New / Revised Syllabus for

M.PHIL /PH.D BIOINFORMATICS

SUBMITTED TO

University Grants Commission
(UGC XIIth PLAN)

New Delhi- 110 002

(Introduced from June 2012 onwards)

STRUCTURE OF THE COURSE WORK FOR M.Phil /Ph.D.

<u>(NO.OF PAPERS THREE)</u>

Sr. No.	Subjects/Papers	Marks
1.	Research Methodology	100
2.	Recent Trends in Bioinformatics	100
3.	Structural Bioinformatics	100
	Total	**300**

M.Phil./Ph.D. Course Work

**(Introduced from June 2012
onwards)**

Syllabus for Bioinformatics

i) **Paper – I:**   **(60 Lectures, 100 marks)**

ii) **Title of the Paper: Research Methodology**

iii) **Specific Objectives if any: To trend the research students in the analytical tools required during the M.Phil./Ph.D. Course and to develop computational skills.**

Topic No.	Research Methodology	Lectures 60
	Unit- I	
1.	**Basic Concepts of Computer**	15
	History of Computer, Concept of Computer hardware, Concept of Computer languages, Concept of Computer Softwares **Computer applications in Biology** Spreadsheet tools : Introduction to spreadsheet applications, features, Using formulas and functions, Data storing, Features for Statistical data analysis, Generating charts / graph and other features, Tools – Microsoft Excel or similar. Presentation tools: Introduction, features and functions, Presentation of Power Point Presentation, Customizing presentation, Showing presentation, Tools – Microsoft Power Point	

	or Similar.	
	Web Search: Introduction to Internet, Use of Internet and WWW, Use of search engines, Biological data bases.	
	Unit-II	
2.	**Biostatistics** and **Quantitative Techniques**:	**15**
	Biostatistics: Measures of Central tendency and Dispersion. Probability distribution: Binomial, Poisson and Normal. Parametric and Nonparametric statistics, Confidence Interval, Errors.	
	Quantitative Techniques: Levels of significance, Regression and Correlation, Use of Statistics in Biosciences, Use of Computers in Quantitative analysis.	
	Unit- III	
3	**Scientific Writing** and **Techniques in Molecular Biology**:	**15**
	Scientific Writing:	

Scientific Writing and **Techniques in Molecular Biology**:

Scientific Writing:

An Insight into Research: Definition and basic concepts, objectives, significance and techniques of research, finding research materials – literature survey, compiling records.

a) Definition and kinds of scientific documents – research paper, review paper, book reviews, theses, conference and project reports (for the scientific community and for funding agencies).

b) Components of a research paper– the IMRAD system, title, authors and addresses, abstract, acknowledgements, references, tables and illustrations.

c) Dealing with publishers – submission of manuscript, ordering reprints.

d) Oral and poster presentation of research papers in conferences/symposia.

e) Preparation and submission of research project proposals to funding agencies

Techniques in Molecular Biology:

Identification and characterization of DNA, RNA, plasmids. Agarose gel electrophoresis, ethidium bromide staining. Southern, Northern, Western Blotting, RAPD, RFLP, DGGE, TGGE, PCR.

	Unit- IV	
4	**Research Techniques:**	**15**
	Enzyme assay, enzyme activity and specific activity determination. Cell disintegration and extraction techniques, separation of proteins by fractionation (ammonium sulphate, organic solvents). Ion exchange chromatography, molecular sieve chromatography, affinity chromatography, paper chromatography, thin layer chromatography, ultra filtration, Ultracentrifugation. Gel electrophoresis, isoelectric focusing and immunoelectrophoresis, capillary electrophoresis, pulse field electrophoresis. Microscopy, HPLC, HPTLC, GC-MS, FTIR, SEM/TEM, NMR, AAS.	

Suggested readings:

1. Biostatistics: A foundation for Analysis in the Health Sciences 7/E Wayne W. Daniel, Wiley Series in Probability and Statistics.

2. Introductory Statistics. Fifth Edition. (2004) Prem S. Mann. John Wiley and Sons (ASIA) Pvt. Ltd.

3. Bioinformatics Methods and Applications Genomics, Proteomics, and Drug Discovery (S. C. Rastogi, N. Mendiratta, and P. Rastogi).

4. Introduction to Bioinformatics, (Atwood, T. K. and Parry-Smith, D. J).

5. Protein Purification by Robert Scopes, Springer Verlag Publication, 1982

6. Tools in Biochemistry David Cooper

7. Methods of Protein and Nucleic acid Research, Osterman Vol I – III

8. Centrifugation D. Rickwood

9. Practical Biochemistry, V th edition, Keith Wilson and Walker.

10. Bioinformatics by David Mound

11. Practical Biochemistry, Vth edition, Keith Wilson and Walker.

12. Protein Purification by Robert Scopes, Springer Verlag Publication, 1982

13. Tools in Biochemistry David Cooper

14. Methods of Protein and Nucleic acid Research, Osterman Vol I – III

15. Centrifugation D. Rickwood

Paper-II: **(60 Lectures, 100 marks)**

Title of the paper: Recent Trends in Bioinformatics

Topic No.	Recent Trends in Bioinformatics	Lectures 60
	Unit- I	
1.	**Genomics**:	**15**
	Genomics: Genes, Genomes, Human Genome Project, Rough and Final Draft of Human Genome Project, Goals of Human Genome Project, Vectors: plasmids, Cosmids, bacteriophage, M13 vectors, BAC, YAC and synthetic plasmids. Enzymes: DNA polymerase, restriction endonucleases, topisomerase I and DNA ligase, reverse transcriptase, kinase, alkaline phosphatase, nuclease, RNAse. DNA sequencing dideoxy chain termination and Sanger's +/- method. cDNA library – screening by oilgonucleotide probe, nick translation, site directed mutagenesis, linkage analysis. Gene cloning- General strategy for gene cloning, transformation. Application of gene technology, Gene Silencing, Geneknock out and gene therapy	
	Unit-II	
2.	**Genome Databases and Gene expression and DNA microarray**	**15**
	Genome Databases Nucleic acid sequences. Sequence databases: GeneBank, European Molecular Biology Laboratory (EMBL) Nucleotide sequence databank, DNA Data Bank of Japan (DDBJ). **Gene expression and DNA microarray** Introduction, Basic steps for gene expression, genome information and special features, coding sequences (CDS), untranslated regions (UTR's), cDNA library, expressed sequence tags (EST). Approach to gene identification; codon-bias detection, detecting functional sites in the DNA. Internet resources for gene identification, detection of functional sites. Types of microarrays; Tools for microarray analysis; soft-finder, xCluster, MADAM, SAGE, Applications of microarray technology.	
	Unit- III	
3	**Proteomics and Protein Databases**	**15**

	Proteomics	
	Proteins and Enzymes; Proteomics classification; tools and techniques in proteomics; gel electrophoresis, gel filtration, PAGE, isoelectric focusing, affinity chromatography, HPLC, ICAT, fixing and spot visualization, Mass spectroscopy for protein analysis, MALDI-TOF, Electrospray ionization (EST), Tandem mass spectroscopy (MS/MS) analysis; tryptic digestion and peptide fingerprinting (PMF). **Protein Databases:** Proteins; Protein sequence databases; primary databases and secondary databases, different formats of databases, composite databases.	
	Unit- IV	
4	**Sequence alignments and Immunoinformatics:**	**15**
	Sequence alignments Introduction, Protein sequences, physicochemical properties based on sequence, sequence comparison. Pair-wise sequence alignment, gaps, gap-penalties, scoring matrices, Smith-Waterman and Needleman-Wunsch algorithms for sequence alignments, multiple sequence alignment, comparision, composition and properties, useful programs, ClustalW, BioEDIT, BLASTp, Phylogenetic analysis tools- Phylip, ClustalW, Online phylogenetic analysis. **Immunoinformatics:** Complement fixation, structure and classes of antibodies, genetic basis of antibody diversity. Understanding MHC I and II: structure and antigen presentation, T and B lymphocytes activation and role in humoral and cell mediated immunity. Vaccines live and attenuated, killed, multi-subunit and DNA vaccines. Hypersensitivity and auto immune diseases. ELISA, RIA, Hybridoma Technology. Computational vaccinology; B cell epitope prediction, T cell epitope prediction, discovery of conserved epitopes through sequence variablility analysis, isotope prediction,,immunopolymorphism; study of polymorphic gene in immuno system,.	

Suggested readings:

1. Biotechnology: Current Progress Volume 1 by P. N. Cheremisinoff and L. M. Ferrante. Technomic Publishing Co. Inc

2. Bergey's Manual of Systematic Bacteriology (2nd Ed.), Volumes1 to 4 Springer

3. The Search for Bioactive Compounds from Microorganisms by S. Omura

4. Advances in Applied Microbiology volumes 6, 10, 17 by D. Perlman and Umbreit (eds). Academic Press.

5. The Physiology and Biochemistry of Procaryotes by D. White. Oxford University Press

6. Sambrook J, Fritsch E. F. and Maniatis (1989) Molecular

   cloning, vol. I, II, III, II nd edition, Cold spring harbor laboratory press, New York.

9. DNA Cloning : A practical approach D.M. Glover and D.B. Hames, RL Press, Oxford, 1995

10. Molecular and cellular methods in Biology and Medicine, P.B. Kaufman, W. Wu , D. Kim and L.J. Cseke, CRC Press Florida 1995

11. Methods in Enzymology Guide to Molecular Cloning Techniques, Vol. 152 S.L. Berger and A. R. Kimmel, Academic Press Inc, San Diego, 1996

12. Methods in Enzymology Gene Expression Technology, Vol. 185D. V. Goedel, Academic Press Inc, San Diego, 1990

13. DNA Science: A First Course in Recombinant Technology, D. A. Mickloss and G. A Freyer, Cold Spring Harbor Laboratory Press, New York, 1990

14. Molecular Biotechnology, 2nd Ed. S. B. Primrose, Blackwell Scientific publishers, Oxford, 1994

15. Route Maps in Gene Technology, M. R. Walker, and R. Rapley, Blakwell Science, Oxford, 1997

16. Genetic Engineering : An Introduction to Gene Analysis and Exploitation in Eukaryotes, S. M. Kingsman, Blackwell Scientific Publications, Oxford, 1998

17. Kuby : Immunology; RA Goldsby, Thomas J. Kindt, Barbara A. Osborne.

18. Immunology by Roitt I. M., Brostoff J. and Male D. Gower medical publishing London.

19. Fundamentals of immunology 4th ed., Paul 1999, Lippencott Raven.

20. Introduction to Bioinformatics, (Atwood, T. K. and Parry-Smith, D. J).

21. An introduction to Computational Biochemistry. (C. Stain Tsai, A. John

   Wiley and Sons, Inc., publications).

22. Bioinformatics; Methods and applications; Genomics, Proteomics and Drug

   Discovery; (Rastogi, S. C. and Mendiratta and Rastogi, P.

23. Bioinformatics; A practical guide to the analysis of genes and proteins.; Edited by, Andreas D. Baxevanis and Francis Oulelette.

24. http://www.ncbi.nlm.nih.gov

25.Bioinformatics for Immunomics Reviews, Springer Publisher, Vol 3, 2010.

Paper – III   (60 Lectures, 100 marks)

Title of the paper: Structural Bioinformatics

Topic No.	Structural Bioinformatics	Lectures 60
	Unit- I	
1.	**Structural biology and Structural databases**	15
	Structural biology Nucleic acid structures, RNA folding, RNA loops, conformational study, various ribose ring conformations, ribose-ring puckering, protein-protein interactions, protein-ligand interactions, DNA-binding proteins, RNA-binding proteins, Ramachandran plot, 3-dimensional structures of membrane proteins, importance of 3^{10} helix and loops, biophysical aspects of proteins and nucleic acids. **Structural databases** Structural databases; Protein Data bank (PDB), Nucleic Acid Data Bank (NDB), Molecular modeling Data Bank (MMDB), Structure classification Databases; SCOP, CATH, PDBSum.	
	Unit-II	
2.	**Protein structure prediction and Fundamentals of UNIX System**	15
	Protein structure prediction Protein Structure Prediction; Homology modeling, prediction of protein structure from sequences, functional sites, Protein folding problem, protein folding classes, protein identification and characterization; structure determination by X-ray and NMR	

	Fundamentals of UNIX System: Introduction about UNIX, differentiation between UNIX and other Operating systems, various programs in the UNIX System, structure of the UNIX system, applications of the UNIX systems, basic UNIX commands, file access permissions, the file system hierarchy, terminating process, running jobs at background, controlling running programs, overview of system administration, managing deisk space, shutting down UNIX system.	
	Unit- III	
3	**Molecular modeling and Molecular mechanics**	**15**
	Molecular modeling Introduction, force field, quantum chemistry, Schrödinger equation, potential energy functions, energy minimization, local and global minima, saddle point, grid search, , various approximations; LCAO, HF, semi-empirical calculations; single point calculations, full-geometry optimization methods, ZDO, MNDO, CNDO, NDDO, AM1, PM3, RM1, conformational search, Z-matrix, docking, molecular modeling packages. **Molecular mechanics** Definition, balls and springs, force fields, bond-stretching, bond-bending, dihedral motions, out of plane angle potential, non-bonded interaction, coulomb interactions, conformational search, united atoms and cut-offs, Derivative methods; First-order methods; Steepest descent, conjugate gradient, Second order methods; Newton-Raphson method.	
	Unit- IV	
4	**Molecular dynamics and Bioinformatics applications**	**15**
	Molecular dynamics Introduction, Newton's equation of motion, equilibrium point, water models, thermodynamic ensembles, quilibration, radial distribution function, pair correlation functions, MD methodology, periodic box (PBC), algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, basic steps in molecular dynamics simulations; starting structures, duration of the MD run, final MD simulation structure. Visualization and analysis of trajectories. **Bioinformatics applications**	

	Agriculture, Molecular biology, Environment, Biotechnology, Food Science Neurobiology, Drug Designing, Biomedical genome medicines.	

Suggested readings:

1. Bioinformatics Sequence and Genome Analysis (David Mount) CBS Publishers and Distributors.

2. Bioinformatics Methods and Applications Genomics, Proteomics, and Drug Discovery (S. C. Rastogi, N. Mendiratta, and P. Rastogi).

3. Introduction to Bioinformatics, (Atwood, T. K. and Parry-Smith, D. J).

4. An introduction to Computational Biochemistry. (C. Stain Tsai, A John Wiley and Sons, Inc., publications).

5. Developing Bioinformatics Computer Skills. (Cynthia Gibas and Per Jambeck).

6. Molecular Modelling for Beginners (Alan Hinchliffe).

7. Molecular Modelling by Alxander Rich

8. A user guide to the UNIX system (Rebecca Thomas and Jean Yates)

9. http://www.ncbi.nlm.nih.gov

Required Financial Support

Annexure-I

Budget: Non-recurring (e.g. Equipments, software, accessories, Books/Journals etc.)

(Rupees in Lacs)

A) **Equipments/Computer and Accessories:**

Sr. Nos.	Item Name	Required Nos.	Cost (Rupees in Lacs)
1.	Desktop PC	40	16.0
2.	LINUX – Rack/Blade Servers with multiple cores	01	10.0
3.	Quard Core PC's	20	7.00
4.	UPS (3 KVA) with batteries (12 hrs backup)	01	2.0
5.	Other computer accessories	-	5.00
6.	Air Conditioners (Server Cooling System)	02	1.0
7.	LCD Projector	01	0.50
	Total		**41.50**

Justification:

This facility would be useful for all the faculties of this university who wish to do computational biology related work. This would also be useful to provide advanced training in bioinformatics to students and teachers of our university as well as affiliated colleges.

1. **Desktop PC:** Desktop computers are necessary to carry out routine bioinformatics practicals.

2. **LINUX Blade Server:** It has planned to use Linux Blade Server with multiple nodes to install various bioinformatics software (commercial and freely available software), molecular modeling software and also to run molecular dynamics simulations practicals for longer time duration by MD simulation packages such as AMBER, GROMACS, SYBYL, Insight-II, CHARMM, QUANTA, SPARTAN, etc.

3. **Quard Core PC's:** These 20 QC PC's are required for training students from our university as well as affiliated colleges to conduct regular bioinformatics workshops, seminars, practicals and for research

4. **Uninterrupted Power Supply (UPS):** UPS is must to avoid fluctuations of electricity and thereby increase durability of Rack/Blade servers, computer PC's and workstations.

5. **LCD Projector:** Department needs one LCD projector to arrange seminars / workshops / guest lectures.

6. **Other accessories:** For upgradation and maintenance of Blade server and other computers.

7. **Air Conditioners:** Required to maintain cold temperature for Blade server and other computers.

B) REQUIRED SOFTWARES:

Sr. No.	Name	Required Nos.	Amount (Rupees in lacs)
1.	Insight II	01	10.0
2.	Maestro	01	10.0
3.	Discovery Studio	01	10.0
4.	PC Pro SPARTAN	02	3.0
5.	MATLAB	01	4.0
6.	GENO-CLUSTER	01	5.0
7	GCG Winsconsin package	01	5.0
8.	GUASSIAN	01	3.0
		Total	**50.00**

Justification: Following points justifies our need for particular software:

1. **Insight II:** This software for energy minimization and MD simulations of various biomolecules. This would also be useful to do graphical visulalization of proteins, nucleic acids, carbohydrates, lipids, drug molecules, etc. during regular bioinformatics practicals.

2. **Maestro:** This software would be useful for energy calculations and molecular docking process**.**

3. **Discovery Studio**: Particularly to use graphical version of MODELLER and CHARMM through which sequence alignments, model building, energy minimization, protein-ligand interactions and refinement could be done.

4. **PC Pro SPARTAN:** Would be useful for each and every student to do quantum chemical, molecular mechanical, *ab-intio,* and density functional calculations of drug molecules.

5. **MATLAB:** For biostatistics purpose.

6. **GENO-CLUSTER:** Would be useful in identifying various gene functions, sequence analysis, vaccine designing, drug receptors and to do some bioinformatics related activities by assigning project work to the students at the time of workshops and seminars.

7. **GCG Winsconsin package**: For sequence analysis, conversion of DNA sequence to protein and vice versa, phylogenetic tree construction and analysis, primer designing, etc.

8. **GUASSIAN:** For charge calculations and molecular modeling studies.

C) Building/Books/Journals:

Sr. Nos.	Item Names	Required nos.	Cost (Rupees in lacs)
1.	Building construction	2500 sp. ft. construction	50.00
1.	Library Material (Books)	As per need	3.0
2.	Journals	As per need	2.0
		Total	**55.0**

Justification: Proposed Department of Bioinformatics requires separate building. Department would also require some library materials and journal subscription fee for the students.

A + B + C = Total Non Recurring Grant

(44.50 + 50.0 + 55.0 = 146.50 Lacs

Annexure- II

Recurring Grants: (Rupees in lacs)

1. **Man Power:**

Sr. Nos.	Name	Required Numbers (for 5 years)	Cost (Rupees in lacs) (for 5 years)
2.	Assistant Professor	04	188.00
3.	Technician-2 @ Rs.10,000/- per month.	01	6.00
4.	Clerk @ Rs.4,000/- per month.	01	3.0
5.	Peon @ Rs.3,000/- per month.	01	1.80
5.	Laboratory Assistant	01	2.10
		Total	**200.90**

Justification:

At present Department of Biochemistry has one faculty **(Dr. K. D. Sonawane, Asso. Prof. and Coordinator Post Graduate Diploma in Bioinformatics; Biodata Attached)** working in Bioinformatics area, but department would require four more faculties for teaching and practical purposes and also to conduct regular workshops and seminars, etc. The technical assistant has to support the system and keep the machinery in working condition. He has to attend the minor repairs and look after the overall maintenance of the unit. An office clerk, peon and laboratory assistant are needed to look after the day-to-day office and lab work. They will assist the Co-ordinator or Head (I/c) in maintaining office record, purchase of the goods and general administration of the department.

Annexure-III

Budgetary Provision/year:

Sr. No.	Budget Head	Amount (Rs. in Lacs)
1.	Laboratory expenses	5.0
2.	Purchase of teaching aids, computer hard wares, software, etc.	10.00
3	Honorarium to contributory teachers and T. A. to visiting professors	0.50
4	Internet bills/stationary	0.02
5	Miscellaneous	0.01
	Total	**15.53**

Total Budgetary Provision for the department:

Sr. No.	Budgetary Provision	Amount (Rs. in Lacs)
1.	Total of **Annexure I** (Non-recurring):	**146.50**
2.	Total of **Annexure II** (Recurring):	**200.90**
3.	Total of **Annexure III** (Budgetary Provision/ year):	**15.53**
	Total Budgetary Amount:	**362.93**

CURRICULUM VITAE

15

1.	Name of the Applicant	Dr. Kailas Dashrath Sonawane

2. Present Position and
   Address: Associate Professor and Coordinator,
   Post Graduate Diploma in Bioinformatics
   Department of Biochemistry,
   Shivaji University, Vidyanagar,
   Kolhapur – 416 004, India, (MS).

	Telephone	+ 91–231-2609153, Mobile: 9881320719
	Fax.	+ 91-231-2692333, 2691523
	E-mail	kds_biochem@unishivaji.ac.in, kds19@rediffmail.com
3.	Date of Birth	19th March, 1973
4.	Nationality	Indian

5. **Educational Qualification (Starting from Graduate onwards):**

Sr. No.	Degree	University	Year	Subject	Class
i.	B. Sc.	Shivaji University, Kolhapur	1994	Chemistry	Ist
ii.	M. Sc.	Shivaji University, Kolhapur	1996	Biochemistry	Ist
iii.	Ph. D.	University of Pune	2003	Biochemistry	-

Ph.D. Thesis title: "Structural Significance of the 3'– adjacent N6-(Δ^2-isopentenyl adenosine) and related modifications in tRNA".

Work place: **National Chemical Laboratory (NCL), Pune, India**.

POST DOCTORAL FELLOWSHIP

DURATION	INSTITUTION	DESIGNATION	NATURE OF WORK DONE
March 2003-Oct. 2005	National Institute of Health (NIH), Bethesda, MD, USA.	Post Doctoral Fellow	Homology modeling, sequence analysis, molecular docking and molecular dynamics simulation studies on K^+ ion channels.

DOCTORAL/ FELLOWSHIP

1999-2003	National Chemical Laboratory, Pune, India	Senior Research Fellow (CSIR, New Delhi).	Molecular modeling; Quantum chemical, molecular mechanics, molecular dynamics simulations study of hypermodified nucleosides present in anticodon loop of tRNA.
1996-1999	National Chemical Laboratory (NCL), Pune, India	Project Assistant-II, (Indo-French Project), IFCPAR, New Delhi	Conformational preferences of hypermodified bases, i^6A, ms^2i^6A. Protonation induced conformational preferences of hypermodified nucleosides (g^6A, t^6A, ms^2t^6A) present in anticodon loop of tRNA using various modeling techniques.

ii. Research student working under the guidance for their Ph. D. programme:
- 01 Thesis Submitted.
- 08 Working.

iii. Research Schemes/Projects: (Ongoing/Completed)

Title of Project/Scheme	Funding agency	Funds received (Rs.)	Date of starting	Date of ending	Worked as Principal Investigator/ Co-investigator
1. "Molecular modeling study of hypermodified nucleoside lysidine present at wobble position in anticodon loop of E. coli tRNA^{Ile} and its role in proper codon-anticodon recognition" SERC - Fast Track Young Scientist Scheme.	DST, New Delhi	18,32,000/-	January 2008	April, 2011	Principal Investigator
2. UGC SAP DRS I Infrastructure Grant Sanctioned to Department of Biochemistry, Shivaji University, Kolhapur	UGC SAP DRS I	32,00,000/- + 2 Project Fellows	April, 2009	March, 2013	Dy. Coordinator
3. "Structural Significance of	UGC,	10,41,800/-	July,	March,	Principal

hypermodified nucleosides 5-taurinomethyluridine ($\tau m^5 U$) and its derivative 5-taurinomethyl-2-thiouridine, ($\tau m^5 s^2 U$) present at 'wobble' position in anticodon loop of tRNA"	New Delhi	2011	2014	Investigator

Research Specialization:

   Bioinformatics/Computational Biology:- Molecular modeling**.**
- Structural biology of hypermodified nucleic acids, Molecular modeling, homology modeling.
- RNA-Protein interactions, Prediction of three-dimensional structures of enzymes involved in Alzheimer's disease; molecular docking, and drug designing.

   Antimicrobial activity and Enzymology

Research Experience: (16 Years)

- **Post-Doctoral Fellow** at the **National Institutes of Health (NIH), Bethesda, MD, USA** from March 2003 to Oct. 2005. During this period worked on sequence analysis, homology modeling and molecular dynamics (MD) simulations of potassium ion Channels. **Software used during the period:** Modeler (Insight-II), CHARMM, GROMACS (MD Simulations using dual xeon processor and *Helix* NIH supercomputer system), BLAST, FASTA, Sequence alignment using ClustalW & GCG Wisconsin package, DS viewer Pro (Accelrys), Chimera, programming languages; PERL, HTML. Java, Java Script etc.
- **National Chemical Laboratory (NCL), Pune, India**, from 1996 to 2003 during Ph.D. During this period got an opportunity to learn: UNIX; Molecular modeling techniques such as, *ab-initio*; Semi-empirical quantum chemical calculations using PCILO, PM3, MNDO, AM1; Molecular mechanics (MMFF) and Molecular Dynamics (MD) Simulations. **Professional software**: SYBYL, SPARTAN, HYPERCHEM, WINMOPAC; programming languages; FORTRAN, C, etc. Structural significance of hypermodified nucleosides present in the anticodon loop of tRNA. Transfer RNA sequence analysis.

Research Guidance:

- **U.G.:-** Guidance to graduate student for his project work during the **post-doctoral fellowship** period from March 2003 to Oct. 2005 at **National Institutes of Health, Bethesda (NIH), MD, USA**. During this period worked on sequence analysis, homology modeling and molecular dynamics (MD) simulations of K^+ ion Channels (Protein folding).

- **P.G.:-** Guidance to M. Sc (Bioinformatics) student for his project work at **NCL, Pune**, **India** (2000).

- **P.G.**:- Guidance to M. Sc Biochemistry, Biotechnology and PG Diploma in Bioinformatics students for their project work in the Department of Biochemistry, Shivaji University, Kolhapur, since (2006).

- **Ph. D**:- Guidance to Ph. D. students in the subject of Biochemistry, Biotechnology and Microbiology, (Total no. of Ph.D. students working; 06).

Membership/Other Charge:

- Presently working as a Head (I/c), Department of Microbiology, Shivaji University, Kolhapur since August 2007.

- Co-ordinator, PG Diploma in Bioinformatics, Department of Biochemistry, Shivaji University, Kolhapur since 2008.
- Dy. Coordinator; UGC SAP DRS-I, sanctioned to Department of Biochemistry, Shivaji University, Kolhapur (2009-2014).
- Worked as Director, CAP (Microbiology Examination; Kolhapur, Karad and Satara centers), since August 2007, Department of Microbiology, Shivaji University, Kolhapur.
- Life member, Association of Microbiologist of India (AMI).
- Reviewer: Biochimica et Biophysica Acta
- Editorial Board Member, Journal of Microbial World
- Member, Editorial Board "SHIVSANDESH" an E-Bulletin of Shivaji University, Kolhapur.
- Chairman, B.Sc**.** Bioinformatics Syllabus Sub-Committee, under BOS Biotechnology, Shivaji University, Kolhapur.
- Member BUTR**,** Shivaji University, Kolhapur
- BOS member, Biotechnology, Solapur University, Solapur.
- BOS member, Biotechnology, Dr. Babasaheb Ambedkar Marathwada University, Aurangabad.

iv. Administrative experience:

a) Head (I/c) Department of Microbiology,
   Shivaji University, Kolhapur, India
   (Since August, 2007).
b) Coordinator; Post Graduate Diploma in Bioinformatics
   Department of Biochemistry,
   Shivaji University, Kolhapur, India
   (Since August, 2008).

v. Teaching and Research Experience:
a) Teaching experience: Since April, 2006.
b) Research experience: 16 years

vi. Publications:
A) **List of Research Publications: Total (17)**

1. Rohit S. Bavi, Asmita D. Kamble, Navanath M. Kumbhar, Bajarang V. Kumbhar and **Kailas D**. **Sonawane**, "Conformational preferences of modified nucleoside N^2-methylguanosine (m^2G) and its derivative N^2, N^2-dimethylguanosine (m^2_2G) occur at 26th position (hinge region) in tRNA"
Cell Biochemistry and Biophysics, 507-521, 61, 2011.
(Impact Factor 4.321)

2. Navanath M. Kumbhar and **Kailas D. Sonawane** "Iso-energetic multiple conformations of hypermodified nucleic acid base Wybutine (yW) which occur at 37th position in anticodon loop of tRNA[Phe]".
J. of Molecular Graphics and Modelling, 29, 935-946, 2011
(Impact Factor 2.033)

3. Bajarang V Kumbhar[1] and **Kailas D Sonawane[1]∗** "Molecular modeling study of hypermodified nucleic acid base 3-hydroxynorvalylcarbamoyl adenine, hn6Ade present at 3'-adjacent position in anticodon loop of hyperthermophilic tRNAs"
IRSAPS Bulletin (1) 3, 2011, -8-15, 2011.

4. R.T. Sapkal, S.S. Shinde, A.R. Babar, C.B. Jalkute ,K.Y. Rajpure , **K.D. Sonawane** ,C.H. Bhosale. Photoelectrocatalytic purification of fecal, tap and *E.coli* contained water using ZnO thin films: A comparative study.
International Journal of Basic and Applied Research, 1, 42-49, 2011.

5. Maruti J. Dhanawade, Chidamber B. Jalkute, Jai S. Ghosh and **Kailas D. Sonawane** "Study Antimicrobial Activity of Lemon (*Citrus lemon* L.) Peel Extract"
British J. of Pharmacology and Toxicology, 2, 119-122, 2011.

6. Sapkal, R. T., Shinde, S. S., Sapkal, M. R., Babar, A. R. Sakpal, D. M., Jalkute, C. B., Rajpure, K. Y., Patil, P. S., **Sonawane, K. D**. and Bhosale, C. B. "Photoelectrocatalytic Hydrolysis of Starch By Sprayed Zno Thin Film**"**
Material Science, **7**, **2011.**

7. Susmit B. Sambhare, Navanath M. Kumbhar, Asmita D. Kamble, Bajarang V. Kumbhar and **Kailas D. Sonawane "**Molecular modeling study to investigate conformational preferences and base stacking interactions of hypermodified nucleoside lysidine (k^2C) incorporated in the trinucleotide segment of anticodon loop of tRNA[Ile]"
Bionanofrontier, 4, 191-196, 2011.
(Impact Factor 0.237)

8. **Kailas D. Sonawane,** Bajarang V. Kumbhar, Navanath M. Kumbhar, Susmit B. Sambhare and Asmita D. Kamble. "Consequences of 5' -3' diphosphate backbone on the conformation of hypermodified nucleotide lysidine (k^2C) occur at wobble (34th) position in the anticodon loop of tRNA[Ile]", **International J Bioinformatics Research,** 3, 148-160, **2011.**

9. **Sonawane, K. D.**, Tewari, R. "Conformational preferences of hypermodified nucleoside lysidine (k^2C) occurring at 'wobble' position in anticodon loop of tRNA[Ile]".
Nucleosides, Nucleotides and Nucleic Acids. 27, 1158-1174, 2008.
(Impact Factor 1.3)

10. Gea-Ny, Tseng., **Sonawane, K. D**., Korolkova, Y. V., Zhang, M., Liu, J., Grishin, E. V., and Guy, H. R. "Probing outer mouth structure of hERG channel with peptide toxin foot printing and molecular modeling.

Biophysical J. 92, 3524-3540, 2007.
(Impact Factor 4.8)

11. Zhang, M., Liu, J., Jiang, M, Wu, D. M., **Sonawane K**., Guy, H. R. and Tseng, G. N. "Interactions between charged residues in the transmembrane segments of voltage-sensing domain in the hERG channel.
J. Memb. Biol. 207, 169-181, 2005.
(Impact Factor 2.8)

12. Sonavane, U. B., **Sonawane, K. D.** and Tewari, R. Modified Nucleotides and across the anticdon loop interaction in tRNA. **Europ. Biophysics Lett., 34, 581-581, 2005.**

13. Sonavane, U.B., **Sonawane, K. D**. and Tewari, R. "Conformational preferences of the base substituent in hypermodified nucleoside queuisine 5'monophosphate 'pQ' and protonated variant 'pQH^{+}'". **J. Biomol. Struct. Dyn. 20, 437-485, 2002.**
(Impact Factor 4.923)

14. **Sonawane, K. D**., Sonavane, U.B., and Tewari, R. "Conformational preferences of anticodon 3'-adjacent hypermodified nucleic acid base cis- or trans-Zeatin and its 2-methylthio derivative, cis- or trans-ms^{2}Zeatin". **J. Biomol. Struct. Dyn. 19, 637-648, 2002.**
(Impact Factor 4.923)

15. **Sonawane, K. D.**, Sonavane, U.B. and Tewari, R. "Conformational flipping of the N(6) substitutent in diprotonated N6-(N-glycylcarbonyl) adenines: The role of N(6) H in purine ring protonated ureido adenines. **Intl. J. Quantum Chem. 78, 398-405, 2000.**
(Impact Factor 1.317)

16. Sonavane, U.B., **Sonawane, K.D.**, Morin, A., Grosjean, H. and Tewari, R. "N(7)-protonation induced conformational flipping in hypermodified nucleic acid bases N6-(N-threonylcarbonyl) adenine and its 2-methylthio- or N(6)-methyl-derivatives. **Intl. J. Quantum Chem. 75, 223-229, 1999.**
(Impact Factor 1.317)

17. **Sonawane, K.D.**, Grosjean, H. and Tewari, R. "Conformation of anticodon adjacent hypermodified nucleoside N6-hydroxylisopentenyl adenosine, io6A. **J. Biosci. 24, 183-183, 1999.**
(Impact Factor 1.96).

B) Invited Talks:
1. National conference on **"TRANSCRITION2K12"** on **Advances in Biotechnology** on 16th March 2012 organized by Department of Biotechnology, College of Engineering and Technology Bhambori, Jalgaon, India.
2. "**Symposium on Accelerating Biology 2012: Computing to decipher"**, organized by **Bioinformatics group, Center for Development of Advanced Computing C-DAC Pune, India** 15-17th February 2012 C-DAC Pune.
3. UGC sponsored State Level Seminar on Application of Computer in Biological Sciences, on 21st-22nd December, 2011, Organized by Department of Zoology and Botany, Karmveer Bhaurao Patil Mahavidyalya, Pandharpur, India.
4. **International Interdisciplinary Science Conference on: Bioinformatics**; an Interface between Computer Science and Biology, organized by Centre for

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Interdisciplinary Research in Basic Sciences, Jamia Milia Islamia Unversity, New Delhi, 15-17, November, 2011.

5. One day Workshope on, **"e-learning in Microbiology"**, organized by Department of Microbiology, Dr. Babasaheb Ambedkar Marathwada University, Aurangabad, Sub centre Osmanabad, on 21st August, 2011.

6. Challenges and Opportunities in Information Technology and Bioinformatics **(NCCOITBT-09)**, Swami Vivekanand Mahavidyalaya, Udgir, Maharashtra, India, 27 – 28th February, 2009.

C) <u>Conference organized:</u>

1. Organizing Secretary, UGC SAP DRS-I Sponsored, conference on **"Recent Trends in Life Sciences-2011'** organized by Department of Biochemistry, Shivaji University, Kolhapur, on 4-5 March 2011.

2. Convener, DST PURSE Sponsored, one day "**International Webinar on Advances in Life Science" (WebLS-2012)** organized by Department of Microbiology, Shivaji University, Kolhapur, on 21st January, 2012.

D) <u>Conference attended/Papers presented:</u> (Total: 47)

<u>National:</u> (Total 28)

1. Asmita D Kamble, Susmit B Sambhare, Bajarang V. Kumbhar Navanath M Kumbhar, Rohit S. Bavi and **Kailas D. Sonawane[1*]** "Conformational study of hypermodified nucleosides 5-taurinomethyluridine (tm^5U) and its derivative 5-taurinomethyl-2-thiouridine (tm^5S^2U) using RM1 method. **Second national conference on "Biotechnology, Bioinformatics and Bioengineering"** organized by **Society for Applied Biotechnology (India)** 24-25th February, 2012, Page-49-50.

2. Bajarang V. Kumbhar and **Kailas D. Sonawane** "Molecular dynamics simulation study of model anticodon stem loop structure of tRNA containing hypermodified nucleosides ac^4C at 34th and mS^2hn^6Ade at 37th position" in "**Symposium on Accelerating Biology 2012: Computing to decipher"**, organized by **Bioinformatics group, Center for Development of Advanced Computing C-DAC Pune, India** 15-17th February 2012 Page-68-69.

3. Rohit S. Bavi, Asmita D Kamble, Susmit B Sambhare, Bajarang V. Kumbhar Navanath M Kumbhar and **Kailas D. Sonawane[1*]** "Molecular dynamics simulation study of modified nucleosides N2-methylgaunosine, m^2G present at the hinge region (26th position) of tRNA" in **"Symposium on Accelerating Biology 2012: Computing to decipher"** organized by **Bioinformatics group, Center for Development of Advanced Computing Pune India** 15-17th February 2012 Page 92.

4. Sagar H Barage, Chidamber B Jalkute, Maruti J Dhanwade and Kailas D Sonawane
"Molecular dynamic simulation of whole ECE-1 enzyme with lipid bilayer" **"Symposium on Accelerating Biology 2012: Computing to decipher"**

organized by **Bioinformatics group, Center for Development of Advanced Computing Pune India** 15-17th February 2012, Page-93.

5. Maruti J Dhanwade Sagar H Barage, Chidamber B Jalkute, and Kailas D Sonawane **"Molecular Docking and MD simulation study of aminopeptidase and Aβ peptide"** Symposium on **"Accelerating Biology 2012: Computing to decipher"** organized by **Bioinformatics group, Center for Development of Advanced Computing Pune India** 15-17th February 2012, Page-78.

6. Susmit B Sambhare, Navanath M Kumbhar, Bajarang V. Kumbhar and **Kailas D. Sonawane**[1*] "MD simulation study to investigate role of hypermodified nucleoside lysidine, (k^2C) in proper codon-anticodon recognition" in **"Symposium on Accelerating Biology 2012: Computing to decipher"** organized by **Bioinformatics group, Center for Development of Advanced Computing Pune India** 15-17th February 2012, Page-105-106.

7. Chidambar B. Jalkute, Sagar H. Barage, Maruti J. Dhanawade and **Kailas D. Sonawane** "Virtual screening and molecular dynamics simulation study of ACE inhibitors" P24, '**Conference on Informatics & Integrative Biology (CIIB-2011)' organized by Bioinformatics centre, Bose institute, Kolkata,** India. 14-16 December 2011.

8. Asmita D. Kamble, Susmit B. Sambhare, Bajarang V. Kumbhar, Navanath V. Kumbhar, Rohit. S. Bavi, and **Kailas D. Sonawane** "Molecular dynamics simulation study of hypermodified nucleoside 5- taurinomethyluridine (τm^5U) and its derivative 5-taurinomethyl-2-thiouridine (τm^5s^2U) occur at 'wobble' position in the anticodon loop of tRNA." P25, '**Conference on Informatics & Integrative Biology (CIIB-2011)' organized by Bioinformatics centre, Bose institute, Kolkata**, India 14-16 December 2011.

9. Navanath M. Kumbhar and **Kailas D. Sonawane** "Analysis of compiled tRNA sequence database containing modified nucleoside in anticodon loop of tRNA" in **'Recent Trends in Life Sciences-2011'** Page no.81, organized by Department of Biochemistry, **Shivaji University, Kolhapur**, 4-5 March 2011.

10. Sagar H. Barage, Chidambar C. Jalkute and **Kailas D. Sonawane** "Virtual screening and molecular dynamics simulation study of ECE protease inhibitors" Page No 84, BIF-7, **'Recent Trends in Life Sciences-2011'**, Department of Biochemistry, **Shivaji University, Kolhapur**, March 4-5, 2011.

11. Susmit B. Sambhare, Navanath M. Kumbhar and **Kailas D. Sonawane** "Structural Bioinformatics Unit, Department of Biochemistry, Shivaji University kolhapur- 416 004. "Role of hypermodified nucleoside lysidine (k^2C) in proper codon-antocodon recognition", in **'Recent Trends in Life Sciences-2011'** page no.82, organized by Department of Biochemistry, **Shivaji University, Kolhapur**. 4-5 March 2011.

12. Bajarang V. Kumbhar, Navanath V. Kumbhar, Asmita D. Kamble and **Kailas D. Sonawnae**. "Conformational preferences of the hypermodified nucleosides hn^6A and ac^4C present in the model anticodon loop segment of tRNA." in **'Recent Trends in Life Sciences-2011'** Page no.-80, organized by Department of Biochemistry, **Shivaji University ,Kolhapur**. 4-5 march 2011.

13. Susmit B. Sambhare, Bajarang V. Kumbhar, Navanath V. Kumbhar, Asmita D. Kamble and **Kailas D. Sonawane** "Conformational study and base stacking interactions of hypermodified nucleoside lysidine (k^2C) incorporated in the

trinucleotide segment of anticodon loop of tRNA^{Ile}" **"Accelerating Biology**", **Center for Development of Advanced Computing (C-DAC)** Pune, India, December 14-16, 2010.

14. Rohit S. Bavi, Asmita D. Kamble, Susmit B. Sambhare, Navanath V. Kumbhar, Bajarang V. Kumbhar, and **Kailas D. Sonawane** "Structural role of modified nucleotide m^{2}G and m$^2_2$G inserted in the model diphosphate nucleotide segment of hyperthermophilic tRNAs", **"Accelerating Biology**", **Center for Development of Advanced Computing (C-DAC) Pune**, India, December 14-16, 2010.

15. Sagar H. Barage, Chidambar C. Jalkute and **Kailas D. Sonawane**, "Molecular Dynamics (MD) Simulation Study of Endothelin Converting Enzyme (ECE) with its Inhibitor Phosphoramidon and β-Amyloid Peptide, **"Accelerating Biology", Center for Development of Advanced Computing (C-DAC) Pune**, India, December 14-16, 2010.

16. Asmita D. Kamble, Bajarang V. Kumbhar, Navanath V. Kumbhar, Rohit. S. Bavi, Kailas D. Sonawane, "Conformational preferences of hypermodified nucleoside 5-taurinomethyluridine (τm^{5}U) and its derivative 5-taurinomethyl-2-thiouridine (τm^{5}s^{2}U) occur at 'wobble' position in the anticodon loop of tRNA", **"Accelerating Biology", Center for Development of Advanced Computing (C-DAC) Pune**, India, December 14-16, 2010.

17. Bajarang V. Kumbhar, Navanath V. Kumbhar, Asmita D. Kamble, Rohit S. Bavi, Susmit B. Sambhare and Kailas D. Sonawane, "Structural significance of hypermodified nucleoside N^6-hydroxynorvalylcarbamoyl adenine, hn^{6}Ade and ms^{2}hn^{6}Ade inserted in the trinucleotide segment of anticodon loop of tRNA, **"Accelerating Biology", Center for Development of Advanced Computing (C-DAC) Pune,** India, December 14-16, 2010.

18. Bavi R. S., Kumbhar B. V., Kumbhar N. M. and Sonawane K. D. "Conformational preferences of modified nucleoside 2-methylguanosine (m^{2}G) and its related derivatives occur at 26th position in tRNA of hyperthermophiles" **50th Annual Conference of Association of Microbiologists in India (AMI), National Chemical Laboratory (NCL), Pune,** (GM088), Page no. 197, 18 Dec.2009.

19. Jalkute C.B., Barage S.H., Sonawane K.D. "Homology modeling study of Angiotensin Converting Enzyme from Stigmatella aurantiaca". **50th annual conference of Association of Microbiologists in India (AMI), National Chemical Laboratory (NCL), Pune,** (GM087), Page no. 197, 15-18 Dec.2009.

20. Navanath M. Kumbhar, Abhinandan B. kadam, Bajarang V. Kumbhar, Kailas D. Sonawane. "Quantum chemical study of hypermodified nucleoside, Hydroxywybutosine (yWOH) present in the anticodon loop of tRNA^{phe}" **Challenges and Opportunities in Information Technology and Bioinformatics (NCCOITBT-09), Swami Vivekanand Mahavidyalaya, Udgir,** Latur, India, February, 27-28, 2009.

21. Abhinandan B. Kadam, Navanath M. Kumbhar, Bajarang V, Kumbhar, Kailas D. Sonawane. "Structural study of modified nucleosides m$^2_2$G and m$^2_2$Gm occur at 26th position in tRNA of hyperthermophilic bacteria" **Challenges and Opportunities in Information Technology and Bioinformatics (NCCOITBT-09), Swami Vivekanand Mahavidyalaya, Udgir**, Latur, India, February, 27-28, 2009.

22. Bajarang V. Kumbhar and Kailas D. Sonawane. "Conformational preferences of Hypermodified Nucelotides Present in the Anticodon Loop of tRNA**".**

"Frontiers in Computational Biology", Center for Development of Advanced Computing (C-DAC) Pune, India, July 23-24, 2009.

23. Kailas D. Sonawane. Symposium on Genes to Drugs: In-Silico Approaches, **C-DAC, University of Pune Campus, Pune**, India, April 29-30, 2008.

24. Uddhavesh B. Sonavane, Kailas D. Sonawane and Ravindra Tewari. "Hypermodified Wobble Nucleoside Queuosine in tRNA^{Asp} Anticodon Loop and Significance of Modified Nucleoside Lysidine in Mycoplasma Capricolum tRNA^{Ile}, **National Symposium on Biophysics, TIFR, Mumbai,** India, 21-23 February, 2003.

25. Kailas D. Sonawane, Uddhavesh B. Sonawane and Tewari Ravindra, Discussion **Meeting On Structural Biology And Symposium On Biophysics, University of Madras, Chennai,** India, P83 and P78, January 21-23, 2002.

26. National Symposium on Magnetic Resonance and Biomolecular Structure and Function, **TIFR, Mumbai**, January 17 – 20, 2000.

27. Golden Jubilee Symposium on "Small Scales in Space and Time", **NCL, Pune**, India, November 3 – 5, 1999.

28. National Symposium on Radiation and Molecular Biophysics, **BARC, Mumbai**, India, January 21 – 24, 1998.

International: (Total 19)

29. Apurva D. Kodolikar, Dhanashri S. Patil, Asmita D Kamble, Sagar H. Barage, Chidambar B. Jalkute and **Kailas D. Sonawane**. "Homology modeling study of Chitinase from *Thermomyces lanuginosus*" in **International Conference on "Biotechnology for Better Tomorrow"**(BTBT-2011)at The Department of Microbiology, **Dr. Babasaheb Ambedkar Marathwada University**, **Aurangabad**, Sub-center Osmanabad, Maharashtra, (INDIA), Feb 6-9, 2011.

30. Maruti J. Dhanavade, Sagar H. Barage, Chidambar B. Jalkute and **Kailas D. Sonawane** "Homology modeling study of Cathepsin B (CatB) from Rhodopirellula baltica" in **International Conference on "Biotechnology for Better Tomorrow"(BTBT 2011)** at Department of Microbiology, **Dr. Babasaheb Ambedkar Marathwada University, Aurangabad,** Sub-center Osmanabad, Maharashtra, (INDIA). Feb 6-9, 2011,OMM-13, page-78

31. Chidambar C. Jalkute Sagar H. Barage and **Kailas D. Sonawane**, "Molecular dynamic (MD) of angiotensin converting enzyme (ace) with its inhibitor and β-amyloid peptide." **International Conference on "Biotechnology for Better Tomorrow"(BTBT 2011)** at Department of Microbiology, **Dr. Babasaheb Ambedkar Marathwada University, Aurangabad,** Sub-center Osmanabad, Aurangabad University, Aurangabad.6-9 feb-2011.

32. Jadhav N. R., Bhende S. A., Bhawale B. K., **Sonawnae, K. D**., " Investigation of interactions between Poorly soluble drugs and Moringa coagulant enhancing dissolution", **11th International Symposium on Advances in Technology and Business Potential of New Drug Delivery Systems, organized by Controlled Release Society Indian Chapter, Mumbai**, 16-17, February, 2011.

33. Sagar H. Barage, Priya V. Ayyar, Chidambar B. Jalkute and **Kailas D. Sonawane**,"Structural study of Cathepsin B and its inhibitors produced by plant pathogens", **XXXIII Conference on Indian Botanical Society and International Symposium on the New Horizons of Botany**, Department of Botany, **Shivaji University, Kolhapur,** India, November 10-12, 2010.

34. Sambhare, S.B., Kumbhar, B.V., Kumbhar, N. M, Kamble, A.D. and **Sonawane, K.D.** "Structural significance of hypermodified nucleic acid base 'lysidine' (k^2C) Present at wobble position in the model diphosphate segment (Me-p-k2c-p-me) of E.coli tRNA^{phe} anticodon loop." **International conference on Bioinformatics and System Biology**. Zoology wing –DDE, **Annamalai University, Annamalai Nagar**-608002 India. Page-247, February 19-21, 2010.

35. Sagar H. Barage, Chidambar, B Jalkute, and **Kailas. D. Sonawane**, "Molecular modeling study of endothelin converting enzyme (ECE) embedded in lipid bilayer membrane." **International conference on Bioinformatics and System Biology**. Zoology wing –DDE, **Annamalai University, Annamalai Nagar**-608002 India, Page-60, February 19-21, 2010.

36. Sambhaji. B. Thakar and Kailas. D. Sonawane, "Mangroves plant resource database (MPRDB)" **International conference on Bioinformatics and System Biology**. Zoology wing –DDE, **Annamalai University, Annamalai** Nagar-608002 India, Page-60, February 19-21, 2010.

37. Bajarang V Kumbhar, Navanath M. Kumbhar, and **Kailas D. Sonawane** "Conformational preferences of N6- hydroxynorvalylcarbamoyl adenine, hn^{6}Ade and ms^{2}hn^{6}Ade present at 37th position in the anticodon loop of tRNA" **8th Asia Pacific Bioinformatics conference (APBC), Bangalore**. India, January 18-21, 2010

38. Bajarang V. Kumbhar, Navanath M. Kumbhar and **Kailas D. Sonawane,** "Structural significance of anticodon adjacent hypermodified nucleoside N6-hydroxynorvalylcarbamoyl adenosine, hn^{6}A", **BioConvene: International Conference on Bioinformatics & Drug Discovery, pp. 145, University of Hyderabad, Hyderabad,** December 19-22, 2007.

39. Navanath M. Kumbhar, Bajarang V. Kumbhar and **Kailas D. Sonawane** Conformational study of hypermodified nucleoside Wybutosine occurs at the 3'-adjacent position in the anticodon loop tRNA^{Phe}. **BioConvene: International Conference on Bioinformatics & Drug Discovery, pp. 151, University of Hyderabad, Hyderabad**, December 19-22, 2007.

40. Tewari, R., Sonavane, U. V., **Sonawane, K. D.** and Karpoormath, R. Deficient Wobble Nucleoside Modifications In tRNA: Implications for Decoding and Human Diseases. **Fourth Indo-Australian Conference on Biotechnology, Queensland Institute of Medical Research, Brisbane, Australia**. May 7-9 2007.

41. **Sonawane, K.,** Shrivastava, I., and Guy, H.R. Models of the structure and gating mechanism of the hERG channel. **Biophysical Society 49th Annual Meeting, Long Beach, California, USA**, February 12-16, 2005.

42. **Sonawane, K.D.,** Gea-Ny, Tseng. and H. Robert Guy. Models of the structure and gating mechanism of hERG K$^+$ channels developed from models of KvAP. **Biophysical Society 48th Annual Meeting, Baltimore, MD, USA**. (B363), February 14-18, 2004.

43. Mei Zhang, Jie Liu, **Kailas Sonawane**, Min Jiang, H. Robert Guy, Gea-Ny Tseng. Interactions Between Charged Residues In The Transmembrane Helices Of Herg's Voltage-sensing Domain. **Biophysical Society 48th Annual Meeting, Baltimore, MD, USA.** (B424), February 14-18, 2004.

44. Min Jiang, Mei Zhang, Jie Liu, Innokenty Maslennikov, Yuliya V Korolkova, Alexander S Arseniev, Eugene V Grishin, **Kailas Sonawane**, H. Robert Guy, Gea-Ny Tseng. Probing Dynamic Interactions Between Extracellular S5-p Linker And Other Domains Of The Herg Channel Using Disulfide Formation,

Biophysical Society 48th Annual Meeting, Baltimore, MD, USA. (B426), February 14-18, 2004.

45. **Kailas D. Sonawane**, Uddhavesh B. Sonavane and Ravindra Tewari. "Protonation Induced Conformational Flipping of Hypermodified Nucleosides and Maintenance of the Reading Frame for Codon - Anticodon Interactions" **Physical Aspects of Photobiological Processes: Photobiology and Energy Conversion, Nagoya University, Nagoya Japan,** P23, July 27 – 28, 2001.

46. **Kailas D. Sonawane**, Uddhavesh B. Sonavane and Ravindra Tewari, ICBP 2001, **4th International Conference on Biological Physics, Kyoto International Conference Hall, Kyoto, Japan**, July 30 – August 3, 2001.

47. **Fifth IUPAC International Symposium on Bio-Organic Chemistry, SBOC – 5, NCL, Pune,** India, 30th January- 4th February, 2000.