

# Research and Reviews: Journal of Botanical Science

## Extraction and Molecular Modeling of Phytohormones from Medicinal Plants

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### Review Article

### ABSTRACT

Received: 20/03/2017

Revised: 24/03/2017

Accepted: 29/03/2017

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**Keywords:** Phytohormones, Extraction,  
biomaterials, Medicinal Plants

In recent decades, phytohormones came up as suitable alternate for various severe diseases but as amount of phytohormone present and less availability of medicinal plants has made extraction as well as molecular modeling and chemical synthesis of the drug like molecule with the help of protein bioinformatics, modeling techniques and molecular dynamics simulation. Current review article focuses a brief insight on the process and possible step associated with it.

### INTRODUCTION

Phytohormones are the plant growth substances, which actually controls compete growth and form of a plant. These regulators plays vital role in growth of leaves, stems, sex differentiation of flowers and senescence of leaves, or fruit. They are present in a plant with very low concentration. These are mostly concerned with higher plants, but their presence cannot be ignored in lower plants like algae, fungi and even microorganisms like bacteria. But in these cases, these do not play a significant role in direct physiological activities and hence termed as secondary metabolite <sup>[1-8]</sup>.

#### Medicinal Aspect

Modern molecular and genetic analysis gives us an idea about understanding of techniques and possible application of these phytohormones. These phytohormones are biomolecules possessing same kind of effect to alter physiological activities at cellular level. These molecules resemble with many drug like molecules or in most of the cases almost same structure compatible to target sites <sup>[9,10]</sup>.

#### Review of literature

Melatonin is known to be produced by plants and to exert numerous effects, which overlap with actions of known phytohormones, including auxins, ethylene, abscisic, jasmonic and salicylic acids. It exhibits growth effects, alleviates stress by heat, cold, drought, and toxic chemicals, counteracts infections by bacterial or fungal pathogens, favours wound healing, delays senescence and acts as an antioxidant and photoprotectant. Stressors and intense radiation frequently induce substantial increases in melatonin. High levels are particularly found in oily seeds. The criteria are discussed which have to be fulfilled before melatonin might be classified as a phytohormone. These include, in particular, the identification of high-affinity binding sites, of components of signal transduction pathways, the determination of freely movable melatonin and its movements within the organism <sup>[11-17]</sup>.

Abiotic stresses, primarily drought, salinity, heat, cold, flooding and ultra-violet rays are causing widespread crop losses worldwide. Because of the complexity of the stress-tolerance traits, conventional breeding techniques have met with little success in fulfilling the world food demands. Therefore, to face the abiotic stresses, novel and potent approaches should be devised and engineering of phytohormones could be a method of choice to increase the crop productivity [18-21].

Development of more advanced and functional biomaterials has been an ongoing challenge in the last decades towards the benefit of millions of patients worldwide that need to be treated with biomaterial-based therapies. The ability of individual polymers to respond to changes in pH, temperature, electric or magnetic fields, together with the possibility of combining different polymers, is a strategy largely pursued in the field [22-25].

This review examines contemporary views of the role of plant hormones in the control of physiological processes. Past and present difficulties with nomenclature encapsulate the problems inherent in using the 'classic' hormone concept in plants, with their distinctive multicellular organization. Chemical control may be a more relevant notion. However, control may also reside in the responding tissue via changes in sensitivity, or as combined control, where response is dictated by both sensitivity and concentration [26-29].

While animals and plants appear to have coinherited homologous intracellular signalling systems, at the whole organism level modes of hormone action may diverge. It is postulated that the synthesis-transport-action mechanism of action may be just one of several possible ways that phytohormones could control physiological processes. Twelve separate roles are discussed, and it is suggested that some of these could operate simultaneously to the plant's advantage [30-36].

## Molecular modeling

Molecular modeling is one of the basic and preliminary steps for target based drug designing or medicinal research. In this step we need to model a ligand molecule according to the target site compatibility. The designed chemical formula is first exposed to 2-D formulation and structure, after that we convert that two-dimensional structure to 3-D models. After determination of chemical molecules structure in 3-D, the process of rotation starts, where we check most stable conformation space where binding with molecule would be most thermodynamic stable in terms of free energy [37-41].

Another aspect would be computational chemistry calculation where we check compatibility according to the quantum mechanics as well as classical mechanics. During which quantum mechanics can be based on the method like ab initio, density functional theory or semi-empirical method, while classical mechanics would be primarily based on molecular mechanic and molecular dynamics study or monte carlo methods [42-56].

After all, prediction of molecular property would be based on mainly structural, chemical, physical and biological. So, that we can easily understand, explain and predict about chemical process [47]. Next step we go for a force field calculation, which differs from molecule to molecule. Force fields are mathematical expression that describes the dependence of the energy of a molecule on the coordinates of the atoms in the molecule (**Table 1**).

MM2/MM3/MM4	Molecular Mechanic Force field for small organic molecules
CHARMM	Chemistry at Harvard Macromolecular Mechanics
AMBER	Assisted Model Building with Energy Refinement
OPLS	Optimized Parameters for Liquid Simulation
CFF	Consistent Force Field
CVFF	Valence Consistent Force Field
MMFF94	Merck Molecular Force Field 94
DREIDING	Generic rules based force field
UFF	Universal Force Field
ReaxFF	Speciality force-field to allow bond breaking

**Table 1.** Common Force Fields.

Force Fields differ in their parameters, terms and the method of development, according to that we may classify them as below:

1. Class I - simple functional form with data fitted to quantum mechanical calculations and/or experiment (AMBER, CHARMM)
2. Class II - more complicated functional form using cross terms and data fitted to quantum mechanical calculations and/or experiment (CFF, PCFF)
3. Class III - new generation force fields that incorporate polarizability (AMOEBA, AMBER ff02, CHARMM Drude)
4. Rules Based - covers most of the periodic table – UFF, DREIDING
5. Fundamental quantities are derived for each atom type: electronegativity, hardness, atomic radius
6. Forcefield parameters are derived at runtime using a series of theoretically or empirically derived rules  
Specialist - developed for a particular family of compounds fluorinated polymers, zeolites
7. Reaction Forcefields - ReaxFF

## Energy minimization strategies and methods

Energy minimization strategies and methods can be implemented and understood at two different levels of local minima and global minima. Minimization methods mainly optimize the molecule and provide the closest local minimum possible (**Figure 1**). To find global minimum we may use systematic conformational searches, but it is very time consuming and nearly impossible to imply with smaller molecules. Another method may be molecular dynamics, Monte Carlo method, random sampling [57-77].

- Minimize the potential energy

$$E = E_{\text{bond}} + E_{\text{angle}} + E_{\text{torsion}} + E_{\text{oop}} + E_{\text{nonbond}} + E_{\text{other}}$$

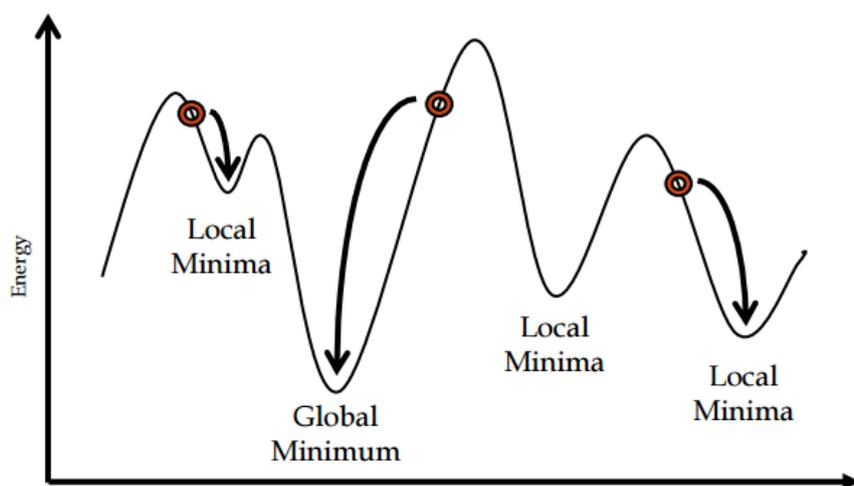


Figure 1. Energy minimization in terms of potential energy.

## Molecular dynamic simulation

Molecular dynamics can also be better understood in terms of high temperature dynamics, which can be checked under simulated annealing and quench dynamics. Molecular Dynamics Variations can also be measured on basis of three basic classifications as

- Constant Volume - Constant Temperature (NVT)
- Constant Volume - Constant Energy (NVE)
- Constant Pressure – Constant Temperature (NPT)

Most simulations are on the order of picoseconds (10<sup>-12</sup> s) or nanoseconds (10<sup>-9</sup> s) while running on system. Overall during process we prepare the model, then minimization process is done, heating would also be implement and checked for equilibrium with NVE and simulation would be run for all NVT, NVE, and NPT.

After this process solvation test would be performed for both explicit as well as dielectric models. Next would be informatics searches and bioinformatics implementation to the study [78-95].

We would make a cross check with already available databases for phytohormones and on the basis of structure, properties and activities. After that we can go for Combinatorial Chemistry and start comparing structure with modeled molecules. Protein bioinformatics and QSAR- Quantitative Structure Activity Relationships will also play major role in designing with help of comparative studies of biological activity and structural similarity along with conformational stability and structural compatibility [96-100].

## Conclusion

Molecular modeling and molecular dynamics simulation plays a driving role in designing and extraction from medicinal plants. We cannot rely much on the extraction, as number of plants is very less and moreover the amount of phytohormones getting extracted also is very low. Mostly we go for a molecular modeling for higher amount of these chemical molecules at production level.

## Acknowledgements

I would like to acknowledge help and continuous support from my co-authors Anurashree verma and Deepti Kumari during complete drafting of the review and valuable inputs from them.

## References

1. Sheehan D. Next-generation genome sequencing makes non-model organisms increasingly accessible for proteomic studies: some implications for ecotoxicology. *J Proteomics Bioinform.* 2013;6:e21.
2. Morya VK. Open access biological information: deeds of need. *J Proteomics Bioinform.* 2012;5: i-i.
3. Weier HUG. Bioinformatics for high throughput sequencing. *J Data Mining Genomics Proteomics.* 2013;4:e108.
4. Amigo J, et al. GDF: Dealing with Highthroughput Genotyping Multiplatform Data for Medical and Population Genetic Applications. *J Proteomics Bioinform.* 2012;5:001-006.
5. Hsiao ESL, et al. Proteomics investigation reveals apoptosis-associated proteins in aryl hydrocarbon receptor-deficient human lung cells treated with 2,3,7,8-tetrachlorobenzo-p-dioxin. *J Proteomics Bioinform* 2012;5:015-023.
6. Naghizadeh S, et al. A modified hidden markov model and its application in protein secondary structure prediction. *J Proteomics Bioinform* 2012;5:024-030.
7. Simpson RJ and Mathivanan S. Extracellular microvesicles: the need for internationally recognised nomenclature and stringent purification criteria. *J Proteomics Bioinform* 2012;5: ii-ii.
8. Petushkova NA, et al. Optimization of the SDS-PAGE gel slicing approach for identification of human liver microsomal proteins via MALDI-TOF mass spectrometry. *J Proteomics Bioinform* 2012;5:040-049.
9. Hashemi M, et al. Evaluating new targets of natural anticancer molecules through bioinformatics tools. *J Proteomics Bioinform* 2012;5:050-053.
10. Bora L. Homology modeling and docking to potential novel inhibitor for chikungunya (37997) protein nsP2 protease. *J Proteomics Bioinform* 2012;5:054-059.
11. Khan A and Khan AU. Biomarker discovery and drug development: a proteomics approach. *J Proteomics Bioinform* 2012;5:v-vi.
12. Luo M, et al. High fat diet- induced changes in hepatic protein abundance in Mice. *J Proteomics Bioinform.* 2012;5:060-066.
13. Wang Z, et al. Identifying differential gene sets using the linear combination of genes with maximum AUC. *J Proteomics Bioinform.* 2012;5:073-083.
14. Sharma OP, et al. Structural epitope database (SEDB): a web-based database for the epitope, and its intermolecular interaction along with the tertiary structure information. *J Proteomics Bioinform.* 2012;5:084-089.

15. Nadarajah VD, et al. Serum peptide profiles of duchenne muscular dystrophy (DMD) patients evaluated by data handling strategies for high resolution content. *J Proteomics Bioinform.* 2012;5: 096-103.
16. Edwards AVG, et al. Reportsites - a computational method to extract positional and physico-chemical information from large-scale proteomic post-translational modification datasets. *J Proteomics Bioinform.* 2012;5:104-107.
17. Galindo RC and de la Fuente J. Transcriptomics data integration reveals jak-STAT as a common pathway affected by pathogenic intracellular bacteria in natural reservoir hosts. *J Proteomics Bioinform.* 2012;5:108-115.
18. Erdoğan H and Apaydın MS. Incorporating amino acid typing into nuclear magnetic resonance protein structure-based assignments. *J Proteomics Bioinform.* 2012;5:116-121.
19. Lakshmanan J, et al. Proteomic analysis of rat prefrontal cortex after chronic lithium treatment. *J Proteomics Bioinform.* 2012;5: 140-146.
20. Xian GM. Prediction of membrane spanning  $\beta$  strands in bacterial porins by using wavelet support vector machine algorithm. *J Proteomics Bioinform.* 2012;5:135-139.
21. Chadha T and Alexandre TA. Phylogenetic analysis of genetic diversity of hemolysins in leptospira. *J Proteomics Bioinform.* 2012;5:152-154.
22. Zanatta G et al. Quantum biochemistry description of the human dopamine D3 receptor in complex with the selective antagonist eticlopride. *J Proteomics Bioinform.* 2012;5:155-162.
23. Lai Y. Quantitative membrane proteomics and its application in translational pharmacology. *J Proteomics Bioinform.* 2012;5:vii-viii.
24. Saha S, et al. Fractional precipitation of plasma proteome by ammonium sulphate: case studies in leukemia and thalassemia. *J Proteomics Bioinform.* 2012;5:163-171.
25. Vipin Kumar S, et al. Comparative analysis of non-synonymous and synonymous substitution of capsid proteins of human herpes virus. *J Proteomics Bioinform.* 2012;5:172-176.
26. El-Haibi CP, et al. Antibody microarray analysis of signaling networks regulated by Cxcl13 and Cxcr5 in prostate cancer. *J Proteomics Bioinform.* 2012;5:177-184.
27. Sjöberg R, et al. Biosensor based protein profiling on reverse phase serum microarray. *J Proteomics Bioinform.* 2012;5:185-189.
28. Sharma N, et al. Comparative genomic and proteomic phylogenetic analysis of indian isolate of partial coat protein gene sequence of zucchini yellow mosaic virus (ZYMV) using data mining. *J Proteomics Bioinform.* 2012;5:196-203.
29. Peng L. Tandem mass spectrometry: a new platform for fluxomics. *J Proteomics Bioinform.* 2012;5:ix-x.
30. Davoudi-Dehaghani E, et al. Amplicon secondary structure formation and elongation during the process of sequencing. *J Proteomics Bioinform.* 2012;5:204-207.
31. Shobana S, et al. evolutionary trace analysis of azoreductase at the ligand binding site and enhancing the active site through site directed mutagenesis. *J Proteomics Bioinform.* 2012;5:222-225.
32. Mostovenko E, et al. Protein fractionation for quantitative plasma proteomics by semi-selective precipitation. *J Proteomics Bioinform.* 2012;5:217-221.
33. Nebel JC. Proteomics and bioinformatics soon to resolve the human structural interactome. *J Proteomics Bioinform.* 2012;5:xi-xii.
34. Bhaskar A, et al. Characterization of keratitis disease causing 56k cysteine protease encoding gene from *serratia marcescens*. *J Proteomics Bioinform.* 2012;5:226-229.
35. Sumathy R, et al. Theoretical modeling and docking studies of silkworm serotonin receptor. *J Proteomics Bioinform.* 2012;5:230-234.
36. Sameer Kumar GS, et al. gene expression profiling of tuberculous meningitis co-infected with HIV. *J Proteomics Bioinform.* 2012;5:235-244.
37. Cooley P, et al. Conducting genome- wide association studies: epistasis scenarios. *J Proteomics Bioinform.* 2012;5:245-251.
38. Gridley DS, et al. Effects of space flight on the expression of liver proteins in the mouse. *J Proteomics Bioinform.* 2012;5:256-261.
39. Rauf S and Mir A. Phylogenetic analysis of ASPM, a major contributor gene of microcephaly. *J Proteomics Bioinform.* 2012;5:252-255.

40. Mathivanan S. Quest for cancer biomarkers: assaying mutant proteins and rna that provides the much needed specificity. *J Proteomics Bioinform.* 2012;5:xiii-xvii.
41. Morya VK. Omics for Metabolic reconstruction engineering: the current trend. *J Proteomics Bioinform.* 2012;5:xviii-xix.
42. Cheng F. Blood microRNAs: novel omics biomarkers for ovarian cancer early detection. *J Proteomics Bioinform.* 2012;5:xx-xxi.
43. Chaudhary M and Payasi A. Molecular characterization and antimicrobial susceptibility study of acinetobacter baumannii clinical isolates from middle East, african and indian patients. *J Proteomics Bioinform.* 2012;5:265-269.
44. Hernández S, et al. Do moonlighting proteins belong to the intrinsically disordered protein class? *J Proteomics Bioinform.* 2012;5:262-264.
45. Kumavath RN and Pratap D. Comparative network analysis of two- component signal transducing protein-protein interactions in enterococcus faecalis Sp. *J Proteomics Bioinform.* 2012;5:270-278.
46. Ladame S. Looking at the genome and the proteome with the eyes of a chemist: engineered molecular and chemical tools for sensing and therapeutic applications. *J Proteomics Bioinform.* 2012;5:xxii-xxiv.
47. Trudgian DC, et al. ModLS: post-translational modification localization scoring with automatic specificity expansion. *J Proteomics Bioinform.* 2012;5:283-289.
48. Kumar A, et al. Identification of milk protein polymorphism in indian goats by 2d gel electrophoresis. *J Proteomics Bioinform.* 2013;6:001-004.
49. Chaudhary M and Payasi A. rising antimicrobial resistance of pseudomonas aeruginosa isolated from clinical specimens in India. *J Proteomics Bioinform.* 2013;6:005-009.
50. Tahir M and Shakeel SN. Buffer optimization for cynodon dactylon proteome. *J Proteomics Bioinform.* 2013;6:010-014.
51. Perez G, et al. Peptides binding cocaine: a strategy to design biomimetic receptors. *J Proteomics Bioinform.* 2013;6:015-022.
52. Sohpal VK, et al. Computational analysis of distance and character based phylogenetic tree for capsid proteins of human herpes virus. *J Data Mining Genomics Proteomics.* 2013;4:128.
53. Tiwari K and Thakur HK. Diversity and molecular characterization of dominant bacillus amyloliquefaciens (JNU-001) endophytic bacterial strains isolated from native neem varieties of sanganer region of rajasthan. *J Biodivers Biopros Dev.* 2014;1:115.
54. Kuznetsov A. VMD: genetic networks described in stochastic pi machine (SPiM) programming language: compositional design. *J Comput Sci Syst Biol.* 2009;2:272-282.
55. Natarajan S. Highlights of recent articles on data mining in genomics and proteomics. *j data mining genomics proteomics.* 2013;4:e104.
56. Daefler S. Using datasets for modeling of infectious diseases. *J Data Mining Genomics Proteomics.* 2013;4:e103.
57. Karasawa R, et al. Validation of a new biomarker in patients with kawasaki disease identified by proteomics. *J Data Mining Genomics Proteomics.* 2013;4:124.
58. Attie O and Daefler S. An agent based model of tularemia. *J Data Mining Genomics Proteomics.* 2013;4:125.
59. Josic D and Giacometti J. Foodomics-use of integrated omics in nutrition, food technology and biotechnology. *J Data Mining Genomics Proteomics.* 2013;4:e106.
60. Wood PI and Braverman NE. Lipidomics analysis of peroxisomal disorders: discovery of deficits in phosphatidylglycerol levels in rhizomelic chondrodysplasia type 1. *J Data Mining Genomics Proteomics.* 2014;S1:001.
61. Brindley SM, et al. Attempted validation of surface enhanced laser desorption ionization-time of flight derived kinesin biomarkers in malignant mesothelioma. *J Data Mining Genomics Proteomics.* 2013;S1:002.
62. Lee S, et al. Exploration of biomarkers for asbestos exposure and occurrence of malignant mesothelioma based on the immunological effects of asbestos. *J Data Mining Genomics Proteomics.* 2013;S2:001.
63. Vipin Kumar S, et al. N-W algorithm and anfis modeling on alignment similarity of triplex capsid protein of human herpes simplex virus. *J Data Mining Genomics Proteomics.* 2013;S3:001.
64. Roy A, et al. A case study on discovery of novel citrus leprosis virus cytoplasmic type 2 utilizing small RNA libraries by next generation sequencing and bioinformatic analyses. *J Data Mining Genomics Proteomics.* 2013;4:129.

65. Oliveira JS, et al. A computational approach for microRNA identification in plants: combining genome-based predictions with rna-seq data. *J Data Mining Genomics Proteomics*. 2013;4:130.
66. Natsoulis G, et al. Identification of insertion deletion mutations from deep targeted resequencing. *J Data Mining Genomics Proteomics*. 2013;4:132.
67. Al-Haggag MMS, et al. Bioinformatics in high throughput sequencing: application in evolving genetic diseases. *J Data Mining Genomics Proteomics*. 2013;4:131.
68. Davis C, et al. mblast: keeping up with the sequencing explosion for (Meta) genome analysis. *J Data Mining Genomics Proteomics*. 2013;4:135.
69. Jiao X, et al. A benchmark study on error assessment and quality control of ccs reads derived from the PacBio RS. *J Data Mining Genomics Proteomics*. 2013;4:136.
70. Avsar-Ban E, et al. High-throughput injection system for zebrafish fertilized eggs. *J Data Mining Genomics Proteomics*. 2013;4:137.
71. Weier HUG. New algorithms for genome characterization, epigenetic profiling analysis, data mining and population-based studies. *J Data Mining Genomics Proteomics*. 2013;4:e109.
72. Yin T, et al. Visual mining methods for RNA-seq data: data structure, dispersion estimation and significance testing. *J Data Mining Genomics Proteomics*. 2013;4:139.
73. Ophir D. An analysis of palindromes and n-ary tract frequencies found in a genomic sequence. *J Data Mining Genomics Proteomics*. 2013;4:140.
74. Blum HE and Oexle K. Clinical interpretation and implications of whole genome sequencing. *Next Generat Sequenc & Applic*. 2014;1:105.
75. Srinivasan S and Batra J. Four generations of sequencing- is it ready for the clinic yet?. *Next Generat Sequenc & Applic*. 2014;1:107.
76. Gryganskyi AP and Muszewska A. Whole genome sequencing and the zygomycota. *Fungal Genom Biol*. 2014;4:e116.
77. Bhensdadia DV, et al. Isolation, molecular characterization and insight into the genome sequence of e.coli bacteriophage adb-2 from poultry fecal sample. *Next Generat Sequenc & Applic*. 2014;1:101.
78. Alharbi KK, et al. The role of genome sequencing in the identification of novel therapeutic targets. *J Glycomics Lipidomics*. 2014;4:112.
79. Martins MD and Castilho RM. Histones: controlling tumor signaling circuitry. *J Carcinogene Mutagene*. 2013;S5:001.
80. Chenoll E, et al. Genomic sequence and pre-clinical safety assessment of bifi dobacterium longum cect 7347, a probiotic able to reduce the toxicity and infl ammatory potential of gliadin-derived peptides. *J Prob Health*. 2013;1:106.
81. Arora N, et al. In silico characterization of shikimate kinase of shigella flexneri: a potential drug target. *Interdiscip Sci*. 2010;3:280-290.
82. Banerjee AK, et al. Classification and regression tree (CART) analysis for deriving variable importance of parameters influencing average flexibility of CaMK kinase family. *Electronic Journal of Biology*. 2008;4:27-33.
83. Arora N, et al. Homology model of 2C-methyl-d-erythritol 2, 4-cyclodiphosphate (MECP) synthase of plasmodium falciparum 3D7. *Electronic Journal of Biology*. 2010;6:52-57.
84. Duddela S, et al. Probing the structure of human glucose transporter 2 and analysis of protein ligand interactions. *Medicinal chemistry research*. 2010;19:836-853.
85. Banerjee AK, et al. Aspartate carbamoyltransferase of plasmodium falciparum as a potential drug target for designing anti-malarial chemotherapeutic agents. *Medicinal chemistry research*. 2012;21:2480-2493.
86. Arora N, et al. A computational approach to explore plasmodium falciparum 3D7 chorismate synthase. *Internet J Genomics Proteomics*. 2007;3.
87. Banerjee AK and Murty US. Extracting the significant descriptors by 2D QSAR and docking efficiency of NRTI drugs: a molecular modeling approach. *Internet J Genomics Proteomics*. 2007;2.
88. Chen D, et al. Analyzing and modeling spatial and temporal dynamics of infectious diseases. *John Wiley & Sons*; 2014;478.
89. Arora N, et al. Shikimate kinase of yersinia pestis: a sequence, structural and functional analysis. *Int J Biomed Data Min*. 2016;5:4-11.

90. Banerjee AK. Computation in analyzing inflammation: a general perspective. *Interdiscip J Microinflammation*. 2015;2:2.
91. Marjeta U. Chemo proteomics, a valuable tool for biomarker and drug discovery. *Mol Biol*. 2014;3:e117.
92. Takis A. Celebrating 30 years since the conception of the human genome project (hgp): new concepts ahead-molecular biology tools to efficiently modify the hg and/or other species-genomes-implications for health and disease. *Mol Biol*. 2014;3:e119.
93. Bhowmick S and Tripathy S. A tale of effectors; their secretory mechanisms and computational discovery in pathogenic, non-pathogenic and commensal microbes. *Mol Biol*. 2014;3:118.
94. Remes AM, et al. Functional MRI in patients with the C9ORF72 expansion associate frontotemporal dementia. *Mol Biol*. 2014;3:117.
95. Perepechaeva M, et al. Altered mRNA expression of “Ahr-Nrf2 gene batteries” in the retinas of senescence-accelerated oxys rats during development of amd-like retinopathy. *J Mol Genet Med*. 2014;8:105.
96. Saxena SK, et al. Current scenario of antiviral drugs for japanese encephalitis. *J Med Microb Diagn*. 2014;3:133.
97. Zhou G, et al. Chemical characterization and antioxidant activities of different sulfate content of  $\lambda$ -carrageenan fractions from edible red seaweed *chondrus ocellatus*. *Cell Mol Biol*. 2014;60: 107.
98. Zhang H, et al. Panax notoginsenosides attenuates pleural inflammation in rabbit model. *Cell Mol Biol*. 2014;60:106.
99. Yamane T, et al. Identification of DJ-1-associated regions on human genes from sh-sy5y cells using chromatin immunoprecipitation sequence technique. *Mol Biol*. 2013;3:115.
100. Rajat KS, et al. In Silico inhibition of chitinase enzyme in filariasis and lead optimization by pharmacophore studies. *J Biosci* 2014;3:485-496.