	5.99	2	939 798 1	661	11 4.3 6	6.84	2. 85	Predicted Rossmann fold nucleotide-binding protein involved in DNA uptake	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2290 GeneM ark.hmm 99_nt - 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2291 GeneM ark.hmm 96_nt + 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2292 GeneM ark.hmm 96_nt - 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2293 GeneM ark.hmm 96_nt - 3 98	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2294 GeneM ark.hmm 99_nt - 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2295 GeneM ark.hmm 99_nt - 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2296 GeneM ark.hmm 99_nt - 3 101	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2297 GeneM ark.hmm 99_nt - 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2298 GeneM ark.hmm 99_nt + 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2299 GeneM ark.hmm 99_nt + 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_229 GeneMa rk.hmm 186_nt -	18	399 220	70	94.	6.56	117 411	104	47.	5.57	- 0.	939 798	113	64.	6.01	- 0.	---	---	---	---

[1193 1378	6	7		27		44		62		99	1		64		55				
gene_22 GeneMar k.hmm 1125_nt - 13713 14837	11 25	399 220 7	84	18. 7	4.23	117 411 44	488	36. 95	5.21	0. 98	939 798 1	191	18. 07	4.18	- 0. 05	O-acetylhomoserine sulfhydrylase	METABOLISM	Amino acid transport and metabolism	E
gene_2300 GeneM ark.hmm 99_nt - 3 101	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2301 GeneM ark.hmm 99_nt - 1 99	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2302 GeneM ark.hmm 102_nt + 1 102	10 2	399 220 7	4	9.8 2	3.3	117 411 44	39	32. 57	5.03	1. 73	939 798 1	73	76. 15	6.25	2. 95	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2303 GeneM ark.hmm 99_nt - 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2304 GeneM ark.hmm 99_nt + 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2305 GeneM ark.hmm 99_nt + 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2306 GeneM ark.hmm 102_nt + 1 102	10 2	399 220 7	0	0	0	117 411 44	5	4.1 8	2.06	2. 06	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2307 GeneM ark.hmm 96_nt + 1 96	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2308 GeneM ark.hmm 99_nt - 3 101	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2309 GeneM ark.hmm 102_nt + 2 103	10 2	399 220 7	0	0	0	117 411 44	2	1.6 7	0.74	0. 74	939 798 1	8	8.3 5	3.06	3. 06	NA			
gene_230 GeneMa rk.hmm 768_nt - 1641 2408	76 8	399 220 7	744	24 2.6 6	7.92	117 411 44	205 8	22 8.2 3	7.83	- 0. 09	939 798 1	156 0	21 6.1 4	7.76	- 0. 16	Acetyl-CoA carboxylase alpha subunit	METABOLISM	Lipid transport and metabolism	I
gene_2471 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	1	2.0 9	1.06	117 411 44	24	17. 03	4.09	3. 03	939 798 1	17	15. 07	3.91	2. 85	---	---	---	---
gene_294 GeneMa rk.hmm 402_nt - 66407 66808	40 2	399 220 7	2	1.2 5	0.32	117 411 44	55	11. 65	3.54	3. 22	939 798 1	34	9	3.17	2. 85	Capsular polysaccharide biosynthesis protein	METABOLISM	Carbohydrate transport and metabolism	G
gene_77 GeneMar k.hmm 228_nt - 54609 54836	22 8	399 220 7	4	4.3 9	2.14	117 411 44	92	34. 37	5.1	2. 96	939 798 1	68	31. 74	4.99	2. 85	NA			

gene_1884 GeneMark.hmm 558_nt - 10856 11413	55 8	399 220 7	17	7.6 3	2.93	117 411 44	315	48. 08	5.59	2. 66	939 798 1	290	55. 3	5.79	2. 86	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZED	General function prediction only	R
gene_427 GeneMark.hmm 147_nt - 17870 18016	14 7	399 220 7	0	0	0	117 411 44	15	8.6 9	3.12	3. 12	939 798 1	10	7.2 4	2.86	2. 86	NA			
gene_1597 GeneMark.hmm 300_nt - 15035 15334	30 0	399 220 7	48	40. 08	5.32	117 411 44	720	20 4.4 1	7.68	2. 36	939 798 1	823	29 1.9 1	8.19	2. 87	Ribosomal protein HS6-type (S12/L30/L7a)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1736 GeneMark.hmm 423_nt + 6435 6857	42 3	399 220 7	0	0	0	117 411 44	90	18. 12	4.18	4. 18	939 798 1	29	7.2 9	2.87	2. 87	NA			
gene_2318 GeneMark.hmm 102_nt - 2 103	10 2	399 220 7	0	0	0	117 411 44	6	5.0 1	2.32	2. 32	939 798 1	7	7.3	2.87	2. 87	NA			
gene_1927 GeneMark.hmm 195_nt + 53738 53932	19 5	399 220 7	37	47. 53	5.57	117 411 44	523	22 8.4 3	7.84	2. 27	939 798 1	640	34 9.2 3	8.45	2. 88	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_2234 GeneMark.hmm 285_nt - 49744 50028	28 5	399 220 7	5	4.3 9	2.14	117 411 44	98	29. 29	4.87	2. 73	939 798 1	87	32. 48	5.02	2. 88	Phosphotransferase system, galactitol-specific IIB component	METABOLISM	Carbohydrate transport and metabolism	G
gene_231 GeneMark.hmm 867_nt - 2405 3271	86 7	399 220 7	102 0	29 4.6 9	8.2	117 411 44	254 4	24 9.9 1	7.97	- 0. 23	939 798 1	239 9	29 4.4 3	8.2	0	Acetyl-CoA carboxylase beta subunit	METABOLISM	Lipid transport and metabolism	I
gene_1634 GeneMark.hmm 798_nt + 45764 46561	79 8	399 220 7	46	14. 44	3.85	117 411 44	102 0	10 8.8 6	6.77	2. 92	939 798 1	801	10 6.8 1	6.74	2. 89	Integrase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1732 GeneMark.hmm 1002_nt + 1005 2006	10 02	399 220 7	0	0	0	117 411 44	213	18. 11	4.18	4. 18	939 798 1	70	7.4 3	2.89	2. 89	Cell wall-associated hydrolases (invasion-associated proteins)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2322 GeneMark.hmm 102_nt - 2 103	10 2	399 220 7	0	0	0	117 411 44	1	0.8 4	- 0.26	- 0. 26	939 798 1	2	2.0 9	1.06	1. 06	NA			
gene_2323 GeneMark.hmm 102_nt - 2 103	10 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	2.0 9	1.06	1. 06	NA			
gene_2324 GeneMark.hmm 102_nt - 2 103	10 2	399 220 7	0	0	0	117 411 44	3	2.5 1	1.32	1. 32	939 798 1	4	4.1 7	2.06	2. 06	NA			
gene_2325 GeneMark.hmm 102_nt - 2 103	10 2	399 220 7	0	0	0	117 411 44	2	1.6 7	0.74	0. 74	939 798 1	0	0	0	0	NA			
gene_1428 GeneMark.hmm 465_nt - 23831 24295	46 5	399 220 7	216	11 6.3 6	6.86	117 411 44	299 7	54 8.9 4	9.1	2. 24	939 798 1	378 6	86 6.3 5	9.76	2. 9	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K

gene_1683 GeneM ark.hmm 1701_nt + 10718 12418	17 01	399 220 7	305	44. 91	5.49	117 411 44	361 3	18 0.9 1	7.5	2. 01	939 798 1	546 4	34 1.8	8.42	2. 93	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carbolicgase, phosphonopyruvate decarboxylase]	METABOLISM	Amino acid transport and metabolism	E
gene_1892 GeneM ark.hmm 663_nt - 17259 17921	66 3	399 220 7	7	2.6 4	1.4	117 411 44	255	32. 76	5.03	3. 63	939 798 1	125	20. 06	4.33	2. 93	Predicted amidophosphoribosyltransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_410 GeneMa rk.hmm 222_nt - 4505 4726	22 2	399 220 7	0	0	0	117 411 44	39	14. 96	3.9	3. 9	939 798 1	16	7.6 7	2.94	2. 94	NA			
gene_232 GeneMa rk.hmm 1368_nt - 3308 4675	13 68	399 220 7	222 5	40 7.4 1	8.67	117 411 44	503 1	31 3.2 3	8.29	- 0. 38	939 798 1	435 0	33 8.3 5	8.4	- 0. 27	Biotin carboxylase	METABOLISM	Lipid transport and metabolism	I
gene_2330 GeneM ark.hmm 102_nt + 3 104	10 2	399 220 7	0	0	0	117 411 44	1	0.8 4	- 0.26	- 0. 26	939 798 1	12	12. 52	3.65	3. 65	NA			
gene_534 GeneMa rk.hmm 360_nt - 40518 40877	36 0	399 220 7	17	11. 83	3.56	117 411 44	372	88. 01	6.46	2. 9	939 798 1	307	90. 74	6.5	2. 94	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2332 GeneM ark.hmm 102_nt + 3 104	10 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	3	3.1 3	1.65	1. 65	NA			
gene_2333 GeneM ark.hmm 105_nt + 1 105	10 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2334 GeneM ark.hmm 105_nt + 2 106	10 5	399 220 7	8	19. 08	4.25	117 411 44	8	6.4 9	2.7	- 1. 55	939 798 1	17	17. 23	4.11	- 0. 14	---	---	---	---
gene_421 GeneMa rk.hmm 456_nt - 11910 12365	45 6	399 220 7	3	1.6 5	0.72	117 411 44	118	22. 04	4.46	3. 74	939 798 1	54	12. 6	3.66	2. 94	Surface antigen	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2511 GeneM ark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	13	9	3.17	3. 17	939 798 1	9	7.7 9	2.96	2. 96	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_1380 GeneM ark.hmm 504_nt - 93310 93813	50 4	399 220 7	103	51. 19	5.68	117 411 44	136 2	23 0.1 6	7.85	2. 17	939 798 1	190 2	40 1.5 6	8.65	2. 97	Aspartate-semialdehyde dehydrogenase	METABOLISM	Amino acid transport and metabolism	E
gene_2338 GeneM ark.hmm 105_nt - 2 106	10 5	399 220 7	3	7.1 6	2.84	117 411 44	24	19. 47	4.28	1. 44	939 798 1	17	17. 23	4.11	1. 27	---	---	---	---
gene_415 GeneMa rk.hmm 378_nt - 8474 8851	37 8	399 220 7	0	0	0	117 411 44	89	20. 05	4.33	4. 33	939 798 1	28	7.8 8	2.98	2. 98	Putative phage replication protein RstA	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_233 GeneMa rk.hmm 423_nt -	42 3	399 220	376	22 2.6	7.8	117 411	978	19 6.9	7.62	- 0.	939 798	877	22 0.6	7.79	- 0.	3-hydroxymyristoyl/3- hydroxydecanoyl-(acyl carrier	METABOLISM	Lipid transport and metabolism	I

[4687 5109		7		6		44		2		18	1		1		01	protein) dehydratases			
gene_2240 GeneM ark.hmm 1881_nt - 54384 56264	18 81	399 220 7	93	12. 38	3.63	117 411 44	117 8	53. 34	5.74	2. 11	939 798 1	172 7	97. 69	6.61	2. 98	---	---	---	---
gene_535 GeneMa rk.hmm 426_nt - 40888 41313	42 6	399 220 7	23	13. 52	3.76	117 411 44	369	73. 77	6.21	2. 45	939 798 1	427	10 6.6 6	6.74	2. 98	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2260 GeneM ark.hmm 1779_nt - 84029 85807	17 79	399 220 7	34	4.7 9	2.26	117 411 44	129 4	61. 95	5.95	3. 69	939 798 1	638	38. 16	5.25	2. 99	NA			
gene_1144 GeneM ark.hmm 210_nt + 62479 62688	21 0	399 220 7	130	15 5.0 6	7.28	117 411 44	222 0	90 0.3 7	9.81	2. 53	939 798 1	247 1	12 52. 04	10.2 9	3. 01	Lactoylglutathione lyase and related lyases	METABOLISM	Amino acid transport and metabolism	E
gene_2344 GeneM ark.hmm 108_nt + 2 109	10 8	399 220 7	7	16. 24	4.02	117 411 44	19	14. 98	3.91	- 0. 11	939 798 1	18	17. 73	4.15	0. 13	---	---	---	---
gene_2345 GeneM ark.hmm 105_nt - 3 107	10 5	399 220 7	11	26. 24	4.71	117 411 44	15	12. 17	3.6	- 1. 11	939 798 1	14	14. 19	3.83	- 0. 88	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_82 GeneMar k.hmm 1038_nt - 55915 56952	10 38	399 220 7	52	12. 55	3.65	117 411 44	119 1	97. 72	6.61	2. 96	939 798 1	986	10 1.0 8	6.66	3. 01	Isocitrate/isopropylmalate dehydrogenase	METABOLISM	Energy production and conversion	C
gene_888 GeneMa rk.hmm 246_nt - 37464 37709	24 6	399 220 7	1	1.0 2	0.03	117 411 44	76	26. 31	4.72	4. 69	939 798 1	19	8.2 2	3.04	3. 01	ABC-type cobalt transport system, permease component CbiQ and related transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_2348 GeneM ark.hmm 105_nt + 3 107	10 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_958 GeneMa rk.hmm 954_nt + 5 7587 58540	95 4	399 220 7	275	72. 21	6.17	117 411 44	693 5	61 9.1 4	9.27	3. 1	939 798 1	526 5	58 7.2 4	9.2	3. 03	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_234 GeneMa rk.hmm 486_nt - 5106 5591	48 6	399 220 7	930	47 9.3 3	8.9	117 411 44	165 2	28 9.5 1	8.18	- 0. 72	939 798 1	167 2	36 6.0 7	8.52	- 0. 38	Biotin carboxyl carrier protein	METABOLISM	Lipid transport and metabolism	I
gene_473 GeneMa rk.hmm 1179_nt - 62598 63776	11 79	399 220 7	67	14. 23	3.83	117 411 44	887	64. 08	6	2. 17	939 798 1	128 5	11 5.9 7	6.86	3. 03	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_79 GeneMar k.hmm 144_nt - 54924 55067	14 4	399 220 7	5	8.7	3.12	117 411 44	118	69. 79	6.13	3. 01	939 798 1	96	70. 94	6.15	3. 03	---	---	---	---
gene_336 GeneMa rk.hmm 111_nt - 28277 28387	11 1	399 220 7	3	6.7 7	2.76	117 411 44	100	76. 73	6.26	3. 5	939 798 1	58	55. 6	5.8	3. 04	Thymidylate synthase	METABOLISM	Nucleotide transport and metabolism	F
gene_1426 GeneM ark.hmm 306_nt - 22565 22870	30 6	399 220 7	65	53. 21	5.73	117 411 44	890	24 7.7 2	7.95	2. 22	939 798 1	126 7	44 0.5 8	8.78	3. 05	Transposase and inactivated derivatives, IS30 family	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_1830 GeneM ark.hmm 648_nt + 32899 33546	64 8	399 220 7	5	1.9 3	0.95	117 411 44	152	19. 98	4.32	3. 37	939 798 1	98	16. 09	4.01	3. 06	---	---	---	---
gene_2793 GeneM ark.hmm 186_nt - 2 187	18 6	399 220 7	7	9.4 3	3.24	117 411 44	121	55. 41	5.79	2. 55	939 798 1	139	79. 52	6.31	3. 07	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_86 GeneMar k.hmm 348_nt - 58448 58795	34 8	399 220 7	9	6.4 8	2.7	117 411 44	246	60. 21	5.91	3. 21	939 798 1	178	54. 43	5.77	3. 07	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2357 GeneM ark.hmm 78_nt - 3 80	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_1759 GeneM ark.hmm 228_nt + 30427 30654	22 8	399 220 7	0	0	0	117 411 44	54	20. 17	4.33	4. 33	939 798 1	18	8.4	3.07	3. 07	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2359 GeneM ark.hmm 111_nt + 2 112	11 1	399 220 7	0	0	0	117 411 44	4	3.0 7	1.62	1. 62	939 798 1	5	4.7 9	2.26	2. 26	NA			
gene_235 GeneMa rk.hmm 1236_nt - 5594 6829	12 36	399 220 7	137 2	27 8.0 5	8.12	117 411 44	402 3	27 7.2 2	8.11	- 0. 01	939 798 1	386 6	33 2.8 2	8.38	0. 26	3-oxoacyl-(acyl-carrier-protein) synthase	METABOLISM	Lipid transport and metabolism	I
gene_2360 GeneM ark.hmm 111_nt - 1 111	11 1	399 220 7	75	16 9.2 5	7.4	117 411 44	683	52 4.0 7	9.03	1. 63	939 798 1	784	75 1.5 5	9.55	2. 15	NA			
gene_1326 GeneM ark.hmm 630_nt - 35943 36572	63 0	399 220 7	4	1.5 9	0.67	117 411 44	136	18. 39	4.2	3. 53	939 798 1	80	13. 51	3.76	3. 09	NA			
gene_327 GeneMa rk.hmm 150_nt + 2 3185 23334	15 0	399 220 7	0	0	0	117 411 44	24	13. 63	3.77	3. 77	939 798 1	12	8.5 1	3.09	3. 09	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_506 GeneMa rk.hmm 864_nt - 18905 19768	86 4	399 220 7	8	2.3 2	1.21	117 411 44	384	37. 85	5.24	4. 03	939 798 1	160	19. 7	4.3	3. 09	Putative L-xylulose-5-phosphate 3- epimerase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1329 GeneM ark.hmm 225_nt - 38120 38344	22 5	399 220 7	1	1.1 1	0.15	117 411 44	59	22. 33	4.48	4. 33	939 798 1	20	9.4 6	3.24	3. 09	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_1885 GeneM ark.hmm 225_nt - 11482 11706	22 5	399 220 7	4	4.4 5	2.15	117 411 44	78	29. 53	4.88	2. 73	939 798 1	80	37. 83	5.24	3. 09	Surface antigen	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1176 GeneM ark.hmm 141_nt + 3 143	14 1	399 220 7	4	7.1 1	2.83	117 411 44	59	35. 64	5.16	2. 33	939 798 1	81	61. 13	5.93	3. 1	Collagenase and related proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_1381 GeneM ark.hmm 150_nt - 93874 94023	15 0	399 220 7	6	10. 02	3.32	117 411 44	112	63. 59	5.99	2. 67	939 798 1	121	85. 83	6.42	3. 1	Aspartate-semialdehyde dehydrogenase	METABOLISM	Amino acid transport and metabolism	E

gene_503 GeneMark.hmm 1134_nt - 15104 16237	11 34	399 220 7	8	1.7 7	0.82	117 411 44	341	25. 61	4.68	3. 86	939 798 1	163	15. 29	3.93	3. 11	Predicted Zn-dependent hydrolases of the beta-lactamase fold	POORLY CHARACTERIZED	General function prediction only	R
gene_2369 GeneMark.hmm 114_nt - 2 115	11 4	399 220 7	0	0	0	117 411 44	4	2.9 9	1.58	1. 58	939 798 1	10	9.3 3	3.22	3. 22	NA			
gene_236 GeneMark.hmm 732_nt - 6851 7582	73 2	399 220 7	547	18 7.1 8	7.55	117 411 44	149 9	17 4.4 1	7.45	- 0. 1	939 798 1	172 4	25 0.6 1	7.97	0. 42	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	METABOLISM	Lipid transport and metabolism	I
gene_1268 GeneMark.hmm 171_nt + 72466 72636	17 1	399 220 7	0	0	0	117 411 44	20	9.9 6	3.32	3. 32	939 798 1	14	8.7 1	3.12	3. 12	---	---	---	---
gene_1980 GeneMark.hmm 1464_nt - 6247 7710	14 64	399 220 7	31	5.3	2.41	117 411 44	697	40. 55	5.34	2. 93	939 798 1	635	46. 15	5.53	3. 12	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_600 GeneMark.hmm 1416_nt - 51542 52957	14 16	399 220 7	37	6.5 5	2.71	117 411 44	115 7	69. 59	6.12	3. 41	939 798 1	759	57. 04	5.83	3. 12	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2373 GeneMark.hmm 114_nt + 2 115	11 4	399 220 7	12	26. 37	4.72	117 411 44	36	26. 9	4.75	0. 03	939 798 1	77	71. 87	6.17	1. 45	NA			
gene_2374 GeneMark.hmm 99_nt - 17 115	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_727 GeneMark.hmm 981_nt + 100168 101148	98 1	399 220 7	51	13. 02	3.7	117 411 44	245 9	21 3.4 9	7.74	4. 04	939 798 1	105 6	11 4.5 4	6.84	3. 14	Transcriptional regulator, contains sigma factor-related N-terminal domain	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_840 GeneMark.hmm 141_nt + 2 142	14 1	399 220 7	1	1.7 8	0.83	117 411 44	26	15. 71	3.97	3. 14	939 798 1	21	15. 85	3.99	3. 16	NA			
gene_2377 GeneMark.hmm 114_nt + 2 115	11 4	399 220 7	0	0	0	117 411 44	2	1.4 9	0.58	0. 58	939 798 1	3	2.8	1.49	1. 49	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_905 GeneMark.hmm 288_nt - 10108 10395	28 8	399 220 7	2	1.7 4	0.8	117 411 44	54	15. 97	4	3. 2	939 798 1	42	15. 52	3.96	3. 16	---	---	---	---
gene_2379 GeneMark.hmm 114_nt - 2 115	11 4	399 220 7	4	8.7 9	3.14	117 411 44	7	5.2 3	2.39	- 0. 75	939 798 1	9	8.4	3.07	- 0. 07	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_237 GeneMark.hmm 921_nt - 7616 8536	92 1	399 220 7	157 6	42 8.6 3	8.74	117 411 44	171 6	15 8.6 9	7.31	- 1. 43	939 798 1	225 7	26 0.7 6	8.03	- 0. 71	(acyl-carrier-protein) S-malonyltransferase	METABOLISM	Lipid transport and metabolism	I
gene_2380 GeneMark.hmm 114_nt - 3 116	11 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	6	5.6	2.49	2. 49	NA			
gene_2046 GeneMark.hmm 834_nt -	83	399 220	8	2.4	1.26	117 411	352	35.	5.17	3.	939 798	169	21.	4.43	3.	ABC-type sugar transport system,	METABOLISM	Carbohydrate transport and	G

73119 73952	4	7				44		95		91	1		56		17	permease component		metabolism	
gene_1611 GeneM ark.hmm 678_nt + 23798 24475	67 8	399 220 7	26	9.6 1	3.26	117 411 44	981	12 3.2 3	6.95	3. 69	939 798 1	560	87. 89	6.46	3. 2	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_430 GeneMa rk.hmm 1806_nt 19098 20903	18 06	399 220 7	6	0.8 3	- 0.27	117 411 44	314	14. 81	3.89	4. 16	939 798 1	130	7.6 6	2.94	3. 21	Type IV secretory pathway, VirD4 components	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_601 GeneMa rk.hmm 1839_nt 52970 54808	18 39	399 220 7	55	7.4 9	2.91	117 411 44	168 9	78. 22	6.29	3. 38	939 798 1	119 9	69. 37	6.12	3. 21	Phosphotransferase system IIC components, glucose/maltose/N- acetylglucosamine-specific	METABOLISM	Carbohydrate transport and metabolism	G
gene_2385 GeneM ark.hmm 93_nt + 1 93	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1403 GeneM ark.hmm 960_nt 4428 5387	96 0	399 220 7	25	6.5 2	2.71	117 411 44	727	64. 5	6.01	3. 3	939 798 1	549	60. 85	5.93	3. 22	---	---	---	---
gene_1593 GeneM ark.hmm 183_nt 10383 10565	18 3	399 220 7	0	0	0	117 411 44	20	9.3 1	3.22	3. 22	939 798 1	16	9.3	3.22	3. 22	---	---	---	---
gene_1552 GeneM ark.hmm 1023_nt + 29011 30033	10 23	399 220 7	16	3.9 2	1.97	117 411 44	591	49. 2	5.62	3. 65	939 798 1	352	36. 61	5.19	3. 22	Phosphoribosylaminoimidazole (AIR) synthetase	METABOLISM	Nucleotide transport and metabolism	F
gene_537 GeneMa rk.hmm 624_nt 42940 43563	62 4	399 220 7	82	32. 92	5.04	117 411 44	105 0	14 3.3 2	7.16	2. 12	939 798 1	181 4	30 9.3 3	8.27	3. 23	Predicted phosphatases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_238 GeneMa rk.hmm 618_nt 8529 9146	61 8	399 220 7	403	16 3.3 4	7.35	117 411 44	741	10 2.1 2	6.67	- 0. 68	939 798 1	770	13 2.5 8	7.05	- 0. 3	Dioxygenases related to 2- nitropropane dioxygenase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_779 GeneMa rk.hmm 240_nt + 1 56802 157041	24 0	399 220 7	1	1.0 4	0.06	117 411 44	52	18. 45	4.21	4. 15	939 798 1	22	9.7 5	3.29	3. 23	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2391 GeneM ark.hmm 87_nt + 3 119	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_228 GeneMa rk.hmm 270_nt 3 272	27 0	399 220 7	15	13. 92	3.8	117 411 44	211	66. 56	6.06	2. 26	939 798 1	331	13 0.4 5	7.03	3. 23	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1731 GeneM ark.hmm 1008_nt + 1 1008	10 08	399 220 7	0	0	0	117 411 44	191	16. 14	4.01	4. 01	939 798 1	90	9.5	3.25	3. 25	NA			
gene_596 GeneMa rk.hmm 510_nt 47615 48124	51 0	399 220 7	46	22. 59	4.5	117 411 44	662	11 0.5 5	6.79	2. 29	939 798 1	104 1	21 7.1 9	7.76	3. 26	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2395 GeneM ark.hmm 78_nt	78	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

[43 120		7				44					1								
gene_205 GeneMa rk.hmm 219_nt + 6 1925 62143	21 9	399 220 7	4	4.5 8	2.19	117 411 44	126	49	5.61	3. 42	939 798 1	90	43. 73	5.45	3. 26	---	---	---	
gene_2397 GeneM ark.hmm 78_nt + 2 79	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1405 GeneM ark.hmm 135_nt 6611 6745	13 5	399 220 7	1	1.8 6	0.89	117 411 44	25	15. 77	3.98	3. 09	939 798 1	23	18. 13	4.18	3. 29	NA			
gene_1852 GeneM ark.hmm 120_nt + 13845 13964	12 0	399 220 7	0	0	0	117 411 44	20	14. 2	3.83	3. 83	939 798 1	11	9.7 5	3.29	3. 29	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_239 GeneMa rk.hmm 486_nt 9064 9549	48 6	399 220 7	179	92. 26	6.53	117 411 44	625	10 9.5 3	6.78	0. 25	939 798 1	514	11 2.5 4	6.81	0. 28	Dioxygenases related to 2- nitropropane dioxygenase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_23 GeneMar k.hmm 123_nt 14850 14972	12 3	399 220 7	6	12. 22	3.61	117 411 44	7	4.8 5	2.28	- 1. 33	939 798 1	3	2.6	1.38	- 2. 23	O-acetylhomoserine sulfhydrylase	METABOLISM	Amino acid transport and metabolism	E
gene_884 GeneMa rk.hmm 261_nt + 3 3428 33688	26 1	399 220 7	1	0.9 6	- 0.06	117 411 44	38	12. 4	3.63	3. 69	939 798 1	23	9.3 8	3.23	3. 29	---	---	---	---
gene_2401 GeneM ark.hmm 93_nt + 1 93	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_801 GeneMa rk.hmm 1902_nt + 177777 179678	19 02	399 220 7	15	1.9 8	0.98	117 411 44	777	34. 79	5.12	4. 14	939 798 1	347	19. 41	4.28	3. 3	---	---	---	---
gene_2136 GeneM ark.hmm 297_nt 68889 69185	29 7	399 220 7	5	4.2 2	2.08	117 411 44	196	56. 21	5.81	3. 73	939 798 1	117	41. 92	5.39	3. 31	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2404 GeneM ark.hmm 120_nt 3 122	12 0	399 220 7	0	0	0	117 411 44	5	3.5 5	1.83	1. 83	939 798 1	14	12. 41	3.63	3. 63	NA			
gene_1327 GeneM ark.hmm 741_nt 36849 37589	74 1	399 220 7	4	1.3 5	0.44	117 411 44	219	25. 17	4.65	4. 21	939 798 1	94	13. 5	3.75	3. 31	Site-specific recombinases, DNA invertase Pin homologs	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2538 GeneM ark.hmm 117_nt 3 119	11 7	399 220 7	0	0	0	117 411 44	18	13. 1	3.71	3. 71	939 798 1	11	10	3.32	3. 32	NA			
gene_2407 GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	126	26 3.0 1	8.04	117 411 44	93	66. 01	6.04	-2	939 798 1	84	74. 48	6.22	- 1. 82	NA			
gene_81 GeneMar k.hmm 270_nt 	27 0	399 220	11	10. 21	3.35	117 411	301	94. 95	6.57	3. 22	939 798	259	10 2.0	6.67	3. 32	Predicted membrane protein	POORLY CHARACTERIZ	Function unknown	S

[55649 55918		7				44					1		7				ED		
gene_777 GeneMa rk.hmm 339_nt + 1 54786 155124	33 9	399 220 7	0	0	0	117 411 44	57	14. 32	3.84	3. 84	939 798 1	32	10. 04	3.33	3. 33	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_240 GeneMa rk.hmm 225_nt 9668 9892	22 5	399 220 7	192 0	21 37. 5	11.0 6	117 411 44	370 9	14 03. 99	10.4 6	- 0. 6	939 798 1	213 2	10 08. 25	9.98	- 1. 08	Acyl carrier protein	METABOLISM	Lipid transport and metabolism	I
gene_2341 GeneM ark.hmm 105_nt 2 106	10 5	399 220 7	0	0	0	117 411 44	7	5.6 8	2.51	2. 51	939 798 1	10	10. 13	3.34	3. 34	Transposase and inactivated derivatives, IS30 family	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_393 GeneMa rk.hmm 306_nt + 8 465 8770	30 6	399 220 7	2	1.6 4	0.71	117 411 44	217	60. 4	5.92	5. 21	939 798 1	49	17. 04	4.09	3. 38	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_388 GeneMa rk.hmm 576_nt + 5 160 5735	57 6	399 220 7	13	5.6 5	2.5	117 411 44	257 2	38 0.3 1	8.57	6. 07	939 798 1	320	59. 11	5.89	3. 39	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_498 GeneMa rk.hmm 2652_nt 8760 11411	26 52	399 220 7	221 2	20 8.9 3	7.71	117 411 44	669 72	21 50. 85	11.0 7	3. 36	939 798 1	549 13	22 03. 27	11.1 1	3. 4	NAD-dependent aldehyde dehydrogenases	METABOLISM	Energy production and conversion	C
gene_2364 GeneM ark.hmm 111_nt + 3 113	11 1	399 220 7	0	0	0	117 411 44	13	9.9 7	3.32	3. 32	939 798 1	11	10. 54	3.4	3. 4	NA			
gene_1733 GeneM ark.hmm 915_nt + 2021 2935	91 5	399 220 7	0	0	0	117 411 44	277	25. 78	4.69	4. 69	939 798 1	92	10. 7	3.42	3. 42	NA			
gene_1916 GeneM ark.hmm 339_nt 43488 43826	33 9	399 220 7	6	4.4 3	2.15	117 411 44	169	42. 46	5.41	3. 26	939 798 1	155	48. 65	5.6	3. 45	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2417 GeneM ark.hmm 78_nt 46 123	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2418 GeneM ark.hmm 90_nt + 2 91	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_416 GeneMa rk.hmm 717_nt 9086 9802	71 7	399 220 7	4	1.4	0.48	117 411 44	176	20. 91	4.39	3. 91	939 798 1	103	15. 29	3.93	3. 45	DNA segregation ATPase FtsK/SpoIIIE and related proteins	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_241 GeneMa rk.hmm 975_nt 9952 10926	97 5	399 220 7	256 4	65 8.7 2	9.36	117 411 44	157 94	13 79. 68	10.4 3	1. 07	939 798 1	116 75	12 74. 14	10.3 2	0. 96	3-oxoacyl-[acyl-carrier-protein] synthase III	METABOLISM	Lipid transport and metabolism	I
gene_2420 GeneM ark.hmm 120_nt 3 122	12 0	399 220 7	3	6.2 6	2.65	117 411 44	29	20. 58	4.36	1. 71	939 798 1	11	9.7 5	3.29	0. 64	---	---	---	---
gene_2421 GeneM ark.hmm 123_nt	12 3	399 220	31	63. 13	5.98	117 411	87	60. 24	5.91	- 0.	939 798	71	61. 42	5.94	- 0.	---	---	---	---

1 123		7				44				07	1				04				
gene_1270 GeneM ark.hmm 324_nt + 72898 73221	32 4	399 220 7	2	1.5 5	0.63	117 411 44	135	35. 49	5.15	4. 52	939 798 1	52	17. 08	4.09	3. 46	---	---	---	
gene_2423 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	2	4.1 7	2.06	117 411 44	19	13. 49	3.75	1. 69	939 798 1	22	19. 51	4.29	2. 23	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1401 GeneM ark.hmm 351_nt - 3665 4015	35 1	399 220 7	2	1.4 3	0.51	117 411 44	66	16. 01	4	3. 49	939 798 1	52	15. 76	3.98	3. 47	---	---	---	
gene_638 GeneMa rk.hmm 657_nt + 3 4313 34969	65 7	399 220 7	6	2.2 9	1.19	117 411 44	205	26. 58	4.73	3. 54	939 798 1	161	26. 08	4.7	3. 51	Predicted branched-chain amino acid permease (azaleucine resistance)	METABOLISM	Amino acid transport and metabolism	E
gene_2768 GeneM ark.hmm 111_nt - 1 111	11 1	399 220 7	0	0	0	117 411 44	15	11. 51	3.52	3. 52	939 798 1	12	11. 5	3.52	3. 52	NA			
gene_2427 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	266	55 5.2 5	9.12	117 411 44	104 0	73 8.1 4	9.53	0. 41	939 798 1	803	71 2.0 3	9.48	0. 36	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2428 GeneM ark.hmm 111_nt - 3 113	11 1	399 220 7	14	31. 59	4.98	117 411 44	165	12 6.6	6.98	2	939 798 1	62	59. 43	5.89	0. 91	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_723 GeneMa rk.hmm 195_nt - 97414 97608	19 5	399 220 7	1	1.2 8	0.36	117 411 44	46	20. 09	4.33	3. 97	939 798 1	27	14. 73	3.88	3. 52	ABC-type Fe3+ transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_242 GeneMa rk.hmm 435_nt - 10926 11360	43 5	399 220 7	183 7	10 57. 81	10.0 5	117 411 44	877 1	17 17. 31	10.7 5	0. 7	939 798 1	613 5	15 00. 69	10.5 5	0. 5	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_193 GeneMa rk.hmm 171_nt - 49790 49960	17 1	399 220 7	1	1.4 6	0.55	117 411 44	74	36. 86	5.2	4. 65	939 798 1	27	16. 8	4.07	3. 52	---	---	---	---
gene_2405 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	9	6.3 9	2.68	2. 68	939 798 1	13	11. 53	3.53	3. 53	NA			
gene_1550 GeneM ark.hmm 3726_nt + 23714 27439	37 26	399 220 7	19	1.2 8	0.35	117 411 44	928	21. 21	4.41	4. 06	939 798 1	520	14. 85	3.89	3. 54	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	METABOLISM	Nucleotide transport and metabolism	F
gene_1160 GeneM ark.hmm 954_nt + 77512 78465	95 4	399 220 7	15	3.9 4	1.98	117 411 44	312	27. 85	4.8	2. 82	939 798 1	414	46. 18	5.53	3. 55	Competence protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_1391 GeneM ark.hmm 258_nt - 99817 100074	25 8	399 220 7	10	9.7 1	3.28	117 411 44	198	65. 36	6.03	2. 75	939 798 1	278	11 4.6 5	6.84	3. 56	NA			
gene_2435 GeneM ark.hmm 90_nt + 3 92	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			

gene_1742 GeneM ark.hmm 1644_nt + 12969 14612	16 44	399 220 7	0	0	0	117 411 44	392	20. 31	4.34	4. 34	939 798 1	184	11. 91	3.57	3. 57	Adenine-specific DNA methylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1977 GeneM ark.hmm 312_nt - 5060 5371	31 2	399 220 7	6	4.8 2	2.27	117 411 44	201	54. 87	5.78	3. 51	939 798 1	168	57. 3	5.84	3. 57	Phosphotransferase system fructose-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_1974 GeneM ark.hmm 339_nt - 2868 3206	33 9	399 220 7	11	8.1 3	3.02	117 411 44	269	67. 58	6.08	3. 06	939 798 1	314	98. 56	6.62	3. 6	Transketolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_1331 GeneM ark.hmm 225_nt - 39890 40114	22 5	399 220 7	0	0	0	117 411 44	44	16. 66	4.06	4. 06	939 798 1	26	12. 3	3.62	3. 62	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_243 GeneMa rk.hmm 786_nt - 11454 12239	78 6	399 220 7	593	18 8.9 8	7.56	117 411 44	116 4	12 6.1 3	6.98	- 0. 58	939 798 1	102 5	13 8.7 6	7.12	- 0. 44	Enoyl-CoA hydratase/carnithine racemase	METABOLISM	Lipid transport and metabolism	I
gene_1737 GeneM ark.hmm 231_nt + 6854 7084	23 1	399 220 7	1	1.0 8	0.12	117 411 44	51	18. 8	4.23	4. 11	939 798 1	29	13. 36	3.74	3. 62	---	---	---	---
gene_407 GeneMa rk.hmm 681_nt - 1170 1850	68 1	399 220 7	2	0.7 4	- 0.44	117 411 44	154	19. 26	4.27	4. 71	939 798 1	58	9.0 6	3.18	3. 62	---	---	---	---
gene_2491 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	10	7.1	2.83	2. 83	939 798 1	14	12. 41	3.63	3. 63	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2314 GeneM ark.hmm 102_nt - 3 104	10 2	399 220 7	0	0	0	117 411 44	5	4.1 8	2.06	2. 06	939 798 1	12	12. 52	3.65	3. 65	NA			
gene_1390 GeneM ark.hmm 294_nt - 99276 99569	29 4	399 220 7	8	6.8 2	2.77	117 411 44	190	55. 04	5.78	3. 01	939 798 1	238	86. 14	6.43	3. 66	---	---	---	---
gene_2347 GeneM ark.hmm 108_nt - 2 109	10 8	399 220 7	0	0	0	117 411 44	6	4.7 3	2.24	2. 24	939 798 1	13	12. 81	3.68	3. 68	NA			
gene_2799 GeneM ark.hmm 108_nt + 3 110	10 8	399 220 7	0	0	0	117 411 44	8	6.3 1	2.66	2. 66	939 798 1	13	12. 81	3.68	3. 68	NA			
gene_509 GeneMa rk.hmm 282_nt - 21016 21297	28 2	399 220 7	2	1.7 8	0.83	117 411 44	92	27. 79	4.8	3. 97	939 798 1	63	23. 77	4.57	3. 74	Phosphotransferase system, galactitol-specific IIB component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2272 GeneM ark.hmm 1269_nt - 97540 98808	12 69	399 220 7	23	4.5 4	2.18	117 411 44	174 26	11 69. 57	10.1 9	8. 01	939 798 1	732	61. 38	5.94	3. 76	Protein involved in D-alanine esterification of lipoteichoic acid and wall teichoic acid (D-alanine transfer protein)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1032 GeneM ark.hmm 582_nt + 124257 124838	58 2	399 220 7	10	4.3	2.11	117 411 44	262	38. 34	5.26	3. 15	939 798 1	329	60. 15	5.91	3. 8	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	METABOLISM	Nucleotide transport and metabolism	F

gene_244 GeneMa rk.hmm 1278_nt + 12564 13841	12 78	399 220 7	132 0	25 8.7 2	8.02	117 411 44	703 6	46 8.9	8.87	0. 85	939 798 1	427 7	35 6.1	8.48	0. 46	Aspartokinases	METABOLISM	Amino acid transport and metabolism	E
gene_580 GeneMa rk.hmm 456_nt - 31668 32123	45 6	399 220 7	22	12. 08	3.6	117 411 44	428	79. 94	6.32	2. 72	939 798 1	731	17 0.5 8	7.41	3. 81	---	---	---	---
gene_439 GeneMa rk.hmm 1359_nt - 25200 26558	13 59	399 220 7	7	1.2 9	0.37	117 411 44	445	27. 89	4.8	4. 43	939 798 1	234	18. 32	4.2	3. 83	Site-specific DNA methylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2452 GeneM ark.hmm 90_nt - 33 122	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_593 GeneMa rk.hmm 225_nt - 43692 43916	22 5	399 220 7	19	21. 15	4.4	117 411 44	242	91. 61	6.52	2. 12	939 798 1	635	30 0.3	8.23	3. 83	Transposase and inactivated derivatives, IS30 family	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1748 GeneM ark.hmm 1086_nt + 21033 22118	10 86	399 220 7	2	0.4 6	- 1.12	117 411 44	182	14. 27	3.84	4. 96	939 798 1	68	6.6 6	2.74	3. 86	NA			
gene_1594 GeneM ark.hmm 780_nt - 10567 11346	78 0	399 220 7	4	1.2 8	0.36	117 411 44	257	28. 06	4.81	4. 45	939 798 1	138	18. 83	4.23	3. 87	---	---	---	---
gene_147 GeneMa rk.hmm 1098_nt + 2687 3784	10 98	399 220 7	113	25. 78	4.69	117 411 44	161 1	12 4.9 6	6.97	2. 28	939 798 1	395 0	38 2.7 9	8.58	3. 89	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_211 GeneMa rk.hmm 297_nt + 3 299	29 7	399 220 7	4	3.3 7	1.75	117 411 44	88	25. 24	4.66	2. 91	939 798 1	139	49. 8	5.64	3. 89	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2458 GeneM ark.hmm 84_nt + 3 86	84	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_295 GeneMa rk.hmm 318_nt - 66820 67137	31 8	399 220 7	1	0.7 9	- 0.34	117 411 44	74	19. 82	4.31	4. 65	939 798 1	35	11. 71	3.55	3. 89	Capsular polysaccharide biosynthesis protein	METABOLISM	Carbohydrate transport and metabolism	G
gene_245 GeneMa rk.hmm 372_nt + 1 3990 14361	37 2	399 220 7	827	55 6.8 6	9.12	117 411 44	285 6	65 3.8 9	9.35	0. 23	939 798 1	207 9	59 4.6 7	9.22	0. 1	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2393 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	6	4.2 6	2.09	2. 09	939 798 1	17	15. 07	3.91	3. 91	NA			
gene_2508 GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	8	5.6 8	2.51	2. 51	939 798 1	17	15. 07	3.91	3. 91	NA			
gene_520 GeneMa rk.hmm 462_nt - 29283 29744	46 2	399 220 7	2	1.0 8	0.12	117 411 44	231	42. 59	5.41	5. 29	939 798 1	71	16. 35	4.03	3. 91	Competence protein ComGF	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U

gene_2410 GeneM ark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	6	4.1 5	2.05	2. 05	939 798 1	18	15. 57	3.96	3. 96	NA			
gene_420 GeneMa rk.hmm 315_nt - 11029 11343	31 5	399 220 7	0	0	0	117 411 44	73	19. 74	4.3	4. 3	939 798 1	46	15. 54	3.96	3. 96	---	---	---	---
gene_2465 GeneM ark.hmm 93_nt - 29 121	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_508 GeneMa rk.hmm 486_nt - 20454 20939	48 6	399 220 7	0	0	0	117 411 44	99	17. 35	4.12	4. 12	939 798 1	71	15. 54	3.96	3. 96	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_2467 GeneM ark.hmm 81_nt + 4 3 123	81	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2468 GeneM ark.hmm 78_nt - 2 79	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_965 GeneMa rk.hmm 147_nt - 62626 62772	14 7	399 220 7	0	0	0	117 411 44	24	13. 91	3.8	3. 8	939 798 1	22	15. 92	3.99	3. 99	NA			
gene_246 GeneMa rk.hmm 1275_nt + 14575 15849	12 75	399 220 7	194 1	38 1.3 3	8.57	117 411 44	567 9	37 9.3 6	8.57	0	939 798 1	827 8	69 0.8 5	9.43	0. 86	Seryl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_1352 GeneM ark.hmm 225_nt - 67630 67854	22 5	399 220 7	0	0	0	117 411 44	50	18. 93	4.24	4. 24	939 798 1	34	16. 08	4.01	4. 01	Glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_639 GeneMa rk.hmm 324_nt + 3 4959 35282	32 4	399 220 7	0	0	0	117 411 44	74	19. 45	4.28	4. 28	939 798 1	50	16. 42	4.04	4. 04	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_592 GeneMa rk.hmm 213_nt - 43121 43333	21 3	399 220 7	6	7.0 6	2.82	117 411 44	89	35. 59	5.15	2. 33	939 798 1	234	11 6.9	6.87	4. 05	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2473 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2310 GeneM ark.hmm 102_nt + 1 102	10 2	399 220 7	0	0	0	117 411 44	5	4.1 8	2.06	2. 06	939 798 1	16	16. 69	4.06	4. 06	NA			
gene_2475 GeneM ark.hmm 87_nt - 1 87	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2352 GeneM ark.hmm 108_nt - 2 109	10 8	399 220 7	0	0	0	117 411 44	11	8.6 7	3.12	3. 12	939 798 1	17	16. 75	4.07	4. 07	NA			
gene_1523 GeneM ark.hmm 237_nt +	23	399 220	7	7.4	2.89	117 411	145	52.	5.7	2.	939 798	282	12 6.6	6.98	4.	---	---	---	---

462 698	7	7				44		11		81	1		1		09				
gene_441 GeneMa rk.hmm 249_nt - 26657 26905	24 9	399 220 7	0	0	0	117 411 44	53	18. 13	4.18	4. 18	939 798 1	41	17. 52	4.13	4. 13	---	---	---	
gene_1662 GeneM ark.hmm 351_nt - 73921 74271	35 1	399 220 7	3	2.1 4	1.1	117 411 44	172	41. 74	5.38	4. 28	939 798 1	125	37. 89	5.24	4. 14	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_247 GeneMa rk.hmm 900_nt - 15874 16773	90 0	399 220 7	184 2	51 2.6 7	9	117 411 44	786 8	74 4.5 8	9.54	0. 54	939 798 1	450 3	53 2.3 8	9.06	0. 06	Tellurite resistance protein and related permeases	METABOLISM	Inorganic ion transport and metabolism	P
gene_2368 GeneM ark.hmm 114_nt - 2 115	11 4	399 220 7	0	0	0	117 411 44	11	8.2 2	3.04	3. 04	939 798 1	19	17. 73	4.15	4. 15	NA			
gene_2512 GeneM ark.hmm 126_nt - 1 126	12 6	399 220 7	0	0	0	117 411 44	7	4.7 3	2.24	2. 24	939 798 1	21	17. 73	4.15	4. 15	NA			
gene_437 GeneMa rk.hmm 381_nt - 24394 24774	38 1	399 220 7	0	0	0	117 411 44	159	35. 54	5.15	5. 15	939 798 1	64	17. 87	4.16	4. 16	Arsenate reductase and related proteins, glutaredoxin family	METABOLISM	Inorganic ion transport and metabolism	P
gene_146 GeneMa rk.hmm 738_nt + 1 950 2687	73 8	399 220 7	48	16. 29	4.03	117 411 44	717	82. 75	6.37	2. 34	939 798 1	205 7	29 6.5 8	8.21	4. 18	ABC-type multidrug transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2275 GeneM ark.hmm 1353_nt - 100295 101647	13 53	399 220 7	16	2.9 6	1.57	117 411 44	215 59	13 57. 13	10.4 1	8. 84	939 798 1	688	54. 11	5.76	4. 19	Non-ribosomal peptide synthetase modules and related proteins	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_2485 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	299	62 4.1 3	9.29	117 411 44	725	51 4.5 7	9.01	- 0. 28	939 798 1	781	69 2.5 2	9.44	0. 15	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1607 GeneM ark.hmm 384_nt - 20731 21114	38 4	399 220 7	7	4.5 7	2.19	117 411 44	583	12 9.3 1	7.01	4. 82	939 798 1	308	85. 35	6.42	4. 23	---	---	---	---
gene_604 GeneMa rk.hmm 264_nt + 2 056 2319	26 4	399 220 7	0	0	0	117 411 44	16	5.1 6	2.37	2. 37	939 798 1	48	19. 35	4.27	4. 27	NA			
gene_632 GeneMa rk.hmm 345_nt + 2 8865 29209	34 5	399 220 7	0	0	0	117 411 44	101	24. 93	4.64	4. 64	939 798 1	63	19. 43	4.28	4. 28	Predicted UDP-glucose 6- dehydrogenase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_1361 GeneM ark.hmm 162_nt - 73960 74121	16 2	399 220 7	0	0	0	117 411 44	14	7.3 6	2.88	2. 88	939 798 1	30	19. 7	4.3	4. 3	---	---	---	---
gene_248 GeneMa rk.hmm 549_nt - 16883 17431	54 9	399 220 7	187 7	85 6.4	9.74	117 411 44	122 55	19 01. 21	10.8 9	1. 15	939 798 1	562 4	10 90. 03	10.0 9	0. 35	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_1735 GeneM ark.hmm 354_nt -	35	399 220	3	2.1	1.09	117 411	98	23.	4.56	3.	939 798	140	42.	5.4	4.	NA			

5577 5930	4	7		2		44		58		47	1		08		31				
gene_607 GeneMa rk.hmm 246_nt - 6613 6858	24 6	399 220 7	2	2.0 4	1.03	117 411 44	57	19. 73	4.3	3. 27	939 798 1	96	41. 52	5.38	4. 35	Heme/copper-type cytochrome/quinol oxidase, subunit 3	METABOLISM	Energy production and conversion	C
gene_2429 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	18	12. 78	3.68	3. 68	939 798 1	24	21. 28	4.41	4. 41	NA			
gene_422 GeneMa rk.hmm 2073_nt - 12423 14495	20 73	399 220 7	6	0.7 3	- 0.46	117 411 44	726	29. 83	4.9	5. 36	939 798 1	315	16. 17	4.02	4. 48	---	---	---	---
gene_1033 GeneM ark.hmm 1263_nt + 124838 126100	12 63	399 220 7	17	3.3 7	1.75	117 411 44	739	49. 83	5.64	3. 89	939 798 1	889	74. 9	6.23	4. 48	Xanthine/uracil permeases	METABOLISM	Nucleotide transport and metabolism	F
gene_2495 GeneM ark.hmm 99_nt - 25 123	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2228 GeneM ark.hmm 852_nt - 43134 43985	85 2	399 220 7	41	12. 05	3.59	117 411 44	796	79. 57	6.31	2. 72	939 798 1	217 2	27 1.2 6	8.08	4. 49	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2335 GeneM ark.hmm 105_nt + 2 106	10 5	399 220 7	0	0	0	117 411 44	8	6.4 9	2.7	2. 7	939 798 1	23	23. 31	4.54	4. 54	NA			
gene_2342 GeneM ark.hmm 105_nt - 3 107	10 5	399 220 7	0	0	0	117 411 44	5	4.0 6	2.02	2. 02	939 798 1	24	24. 32	4.6	4. 6	NA			
gene_2499 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	193	40 2.8 7	8.65	117 411 44	917	65 0.8 5	9.35	0. 7	939 798 1	730	64 7.3	9.34	0. 69	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_249 GeneMa rk.hmm 1323_nt - 17649 18971	13 23	399 220 7	116	21. 96	4.46	117 411 44	118 8	76. 48	6.26	1. 8	939 798 1	180 3	14 5.0 1	7.18	2. 72	Na+/alanine symporter	METABOLISM	Amino acid transport and metabolism	E
gene_24 GeneMar k.hmm 798_nt - 15120 15917	79 8	399 220 7	99	31. 08	4.96	117 411 44	195 8	20 8.9 8	7.71	2. 75	939 798 1	668	89. 07	6.48	1. 52	Formate/nitrite family of transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_76 GeneMar k.hmm 162_nt - 54458 54619	16 2	399 220 7	2	3.0 9	1.63	117 411 44	124	65. 19	6.03	4. 4	939 798 1	115	75. 54	6.24	4. 61	---	---	---	---
gene_2501 GeneM ark.hmm 90_nt + 3 92	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1700 GeneM ark.hmm 117_nt - 3 119	11 7	399 220 7	0	0	0	117 411 44	20	14. 56	3.86	3. 86	939 798 1	27	24. 56	4.62	4. 62	NA			
gene_625 GeneMa rk.hmm 186_nt - 18835 19020	18 6	399 220 7	1	1.3 5	0.43	117 411 44	69	31. 6	4.98	4. 55	939 798 1	58	33. 18	5.05	4. 62	---	---	---	---

gene_2504 GeneM ark.hmm 99_nt - 25 123	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1609 GeneM ark.hmm 198_nt - 22739 22936	19 8	399 220 7	15	18. 98	4.25	117 411 44	450	19 3.5 7	7.6	3. 35	939 798 1	891	47 8.8 3	8.9	4. 65	---	---	---	---
gene_1757 GeneM ark.hmm 282_nt + 27856 28137	28 2	399 220 7	0	0	0	117 411 44	168	50. 74	5.67	5. 67	939 798 1	67	25. 28	4.66	4. 66	---	---	---	---
gene_2507 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	47	98. 11	6.62	117 411 44	305	21 6.4 8	7.76	1. 14	939 798 1	210	18 6.2 1	7.54	0. 92	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2376 GeneM ark.hmm 114_nt + 3 116	11 4	399 220 7	0	0	0	117 411 44	19	14. 2	3.83	3. 83	939 798 1	27	25. 2	4.66	4. 66	NA			
gene_2509 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	10	20. 87	4.38	117 411 44	59	41. 88	5.39	1. 01	939 798 1	46	40. 79	5.35	0. 97	NA			
gene_250 GeneMa rk.hmm 618_nt - 19314 19931	61 8	399 220 7	519	21 0.3 6	7.72	117 411 44	249 9	34 4.4	8.43	0. 71	939 798 1	269 6	46 4.1 9	8.86	1. 14	Mismatch repair ATPase (MutS family)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2510 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	5	10. 44	3.38	117 411 44	14	9.9 4	3.31	- 0. 07	939 798 1	2	1.7 7	0.83	- 2. 55	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_428 GeneMa rk.hmm 597_nt - 18100 18696	59 7	399 220 7	1	0.4 2	- 1.25	117 411 44	136	19. 4	4.28	5. 53	939 798 1	60	10. 69	3.42	4. 67	NA			
gene_2488 GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	22	15. 61	3.96	3. 96	939 798 1	29	25. 71	4.68	4. 68	NA			
gene_2513 GeneM ark.hmm 126_nt + 3 128	12 6	399 220 7	33	65. 6	6.04	117 411 44	130	87. 87	6.46	0. 42	939 798 1	141	11 9.0 7	6.9	0. 86	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_1747 GeneM ark.hmm 642_nt + 20382 21023	64 2	399 220 7	1	0.3 9	- 1.36	117 411 44	140	18. 57	4.22	5. 58	939 798 1	61	10. 11	3.34	4. 7	NA			
gene_145 GeneMa rk.hmm 636_nt + 1 313 1948	63 6	399 220 7	33	13	3.7	117 411 44	713	95. 48	6.58	2. 88	939 798 1	209 6	35 0.6 7	8.45	4. 75	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2516 GeneM ark.hmm 129_nt + 3 131	12 9	399 220 7	4	7.7 7	2.96	117 411 44	36	23. 77	4.57	1. 61	939 798 1	25	20. 62	4.37	1. 41	NA			
gene_2517 GeneM ark.hmm 132_nt + 2 133	13 2	399 220 7	75	14 2.3 2	7.15	117 411 44	515	33 2.2 9	8.38	1. 23	939 798 1	623	50 2.2	8.97	1. 82	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_2518 GeneM ark.hmm 93_nt + 4 1 133	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	---	---	---	---
gene_2519 GeneM ark.hmm 132_nt + 3 134	13 2	399 220 7	6	11. 39	3.51	117 411 44	10	6.4 5	2.69	- 0. 82	939 798 1	8	6.4 5	2.69	- 0. 82	Phosphotransferase system, galactitol-specific IIB component	METABOLISM	Carbohydrate transport and metabolism	G
gene_251 GeneMa rk.hmm 1770_nt - 19922 21691	17 70	399 220 7	115 1	16 2.8 9	7.35	117 411 44	667 1	32 1	8.33	0. 98	939 798 1	639 6	38 4.5	8.59	1. 24	Mismatch repair ATPase (MutS family)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2520 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	4	8.3 5	3.06	117 411 44	38	26. 97	4.75	1. 69	939 798 1	127	11 2.6 1	6.82	3. 76	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2521 GeneM ark.hmm 135_nt - 2 136	13 5	399 220 7	180	33 3.9 8	8.38	117 411 44	550	34 6.9 9	8.44	0. 06	939 798 1	571	45 0.0 6	8.81	0. 43	---	---	---	---
gene_2363 GeneM ark.hmm 111_nt - 3 113	11 1	399 220 7	0	0	0	117 411 44	17	13. 04	3.71	3. 71	939 798 1	28	26. 84	4.75	4. 75	NA			
gene_2523 GeneM ark.hmm 141_nt - 3 143	14 1	399 220 7	13	23. 09	4.53	117 411 44	57	34. 43	5.11	0. 58	939 798 1	77	58. 11	5.86	1. 33	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2524 GeneM ark.hmm 141_nt - 3 143	14 1	399 220 7	44	78. 17	6.29	117 411 44	237	14 3.1 6	7.16	0. 87	939 798 1	238	17 9.6 1	7.49	1. 2	Collagenase and related proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2525 GeneM ark.hmm 141_nt + 3 143	14 1	399 220 7	4	7.1 1	2.83	117 411 44	51	30. 81	4.95	2. 12	939 798 1	21	15. 85	3.99	1. 16	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2526 GeneM ark.hmm 144_nt - 2 145	14 4	399 220 7	5	8.7	3.12	117 411 44	16	9.4 6	3.24	0. 12	939 798 1	11	8.1 3	3.02	- 0. 1	NA			
gene_2527 GeneM ark.hmm 147_nt - 1 147	14 7	399 220 7	27	46. 01	5.52	117 411 44	27	15. 64	3.97	- 1. 55	939 798 1	93	67. 32	6.07	0. 55	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2528 GeneM ark.hmm 147_nt - 1 147	14 7	399 220 7	54	92. 02	6.52	117 411 44	377	21 8.4 3	7.77	1. 25	939 798 1	347	25 1.1 8	7.97	1. 45	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2529 GeneM ark.hmm 147_nt - 2 148	14 7	399 220 7	117	19 9.3 7	7.64	117 411 44	657	38 0.6 6	8.57	0. 93	939 798 1	359	25 9.8 6	8.02	0. 38	NA			
gene_252 GeneMa rk.hmm 549_nt - 21795 22343	54 9	399 220 7	355 0	16 19. 73	10.6 6	117 411 44	505 1	78 3.6	9.61	- 1. 05	939 798 1	300 6	58 2.6 2	9.19	- 1. 47	Uncharacterized membrane protein, required for colicin V production	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2530 GeneM ark.hmm 150_nt + 1 150	15 0	399 220 7	6	10. 02	3.32	117 411 44	30	17. 03	4.09	0. 77	939 798 1	49	34. 76	5.12	1. 8	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_2531 GeneM ark.hmm 111_nt + 41 151	11 1	399 220 7	6	13. 54	3.76	117 411 44	24	18. 42	4.2	0. 44	939 798 1	6	5.7 5	2.52	- 1. 24	Di- and tricarboxylate transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_2532 GeneM ark.hmm 150_nt + 3 152	15 0	399 220 7	17	28. 39	4.83	117 411 44	135	76. 65	6.26	1. 43	939 798 1	145	10 2.8 6	6.68	1. 85	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2533 GeneM ark.hmm 162_nt - 2 163	16 2	399 220 7	13	20. 1	4.33	117 411 44	88	46. 27	5.53	1. 2	939 798 1	59	38. 75	5.28	0. 95	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2534 GeneM ark.hmm 162_nt + 3 164	16 2	399 220 7	35	54. 12	5.76	117 411 44	236	12 4.0 8	6.96	1. 2	939 798 1	176	11 5.6	6.85	1. 09	---	---	---	---
gene_2535 GeneM ark.hmm 162_nt + 2 163	16 2	399 220 7	18	27. 83	4.8	117 411 44	113	59. 41	5.89	1. 09	939 798 1	98	64. 37	6.01	1. 21	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2536 GeneM ark.hmm 138_nt - 20 157	13 8	399 220 7	30	54. 45	5.77	117 411 44	210	12 9.6 1	7.02	1. 25	939 798 1	164	12 6.4 5	6.98	1. 21	NA			
gene_2537 GeneM ark.hmm 168_nt - 2 169	16 8	399 220 7	5	7.4 6	2.9	117 411 44	30	15. 21	3.93	1. 03	939 798 1	28	17. 73	4.15	1. 25	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2337 GeneM ark.hmm 105_nt - 2 106	10 5	399 220 7	0	0	0	117 411 44	14	11. 36	3.51	3. 51	939 798 1	27	27. 36	4.77	4. 77	NA			
gene_2539 GeneM ark.hmm 168_nt - 2 169	16 8	399 220 7	4	5.9 6	2.58	117 411 44	35	17. 74	4.15	1. 57	939 798 1	11	6.9 7	2.8	0. 22	---	---	---	---
gene_253 GeneMa rk.hmm 303_nt - 22340 22642	30 3	399 220 7	849	70 1.8 6	9.46	117 411 44	500 4	14 06. 58	10.4 6	1	939 798 1	169 3	59 4.5 4	9.22	- 0. 24	---	---	---	---
gene_2540 GeneM ark.hmm 168_nt - 2 169	16 8	399 220 7	5	7.4 6	2.9	117 411 44	40	20. 28	4.34	1. 44	939 798 1	20	12. 67	3.66	0. 76	---	---	---	---
gene_2541 GeneM ark.hmm 168_nt + 3 170	16 8	399 220 7	13	19. 38	4.28	117 411 44	71	35. 99	5.17	0. 89	939 798 1	48	30. 4	4.93	0. 65	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2542 GeneM ark.hmm 78_nt + 9 4 171	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2543 GeneM ark.hmm 78_nt - 2 79	78	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2544 GeneM ark.hmm 174_nt - 3 176	17 4	399 220 7	16	23. 03	4.53	117 411 44	105	51. 4	5.68	1. 15	939 798 1	43	26. 3	4.72	0. 19	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2545 GeneM ark.hmm 174_nt +	17	399 220	31	44.	5.48	117 411	155	75.	6.25	0.	939 798	94	57.	5.85	0.	Transposase and inactivated	INFORMATION STORAGE AND	Replication, recombination and	L

3 176	4	7		63		44		87		77	1		48		37	derivatives	PROCESSING	repair	
gene_2546 GeneM ark.hmm 141_nt + 42 182	14 1	399 220 7	107	19 0.0 9	7.57	117 411 44	634	38 2.9 7	8.58	1. 01	939 798 1	72	54. 33	5.76	- 1. 81	NA			
gene_2547 GeneM ark.hmm 147_nt - 37 183	14 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2548 GeneM ark.hmm 180_nt - 3 182	18 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2549 GeneM ark.hmm 177_nt - 8 184	17 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.6	- 0.73	- 0. 73	NA			
gene_254 GeneMa rk.hmm 882_nt + 2 2729 23610	88 2	399 220 7	342 0	97 1.2 8	9.92	117 411 44	159 47	15 39. 93	10.5 9	0. 67	939 798 1	109 75	13 24. 04	10.3 7	0. 45	Ribonuclease HIII	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2550 GeneM ark.hmm 183_nt + 1 183	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			
gene_2551 GeneM ark.hmm 99_nt - 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2552 GeneM ark.hmm 84_nt + 9 9 182	84	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2553 GeneM ark.hmm 183_nt - 2 184	18 3	399 220 7	0	0	0	117 411 44	1	0.4 7	-1.1	- 1. 1	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			
gene_2554 GeneM ark.hmm 183_nt - 2 184	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2555 GeneM ark.hmm 183_nt + 2 184	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2556 GeneM ark.hmm 183_nt + 2 184	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 6	0.22	0. 22	NA			
gene_2557 GeneM ark.hmm 180_nt - 3 182	18 0	399 220 7	37	51. 49	5.69	117 411 44	480	22 7.1 2	7.83	2. 14	939 798 1	348	20 5.7 2	7.68	1. 99	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2558 GeneM ark.hmm 183_nt - 1 183	18 3	399 220 7	0	0	0	117 411 44	1	0.4 7	-1.1	- 1. 1	939 798 1	0	0	0	0	NA			
gene_2559 GeneM ark.hmm 183_nt + 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			

gene_255 GeneMa rk.hmm 501_nt + 2 3728 24228	50 1	399 220 7	328 8	16 43. 92	10.6 8	117 411 44	980 0	16 66. 01	10.7	0. 02	939 798 1	721 0	15 31. 31	10.5 8	- 0. 1	Signal peptidase I	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_2560 GeneM ark.hmm 183_nt - 1 183	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 6	0.22	0. 22	NA			
gene_2561 GeneM ark.hmm 183_nt - 3 185	18 3	399 220 7	0	0	0	117 411 44	1	0.4 7	-1.1	- 1. 1	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			
gene_2562 GeneM ark.hmm 183_nt - 2 184	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			
gene_2563 GeneM ark.hmm 183_nt - 1 183	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2564 GeneM ark.hmm 183_nt + 2 184	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	5	2.9 1	1.54	1. 54	ABC-type xylose transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_2565 GeneM ark.hmm 183_nt + 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			
gene_2566 GeneM ark.hmm 183_nt + 1 183	18 3	399 220 7	0	0	0	117 411 44	1	0.4 7	-1.1	- 1. 1	939 798 1	0	0	0	0	NA			
gene_2567 GeneM ark.hmm 183_nt + 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2568 GeneM ark.hmm 186_nt + 1 186	18 6	399 220 7	0	0	0	117 411 44	1	0.4 6	- 1.13	- 1. 13	939 798 1	0	0	0	0	NA			
gene_2569 GeneM ark.hmm 183_nt - 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_256 GeneMa rk.hmm 2367_nt + 24355 26721	23 67	399 220 7	311 9	33 0.0 7	8.37	117 411 44	947 7	34 1.0 1	8.41	0. 04	939 798 1	951 7	42 7.8 3	8.74	0. 37	ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2570 GeneM ark.hmm 183_nt + 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			
gene_2571 GeneM ark.hmm 150_nt - 3 152	15 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2572 GeneM ark.hmm 183_nt - 3 185	18 3	399 220 7	0	0	0	117 411 44	2	0.9 3	-0.1	- 0. 1	939 798 1	1	0.5 8	- 0.78	- 0. 78	NA			

gene_2573 GeneM ark.hmm 186_nt - 1 186	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 7	- 0.81	- 0.81	NA			
gene_2574 GeneM ark.hmm 183_nt - 2 184	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2575 GeneM ark.hmm 186_nt - 1 186	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 7	- 0.81	- 0.81	NA			
gene_2576 GeneM ark.hmm 183_nt - 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 6	0.22	0.22	NA			
gene_2577 GeneM ark.hmm 186_nt + 1 186	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2578 GeneM ark.hmm 186_nt + 2 187	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 4	0.19	0.19	NA			
gene_2579 GeneM ark.hmm 186_nt - 1 186	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Predicted flavin-nucleotide-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_257 GeneMa rk.hmm 1284_nt - 26769 28052	12 84	399 220 7	131 58	25 66. 92	11.3 3	117 411 44	536 54	35 58. 99	11.8	0. 47	939 798 1	208 63	17 28. 93	10.7 6	- 0. 57	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2580 GeneM ark.hmm 147_nt - 41 187	14 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.7 2	- 0.47	- 0.47	NA			
gene_2581 GeneM ark.hmm 183_nt - 3 185	18 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2582 GeneM ark.hmm 186_nt - 3 188	18 6	399 220 7	0	0	0	117 411 44	1	0.4 6	- 1.13	- 1.13	939 798 1	1	0.5 7	- 0.81	- 0.81	NA			
gene_2583 GeneM ark.hmm 186_nt - 3 188	18 6	399 220 7	0	0	0	117 411 44	1	0.4 6	- 1.13	- 1.13	939 798 1	4	2.2 9	1.19	1.19	NA			
gene_2584 GeneM ark.hmm 186_nt + 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2585 GeneM ark.hmm 186_nt + 1 186	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	3	1.7 2	0.78	0.78	NA			
gene_2586 GeneM ark.hmm 186_nt - 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			

gene_2587 GeneM ark.hmm 186_nt - 1 186	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2588 GeneM ark.hmm 186_nt - 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 7	- 0.81	- 0.81	NA			
gene_2589 GeneM ark.hmm 186_nt + 1 186	18 6	399 220 7	0	0	0	117 411 44	1	0.4 6	- 1.13	- 1.13	939 798 1	1	0.5 7	- 0.81	- 0.81	NA			
gene_258 GeneMa rk.hmm 594_nt - 28904 29497	59 4	399 220 7	242	10 2.0 5	6.67	117 411 44	140 8	20 1.8 9	7.66	0. 99	939 798 1	657	11 7.6 9	6.88	0. 21	V8-like Glu-specific endopeptidase	METABOLISM	Amino acid transport and metabolism	E
gene_2590 GeneM ark.hmm 186_nt - 2 187	18 6	399 220 7	0	0	0	117 411 44	1	0.4 6	- 1.13	- 1.13	939 798 1	2	1.1 4	0.19	0. 19	NA			
gene_2591 GeneM ark.hmm 186_nt - 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	5	2.8 6	1.52	1. 52	NA			
gene_2592 GeneM ark.hmm 186_nt + 2 187	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2593 GeneM ark.hmm 186_nt + 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2594 GeneM ark.hmm 189_nt - 1 189	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 6	- 0.83	- 0.83	NA			
gene_2595 GeneM ark.hmm 186_nt + 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 7	- 0.81	- 0.81	ABC-type uncharacterized transport systems, ATPase components	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2596 GeneM ark.hmm 189_nt + 1 189	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2597 GeneM ark.hmm 114_nt + 3 116	11 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2598 GeneM ark.hmm 189_nt - 1 189	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	ATPases involved in chromosome partitioning	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2599 GeneM ark.hmm 186_nt + 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_259 GeneMa rk.hmm 240_nt - 29578 29817	24 0	399 220 7	108	11 2.7 2	6.82	117 411 44	637	22 6.0 6	7.82	1	939 798 1	150	66. 5	6.06	- 0.76	---	---	---	---

gene_25 GeneMark.hmm 747_nt - 16161 16907	74 7	399 220 7	279 3	93 6.5 6	9.87	117 411 44	554 1	63 1.7 7	9.3	- 0. 57	939 798 1	335 1	47 7.3 3	8.9	- 0. 97	Sortase (surface protein transpeptidase)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2600 GeneMark.hmm 189_nt + 1 189	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 6	- 0.83	- 0. 83	NA			
gene_2601 GeneMark.hmm 189_nt + 1 189	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 6	- 0.83	- 0. 83	NA			
gene_2602 GeneMark.hmm 189_nt + 1 189	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 6	- 0.83	- 0. 83	NA			
gene_2603 GeneMark.hmm 189_nt - 2 190	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2604 GeneMark.hmm 189_nt - 2 190	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2605 GeneMark.hmm 186_nt - 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2606 GeneMark.hmm 99_nt + 2 100	99	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2607 GeneMark.hmm 189_nt - 2 190	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2608 GeneMark.hmm 186_nt + 3 188	18 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2609 GeneMark.hmm 189_nt - 2 190	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 6	- 0.83	- 0. 83	NA			
gene_260 GeneMark.hmm 177_nt - 29967 30143	17 7	399 220 7	57	80. 67	6.33	117 411 44	207	99. 61	6.64	0. 31	939 798 1	72	43. 28	5.44	- 0. 89	Predicted DNA alkylation repair enzyme	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2610 GeneMark.hmm 189_nt - 3 191	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2611 GeneMark.hmm 129_nt + 3 131	12 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2612 GeneMark.hmm 189_nt + 3 191	18 9	399 220 7	20	26. 51	4.73	117 411 44	105	47. 32	5.56	0. 83	939 798 1	44	24. 77	4.63	- 0. 1	Di- and tricarboxylate transporters	METABOLISM	Inorganic ion transport and metabolism	P

gene_2613 GeneM ark.hmm 189_nt + 3 191	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2614 GeneM ark.hmm 189_nt + 3 191	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 3	0.17	0. 17	NA			
gene_2615 GeneM ark.hmm 189_nt + 3 191	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2616 GeneM ark.hmm 192_nt - 1 192	19 2	399 220 7	0	0	0	117 411 44	1	0.4 4	- 1.17	- 1. 17	939 798 1	1	0.5 5	- 0.85	- 0. 85	NA			
gene_2617 GeneM ark.hmm 117_nt + 3 119	11 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2618 GeneM ark.hmm 192_nt + 2 193	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2619 GeneM ark.hmm 192_nt - 1 192	19 2	399 220 7	0	0	0	117 411 44	2	0.8 9	- 0.17	- 0. 17	939 798 1	0	0	0	0	NA			
gene_261 GeneMa rk.hmm 255_nt - 30258 30512	25 5	399 220 7	67	65. 81	6.04	117 411 44	268	89. 51	6.48	0. 44	939 798 1	131	54. 66	5.77	- 0. 27	NA			
gene_2620 GeneM ark.hmm 192_nt - 1 192	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 5	- 0.85	- 0. 85	NA			
gene_2621 GeneM ark.hmm 192_nt - 1 192	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 1	0.15	0. 15	NA			
gene_2622 GeneM ark.hmm 192_nt + 2 193	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 1	0.15	0. 15	NA			
gene_780 GeneMa rk.hmm 315_nt +1 57171 157485	31 5	399 220 7	1	0.8	- 0.33	117 411 44	162	43. 8	5.45	5. 78	939 798 1	66	22. 29	4.48	4. 81	Phosphotransferase system cellobiose-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_2624 GeneM ark.hmm 192_nt + 3 194	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	4	2.2 2	1.15	1. 15	NA			
gene_2625 GeneM ark.hmm 192_nt - 2 193	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 1	0.15	0. 15	NA			
gene_2626 GeneM ark.hmm 132_nt - 62 193	13 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2627 GeneM ark.hmm 192_nt + 3 191	19	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

2 193	2	7				44					1								
gene_2628 GeneMark.hmm 192_nt - 3 194	192	3992207	0	0	0	11741144	1	0.44	-1.17	-1.17	9397981	0	0	0	0	NA			
gene_2629 GeneMark.hmm 192_nt + 2 193	192	3992207	0	0	0	11741144	1	0.44	-1.17	-1.17	9397981	1	0.55	-0.85	-0.85	NA			
gene_262 GeneMark.hmm 243_nt - 30494 30736	243	3992207	38	39.17	5.29	11741144	230	80.61	6.33	1.04	9397981	119	52.11	5.7	0.41	---	---	---	
gene_2630 GeneMark.hmm 162_nt + 2 163	162	3992207	885	1368.41	10.42	11741144	1968	1034.66	10.01	-0.41	9397981	2368	1555.36	10.6	0.18	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2631 GeneMark.hmm 192_nt + 2 193	192	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2632 GeneMark.hmm 192_nt + 2 193	192	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2633 GeneMark.hmm 132_nt + 1 132	132	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2634 GeneMark.hmm 192_nt + 2 193	192	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2635 GeneMark.hmm 192_nt - 2 193	192	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2636 GeneMark.hmm 195_nt - 1 195	195	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2637 GeneMark.hmm 192_nt - 2 193	192	3992207	0	0	0	11741144	0	0	0	0	9397981	1	0.55	-0.85	-0.85	NA			
gene_2638 GeneMark.hmm 135_nt + 1 135	135	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2639 GeneMark.hmm 195_nt + 2 196	195	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_263 GeneMark.hmm 633_nt - 30737 31369	633	3992207	492	194.69	7.61	11741144	945	127.15	6.99	-0.62	9397981	499	83.88	6.39	-1.22	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2640 GeneMark.hmm 192_nt -	192	399220	0	0	0	117411	0	0	0	0	939798	0	0	0	0	NA			

3 194		7				44					1								
gene_2641 GeneM ark.hmm 192_nt + 3 194	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.1 1	0.15	0. 15	NA			
gene_2642 GeneM ark.hmm 195_nt 1 195	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	3	1.6 4	0.71	0. 71	NA			
gene_2643 GeneM ark.hmm 195_nt 2 196	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 5	- 0.87	- 0. 87	NA			
gene_2644 GeneM ark.hmm 195_nt 1 195	19 5	399 220 7	0	0	0	117 411 44	1	0.4 4	-1.2	- 1. 2	939 798 1	3	1.6 4	0.71	0. 71	NA			
gene_2408 GeneM ark.hmm 120_nt 3 122	12 0	399 220 7	0	0	0	117 411 44	11	7.8 1	2.96	2. 96	939 798 1	32	28. 37	4.83	4. 83	NA			
gene_2646 GeneM ark.hmm 195_nt + 2 196	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2647 GeneM ark.hmm 195_nt + 1 195	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.0 9	0.13	0. 13	NA			
gene_2648 GeneM ark.hmm 195_nt 3 197	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 5	- 0.87	- 0. 87	NA			
gene_2649 GeneM ark.hmm 195_nt + 1 195	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_264 GeneMa rk.hmm 996_nt 3 1383 32378	99 6	399 220 7	484	12 1.7 2	6.93	117 411 44	134 5	11 5.0 1	6.85	- 0. 08	939 798 1	879	93. 91	6.55	- 0. 38	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2650 GeneM ark.hmm 195_nt 2 196	19 5	399 220 7	0	0	0	117 411 44	1	0.4 4	-1.2	- 1. 2	939 798 1	0	0	0	0	NA			
gene_2651 GeneM ark.hmm 195_nt 3 197	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2652 GeneM ark.hmm 195_nt + 1 195	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2653 GeneM ark.hmm 195_nt + 2 196	19 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	1.0 9	0.13	0. 13	NA			
gene_2654 GeneM ark.hmm 195_nt	19 5	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

3 197		7				44					1								
gene_2655 GeneMark.hmm 186_nt - 13 198	186	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2656 GeneMark.hmm 90_nt - 2 91	90	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2657 GeneMark.hmm 195_nt - 2 196	195	3992207	0	0	0	11741144	0	0	0	0	9397981	1	0.55	-0.87	-0.87	NA			
gene_2658 GeneMark.hmm 198_nt - 1 198	198	3992207	0	0	0	11741144	1	0.43	-1.22	-1.22	9397981	5	2.69	1.43	1.43	NA			
gene_2659 GeneMark.hmm 198_nt - 1 198	198	3992207	0	0	0	11741144	2	0.86	-0.22	-0.22	9397981	1	0.54	-0.9	-0.9	NA			
gene_265 GeneMark.hmm 699_nt - 32375 33073	699	3992207	1167	418.2	8.71	11741144	1690	205.92	7.69	-1.02	9397981	1271	193.48	7.6	-1.11	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_2660 GeneMark.hmm 135_nt + 62 196	135	3992207	0	0	0	11741144	0	0	0	0	9397981	1	0.79	-0.34	-0.34	NA			
gene_2661 GeneMark.hmm 150_nt - 2 151	150	3992207	0	0	0	11741144	0	0	0	0	9397981	2	1.42	0.5	0.5	NA			
gene_2662 GeneMark.hmm 198_nt - 1 198	198	3992207	0	0	0	11741144	3	1.29	0.37	0.37	9397981	0	0	0	0	---	---	---	---
gene_2663 GeneMark.hmm 195_nt + 3 197	195	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2664 GeneMark.hmm 198_nt - 1 198	198	3992207	0	0	0	11741144	2	0.86	-0.22	-0.22	9397981	1	0.54	-0.9	-0.9	NA			
gene_2665 GeneMark.hmm 198_nt - 1 198	198	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2666 GeneMark.hmm 198_nt - 3 200	198	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2667 GeneMark.hmm 198_nt + 1 198	198	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2668 GeneMark.hmm 198_nt + 2 199	198	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			

gene_2669 GeneM ark.hmm 198_nt[+] 2 199	19 8	399 220 7	0	0	0	117 411 44	2	0.8 6	- 0.22	- 0.22	939 798 1	4	2.1 5	1.1	1. 1	NA			
gene_266 GeneMa rk.hmm 87_nt[-] 33151 33237	87	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	L-lactate dehydrogenase (FMN- dependent) and related alpha- hydroxy acid dehydrogenases	METABOLISM	Energy production and conversion	C
gene_2670 GeneM ark.hmm 201_nt[-] 1 201	20 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2671 GeneM ark.hmm 201_nt[-] 1 201	20 1	399 220 7	0	0	0	117 411 44	2	0.8 5	- 0.24	- 0.24	939 798 1	3	1.5 9	0.67	0. 67	NA			
gene_2672 GeneM ark.hmm 198_nt[+] 3 200	19 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2673 GeneM ark.hmm 147_nt[+] 2 148	14 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2674 GeneM ark.hmm 198_nt[-] 3 200	19 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_2455 GeneM ark.hmm 120_nt[+] 2 121	12 0	399 220 7	0	0	0	117 411 44	19	13. 49	3.75	3. 75	939 798 1	32	28. 37	4.83	4. 83	NA			
gene_2676 GeneM ark.hmm 198_nt[+] 3 200	19 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2677 GeneM ark.hmm 198_nt[-] 3 200	19 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 4	-0.9	- 0. 9	NA			
gene_2678 GeneM ark.hmm 129_nt[+] 1 129	12 9	399 220 7	0	0	0	117 411 44	1	0.6 6	-0.6	- 0. 6	939 798 1	0	0	0	0	NA			
gene_2679 GeneM ark.hmm 198_nt[-] 3 200	19 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_267 GeneMa rk.hmm 918_nt[-] 33294 34211	91 8	399 220 7	447	12 1.9 7	6.93	117 411 44	208 0	19 2.9 8	7.59	0. 66	939 798 1	245 3	28 4.3 3	8.15	1. 22	L-lactate dehydrogenase (FMN- dependent) and related alpha- hydroxy acid dehydrogenases	METABOLISM	Energy production and conversion	C
gene_2680 GeneM ark.hmm 201_nt[+] 1 201	20 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2681 GeneM ark.hmm 186_nt[-] 18 203	18 6	399 220 7	0	0	0	117 411 44	2	0.9 2	- 0.13	- 0. 13	939 798 1	2	1.1 4	0.19	0. 19	NA			

gene_2682 GeneM ark.hmm 189_nt - 14 202	18 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 6	- 0.83	- 0.83	NA			
gene_2683 GeneM ark.hmm 201_nt + 2 202	20 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2684 GeneM ark.hmm 204_nt - 1 204	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2685 GeneM ark.hmm 201_nt - 2 202	20 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2686 GeneM ark.hmm 201_nt - 2 202	20 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 3	- 0.92	- 0.92	NA			
gene_2687 GeneM ark.hmm 204_nt + 2 205	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 2	- 0.94	- 0.94	Choline dehydrogenase and related flavoproteins	METABOLISM	Amino acid transport and metabolism	E
gene_2688 GeneM ark.hmm 204_nt + 2 205	20 4	399 220 7	0	0	0	117 411 44	1	0.4 2	- 1.26	- 1.26	939 798 1	0	0	0	0	NA			
gene_2689 GeneM ark.hmm 147_nt + 3 149	14 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_268 GeneMa rk.hmm 1008_nt - 34195 35202	10 08	399 220 7	284	70. 57	6.14	117 411 44	163 4	13 8.0 6	7.11	0. 97	939 798 1	186 3	19 6.6 6	7.62	1. 48	Mevalonate kinase	METABOLISM	Lipid transport and metabolism	I
gene_2690 GeneM ark.hmm 204_nt + 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	4	2.0 9	1.06	1. 06	NA			
gene_2691 GeneM ark.hmm 204_nt - 1 204	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 2	- 0.94	- 0.94	NA			
gene_2692 GeneM ark.hmm 204_nt - 2 205	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 2	- 0.94	- 0.94	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2460 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	17	12. 07	3.59	3. 59	939 798 1	32	28. 37	4.83	4. 83	NA			
gene_2694 GeneM ark.hmm 204_nt - 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2695 GeneM ark.hmm 204_nt + 3 206	20 4	399 220 7	0	0	0	117 411 44	2	0.8 4	- 0.26	- 0.26	939 798 1	0	0	0	0	NA			
gene_2696 GeneM ark.hmm 204_nt -	20	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

[3 206	4	7				44					1								
gene_2697 GeneM ark.hmm 204_nt + 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2698 GeneM ark.hmm 204_nt 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	5	2.6 1	1.38	1. 38	NA			
gene_2366 GeneM ark.hmm 114_nt + 2 115	11 4	399 220 7	0	0	0	117 411 44	22	16. 44	4.04	4. 04	939 798 1	31	28. 93	4.85	4. 85	NA			
gene_269 GeneMa rk.hmm 954_nt 35189 36142	95 4	399 220 7	494	12 9.7 1	7.02	117 411 44	132 8	11 8.5 6	6.89	- 0. 13	939 798 1	110 1	12 2.8	6.94	- 0. 08	Mevalonate pyrophosphate decarboxylase	METABOLISM	Lipid transport and metabolism	I
gene_26 GeneMar k.hmm 1890_nt 16907 18796	18 90	399 220 7	364 5	48 3.0 8	8.92	117 411 44	865 3	38 9.9 4	8.61	- 0. 31	939 798 1	668 0	37 6.0 8	8.55	- 0. 37	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2700 GeneM ark.hmm 204_nt 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 2	- 0.94	- 0. 94	NA			
gene_2701 GeneM ark.hmm 204_nt + 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 2	- 0.94	- 0. 94	NA			
gene_2702 GeneM ark.hmm 207_nt 2 208	20 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2703 GeneM ark.hmm 207_nt + 1 207	20 7	399 220 7	0	0	0	117 411 44	1	0.4 1	- 1.28	- 1. 28	939 798 1	2	1.0 3	0.04	0. 04	NA			
gene_2704 GeneM ark.hmm 204_nt 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2705 GeneM ark.hmm 204_nt 3 206	20 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2706 GeneM ark.hmm 207_nt + 3 209	20 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2707 GeneM ark.hmm 207_nt + 3 209	20 7	399 220 7	0	0	0	117 411 44	1	0.4 1	- 1.28	- 1. 28	939 798 1	0	0	0	0	ATP-dependent Lon protease, bacterial type	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2708 GeneM ark.hmm 207_nt + 3 209	20 7	399 220 7	0	0	0	117 411 44	1	0.4 1	- 1.28	- 1. 28	939 798 1	0	0	0	0	NA			
gene_2709 GeneM ark.hmm 210_nt 3 206	21 0	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

1 210		7				44					1								
gene_270 GeneMa rk.hmm 879_nt 36124 37002	87 9	399 220 7	338	96. 32	6.59	117 411 44	158 9	15 3.9 7	7.27	0. 68	939 798 1	115 4	13 9.7	7.13	0. 54	Mevalonate kinase	METABOLISM	Lipid transport and metabolism	I
gene_2710 GeneM ark.hmm 210_nt 1 210	21 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2711 GeneM ark.hmm 102_nt 102 203	10 2	399 220 7	0	0	0	117 411 44	2	1.6 7	0.74	0. 74	939 798 1	4	4.1 7	2.06	2. 06	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_144 GeneMa rk.hmm 288_nt + 1 029 1316	28 8	399 220 7	6	5.2 2	2.38	117 411 44	123	36. 37	5.18	2. 8	939 798 1	411	15 1.8 5	7.25	4. 87	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2713 GeneM ark.hmm 210_nt 1 210	21 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5 1	- 0.98	- 0. 98	NA			
gene_2339 GeneM ark.hmm 105_nt + 3 107	10 5	399 220 7	0	0	0	117 411 44	28	22. 71	4.51	4. 51	939 798 1	29	29. 39	4.88	4. 88	NA			
gene_2715 GeneM ark.hmm 210_nt 2 211	21 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2716 GeneM ark.hmm 213_nt + 1 213	21 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2717 GeneM ark.hmm 210_nt 3 212	21 0	399 220 7	19	22. 66	4.5	117 411 44	218	88. 42	6.47	1. 97	939 798 1	144	72. 96	6.19	1. 69	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2718 GeneM ark.hmm 213_nt 2 214	21 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2719 GeneM ark.hmm 213_nt + 1 213	21 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.5	-1	-1	NA			
gene_271 GeneMa rk.hmm 330_nt 37124 37453	33 0	399 220 7	17	12. 9	3.69	117 411 44	185	47. 75	5.58	1. 89	939 798 1	73	23. 54	4.56	0. 87	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2720 GeneM ark.hmm 213_nt + 3 215	21 3	399 220 7	0	0	0	117 411 44	1	0.4	- 1.32	- 1. 32	939 798 1	0	0	0	0	Preprotein translocase subunit SecA (ATPase, RNA helicase)	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_2721 GeneM ark.hmm 216_nt 1 216	21 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.4 9	- 1.02	- 1. 02	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2722 GeneM ark.hmm 111_nt +	11	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

2 112	1	7				44					1								
gene_2723 GeneM ark.hmm 93_nt - 123 215	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2724 GeneM ark.hmm 147_nt - 68 214	14 7	399 220 7	241	41 0.6 6	8.68	117 411 44	105 1	60 8.9 4	9.25	0. 57	939 798 1	519	37 5.6 8	8.55	- 0. 13	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2725 GeneM ark.hmm 159_nt + 53 211	15 9	399 220 7	0	0	0	117 411 44	1	0.5 4	-0.9	- 0. 9	939 798 1	2	1.3 4	0.42	0. 42	NA			
gene_2726 GeneM ark.hmm 216_nt - 2 217	21 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.4 9	- 1.02	- 1. 02	NA			
gene_2727 GeneM ark.hmm 216_nt - 1 216	21 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	0.9 9	- 0.02	- 0. 02	NA			
gene_2382 GeneM ark.hmm 114_nt + 3 116	11 4	399 220 7	0	0	0	117 411 44	17	12. 7	3.67	3. 67	939 798 1	32	29. 87	4.9	4. 9	NA			
gene_2729 GeneM ark.hmm 219_nt - 1 219	21 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	0.9 7	- 0.04	- 0. 04	NA			
gene_272 GeneMa rk.hmm 282_nt + 3 8705 38986	28 2	399 220 7	37	32. 87	5.04	117 411 44	187	56. 48	5.82	0. 78	939 798 1	92	34. 71	5.12	0. 08	Lantibiotic modifying enzyme	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_1954 GeneM ark.hmm 138_nt - 626 763	13 8	399 220 7	1	1.8 2	0.86	117 411 44	57	35. 18	5.14	4. 28	939 798 1	76	58. 6	5.87	5. 01	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2731 GeneM ark.hmm 219_nt - 1 219	21 9	399 220 7	0	0	0	117 411 44	1	0.3 9	- 1.36	- 1. 36	939 798 1	0	0	0	0	NA			
gene_2328 GeneM ark.hmm 105_nt + 2 106	10 5	399 220 7	0	0	0	117 411 44	15	12. 17	3.6	3. 6	939 798 1	32	32. 43	5.02	5. 02	NA			
gene_2733 GeneM ark.hmm 222_nt - 1 222	22 2	399 220 7	0	0	0	117 411 44	2	0.7 7	- 0.38	- 0. 38	939 798 1	0	0	0	0	NA			
gene_2734 GeneM ark.hmm 222_nt - 1 222	22 2	399 220 7	0	0	0	117 411 44	1	0.3 8	- 1.38	- 1. 38	939 798 1	2	0.9 6	- 0.06	- 0. 06	NA			
gene_2735 GeneM ark.hmm 219_nt - 3 221	21 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	ABC-type transport system involved in resistance to organic solvents, periplasmic component	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_2736 GeneM ark.hmm 222_nt -	22 2	399 220	0	0	0	117 411	0	0	0	0	939 798	2	0.9 6	- 0.06	- 0.	NA			

2 223		7				44					1				06				
gene_2737 GeneM ark.hmm 225_nt - 1 225	22 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	0.9 5	- 0.08	- 0.08	NA			
gene_2738 GeneM ark.hmm 222_nt - 2 223	22 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	0.9 6	- 0.06	- 0.06	NA			
gene_2823 GeneM ark.hmm 108_nt - 2 109	10 8	399 220 7	0	0	0	117 411 44	31	24. 45	4.61	4. 61	939 798 1	33	32. 51	5.02	5. 02	Collagenase and related proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_273 GeneMa rk.hmm 1233_nt + 39029 40261	12 33	399 220 7	265	53. 84	5.75	117 411 44	169 6	11 7.1 5	6.87	1. 12	939 798 1	118 9	10 2.6 1	6.68	0. 93	Permeases of the major facilitator superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_2740 GeneM ark.hmm 225_nt + 2 226	22 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2741 GeneM ark.hmm 222_nt - 3 224	22 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2742 GeneM ark.hmm 105_nt - 2 106	10 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2743 GeneM ark.hmm 105_nt - 123 227	10 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2744 GeneM ark.hmm 225_nt + 1 225	22 5	399 220 7	0	0	0	117 411 44	1	0.3 8	-1.4	- 1. 4	939 798 1	0	0	0	0	NA			
gene_2745 GeneM ark.hmm 171_nt + 3 173	17 1	399 220 7	31	45. 41	5.5	117 411 44	201	10 0.1 1	6.65	1. 15	939 798 1	276	17 1.7 4	7.42	1. 92	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2746 GeneM ark.hmm 96_nt - 2 97	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2356 GeneM ark.hmm 108_nt - 3 110	10 8	399 220 7	0	0	0	117 411 44	19	14. 98	3.91	3. 91	939 798 1	35	34. 48	5.11	5. 11	NA			
gene_2748 GeneM ark.hmm 108_nt - 123 230	10 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2749 GeneM ark.hmm 231_nt - 3 233	23 1	399 220 7	9	9.7 6	3.29	117 411 44	88	32. 45	5.02	1. 73	939 798 1	103	47. 45	5.57	2. 28	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_274 GeneMa rk.hmm 420_nt -	42 0	399 220	570	33 9.9	8.41	117 411	605	12 2.6	6.94	- 1.	939 798	571	14 4.6	7.18	- 1.	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ	General function prediction only	R

[40379 40798		7		5		44		9		47	1		6		23		ED		
gene_1608 GeneM ark.hmm 150_nt - 22123 22272	15 0	399 220 7	0	0	0	117 411 44	35	19. 87	4.31	4. 31	939 798 1	51	36. 18	5.18	5. 18	---	---	---	---
gene_2751 GeneM ark.hmm 234_nt - 1 234	23 4	399 220 7	0	0	0	117 411 44	3	1.0 9	0.13	0. 13	939 798 1	0	0	0	0	NA			
gene_2752 GeneM ark.hmm 234_nt + 2 235	23 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.4 5	- 1.14	- 1. 14	NA			
gene_2753 GeneM ark.hmm 144_nt - 3 146	14 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.7 4	- 0.44	- 0. 44	NA			
gene_2754 GeneM ark.hmm 90_nt - 147 236	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2755 GeneM ark.hmm 237_nt + 2 238	23 7	399 220 7	0	0	0	117 411 44	1	0.3 6	- 1.48	- 1. 48	939 798 1	0	0	0	0	NA			
gene_2756 GeneM ark.hmm 240_nt + 2 241	24 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2757 GeneM ark.hmm 186_nt - 59 244	18 6	399 220 7	183	24 6.4 5	7.95	117 411 44	141 5	64 7.9 4	9.34	1. 39	939 798 1	131	74. 94	6.23	- 1. 72	NA			
gene_2758 GeneM ark.hmm 246_nt - 1 246	24 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	---	---	---	---
gene_2759 GeneM ark.hmm 246_nt + 2 247	24 6	399 220 7	284	28 9.1 8	8.18	117 411 44	154 3	53 4.2 2	9.06	0. 88	939 798 1	121 2	52 4.2 4	9.03	0. 85	---	---	---	---
gene_275 GeneMa rk.hmm 702_nt - 40981 41682	70 2	399 220 7	383	13 6.6 6	7.09	117 411 44	126 5	15 3.4 8	7.26	0. 17	939 798 1	915	13 8.6 9	7.12	0. 03	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2760 GeneM ark.hmm 246_nt - 1 246	24 6	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2761 GeneM ark.hmm 102_nt - 145 246	10 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2762 GeneM ark.hmm 201_nt + 3 203	20 1	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	3	1.5 9	0.67	0. 67	NA			
gene_2763 GeneM ark.hmm 249_nt + 1 249	24 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			

gene_1404 GeneM ark.hmm 300_nt - 6092 6391	30 0	399 220 7	1	0.8 3	- 0.26	117 411 44	155	44	5.46	5. 72	939 798 1	86	30. 5	4.93	5. 19	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2765 GeneM ark.hmm 252_nt - 2 253	25 2	399 220 7	0	0	0	117 411 44	1	0.3 4	- 1.56	- 1. 56	939 798 1	2	0.8 4	- 0.24	- 0. 24	NA			
gene_2766 GeneM ark.hmm 255_nt - 3 257	25 5	399 220 7	0	0	0	117 411 44	1	0.3 3	- 1.58	- 1. 58	939 798 1	1	0.4 2	- 1.26	- 1. 26	NA			
gene_2375 GeneM ark.hmm 114_nt + 3 116	11 4	399 220 7	0	0	0	117 411 44	16	11. 95	3.58	3. 58	939 798 1	39	36. 4	5.19	5. 19	NA			
gene_2484 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	22	15. 61	3.96	3. 96	939 798 1	43	38. 13	5.25	5. 25	NA			
gene_2769 GeneM ark.hmm 255_nt - 3 257	25 5	399 220 7	0	0	0	117 411 44	1	0.3 3	- 1.58	- 1. 58	939 798 1	4	1.6 7	0.74	0. 74	NA			
gene_276 GeneMa rk.hmm 1023_nt - 41701 42723	10 23	399 220 7	647	15 8.4 2	7.31	117 411 44	154 2	12 8.3 8	7	- 0. 31	939 798 1	135 3	14 0.7 3	7.14	- 0. 17	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2770 GeneM ark.hmm 126_nt + 136 261	12 6	399 220 7	0	0	0	117 411 44	64	43. 26	5.44	5. 44	939 798 1	46	38. 85	5.28	5. 28	NA			
gene_2771 GeneM ark.hmm 264_nt - 1 264	26 4	399 220 7	0	0	0	117 411 44	1	0.3 2	- 1.63	- 1. 63	939 798 1	0	0	0	0	Trehalose and maltose hydrolases (possible phosphorylases)	METABOLISM	Carbohydrate transport and metabolism	G
gene_2772 GeneM ark.hmm 96_nt - 170 265	96	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2773 GeneM ark.hmm 267_nt + 1 267	26 7	399 220 7	48	45. 03	5.49	117 411 44	313	99. 84	6.64	1. 15	939 798 1	499	19 8.8 6	7.64	2. 15	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2774 GeneM ark.hmm 243_nt + 23 265	24 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	1	0.4 4	- 1.19	- 1. 19	NA			
gene_2403 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	0	0	0	117 411 44	26	18. 45	4.21	4. 21	939 798 1	44	39. 02	5.29	5. 29	NA			
gene_2776 GeneM ark.hmm 192_nt + 3 194	19 2	399 220 7	0	0	0	117 411 44	1	0.4 4	- 1.17	- 1. 17	939 798 1	8	4.4 3	2.15	2. 15	NA			
gene_2777 GeneM ark.hmm 270_nt + 2 271	27 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	2	0.7 9	- 0.34	- 0. 34	NA			
gene_2346 GeneM ark.hmm 105_nt + 	10	399 220	0	0	0	117 411	17	13.	3.79	3.	939 798	39	39.	5.3	5.	NA			

3 107	5	7				44		79		79	1		52		3				
gene_423 GeneMa rk.hmm 2316_nt - 14789 17104	23 16	399 220 7	4	0.4 3	- 1.21	117 411 44	106 7	39. 24	5.29	6. 5	939 798 1	370	17	4.09	5. 3	Type IV secretory pathway, VirB4 components	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_277 GeneMa rk.hmm 690_nt - 42822 43511	69 0	399 220 7	763 0	27 69. 89	11.4 4	117 411 44	139 25	17 18. 84	10.7 5	- 0. 69	939 798 1	100 75	15 53. 68	10.6	- 0. 84	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_1758 GeneM ark.hmm 1830_nt + 28494 30323	18 30	399 220 7	2	0.2 7	- 1.87	117 411 44	353	16. 43	4.04	5. 91	939 798 1	187	10. 87	3.44	5. 31	Type IV secretory pathway, VirD2 components (relaxase)	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_2781 GeneM ark.hmm 108_nt + 1 108	10 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_602 GeneMa rk.hmm 675_nt - 54826 55500	67 5	399 220 7	2	0.7 4	- 0.43	117 411 44	236	29. 78	4.9	5. 33	939 798 1	188	29. 64	4.89	5. 32	Transcriptional antiterminator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2783 GeneM ark.hmm 90_nt + 1 90	90	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_1549 GeneM ark.hmm 708_nt + 22805 23512	70 8	399 220 7	1	0.3 5	-1.5	117 411 44	192	23. 1	4.53	6. 03	939 798 1	98	14. 73	3.88	5. 38	Phosphoribosylaminoimidazolesucci nocarboxamide (SAICAR) synthase	METABOLISM	Nucleotide transport and metabolism	F
gene_2775 GeneM ark.hmm 192_nt + 79 270	19 2	399 220 7	0	0	0	117 411 44	104	46. 13	5.53	5. 53	939 798 1	76	42. 12	5.4	5. 4	NA			
gene_2786 GeneM ark.hmm 300_nt + 3 302	30 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_142 GeneMa rk.hmm 180_nt + 6 72 851	18 0	399 220 7	1	1.3 9	0.48	117 411 44	51	24. 13	4.59	4. 11	939 798 1	102	60. 3	5.91	5. 43	---	---	---	---
gene_2326 GeneM ark.hmm 102_nt - 3 104	10 2	399 220 7	0	0	0	117 411 44	27	22. 55	4.49	4. 49	939 798 1	42	43. 81	5.45	5. 45	NA			
gene_2789 GeneM ark.hmm 84_nt - 1 84	84	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_278 GeneMa rk.hmm 1425_nt - 43523 44947	14 25	399 220 7	150 94	26 53. 24	11.3 7	117 411 44	221 54	13 24. 12	10.3 7	-1	939 798 1	150 70	11 25. 29	10.1 4	- 1. 23	6-phosphogluconate dehydrogenase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2790 GeneM ark.hmm 108_nt - 202 309	10 8	399 220 7	0	0	0	117 411 44	6	4.7 3	2.24	2. 24	939 798 1	4	3.9 4	1.98	1. 98	NA			

gene_2791 GeneM ark.hmm 105_nt + 209 313	10 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2329 GeneM ark.hmm 105_nt - 2 106	10 5	399 220 7	0	0	0	117 411 44	23	18. 66	4.22	4. 22	939 798 1	43	43. 58	5.45	5. 45	NA			
gene_2778 GeneM ark.hmm 198_nt - 74 271	19 8	399 220 7	0	0	0	117 411 44	81	34. 84	5.12	5. 12	939 798 1	82	44. 07	5.46	5. 46	---	---	---	---
gene_2794 GeneM ark.hmm 135_nt - 3 137	13 5	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2795 GeneM ark.hmm 123_nt + 197 319	12 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2155 GeneM ark.hmm 459_nt - 232 690	45 9	399 220 7	11	6	2.59	117 411 44	683	12 6.7 4	6.99	4. 4	939 798 1	118 9	27 5.6 4	8.11	5. 52	Serine/threonine protein kinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2623 GeneM ark.hmm 189_nt - 3 191	18 9	399 220 7	0	0	0	117 411 44	104	46. 87	5.55	5. 55	939 798 1	82	46. 17	5.53	5. 53	NA			
gene_2798 GeneM ark.hmm 339_nt - 3 341	33 9	399 220 7	0	0	0	117 411 44	4	1	0.01	0. 01	939 798 1	3	0.9 4	- 0.09	- 0. 09	NA			
gene_2805 GeneM ark.hmm 219_nt - 147 365	21 9	399 220 7	0	0	0	117 411 44	55	21. 39	4.42	4. 42	939 798 1	95	46. 16	5.53	5. 53	NA			
gene_279 GeneMa rk.hmm 1395_nt - 45023 46417	13 95	399 220 7	115 3	20 7.0 3	7.69	117 411 44	687 2	41 9.5 6	8.71	1. 02	939 798 1	694 9	53 0.0 5	9.05	1. 36	---	---	---	---
gene_27 GeneMar k.hmm 480_nt - 18971 19450	48 0	399 220 7	161 2	84 1.2 2	9.72	117 411 44	257 3	45 6.5 5	8.83	- 0. 89	939 798 1	289 5	64 1.7 6	9.33	- 0. 39	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2800 GeneM ark.hmm 339_nt - 3 341	33 9	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2801 GeneM ark.hmm 342_nt - 2 343	34 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	5	1.5 6	0.64	0. 64	Nitroreductase	METABOLISM	Energy production and conversion	C
gene_2370 GeneM ark.hmm 114_nt - 3 116	11 4	399 220 7	0	0	0	117 411 44	38	28. 39	4.83	4. 83	939 798 1	51	47. 6	5.57	5. 57	NA			
gene_2358 GeneM ark.hmm 111_nt + 1 111	11 1	399 220 7	0	0	0	117 411 44	32	24. 55	4.62	4. 62	939 798 1	51	48. 89	5.61	5. 61	NA			
gene_2804 GeneM ark.hmm 96_nt + 1	96	399 220	0	0	0	117 411	0	0	0	0	939 798	0	0	0	0	NA			

96		7				44					1								
gene_2693 GeneMark.hmm 147_nt - 3 149	147	3992207	0	0	0	11741144	88	50.99	5.67	5.67	9397981	69	49.95	5.64	5.64	---	---	---	
gene_2806 GeneMark.hmm 378_nt + 3 380	378	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	---	---	---	
gene_2732 GeneMark.hmm 183_nt + 39 221	183	3992207	0	0	0	11741144	102	47.47	5.57	5.57	9397981	94	54.66	5.77	5.77	NA			
gene_2808 GeneMark.hmm 87_nt + 3 89	87	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2809 GeneMark.hmm 87_nt + 131 217	87	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_280 GeneMark.hmm 1158_nt - 46430 47587	1158	3992207	427	92.36	6.53	11741144	3638	267.57	8.06	1.53	9397981	3588	329.69	8.36	1.83	Predicted N6-adenine-specific DNA methylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2810 GeneMark.hmm 105_nt + 285 389	105	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2811 GeneMark.hmm 183_nt - 2 184	183	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2812 GeneMark.hmm 138_nt - 259 396	138	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2340 GeneMark.hmm 105_nt + 3 107	105	3992207	0	0	0	11741144	31	25.15	4.65	4.65	9397981	59	59.79	5.9	5.9	NA			
gene_2814 GeneMark.hmm 363_nt - 66 428	363	3992207	0	0	0	11741144	2	0.47	-1.09	-1.09	9397981	2	0.59	-0.77	-0.77	NA			
gene_2815 GeneMark.hmm 450_nt - 3 452	450	3992207	224	124.69	6.96	11741144	2071	391.97	8.61	1.65	9397981	1912	452.11	8.82	1.86	Collagenase and related proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2816 GeneMark.hmm 489_nt + 3 491	489	3992207	598	306.32	8.26	11741144	4425	770.72	9.59	1.33	9397981	3456	752.02	9.55	1.29	---	---	---	---
gene_2817 GeneMark.hmm 87_nt - 406 492	87	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2818 GeneMark.hmm 84_nt + 2	84	399220	0	0	0	117411	0	0	0	0	939798	0	0	0	0	NA			

185		7									1								
gene_2819 GeneMark.hmm 150_nt + 337 486	150	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_281 GeneMark.hmm 84_nt - 47921 48004	84	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2443 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	36	25.55	4.68	4.68	9397981	68	60.3	5.91	5.91	NA			
gene_2699 GeneMark.hmm 204_nt + 2 205	204	3992207	0	0	0	11741144	148	61.79	5.95	5.95	9397981	115	59.98	5.91	5.91	DNA-directed RNA polymerase, beta' subunit/160 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2822 GeneMark.hmm 537_nt + 2 538	537	3992207	261	121.75	6.93	11741144	975	154.64	7.27	0.34	9397981	766	151.78	7.25	0.32	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2466 GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	28	19.87	4.31	4.31	9397981	70	62.07	5.96	5.96	NA			
gene_2824 GeneMark.hmm 144_nt - 630 773	144	3992207	43	74.8	6.22	11741144	606	358.43	8.49	2.27	9397981	182	134.49	7.07	0.85	NA			
gene_2825 GeneMark.hmm 288_nt - 464 751	288	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2826 GeneMark.hmm 981_nt + 2 982	981	3992207	1503	383.78	8.58	11741144	8227	714.27	9.48	0.9	9397981	6318	685.29	9.42	0.84	---	---	---	---
gene_2438 GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	47	33.36	5.06	5.06	9397981	71	62.96	5.98	5.98	NA			
gene_2828 GeneMark.hmm 282_nt + 288 569	282	3992207	64	56.85	5.83	11741144	241	72.79	6.19	0.36	9397981	228	86.03	6.43	0.6	---	---	---	---
gene_2829 GeneMark.hmm 717_nt + 604 1320	717	3992207	253	88.39	6.47	11741144	797	94.67	6.56	0.09	9397981	754	111.9	6.81	0.34	---	---	---	---
gene_282 GeneMark.hmm 330_nt - 48073 48402	330	3992207	1121	850.9	9.73	11741144	4564	1177.93	10.2	0.47	9397981	1462	471.41	8.88	-0.85	Cell division initiation protein	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2830 GeneMark.hmm 768_nt - 1450 2217	768	3992207	3125	1019.24	9.99	11741144	13430	1489.38	10.54	0.55	9397981	6304	873.41	9.77	-0.22	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_2831 GeneMark.hmm 114_nt +	114	399220	0	0	0	117411	0	0	0	0	939798	0	0	0	0	NA			

332 645			7				44					1							
gene_2832 GeneM ark.hmm 108_nt + 774 881	10 8	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2833 GeneM ark.hmm 93_nt + 1 240 1332	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2834 GeneM ark.hmm 192_nt - 1396 1587	19 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2835 GeneM ark.hmm 267_nt - 2397 2663	26 7	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_283 GeneMa rk.hmm 528_nt - 48472 48999	52 8	399 220 7	62	29. 41	4.88	117 411 44	558	90. 01	6.49	1. 61	939 798 1	469	94. 52	6.56	1. 68	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_284 GeneMa rk.hmm 597_nt + 4 9065 49661	59 7	399 220 7	124 2	52 1.1 2	9.03	117 411 44	601 9	85 8.7	9.75	0. 72	939 798 1	368 3	65 6.4 4	9.36	0. 33	Penicillin-binding protein-related factor A, putative recombinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_285 GeneMa rk.hmm 2160_nt + 49658 51817	21 60	399 220 7	300 93	34 89. 79	11.7 7	117 411 44	619 84	24 44. 08	11.2 6	- 0. 51	939 798 1	562 64	27 71. 67	11.4 4	- 0. 33	Membrane carboxypeptidase (penicillin-binding protein)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_286 GeneMa rk.hmm 5232_nt - 51983 57214	52 32	399 220 7	955	45. 72	5.51	117 411 44	461 3	75. 09	6.23	0. 72	939 798 1	418 6	85. 13	6.41	0. 9	NA			
gene_287 GeneMa rk.hmm 921_nt - 57587 58507	92 1	399 220 7	817 6	22 23. 66	11.1 2	117 411 44	560 29	51 81. 35	12.3 4	1. 22	939 798 1	103 056	11 90 6.3 6	13.5 4	2. 42	ABC-type oligopeptide transport system, periplasmic component	METABOLISM	Amino acid transport and metabolism	E
gene_288 GeneMa rk.hmm 1218_nt - 59159 60376	12 18	399 220 7	108 82	22 37. 94	11.1 3	117 411 44	598 02	41 81. 75	12.0 3	0. 9	939 798 1	959 54	83 82. 65	13.0 3	1. 9	Phosphomannomutase	METABOLISM	Carbohydrate transport and metabolism	G
gene_289 GeneMa rk.hmm 921_nt - 60373 61293	92 1	399 220 7	317 5	86 3.5 2	9.75	117 411 44	254 24	23 51. 11	11.2	1. 45	939 798 1	331 04	38 24. 6	11.9	2. 15	UDP-glucose pyrophosphorylase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_28 GeneMar k.hmm 987_nt + 19 644 20630	98 7	399 220 7	135 31	34 34	11.7 5	117 411 44	484 27	41 78. 88	12.0 3	0. 28	939 798 1	123 82	13 34. 87	10.3 8	- 1. 37	Malate/lactate dehydrogenases	METABOLISM	Energy production and conversion	C
gene_290 GeneMa rk.hmm 924_nt - 61591 62514	92 4	399 220 7	247 7	67 1.4 9	9.39	117 411 44	163 93	15 11. 04	10.5 6	1. 17	939 798 1	136 19	15 68. 33	10.6 2	1. 23	Glycosyltransferases, probably involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_291 GeneMa rk.hmm 1185_nt - 62860 64044	11 85	399 220 7	628 6	13 28. 75	10.3 8	117 411 44	351 34	25 25. 22	11.3	0. 92	939 798 1	161 99	14 54. 57	10.5 1	0. 13	Predicted UDP-glucose 6- dehydrogenase	CELLULAR PROCESSES AND	Cell wall/membrane/envelope biogenesis	M

																	SIGNALING		
gene_292 GeneMark.hmm 480_nt - 64123 64602	480	3992207	17	8.87	3.15	11741144	135	23.95	4.58	1.43	9397981	82	18.18	4.18	1.03	Transposase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2645 GeneMark.hmm 195_nt - 3 197	195	3992207	0	0	0	11741144	161	70.32	6.14	6.14	9397981	122	66.57	6.06	6.06	Acetyl-CoA carboxylase beta subunit	METABOLISM	Lipid transport and metabolism	I
gene_2712 GeneMark.hmm 210_nt - 1 210	210	3992207	0	0	0	11741144	165	66.92	6.06	6.06	9397981	133	67.39	6.07	6.07	---	---	---	---
gene_2327 GeneMark.hmm 105_nt - 1 105	105	3992207	0	0	0	11741144	36	29.2	4.87	4.87	9397981	67	67.9	6.09	6.09	NA			
gene_296 GeneMark.hmm 723_nt - 67139 67861	723	3992207	14	4.85	2.28	11741144	199	23.44	4.55	2.27	9397981	111	16.34	4.03	1.75	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_297 GeneMark.hmm 291_nt - 68052 68342	291	3992207	6	5.16	2.37	11741144	33	9.66	3.27	0.9	9397981	21	7.68	2.94	0.57	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_298 GeneMark.hmm 99_nt - 2 100	99	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	METABOLISM	Energy production and conversion	C
gene_299 GeneMark.hmm 1491_nt - 724 2214	1491	3992207	8846	1486.13	10.54	11741144	31086	1775.73	10.79	0.25	9397981	15962	1139.13	10.15	-0.39	Lysyl-tRNA synthetase (class II)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_29 GeneMark.hmm 696_nt - 20979 21674	696	3992207	75	26.99	4.75	11741144	295	36.1	5.17	0.42	9397981	162	24.77	4.63	-0.12	Kef-type K+ transport systems, predicted NAD-binding component	METABOLISM	Inorganic ion transport and metabolism	P
gene_2 GeneMark.hmm 93_nt - 3 95	93	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	---	---	---	---
gene_300 GeneMark.hmm 147_nt - 2341 2487	147	3992207	153	260.71	8.03	11741144	143	82.85	6.37	-1.66	9397981	68	49.22	5.62	-2.41	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	METABOLISM	Energy production and conversion	C
gene_2675 GeneMark.hmm 201_nt + 2 202	201	3992207	0	0	0	11741144	115	48.73	5.61	5.61	9397981	132	69.88	6.13	6.13	DNA-directed RNA polymerase, beta subunit/140 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2354 GeneMark.hmm 111_nt - 2 112	111	3992207	0	0	0	11741144	52	39.9	5.32	5.32	9397981	76	72.85	6.19	6.19	NA			
gene_303 GeneMark.hmm 111_nt + 4020 4130	111	3992207	0	0	0	11741144	4	3.07	1.62	1.62	9397981	0	0	0	0	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_304 GeneMark.hmm 507_nt + 4320 4826	507	3992207	86	42.49	5.41	11741144	416	69.88	6.13	0.72	9397981	307	64.43	6.01	0.6	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E

gene_305[GeneMark.hmm 867_nt + 4838 5704	867	3992207	50	14.45	3.85	11741144	577	56.68	5.82	1.97	9397981	399	48.97	5.61	1.76	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_306[GeneMark.hmm 648_nt - 5791 6438	648	3992207	193	74.61	6.22	11741144	898	118.03	6.88	0.66	9397981	424	69.62	6.12	-0.1	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_307[GeneMark.hmm 765_nt - 7895 8659	765	3992207	75	24.56	4.62	11741144	980	109.11	6.77	2.15	9397981	470	65.37	6.03	1.41	---	---	---	---
gene_308[GeneMark.hmm 300_nt - 8755 9054	300	3992207	595	496.8	8.96	11741144	1014	287.88	8.17	-0.79	9397981	648	229.84	7.84	-1.12	---	---	---	---
gene_309[GeneMark.hmm 633_nt - 9338 9970	633	3992207	267	105.66	6.72	11741144	551	74.14	6.21	-0.51	9397981	438	73.63	6.2	-0.52	Orotate phosphoribosyltransferase	METABOLISM	Nucleotide transport and metabolism	F
gene_30[GeneMark.hmm 264_nt - 21721 21984	264	3992207	72	68.31	6.09	11741144	251	80.98	6.34	0.25	9397981	219	88.27	6.46	0.37	Cytotoxic translational repressor of toxin-antitoxin stability system	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_310[GeneMark.hmm 702_nt - 10004 10705	702	3992207	301	107.4	6.75	11741144	716	86.87	6.44	-0.31	9397981	505	76.55	6.26	-0.49	Orotidine-5'-phosphate decarboxylase	METABOLISM	Nucleotide transport and metabolism	F
gene_311[GeneMark.hmm 1200_nt - 10938 12137	1200	3992207	1429	298.29	8.22	11741144	5761	408.89	8.68	0.46	9397981	6299	558.54	9.13	0.91	Cell division septal protein	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_312[GeneMark.hmm 609_nt - 12147 12755	609	3992207	374	153.83	7.27	11741144	1397	195.37	7.61	0.34	9397981	1657	289.51	8.18	0.91	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_313[GeneMark.hmm 444_nt - 12813 13256	444	3992207	188	106.06	6.73	11741144	855	164.01	7.36	0.63	9397981	797	191	7.58	0.85	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_314[GeneMark.hmm 1341_nt - 13258 14598	1341	3992207	2082	388.9	8.6	11741144	5374	341.32	8.41	-0.19	9397981	4971	394.44	8.62	0.02	UDP-N-acetylmuramoylalanine-D-glutamate ligase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_315[GeneMark.hmm 642_nt - 14702 15343	642	3992207	29	11.31	3.5	11741144	159	21.09	4.4	0.9	9397981	434	71.93	6.17	2.67	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2500[GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	41	29.1	4.86	4.86	9397981	83	73.6	6.2	6.2	NA			
gene_317[GeneMark.hmm 300_nt -	300	399220	16	13.36	3.74	117411	95	26.97	4.75	1.01	939798	46	16.32	4.03	0.29	NA			

[17437 17736		7				44					1								
gene_318 GeneMa rk.hmm 255_nt 18101 18355	25 5	399 220 7	170 1	16 70. 9	10.7 1	117 411 44	467 9	15 62. 8	10.6 1	- 0. 1	939 798 1	325 8	13 59. 49	10.4 1	- 0. 3	---	---	---	
gene_319 GeneMa rk.hmm 1023_nt 18375 19397	10 23	399 220 7	418 9	10 25. 7	10	117 411 44	183 08	15 24. 25	10.5 7	0. 57	939 798 1	124 30	12 92. 89	10.3 4	0. 34	Predicted membrane GTPase involved in stress response	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_31 GeneMar k.hmm 243_nt 21977 22219	24 3	399 220 7	54	55. 66	5.8	117 411 44	119	41. 71	5.38	- 0. 42	939 798 1	150	65. 68	6.04	0. 24	---	---	---	
gene_320 GeneMa rk.hmm 126_nt 19479 19604	12 6	399 220 7	44	87. 47	6.45	117 411 44	343	23 1.8 5	7.86	1. 41	939 798 1	172	14 5.2 5	7.18	0. 73	Predicted membrane GTPase involved in stress response	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_321 GeneMa rk.hmm 666_nt 19746 20411	66 6	399 220 7	276 0	10 38. 06	10.0 2	117 411 44	181 75	23 24. 29	11.1 8	1. 16	939 798 1	686 7	10 97. 13	10.1	0. 08	Predicted membrane GTPase involved in stress response	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2156 GeneM ark.hmm 105_nt 1310 1414	10 5	399 220 7	0	0	0	117 411 44	42	34. 07	5.09	5. 09	939 798 1	76	77. 02	6.27	6. 27	NA			
gene_2767 GeneM ark.hmm 255_nt 3 257	25 5	399 220 7	0	0	0	117 411 44	215	71. 81	6.17	6. 17	939 798 1	185	77. 2	6.27	6. 27	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases	METABOLISM	Energy production and conversion	C
gene_324 GeneMa rk.hmm 381_nt 21654 22034	38 1	399 220 7	238	15 6.4 7	7.29	117 411 44	943	21 0.8	7.72	0. 43	939 798 1	480	13 4.0 5	7.07	- 0. 22	Rhodanese-related sulfurtransferase	METABOLISM	Inorganic ion transport and metabolism	P
gene_325 GeneMa rk.hmm 270_nt 22034 22303	27 0	399 220 7	107 4	99 6.3 9	9.96	117 411 44	398 2	12 56. 11	10.2 9	0. 33	939 798 1	999	39 3.7	8.62	- 1. 34	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_326 GeneMa rk.hmm 816_nt + 2 2307 23122	81 6	399 220 7	181 1	55 5.9 2	9.12	117 411 44	661 4	69 0.3 4	9.43	0. 31	939 798 1	419 2	54 6.6 3	9.09	- 0. 03	Transcriptional regulator	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2497 GeneM ark.hmm 120_nt 2 121	12 0	399 220 7	2	4.1 7	2.06	117 411 44	160	11 3.5 6	6.83	4. 77	939 798 1	384	34 0.5	8.41	6. 35	NA			
gene_328 GeneMa rk.hmm 756_nt 23388 24143	75 6	399 220 7	115 0	38 1.0 3	8.57	117 411 44	221 7	24 9.7 7	7.96	- 0. 61	939 798 1	270 6	38 0.8 7	8.57	0	Short-chain dehydrogenases of various substrate specificities	POORLY CHARACTERIZ ED	General function prediction only	R
gene_329 GeneMa rk.hmm 249_nt 24164 24412	24 9	399 220 7	63	63. 38	5.99	117 411 44	228	77. 99	6.29	0. 3	939 798 1	193	82. 48	6.37	0. 38	Metal-dependent hydrolases of the beta-lactamase superfamily III	POORLY CHARACTERIZ ED	General function prediction only	R
gene_32 GeneMar k.hmm 720_nt 22310 23029	72 0	399 220 7	210 0	73 0.5 9	9.51	117 411 44	328 2	38 8.2 4	8.6	- 0. 91	939 798 1	326 5	48 2.5 2	8.91	- 0. 6	Metal-dependent hydrolases of the beta-lactamase superfamily I	POORLY CHARACTERIZ ED	General function prediction only	R

gene_330 GeneMark.hmm 810_nt - 24330 25139	810	3992207	650	201.01	7.65	11741144	1451	152.57	7.25	-0.4	9397981	1508	198.1	7.63	-0.02	Metal-dependent hydrolases of the beta-lactamase superfamily III	POORLY CHARACTERIZED	General function prediction only	R
gene_331 GeneMark.hmm 624_nt - 25154 25777	624	3992207	350	140.5	7.13	11741144	1282	174.98	7.45	0.32	9397981	1456	248.28	7.96	0.83	---	---	---	---
gene_332 GeneMark.hmm 1239_nt - 25770 27008	1239	3992207	705	142.53	7.16	11741144	1882	129.37	7.02	-0.14	9397981	2191	188.16	7.56	0.4	GTPases	POORLY CHARACTERIZED	General function prediction only	R
gene_333 GeneMark.hmm 114_nt - 27001 27114	114	3992207	2	4.39	2.14	11741144	14	10.46	3.39	1.25	9397981	8	7.47	2.9	0.76	tRNA delta(2)-isopentenylpyrophosphate transferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_334 GeneMark.hmm 765_nt - 27174 27938	765	3992207	335	109.69	6.78	11741144	1330	148.07	7.21	0.43	9397981	1185	164.82	7.36	0.58	tRNA delta(2)-isopentenylpyrophosphate transferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_335 GeneMark.hmm 171_nt + 28059 28229	171	3992207	1598	2340.82	11.19	11741144	8950	4457.76	12.12	0.93	9397981	1254	780.31	9.61	-1.58	---	---	---	---
gene_2434 GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	58	41.17	5.36	5.36	9397981	93	82.46	6.37	6.37	NA			
gene_337 GeneMark.hmm 723_nt - 28448 29170	723	3992207	1158	401.2	8.65	11741144	8058	949.25	9.89	1.24	9397981	4222	621.36	9.28	0.63	Thymidylate synthase	METABOLISM	Nucleotide transport and metabolism	F
gene_338 GeneMark.hmm 960_nt - 29267 30226	960	3992207	1299	338.94	8.4	11741144	3344	296.68	8.21	-0.19	9397981	4059	449.9	8.81	0.41	Transcriptional regulator/sugar kinase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_339 GeneMark.hmm 927_nt - 30425 31351	927	3992207	462	124.84	6.96	11741144	2565	235.67	7.88	0.92	9397981	2762	317.04	8.31	1.35	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZED	General function prediction only	R
gene_33 GeneMark.hmm 1350_nt - 23121 24470	1350	3992207	3250	603.03	9.24	11741144	6809	429.58	8.75	-0.49	9397981	5474	431.46	8.75	-0.49	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_340 GeneMark.hmm 618_nt - 31401 32018	618	3992207	464	188.07	7.56	11741144	3123	430.4	8.75	1.19	9397981	4014	691.12	9.43	1.87	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	POORLY CHARACTERIZED	General function prediction only	R
gene_341 GeneMark.hmm 1650_nt - 32019 33668	1650	3992207	1442	218.91	7.77	11741144	6175	318.74	8.32	0.55	9397981	8293	534.8	9.06	1.29	Anthranilate/para-aminobenzoate synthases component I	METABOLISM	Amino acid transport and metabolism	E
gene_342 GeneMark.hmm 5436_nt - 33809 39244	5436	3992207	22703	1046.14	10.03	11741144	51324	804.14	9.65	-0.38	9397981	52189	1021.56	10	-0.03	---	---	---	---
gene_343 GeneMark.hmm 564_nt - 39266 39829	564	3992207	557	247.38	7.95	11741144	1904	287.53	8.17	0.22	9397981	2113	398.64	8.64	0.69	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S

gene_344[GeneMa rk.hmm 1692_nt 39945 41636	16 92	399 220 7	192 9	28 5.5 7	8.16	117 411 44	691 4	34 8.0 3	8.44	0. 28	939 798 1	563 2	35 4.1 8	8.47	0. 31	Predicted signal transduction protein with a C-terminal ATPase domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_345[GeneMa rk.hmm 213_nt 41705 41917	21 3	399 220 7	93	10 9.3 7	6.77	117 411 44	293	11 7.1 6	6.87	0. 1	939 798 1	191	95. 42	6.58	- 0. 19	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_346[GeneMa rk.hmm 510_nt 42002 42511	51 0	399 220 7	523	25 6.8 7	8	117 411 44	240 6	40 1.8	8.65	0. 65	939 798 1	152 5	31 8.1 7	8.31	0. 31	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_2350[GeneM ark.hmm 108_nt 2 109	10 8	399 220 7	0	0	0	117 411 44	15	11. 83	3.56	3. 56	939 798 1	85	83. 75	6.39	6. 39	NA			
gene_2714[GeneM ark.hmm 207_nt 3 209	20 7	399 220 7	0	0	0	117 411 44	205	84. 35	6.4	6. 4	939 798 1	168	86. 36	6.43	6. 43	DNA-directed RNA polymerase, beta subunit/140 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_2780[GeneM ark.hmm 288_nt 2 289	28 8	399 220 7	0	0	0	117 411 44	326	96. 41	6.59	6. 59	939 798 1	237	87. 56	6.45	6. 45	DNA-directed RNA polymerase, beta' subunit/160 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_34[GeneMar k.hmm 705_nt 24463 25167	70 5	399 220 7	144 2	51 2.3 5	9	117 411 44	332 8	40 2.0 5	8.65	- 0. 35	939 798 1	273 9	41 3.4	8.69	- 0. 31	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_350[GeneMa rk.hmm 711_nt 44578 45288	71 1	399 220 7	499	17 5.8	7.46	117 411 44	337	40. 37	5.34	- 2. 12	939 798 1	322	48. 19	5.59	- 1. 87	Cytochrome c biogenesis protein	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_351[GeneMa rk.hmm 861_nt 45507 46367	86 1	399 220 7	278	80. 88	6.34	117 411 44	118 5	11 7.2 2	6.87	0. 53	939 798 1	131 6	16 2.6 4	7.35	1. 01	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_352[GeneMa rk.hmm 2055_nt 46546 48600	20 55	399 220 7	860	10 4.8 3	6.71	117 411 44	328 6	13 6.1 9	7.09	0. 38	939 798 1	378 9	19 6.1 9	7.62	0. 91	NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_353[GeneMa rk.hmm 255_nt 48612 48866	25 5	399 220 7	42	41. 26	5.37	117 411 44	269	89. 85	6.49	1. 12	939 798 1	176	73. 44	6.2	0. 83	---	---	---	---
gene_354[GeneMa rk.hmm 399_nt 48859 49257	39 9	399 220 7	242	15 1.9 3	7.25	117 411 44	611	13 0.4 2	7.03	- 0. 22	939 798 1	837	22 3.2 1	7.8	0. 55	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_355[GeneMa rk.hmm 156_nt 49358 49513	15 6	399 220 7	14	22. 48	4.49	117 411 44	55	30. 03	4.91	0. 42	939 798 1	81	55. 25	5.79	1. 3	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_356[GeneMa rk.hmm 378_nt 49634 50011	37 8	399 220 7	77	51. 03	5.67	117 411 44	387	87. 2	6.45	0. 78	939 798 1	345	97. 12	6.6	0. 93	Predicted Fe-S oxidoreductase	POORLY CHARACTERIZ ED	General function prediction only	R

gene_357 GeneMark.hmm 510_nt - 50012 50521	510	3992207	240	117.88	6.88	11741144	735	122.75	6.94	0.06	9397981	639	133.32	7.06	0.18	Predicted Fe-S oxidoreductase	POORLY CHARACTERIZED	General function prediction only	R
gene_358 GeneMark.hmm 360_nt + 50613 50972	360	3992207	305	212.22	7.73	11741144	3583	847.68	9.73	2	9397981	1136	335.77	8.39	0.66	---	---	---	---
gene_359 GeneMark.hmm 246_nt + 51183 51428	246	3992207	13	13.24	3.73	11741144	117	40.51	5.34	1.61	9397981	44	19.03	4.25	0.52	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_35 GeneMark.hmm 186_nt - 25222 25407	186	3992207	173	232.98	7.86	11741144	286	130.96	7.03	-0.83	9397981	277	158.46	7.31	-0.55	A/G-specific DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_360 GeneMark.hmm 624_nt + 51416 52039	624	3992207	35	14.05	3.81	11741144	287	39.17	5.29	1.48	9397981	153	26.09	4.71	0.9	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_361 GeneMark.hmm 3531_nt - 52287 55817	3531	3992207	953	67.61	6.08	11741144	4704	113.46	6.83	0.75	9397981	1817	54.75	5.77	-0.31	---	---	---	---
gene_362 GeneMark.hmm 1656_nt - 55878 57533	1656	3992207	215	32.52	5.02	11741144	2191	112.69	6.82	1.8	9397981	615	39.52	5.3	0.28	Beta-galactosidase/beta-glucuronidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_363 GeneMark.hmm 465_nt - 57603 58067	465	3992207	88	47.4	5.57	11741144	376	68.87	6.11	0.54	9397981	104	23.8	4.57	-1	Beta-galactosidase/beta-glucuronidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_364 GeneMark.hmm 1032_nt - 58133 59164	1032	3992207	123	29.85	4.9	11741144	1152	95.07	6.57	1.67	9397981	428	44.13	5.46	0.56	Beta-galactosidase/beta-glucuronidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_365 GeneMark.hmm 117_nt - 59252 59368	117	3992207	6	12.85	3.68	11741144	27	19.65	4.3	0.62	9397981	5	4.55	2.18	-1.5	NA			
gene_366 GeneMark.hmm 1476_nt - 59559 61034	1476	3992207	291	49.38	5.63	11741144	1149	66.3	6.05	0.42	9397981	362	26.1	4.71	-0.92	Phosphotransferase system, galactitol-specific IIC component	METABOLISM	Carbohydrate transport and metabolism	G
gene_367 GeneMark.hmm 183_nt - 61082 61264	183	3992207	39	53.38	5.74	11741144	173	80.52	6.33	0.59	9397981	44	25.58	4.68	-1.06	Phosphotransferase system, galactitol-specific IIB component	METABOLISM	Carbohydrate transport and metabolism	G
gene_368 GeneMark.hmm 444_nt - 61463 61906	444	3992207	21	11.85	3.57	11741144	223	42.78	5.42	1.85	9397981	71	17.02	4.09	0.52	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_2739 GeneMark.hmm 225_nt - 1 225	225	3992207	0	0	0	11741144	277	104.85	6.71	6.71	9397981	191	90.33	6.5	6.5	DNA-directed RNA polymerase, beta' subunit/160 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_36 GeneMark.hmm 639_nt - 25462 26100	639	3992207	669	262.25	8.03	11741144	1669	222.46	7.8	-0.23	9397981	1846	307.39	8.26	0.23	A/G-specific DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_370 GeneMark.hmm 198_nt -	198	399220	24	30.	4.92	117411	94	40.	5.34	0.	939798	71	38.	5.25	0.	Acetyltransferases	POORLY CHARACTERIZ	General function prediction only	R

[69724 69921	8	7		36		44		43		42	1		16		33		ED		
gene_371 GeneMa rk.hmm 279_nt - 69906 70184	27 9	399 220 7	212	19 0.3 3	7.57	117 411 44	486	14 8.3 6	7.21	- 0. 36	939 798 1	460	17 5.4 4	7.45	- 0. 12	---	---	---	---
gene_372 GeneMa rk.hmm 786_nt - 70223 71008	78 6	399 220 7	213	67. 88	6.08	117 411 44	719	77. 91	6.28	0. 2	939 798 1	492	66. 61	6.06	- 0. 02	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_373 GeneMa rk.hmm 819_nt - 71010 71828	81 9	399 220 7	108	33. 03	5.05	117 411 44	596	61. 98	5.95	0. 9	939 798 1	443	57. 56	5.85	0. 8	ABC-type uncharacterized transport system, permease component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_374 GeneMa rk.hmm 612_nt - 71830 72441	61 2	399 220 7	248	10 1.5	6.67	117 411 44	716	99. 64	6.64	- 0. 03	939 798 1	730	12 6.9 2	6.99	0. 32	ABC-type uncharacterized transport system, ATPase component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_375 GeneMa rk.hmm 351_nt - 72519 72869	35 1	399 220 7	321	22 9.0 8	7.84	117 411 44	509	12 3.5 1	6.95	- 0. 89	939 798 1	450	13 6.4 2	7.09	- 0. 75	ABC-type uncharacterized transport system, ATPase component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_376 GeneMa rk.hmm 327_nt + 7 4289 74615	32 7	399 220 7	12	9.1 9	3.2	117 411 44	101	26. 31	4.72	1. 52	939 798 1	55	17. 9	4.16	0. 96	NA			
gene_377 GeneMa rk.hmm 690_nt - 75298 75987	69 0	399 220 7	343 2	12 45. 91	10.2 8	117 411 44	173 01	21 35. 56	11.0 6	0. 78	939 798 1	168 03	25 91. 21	11.3 4	1. 06	Ribosomal protein L1	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_378 GeneMa rk.hmm 426_nt - 76195 76620	42 6	399 220 7	673 8	39 61. 94	11.9 5	117 411 44	249 81	49 94. 47	12.2 9	0. 34	939 798 1	293 76	73 37. 51	12.8 4	0. 89	Ribosomal protein L11	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_379 GeneMa rk.hmm 717_nt - 76929 77645	71 7	399 220 7	152 2	53 1.7 2	9.05	117 411 44	556 0	66 0.4 6	9.37	0. 32	939 798 1	750 5	11 13. 77	10.1 2	1. 07	D-alanyl-D-alanine carboxypeptidase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_37 GeneMar k.hmm 336_nt - 26157 26492	33 6	399 220 7	79	58. 89	5.88	117 411 44	372	94. 3	6.56	0. 68	939 798 1	442	13 9.9 7	7.13	1. 25	A/G-specific DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2355 GeneM ark.hmm 111_nt + 1 111	11 1	399 220 7	0	0	0	117 411 44	51	39. 13	5.29	5. 29	939 798 1	98	93. 94	6.55	6. 55	NA			
gene_381 GeneMa rk.hmm 426_nt + 1 315 1740	42 6	399 220 7	242	14 2.3	7.15	117 411 44	990	19 7.9 3	7.63	0. 48	939 798 1	471	11 7.6 5	6.88	- 0. 27	Ribose 5-phosphate isomerase RpiB	METABOLISM	Carbohydrate transport and metabolism	G
gene_382 GeneMa rk.hmm 168_nt + 1 876 2043	16 8	399 220 7	24	35. 78	5.16	117 411 44	75	38. 02	5.25	0. 09	939 798 1	25	15. 83	3.98	- 1. 18	Ribose 5-phosphate isomerase RpiB	METABOLISM	Carbohydrate transport and metabolism	G
gene_383 GeneMa rk.hmm 171_nt + 2 273 2443	17 1	399 220 7	16	23. 44	4.55	117 411 44	45	22. 41	4.49	- 0. 06	939 798 1	19	11. 82	3.56	- 0. 99	Ribose 5-phosphate isomerase RpiB	METABOLISM	Carbohydrate transport and metabolism	G
gene_384 GeneMa rk.hmm 129_nt + 2	12 9	399 220	46	89. 32	6.48	117 411	57	37. 63	5.23	- 1.	939 798	22	18. 15	4.18	- 2.	Ribose 5-phosphate isomerase RpiB	METABOLISM	Carbohydrate transport and metabolism	G

734 2862		7				44				25	1				3				
gene_385 GeneMa rk.hmm 624_nt + 2 989 3612	62 4	399 220 7	448	17 9.8 4	7.49	117 411 44	730	99. 64	6.64	- 0. 85	939 798 1	508	86. 63	6.44	- 1. 05	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	METABOLISM	Carbohydrate transport and metabolism	G
gene_386 GeneMa rk.hmm 279_nt + 3 666 3944	27 9	399 220 7	101	90. 68	6.5	117 411 44	304	92. 8	6.54	0. 04	939 798 1	171	65. 22	6.03	- 0. 47	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	METABOLISM	Carbohydrate transport and metabolism	G
gene_387 GeneMa rk.hmm 981_nt + 3 946 4926	98 1	399 220 7	554	14 1.4 6	7.14	117 411 44	139 5	12 1.1 1	6.92	- 0. 22	939 798 1	659	71. 48	6.16	- 0. 98	Tagatose-1,6-bisphosphate aldolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2440 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	0	0	0	117 411 44	60	42. 59	5.41	5. 41	939 798 1	106	93. 99	6.55	6. 55	NA			
gene_1666 GeneM ark.hmm 162_nt - 2 163	16 2	399 220 7	0	0	0	117 411 44	72	37. 85	5.24	5. 24	939 798 1	144	94. 58	6.56	6. 56	NA			
gene_38 GeneMar k.hmm 258_nt - 26905 27162	25 8	399 220 7	70	67. 96	6.09	117 411 44	413	13 6.3 4	7.09	1	939 798 1	293	12 0.8 4	6.92	0. 83	Formyltetrahydrofolate synthetase	METABOLISM	Nucleotide transport and metabolism	F
gene_2469 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	67	47. 55	5.57	5. 57	939 798 1	108	95. 77	6.58	6. 58	NA			
gene_391 GeneMa rk.hmm 1287_nt + 6485 7771	12 87	399 220 7	107	20. 83	4.38	117 411 44	355 2	23 5.0 6	7.88	3. 5	939 798 1	611	50. 52	5.66	1. 28	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_1952 GeneM ark.hmm 321_nt - 402 722	32 1	399 220 7	0	0	0	117 411 44	275	72. 97	6.19	6. 19	939 798 1	291	96. 46	6.59	6. 59	F0F1-type ATP synthase, subunit a	METABOLISM	Energy production and conversion	C
gene_2396 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	76	53. 94	5.75	5. 75	939 798 1	109	96. 65	6.59	6. 59	NA			
gene_394 GeneMa rk.hmm 213_nt + 8 882 9094	21 3	399 220 7	19	22. 34	4.48	117 411 44	436	17 4.3 4	7.45	2. 97	939 798 1	44	21. 98	4.46	- 0. 02	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_395 GeneMa rk.hmm 870_nt + 9 166 10035	87 0	399 220 7	33	9.5	3.25	117 411 44	149 3	14 6.1 6	7.19	3. 94	939 798 1	220	26. 91	4.75	1. 5	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_396 GeneMa rk.hmm 762_nt - 10614 11375	76 2	399 220 7	203 6	66 9.2 8	9.39	117 411 44	459 4	51 3.4 8	9	- 0. 39	939 798 1	278 4	38 8.7 6	8.6	- 0. 79	Transcriptional regulators of sugar metabolism	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_397 GeneMa rk.hmm 963_nt - 11557 12519	96 3	399 220 7	881 1	22 91. 85	11.1 6	117 411 44	214 22	18 94. 63	10.8 9	- 0. 27	939 798 1	138 79	15 33. 55	10.5 8	- 0. 58	Ribonucleotide reductase, beta subunit	METABOLISM	Nucleotide transport and metabolism	F
gene_398 GeneMa rk.hmm 825_nt - 12707 13531	82 5	399 220 7	155 97	47 35. 59	12.2 1	117 411 44	260 33	26 87. 57	11.3 9	- 0. 82	939 798 1	223 41	28 81. 47	11.4 9	- 0. 72	Ribonucleotide reductase, alpha subunit	METABOLISM	Nucleotide transport and metabolism	F

gene_399 GeneMark.hmm 1332_nt - 13594 14925	13 32	399 220 7	779 5	14 65. 88	10.5 2	117 411 44	157 87	10 09. 45	9.98	- 0. 54	939 798 1	124 56	99 5.0 4	9.96	- 0. 56	Ribonucleotide reductase, alpha subunit	METABOLISM	Nucleotide transport and metabolism	F
gene_39 GeneMark.hmm 1428_nt - 27159 28586	14 28	399 220 7	373	65. 43	6.03	117 411 44	225 5	13 4.5	7.07	1. 04	939 798 1	207 7	15 4.7 7	7.27	1. 24	Formyltetrahydrofolate synthetase	METABOLISM	Nucleotide transport and metabolism	F
gene_3 GeneMark.hmm 279_nt - 393 671	27 9	399 220 7	47	42. 2	5.4	117 411 44	130	39. 69	5.31	- 0. 09	939 798 1	62	23. 65	4.56	- 0. 84	Phosphotransferase system, galactitol-specific IIB component	METABOLISM	Carbohydrate transport and metabolism	G
gene_400 GeneMark.hmm 219_nt - 15006 15224	21 9	399 220 7	253 6	29 00. 63	11.5	117 411 44	617 2	24 00. 33	11.2 3	- 0. 27	939 798 1	721 8	35 07. 02	11.7 8	0. 28	Glutaredoxin and related proteins	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_401 GeneMark.hmm 264_nt + 15575 15838	26 4	399 220 7	486 5	46 16	12.1 7	117 411 44	698 9	22 54. 76	11.1 4	- 1. 03	939 798 1	204 3	82 3.4 4	9.69	- 2. 48	Phosphotransferase system, HPr-related proteins	METABOLISM	Carbohydrate transport and metabolism	G
gene_402 GeneMark.hmm 1734_nt + 15844 17577	17 34	399 220 7	247 12	35 69. 82	11.8	117 411 44	775 86	38 10. 87	11.9	0. 1	939 798 1	469 63	28 81. 86	11.4 9	- 0. 31	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	METABOLISM	Carbohydrate transport and metabolism	G
gene_403 GeneMark.hmm 876_nt + 17832 18707	87 6	399 220 7	888	25 3.9 2	7.99	117 411 44	359 8	34 9.8 2	8.45	0. 46	939 798 1	951	11 5.5 2	6.85	- 1. 14	---	---	---	---
gene_404 GeneMark.hmm 168_nt + 18896 19063	16 8	399 220 7	106	15 8.0 5	7.3	117 411 44	244	12 3.7	6.95	- 0. 35	939 798 1	174	11 0.2 1	6.78	- 0. 52	---	---	---	---
gene_2494 GeneMark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	39	27. 68	4.79	4. 79	939 798 1	110	97. 54	6.61	6. 61	NA			
gene_2787 GeneMark.hmm 303_nt - 3 305	30 3	399 220 7	0	0	0	117 411 44	349	98. 1	6.62	6. 62	939 798 1	293	10 2.8 9	6.69	6. 69	Protease subunit of ATP-dependent Clp proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2441 GeneMark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	55	39. 04	5.29	5. 29	939 798 1	118	10 4.6 3	6.71	6. 71	NA			
gene_408 GeneMark.hmm 1455_nt - 1928 3382	14 55	399 220 7	12	2.0 7	1.05	117 411 44	313	18. 32	4.2	3. 15	939 798 1	102	7.4 6	2.9	1. 85	---	---	---	---
gene_2750 GeneMark.hmm 231_nt - 3 233	23 1	399 220 7	0	0	0	117 411 44	290	10 6.9 2	6.74	6. 74	939 798 1	234	10 7.7 9	6.75	6. 75	F0F1-type ATP synthase, beta subunit	METABOLISM	Energy production and conversion	C
gene_40 GeneMark.hmm 705_nt + 28801 29505	70 5	399 220 7	842	29 9.1 6	8.22	117 411 44	568 1	68 6.3 2	9.42	1. 2	939 798 1	984	14 8.5 2	7.21	- 1. 01	Phosphopantothenoylcysteine synthetase/decarboxylase	METABOLISM	Coenzyme transport and metabolism	H
gene_2409 GeneMark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	93	64. 4	6.01	6. 01	939 798 1	125	10 8.1 4	6.76	6. 76	NA			

gene_411 GeneMark.hmm 1248_nt + 4906 6153	1248	3992207	145	29.1	4.86	11741144	1762	120.25	6.91	2.05	9397981	1050	89.52	6.48	1.62	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_412 GeneMark.hmm 738_nt - 6410 7147	738	3992207	7928	2690.88	11.39	11741144	10012	1155.46	10.17	-1.22	9397981	4833	696.83	9.44	-1.95	Dimethyladenosine transferase (rRNA methylation)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_413 GeneMark.hmm 84_nt - 7272 7355	84	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_414 GeneMark.hmm 939_nt - 7404 8342	939	3992207	112	29.88	4.9	11741144	663	60.14	5.91	1.01	9397981	269	30.48	4.93	0.03	Putative phage replication protein RstA	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2425 GeneMark.hmm 123_nt + 1 123	123	3992207	0	0	0	11741144	73	50.55	5.66	5.66	9397981	129	111.6	6.8	6.8	NA			
gene_610 GeneMark.hmm 855_nt + 2788 3642	855	3992207	0	0	0	11741144	446	44.43	5.47	5.47	9397981	910	113.25	6.82	6.82	Retron-type reverse transcriptase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_417 GeneMark.hmm 417_nt - 9868 10284	417	3992207	4	2.4	1.26	11741144	55	11.23	3.49	2.23	9397981	21	5.36	2.42	1.16	DNA segregation ATPase FtsK/SpoIIIE and related proteins	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_2764 GeneMark.hmm 252_nt + 2 253	252	3992207	0	0	0	11741144	306	103.42	6.69	6.69	9397981	270	114.01	6.83	6.83	NA			
gene_2797 GeneMark.hmm 246_nt - 21 266	246	3992207	0	0	0	11741144	284	98.33	6.62	6.62	9397981	265	114.62	6.84	6.84	F ₀ F ₁ -type ATP synthase, subunit c/Archaeal/vacuolar-type H ⁺ -ATPase, subunit K	METABOLISM	Energy production and conversion	C
gene_41 GeneMark.hmm 552_nt + 29517 30068	552	3992207	1179	535.01	9.06	11741144	4948	763.45	9.58	0.52	9397981	1376	265.24	8.05	-1.01	Phosphopantothenoilcysteine synthetase/decarboxylase	METABOLISM	Coenzyme transport and metabolism	H
gene_2456 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	82	58.2	5.86	5.86	9397981	132	117.05	6.87	6.87	NA			
gene_2730 GeneMark.hmm 216_nt - 2 217	216	3992207	0	0	0	11741144	243	95.82	6.58	6.58	9397981	238	117.24	6.87	6.87	Ribulose 1,5-bisphosphate carboxylase, large subunit	METABOLISM	Carbohydrate transport and metabolism	G
gene_2383 GeneMark.hmm 117_nt - 2 118	117	3992207	0	0	0	11741144	29	21.11	4.4	4.4	9397981	130	118.23	6.89	6.89	NA			
gene_2388 GeneMark.hmm 117_nt - 2 118	117	3992207	0	0	0	11741144	67	48.77	5.61	5.61	9397981	132	120.05	6.91	6.91	NA			
gene_2398 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	133	94.4	6.56	6.56	9397981	137	121.48	6.92	6.92	NA			

gene_425 GeneMa rk.hmm 120_nt - 17414 17533	12 0	399 220 7	0	0	0	117 411 44	7	4.9 7	2.31	2. 31	939 798 1	4	3.5 5	1.83	1. 83	NA			
gene_426 GeneMa rk.hmm 102_nt - 17587 17688	10 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2424 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	88	62. 46	5.96	5. 96	939 798 1	137	12 1.4 8	6.92	6. 92	NA			
gene_2362 GeneM ark.hmm 111_nt + 3 113	11 1	399 220 7	0	0	0	117 411 44	61	46. 81	5.55	5. 55	939 798 1	128	12 2.7	6.94	6. 94	NA			
gene_429 GeneMa rk.hmm 243_nt - 18713 18955	24 3	399 220 7	3	3.0 9	1.63	117 411 44	36	12. 62	3.66	2. 03	939 798 1	23	10. 07	3.33	1. 7	NA			
gene_42 GeneMar k.hmm 297_nt + 30 052 30348	29 7	399 220 7	413	34 8.3 2	8.44	117 411 44	193 2	55 4.0 4	9.11	0. 67	939 798 1	544	19 4.9	7.61	- 0. 83	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_2747 GeneM ark.hmm 228_nt - 1 228	22 8	399 220 7	0	0	0	117 411 44	327	12 2.1 5	6.93	6. 93	939 798 1	266	12 4.1 4	6.96	6. 96	NA			
gene_431 GeneMa rk.hmm 489_nt - 20900 21388	48 9	399 220 7	14	7.1 7	2.84	117 411 44	128	22. 29	4.48	1. 64	939 798 1	94	20. 45	4.35	1. 51	NA			
gene_432 GeneMa rk.hmm 300_nt - 21378 21677	30 0	399 220 7	86	71. 81	6.17	117 411 44	299	84. 89	6.41	0. 24	939 798 1	266	94. 35	6.56	0. 39	NA			
gene_433 GeneMa rk.hmm 837_nt - 22004 22840	83 7	399 220 7	234	70. 03	6.13	117 411 44	843	85. 78	6.42	0. 29	939 798 1	495	62. 93	5.98	- 0. 15	---	---	---	---
gene_434 GeneMa rk.hmm 591_nt - 22840 23430	59 1	399 220 7	188	79. 68	6.32	117 411 44	700	10 0.8 8	6.66	0. 34	939 798 1	456	82. 1	6.36	0. 04	NA			
gene_2820 GeneM ark.hmm 399_nt - 2 400	39 9	399 220 7	0	0	0	117 411 44	508	10 8.4 4	6.76	6. 76	939 798 1	468	12 4.8 1	6.96	6. 96	NA			
gene_2361 GeneM ark.hmm 111_nt + 3 113	11 1	399 220 7	0	0	0	117 411 44	84	64. 45	6.01	6. 01	939 798 1	131	12 5.5 8	6.97	6. 97	NA			
gene_2371 GeneM ark.hmm 114_nt + 2 115	11 4	399 220 7	0	0	0	117 411 44	70	52. 3	5.71	5. 71	939 798 1	135	12 6.0 1	6.98	6. 98	NA			
gene_2406 GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	120	85. 17	6.41	6. 41	939 798 1	145	12 8.5 7	7.01	7. 01	NA			
gene_2803 GeneM ark.hmm 354_nt -	35	399 220	0	0	0	117 411	625	15 0.3	7.23	7.	939 798	434	13 0.4	7.03	7.	NA			

[3 356	4	7				44		7		23	1		5		03				
gene_43 GeneMark.hmm 258_nt + 30435 30692	258	3992207	1042	1011.66	9.98	11741144	2114	697.87	9.45	-0.53	9397981	754	310.97	8.28	-1.7	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_440 GeneMark.hmm 102_nt - 26555 26656	102	3992207	0	0	0	11741144	0	0	0	0	9397981	1	1.04	0.06	0.06	NA			
gene_2336 GeneMark.hmm 105_nt - 1 105	105	3992207	0	0	0	11741144	34	27.58	4.79	4.79	9397981	133	134.78	7.07	7.07	NA			
gene_442 GeneMark.hmm 327_nt - 27153 27479	327	3992207	2	1.53	0.62	11741144	49	12.76	3.67	3.05	9397981	7	2.28	1.19	0.57	---	---	---	---
gene_443 GeneMark.hmm 174_nt - 27476 27649	174	3992207	0	0	0	11741144	8	3.92	1.97	1.97	9397981	2	1.22	0.29	0.29	NA			
gene_444 GeneMark.hmm 270_nt - 28495 28764	270	3992207	221	205.03	7.68	11741144	528	166.56	7.38	-0.3	9397981	374	147.39	7.2	-0.48	---	---	---	---
gene_445 GeneMark.hmm 201_nt - 28873 29073	201	3992207	1106	1378.31	10.43	11741144	919	389.41	8.61	-1.82	9397981	536	283.75	8.15	-2.28	---	---	---	---
gene_446 GeneMark.hmm 735_nt - 29130 29864	735	3992207	1910	650.93	9.35	11741144	3532	409.28	8.68	-0.67	9397981	2412	349.18	8.45	-0.9	---	---	---	---
gene_447 GeneMark.hmm 3372_nt - 29900 33271	3372	3992207	6776	503.35	8.98	11741144	14051	354.9	8.47	-0.51	9397981	8025	253.23	7.98	-1	---	---	---	---
gene_448 GeneMark.hmm 1203_nt - 33441 34643	1203	3992207	2115	440.38	8.78	11741144	6889	487.73	8.93	0.15	9397981	2591	229.17	7.84	-0.94	---	---	---	---
gene_449 GeneMark.hmm 1179_nt - 34852 36030	1179	3992207	842	178.89	7.48	11741144	2828	204.29	7.67	0.19	9397981	2964	267.5	8.06	0.58	---	---	---	---
gene_44 GeneMark.hmm 501_nt + 31001 31501	501	3992207	153	76.5	6.26	11741144	681	115.77	6.86	0.6	9397981	516	109.59	6.78	0.52	---	---	---	---
gene_450 GeneMark.hmm 1269_nt - 36305 37573	1269	3992207	623	122.97	6.94	11741144	2056	137.99	7.11	0.17	9397981	2010	168.54	7.4	0.46	ATP-dependent exoDNase (exonuclease V) beta subunit (contains helicase and exonuclease domains)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_451 GeneMark.hmm 2370_nt - 37839 40208	2370	3992207	1510	159.59	7.32	11741144	5728	205.85	7.69	0.37	9397981	6461	290.08	8.18	0.86	ATP-dependent exoDNase (exonuclease V) beta subunit (contains helicase and exonuclease domains)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_452 GeneMark.hmm 978_nt -	97	399220	566	144.9	7.18	117411	207	180.4	7.5	0.	939798	266	289.7	8.18	1	ATP-dependent nuclease, subunit B	INFORMATION STORAGE AND	Replication, recombination and	L

[40205 41182	8	7		7		44	2	4		32	1	3	3				PROCESSING	repair		
gene_453 GeneMa rk.hmm 519_nt 41242 41760	51 9	399 220 7	87	41. 99	5.39	117 411 44	645	10 5.8 5	6.73	1. 34	939 798 1	651	13 3.4 7	7.06	1. 67		ATP-dependent nuclease, subunit B	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_454 GeneMa rk.hmm 1770_nt 41829 43598	17 70	399 220 7	761	10 7.7	6.75	117 411 44	315 1	15 1.6 2	7.24	0. 49	939 798 1	278 7	16 7.5 4	7.39	0. 64		ATP-dependent nuclease, subunit B	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_455 GeneMa rk.hmm 1173_nt 45489 46661	11 73	399 220 7	378 58	80 84. 38	12.9 8	117 411 44	109 132	79 23. 99	12.9 5	- 0. 03	939 798 1	330 49	29 97. 96	11.5 5	- 1. 43		Enolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_456 GeneMa rk.hmm 126_nt 46731 46856	12 6	399 220 7	213	42 3.4 4	8.73	117 411 44	829	56 0.3 7	9.13	0. 4	939 798 1	100	84. 45	6.4	- 2. 33		Enolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_457 GeneMa rk.hmm 135_nt + 4 7317 47451	13 5	399 220 7	21	38. 96	5.28	117 411 44	198	12 4.9 2	6.96	1. 68	939 798 1	26	20. 49	4.36	- 0. 92		Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_458 GeneMa rk.hmm 1116_nt 47695 48810	11 16	399 220 7	101	22. 67	4.5	117 411 44	129 4	98. 76	6.63	2. 13	939 798 1	518	49. 39	5.63	1. 13		Glycerate kinase	METABOLISM	Carbohydrate transport and metabolism	G
gene_459 GeneMa rk.hmm 372_nt 49093 49464	37 2	399 220 7	16	10. 77	3.43	117 411 44	225	51. 51	5.69	2. 26	939 798 1	135	38. 62	5.27	1. 84		Phosphoserine phosphatase	METABOLISM	Amino acid transport and metabolism	E
gene_45 GeneMar k.hmm 342_nt + 31 513 31854	34 2	399 220 7	172	12 5.9 8	6.98	117 411 44	111 9	27 8.6 7	8.12	1. 14	939 798 1	514	15 9.9 2	7.32	0. 34		Predicted small molecule binding protein (contains 3H domain)	POORLY CHARACTERIZ ED	General function prediction only	R
gene_460 GeneMa rk.hmm 1410_nt 49523 50932	14 10	399 220 7	259	46. 01	5.52	117 411 44	883	53. 34	5.74	0. 22	939 798 1	528	39. 85	5.32	- 0. 2		Glycogen synthase	METABOLISM	Carbohydrate transport and metabolism	G
gene_461 GeneMa rk.hmm 150_nt + 5 0875 51024	15 0	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0		NA			
gene_462 GeneMa rk.hmm 1140_nt 50996 52135	11 40	399 220 7	443	97. 34	6.6	117 411 44	846	63. 21	5.98	- 0. 62	939 798 1	522	48. 72	5.61	- 0. 99		ADP-glucose pyrophosphorylase	METABOLISM	Carbohydrate transport and metabolism	G
gene_463 GeneMa rk.hmm 750_nt 52125 52874	75 0	399 220 7	366	12 2.2 4	6.93	117 411 44	516	58. 6	5.87	- 1. 06	939 798 1	305	43. 27	5.44	- 1. 49		ADP-glucose pyrophosphorylase	METABOLISM	Carbohydrate transport and metabolism	G
gene_464 GeneMa rk.hmm 216_nt 53103 53318	21 6	399 220 7	33	38. 27	5.26	117 411 44	82	32. 33	5.01	- 0. 25	939 798 1	49	24. 14	4.59	- 0. 67		ADP-glucose pyrophosphorylase	METABOLISM	Carbohydrate transport and metabolism	G
gene_465 GeneMa rk.hmm 1899_nt 53338 55236	18 99	399 220 7	279	36. 8	5.2	117 411 44	118 6	53. 19	5.73	0. 53	939 798 1	555	31. 1	4.96	- 0. 24		1,4-alpha-glucan branching enzyme	METABOLISM	Carbohydrate transport and metabolism	G
gene_466 GeneMa rk.hmm 1425_nt 55945 57369	14 25	399 220 7	126 0	22 1.4 8	7.79	117 411 44	312 6	18 6.8 4	7.55	- 0. 24	939 798 1	277 3	20 7.0 6	7.69	- 0. 1		NAD-dependent aldehyde dehydrogenases	METABOLISM	Energy production and conversion	C

gene_467 GeneMark.hmm 1707_nt - 57914 59620	17 07	399 220 7	241 6	35 4.5 3	8.47	117 411 44	539 1	26 8.9 8	8.07	- 0. 4	939 798 1	680 7	42 4.3 1	8.73	0. 26	Type II secretory pathway, pullulanase PulA and related glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_468 GeneMark.hmm 237_nt - 59709 59945	23 7	399 220 7	80	84. 55	6.4	117 411 44	187	67. 2	6.07	- 0. 33	939 798 1	192	86. 2	6.43	0. 03	Type II secretory pathway, pullulanase PulA and related glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_469 GeneMark.hmm 450_nt - 59870 60319	45 0	399 220 7	184	10 2.4 2	6.68	117 411 44	382	72. 3	6.18	- 0. 5	939 798 1	374	88. 44	6.47	- 0. 21	Type II secretory pathway, pullulanase PulA and related glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_46 GeneMark.hmm 171_nt + 31922 32092	17 1	399 220 7	41	60. 06	5.91	117 411 44	312	15 5.4	7.28	1. 37	939 798 1	173	10 7.6 5	6.75	0. 84	Predicted small molecule binding protein (contains 3H domain)	POORLY CHARACTERIZED	General function prediction only	R
gene_470 GeneMark.hmm 735_nt - 60431 61165	73 5	399 220 7	702	23 9.2 4	7.9	117 411 44	125 9	14 5.8 9	7.19	- 0. 71	939 798 1	102 9	14 8.9 7	7.22	- 0. 68	NAD-dependent DNA ligase (contains BRCT domain type II)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_471 GeneMark.hmm 546_nt - 61194 61739	54 6	399 220 7	207	94. 97	6.57	117 411 44	432	67. 39	6.07	- 0. 5	939 798 1	280	54. 57	5.77	- 0. 8	NAD-dependent DNA ligase (contains BRCT domain type II)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_472 GeneMark.hmm 612_nt - 61894 62505	61 2	399 220 7	478	19 5.6 4	7.61	117 411 44	130 5	18 1.6 1	7.5	- 0. 11	939 798 1	572	99. 45	6.64	- 0. 97	NAD-dependent DNA ligase (contains BRCT domain type II)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2479 GeneMark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	94	66. 72	6.06	6. 06	939 798 1	153	13 5.6 7	7.08	7. 08	NA			
gene_474 GeneMark.hmm 579_nt - 63856 64434	57 9	399 220 7	330	14 2.7 7	7.16	117 411 44	163 0	23 9.7 7	7.91	0. 75	939 798 1	158 8	29 1.8 3	8.19	1. 03	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_475 GeneMark.hmm 282_nt - 64497 64778	28 2	399 220 7	65	57. 74	5.85	117 411 44	434	13 1.0 8	7.03	1. 18	939 798 1	393	14 8.2 9	7.21	1. 36	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_476 GeneMark.hmm 177_nt - 64781 64957	17 7	399 220 7	79	11 1.8	6.8	117 411 44	396	19 0.5 5	7.57	0. 77	939 798 1	418	25 1.2 9	7.97	1. 17	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZED	General function prediction only	R
gene_477 GeneMark.hmm 588_nt - 65011 65598	58 8	399 220 7	100 6	42 8.5 6	8.74	117 411 44	283 5	41 0.6 4	8.68	- 0. 06	939 798 1	309 9	56 0.8	9.13	0. 39	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZED	General function prediction only	R
gene_478 GeneMark.hmm 138_nt - 65742 65879	13 8	399 220 7	26	47. 19	5.56	117 411 44	63	38. 88	5.28	- 0. 28	939 798 1	56	43. 18	5.43	- 0. 13	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZED	General function prediction only	R
gene_479 GeneMark.hmm 384_nt - 65985 66368	38 4	399 220 7	270	17 6.1 2	7.46	117 411 44	113 8	25 2.4 1	7.98	0. 52	939 798 1	105 0	29 0.9 5	8.18	0. 72	ATPase components of ABC transporters with duplicated ATPase domains	POORLY CHARACTERIZED	General function prediction only	R
gene_47 GeneMark.hmm 468_nt - 32089 32556	46 8	399 220 7	350	18 7.3 3	7.55	117 411 44	179 1	32 5.9 4	8.35	0. 8	939 798 1	153 7	34 9.4 6	8.45	0. 9	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_480 GeneMark.hmm 588_nt -	58	399 220	179	76.	6.25	117 411	838	12 1.3	6.92	0.	939 798	619	11 2.0	6.81	0.	ATPase components of ABC transporters with duplicated ATPase	POORLY CHARACTERIZ	General function prediction only	R

[66440]67027	8	7		25		44		8		67	1		2		56	domains	ED		
gene_481 GeneMa rk.hmm 276_nt - [67453]67728	27 6	399 220 7	123 14	11 17 5.7 6	13.4 5	117 411 44	883 99	27 27 8.9 6	14.7 4	1. 29	939 798 1	641 08	24 71 5.4 5	14.5 9	1. 14	Bacterial nucleoid DNA-binding protein	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_482 GeneMa rk.hmm 840_nt - [67835]68674	84 0	399 220 7	301 1	89 7.8 8	9.81	117 411 44	479 7	48 6.3 8	8.93	- 0. 88	939 798 1	226 3	28 6.6 6	8.16	- 1. 65	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_483 GeneMa rk.hmm 849_nt + 6 8816]69664	84 9	399 220 7	514	15 1.6 5	7.24	117 411 44	106 1	10 6.4 4	6.73	- 0. 51	939 798 1	756	94. 75	6.57	- 0. 67	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_484 GeneMa rk.hmm 918_nt - [69757]70674	91 8	399 220 7	128 8	35 1.4 5	8.46	117 411 44	304 0	28 2.0 5	8.14	- 0. 32	939 798 1	898	10 4.0 9	6.7	- 1. 76	FAD synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_2792 GeneM ark.hmm 312_nt - [2]313	31 2	399 220 7	0	0	0	117 411 44	502	13 7.0 4	7.1	7. 1	939 798 1	397	13 5.3 9	7.08	7. 08	NADH:ubiquinone oxidoreductase 49 kD subunit 7	METABOLISM	Energy production and conversion	C
gene_486 GeneMa rk.hmm 294_nt - [71669]71962	29 4	399 220 7	284 0	24 19. 68	11.2 4	117 411 44	156 73	45 40. 4	12.1 5	0. 91	939 798 1	802 2	29 03. 36	11.5	0. 26	Ribosomal protein L27	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_487 GeneMa rk.hmm 345_nt - [71979]72323	34 5	399 220 7	763 5	55 43. 41	12.4 4	117 411 44	348 52	86 03. 96	13.0 7	0. 63	939 798 1	188 14	58 02. 66	12.5	0. 06	Predicted ribosomal protein	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_488 GeneMa rk.hmm 315_nt - [72339]72653	31 5	399 220 7	389 0	30 93. 33	11.5 9	117 411 44	233 31	63 08. 3	12.6 2	1. 03	939 798 1	121 47	41 03. 21	12	0. 41	Ribosomal protein L21	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_489 GeneMa rk.hmm 579_nt - [72872]73450	57 9	399 220 7	73	31. 58	4.98	117 411 44	502	73. 84	6.21	1. 23	939 798 1	195	35. 84	5.16	0. 18	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_48 GeneMar k.hmm 489_nt - [32630]33118	48 9	399 220 7	220	11 2.6 9	6.82	117 411 44	127 1	22 1.3 7	7.79	0. 97	939 798 1	101 4	22 0.6 5	7.79	0. 97	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_490 GeneMa rk.hmm 300_nt + 7 3942]74241	30 0	399 220 7	289 7	24 18. 88	11.2 4	117 411 44	389 0	11 04. 38	10.1 1	- 1. 13	939 798 1	221 6	78 5.9 8	9.62	- 1. 62	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_491 GeneMa rk.hmm 873_nt - [228]1100	87 3	399 220 7	666	19 1.0 9	7.58	117 411 44	326 4	31 8.4 4	8.31	0. 73	939 798 1	267 5	32 6.0 4	8.35	0. 77	Nicotinate-nucleotide pyrophosphorylase	METABOLISM	Coenzyme transport and metabolism	H
gene_492 GeneMa rk.hmm 1296_nt + 1352]2647	12 96	399 220 7	113 0	21 8.4	7.77	117 411 44	403 9	26 5.4 4	8.05	0. 28	939 798 1	297 4	24 4.1 8	7.93	0. 16	Di- and tricarboxylate transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_493 GeneMa rk.hmm 663_nt - [3667]4329	66 3	399 220 7	489	18 4.7 5	7.53	117 411 44	652 4	83 8.0 9	9.71	2. 18	939 798 1	160 3	25 7.2 7	8.01	0. 48	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_494 GeneMa rk.hmm 1410_nt +	14 10	399 220	194 5	34 5.5	8.43	117 411	326 48	19 72.	10.9 5	2. 52	939 798	117 49	88 6.6	9.79	1. 36	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G

4553 5962		7		3		44		09			1		4						
gene_495 GeneMark.hmm 1296_nt + 5980 7275	1296	3992207	2049	396.03	8.63	11741144	43681	2870.63	11.49	2.86	9397981	8136	667.99	9.38	0.75	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_496 GeneMark.hmm 309_nt + 7280 7588	309	3992207	1435	1163.27	10.18	11741144	40039	11036.07	13.43	3.25	9397981	5566	1916.68	10.9	0.72	Phosphotransferase system cellobiose-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_497 GeneMark.hmm 309_nt + 7585 7893	309	3992207	865	701.2	9.45	11741144	12978	3577.16	11.8	2.35	9397981	2064	710.75	9.47	0.02	Phosphotransferase system cellobiose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G
gene_2782 GeneMark.hmm 291_nt - 2 292	291	3992207	0	0	0	11741144	525	153.66	7.26	7.26	9397981	376	137.49	7.1	7.1	NADH:ubiquinone oxidoreductase 49 kD subunit 7	METABOLISM	Energy production and conversion	C
gene_499 GeneMark.hmm 411_nt - 11711 12121	411	3992207	1003	611.29	9.26	11741144	3095	641.37	9.33	0.07	9397981	1678	434.43	8.76	-0.5	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_2482 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	79	56.07	5.81	5.81	9397981	159	140.99	7.14	7.14	NA			
gene_4 GeneMark.hmm 321_nt - 709 1029	321	3992207	6	4.68	2.23	11741144	55	14.59	3.87	1.64	9397981	29	9.61	3.26	1.03	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	METABOLISM	Carbohydrate transport and metabolism	G
gene_500 GeneMark.hmm 429_nt - 12123 12551	429	3992207	489	285.52	8.16	11741144	2215	439.75	8.78	0.62	9397981	1280	317.48	8.31	0.15	Protein-tyrosine-phosphatase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_501 GeneMark.hmm 300_nt - 12598 12897	300	3992207	2904	2424.72	11.24	11741144	10218	2900.91	11.5	0.26	9397981	4996	1772.01	10.79	-0.45	Preprotein translocase subunit YajC	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_502 GeneMark.hmm 1983_nt - 13008 14990	1983	3992207	6851	865.4	9.76	11741144	14501	622.82	9.28	-0.48	9397981	10061	539.86	9.08	-0.68	Transketolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2389 GeneMark.hmm 120_nt - 1 120	120	3992207	0	0	0	11741144	107	75.94	6.25	6.25	9397981	161	142.76	7.16	7.16	NA			
gene_2784 GeneMark.hmm 294_nt - 2 295	294	3992207	0	0	0	11741144	554	160.49	7.33	7.33	9397981	418	151.28	7.24	7.24	NA			
gene_505 GeneMark.hmm 705_nt - 18199 18903	705	3992207	28	9.95	3.31	11741144	212	25.61	4.68	1.37	9397981	124	18.72	4.23	0.92	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	METABOLISM	Carbohydrate transport and metabolism	G
gene_1667 GeneMark.hmm 687_nt - 413 1099	687	3992207	0	0	0	11741144	558	69.18	6.11	6.11	9397981	997	154.42	7.27	7.27	NA			

gene_2386 GeneM ark.hmm 117_nt - 3 119	11 7	399 220 7	1	2.1 4	1.1	117 411 44	140	10 1.9 1	6.67	5. 57	939 798 1	363	33 0.1 3	8.37	7. 27	NA			
gene_2785 GeneM ark.hmm 300_nt - 2 301	30 0	399 220 7	0	0	0	117 411 44	526	14 9.3 3	7.22	7. 22	939 798 1	438	15 5.3 5	7.28	7. 28	NA			
gene_2351 GeneM ark.hmm 108_nt + 3 110	10 8	399 220 7	0	0	0	117 411 44	91	71. 76	6.17	6. 17	939 798 1	161	15 8.6 2	7.31	7. 31	NA			
gene_50 GeneMar k.hmm 456_nt - 33657 34112	45 6	399 220 7	210	11 5.3 6	6.85	117 411 44	840	15 6.8 9	7.29	0. 44	939 798 1	781	18 2.2 4	7.51	0. 66	Helicase subunit of the DNA excision repair complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_510 GeneMa rk.hmm 1458_nt - 21320 22777	14 58	399 220 7	38	6.5 3	2.71	117 411 44	490	28. 62	4.84	2. 13	939 798 1	309	22. 55	4.5	1. 79	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_511 GeneMa rk.hmm 624_nt - 22908 23531	62 4	399 220 7	164	65. 83	6.04	117 411 44	142 3	19 4.2 3	7.6	1. 56	939 798 1	141 7	24 1.6 3	7.92	1. 88	---	---	---	---
gene_512 GeneMa rk.hmm 987_nt - 23582 24568	98 7	399 220 7	155 2	39 3.8 8	8.62	117 411 44	867 8	74 8.8 5	9.55	0. 93	939 798 1	580 7	62 6.0 4	9.29	0. 67	Predicted RNA-binding protein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_513 GeneMa rk.hmm 825_nt - 24587 25411	82 5	399 220 7	491	14 9.0 8	7.22	117 411 44	318 3	32 8.6	8.36	1. 14	939 798 1	235 3	30 3.4 8	8.25	1. 03	Preprotein translocase subunit YidC	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_514 GeneMa rk.hmm 372_nt - 25386 25757	37 2	399 220 7	691	46 5.2 9	8.86	117 411 44	446 9	10 23. 19	10	1. 14	939 798 1	266 9	76 3.4 3	9.58	0. 72	RNase P protein component	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_515 GeneMa rk.hmm 1191_nt - 25906 27096	11 91	399 220 7	419 4	88 2.0 7	9.78	117 411 44	896 2	64 0.8 9	9.32	- 0. 46	939 798 1	476 6	42 5.8	8.73	- 1. 05	Acetate kinase	METABOLISM	Energy production and conversion	C
gene_516 GeneMa rk.hmm 954_nt - 27147 28100	95 4	399 220 7	546	14 3.3 6	7.16	117 411 44	193 4	17 2.6 6	7.43	0. 27	939 798 1	107 9	12 0.3 5	6.91	- 0. 25	Adenine-specific DNA methylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2390 GeneM ark.hmm 117_nt - 3 119	11 7	399 220 7	0	0	0	117 411 44	97	70. 61	6.14	6. 14	939 798 1	177	16 0.9 7	7.33	7. 33	NA			
gene_518 GeneMa rk.hmm 183_nt - 28573 28755	18 3	399 220 7	1	1.3 7	0.45	117 411 44	21	9.7 7	3.29	2. 84	939 798 1	8	4.6 5	2.22	1. 77	NA			
gene_2807 GeneM ark.hmm 303_nt + 87 389	30 3	399 220 7	0	0	0	117 411 44	610	17 1.4 7	7.42	7. 42	939 798 1	459	16 1.1 9	7.33	7. 33	Ribosomal protein S7	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_51 GeneMar k.hmm 171_nt - 34225 34395	17 1	399 220 7	26	38. 09	5.25	117 411 44	73	36. 36	5.18	- 0. 07	939 798 1	73	45. 42	5.51	0. 26	Helicase subunit of the DNA excision repair complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_2478 GeneM ark.hmm 123_nt - 1 123	12 3	399 220 7	0	0	0	117 411 44	117	81. 02	6.34	6. 34	939 798 1	188	16 2.6 4	7.35	7. 35	NA			
gene_521 GeneMa rk.hmm 303_nt - 29707 30009	30 3	399 220 7	11	9.0 9	3.18	117 411 44	169	47. 5	5.57	2. 39	939 798 1	82	28. 8	4.85	1. 67	Type II secretory pathway, pseudopilin PulG	CELLULAR PROCESSES AND SIGNALING	Cell motility	N
gene_2515 GeneM ark.hmm 129_nt + 3 131	12 9	399 220 7	0	0	0	117 411 44	95	62. 72	5.97	5. 97	939 798 1	205	16 9.0 9	7.4	7. 4	NA			
gene_523 GeneMa rk.hmm 327_nt - 30369 30695	32 7	399 220 7	12	9.1 9	3.2	117 411 44	190	49. 49	5.63	2. 43	939 798 1	62	20. 17	4.33	1. 13	Competence protein ComGC	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_2796 GeneM ark.hmm 318_nt + 3 320	31 8	399 220 7	0	0	0	117 411 44	642	17 1.9 5	7.43	7. 43	939 798 1	513	17 1.6 5	7.42	7. 42	NADH:ubiquinone oxidoreductase subunit 1 (chain H)	METABOLISM	Energy production and conversion	C
gene_2311 GeneM ark.hmm 102_nt - 2 103	10 2	399 220 7	0	0	0	117 411 44	34	28. 39	4.83	4. 83	939 798 1	172	17 9.4 3	7.49	7. 49	NA			
gene_526 GeneMa rk.hmm 366_nt - 32679 33044	36 6	399 220 7	330	22 5.8 5	7.82	117 411 44	303 0	70 5.1	9.46	1. 64	939 798 1	307 4	89 3.6 9	9.8	1. 98	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_527 GeneMa rk.hmm 1059_nt - 33195 34253	10 59	399 220 7	158 33	37 45. 02	11.8 7	117 411 44	154 92	12 45. 95	10.2 8	- 1. 59	939 798 1	836 2	84 0.1 9	9.71	- 2. 16	Threonine dehydrogenase and related Zn-dependent dehydrogenases	METABOLISM	Amino acid transport and metabolism	E
gene_528 GeneMa rk.hmm 1152_nt - 34416 35567	11 52	399 220 7	372 5	80 9.9 5	9.66	117 411 44	796 1	58 8.5 8	9.2	- 0. 46	939 798 1	753 0	69 5.5 2	9.44	- 0. 22	N-acetylglucosamine-6-phosphate deacetylase	METABOLISM	Carbohydrate transport and metabolism	G
gene_529 GeneMa rk.hmm 1818_nt - 35720 37537	18 18	399 220 7	451 9	62 2.6 4	9.28	117 411 44	118 46	55 4.9 7	9.12	- 0. 16	939 798 1	744 1	43 5.5 1	8.77	- 0. 51	Predicted acyltransferases	METABOLISM	Lipid transport and metabolism	I
gene_52 GeneMar k.hmm 120_nt - 34579 34698	12 0	399 220 7	3	6.2 6	2.65	117 411 44	24	17. 03	4.09	1. 44	939 798 1	12	10. 64	3.41	0. 76	Helicase subunit of the DNA excision repair complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_530 GeneMa rk.hmm 1143_nt - 37638 38780	11 43	399 220 7	360 3	78 9.6	9.62	117 411 44	864 6	64 4.2 6	9.33	- 0. 29	939 798 1	110 92	10 32. 59	10.0 1	0. 39	Queuine/archaeosine tRNA- ribosyltransferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_531 GeneMa rk.hmm 858_nt + 3 8910 39767	85 8	399 220 7	225 9	65 9.5	9.37	117 411 44	892 9	88 6.3 5	9.79	0. 42	939 798 1	555 3	68 8.6 6	9.43	0. 06	Predicted integral membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_532 GeneMa rk.hmm 213_nt - 39794 40006	21 3	399 220 7	68	79. 97	6.32	117 411 44	310	12 3.9 6	6.95	0. 63	939 798 1	414	20 6.8 2	7.69	1. 37	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_533 GeneMa rk.hmm 384_nt -	38 4	399 220	332	21 6.5	7.76	117 411	803	17 8.1	7.48	- 0.	939 798	142 6	39 5.1	8.63	0. 87	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	CELLULAR PROCESSES AND	Posttranslational modification, protein turnover, chaperones	O

[40006 40389		7		7		44				28	1		4				SIGNALING		
gene_2447 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	82	58. 2	5.86	5. 86	939 798 1	215	19 0.6 4	7.57	7. 57	NA			
gene_2448 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	69	48. 97	5.61	5. 61	939 798 1	242	21 4.5 9	7.75	7. 75	NA			
gene_536 GeneMa rk.hmm 1131_nt - 41636 42766	11 31	399 220 7	271 48	60 12. 6	12.5 5	117 411 44	103 376	77 84. 79	12.9 3	0. 38	939 798 1	494 54	46 52. 69	12.1 8	- 0. 37	---	---	---	---
gene_2470 GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	107	75. 94	6.25	6. 25	939 798 1	244	21 6.3 6	7.76	7. 76	NA			
gene_538 GeneMa rk.hmm 1281_nt - 43567 44847	12 81	399 220 7	223	43. 61	5.45	117 411 44	154 9	10 2.9 9	6.69	1. 24	939 798 1	298 7	24 8.1 1	7.95	2. 5	Na+-driven multidrug efflux pump	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_539 GeneMa rk.hmm 1485_nt - 44908 46392	14 85	399 220 7	138 8	23 4.1 3	7.87	117 411 44	747 9	42 8.9 5	8.74	0. 87	939 798 1	996 8	71 4.2 4	9.48	1. 61	Threonine synthase	METABOLISM	Amino acid transport and metabolism	E
gene_53 GeneMar k.hmm 147_nt - 34817 34963	14 7	399 220 7	18	30. 67	4.94	117 411 44	125	72. 42	6.18	1. 24	939 798 1	109	78. 9	6.3	1. 36	Helicase subunit of the DNA excision repair complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_540 GeneMa rk.hmm 1215_nt - 46468 47682	12 15	399 220 7	326	67. 21	6.07	117 411 44	330 9	23 1.9 6	7.86	1. 79	939 798 1	458 0	40 1.1	8.65	2. 58	Gamma-glutamylcysteine synthetase	METABOLISM	Coenzyme transport and metabolism	H
gene_541 GeneMa rk.hmm 135_nt - 48007 48141	13 5	399 220 7	8	14. 84	3.89	117 411 44	204	12 8.7	7.01	3. 12	939 798 1	37	29. 16	4.87	0. 98	NA			
gene_542 GeneMa rk.hmm 108_nt - 48235 48342	10 8	399 220 7	5	11. 6	3.54	117 411 44	89	70. 19	6.13	2. 59	939 798 1	23	22. 66	4.5	0. 96	NA			
gene_543 GeneMa rk.hmm 183_nt + 4 8861 49043	18 3	399 220 7	110	15 0.5 7	7.23	117 411 44	180 8	84 1.4 7	9.72	2. 49	939 798 1	661	38 4.3 4	8.59	1. 36	NA			
gene_544 GeneMa rk.hmm 135_nt - 1 135	13 5	399 220 7	24	44. 53	5.48	117 411 44	73	46. 06	5.53	0. 05	939 798 1	103	81. 18	6.34	0. 86	---	---	---	---
gene_545 GeneMa rk.hmm 234_nt - 387 620	23 4	399 220 7	660	70 6.5	9.46	117 411 44	131 6	47 8.9 9	8.9	- 0. 56	939 798 1	177 6	80 7.5 9	9.66	0. 2	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	METABOLISM	Nucleotide transport and metabolism	F
gene_546 GeneMa rk.hmm 1038_nt - 818 1855	10 38	399 220 7	116 7	28 1.6 2	8.14	117 411 44	363 4	29 8.1 8	8.22	0. 08	939 798 1	442 4	45 3.5 1	8.82	0. 68	Cellulase M and related proteins	METABOLISM	Carbohydrate transport and metabolism	G
gene_547 GeneMa rk.hmm 540_nt -	54 0	399 220	875	40 5.8	8.66	117 411	681 7	10 75.	10.0 7	1. 41	939 798	149 9	29 5.3	8.21	- 0.	Branched-chain amino acid permeases	METABOLISM	Amino acid transport and metabolism	E

1953 2492			7		8		44		2			1		7		45			
gene_548 GeneMark.hmm 783_nt - 2548 3330	78 3	399 220 7	215 5	68 9.4	9.43	117 411 44	162 14	17 63. 67	10.7 8	1. 35	939 798 1	268 7	36 5.1 5	8.51	- 0. 92	Branched-chain amino acid permeases	METABOLISM	Amino acid transport and metabolism	E
gene_549 GeneMark.hmm 153_nt - 3636 3788	15 3	399 220 7	34	55. 66	5.8	117 411 44	237	13 1.9 3	7.04	1. 24	939 798 1	174	12 1.0 1	6.92	1. 12	NA			
gene_54 GeneMark.hmm 480_nt - 35091 35570	48 0	399 220 7	224	11 6.8 9	6.87	117 411 44	126 8	22 4.9 9	7.81	0. 94	939 798 1	119 3	26 4.4 6	8.05	1. 18	Helicase subunit of the DNA excision repair complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_550 GeneMark.hmm 585_nt - 3941 4525	58 5	399 220 7	572	24 4.9 2	7.94	117 411 44	127 5	18 5.6 3	7.54	- 0. 4	939 798 1	924	16 8.0 7	7.39	- 0. 55	Uracil-DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_551 GeneMark.hmm 468_nt - 4579 5046	46 8	399 220 7	346 3	18 53. 5	10.8 6	117 411 44	879 3	16 00. 22	10.6 4	- 0. 22	939 798 1	668 7	15 20. 38	10.5 7	- 0. 29	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	METABOLISM	Amino acid transport and metabolism	E
gene_552 GeneMark.hmm 930_nt - 5109 6038	93 0	399 220 7	344 0	92 6.5 4	9.86	117 411 44	132 80	12 16. 2	10.2 5	0. 39	939 798 1	861 8	98 6.0 3	9.95	0. 09	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	METABOLISM	Amino acid transport and metabolism	E
gene_553 GeneMark.hmm 606_nt - 6051 6656	60 6	399 220 7	299 6	12 38. 39	10.2 7	117 411 44	126 26	17 74. 53	10.7 9	0. 52	939 798 1	567 8	99 6.9 8	9.96	- 0. 31	Nitroreductase	METABOLISM	Energy production and conversion	C
gene_554 GeneMark.hmm 801_nt + 6827 7627	80 1	399 220 7	174	54. 41	5.77	117 411 44	163 9	17 4.2 8	7.45	1. 68	939 798 1	115 1	15 2.9	7.26	1. 49	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_555 GeneMark.hmm 834_nt - 7809 8642	83 4	399 220 7	163 7	49 1.6 7	8.94	117 411 44	287 1	29 3.2	8.2	- 0. 74	939 798 1	254 3	32 4.4 5	8.34	- 0. 6	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_556 GeneMark.hmm 1101_nt - 8632 9732	11 01	399 220 7	121 6	27 6.6 5	8.11	117 411 44	294 1	22 7.5 1	7.83	- 0. 28	939 798 1	282 2	27 2.7 3	8.09	- 0. 02	Nuclease subunit of the excinuclease complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_557 GeneMark.hmm 162_nt - 9828 9989	16 2	399 220 7	23	35. 56	5.15	117 411 44	117	61. 51	5.94	0. 79	939 798 1	51	33. 5	5.07	- 0. 08	Nuclease subunit of the excinuclease complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_558 GeneMark.hmm 213_nt - 10143 10355	21 3	399 220 7	255	29 9.8 8	8.23	117 411 44	590	23 5.9 2	7.88	- 0. 35	939 798 1	416	20 7.8 2	7.7	- 0. 53	Nuclease subunit of the excinuclease complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_559 GeneMark.hmm 345_nt - 10432 10776	34 5	399 220 7	123	89. 3	6.48	117 411 44	542	13 3.8	7.06	0. 58	939 798 1	269	82. 97	6.37	- 0. 11	Nuclease subunit of the excinuclease complex	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2454 GeneMark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	62	42. 93	5.42	5. 42	939 798 1	252	21 8	7.77	7. 77	NA			

gene_560[GeneMa rk.hmm 702_nt]- 10816 11517	70 2	399 220 7	129 9	46 3.5 1	8.86	117 411 44	372 5	45 1.9 4	8.82	- 0. 04	939 798 1	574 2	87 0.3 5	9.77	0. 91	Predicted Zn-dependent protease	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_561[GeneMa rk.hmm 1233_nt]- 11596 12828	12 33	399 220 7	150 0	30 4.7 3	8.25	117 411 44	838 9	57 9.4 8	9.18	0. 93	939 798 1	645 4	55 6.9 7	9.12	0. 87	Uncharacterized protein involved in methicillin resistance	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_562[GeneMa rk.hmm 1221_nt]- 12833 14053	12 21	399 220 7	912	18 7.1	7.55	117 411 44	624 1	43 5.3 4	8.77	1. 22	939 798 1	526 1	45 8.4 8	8.84	1. 29	Uncharacterized protein involved in methicillin resistance	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_563[GeneMa rk.hmm 780_nt]- 14165 14944	78 0	399 220 7	445	14 2.9 1	7.16	117 411 44	210 1	22 9.4 1	7.84	0. 68	939 798 1	393 0	53 6.1 2	9.07	1. 91	Predicted esterase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_564[GeneMa rk.hmm 1662_nt]- 15013 16674	16 62	399 220 7	258 2	38 9.1 5	8.6	117 411 44	957 2	49 0.5 3	8.94	0. 34	939 798 1	838 2	53 6.6 4	9.07	0. 47	Predicted hydrolase of the metallo- beta-lactamase superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_565[GeneMa rk.hmm 2235_nt]- 16849 19083	22 35	399 220 7	604	67. 69	6.08	117 411 44	400 7	15 2.7	7.25	1. 17	939 798 1	330 8	15 7.4 9	7.3	1. 22	Single-stranded DNA-specific exonuclease	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_566[GeneMa rk.hmm 759_nt + 1 9348 20106	75 9	399 220 7	137	45. 21	5.5	117 411 44	926	10 3.9 1	6.7	1. 2	939 798 1	151 3	21 2.1 1	7.73	2. 23	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_567[GeneMa rk.hmm 795_nt + 2 0117 20911	79 5	399 220 7	109	34. 34	5.1	117 411 44	109 5	11 7.3 1	6.87	1. 77	939 798 1	133 6	17 8.8 2	7.48	2. 38	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_568[GeneMa rk.hmm 678_nt + 2 0924 21601	67 8	399 220 7	89	32. 88	5.04	117 411 44	775	97. 36	6.61	1. 57	939 798 1	606	95. 11	6.57	1. 53	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_569[GeneMa rk.hmm 204_nt + 2 1611 21814	20 4	399 220 7	16	19. 65	4.3	117 411 44	120	50. 1	5.65	1. 35	939 798 1	118	61. 55	5.94	1. 64	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_56[GeneMar k.hmm 849_nt]- 36249 37097	84 9	399 220 7	811	23 9.2 8	7.9	117 411 44	271 4	27 2.2 6	8.09	0. 19	939 798 1	165 0	20 6.8	7.69	- 0. 21	Predicted metal-dependent membrane protease	POORLY CHARACTERIZ ED	General function prediction only	R
gene_570[GeneMa rk.hmm 420_nt + 2 1912 22331	42 0	399 220 7	101	60. 24	5.91	117 411 44	903	18 3.1 2	7.52	1. 61	939 798 1	631	15 9.8 6	7.32	1. 41	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_2431[GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	107	75. 94	6.25	6. 25	939 798 1	261	23 1.4 3	7.85	7. 85	NA			
gene_572[GeneMa rk.hmm 882_nt]- 24090 24971	88 2	399 220 7	313 35	88 99. 14	13.1 2	117 411 44	585 01	56 49. 17	12.4 6	- 0. 66	939 798 1	184 42	22 24. 87	11.1 2	-2	Fructose/tagatose bisphosphate aldolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_573[GeneMa rk.hmm 990_nt]-	99	399 220	797	20 1.6	7.66	117 411	253	21 7.8	7.77	0.	939 798	232	24 9.5	7.96	0.	Signal transduction histidine kinase	CELLULAR PROCESSES	Signal transduction mechanisms	T

[25112][26101]	0	7		6		44	2	3		11	1	2	7		3		AND SIGNALING		
gene_574[GeneMark.hmm 372_nt -[26112][26483]	37 2	399 220 7	116	78. 11	6.29	117 411 44	665	15 2.2 5	7.25	0. 96	939 798 1	428	12 2.4 2	6.94	0. 65	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_575[GeneMark.hmm 657_nt -[26480][27136]	65 7	399 220 7	285	10 8.6 6	6.76	117 411 44	141 7	18 3.6 9	7.52	0. 76	939 798 1	859	13 9.1 2	7.12	0. 36	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_576[GeneMark.hmm 1380_nt -[27449][28828]	13 80	399 220 7	152 2	27 6.2 6	8.11	117 411 44	255 5	15 7.6 9	7.3	- 0. 81	939 798 1	493 4	38 0.4 4	8.57	0. 46	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_577[GeneMark.hmm 648_nt -[28880][29527]	64 8	399 220 7	228	88. 13	6.46	117 411 44	602	79. 12	6.31	- 0. 15	939 798 1	164 8	27 0.6 1	8.08	1. 62	ABC-type antimicrobial peptide transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_578[GeneMark.hmm 1278_nt -[29540][30817]	12 78	399 220 7	291	57. 04	5.83	117 411 44	819	54. 58	5.77	- 0. 06	939 798 1	191 3	15 9.2 8	7.32	1. 49	ABC-type antimicrobial peptide transport system, permease component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_579[GeneMark.hmm 147_nt -[31525][31671]	14 7	399 220 7	12	20. 45	4.35	117 411 44	62	35. 92	5.17	0. 82	939 798 1	163	11 7.9 9	6.88	2. 53	---	---	---	---
gene_57[GeneMark.hmm 609_nt +][37375][37983]	60 9	399 220 7	128 4	52 8.1 2	9.04	117 411 44	715 9	10 01. 21	9.97	0. 93	939 798 1	117 66	20 55. 78	11.0 1	1. 97	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_2821[GeneMark.hmm 504_nt -[1][504]	50 4	399 220 7	0	0	0	117 411 44	124 9	21 1.0 7	7.72	7. 72	939 798 1	109 5	23 1.1 8	7.85	7. 85	NA			
gene_581[GeneMark.hmm 885_nt -[32260][33144]	88 5	399 220 7	309 2	87 5.1 5	9.77	117 411 44	489 2	47 0.8	8.88	- 0. 89	939 798 1	892 6	10 73. 2	10.0 7	0. 3	Regulator of polyketide synthase expression	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_582[GeneMark.hmm 387_nt -[33148][33534]	38 7	399 220 7	933	60 3.8 9	9.24	117 411 44	161 8	35 6.0 9	8.48	- 0. 76	939 798 1	281 1	77 2.8 9	9.59	0. 35	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_583[GeneMark.hmm 1344_nt -[33527][34870]	13 44	399 220 7	274 0	51 0.6 7	9	117 411 44	510 5	32 3.5 1	8.34	- 0. 66	939 798 1	816 2	64 6.1 9	9.34	0. 34	CysteinyI-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_584[GeneMark.hmm 885_nt -[34957][35841]	88 5	399 220 7	116 7	33 0.3	8.37	117 411 44	300 0	28 8.7 1	8.17	- 0. 2	939 798 1	476 3	57 2.6 7	9.16	0. 79	Acetyltransferases	POORLY CHARACTERIZED	General function prediction only	R
gene_585[GeneMark.hmm 618_nt -[35853][36470]	61 8	399 220 7	851	34 4.9 3	8.43	117 411 44	252 4	34 7.8 5	8.44	0. 01	939 798 1	381 5	65 6.8 6	9.36	0. 93	Serine acetyltransferase	METABOLISM	Amino acid transport and metabolism	E

gene_586 GeneMa rk.hmm 141_nt 36486 36626	14 1	399 220 7	70	12 4.3 6	6.96	117 411 44	205	12 3.8 3	6.95	- 0. 01	939 798 1	526	39 6.9 5	8.63	1. 67	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_587 GeneMa rk.hmm 129_nt 36722 36850	12 9	399 220 7	369	71 6.5 1	9.48	117 411 44	627	41 3.9 7	8.69	- 0. 79	939 798 1	786	64 8.3 3	9.34	- 0. 14	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_588 GeneMa rk.hmm 1938_nt 36977 38914	19 38	399 220 7	338 1	43 7	8.77	117 411 44	872 6	38 3.4 9	8.58	- 0. 19	939 798 1	101 05	55 4.8 1	9.12	0. 35	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_589 GeneMa rk.hmm 867_nt 39599 40465	86 7	399 220 7	83	23. 98	4.58	117 411 44	436	42. 83	5.42	0. 84	939 798 1	487	59. 77	5.9	1. 32	5,10-methylenetetrahydrofolate reductase	METABOLISM	Amino acid transport and metabolism	E
gene_58 GeneMar k.hmm 1449_nt + 3 8037 39485	14 49	399 220 7	171 0	29 5.6 1	8.21	117 411 44	928 2	54 5.5 9	9.09	0. 88	939 798 1	140 37	10 30. 79	10.0 1	1. 8	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_590 GeneMa rk.hmm 540_nt 40529 41068	54 0	399 220 7	20	9.2 8	3.21	117 411 44	179	28. 23	4.82	1. 61	939 798 1	166	32. 71	5.03	1. 82	Methionine synthase II (cobalamin- independent)	METABOLISM	Amino acid transport and metabolism	E
gene_2464 GeneM ark.hmm 120_nt 2 121	12 0	399 220 7	0	0	0	117 411 44	134	95. 11	6.57	6. 57	939 798 1	290	25 7.1 5	8.01	8. 01	NA			
gene_2449 GeneM ark.hmm 120_nt 2 121	12 0	399 220 7	0	0	0	117 411 44	75	53. 23	5.73	5. 73	939 798 1	292	25 8.9 2	8.02	8. 02	NA			
gene_2503 GeneM ark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	103	71. 32	6.16	6. 16	939 798 1	329	28 4.6 1	8.15	8. 15	NA			
gene_594 GeneMa rk.hmm 1002_nt + 44064 45065	10 02	399 220 7	396	99	6.63	117 411 44	308 2	26 1.9 7	8.03	1. 4	939 798 1	290 9	30 8.9 2	8.27	1. 64	---	---	---	---
gene_595 GeneMa rk.hmm 2406_nt 45133 47538	24 06	399 220 7	623	64. 86	6.02	117 411 44	448 5	15 8.7 7	7.31	1. 29	939 798 1	100 59	44 4.8 6	8.8	2. 78	Phenylalanyl-tRNA synthetase beta subunit	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2442 GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	78	55. 36	5.79	5. 79	939 798 1	335	29 7.0 5	8.21	8. 21	NA			
gene_597 GeneMa rk.hmm 1089_nt 48124 49212	10 89	399 220 7	142	32. 66	5.03	117 411 44	147 0	11 4.9 7	6.85	1. 82	939 798 1	237 8	23 2.3 5	7.86	2. 83	Phenylalanyl-tRNA synthetase alpha subunit	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_598 GeneMa rk.hmm 93_nt + 49 211 49303	93	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_599 GeneMa rk.hmm 1347_nt 49897 51243	13 47	399 220 7	72	13. 39	3.74	117 411 44	748	47. 3	5.56	1. 82	939 798 1	332	26. 23	4.71	0. 97	---	---	---	---

gene_59 GeneMark.hmm 120_nt + 39555 39674	120	3992207	20	41.75	5.38	11741144	62	44	5.46	0.08	9397981	47	41.68	5.38	0	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_5 GeneMark.hmm 69_nt - 1242 1310	69	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2728 GeneMark.hmm 150_nt + 2 151	150	3992207	0	0	0	11741144	170	96.53	6.59	6.59	9397981	428	303.61	8.25	8.25	NA			
gene_2492 GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	193	136.98	7.1	7.1	9397981	358	317.44	8.31	8.31	NA			
gene_2457 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	114	80.91	6.34	6.34	9397981	365	323.65	8.34	8.34	NA			
gene_603 GeneMark.hmm 84_nt + 1203 1286	84	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2430 GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	180	127.76	7	7	9397981	397	352.03	8.46	8.46	NA			
gene_605 GeneMark.hmm 126_nt - 2975 3100	126	3992207	0	0	0	11741144	6	4.06	2.02	2.02	9397981	4	3.38	1.76	1.76	NA			
gene_606 GeneMark.hmm 354_nt + 4872 5225	354	3992207	8	5.66	2.5	11741144	61	14.68	3.88	1.38	9397981	92	27.65	4.79	2.29	NA			
gene_1395 GeneMark.hmm 159_nt - 756 914	159	3992207	0	0	0	11741144	151	80.89	6.34	6.34	9397981	535	358.03	8.48	8.48	NA			
gene_608 GeneMark.hmm 96_nt + 9089 9184	96	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_609 GeneMark.hmm 90_nt + 13395 13484	90	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_60 GeneMark.hmm 741_nt + 39674 40414	741	3992207	5882	1988.35	10.96	11741144	11403	1310.66	10.36	-0.6	9397981	14825	2128.83	11.06	0.1	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_2496 GeneMark.hmm 123_nt - 1 123	123	3992207	0	0	0	11741144	155	107.33	6.75	6.75	9397981	413	357.28	8.48	8.48	NA			
gene_611 GeneMark.hmm 372_nt + 746 1117	372	3992207	46	30.97	4.95	11741144	232	53.12	5.73	0.78	9397981	138	39.47	5.3	0.35	---	---	---	---
gene_612 GeneMark.hmm 126_nt + 1	12	399220	11	21.	4.45	117411	31	20.	4.39	-0.	939798	34	28.	4.84	0.	NA			

711 1836	6	7		87		44		95		06	1		71		39				
gene_613 GeneMark.hmm 375_nt + 5041 5415	375	3992207	325	217.09	7.76	11741144	951	215.99	7.75	-0.01	9397981	782	221.89	7.79	0.03	---	---	---	---
gene_614 GeneMark.hmm 354_nt + 6581 6934	354	3992207	185	130.9	7.03	11741144	878	211.24	7.72	0.69	9397981	594	178.55	7.48	0.45	NA			
gene_615 GeneMark.hmm 354_nt + 9593 9946	354	3992207	13950	9870.93	13.27	11741144	45928	11050.04	13.43	0.16	9397981	24717	7429.47	12.86	-0.41	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZED	General function prediction only	R
gene_616 GeneMark.hmm 1650_nt + 9906 11555	1650	3992207	54925	8338.21	13.03	11741144	106536	5499.23	12.43	-0.6	9397981	73961	4769.63	12.22	-0.81	FOG: Glucan-binding domain (YG repeat)	POORLY CHARACTERIZED	General function prediction only	R
gene_617 GeneMark.hmm 102_nt - 11856 11957	102	3992207	0	0	0	11741144	2	1.67	0.74	0.74	9397981	2	2.09	1.06	1.06	NA			
gene_618 GeneMark.hmm 1122_nt + 11956 13077	1122	3992207	2095	467.71	8.87	11741144	4324	328.23	8.36	-0.51	9397981	7179	680.83	9.41	0.54	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_619 GeneMark.hmm 351_nt + 13218 13568	351	3992207	653	466.01	8.86	11741144	747	181.26	7.5	-1.36	9397981	806	244.34	7.93	-0.93	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_61 GeneMark.hmm 1488_nt + 40563 42050	1488	3992207	8905	1499.06	10.55	11741144	27001	1545.49	10.59	0.04	9397981	23881	1707.71	10.74	0.19	Glucose-6-phosphate 1-dehydrogenase	METABOLISM	Carbohydrate transport and metabolism	G
gene_620 GeneMark.hmm 1914_nt + 13683 15596	1914	3992207	4619	604.5	9.24	11741144	3408	151.65	7.24	-2	9397981	5619	312.38	8.29	-0.95	NAD/FAD-utilizing enzyme apparently involved in cell division	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_621 GeneMark.hmm 1680_nt - 15949 17628	1680	3992207	9964	1485.63	10.54	11741144	42810	2170.33	11.08	0.54	9397981	26091	1652.52	10.69	0.15	Predicted hydrolase of the metallo-beta-lactamase superfamily	POORLY CHARACTERIZED	General function prediction only	R
gene_622 GeneMark.hmm 234_nt - 17630 17863	234	3992207	430	460.3	8.85	11741144	5352	1948	10.93	2.08	9397981	1806	821.23	9.68	0.83	Uncharacterized conserved small protein	POORLY CHARACTERIZED	Function unknown	S
gene_623 GeneMark.hmm 108_nt + 18143 18250	108	3992207	3	6.96	2.8	11741144	24	18.93	4.24	1.44	9397981	18	17.73	4.15	1.35	NA			
gene_2462 GeneMark.hmm 123_nt + 1 123	123	3992207	0	0	0	11741144	99	68.55	6.1	6.1	9397981	418	361.61	8.5	8.5	NA			
gene_2439 GeneMark.hmm 123_nt + 1 123	123	3992207	0	0	0	11741144	212	146.8	7.2	7.2	9397981	485	419.57	8.71	8.71	NA			

gene_626[GeneMa rk.hmm 684_nt + 1 9197 19880	68 4	399 220 7	336	12 3.0 5	6.94	117 411 44	103 5	12 8.8 8	7.01	0. 07	939 798 1	834	12 9.7 4	7.02	0. 08	Inactive homolog of metal- dependent proteases, putative molecular chaperone	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_627[GeneMa rk.hmm 438_nt + 1 9877 20314	43 8	399 220 7	233	13 3.2 5	7.06	117 411 44	669	13 0.0 9	7.02	- 0. 04	939 798 1	829	20 1.3 9	7.65	0. 59	Acetyltransferases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_628[GeneMa rk.hmm 1011_nt + 20304 21314	10 11	399 220 7	100 7	24 9.5	7.96	117 411 44	228 1	19 2.1 6	7.59	- 0. 37	939 798 1	212 0	22 3.1 3	7.8	- 0. 16	Metal-dependent proteases with possible chaperone activity	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_629[GeneMa rk.hmm 387_nt - 21354 21740	38 7	399 220 7	14	9.0 6	3.18	117 411 44	107	23. 55	4.56	1. 38	939 798 1	94	25. 85	4.69	1. 51	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_62[GeneMar k.hmm 1086_nt - 42094 43179	10 86	399 220 7	906	20 8.9 7	7.71	117 411 44	231 8	18 1.7 9	7.51	- 0. 2	939 798 1	218 6	21 4.1 8	7.74	0. 03	Signal recognition particle GTPase	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_630[GeneMa rk.hmm 930_nt - 21731 22660	93 0	399 220 7	74	19. 93	4.32	117 411 44	435	39. 84	5.32	1	939 798 1	260	29. 75	4.89	0. 57	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2313[GeneM ark.hmm 102_nt + 1 102	10 2	399 220 7	0	0	0	117 411 44	136	11 3.5 6	6.83	6. 83	939 798 1	455	47 4.6 5	8.89	8. 89	NA			
gene_2394[GeneM ark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	258	18 3.1 2	7.52	7. 52	939 798 1	579	51 3.4 1	9	9	NA			
gene_633[GeneMa rk.hmm 126_nt + 3 0432 30557	12 6	399 220 7	0	0	0	117 411 44	19	12. 84	3.68	3. 68	939 798 1	4	3.3 8	1.76	1. 76	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_634[GeneMa rk.hmm 735_nt + 3 0561 31295	73 5	399 220 7	62	21. 13	4.4	117 411 44	590	68. 37	6.1	1. 7	939 798 1	935	13 5.3 6	7.08	2. 68	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_635[GeneMa rk.hmm 198_nt + 3 1586 31783	19 8	399 220 7	35	44. 28	5.47	117 411 44	195	83. 88	6.39	0. 92	939 798 1	274	14 7.2 5	7.2	1. 73	NA			
gene_2312[GeneM ark.hmm 102_nt + 2 103	10 2	399 220 7	1	2.4 6	1.3	117 411 44	315	26 3.0 3	8.04	6. 74	939 798 1	152 6	15 91. 91	10.6 4	9. 34	NA			
gene_2331[GeneM ark.hmm 105_nt - 2 106	10 5	399 220 7	0	0	0	117 411 44	122	98. 96	6.63	6. 63	939 798 1	707	71 6.4 7	9.48	9. 48	NA			
gene_2387[GeneM ark.hmm 117_nt - 2 118	11 7	399 220 7	0	0	0	117 411 44	217	15 7.9 7	7.3	7. 3	939 798 1	785	71 3.9 2	9.48	9. 48	NA			
gene_2365[GeneM ark.hmm 102_nt +	10 2	399 220	0	0	0	117 411	154	12 8.5	7.01	7. 01	939 798	733	76 4.6	9.58	9. 58	NA			

1 102		7				44		9			1		6						
gene_63 GeneMark.hmm 183_nt - 43233 43415	183	3992207	29	39.69	5.31	11741144	107	49.8	5.64	0.33	9397981	72	41.86	5.39	0.08	Signal recognition particle GTPase	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_640 GeneMark.hmm 831_nt + 35386 36216	831	3992207	8225	2479.26	11.28	11741144	19198	1967.64	10.94	-0.34	9397981	8560	1096.07	10.1	-1.18	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	METABOLISM	Amino acid transport and metabolism	E
gene_641 GeneMark.hmm 855_nt + 36370 37224	855	3992207	1176	344.53	8.43	11741144	9101	906.59	9.82	1.39	9397981	5845	727.42	9.51	1.08	ABC-type metal ion transport system, periplasmic component/surface antigen	METABOLISM	Inorganic ion transport and metabolism	P
gene_642 GeneMark.hmm 840_nt + 37324 38163	840	3992207	146	43.54	5.44	11741144	1203	121.98	6.93	1.49	9397981	1291	163.54	7.35	1.91	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	METABOLISM	Amino acid transport and metabolism	E
gene_643 GeneMark.hmm 588_nt + 38151 38738	588	3992207	789	336.11	8.39	11741144	1793	259.71	8.02	-0.37	9397981	2287	413.86	8.69	0.3	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	METABOLISM	Amino acid transport and metabolism	E
gene_644 GeneMark.hmm 1062_nt + 38731 39792	1062	3992207	929	219.12	7.78	11741144	3701	296.81	8.21	0.43	9397981	4050	405.78	8.66	0.88	ABC-type metal ion transport system, ATPase component	METABOLISM	Inorganic ion transport and metabolism	P
gene_645 GeneMark.hmm 255_nt + 39794 40048	255	3992207	36	35.36	5.14	11741144	199	66.47	6.05	0.91	9397981	231	96.39	6.59	1.45	ABC-type metal ion transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_646 GeneMark.hmm 429_nt + 40102 40530	429	3992207	98	57.22	5.84	11741144	429	85.17	6.41	0.57	9397981	442	109.63	6.78	0.94	ABC-type metal ion transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_647 GeneMark.hmm 570_nt - 40560 41129	570	3992207	294	129.2	7.01	11741144	1115	166.61	7.38	0.37	9397981	508	94.83	6.57	-0.44	---	---	---	---
gene_648 GeneMark.hmm 615_nt + 41264 41878	615	3992207	376	153.14	7.26	11741144	1169	161.89	7.34	0.08	9397981	757	130.97	7.03	-0.23	Predicted integral membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_649 GeneMark.hmm 1671_nt + 41856 43526	1671	3992207	955	143.16	7.16	11741144	4114	209.69	7.71	0.55	9397981	2727	173.65	7.44	0.28	Predicted signal transduction protein with a C-terminal ATPase domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_64 GeneMark.hmm 819_nt - 43419 44237	819	3992207	233	71.26	6.16	11741144	1383	143.82	7.17	1.01	9397981	1290	167.6	7.39	1.23	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZED	General function prediction only	R
gene_650 GeneMark.hmm 1287_nt + 43538 44824	1287	3992207	2322	451.93	8.82	11741144	5122	338.96	8.4	-0.42	9397981	3071	253.9	7.99	-0.83	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_651 GeneMark.hmm 534_nt + 4	534	399220	151	711.5	9.47	117411	120	1925.	10.9	1.	939798	100	2000.	10.9	1.	---	---	---	---

4876 45409	4	7	7	9		44	73	59	1	44	1	40	59	7	5				
gene_652 GeneMark.hmm 471_nt + 45487 45957	471	3992207	389	206.88	7.69	11741144	1919	347.01	8.44	0.75	9397981	1587	358.53	8.49	0.8	Protein involved in ribonucleotide reduction	METABOLISM	Nucleotide transport and metabolism	F
gene_653 GeneMark.hmm 87_nt + 45964 46050	87	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_654 GeneMark.hmm 1263_nt - 46250 47512	1263	3992207	737	146.17	7.19	11741144	3597	242.56	7.92	0.73	9397981	3491	294.11	8.2	1.01	Mn2+ and Fe2+ transporters of the NRAMP family	METABOLISM	Inorganic ion transport and metabolism	P
gene_655 GeneMark.hmm 459_nt - 47822 48280	459	3992207	103	56.21	5.81	11741144	700	129.89	7.02	1.21	9397981	902	209.1	7.71	1.9	---	---	---	---
gene_656 GeneMark.hmm 441_nt - 48277 48717	441	3992207	126	71.57	6.16	11741144	628	121.29	6.92	0.76	9397981	650	156.83	7.29	1.13	Response regulator of the LytR/AlgR family	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_657 GeneMark.hmm 1950_nt + 49073 51022	1950	3992207	2433	312.53	8.29	11741144	9363	408.95	8.68	0.39	9397981	7328	399.87	8.64	0.35	DNA mismatch repair enzyme (predicted ATPase)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_658 GeneMark.hmm 468_nt - 51347 51814	468	3992207	51	27.3	4.77	11741144	536	97.55	6.61	1.84	9397981	468	106.41	6.73	1.96	Riboflavin synthase beta-chain	METABOLISM	Coenzyme transport and metabolism	H
gene_659 GeneMark.hmm 1236_nt - 51815 53050	1236	3992207	245	49.65	5.63	11741144	2183	150.43	7.23	1.6	9397981	1567	134.9	7.08	1.45	3,4-dihydroxy-2-butanone 4-phosphate synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_65 GeneMark.hmm 153_nt - 44237 44389	153	3992207	32	52.39	5.71	11741144	203	113	6.82	1.11	9397981	222	154.39	7.27	1.56	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZED	General function prediction only	R
gene_660 GeneMark.hmm 636_nt - 53040 53675	636	3992207	111	43.72	5.45	11741144	876	117.31	6.87	1.42	9397981	598	100.05	6.64	1.19	Riboflavin synthase alpha chain	METABOLISM	Coenzyme transport and metabolism	H
gene_661 GeneMark.hmm 1101_nt - 53660 54760	1101	3992207	233	53.01	5.73	11741144	2098	162.3	7.34	1.61	9397981	1505	145.45	7.18	1.45	Pyrimidine reductase, riboflavin biosynthesis	METABOLISM	Coenzyme transport and metabolism	H
gene_662 GeneMark.hmm 594_nt + 55165 55758	594	3992207	445	187.66	7.55	11741144	1555	222.96	7.8	0.25	9397981	1198	214.6	7.75	0.2	Holliday junction resolvosome, DNA-binding subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_663 GeneMark.hmm 564_nt + 55768 56331	564	3992207	1217	540.5	9.08	11741144	2316	349.74	8.45	0.63	9397981	1805	340.54	8.41	0.67	3-methyladenine DNA glycosylase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_664 GeneMark.hmm 678_nt + 56328 57005	678	3992207	248	91.62	6.52	11741144	874	109.79	6.78	0.26	9397981	672	105.46	6.72	0.2	Predicted metal-dependent membrane protease	POORLY CHARACTERIZED	General function prediction only	R
gene_665 GeneMark.hmm 1032_nt - 57160 58191	1032	3992207	524	127.19	6.99	11741144	3265	269.46	8.07	1.08	9397981	3867	398.71	8.64	1.65	Uncharacterized proteins, homologs of microcin C7 resistance protein MccF	CELLULAR PROCESSES AND	Defense mechanisms	V

																	SIGNALING		
gene_666 GeneMa rk.hmm 684_nt - 58446 59129	68 4	399 220 7	269 5	98 6.9 4	9.95	117 411 44	682 6	84 9.9 6	9.73	- 0. 22	939 798 1	407 4	63 3.7 7	9.31	- 0. 64	Uncharacterized membrane-bound protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_667 GeneMa rk.hmm 945_nt - 59141 60085	94 5	399 220 7	404 5	10 72. 19	10.0 7	117 411 44	135 82	12 24. 11	10.2 6	0. 19	939 798 1	767 8	86 4.5 3	9.76	- 0. 31	Mg2+ and Co2+ transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_668 GeneMa rk.hmm 2832_nt + 60217 63048	28 32	399 220 7	202 6	17 9.2	7.49	117 411 44	521 4	15 6.8 1	7.29	- 0. 2	939 798 1	375 9	14 1.2 4	7.14	- 0. 35	Excinuclease ATPase subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_669 GeneMa rk.hmm 1062_nt + 63041 64102	10 62	399 220 7	144 6	34 1.0 6	8.41	117 411 44	312 2	25 0.3 8	7.97	- 0. 44	939 798 1	233 8	23 4.2 5	7.87	- 0. 54	Xaa-Pro aminopeptidase	METABOLISM	Amino acid transport and metabolism	E
gene_66 GeneMar k.hmm 186_nt - 44455 44640	18 6	399 220 7	25	33. 67	5.07	117 411 44	100	45. 79	5.52	0. 45	939 798 1	68	38. 9	5.28	0. 21	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_670 GeneMa rk.hmm 399_nt + 6 4234 64632	39 9	399 220 7	161 92	10 16 5.1 7	13.3 1	117 411 44	237 12	50 61. 57	12.3 1	-1	939 798 1	416 04	11 09 5.0 1	13.4 4	0. 13	Arsenate reductase and related proteins, glutaredoxin family	METABOLISM	Inorganic ion transport and metabolism	P
gene_671 GeneMa rk.hmm 570_nt + 6 4698 65267	57 0	399 220 7	318 6	14 00. 1	10.4 5	117 411 44	707 9	10 57. 76	10.0 5	- 0. 4	939 798 1	112 58	21 01. 61	11.0 4	0. 59	---	---	---	---
gene_672 GeneMa rk.hmm 267_nt + 6 5354 65620	26 7	399 220 7	155 5	14 58. 83	10.5 1	117 411 44	361 6	11 53. 47	10.1 7	- 0. 34	939 798 1	462 0	18 41. 18	10.8 5	0. 34	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_673 GeneMa rk.hmm 411_nt + 6 5633 66043	41 1	399 220 7	389 6	23 74. 46	11.2 1	117 411 44	103 75	21 49. 99	11.0 7	- 0. 14	939 798 1	106 64	27 60. 86	11.4 3	0. 22	Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_674 GeneMa rk.hmm 306_nt + 6 6059 66364	30 6	399 220 7	891 0	72 93. 62	12.8 3	117 411 44	188 01	52 32. 98	12.3 5	- 0. 48	939 798 1	159 02	55 29. 63	12.4 3	- 0. 4	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_675 GeneMa rk.hmm 1251_nt + 66671 67921	12 51	399 220 7	176 5	35 3.4 1	8.47	117 411 44	416 7	28 3.7	8.15	- 0. 32	939 798 1	526 2	44 7.5 7	8.81	0. 34	Folylpolyglutamate synthase	METABOLISM	Coenzyme transport and metabolism	H
gene_676 GeneMa rk.hmm 432_nt + 6 8005 68436	43 2	399 220 7	255 1	14 79. 15	10.5 3	117 411 44	724 5	14 28. 38	10.4 8	- 0. 05	939 798 1	559 3	13 77. 61	10.4 3	- 0. 1	---	---	---	---
gene_677 GeneMa rk.hmm 1506_nt + 68609 70114	15 06	399 220 7	406	67. 53	6.08	117 411 44	272 0	15 3.8 3	7.27	1. 19	939 798 1	167 8	11 8.5 6	6.89	0. 81	Phosphatidylserine/phosphatidylglyc erophosphate/cardioliipin synthases and related enzymes	METABOLISM	Lipid transport and metabolism	I
gene_678 GeneMa rk.hmm 144_nt + 7 0192 70335	14 4	399 220 7	10	17. 4	4.12	117 411 44	68	40. 22	5.33	1. 21	939 798 1	48	35. 47	5.15	1. 03	NA			
gene_679 GeneMa rk.hmm 1539_nt +	15	399 220	498	81.	6.34	117 411	523	28 9.7	8.18	1.	939 798	269	18 6.3	7.54	1.	---	---	---	---

70372 71910	39	7		05		44	5	1		84	1	5	3		2				
gene_67 GeneMark.hmm 222_nt - 44746 44967	22 2	399 220 7	34	38. 36	5.26	117 411 44	213	81. 72	6.35	1. 09	939 798 1	166	79. 56	6.31	1. 05	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZED	General function prediction only	R
gene_680 GeneMark.hmm 2214_nt + 72024 74237	22 14	399 220 7	657 0	74 3.3 2	9.54	117 411 44	153 60	59 0.8 9	9.21	- 0. 33	939 798 1	102 70	49 3.5 8	8.95	- 0. 59	Oxygen-sensitive ribonucleoside-triphosphate reductase	METABOLISM	Nucleotide transport and metabolism	F
gene_2353 GeneMark.hmm 111_nt - 1 111	11 1	399 220 7	0	0	0	117 411 44	203	15 5.7 6	7.28	7. 28	939 798 1	890	85 3.1 6	9.74	9. 74	NA			
gene_682 GeneMark.hmm 507_nt + 74433 74939	50 7	399 220 7	139	68. 67	6.1	117 411 44	850	14 2.7 9	7.16	1. 06	939 798 1	655	13 7.4 7	7.1	1	Predicted acetyltransferase	POORLY CHARACTERIZED	General function prediction only	R
gene_683 GeneMark.hmm 591_nt + 74932 75522	59 1	399 220 7	160	67. 81	6.08	117 411 44	116 3	16 7.6	7.39	1. 31	939 798 1	880	15 8.4 4	7.31	1. 23	Organic radical activating enzymes	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_684 GeneMark.hmm 618_nt + 75519 76136	61 8	399 220 7	333	13 4.9 7	7.08	117 411 44	179 9	24 7.9 3	7.95	0. 87	939 798 1	108 4	18 6.6 4	7.54	0. 46	---	---	---	---
gene_685 GeneMark.hmm 309_nt + 76402 76710	30 9	399 220 7	310 7	25 18. 66	11.3	117 411 44	233 81	64 44. 57	12.6 5	1. 35	939 798 1	400 13	13 77 8.6 9	13.7 5	2. 45	Ribosomal protein S10	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_686 GeneMark.hmm 627_nt + 76927 77553	62 7	399 220 7	683 2	27 29. 4	11.4 1	117 411 44	246 79	33 52. 35	11.7 1	0. 3	939 798 1	379 73	64 44. 26	12.6 5	1. 24	Ribosomal protein L3	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_687 GeneMark.hmm 624_nt + 77578 78201	62 4	399 220 7	214 5	86 1.0 5	9.75	117 411 44	185 95	25 38. 06	11.3 1	1. 56	939 798 1	252 50	43 05. 68	12.0 7	2. 32	Ribosomal protein L4	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_688 GeneMark.hmm 297_nt + 78201 78497	29 7	399 220 7	153 4	12 93. 77	10.3 4	117 411 44	109 91	31 51. 88	11.6 2	1. 28	939 798 1	174 59	62 55. 01	12.6 1	2. 27	Ribosomal protein L23	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_689 GeneMark.hmm 834_nt + 78515 79348	83 4	399 220 7	518 1	15 56. 09	10.6	117 411 44	260 04	26 55. 61	11.3 7	0. 77	939 798 1	392 62	50 09. 24	12.2 9	1. 69	Ribosomal protein L2	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_68 GeneMark.hmm 150_nt - 45103 45252	15 0	399 220 7	9	15. 03	3.91	117 411 44	54	30. 66	4.94	1. 03	939 798 1	50	35. 47	5.15	1. 24	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZED	General function prediction only	R
gene_690 GeneMark.hmm 282_nt + 79452 79733	28 2	399 220 7	511 7	45 45. 2	12.1 5	117 411 44	344 86	10 41 5.5 8	13.3 5	1. 2	939 798 1	725 98	27 39 3.0 9	14.7 4	2. 59	Ribosomal protein S19	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_691 GeneMark.hmm 345_nt + 79745 80089	34 5	399 220 7	216 1	15 69	10.6 2	117 411 44	874 8	21 59. 63	11.0 8	0. 46	939 798 1	149 74	46 18. 32	12.1 7	1. 55	Ribosomal protein L22	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J

gene_692[GeneMark.hmm 654_nt + 80102 80755	654	3992207	3152	1207.24	10.24	11741144	17780	2315.49	11.18	0.94	9397981	29896	4864.08	12.25	2.01	Ribosomal protein S3	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_693[GeneMark.hmm 414_nt + 80759 81172	414	3992207	8226	4977.09	12.28	11741144	21490	4421.05	12.11	-0.17	9397981	35391	9096.16	13.15	0.87	Ribosomal protein L16/L10E	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_694[GeneMark.hmm 207_nt + 81182 81388	207	3992207	1744	2110.39	11.04	11741144	8124	3342.64	11.71	0.67	9397981	12286	6315.47	12.62	1.58	Ribosomal protein L29	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_695[GeneMark.hmm 261_nt + 81413 81673	261	3992207	1737	1667.04	10.7	11741144	11359	3706.71	11.86	1.16	9397981	15953	6503.8	12.67	1.97	Ribosomal protein S17	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_696[GeneMark.hmm 369_nt + 81699 82067	369	3992207	5769	3916.17	11.94	11741144	18287	4220.91	12.04	0.1	9397981	28877	8327.05	13.02	1.08	Ribosomal protein L14	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_697[GeneMark.hmm 306_nt + 82145 82450	306	3992207	3002	2457.4	11.26	11741144	8982	2500.01	11.29	0.03	9397981	14934	5193.02	12.34	1.08	Ribosomal protein L24	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_698[GeneMark.hmm 543_nt + 82474 83016	543	3992207	1798	829.42	9.7	11741144	9424	1478.17	10.53	0.83	9397981	15907	3117.12	11.61	1.91	Ribosomal protein L5	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_699[GeneMark.hmm 270_nt + 83034 83303	270	3992207	453	420.26	8.72	11741144	1954	616.38	9.27	0.55	9397981	3884	1530.67	10.58	1.86	Ribosomal protein S14	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_69[GeneMark.hmm 3243_nt - 45249 48491	3243	3992207	1075	83.03	6.38	11741144	4451	116.9	6.87	0.49	9397981	3512	115.23	6.85	0.47	Chromosome segregation ATPases	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_6[GeneMark.hmm 1824_nt - 1837 3660	1824	3992207	2042	280.43	8.13	11741144	4904	228.99	7.84	-0.29	9397981	4764	277.92	8.12	-0.01	Membrane GTPase LepA	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_700[GeneMark.hmm 399_nt + 83588 83986	399	3992207	2481	1557.55	10.61	11741144	7766	1657.73	10.69	0.08	9397981	12989	3463.92	11.76	1.15	Ribosomal protein S8	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_701[GeneMark.hmm 537_nt + 84178 84714	537	3992207	2417	1127.43	10.14	11741144	10055	1594.77	10.64	0.5	9397981	19325	3829.22	11.9	1.76	Ribosomal protein L6P/L9E	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_702[GeneMark.hmm 357_nt + 84798 85154	357	3992207	2222	1559.06	10.61	11741144	9546	2277.42	11.15	0.54	9397981	18461	5502.4	12.43	1.82	Ribosomal protein L18	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_703[GeneMark.hmm 495_nt + 85172 85666	495	3992207	4482	2268.06	11.15	11741144	10996	1891.99	10.89	-0.26	9397981	18984	4080.82	11.99	0.84	Ribosomal protein S5	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_704[GeneMark.hmm 183_nt + 85680 85862	183	3992207	796	1089.55	10.09	11741144	1539	716.27	9.48	-0.61	9397981	1711	994.87	9.96	-0.13	Ribosomal protein L30/L7E	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J

gene_705[GeneMark.hmm 441_nt + 86007 86447	44 1	399 220 7	133 2	75 6.5 8	9.56	117 411 44	520 4	10 05 05	9.97	0. 41	939 798 1	893 7	21 56. 35	11.0 7	1. 51	Ribosomal protein L15	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_706[GeneMark.hmm 1311_nt + 86460 87770	13 11	399 220 7	856 7	16 36. 87	10.6 8	117 411 44	198 01	12 86. 39	10.3 3	- 0. 35	939 798 1	312 22	25 34. 1	11.3 1	0. 63	Preprotein translocase subunit SecY	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_707[GeneMark.hmm 639_nt + 87921 88559	63 9	399 220 7	237 0	92 9.0 4	9.86	117 411 44	104 98	13 99. 25	10.4 5	0. 59	939 798 1	298 4	49 6.8 9	8.96	- 0. 9	Adenylate kinase and related kinases	METABOLISM	Nucleotide transport and metabolism	F
gene_708[GeneMark.hmm 219_nt + 88676 88894	21 9	399 220 7	680 7	77 85. 72	12.9 3	117 411 44	248 53	96 65. 5	13.2 4	0. 31	939 798 1	184 49	89 63. 84	13.1 3	0. 2	Translation initiation factor 1 (IF-1)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_709[GeneMark.hmm 117_nt + 88919 89035	11 7	399 220 7	885	18 94. 72	10.8 9	117 411 44	176 1	12 81. 93	10.3 2	- 0. 57	939 798 1	147 0	13 36. 89	10.3 8	- 0. 51	Ribosomal protein L36	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_70[GeneMark.hmm 303_nt - 48526 48828	30 3	399 220 7	23	19. 01	4.25	117 411 44	146	41. 04	5.36	1. 11	939 798 1	80	28. 09	4.81	0. 56	Chromosome segregation ATPases	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_710[GeneMark.hmm 366_nt + 89053 89418	36 6	399 220 7	641 6	43 91. 07	12.1	117 411 44	228 62	53 20. 14	12.3 8	0. 28	939 798 1	241 03	70 07. 38	12.7 7	0. 67	Ribosomal protein S13	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_711[GeneMark.hmm 384_nt + 89436 89819	38 4	399 220 7	491 2	32 04. 16	11.6 5	117 411 44	137 12	30 41. 3	11.5 7	- 0. 08	939 798 1	149 98	41 55. 92	12.0 2	0. 37	Ribosomal protein S11	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_712[GeneMark.hmm 936_nt + 89862 90797	93 6	399 220 7	126 27	33 79. 18	11.7 2	117 411 44	369 22	33 59. 69	11.7 1	- 0. 01	939 798 1	401 38	45 62. 95	12.1 6	0. 44	DNA-directed RNA polymerase, alpha subunit/40 kD subunit	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_713[GeneMark.hmm 387_nt + 90809 91195	38 7	399 220 7	206 7	13 37. 88	10.3 9	117 411 44	104 81	23 06. 65	11.1 7	0. 78	939 798 1	124 61	34 26. 16	11.7 4	1. 35	Ribosomal protein L17	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_714[GeneMark.hmm 267_nt + 91460 91726	26 7	399 220 7	155	14 5.4 1	7.18	117 411 44	419	13 3.6 6	7.06	- 0. 12	939 798 1	158	62. 97	5.98	- 1. 2	ACT domain-containing protein	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_715[GeneMark.hmm 903_nt + 91736 92638	90 3	399 220 7	600	16 6.4 4	7.38	117 411 44	237 9	22 4.3 9	7.81	0. 43	939 798 1	124 4	14 6.5 9	7.2	- 0. 18	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_716[GeneMark.hmm 432_nt + 92692 93123	43 2	399 220 7	382	22 1.5	7.79	117 411 44	136 1	26 8.3 3	8.07	0. 28	939 798 1	991	24 4.0 9	7.93	0. 14	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_717[GeneMark.hmm 693_nt + 93367 94059	69 3	399 220 7	179 8	64 9.9	9.34	117 411 44	710 2	87 2.8 4	9.77	0. 43	939 798 1	482 6	74 1	9.53	0. 19	Fructose-2,6-bisphosphatase	METABOLISM	Carbohydrate transport and metabolism	G
gene_718[GeneMark.hmm 993_nt -	99 3	399 220	44	11. 1	3.47	117 411	496	42. 54	5.41	1. 94	939 798	312	33. 43	5.06	1. 59	ABC-type Fe3+ transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P

[94162 95154			7				44					1							
gene_719 GeneMark.hmm 369_nt - 95181 95549	36 9	399 220 7	11	7.4 7	2.9	117 411 44	150	34. 62	5.11	2. 21	939 798 1	102	29. 41	4.88	1. 98	ABC-type Fe3+ transport system, permease component	METABOLISM	Inorganic ion transport and metabolism	P
gene_71 GeneMark.hmm 624_nt - 48819 49442	62 4	399 220 7	56	22. 48	4.49	117 411 44	477	65. 11	6.02	1. 53	939 798 1	162	27. 62	4.79	0. 3	dsRNA-specific ribonuclease	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_720 GeneMark.hmm 102_nt - 95706 95807	10 2	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_721 GeneMark.hmm 1092_nt - 95797 96888	10 92	399 220 7	50	11. 47	3.52	117 411 44	614	47. 89	5.58	2. 06	939 798 1	330	32. 16	5.01	1. 49	ABC-type spermidine/putrescine transport systems, ATPase components	METABOLISM	Amino acid transport and metabolism	E
gene_722 GeneMark.hmm 450_nt - 96901 97350	45 0	399 220 7	22	12. 25	3.61	117 411 44	191	36. 15	5.18	1. 57	939 798 1	126	29. 79	4.9	1. 29	ABC-type Fe3+ transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_1394 GeneMark.hmm 144_nt + 1 144	14 4	399 220 7	0	0	0	117 411 44	334	19 7.5 5	7.63	7. 63	939 798 1	121 1	89 4.8 4	9.81	9. 81	NA			
gene_724 GeneMark.hmm 102_nt - 97921 98022	10 2	399 220 7	0	0	0	117 411 44	2	1.6 7	0.74	0. 74	939 798 1	0	0	0	0	ABC-type Fe3+ transport system, periplasmic component	METABOLISM	Inorganic ion transport and metabolism	P
gene_725 GeneMark.hmm 777_nt - 98511 99287	77 7	399 220 7	162	52. 23	5.71	117 411 44	158 6	17 3.8 5	7.44	1. 73	939 798 1	568	77. 78	6.28	0. 57	Pyruvate-formate lyase-activating enzyme	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_2317 GeneMark.hmm 102_nt + 1 102	10 2	399 220 7	0	0	0	117 411 44	223	18 6.2 1	7.54	7. 54	939 798 1	864	90 1.3 2	9.82	9. 82	NA			
gene_2315 GeneMark.hmm 102_nt + 2 103	10 2	399 220 7	0	0	0	117 411 44	282	23 5.4 7	7.88	7. 88	939 798 1	968	10 09. 81	9.98	9. 98	NA			
gene_728 GeneMark.hmm 321_nt + 101343 101663	32 1	399 220 7	18	14. 05	3.81	117 411 44	475	12 6.0 3	6.98	3. 17	939 798 1	147	48. 73	5.61	1. 8	Phosphotransferase system cellobiose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G
gene_729 GeneMark.hmm 309_nt + 101709 102017	30 9	399 220 7	24	19. 46	4.28	117 411 44	316	87. 1	6.44	2. 16	939 798 1	148	50. 96	5.67	1. 39	Phosphotransferase system cellobiose-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_72 GeneMark.hmm 69_nt - 49511 49579	69	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_2392 GeneMark.hmm 117_nt - 3 119	11 7	399 220 7	0	0	0	117 411 44	224	16 3.0 6	7.35	7. 35	939 798 1	118 3	10 75. 88	10.0 7	10 .0 7	NA			
gene_1396 GeneMark.hmm 141_nt +	14 1	399 220	0	0	0	117 411	326	19 6.9	7.62	7. 62	939 798	159 8	12 05.	10.2 4	10 .2	NA			

2 142		7				44		2			1		93		4				
gene_2343 GeneMark.hmm 105_nt - 3 107	105	3992207	0	0	0	11741144	222	180.07	7.49	7.49	9397981	1234	1250.52	10.29	10.29	NA			
gene_2321 GeneMark.hmm 102_nt + 3 104	102	3992207	0	0	0	11741144	324	270.54	8.08	8.08	9397981	1427	1488.64	10.54	10.54	NA			
gene_734 GeneMark.hmm 2502_nt + 108169 110670	2502	3992207	6335	634.23	9.31	11741144	10948	372.68	8.54	-0.77	9397981	9934	422.48	8.72	-0.59	Leucyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_735 GeneMark.hmm 237_nt + 10864 111100	237	3992207	52	54.96	5.78	11741144	392	140.87	7.14	1.36	9397981	168	75.43	6.24	0.46	Acetyltransferases, including N-acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_736 GeneMark.hmm 90_nt + 11209 111298	90	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	Acetyltransferases, including N-acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_737 GeneMark.hmm 345_nt + 11312 111656	345	3992207	46	33.4	5.06	11741144	273	67.4	6.07	1.01	9397981	162	49.96	5.64	0.58	Acetyltransferases, including N-acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_738 GeneMark.hmm 417_nt + 11668 112084	417	3992207	48	28.83	4.85	11741144	351	71.69	6.16	1.31	9397981	228	58.18	5.86	1.01	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_739 GeneMark.hmm 93_nt - 112899 112991	93	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2414 GeneMark.hmm 120_nt + 3 122	120	3992207	2	4.17	2.06	11741144	2067	1467.06	10.52	8.46	9397981	10692	9480.76	13.21	11.15	NA			
gene_740 GeneMark.hmm 972_nt + 13152 114123	972	3992207	499	128.59	7.01	11741144	1433	125.57	6.97	-0.04	9397981	1169	127.97	7	-0.01	Holliday junction resolvosome, helicase subunit	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_741 GeneMark.hmm 252_nt + 14104 114355	252	3992207	80	79.52	6.31	11741144	189	63.88	6	-0.31	9397981	133	56.16	5.81	-0.5	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_742 GeneMark.hmm 276_nt + 14401 114676	276	3992207	150	136.13	7.09	11741144	353	108.93	6.77	-0.32	9397981	353	136.09	7.09	0	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_743 GeneMark.hmm 759_nt + 14907 115665	759	3992207	2445	806.91	9.66	11741144	10217	1146.49	10.16	0.5	9397981	9632	1350.33	10.4	0.74	Undecaprenyl pyrophosphate synthase	METABOLISM	Lipid transport and metabolism	I
gene_744 GeneMark.hmm 804_nt + 15674 116477	804	3992207	386	120.26	6.91	11741144	2866	303.61	8.25	1.34	9397981	2706	358.13	8.48	1.57	CDP-diglyceride synthetase	METABOLISM	Lipid transport and metabolism	I
gene_745 GeneMark.hmm 1260_nt + 116499 117758	1260	3992207	3092	614.69	9.26	11741144	10096	682.45	9.41	0.15	9397981	10603	895.41	9.81	0.55	Predicted membrane-associated Zn-dependent proteases 1	CELLULAR PROCESSES AND	Cell wall/membrane/envelope biogenesis	M

																	SIGNALING		
gene_746 GeneMa rk.hmm 1854_nt + 117771 119624	18 54	399 220 7	641 1	86 6.1 7	9.76	117 411 44	238 66	10 96. 38	10.1	0. 34	939 798 1	221 04	12 68. 61	10.3 1	0. 55	Prolyl-tRNA synthetase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_747 GeneMa rk.hmm 1380_nt + 119724 121103	13 80	399 220 7	351	63. 71	5.99	117 411 44	178 6	11 0.2 3	6.78	0. 79	939 798 1	235 4	18 1.5 1	7.5	1. 51	Beta-glucosidase/6-phospho-beta- glucosidase/beta-galactosidase	METABOLISM	Carbohydrate transport and metabolism	G
gene_2320 GeneM ark.hmm 102_nt + 3 104	10 2	399 220 7	0	0	0	117 411 44	533	44 5.0 6	8.8	8. 8	939 798 1	225 5	23 52. 4	11.2	11 .2	NA			
gene_749 GeneMa rk.hmm 1050_nt + 123259 124308	10 50	399 220 7	291 8	69 6.1 2	9.44	117 411 44	294 0	23 8.4 8	7.9	- 1. 54	939 798 1	299 5	30 3.5 1	8.25	- 1. 19	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	METABOLISM	Energy production and conversion	C
gene_74 GeneMar k.hmm 1320_nt - 51058 52377	13 20	399 220 7	133	25. 24	4.66	117 411 44	551	35. 55	5.15	0. 49	939 798 1	343	27. 65	4.79	0. 13	McrBC 5-methylcytosine restriction system component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_750 GeneMa rk.hmm 3051_nt - 124408 127458	30 51	399 220 7	110 4	90. 64	6.5	117 411 44	632 9	17 6.6 8	7.46	0. 96	939 798 1	378 3	13 1.9 3	7.04	0. 54	Type II secretory pathway, pullulanase PulA and related glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_751 GeneMa rk.hmm 840_nt - 127487 128326	84 0	399 220 7	422	12 5.8 4	6.98	117 411 44	219 0	22 2.0 5	7.79	0. 81	939 798 1	889	11 2.6 1	6.82	- 0. 16	Type II secretory pathway, pullulanase PulA and related glycosidases	METABOLISM	Carbohydrate transport and metabolism	G
gene_752 GeneMa rk.hmm 414_nt + 1 28743 129156	41 4	399 220 7	107 92	65 29. 63	12.6 7	117 411 44	306 94	63 14. 55	12.6 2	- 0. 05	939 798 1	377 00	96 89. 61	13.2 4	0. 57	Ribosomal protein S12	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_753 GeneMa rk.hmm 471_nt + 1 29176 129646	47 1	399 220 7	301 1	16 01. 32	10.6 5	117 411 44	142 81	25 82. 42	11.3 3	0. 68	939 798 1	167 27	37 78. 88	11.8 8	1. 23	Ribosomal protein S7	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_754 GeneMa rk.hmm 2082_nt + 130071 132152	20 82	399 220 7	408 27	49 11. 95	12.2 6	117 411 44	958 57	39 21. 32	11.9 4	- 0. 32	939 798 1	735 57	37 59. 32	11.8 8	- 0. 38	Translation elongation factors (GTPases)	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_755 GeneMa rk.hmm 4392_nt + 132256 136647	43 92	399 220 7	174 7	99. 64	6.64	117 411 44	360 0	69. 81	6.13	0. 51	939 798 1	411 6	99. 72	6.64	0	DNA polymerase III, alpha subunit (gram-positive type)	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_756 GeneMa rk.hmm 264_nt + 1 36749 137012	26 4	399 220 7	170	16 1.3	7.33	117 411 44	424	13 6.7 9	7.1	0. 23	939 798 1	369	14 8.7 3	7.22	- 0. 11	DNA-damage-inducible protein J	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_757 GeneMa rk.hmm 279_nt + 1 37005 137283	27 9	399 220 7	124	11 1.3 3	6.8	117 411 44	549	16 7.5 9	7.39	0. 59	939 798 1	455	17 3.5 3	7.44	0. 64	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_758 GeneMa rk.hmm 153_nt + 1 37304 137456	15 3	399 220 7	20	32. 74	5.03	117 411 44	41	22. 82	4.51	- 0. 52	939 798 1	44	30. 6	4.94	- 0. 09	---	---	---	---

gene_759 GeneMa rk.hmm 1242_nt + 137478 138719	12 42	399 220 7	161 5	32 5.7 2	8.35	117 411 44	295 0	20 2.3	7.66	- 0.69	939 798 1	334 9	28 6.9 2	8.16	- 0.19	Leucyl aminopeptidase (aminopeptidase T)	METABOLISM	Amino acid transport and metabolism	E
gene_75 GeneMar k.hmm 1932_nt - 52361 54292	19 32	399 220 7	162	21	4.39	117 411 44	107 6	47. 43	5.57	1. 18	939 798 1	616	33. 93	5.08	0. 69	GTPase subunit of restriction endonuclease	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_760 GeneMa rk.hmm 231_nt + 1 38729 138959	23 1	399 220 7	181	19 6.2 7	7.62	117 411 44	342	12 6.1	6.98	- 0.64	939 798 1	288	13 2.6 6	7.05	- 0.57	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_761 GeneMa rk.hmm 690_nt + 1 39215 139904	69 0	399 220 7	610	22 1.4 5	7.79	117 411 44	145 7	17 9.8 5	7.49	- 0.3	939 798 1	991	15 2.8 2	7.26	- 0.53	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_762 GeneMa rk.hmm 1335_nt + 140122 141456	13 35	399 220 7	267 92	50 27. 02	12.3	117 411 44	615 82	39 28. 82	11.9 4	- 0.36	939 798 1	269 73	21 49. 88	11.0 7	- 1.23	Aminopeptidase C	METABOLISM	Amino acid transport and metabolism	E
gene_763 GeneMa rk.hmm 912_nt - 141512 142423	91 2	399 220 7	660	18 1.2 7	7.5	117 411 44	527 5	49 2.6 3	8.94	1. 44	939 798 1	664 0	77 4.7 1	9.6	2. 1	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IID	METABOLISM	Carbohydrate transport and metabolism	G
gene_764 GeneMa rk.hmm 804_nt - 142447 143250	80 4	399 220 7	411	12 8.0 5	7	117 411 44	239 7	25 3.9 2	7.99	0. 99	939 798 1	253 2	33 5.1	8.39	1. 39	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_765 GeneMa rk.hmm 990_nt - 143278 144267	99 0	399 220 7	656	16 5.9 8	7.37	117 411 44	384 6	33 0.8 7	8.37	1	939 798 1	253 6	27 2.5 7	8.09	0. 72	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_766 GeneMa rk.hmm 1020_nt - 144500 145519	10 20	399 220 7	128 8	31 6.3	8.31	117 411 44	848 6	70 8.5 9	9.47	1. 16	939 798 1	501 0	52 2.6 4	9.03	0. 72	Zn-dependent alcohol dehydrogenases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_767 GeneMa rk.hmm 813_nt - 145858 146670	81 3	399 220 7	882	27 1.7 5	8.09	117 411 44	757 6	79 3.6 7	9.63	1. 54	939 798 1	303 8	39 7.6 1	8.64	0. 55	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_2316 GeneM ark.hmm 102_nt + 1 102	10 2	399 220 7	0	0	0	117 411 44	355	29 6.4 3	8.21	8. 21	939 798 1	226 6	23 63. 88	11.2 1	11 .2 1	NA			
gene_2319 GeneM ark.hmm 102_nt + 3 104	10 2	399 220 7	0	0	0	117 411 44	512	42 7.5 2	8.74	8. 74	939 798 1	230 4	24 03. 52	11.2 3	11 .2 3	NA			
gene_2463 GeneM ark.hmm 105_nt + 1 105	10 5	399 220 7	0	0	0	117 411 44	622	50 4.5 3	8.98	8. 98	939 798 1	298 9	30 29. 02	11.5 6	11 .5 6	NA			
gene_770 GeneMa rk.hmm 975_nt + 1 49133 150107	97 5	399 220 7	818	21 0.1 5	7.72	117 411 44	357 2	31 2.0 3	8.29	0. 57	939 798 1	250 8	27 3.7 1	8.1	0. 38	Dihydropteroate synthase and related enzymes	METABOLISM	Coenzyme transport and metabolism	H
gene_771 GeneMa rk.hmm 1323_nt +	13	399 220	111	21 1.4	7.72	117 411	349	22	7.81	0.	939 798	348	28 0.3	8.13	0.	Folylpolyglutamate synthase	METABOLISM	Coenzyme transport and	H

150109 151431	23	7	7	9		44	2	4.8		09	1	6	7		41			metabolism	
gene_772 GeneMa rk.hmm 555_nt + 1 51412 151966	55 5	399 220 7	435	19 6.3 3	7.62	117 411 44	172 7	26 5.0 3	8.05	0. 43	939 798 1	203 1	38 9.3 9	8.61	0. 99	GTP cyclohydrolase I	METABOLISM	Coenzyme transport and metabolism	H
gene_773 GeneMa rk.hmm 813_nt + 1 52009 152821	81 3	399 220 7	513	15 8.0 6	7.3	117 411 44	164 4	17 2.2 3	7.43	0. 13	939 798 1	183 0	23 9.5 1	7.9	0. 6	7,8-dihydro-6-hydroxymethylpterin- pyrophosphokinase	METABOLISM	Coenzyme transport and metabolism	H
gene_774 GeneMa rk.hmm 318_nt - 152866 153183	31 8	399 220 7	339 0	26 70. 3	11.3 8	117 411 44	477 3	12 78. 36	10.3 2	- 1. 06	939 798 1	157 9	52 8.3 5	9.05	- 2. 33	---	---	---	---
gene_775 GeneMa rk.hmm 447_nt + 1 53538 153984	44 7	399 220 7	271 39	15 20 8.0 4	13.8 9	117 411 44	406 57	77 46. 71	12.9 2	- 0. 97	939 798 1	295 77	70 40. 64	12.7 8	- 1. 11	Ribosomal protein L13	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_776 GeneMa rk.hmm 393_nt + 1 54003 154395	39 3	399 220 7	215 15	13 71 3.1	13.7 4	117 411 44	343 04	74 34. 33	12.8 6	- 0. 88	939 798 1	251 23	68 02. 12	12.7 3	- 1. 01	Ribosomal protein S9	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2399 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	1	2.0 9	1.06	117 411 44	141 4	10 03. 59	9.97	8. 91	939 798 1	746 2	66 16. 67	12.6 9	11 .6 3	NA			
gene_2419 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	2	4.1 7	2.06	117 411 44	296 8	21 06. 55	11.0 4	8. 98	939 798 1	149 37	13 24 4.8 7	13.6 9	11 .6 3	NA			
gene_2502 GeneM ark.hmm 120_nt - 4 123	12 0	399 220 7	1	2.0 9	1.06	117 411 44	147 9	10 49. 73	10.0 4	8. 98	939 798 1	801 3	71 05. 25	12.7 9	11 .7 3	NA			
gene_2476 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	1	2.0 9	1.06	117 411 44	182 5	12 95. 3	10.3 4	9. 28	939 798 1	828 2	73 43. 78	12.8 4	11 .7 8	NA			
gene_2472 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	761	54 0.1 2	9.08	9. 08	939 798 1	407 2	36 10. 7	11.8 2	11 .8 2	NA			
gene_2413 GeneM ark.hmm 111_nt + 1 111	11 1	399 220 7	0	0	0	117 411 44	746	57 2.4 1	9.16	9. 16	939 798 1	390 6	37 44. 34	11.8 7	11 .8 7	NA			
gene_782 GeneMa rk.hmm 315_nt + 1 59592 159906	31 5	399 220 7	5	3.9 8	1.99	117 411 44	45	12. 17	3.6	1. 61	939 798 1	17	5.7 4	2.52	0. 53	Phosphotransferase system cellobiose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G
gene_783 GeneMa rk.hmm 1347_nt + 160523 161869	13 47	399 220 7	39	7.2 5	2.86	117 411 44	742	46. 92	5.55	2. 69	939 798 1	219	17. 3	4.11	1. 25	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_784 GeneMa rk.hmm 177_nt + 1 62249 162425	17 7	399 220 7	196 2	27 76. 6	11.4 4	117 411 44	107 2	51 5.8 4	9.01	- 2. 43	939 798 1	154 7	93 0	9.86	- 1. 58	---	---	---	---
gene_785 GeneMa rk.hmm 126_nt + 1	12	399 220	127	25 2.4	7.98	117 411	113	76.	6.26	- 1.	939 798	72	60.	5.93	- 2.	NA			

62425 162550	6	7		8		44		38		72	1		8		05				
gene_786 GeneMa rk.hmm 2214_nt + 162826 165039	22 14	399 220 7	210 0	23 7.5 9	7.89	117 411 44	567 9	21 8.4 7	7.77	- 0. 12	939 798 1	403 7	19 4.0 2	7.6	- 0. 29	Alpha-glucosidases, family 31 of glycosyl hydrolases	METABOLISM	Carbohydrate transport and metabolism	G
gene_787 GeneMa rk.hmm 477_nt 165261 165737	47 7	399 220 7	116	60. 92	5.93	117 411 44	663	11 8.3 8	6.89	0. 96	939 798 1	233	51. 98	5.7	- 0. 23	Glutathione peroxidase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_788 GeneMa rk.hmm 381_nt + 1 65960 166340	38 1	399 220 7	43	28. 27	4.82	117 411 44	278	62. 15	5.96	1. 14	939 798 1	160	44. 68	5.48	0. 66	---	---	---	---
gene_789 GeneMa rk.hmm 2736_nt + 166428 169163	27 36	399 220 7	181	16. 57	4.05	117 411 44	164 7	51. 27	5.68	1. 63	939 798 1	148 4	57. 71	5.85	1. 8	---	---	---	---
gene_78 GeneMar k.hmm 144_nt 54775 54918	14 4	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_790 GeneMa rk.hmm 234_nt + 1 69699 169932	23 4	399 220 7	21	22. 48	4.49	117 411 44	51	18. 56	4.21	- 0. 28	939 798 1	14	6.3 7	2.67	- 1. 82	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_791 GeneMa rk.hmm 630_nt 170308 170937	63 0	399 220 7	184	73. 16	6.19	117 411 44	367	49. 62	5.63	- 0. 56	939 798 1	209	35. 3	5.14	- 1. 05	2-keto-3-deoxy-6-phosphogluconate aldolase	METABOLISM	Carbohydrate transport and metabolism	G
gene_792 GeneMa rk.hmm 1002_nt 170947 171948	10 02	399 220 7	150	37. 5	5.23	117 411 44	357	30. 35	4.92	- 0. 31	939 798 1	202	21. 45	4.42	- 0. 81	Sugar kinases, ribokinase family	METABOLISM	Carbohydrate transport and metabolism	G
gene_793 GeneMa rk.hmm 642_nt 171979 172620	64 2	399 220 7	95	37. 07	5.21	117 411 44	270	35. 82	5.16	- 0. 05	939 798 1	156	25. 86	4.69	- 0. 52	Ribose 5-phosphate isomerase RpiB	METABOLISM	Carbohydrate transport and metabolism	G
gene_794 GeneMa rk.hmm 816_nt 172639 173454	81 6	399 220 7	101	31	4.95	117 411 44	246	25. 68	4.68	- 0. 27	939 798 1	120	15. 65	3.97	- 0. 98	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	METABOLISM	Lipid transport and metabolism	I
gene_2436 GeneM ark.hmm 123_nt 1 123	12 3	399 220 7	1	2.0 4	1.03	117 411 44	184 5	12 77. 56	10.3 2	9. 29	939 798 1	970 0	83 91. 35	13.0 3	12	NA			
gene_2451 GeneM ark.hmm 108_nt + 3 110	10 8	399 220 7	0	0	0	117 411 44	767	60 4.8 7	9.24	9. 24	939 798 1	434 5	42 80. 86	12.0 6	12 .0 6	NA			
gene_797 GeneMa rk.hmm 486_nt + 1 75378 175863	48 6	399 220 7	19	9.7 9	3.29	117 411 44	111	19. 45	4.28	0. 99	939 798 1	96	21. 02	4.39	1. 1	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IIB	METABOLISM	Carbohydrate transport and metabolism	G
gene_798 GeneMa rk.hmm 780_nt + 1 75878 176657	78 0	399 220 7	30	9.6 3	3.27	117 411 44	182	19. 87	4.31	1. 04	939 798 1	99	13. 51	3.76	0. 49	Phosphotransferase system, mannose/fructose/N- acetylgalactosamine-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G

gene_799 GeneMark.hmm 819_nt + 176644 177462	819	3992207	124	37.92	5.25	11741144	392	40.77	5.35	0.1	9397981	190	24.69	4.63	-0.62	Phosphotransferase system, mannose/fructose/N-acetylglactosamine-specific component IID	METABOLISM	Carbohydrate transport and metabolism	G
gene_2483 GeneMark.hmm 120_nt - 3 122	120	3992207	1	2.09	1.06	11741144	2205	1565.01	10.61	9.55	9397981	10183	9029.42	13.14	12.08	NA			
gene_7 GeneMark.hmm 729_nt - 3739 4467	729	3992207	320	109.95	6.78	11741144	1216	142.07	7.15	0.37	9397981	1226	178.95	7.48	0.7	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_800 GeneMark.hmm 294_nt + 177462 177755	294	3992207	7	5.96	2.58	11741144	41	11.88	3.57	0.99	9397981	27	9.77	3.29	0.71	Preprotein translocase subunit YajC	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_2505 GeneMark.hmm 117_nt + 1 117	117	3992207	0	0	0	11741144	933	679.18	9.41	9.41	9397981	4995	4542.71	12.15	12.15	NA			
gene_802 GeneMark.hmm 1002_nt + 179738 180739	1002	3992207	4556	1138.95	10.15	11741144	8140	691.9	9.43	-0.72	9397981	3620	384.42	8.59	-1.56	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_803 GeneMark.hmm 336_nt - 180849 181184	336	3992207	344	256.45	8	11741144	651	165.02	7.37	-0.63	9397981	352	111.47	6.8	-1.2	NA			
gene_804 GeneMark.hmm 243_nt - 181195 181437	243	3992207	28	28.86	4.85	11741144	225	78.86	6.3	1.45	9397981	207	90.64	6.5	1.65	---	---	---	---
gene_805 GeneMark.hmm 543_nt - 181448 181990	543	3992207	349	161	7.33	11741144	727	114.03	6.83	-0.5	9397981	610	119.54	6.9	-0.43	---	---	---	---
gene_806 GeneMark.hmm 195_nt - 182006 182200	195	3992207	195	250.49	7.97	11741144	274	119.68	6.9	-1.07	9397981	365	199.17	7.64	-0.33	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_807 GeneMark.hmm 951_nt + 182366 183316	951	3992207	699	184.11	7.52	11741144	3383	302.98	8.24	0.72	9397981	1646	184.17	7.52	0	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_808 GeneMark.hmm 318_nt + 183328 183645	318	3992207	385	303.26	8.24	11741144	1254	335.86	8.39	0.15	9397981	856	286.43	8.16	-0.08	Protein required for the initiation of cell division	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	D
gene_809 GeneMark.hmm 2253_nt + 183649 185901	2253	3992207	4186	465.4	8.86	11741144	10099	381.77	8.58	-0.28	9397981	9637	455.14	8.83	-0.03	Cell division protein FtsI/penicillin-binding protein 2	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_2480 GeneMark.hmm 120_nt + 2 121	120	3992207	1	2.09	1.06	11741144	2201	1562.17	10.61	9.55	9397981	12473	11060	13.43	12.37	NA			

gene_810 GeneMa rk.hmm 981_nt + 1 85903 186883	98 1	399 220 7	307	78. 39	6.29	117 411 44	104 6	90. 81	6.5	0. 21	939 798 1	102 6	11 1.2 9	6.8	0. 51	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-phosphate transferase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_811 GeneMa rk.hmm 2106_nt + 187492 189597	21 06	399 220 7	363 5	43 2.3 5	8.76	117 411 44	186 5	75. 42	6.24	- 2. 52	939 798 1	221 7	11 2.0 1	6.81	- 1. 95	ATPases with chaperone activity, ATP-binding subunit	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_812 GeneMa rk.hmm 483_nt 189893 190375	48 3	399 220 7	443 0	22 97. 44	11.1 7	117 411 44	549 5	96 8.9 7	9.92	- 1. 25	939 798 1	303 8	66 9.2 8	9.39	- 1. 78	LuxS protein involved in autoinducer AI2 synthesis	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_813 GeneMa rk.hmm 1485_nt 190470 191954	14 85	399 220 7	282 3	47 6.1 8	8.9	117 411 44	128 04	73 4.3 6	9.52	0. 62	939 798 1	624 0	44 7.1 2	8.8	- 0. 1	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_2493 GeneM ark.hmm 123_nt 1 123	12 3	399 220 7	0	0	0	117 411 44	114 4	79 2.1 6	9.63	9. 63	939 798 1	629 1	54 42. 27	12.4 1	12 .4 1	NA			
gene_2372 GeneM ark.hmm 114_nt 3 116	11 4	399 220 7	0	0	0	117 411 44	116 2	86 8.1 4	9.76	9. 76	939 798 1	609 6	56 89. 91	12.4 7	12 .4 7	NA			
gene_2498 GeneM ark.hmm 120_nt 3 122	12 0	399 220 7	0	0	0	117 411 44	136 6	96 9.5 3	9.92	9. 92	939 798 1	659 5	58 47. 89	12.5 1	12 .5 1	NA			
gene_817 GeneMa rk.hmm 699_nt + 5 62 1260	69 9	399 220 7	139 8	50 0.9 8	8.97	117 411 44	233 5	28 4.5 1	8.15	- 0. 82	939 798 1	172 6	26 2.7 4	8.04	- 0. 93	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_818 GeneMa rk.hmm 1053_nt + 1257 2309	10 53	399 220 7	109 4	26 0.2 4	8.02	117 411 44	234 6	18 9.7 5	7.57	- 0. 45	939 798 1	149 8	15 1.3 7	7.24	- 0. 78	Signal transduction histidine kinase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_819 GeneMa rk.hmm 612_nt + 2 504 3115	61 2	399 220 7	849 9	34 78. 59	11.7 6	117 411 44	259 23	36 07. 64	11.8 2	0. 06	939 798 1	105 81	18 39. 67	10.8 5	- 0. 91	Ribosomal protein S4 and related proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2384 GeneM ark.hmm 117_nt 2 118	11 7	399 220 7	0	0	0	117 411 44	140 0	10 19. 14	9.99	9. 99	939 798 1	645 9	58 74. 15	12.5 2	12 .5 2	NA			
gene_820 GeneMa rk.hmm 351_nt + 3 854 4204	35 1	399 220 7	849	60 5.8 8	9.24	117 411 44	270 4	65 6.1 3	9.36	0. 12	939 798 1	420	12 7.3 2	6.99	- 2. 25	---	---	---	---
gene_2402 GeneM ark.hmm 120_nt 2 121	12 0	399 220 7	0	0	0	117 411 44	142 8	10 13. 53	9.99	9. 99	939 798 1	675 7	59 91. 54	12.5 5	12 .5 5	NA			
gene_2437 GeneM ark.hmm 120_nt 2 121	12 0	399 220 7	1	2.0 9	1.06	117 411 44	296 2	21 02. 29	11.0 4	9. 98	939 798 1	148 05	13 12 7.8 2	13.6 8	12 .6 2	NA			

gene_823[GeneMark.hmm 1476_nt + 6493 7968	1476	3992207	31	5.26	2.4	11741144	768	44.32	5.47	3.07	9397981	233	16.8	4.07	1.67	ABC-type sugar transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_824[GeneMark.hmm 987_nt + 8240 9226	987	3992207	4709	1195.08	10.22	11741144	15650	1350.48	10.4	0.18	9397981	9604	1035.38	10.02	-0.2	Predicted sulfurtransferase	POORLY CHARACTERIZED	General function prediction only	R
gene_825[GeneMark.hmm 861_nt + 9501 10361	861	3992207	355	103.28	6.69	11741144	965	95.46	6.58	-0.11	9397981	777	96.02	6.59	-0.1	---	---	---	---
gene_826[GeneMark.hmm 126_nt + 12244 12369	126	3992207	15	29.82	4.9	11741144	262	177.1	7.47	2.57	9397981	132	111.47	6.8	1.9	NA			
gene_827[GeneMark.hmm 198_nt + 12394 12591	198	3992207	34	43.01	5.43	11741144	287	123.45	6.95	1.52	9397981	136	73.09	6.19	0.76	NA			
gene_828[GeneMark.hmm 1065_nt - 12859 13923	1065	3992207	4431	1042.17	10.03	11741144	23902	1911.5	10.9	0.87	9397981	18751	1873.44	10.87	0.84	---	---	---	---
gene_829[GeneMark.hmm 912_nt - 13986 14897	912	3992207	1789	491.36	8.94	11741144	16037	1497.68	10.55	1.61	9397981	14560	1698.76	10.73	1.79	---	---	---	---
gene_2411[GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	1470	1043.34	10.03	10.03	9397981	7679	6809.09	12.73	12.73	NA			
gene_2412[GeneMark.hmm 120_nt - 3 122	120	3992207	0	0	0	11741144	1727	1225.75	10.26	10.26	9397981	8316	7373.92	12.85	12.85	NA			
gene_831[GeneMark.hmm 327_nt - 15470 15796	327	3992207	218	166.99	7.38	11741144	1677	436.79	8.77	1.39	9397981	1123	365.42	8.51	1.13	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_832[GeneMark.hmm 1167_nt - 15984 17150	1167	3992207	1552	333.13	8.38	11741144	9236	674.07	9.4	1.02	9397981	8155	743.56	9.54	1.16	Cyanate permease	METABOLISM	Inorganic ion transport and metabolism	P
gene_833[GeneMark.hmm 1065_nt + 17301 18365	1065	3992207	5537	1302.3	10.35	11741144	14819	1185.11	10.21	-0.14	9397981	27132	2710.8	11.4	1.05	Glycosyltransferases involved in cell wall biogenesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_834[GeneMark.hmm 1851_nt + 18407 20257	1851	3992207	14146	1914.32	10.9	11741144	29456	1355.37	10.4	-0.5	9397981	26795	1540.33	10.59	-0.31	Predicted nucleoside-diphosphate sugar epimerases	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_835[GeneMark.hmm 213_nt - 20342 20554	213	3992207	54	63.5	5.99	11741144	280	111.96	6.81	0.82	9397981	266	132.88	7.05	1.06	NA			
gene_836[GeneMark.hmm 633_nt - 20604 21236	633	3992207	2295	908.17	9.83	11741144	1872	251.88	7.98	-1.85	9397981	1526	256.52	8	-1.83	Predicted phosphatases	POORLY CHARACTERIZED	General function prediction only	R

gene_837 GeneMa rk.hmm 873_nt - 21258 22130	87 3	399 220 7	601	17 2.4 4	7.43	117 411 44	129 1	12 5.9 5	6.98	- 0. 45	939 798 1	995	12 1.2 8	6.92	- 0. 51	L-serine deaminase	METABOLISM	Amino acid transport and metabolism	E
gene_838 GeneMa rk.hmm 672_nt - 22139 22810	67 2	399 220 7	147 3	54 9.0 6	9.1	117 411 44	173 2	21 9.5 2	7.78	- 1. 32	939 798 1	825	13 0.6 3	7.03	- 2. 07	L-serine deaminase	METABOLISM	Amino acid transport and metabolism	E
gene_839 GeneMa rk.hmm 573_nt + 2 3052 23624	57 3	399 220 7	193 67	84 66. 32	13.0 5	117 411 44	288 57	42 89. 3	12.0 7	- 0. 98	939 798 1	727 2	13 50. 41	10.4	- 2. 65	---	---	---	---
gene_83 GeneMar k.hmm 435_nt - 56964 57398	43 5	399 220 7	71	40. 88	5.35	117 411 44	576	11 2.7 8	6.82	1. 47	939 798 1	548	13 4.0 5	7.07	1. 72	Isopropylmalate/homocitrate/citram ate synthases	METABOLISM	Amino acid transport and metabolism	E
gene_2400 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	165 1	11 71. 81	10.1 9	10 .1 9	939 798 1	889 4	78 86. 45	12.9 5	12 .9 5	NA			
gene_841 GeneMa rk.hmm 177_nt + 3 60 536	17 7	399 220 7	31	43. 87	5.46	117 411 44	163	78. 43	6.29	0. 83	939 798 1	125	75. 15	6.23	0. 77	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_842 GeneMa rk.hmm 1083_nt - 897 1979	10 83	399 220 7	301 0	69 6.1 9	9.44	117 411 44	647 9	50 9.5 3	8.99	- 0. 45	939 798 1	589 2	57 8.8 9	9.18	- 0. 26	Superfamily II DNA and RNA helicases	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_843 GeneMa rk.hmm 978_nt - 1976 2953	97 8	399 220 7	180 4	46 2.0 5	8.85	117 411 44	501 9	43 7.0 9	8.77	- 0. 08	939 798 1	402 8	43 8.2 4	8.78	- 0. 07	Predicted dehydrogenases and related proteins	POORLY CHARACTERIZ ED	General function prediction only	R
gene_844 GeneMa rk.hmm 156_nt + 3 257 3412	15 6	399 220 7	7	11. 24	3.49	117 411 44	52	28. 39	4.83	1. 34	939 798 1	37	25. 24	4.66	1. 17	NA			
gene_845 GeneMa rk.hmm 252_nt + 3 476 3727	25 2	399 220 7	55	54. 67	5.77	117 411 44	125	42. 25	5.4	- 0. 37	939 798 1	134	56. 58	5.82	0. 05	---	---	---	---
gene_846 GeneMa rk.hmm 1443_nt + 3911 5353	14 43	399 220 7	492 0	85 4.0 5	9.74	117 411 44	110 14	65 0.0 8	9.34	- 0. 4	939 798 1	798 5	58 8.8 1	9.2	- 0. 54	Predicted xylanase/chitin deacetylase	METABOLISM	Carbohydrate transport and metabolism	G
gene_847 GeneMa rk.hmm 843_nt + 5 467 6309	84 3	399 220 7	868	25 7.9 2	8.01	117 411 44	257 2	25 9.8 6	8.02	0. 01	939 798 1	293 9	37 0.9 7	8.54	0. 53	Aldo/keto reductases, related to diketogulonate reductase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_848 GeneMa rk.hmm 762_nt + 6 582 7343	76 2	399 220 7	80	26. 3	4.72	117 411 44	705	78. 8	6.3	1. 58	939 798 1	610	85. 18	6.41	1. 69	---	---	---	---
gene_849 GeneMa rk.hmm 681_nt + 7 538 8218	68 1	399 220 7	148	54. 44	5.77	117 411 44	879	10 9.9 3	6.78	1. 01	939 798 1	121 2	18 9.3 7	7.57	1. 8	Glycyl-tRNA synthetase, alpha subunit	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_2422 GeneM ark.hmm 120_nt - 3 122	12 0	399 220 7	0	0	0	117 411 44	168 4	11 95. 23	10.2 2	10 .2 2	939 798 1	903 7	80 13. 25	12.9 7	12 .9 7	NA			
gene_850 GeneMa rk.hmm 213_nt + 8	21	399 220	73	85.	6.42	117 411	424	16 9.5	7.41	0.	939 798	494	24 6.7	7.95	1.	Glycyl-tRNA synthetase, alpha	INFORMATION STORAGE AND	Translation, ribosomal structure and	J

322 8534	3	7		85		44		4		99	1		8		53	subunit	PROCESSING	biogenesis	
gene_851 GeneMa rk.hmm 1332_nt + 8794 10125	13 32	399 220 7	328	61. 68	5.95	117 411 44	229 0	14 6.4 3	7.19	1. 24	939 798 1	325 7	26 0.1 8	8.02	2. 07	Glycyl-tRNA synthetase, beta subunit	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_852 GeneMa rk.hmm 819_nt + 1 0052 10870	81 9	399 220 7	308	94. 2	6.56	117 411 44	132 6	13 7.9	7.11	0. 55	939 798 1	186 4	24 2.1 7	7.92	1. 36	Glycyl-tRNA synthetase, beta subunit	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_853 GeneMa rk.hmm 258_nt + 1 0912 11169	25 8	399 220 7	649	63 0.1	9.3	117 411 44	261 4	86 2.9 3	9.75	0. 45	939 798 1	316 4	13 04. 91	10.3 5	1. 05	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZ ED	Function unknown	S
gene_854 GeneMa rk.hmm 654_nt - 11392 12045	65 4	399 220 7	69	26. 43	4.72	117 411 44	498	64. 85	6.02	1. 3	939 798 1	227	36. 93	5.21	0. 49	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_855 GeneMa rk.hmm 585_nt - 12105 12689	58 5	399 220 7	19	8.1 4	3.02	117 411 44	277	40. 33	5.33	2. 31	939 798 1	155	28. 19	4.82	1. 8	Predicted flavoprotein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_856 GeneMa rk.hmm 606_nt - 12708 13313	60 6	399 220 7	18	7.4 4	2.9	117 411 44	347	48. 77	5.61	2. 71	939 798 1	152	26. 69	4.74	1. 84	Predicted flavoprotein	POORLY CHARACTERIZ ED	General function prediction only	R
gene_857 GeneMa rk.hmm 924_nt - 13373 14296	92 4	399 220 7	57	15. 45	3.95	117 411 44	734	67. 66	6.08	2. 13	939 798 1	352	40. 54	5.34	1. 39	Membrane-associated lipoprotein involved in thiamine biosynthesis	METABOLISM	Coenzyme transport and metabolism	H
gene_858 GeneMa rk.hmm 1425_nt + 14590 16014	14 25	399 220 7	572 7	10 06. 7	9.98	117 411 44	237 58	14 19. 99	10.4 7	0. 49	939 798 1	173 60	12 96. 28	10.3 4	0. 36	Uncharacterized NAD(FAD)- dependent dehydrogenases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_859 GeneMa rk.hmm 876_nt + 1 6166 17041	87 6	399 220 7	685 8	19 61. 01	10.9 4	117 411 44	101 35	98 5.3 9	9.94	-1	939 798 1	778 7	94 5.8 7	9.89	- 1. 05	Pyridoxine biosynthesis enzyme	METABOLISM	Coenzyme transport and metabolism	H
gene_2446 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	183 7	13 03. 82	10.3 5	10 .3 5	939 798 1	951 6	84 37. 98	13.0 4	13 .0 4	NA			
gene_860 GeneMa rk.hmm 582_nt + 1 7042 17623	58 2	399 220 7	166 7	71 7.4 6	9.49	117 411 44	377 1	55 1.8 5	9.11	- 0. 38	939 798 1	318 8	58 2.8 6	9.19	- 0. 3	Predicted glutamine amidotransferase involved in pyridoxine biosynthesis	METABOLISM	Coenzyme transport and metabolism	H
gene_2461 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	211 1	14 98. 29	10.5 5	10 .5 5	939 798 1	952 7	84 47. 74	13.0 4	13 .0 4	NA			
gene_2506 GeneM ark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	190 4	13 18. 41	10.3 6	10 .3 6	939 798 1	104 09	90 04. 7	13.1 4	13 .1 4	NA			
gene_863 GeneMa rk.hmm 495_nt + 1 8869 19363	49 5	399 220 7	836	42 3.0 5	8.72	117 411 44	220 8	37 9.9 1	8.57	- 0. 15	939 798 1	122 7	26 3.7 6	8.04	- 0. 68	Histone acetyltransferase HPA2 and related acetyltransferases	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_864 GeneMa rk.hmm 531_nt + 1 9363 19893	53 1	399 220 7	583	27 5.0 2	8.1	117 411 44	129 8	20 8.1 9	7.7	- 0. 4	939 798 1	939	18 8.1 6	7.56	- 0. 54	Methylated DNA-protein cysteine methyltransferase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

gene_865[GeneMa rk.hmm 357_nt + 1 9887 20243	35 7	399 220 7	282	19 7.8 6	7.63	117 411 44	117 2	27 9.6 1	8.13	0. 5	939 798 1	737	21 9.6 7	7.78	0. 15	Arsenate reductase and related proteins, glutaredoxin family	METABOLISM	Inorganic ion transport and metabolism	P
gene_866[GeneMa rk.hmm 801_nt + 2 0401 21201	80 1	399 220 7	959	29 9.9	8.23	117 411 44	365 2	38 8.3 2	8.6	0. 37	939 798 1	207 9	27 6.1 8	8.11	- 0. 12	ABC-type amino acid transport system, permease component	METABOLISM	Amino acid transport and metabolism	E
gene_867[GeneMa rk.hmm 66_nt + 21 201 21266	66	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	NA			
gene_868[GeneMa rk.hmm 672_nt + 2 1326 21997	67 2	399 220 7	107 0	39 8.8 4	8.64	117 411 44	370 6	46 9.7 1	8.88	0. 24	939 798 1	228 3	36 1.4 9	8.5	- 0. 14	ABC-type polar amino acid transport system, ATPase component	METABOLISM	Amino acid transport and metabolism	E
gene_869[GeneMa rk.hmm 225_nt + 2 2075 22299	22 5	399 220 7	95	10 5.7 6	6.72	117 411 44	473	17 9.0 5	7.48	0. 76	939 798 1	282	13 3.3 6	7.06	0. 34	---	---	---	---
gene_2432[GeneM ark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	203 5	14 09. 12	10.4 6	10 .4 6	939 798 1	106 33	91 98. 48	13.1 7	13 .1 7	NA			
gene_870[GeneMa rk.hmm 912_nt + 2 2365 23276	91 2	399 220 7	634 6	17 42. 98	10.7 7	117 411 44	118 61	11 07. 68	10.1 1	- 0. 66	939 798 1	509 1	59 3.9 8	9.21	- 1. 56	Thioredoxin reductase	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_871[GeneMa rk.hmm 729_nt - 23314 24042	72 9	399 220 7	141 6	48 6.5 4	8.93	117 411 44	493 9	57 7.0 3	9.17	0. 24	939 798 1	219 1	31 9.8	8.32	- 0. 61	rRNA methylases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_872[GeneMa rk.hmm 567_nt - 24087 24653	56 7	399 220 7	262 5	11 59. 67	10.1 8	117 411 44	748 3	11 24. 04	10.1 3	- 0. 05	939 798 1	255 0	47 8.5 4	8.9	- 1. 28	N-formylmethionyl-tRNA deformylase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_873[GeneMa rk.hmm 123_nt + 2 5251 25373	12 3	399 220 7	3	6.1 1	2.61	117 411 44	13	9	3.17	0. 56	939 798 1	10	8.6 5	3.11	0. 5	---	---	---	---
gene_874[GeneMa rk.hmm 849_nt + 2 5468 26316	84 9	399 220 7	126	37. 17	5.22	117 411 44	808	81. 06	6.34	1. 12	939 798 1	612	76. 7	6.26	1. 04	Putative enzyme of poly-gamma- glutamate biosynthesis (capsule formation)	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_875[GeneMa rk.hmm 828_nt + 2 6338 27165	82 8	399 220 7	176	53. 24	5.73	117 411 44	765	78. 69	6.3	0. 57	939 798 1	672	86. 36	6.43	0. 7	Predicted hydrolases of the HAD superfamily	POORLY CHARACTERIZ ED	General function prediction only	R
gene_876[GeneMa rk.hmm 636_nt + 2 7167 27802	63 6	399 220 7	363	14 2.9 7	7.16	117 411 44	153 4	20 5.4 3	7.68	0. 52	939 798 1	137 4	22 9.8 8	7.84	0. 68	Lysophospholipase L1 and related esterases	METABOLISM	Amino acid transport and metabolism	E
gene_877[GeneMa rk.hmm 726_nt + 2 7886 28611	72 6	399 220 7	577	19 9.0 8	7.64	117 411 44	242 1	28 4.0 2	8.15	0. 51	939 798 1	133 2	19 5.2 2	7.61	- 0. 03	---	---	---	---
gene_878[GeneMa rk.hmm 936_nt + 2 8608 29543	93 6	399 220 7	353	94. 47	6.56	117 411 44	143 4	13 0.4 9	7.03	0. 47	939 798 1	104 8	11 9.1 4	6.9	0. 34	Beta-lactamase class C and other penicillin binding proteins	CELLULAR PROCESSES AND	Defense mechanisms	V

																	SIGNALING		
gene_879 GeneMark.hmm 153_nt + 29552 29704	15 3	399 220 7	0	0	0	117 411 44	0	0	0	0	939 798 1	0	0	0	0	Permeases of the drug/metabolite transporter (DMT) superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_87 GeneMark.hmm 633_nt - 58839 59471	63 3	399 220 7	132	52.23	5.71	117 411 44	226 5	30 4.7 6	8.25	2.54	939 798 1	122 6	20 6.0 9	7.69	1.98	Uncharacterized protein involved in copper resistance	METABOLISM	Inorganic ion transport and metabolism	P
gene_880 GeneMark.hmm 648_nt + 29740 30387	64 8	399 220 7	183	70.74	6.14	117 411 44	953	12 5.2 6	6.97	0.83	939 798 1	671	11 0.1 8	6.78	0.64	Permeases of the drug/metabolite transporter (DMT) superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_881 GeneMark.hmm 231_nt - 30605 30835	23 1	399 220 7	709	76 8.8 1	9.59	117 411 44	126 1	46 4.9 4	8.86	- 0.73	939 798 1	432	19 8.9 9	7.64	- 1.95	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_882 GeneMark.hmm 462_nt - 30913 31374	46 2	399 220 7	383	20 7.6 6	7.7	117 411 44	236 5	43 5.9 9	8.77	1.07	939 798 1	744	17 1.3 5	7.42	- 0.28	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_883 GeneMark.hmm 1563_nt + 31516 33078	15 63	399 220 7	482 6	77 3.4 2	9.6	117 411 44	230 07	12 53.69	10.2 9	0.69	939 798 1	959 6	65 3.2 8	9.35	- 0.25	GMP synthase, PP-ATPase domain/subunit	METABOLISM	Nucleotide transport and metabolism	F
gene_2367 GeneMark.hmm 111_nt - 3 113	11 1	399 220 7	0	0	0	117 411 44	165 8	12 72.19	10.3 1	10.3 1	939 798 1	102 71	98 45.89	13.2 7	13.2 7	NA			
gene_885 GeneMark.hmm 195_nt + 34199 34393	19 5	399 220 7	7	8.9 9	3.17	117 411 44	24	10.48	3.39	0.22	939 798 1	9	4.9 1	2.3	- 0.87	NA			
gene_886 GeneMark.hmm 306_nt + 34380 34685	30 6	399 220 7	59	48.3	5.59	117 411 44	186	51.77	5.69	0.1	939 798 1	118	41.03	5.36	- 0.23	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_887 GeneMark.hmm 450_nt + 34979 35428	45 0	399 220 7	40	22.27	4.48	117 411 44	284	53.75	5.75	1.27	939 798 1	159	37.6	5.23	0.75	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2490 GeneMark.hmm 123_nt - 1 123	12 3	399 220 7	0	0	0	117 411 44	225 8	15 63.54	10.6 1	10.6 1	939 798 1	117 68	10 18 0.3 6	13.3 1	13.3 1	NA			
gene_2450 GeneMark.hmm 120_nt + 2 121	12 0	399 220 7	0	0	0	117 411 44	276 8	19 64.6	10.9 4	10.9 4	939 798 1	120 48	10 68 3.1 5	13.3 8	13.3 8	NA			
gene_88 GeneMark.hmm 360_nt - 59564 59923	36 0	399 220 7	125	86.98	6.44	117 411 44	723	17 1.0 5	7.42	0.98	939 798 1	390	11 5.2 7	6.85	0.41	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_890 GeneMark.hmm 834_nt - 38754 39587	83 4	399 220 7	37	11.11	3.47	117 411 44	626	63.93	6	2.53	939 798 1	247	31.51	4.98	1.51	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V

gene_891 GeneMa rk.hmm 873_nt - 40459 41331	87 3	399 220 7	34	9.7 6	3.29	117 411 44	358	34. 93	5.13	1. 84	939 798 1	101	12. 31	3.62	0. 33	ABC-type multidrug transport system, ATPase and permease components	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_892 GeneMa rk.hmm 183_nt - 45442 45624	18 3	399 220 7	13	17. 79	4.15	117 411 44	146	67. 95	6.09	1. 94	939 798 1	31	18. 03	4.17	0. 02	NA			
gene_893 GeneMa rk.hmm 669_nt + 4 6248 46916	66 9	399 220 7	353	13 2.1 7	7.05	117 411 44	308 9	39 3.2 6	8.62	1. 57	939 798 1	228 4	36 3.2 7	8.5	1. 45	Collagenase and related proteases	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_894 GeneMa rk.hmm 648_nt - 130 777	64 8	399 220 7	100 79	38 96. 09	11.9 3	117 411 44	111 60	14 66. 83	10.5 2	- 1. 41	939 798 1	857 2	14 07. 58	10.4 6	- 1. 47	Acetyl esterase (deacetylase)	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_895 GeneMa rk.hmm 306_nt - 873 1178	30 6	399 220 7	277 4	22 70. 76	11.1 5	117 411 44	277 9	77 3.4 9	9.6	- 1. 55	939 798 1	589 9	20 51. 27	11	- 0. 15	Acetyl esterase (deacetylase)	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_896 GeneMa rk.hmm 555_nt - 1536 2090	55 5	399 220 7	394	17 7.8 2	7.47	117 411 44	926	14 2.1	7.15	- 0. 32	939 798 1	125 6	24 0.8	7.91	0. 44	RecG-like helicase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_897 GeneMa rk.hmm 1452_nt - 2152 3603	14 52	399 220 7	124 8	21 5.3	7.75	117 411 44	276 7	16 2.3 1	7.34	- 0. 41	939 798 1	463 0	33 9.3	8.41	0. 66	RecG-like helicase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_898 GeneMa rk.hmm 1104_nt - 3622 4725	11 04	399 220 7	130 3	29 5.6 4	8.21	117 411 44	227 1	17 5.2	7.45	- 0. 76	939 798 1	388 9	37 4.8 3	8.55	0. 34	Alanine racemase	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_899 GeneMa rk.hmm 369_nt - 4715 5083	36 9	399 220 7	506	34 3.4 9	8.42	117 411 44	108 6	25 0.6 6	7.97	- 0. 45	939 798 1	177 0	51 0.4	9	0. 58	Phosphopantetheinyl transferase (holo-ACP synthase)	METABOLISM	Lipid transport and metabolism	I
gene_89 GeneMar k.hmm 717_nt - 60144 60860	71 7	399 220 7	777	27 1.4 5	8.08	117 411 44	636 4	75 5.9 6	9.56	1. 48	939 798 1	539 0	79 9.9	9.64	1. 56	Zn-finger domain associated with topoisomerase type I	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_8 GeneMark. hmm 441_nt - 4469 4909	44 1	399 220 7	177	10 0.5 4	6.65	117 411 44	464	89. 61	6.49	- 0. 16	939 798 1	441	10 6.4 1	6.73	0. 08	ATPase involved in DNA repair	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_900 GeneMa rk.hmm 1032_nt - 5122 6153	10 32	399 220 7	344 1	83 5.2	9.71	117 411 44	464 1	38 3.0 2	8.58	- 1. 13	939 798 1	634 2	65 3.9	9.35	- 0. 36	3-deoxy-D-arabino-heptulosonate 7- phosphate (DAHP) synthase	METABOLISM	Amino acid transport and metabolism	E
gene_901 GeneMa rk.hmm 1032_nt - 6155 7186	10 32	399 220 7	206 7	50 1.7	8.97	117 411 44	424 1	35 0.0 1	8.45	- 0. 52	939 798 1	450 8	46 4.8	8.86	- 0. 11	3-deoxy-D-arabino-heptulosonate 7- phosphate (DAHP) synthase	METABOLISM	Amino acid transport and metabolism	E
gene_902 GeneMa rk.hmm 708_nt - 7267 7974	70 8	399 220 7	412 2	14 58. 35	10.5 1	117 411 44	676 7	81 4.0 5	9.67	- 0. 84	939 798 1	447 7	67 2.8 5	9.39	- 1. 12	Preprotein translocase subunit SecA (ATPase, RNA helicase)	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_903 GeneMa rk.hmm 342_nt -	34	399 220	374	27 3.9	8.1	117 411	107	26 8.2	8.07	- 0.	939 798	568	17 6.7	7.47	- 0.	Preprotein translocase subunit SecA	CELLULAR PROCESSES	Intracellular trafficking, secretion,	U

[8122 8463	2	7		3		44	7	1		03	1		2		63	(ATPase, RNA helicase)	AND SIGNALING	and vesicular transport	
gene_904 GeneMa rk.hmm 1425_nt - 8538 9962	14 25	399 220 7	470 9	82 7.7 5	9.69	117 411 44	921 1	55 0.5 3	9.1	- 0. 59	939 798 1	642 4	47 9.6 8	8.91	- 0. 78	Preprotein translocase subunit SecA (ATPase, RNA helicase)	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	U
gene_2487 GeneM ark.hmm 123_nt + 1 123	12 3	399 220 7	0	0	0	117 411 44	289 1	20 01. 85	10.9 7	10 .9 7	939 798 1	123 61	10 69 3.3 5	13.3 8	13 .3 8	NA			
gene_906 GeneMa rk.hmm 651_nt - 10406 11056	65 1	399 220 7	55	21. 16	4.4	117 411 44	696	91. 06	6.51	2. 11	939 798 1	452	73. 88	6.21	1. 81	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_2477 GeneM ark.hmm 120_nt - 2 121	12 0	399 220 7	0	0	0	117 411 44	295 9	21 00. 16	11.0 4	11 .0 4	939 798 1	144 01	12 76 9.5 9	13.6 4	13 .6 4	NA			
gene_908 GeneMa rk.hmm 792_nt - 11694 12485	79 2	399 220 7	61	19. 29	4.27	117 411 44	427	45. 92	5.52	1. 25	939 798 1	240	32. 24	5.01	0. 74	---	---	---	---
gene_909 GeneMa rk.hmm 393_nt - 12507 12899	39 3	399 220 7	74	47. 17	5.56	117 411 44	393	85. 17	6.41	0. 85	939 798 1	238	64. 44	6.01	0. 45	NA			
gene_90 GeneMar k.hmm 1365_nt - 60918 62282	13 65	399 220 7	213 1	39 1.0 5	8.61	117 411 44	147 81	92 2.2 8	9.85	1. 24	939 798 1	815 0	63 5.3 2	9.31	0. 7	Topoisomerase IA	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_910 GeneMa rk.hmm 852_nt + 1 3226 14077	85 2	399 220 7	440	12 9.3 6	7.02	117 411 44	976	97. 57	6.61	- 0. 41	939 798 1	503	62. 82	5.97	- 1. 05	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_911 GeneMa rk.hmm 345_nt - 14799 15143	34 5	399 220 7	42	30. 49	4.93	117 411 44	583	14 3.9 3	7.17	2. 24	939 798 1	309	95. 3	6.57	1. 64	---	---	---	---
gene_912 GeneMa rk.hmm 1311_nt - 15225 16535	13 11	399 220 7	973 4	18 59. 84	10.8 6	117 411 44	127 41	82 7.7 3	9.69	- 1. 17	939 798 1	132 42	10 74. 77	10.0 7	- 0. 79	Predicted GTPases	POORLY CHARACTERIZ ED	General function prediction only	R
gene_913 GeneMa rk.hmm 714_nt - 16549 17262	71 4	399 220 7	116 1	40 7.3 1	8.67	117 411 44	310 0	36 9.7 9	8.53	- 0. 14	939 798 1	369 2	55 0.2 1	9.1	0. 43	Nitroreductase	METABOLISM	Energy production and conversion	C
gene_914 GeneMa rk.hmm 897_nt - 17259 18155	89 7	399 220 7	123 0	34 3.4 8	8.42	117 411 44	344 8	32 7.3 9	8.35	- 0. 07	939 798 1	359 8	42 6.8 1	8.74	0. 32	DNA replication protein	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_915 GeneMa rk.hmm 1170_nt - 18156 19325	11 70	399 220 7	174 2	37 2.9 5	8.54	117 411 44	460 2	33 5	8.39	- 0. 15	939 798 1	508 0	46 2	8.85	0. 31	Replication initiation/membrane attachment protein	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_916 GeneMa rk.hmm 474_nt -	47 4	399 220	138 3	73 0.8	9.51	117 411	236 1	42 4.2	8.73	- 0.	939 798	245 2	55 0.4	9.1	- 0.	Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-	INFORMATION STORAGE AND	Transcription	K

[19326]19799		7		5		44		4		78	1		4		41	cone domains	PROCESSING		
gene_917[GeneMa rk.hmm 366_nt + 1 9939 20304	36 6	399 220 7	282 2	19 31. 36	10.9 2	117 411 44	542 2	12 61. 73	10.3	- 0. 62	939 798 1	116 05	33 73. 88	11.7 2	0. 8	Predicted transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_918[GeneMa rk.hmm 696_nt + 2 0309 21004	69 6	399 220 7	116 24	41 83. 44	12.0 3	117 411 44	128 63	15 74. 06	10.6 2	- 1. 41	939 798 1	278 08	42 51. 34	12.0 5	0. 02	ABC-type multidrug transport system, ATPase component	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	V
gene_919[GeneMa rk.hmm 768_nt + 2 1021 21788	76 8	399 220 7	599 7	19 55. 96	10.9 3	117 411 44	833 8	92 4.6 8	9.85	- 1. 08	939 798 1	133 42	18 48. 52	10.8 5	- 0. 08	---	---	---	---
gene_91[GeneMar k.hmm 945_nt - 62449 63393	94 5	399 220 7	647	17 1.5	7.42	117 411 44	250 0	22 5.3 2	7.82	0. 4	939 798 1	197 7	22 2.6 1	7.8	0. 38	Predicted membrane protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_920[GeneMa rk.hmm 1200_nt - 22141 23340	12 00	399 220 7	552	11 5.2 2	6.85	117 411 44	103 0	73. 1	6.19	- 0. 66	939 798 1	190 4	16 8.8 3	7.4	0. 55	ABC-type Na+ efflux pump, permease component	METABOLISM	Energy production and conversion	C
gene_921[GeneMa rk.hmm 894_nt - 23337 24230	89 4	399 220 7	652	18 2.6 8	7.51	117 411 44	797	75. 93	6.25	- 1. 26	939 798 1	172 1	20 4.8 4	7.68	0. 17	ABC-type uncharacterized transport system, ATPase component	POORLY CHARACTERIZ ED	General function prediction only	R
gene_922[GeneMa rk.hmm 618_nt + 2 5601 26218	61 8	399 220 7	118 1	47 8.6 8	8.9	117 411 44	289 6	39 9.1 2	8.64	- 0. 26	939 798 1	282 8	48 6.9 2	8.93	0. 03	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_923[GeneMa rk.hmm 888_nt - 26261 27148	88 8	399 220 7	568	16 0.2 2	7.32	117 411 44	243 1	23 3.1 6	7.87	0. 55	939 798 1	441 3	52 8.7 9	9.05	1. 73	Transcriptional regulator/sugar kinase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_924[GeneMa rk.hmm 1938_nt - 27297 29234	19 38	399 220 7	761	98. 36	6.62	117 411 44	303 7	13 3.4 7	7.06	0. 44	939 798 1	174 17	95 6.2 8	9.9	3. 28	Phosphotransferase system IIC components, glucose/maltose/N- acetylglucosamine-specific	METABOLISM	Carbohydrate transport and metabolism	G
gene_925[GeneMa rk.hmm 1455_nt + 29610 31064	14 55	399 220 7	858	14 7.7 1	7.21	117 411 44	136 8	80. 08	6.32	- 0. 89	939 798 1	149 72	10 94. 92	10.1	2. 89	Beta-fructosidases (levanase/invertase)	METABOLISM	Carbohydrate transport and metabolism	G
gene_926[GeneMa rk.hmm 966_nt + 3 1045 32010	96 6	399 220 7	885	22 9.4 8	7.84	117 411 44	123 3	10 8.7 1	6.76	- 1. 08	939 798 1	220 43	24 28. 06	11.2 5	3. 41	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_927[GeneMa rk.hmm 1275_nt - 32045 33319	12 75	399 220 7	462 9	90 9.4 2	9.83	117 411 44	211 43	14 12. 36	10.4 6	0. 63	939 798 1	173 16	14 45. 12	10.5	0. 67	Hydroxymethylglutaryl-CoA reductase	METABOLISM	Lipid transport and metabolism	I
gene_928[GeneMa rk.hmm 1173_nt - 33319 34491	11 73	399 220 7	178 5	38 1.1 8	8.57	117 411 44	952 7	69 1.7 5	9.43	0. 86	939 798 1	433 4	39 3.1 5	8.62	0. 05	3-hydroxy-3-methylglutaryl CoA synthase	METABOLISM	Lipid transport and metabolism	I
gene_929[GeneMa rk.hmm 288_nt - 34622 34909	28 8	399 220 7	64	55. 66	5.8	117 411 44	517	15 2.8 9	7.26	1. 46	939 798 1	472	17 4.3 9	7.45	1. 65	---	---	---	---
gene_92[GeneMar k.hmm 228_nt -	22 8	399 220	24	26. 37	4.72	117 411	166	62. 01	5.95	1. 23	939 798	224	10 4.5	6.71	1. 99	Predicted Rossmann fold nucleotide-binding protein involved	INFORMATION STORAGE AND	Replication, recombination and repair	L

[64374 64601		7				44					1		4			in DNA uptake	PROCESSING		
gene_930 GeneMa rk.hmm 330_nt - 34938 35267	33 0	399 220 7	282	21 4.0 5	7.74	117 411 44	114 8	29 6.2 9	8.21	0. 47	939 798 1	106 2	34 2.4 3	8.42	0. 68	Transposase and inactivated derivatives	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_931 GeneMa rk.hmm 285_nt - 35341 35625	28 5	399 220 7	173	15 2.0 5	7.25	117 411 44	768	22 9.5 1	7.84	0. 59	939 798 1	414	15 4.5 7	7.27	0. 02	---	---	---	---
gene_932 GeneMa rk.hmm 450_nt - 35690 36139	45 0	399 220 7	321	17 8.6 8	7.48	117 411 44	110 2	20 8.5 7	7.7	0. 22	939 798 1	764	18 0.6 5	7.5	0. 02	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_933 GeneMa rk.hmm 759_nt - 36141 36899	75 9	399 220 7	963	31 7.8 1	8.31	117 411 44	215 2	24 1.4 8	7.92	- 0. 39	939 798 1	116 6	16 3.4 6	7.35	- 0. 96	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_934 GeneMa rk.hmm 1980_nt - 37014 38993	19 80	399 220 7	141 07	17 84. 66	10.8	117 411 44	272 72	11 73. 12	10.2	- 0. 6	939 798 1	263 73	14 17. 29	10.4 7	- 0. 33	Serine/threonine protein kinase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_935 GeneMa rk.hmm 741_nt - 38990 39730	74 1	399 220 7	146 2	49 4.2 2	8.95	117 411 44	355 0	40 8.0 4	8.67	- 0. 28	939 798 1	273 0	39 2.0 2	8.61	- 0. 34	Serine/threonine protein phosphatase	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	T
gene_936 GeneMa rk.hmm 1317_nt - 39745 41061	13 17	399 220 7	115 0	21 8.7 3	7.77	117 411 44	293 8	19 0	7.57	- 0. 2	939 798 1	318 1	25 7.0 1	8.01	0. 24	tRNA and rRNA cytosine-C5- methylases	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_937 GeneMa rk.hmm 936_nt - 41051 41986	93 6	399 220 7	628	16 8.0 6	7.39	117 411 44	126 4	11 5.0 2	6.85	- 0. 54	939 798 1	163 6	18 5.9 8	7.54	0. 15	Methionyl-tRNA formyltransferase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_938 GeneMa rk.hmm 426_nt - 41999 42424	42 6	399 220 7	610	35 8.6 8	8.49	117 411 44	895	17 8.9 4	7.48	- 1. 01	939 798 1	150 3	37 5.4 2	8.55	0. 06	Primosomal protein N' (replication factor Y) - superfamily II helicase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_939 GeneMa rk.hmm 1962_nt - 42485 44446	19 62	399 220 7	776	99. 07	6.63	117 411 44	173 2	75. 19	6.23	- 0. 4	939 798 1	224 9	12 1.9 7	6.93	0. 3	Primosomal protein N' (replication factor Y) - superfamily II helicase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_2486 GeneM ark.hmm 120_nt + 3 122	12 0	399 220 7	0	0	0	117 411 44	273 8	19 43. 31	10.9 2	10 .9 2	939 798 1	147 65	13 09 2.3 5	13.6 8	13 .6 8	NA			
gene_940 GeneMa rk.hmm 315_nt - 44512 44826	31 5	399 220 7	213 2	16 95. 37	10.7 3	117 411 44	365 8	98 9.0 6	9.95	- 0. 78	939 798 1	296 4	10 01. 23	9.97	- 0. 76	DNA-directed RNA polymerase, subunit K/omega	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_941 GeneMa rk.hmm 627_nt - 44851 45477	62 7	399 220 7	281 1	11 23	10.1 3	117 411 44	622 5	84 5.5 9	9.72	- 0. 41	939 798 1	514 1	87 2.4 6	9.77	- 0. 36	Guanylate kinase	METABOLISM	Nucleotide transport and metabolism	F
gene_942 GeneMa rk.hmm 1614_nt - 45607 47220	16 14	399 220 7	116 30	18 04. 94	10.8 2	117 411 44	309 15	16 31. 38	10.6 7	- 0. 15	939 798 1	146 23	96 4.0 5	9.91	- 0. 91	Predicted HD superfamily hydrolase	POORLY CHARACTERIZ ED	General function prediction only	R
gene_943 GeneMa rk.hmm 255_nt -	25	399 220	174	17 0.9	7.42	117 411	949	31 6.9	8.31	0.	939 798	211	88.	6.46	- 0.	Antitoxin of toxin-antitoxin stability	CELLULAR PROCESSES	Cell cycle control, cell division,	D

47669 47923	5	7		2		44		7		89	1		05		96	system	AND SIGNALING	chromosome partitioning	
gene_944 GeneMark.hmm 1098_nt - 48161 49258	1098	3992207	1414	322.58	8.33	11741144	3524	273.35	8.09	-0.24	9397981	3929	380.75	8.57	0.24	Predicted nucleotidyltransferase	POORLY CHARACTERIZED	General function prediction only	R
gene_945 GeneMark.hmm 741_nt - 49268 50008	741	3992207	518	175.1	7.45	11741144	1908	219.31	7.78	0.33	9397981	1911	274.42	8.1	0.65	SAM-dependent methyltransferases	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_946 GeneMark.hmm 354_nt - 50328 50681	354	3992207	352	249.07	7.96	11741144	1178	283.42	8.15	0.19	9397981	1414	425.02	8.73	0.77	Uncharacterized homolog of plant lojap protein	POORLY CHARACTERIZED	Function unknown	S
gene_947 GeneMark.hmm 501_nt - 50694 51194	501	3992207	600	299.99	8.23	11741144	1583	269.11	8.07	-0.16	9397981	2015	427.96	8.74	0.51	Amidases related to nicotinamidase	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	Q
gene_948 GeneMark.hmm 594_nt - 51195 51788	594	3992207	870	366.88	8.52	11741144	1877	269.13	8.07	-0.45	9397981	2709	485.28	8.92	0.4	Predicted HD superfamily hydrolase involved in NAD metabolism	METABOLISM	Coenzyme transport and metabolism	H
gene_949 GeneMark.hmm 630_nt - 51788 52417	630	3992207	873	347.1	8.44	11741144	1677	226.72	7.82	-0.62	9397981	2144	362.12	8.5	0.06	Nicotinic acid mononucleotide adenylyltransferase	METABOLISM	Coenzyme transport and metabolism	H
gene_94 GeneMark.hmm 690_nt - 65354 66043	690	3992207	1747	634.21	9.31	11741144	9950	1228.18	10.26	0.95	9397981	8070	1244.49	10.28	0.97	CTP:phosphocholine cytidyltransferase involved in choline phosphorylation for cell surface LPS epitopes	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_950 GeneMark.hmm 312_nt - 52469 52780	312	3992207	241	193.49	7.6	11741144	844	230.4	7.85	0.25	9397981	912	311.03	8.28	0.68	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_951 GeneMark.hmm 1107_nt - 52995 54101	1107	3992207	1894	428.57	8.74	11741144	5258	404.54	8.66	-0.08	9397981	5512	529.82	9.05	0.31	Predicted GTPases	POORLY CHARACTERIZED	General function prediction only	R
gene_952 GeneMark.hmm 528_nt - 54104 54631	528	3992207	932	442.15	8.79	11741144	1650	266.16	8.06	-0.73	9397981	1648	332.12	8.38	-0.41	Predicted hydrolase of the HAD superfamily	POORLY CHARACTERIZED	General function prediction only	R
gene_953 GeneMark.hmm 909_nt - 54646 55554	909	3992207	1849	509.52	8.99	11741144	5429	508.68	8.99	0	9397981	4523	529.45	9.05	0.06	Mg2+ and Co2+ transporters	METABOLISM	Inorganic ion transport and metabolism	P
gene_954 GeneMark.hmm 561_nt - 55611 56171	561	3992207	501	223.7	7.81	11741144	1795	272.52	8.09	0.28	9397981	884	167.67	7.39	-0.42	Small-conductance mechanosensitive channel	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_955 GeneMark.hmm 81_nt + 56310 56390	81	3992207	0	0	0	11741144	0	0	0	0	9397981	0	0	0	0	NA			
gene_2433 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	3077	2183.92	11.09	11.09	9397981	15567	13803.5	13.75	13.75	NA			

gene_2481 GeneMark.hmm 120_nt + 3 122	120	3992207	0	0	0	11741144	3013	2138.49	11.06	11.06	9397981	15755	13970.2	13.77	13.77	NA			
gene_2459 GeneMark.hmm 120_nt + 2 121	120	3992207	0	0	0	11741144	3110	2207.34	11.11	11.11	9397981	16174	14341.73	13.81	13.81	NA			
gene_959 GeneMark.hmm 381_nt + 58683 59063	381	3992207	989	650.22	9.34	11741144	3659	817.95	9.68	0.34	9397981	2014	562.47	9.14	-0.2	Transcriptional regulators	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_95 GeneMark.hmm 807_nt - 66055 66861	807	3992207	2436	756.12	9.56	11741144	10908	1151.23	10.17	0.61	9397981	8951	1180.22	10.2	0.64	Permeases of the drug/metabolite transporter (DMT) superfamily	METABOLISM	Carbohydrate transport and metabolism	G
gene_960 GeneMark.hmm 222_nt + 59162 59383	222	3992207	15475	17460.82	14.09	11741144	33322	12784.03	13.64	-0.45	9397981	13745	6588.05	12.69	-1.4	---	---	---	---
gene_961 GeneMark.hmm 315_nt + 59400 59714	315	3992207	18193	14467.07	13.82	11741144	26905	7274.65	12.83	-0.99	9397981	8441	2851.34	11.48	-2.34	Thiol-disulfide isomerase and thioredoxins	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	O
gene_962 GeneMark.hmm 534_nt + 60019 60552	534	3992207	441	206.86	7.69	11741144	2100	334.94	8.39	0.7	9397981	1576	314.04	8.29	0.6	Enzyme related to GTP cyclohydrolase I	POORLY CHARACTERIZED	General function prediction only	R
gene_963 GeneMark.hmm 669_nt - 61225 61893	669	3992207	1337	500.6	8.97	11741144	3955	503.51	8.98	0.01	9397981	3014	479.38	8.91	-0.06	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	METABOLISM	Carbohydrate transport and metabolism	G
gene_964 GeneMark.hmm 369_nt - 62190 62558	369	3992207	42	28.51	4.83	11741144	417	96.25	6.59	1.76	9397981	603	173.88	7.44	2.61	---	---	---	---
gene_2445 GeneMark.hmm 123_nt - 1 123	123	3992207	0	0	0	11741144	3526	2441.56	11.25	11.25	9397981	16804	14536.94	13.83	13.83	NA			
gene_966 GeneMark.hmm 486_nt - 62805 63290	486	3992207	217	11.84	6.81	11741144	899	157.5	7.3	0.49	9397981	1302	285.06	8.16	1.35	Oligoendopeptidase F	METABOLISM	Amino acid transport and metabolism	E
gene_967 GeneMark.hmm 1308_nt - 63353 64660	1308	3992207	926	177.33	7.47	11741144	2849	185.51	7.54	0.07	9397981	4896	398.29	8.64	1.17	Oligoendopeptidase F	METABOLISM	Amino acid transport and metabolism	E
gene_968 GeneMark.hmm 744_nt - 64671 65414	744	3992207	430	144.77	7.18	11741144	1252	143.32	7.16	-0.02	9397981	2328	332.95	8.38	1.2	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_969 GeneMark.hmm 978_nt - 65416 66393	978	3992207	252	64.54	6.01	11741144	1010	87.96	6.46	0.45	9397981	1482	161.24	7.33	1.32	Ribosomal protein L11 methylase	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_96 GeneMark.hmm 69_nt -	69	399220	0	0	0	117411	0	0	0	0	939798	0	0	0	0	Permeases of the drug/metabolite	METABOLISM	Carbohydrate transport and	G

[66912 66980		7				44					1					transporter (DMT) superfamily		metabolism	
gene_970 GeneMa rk.hmm 429_nt - 66504 66932	42 9	399 220 7	78	45. 54	5.51	117 411 44	304	60. 35	5.92	0. 41	939 798 1	482	11 9.5 5	6.9	1. 39	NTP pyrophosphohydrolases including oxidative damage repair enzymes	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_971 GeneMa rk.hmm 1089_nt - 66913 68001	10 89	399 220 7	184	42. 32	5.4	117 411 44	106 9	83. 61	6.39	0. 99	939 798 1	131 7	12 8.6 8	7.01	1. 61	---	---	---	---
gene_972 GeneMa rk.hmm 471_nt - 68020 68490	47 1	399 220 7	53	28. 19	4.82	117 411 44	279	50. 45	5.66	0. 84	939 798 1	259	58. 51	5.87	1. 05	---	---	---	---
gene_973 GeneMa rk.hmm 453_nt - 68781 69233	45 3	399 220 7	115 1	63 6.4 5	9.31	117 411 44	241 3	45 3.6 8	8.83	- 0. 48	939 798 1	193 2	45 3.8 1	8.83	- 0. 48	Uncharacterized conserved protein	POORLY CHARACTERIZ ED	Function unknown	S
gene_974 GeneMa rk.hmm 174_nt - 69270 69443	17 4	399 220 7	660	95 0.1 3	9.89	117 411 44	392	19 1.8 8	7.58	- 2. 31	939 798 1	103 7	63 4.1 5	9.31	- 0. 58	---	---	---	---
gene_975 GeneMa rk.hmm 108_nt - 69586 69693	10 8	399 220 7	1	2.3 2	1.21	117 411 44	12	9.4 6	3.24	2. 03	939 798 1	3	2.9 6	1.56	0. 35	NA			
gene_2416 GeneM ark.hmm 123_nt - 1 123	12 3	399 220 7	0	0	0	117 411 44	365 3	25 29. 5	11.3	11 .3	939 798 1	170 31	14 73 3.3 2	13.8 5	13 .8 5	NA			
gene_977 GeneMa rk.hmm 1272_nt + 70439 71710	12 72	399 220 7	185 2	36 4.7	8.51	117 411 44	112 97	75 6.4 2	9.56	1. 05	939 798 1	707 2	59 1.5 9	9.21	0. 7	ATPase related to the helicase subunit of the Holliday junction resolvase	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L
gene_978 GeneMa rk.hmm 534_nt - 72256 72789	53 4	399 220 7	77	36. 12	5.17	117 411 44	549	87. 56	6.45	1. 28	939 798 1	564	11 2.3 8	6.81	1. 64	Beta-fructosidases (levanase/invertase)	METABOLISM	Carbohydrate transport and metabolism	G
gene_979 GeneMa rk.hmm 783_nt - 72852 73634	78 3	399 220 7	195	62. 38	5.96	117 411 44	116 9	12 7.1 6	6.99	1. 03	939 798 1	120 8	16 4.1 6	7.36	1. 4	Beta-fructosidases (levanase/invertase)	METABOLISM	Carbohydrate transport and metabolism	G
gene_97 GeneMar k.hmm 870_nt - 66970 67839	87 0	399 220 7	203 7	58 6.4 9	9.2	117 411 44	122 19	11 96. 21	10.2 2	1. 02	939 798 1	109 08	13 34. 11	10.3 8	1. 18	Predicted choline kinase involved in LPS biosynthesis	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	M
gene_980 GeneMa rk.hmm 1617_nt - 73644 75260	16 17	399 220 7	249	38. 57	5.27	117 411 44	131 5	69. 26	6.11	0. 84	939 798 1	190 1	12 5.0 9	6.97	1. 7	ABC-type sugar transport system, periplasmic component	METABOLISM	Carbohydrate transport and metabolism	G
gene_981 GeneMa rk.hmm 891_nt - 75289 76179	89 1	399 220 7	156	43. 86	5.45	117 411 44	816	78	6.29	0. 84	939 798 1	903	10 7.8 4	6.75	1. 3	ABC-type sugar transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_982 GeneMa rk.hmm 918_nt - 76190 77107	91 8	399 220 7	66	18. 01	4.17	117 411 44	572	53. 07	5.73	1. 56	939 798 1	123 0	14 2.5 7	7.16	2. 99	ABC-type polysaccharide transport system, permease component	METABOLISM	Carbohydrate transport and metabolism	G
gene_983 GeneMa rk.hmm 1002_nt -	10	399 220	965	24 1.2	7.91	117 411	711	60 4.9	9.24	1.	939 798	684	72 6.7	9.51	1.	Transcriptional regulators	INFORMATION STORAGE AND	Transcription	K

[77256 78257	02	7		4		44	7	5		33	1	4	9		6		PROCESSING		
gene_2453 GeneMark.hmm 120_nt - 2 121	120	3992207	0	0	0	11741144	3011	2137.07	11.06	11.06	9397981	16726	14831.2	13.86	13.86	NA			
gene_985 GeneMark.hmm 165_nt + 80543 80707	165	3992207	1098	1666.88	10.7	11741144	2128	1098.44	10.1	0.6	9397981	2345	1512.25	10.56	-0.14	Predicted membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_986 GeneMark.hmm 393_nt + 80965 81357	393	3992207	1131	720.87	9.49	11741144	3616	783.66	9.61	0.12	9397981	3228	873.99	9.77	0.28	---	---	---	---
gene_987 GeneMark.hmm 171_nt + 81369 81539	171	3992207	517	757.32	9.56	11741144	973	484.63	8.92	-0.64	9397981	423	263.21	8.04	-1.52	Small integral membrane protein	POORLY CHARACTERIZED	Function unknown	S
gene_988 GeneMark.hmm 609_nt + 81578 82186	609	3992207	8453	3476.81	11.76	11741144	15019	2100.45	11.04	-0.72	9397981	9570	1672.09	10.71	-1.05	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_989 GeneMark.hmm 204_nt + 82217 82420	204	3992207	3382	4152.7	12.02	11741144	8612	3595.53	11.81	-0.21	9397981	5605	2923.55	11.51	-0.51	Uncharacterized protein conserved in bacteria	POORLY CHARACTERIZED	Function unknown	S
gene_98 GeneMark.hmm 1023_nt - 67856 68878	1023	3992207	1380	337.9	8.4	11741144	11964	996.07	9.96	1.56	9397981	11143	1159.02	10.18	1.78	Threonine dehydrogenase and related Zn-dependent dehydrogenases	METABOLISM	Amino acid transport and metabolism	E
gene_990 GeneMark.hmm 849_nt - 84356 85204	849	3992207	110	32.45	5.02	11741144	410	41.13	5.36	0.34	9397981	343	42.99	5.43	0.41	Uncharacterized conserved protein	POORLY CHARACTERIZED	Function unknown	S
gene_991 GeneMark.hmm 1476_nt - 85201 86676	1476	3992207	258	43.78	5.45	11741144	697	40.22	5.33	-0.12	9397981	450	32.44	5.02	-0.43	Arylsulfatase A and related enzymes	METABOLISM	Inorganic ion transport and metabolism	P
gene_992 GeneMark.hmm 1356_nt - 86999 88354	1356	3992207	60	11.08	3.47	11741144	522	32.79	5.04	1.57	9397981	348	27.31	4.77	1.3	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G
gene_993 GeneMark.hmm 318_nt - 88364 88681	318	3992207	49	38.6	5.27	11741144	314	84.1	6.39	1.12	9397981	144	48.18	5.59	0.32	Phosphotransferase system cellobiose-specific component IIA	METABOLISM	Carbohydrate transport and metabolism	G
gene_994 GeneMark.hmm 111_nt - 88698 88808	111	3992207	0	0	0	11741144	2	1.53	0.62	0.62	9397981	0	0	0	0	NA			
gene_2489 GeneMark.hmm 123_nt - 1 123	123	3992207	0	0	0	11741144	4490	3109.07	11.6	11.6	9397981	21155	18300.94	14.16	14.16	NA			
gene_996 GeneMark.hmm 897_nt - 89099 89995	897	3992207	46	12.85	3.68	11741144	389	36.94	5.21	1.53	9397981	217	25.74	4.69	1.01	---	---	---	---
gene_997 GeneMark.hmm 1263_nt -	1263	399220	32	6.35	2.67	117411	406	27.38	4.77	2.1	939798	205	17.27	4.11	1.44	Phosphotransferase system cellobiose-specific component IIC	METABOLISM	Carbohydrate transport and metabolism	G

89998 91260		7				44					1								
gene_998 GeneMark.hmm 1179_nt + 91540 92718	1179	3992207	238	50.57	5.66	11741144	1166	84.23	6.4	0.74	9397981	390	35.2	5.14	-0.52	Transcriptional regulator/sugar kinase	INFORMATION STORAGE AND PROCESSING	Transcription	K
gene_999 GeneMark.hmm 447_nt - 92946 93392	447	3992207	25	14.01	3.81	11741144	229	43.63	5.45	1.64	9397981	107	25.47	4.67	0.86	Acetyltransferases, including N-acetylases of ribosomal proteins	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	J
gene_99 GeneMark.hmm 708_nt - 68883 69590	708	3992207	1438	508.76	8.99	11741144	8279	995.94	9.96	0.97	9397981	7116	1069.47	10.06	1.07	4-diphosphocytidyl-2-methyl-D-erithritol synthase	METABOLISM	Lipid transport and metabolism	I
gene_9 GeneMark.hmm 198_nt - 5019 5216	198	3992207	43	54.4	5.77	11741144	129	55.49	5.79	0.02	9397981	197	105.87	6.73	0.96	ATPase involved in DNA repair	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	L

SupplementaryTable 2: RPKMO value of each gene Table: RPKMO value of each gene