

CURRICULUM VITAE

Name: **MALLIKA VEERAMALAI**

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Career-Objectives

I am interested in exposing myself to future technologies and shall certainly work hard towards achieving my targets. I am enthusiastic and good team-player as well as an independent researcher. I am interested in dedicated Bioinformatics research work and I would like to utilize my Bioinformatics, Computing skills and Mathematical Knowledge to Solve Complex Biological problems.

Research Interests

Bioinformatics, structural bioinformatics, protein structure and function analysis and prediction, comparison and classification, protein sequence-structural-functional relationships, protein-ligand classification, pattern discovery, pattern matching approaches, fold-recognition, machine learning/ artificial intelligence approaches, systems biology, synthetic biology, translational biology, biochemical pathways modelling and analysis.

Academic Qualifications

- **Post Doctoral Associate** (from Oct 2006), in Prof. Adam Godzik's Lab, Bioinformatics & Systems Biology, Sanford-Burnham Medical Research Institute, La Jolla, San Diego, CA 92037, US.
- **Bioinformatics Consultant** (Feb 2006 – Sep 2006), for database development project, in Prof. Angus Lamond Lab, Wellcome Trust Biocentre, University of Dundee, Scotland, UK.
- **Post Doctoral Research Assistant**, (Aug 2005 – Jan 2006), in the Division of Gene Regulation and Expression lead by Prof. Angus Lamond, Wellcome Trust Biocentre, University of Dundee, Scotland, UK
- **PhD in Computer Science** from Department of Computing Science, University of Glasgow, UK (Oct 2001- Sep 2005). **Title:** "A Novel Method for Comparing Topological Models of Protein Structures Enhanced with Ligand Information" <http://balabio.dcs.gla.ac.uk/mallika/WebTOPS/>
- **Research Assistant**, NCBS (Aug 1999 – Sep 2001) for the *Wellcome Trust Funded Project*, on "Recognition of folds and functions of protein domain superfamilies coded in genome sequences" under supervision of Dr. R. Sowdhamini, Computational Approaches to Protein Science, National Centre for Biological Sciences – TATA Institute for Fundamental Research (NCBS-TIFR), Bangalore, India - <http://www.ncbs.res.in>
- **Post-M.Sc** Advanced Diploma Course in Bioinformatics **First Class** (1998-1999) Bioinformatics Centre, School of Biotechnology, Madurai Kamaraj University, Madurai – 625 021, Tamil Nadu, India.
- **M.Sc.**, Degree in Mathematics **First Class** (1995-1997), Madurai Kamaraj University, Madurai – 625 002, Tamil Nadu, India.

Publications

- Veeramalai M* and Gilbert D, "**Functional analysis of TIM Barrel proteins using TOPS+ Comparison method**", (*Manuscript in preparation*)
- Veeramalai M*, and Godzik A, "**Fast database search for flexible and similar protein structures using TOPS++FATCAT**", (*Manuscript in preparation*)
- Veeramalai M*, Gilbert D and Valiente G "**An Optimized TOPS+ Comparison method for Enhanced TOPS models**", (*Accepted*).
- Veeramalai M* and Gilbert D, "**A Novel Method for Comparing Topological Models of Protein Structures Enhanced with Ligand Information**", (2008), *Bioinformatics*, 24(23):2698-2705
- Veeramalai M*, Ye Y and Godzik A, "**TOPS++FATCAT: fast flexible structural alignment using constraints derived from TOPS+ Strings Model**", (2008), *BMC Bioinformatics*, 9:358.

- Gilbert G, Rosselló F, Valiente G, Veeramalai M. **Alignment-Free Comparison of TOPS Strings**. In J. Daykin, M. Mohamed, K. Steinhöfel (Ed.), London Algorithmics and Stringology, volume 8 of Texts in Algorithmics, Colledge Publications (2007), ch. 11, pp. 177-197.
- Veeramalai M “**A Novel Method for Comparing Topological Models of Protein Structures Enhanced with Ligand Information**”, (2005) Ph.D Thesis, Dept of Computing Science, University of Glasgow, UK.
- Te Ren, Mallika Veeramalai, Aik Choon Tan and David Gilbert, “**MSAT : a Multiple Sequence Alignment tool based on TOPS**”, (2004), *Applied Bioinformatics*, 3(2-3):149-158.
- Nasir L, Gault E, Campbell S, Veeramalai M, Gilbert D, McFarlane R, Munro A and Argyle DJ. “**Isolation and expression of the reverse transcriptase component of the *canis familiaris* telomerase ribonucleoprotein (canTERT)**”, *Gene*, (2004) Jul 7;336(1):105-13.
- Ren T, Veeramalai M, Tan AC and Gilbert D, “**MSAT : a Multiple Sequence Alignment tool based on TOPS**”, *In the Proceedings of the Biological Language Conference (BLC 2003)* J. Klein-Seetharaman, R. Rosenfeld and R. Reddy (editors), BLC., (2003) Nov,p:286-301.
- Veeramalai M and Gilbert D, “**Bioinformatics tools for Protein Structures**”. *Bioinformatics World, Scientific Computing World*, May/June (2002) Issue 64:12-15.
- Mallika V, Anirban Bhaduri and Sowdhamini R., “**PASS2: Semi-Automated database of Protein Alignments Organized as Structural Superfamilies**”. *Nucleic Acids Res.*, (2002), Jan 1;30(1):284-8.
- Bhaduri A, Mallika V and Sowdhamini R., “**Genome analysis of pass2 a semi-automated database of protein alignments organised as structural superfamilies**”. *TheScientificWorldJournal*. (2002) Jan 2;2(1 Suppl 2):9-10.
- Chakrabarti S, Bhavana S, Mallika V and Sowdhamini R., (2002) “**Protein structural similarities and prediction of protein function**”, a book-chapter in 'Trends in Chemistry' (ed. Srivastava, M.M.), India.
→* Corresponding author.

Peer Reviewed International Conference Posters

- Mallika Veeramalai and Adam Godzik, “**Fast database search for flexible & similar structures using TOPS++FATCAT method**”, *International Conference - Genome Biology and Bioinformatics, Nov 12- 14, 2009, Georgia Tech. Atlanta, USA*.
- Mallika Veeramalai, Yuzhen Ye and Adam Godzik, “**TOPS++FATCAT: fast flexible structural alignment using constraints derived from TOPS+ Strings Model**” *16th International Conference ISMB 2008, Toronto, Canada, Poster Abstract: Q46*.
- Mallika Veeramalai and David Gilbert, “**The TOPStrings Protein Structure Comparison Method - A Novel Approach**”. In *Algorithmic Biology Nov 30, 2006, California Institute for Telecommunication and Information Technology, University of California, San Diego, CA, US*.
- Mallika Veeramalai, David Gilbert and David Westhead, “**Incorporating Sequence and Biochemical Information in TOPS models - for Biologically Significant Pattern Matching and Pattern Discovery in Protein Structures**”. In *ECCB 2003 in conjunction with JOBIM 2003, C. Christophe, H.-P. Lenhof and M.-F. Sagot (editors), Poster Abstract: PS-5:p.167-168. ISBN: 2-7261-1257*.
- Mallika Veeramalai, David Gilbert and David Westhead, “**Incorporating Sequence and Biochemical Information in TOPS models - For Biologically Significant Pattern Matching and Pattern Discovery in Proteins**” *11th International Conference ISMB 2003, Brisbane, Australia, Poster Abstract: J-11:p.134*.
- Mallika Veeramalai, David Gilbert and David Westhead, “**Incorporating Sequence and Biochemical Information in Topological Models of Protein Structures Towards Structural and Functional Genomics**” *ECCB 2002 in conjunction with GCB 2002, T. Lengauer, H.-P. Lenhof, R. Christmann (editors), Poster Abstract: P-169:p.249*.
- Mallika Veeramalai, David Gilbert and David Westhead., “**Incorporating Sequence and Biochemical Information in Topological Models of Protein Structure Towards the Structural and Functional Genomics**”. *10th International Conference on Intelligent Systems for Molecular Biology, Edmonton, Canada, August 3-7, 2002, 102-A:p.71*.
- Bhaduri A, Mallika V and Sowdhamini R., “**Genome Analysis of PASS2 A Semi Automated Database of Protein Alignments Organized as Structural Superfamilies**”. *TheScientificWorld*

supplement of the Genome and Beyond Genomics and Structural Biology for Medicine, (Miami Nature Symposium 2002).

- Mallika V, and Sowdhamini R., "PASS2: Semi-Automated database of Protein Alignments Organized as Structural Superfamilies". In *ISMB 2001 – International Conference on Intelligent Systems for Molecular Biology, Poster Abstracts: 257-A*.

Previous Positions

Bioinformatics Consultant (Feb 2006 – Sep 2006), for database development project, for Prof. Angus Lamond Lab, Wellcome Trust Biocentre, University of Dundee, Scotland, UK.

Post Doctoral Research Assistant, (Aug 2005 – Jan 2006), for **Splicing Factor Database (SFD)** in the Division of Gene Regulation and Expression lead by Prof. Angus Lamond, Wellcome Trust Biocentre, University of Dundee, Scotland, UK

PhD Research Student, (Oct 2001 – July 2005), Bioinformatics Research Centre, Department of Computing Science, University of Glasgow. My PhD research work entitled as - “A Novel method for Comparing Topological Models of Protein Structures Enhanced with Ligand Information” under supervision of Prof David Gilbert and Dr. Rob Irwing (second supervisor).

Research Assistant, NCBS (Aug 1999 – Sep 2001) for the *Wellcome Trust Funded Project*, on “Recognition of folds and functions of protein domain superfamilies coded in genome sequences” under supervision of Dr. R. Sowdhamini, Computational Approaches to Protein Science, National Centre for Biological Sciences – TATA Institute for Fundamental Research (NCBS-TIFR), Bangalore, India - <http://www.ncbs.res.in>

Research Experiences

1. In my current postdoctoral work I developed a method, “**TOPS++FATCAT**: fast flexible structural alignment using constraints derived from TOPS+ Strings Model”. This research work has been highly accessed by structural biology and bioinformatics research community and the web-server is available here: <http://fatcat.burnham.org/TOPS/> (Mallika Veeramalai, et.al, (2008) *BMC Bioinformatics*, 9:358; Mallika Veeramalai and Adam Godzik, “Web server - TOPS+FATCAT 3D protein similarity search” – Manuscript in preparation).
2. “Novel Flexible-Templates method for molecular modeling of a given query sequence using FFAS and ProtMod server”. This method uses FFAS (Fold & Function Assignment System) server and generate the inter-mediate models by interpolating two protein structure using FATCAT-DDM (FATCAT Differential Distance Matrix decomposition) approach. Thus, we randomly select 10 inter-mediate models along the trajectory and use them as intermediate templates for a given protein sequence and using the ProtMod we obtain the server models and select the top 5 best models. We have participated in the CASP8 - (8th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction) as a server prediction – “FFASflextemplate”. Initial proof of concept of our novel flexible template method ranked 77 out of 132 predictors, which includes both the server and human predictions. CASP8 assessment results - http://predictioncenter.org/casp8/groups_analysis.cgi. Web server used for CASP8: <http://ffas.burnham.org/protmod/casp/mailmodel.html> (Option: *FlexT_MODEL: flexible templates method*).
3. “Protein molecular modelling and evaluation analysis for choosing the best model from the Suboptimal FFAS Method used in the ProtMod server”. We performed the evaluation analysis on more than 700 models for a given query sequence resulted from the Suboptimal FFAS method used in the ProtMod server. We have utilized different structure comparison and validation tools namely PSQS (Protein Structure Quality Score), DFIRE, Density, TM-Score (Quantitative assessment of protein structure similarities), IF-D (Interaction Finger print derived from the Distance measure) etc., to evaluate all the ProtMod server models and come up with a list of top 5 models which have the best scores consistently from various above mentioned methods. The ProtMod web server can be accessible from the following website: <http://ffas.burnham.org/protmod-cgi/protModHome.pl>. Web server used for CASP8: <http://ffas.burnham.org/protmod/casp/mailmodel.html> (Option: *SubFFAS_MODEL: suboptimal ffas method*). We have participated in the CASP8 as a server prediction - “FFASsuboptimal” and our server ranked as 54 out of 132 predictors, which includes both the server and human predictions.
4. My initial postdoctoral project was, **Splicing Factor Database (SFD)** development and bioinformatics analysis was on splicing factors. This was a proof of concept project – ‘Demonstration of the

- practicality anti-fungal drug discovery from novel RNA processing protein targets'. Our SFD database will support the storage and management of essential data from our drug discovery activities.
5. My PhD Thesis entitled as “*A Novel Method for Comparing Topological Models of Protein Structures Enhanced with Ligand Information*”. This project involves the development of enhanced **TOPS+ Strings models** as well as development of ‘**TOPS+ Comparison**’ protein structure comparison method and implementations. (Mallika Veeramalai and David Gilbert, (2008), *Bioinformatics*, 24(23):2698-2705; ‘**Optimized TOPS+ Comparison**’ Mallika Veeramalai, et.al, (2010) *In press*) <http://balabio.dcs.gla.ac.uk/mallika/WebTOPS/>
 6. Development of “**MSAT – Multiple Sequence Alignment Tool based on TOPS**” collaboration with (Ren et.al., 2004 *Applied Bioinformatics*,3(2-3):149-158).
 7. Bioinformatics sequence and structure prediction and analysis of Reverse Transcriptase component of the *Canis familiaris* telomerase ribonucleoprotein (dogTRET) gene (Nasir et. al., *Gene*. 2004;336(1):105-13).
 8. I was involved in the local system-administration job in the Dr. R. Sowdhamini’s lab, NCBS (1999-2001).
 9. “Genome assignment for more than 75 genome sequences using **PASS2** single and multi-member Superfamily structure based sequence alignments”. This project involved large-scale genome analysis using integration of **BLAST**, **MALIGN**, **PSI-BLAST**, **IMPALA** methods. (Bhaduri et.al., *TheScientificWorldJournal*. 2002 Jan 2;2[1 Suppl 2]:9-10).
 10. “**PASS2:Semi-Automated database of Protein Alignments organised as Structural Superfamilies**”. WWW: <http://www.ncbs.res.in/%7Efaculty/mini/campass/pass.html>. This project involves structure comparison, alignment and Classification methods **SCOP**, **STAMP**, **COMPARER**, **MALIGN** and **JOY**. (Mallika et.al, *Nucleic Acids Res.*, 2002,30(1):284-8).
 11. “Molecular Modelling of Telomeric DNA”. Involves Analysis of Loop Nucleotides in the *G-Quadruplexes* of the Telomeric DNA. We performed the molecular modelling and analysis work by using Biosym Insight-II packages on the Irix operating system. (1999, *BioInformatics Centre, School of Biotechnology, Madurai, Tamil Nadu, India*).

Bioinformatics & Computational Biology Skills

Protein Structure Comparison Servers: Developed algorithms for protein structure comparison and alignments and developed the web servers for same given below:

- TOPS+ Comparison <http://balabio.dcs.gla.ac.uk/mallika/WebTOPS>
- TOPS++FATCAT <http://fatcat.burnham.org/TOPS/>
- PASS2 <http://caps.ncbs.res.in/campass/pass.html>

Relational Databases: Created and worked on TOPS+ relational database using MySQL for my PhD work, also I have hands on experience in TOPS database. Development of SFD - a relational database for splicing factors.

Bioinformatics Databases: Exposed to primary, secondary sequence & structural databases of proteins major analysis work performed based on the TOPS, TOPS+, PASS2, CAMPASS, DDBASE, PDB, CATH, SCOP, PROSITE, UniProt, Pfam, Swiss-Prot, SRS, GenBank, Enzyme, Ligands, PDBSum

Bioinformatics Tools: Exposed to most of the bioinformatics sequence & structural analysis tools

Sequence Analysis: BLAST, FASTA, PHI-BLAST, PSI-BLAST, IMPALA, HMMER, ClustalW, SAM, T-COFFE, MALALIGN, GCG package, Domain Analysis

Protein Structure Predictors: PHD, NNpredict, Jpred, 3D-PSSM, PSI-Pred, TM predictions

Protein Structural Alignments: TOPS, TOPS+, FATCAT, TOPS++FATCAT, COMPARER package, STAMP, CE, DALI, JOY Annotations

Pattern Discovery Tools: TOPS, Pratt.

Molecular Modelling Tools: Homology Modelling, Molecular Modelling & Dynamics package BIOSYM Insight-II, SYBYL, XPLOR, AMBER, MODELLER, ProtMod

Software Skills

Web Tools : HTML, CGI, PHP, Java Scripts
 Programming Languages : Java, Perl
 Databases : MySQL
 Operating Systems : Mac, Linux, Unix, IRIX, COMPAQ, DOS, Windows

Clusters : Hands-on experience with various **Linux clusters** at UofGlasgow and Sanford-Burnham.

Packages : R (Statistical Analysis Tools)

Computer Science Skills

Pattern Discovery, Pattern Matching, Structure Comparison & Classification, Graph Theory, Algorithms and theories over Strings, Sequences, Dynamic Programming, Abstract models, Object Oriented modelling & Programming.

Biological Knowledge

Bioinformatics, Protein Sequence, Structure, Genome Analysis, DNA Structure, Structural Biology, Enzymes, Biochemistry, Molecular Biology, Enzymes, Protein-Ligand information.

Project Supervision

Te Ren “Development of **MSAT:a Multiple Sequence Alignment tool based on TOPS**” (2004), *Applied Bioinformatics*, 3(2-3):149-158. M.Sc. IT Project, University of Glasgow (Co-supervisor).

Teaching & Tutoring Skills

- Tutor for Protein Molecular Modeling & Analysis – practical course for the Scripps Graduate Course, during fall semester 2007, 2008, 2009*. <http://bioinformatics.burnham.org/SSBC/modeling.html>
 - Tutor for Unix/Linux Operating systems (2004) for B.Sc., Computing Students, at University of Glasgow, Scotland, UK.
 - Tutor for Introduction to Bioinformatics for M.Sc., IT students for Spring Term 2003, at University of Glasgow, Scotland, UK* http://www.dcs.gla.ac.uk/~drg/courses/bioinformatics_mscIT/
 - Tutor for Introduction to Bioinformatics (P227) for Graduate students for Spring Term 2002 at City University, London, England, UK*. [http://www.dcs.gla.ac.uk/~drg/courses/bioinformatics_city/]
 - Tutor for Computer Graphics (P214) for Graduate students for Spring Term 2002 at City University, London.
- *Includes preparation of the lecture slides, tutorials, hands-on-website tutorial and delivered lectures related to Protein structure comparison, prediction, molecular modeling etc.

Reviewer

1. Reviewer for Oxford Bioinformatics Journal.
2. Reviewer for BMC Bioinformatics Journal.
3. Reviewer for BMC Structural Biology Journal.
4. Reviewer for IEEE Transactions on Information Technology in Biomedicine.
5. European Conference on Computational Biology - ECCB06, ECCB02
6. Reviewer for ISCB Student Council Symposium, SCS1, Madrid, Spain, SCS2, Brazil.

Research Collaborators

1. Prof. Adam Godzik (Bioinformatics & Systems Biology, Sanford-Burnham Medical Research Institute), Dr. Yuzhen Ye (Now Assistant Professor School of Informatics, Indiana University) – *Development of TOPS++FATCAT: fast flexible structural alignment using constraints derived from TOPS+ Strings Model.*
2. Prof. Adam Godzik, Dr. Piotr Cieplak (Senior Scientist) and Zhanwen Li (Bioinformatics Programmer) at Bioinformatics & Systems Biology, Sanford-Burnham Medical Research Institute; Dr. Lukasz Jaroszewski (Joint Center for Structural Genomics) - *Protein molecular modeling and evaluation analysis of the SuboptimalFFAS approach used in the ProtMod server.*
3. Prof. Adam Godzik, Dr. Piotr Rotkiewicz (now Senior Scientist at Schrödinger), Dr. Piotr Cieplak (Senior Scientist) and Zhanwen Li (Bioinformatics Programmer) at Bioinformatics & Systems Biology, Sanford-Burnham Medical Research Institute; Dr. Lukasz Jaroszewski (Joint Center for Structural Genomics) - *Novel Flexible Templates method for molecular modeling using FFAS, FATCAT-DDM, ProtMod.*
4. Prof. Angus Lamond, Dr. Paul Ajuh, Dr. Andrea Pawellek and Dr. Xiuwen Tang, Division of Gene Regulation and Expression, Wellcome Trust Biocentre, University of Dundee, UK – *Development of Splicing Factors Database.*
5. Prof David Gilbert (Bioinformatics Research Centre, University of Glasgow, UK) and Dr. Rob Irving (Formal Analysis, Theory, and Algorithms group, Department of Computing Science, University of

- Glasgow, UK) –*Algorithm development for enhanced TOPS+ models and protein structure comparison.*
6. Prof. David Westhead, Dr. Ioannis Michalopoulos (Bioinformatics Group, University of Leeds, UK) and Prof. David Gilbert, Mr. Gilleain Torrance (Bioinformatics Research Centre, University of Glasgow, UK) and Dr. Juris Viksna (Institute of Mathematics and Computer Science, Riga, Latvia.) – *Enhanced TOPS+ ligands data and model.*
 7. Dr. Lubna Nasir (Department Veterinary Clinical Studies, Institute of Comparative Medicine, University of Glasgow Veterinary School, Bearsden Road, Glasgow G61 1QH, Scotland, UK) and Prof. David Gilbert (Bioinformatics Research Centre, University of Glasgow, UK) – *on sequence, secondary structure prediction and analysis of the reverse transcriptase component of the Canis familiaris telomerase ribonucleoprotein.*
 8. Dr. R. Sowdhamini and Dr. Anirban Bhadhuri – *on PASS2: Protein Alignments organized as Structural Superfamilies knowledge-base development and Genome Annotations using PASS2: Protein Structural Superfamily Alignments.**
 9. Dr. R. Sowdhamini, Dr. S. Chakarabarti and S. Bhavana – *on Protein structural similarities and prediction of protein function.** [* Computational Approaches to Protein Science, NCBS-TIFR, Bangalore, India]
 10. Dr. Z. A. Rafi, (Bioinformatics Centre, School of Biotechnology, Madurai Kamaraj University, Tamil Nadu, India) – *on Molecular Modelling and Analysis of Loop Nucleotides in G-Quadruplexes of the Telomeric DNA.*

Professional Activities

1. Program committee member for “Joint Automated Function Prediction (AFP) - Biosapiens SIG on Intelligent Systems for Molecular Biology (ISMB) 2008, Toronto, Canada.
2. Supervised and organized the Godzik Lab’s weekly lab meeting. (April 2007 – Jul 2008).
3. Organized the Godzik’s Lab’s Retreat on 28th June 2007, at Mission Bay, San Diego.
4. The Student Council Secretary for the International Society for Computational Biology – Student Council (ISCB-SC) form (20th June 2005 – Sep 2006); Student Council leader (Sep 2006 – present).
5. Program committee member for the 3rd ISCB Student Council Symposium (SCS3), July 21st, 2007, Vienna, Austria.
6. Member of Genome India International (GII) (2005 – present).
7. Member of UK Bioinformatics Forum (2004 – present).
8. Member of Scottish Bioinformatics Forum (2003 - present).
9. Member of the International Society for Computational Biology (ISCB) (2002 – present).
10. Member of the Indian Bioinformatics Society (INBIOS) (2001 – present).
11. Member of the Asia-Pacific Bioinformatics Networks (APBioNet) (2001 – present).

Fellowships / Grants / Awards

- ISMB/ISCB Travel Fellowship Award to attend the 17th International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2009), Stockholm, Sweden, Jun 27 – Jul 2, 2009 (*Declined*).
- ISMB/ISCB Travel Fellowship Award to attend the 16th International Conference on Intelligent Systems for Molecular Biology (ISMB 2008), Toronto, Canada, July 19 – 23, 2008.
- Won iPod shuffle for “The Open Protein Structure Annotation Network” - TOPSAN logo design contest, Oct, 2007.
- Post Doctoral Associate Fellowship (from Oct 2006), Sanford-Burnham Medical Research Institute, San Diego, California, US.
- ISMB/ISCB Travel Fellowship Award to attend the 14th International Conference on Intelligent Systems for Molecular Biology (ISMB 2006), Fortaleza, Brazil, Aug 6 -10, 2006 (*Declined*).
- Post Doctoral Research Fellowship (Aug 2005 – Jan 2006), Division of Gene Regulation and Expression, Wellcome Trust Biocentre, University of Dundee, UK.
- ECCB Travel Fellowship Award to attend 2nd European Conference on Computational Biology (ECCB 2003) in conjunction with JOBIM 2003, Paris, France, September 27 - 30, 2003.
- ISMB/ISCB Travel Fellowship Award to attend the 11th International Conference on Intelligent Systems for Molecular Biology (ISMB 2003), Brisbane, Australia, June 29 - July 3, 2003.

- Research Student Travel Grant, Department of Computing Science, University of Glasgow to attend ISMB 2003, Brisbane, Australia, June 29 - July 3, 2003.
- ISCB Travel Fellowship Award to attend European Conference on Computational Biology (ECCB2002), October 06 – 09, 2002, Saarbrücken, Germany.
- ISMB/ISCB Travel Fellowship Award to attend the 10th International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2002), Edmonton, Canada, Aug 3-7, 2002.
- Research Student Travel Grant, Department of Computing Science, University of Glasgow to attend GPC VII, September 11 – 13, 2002, University of Southampton, Southampton, England, UK.
- Ph.D. Studentships, University of Glasgow, Glasgow, Scotland, UK. (2002-2004).
- Ph.D. Studentships, City University, London, UK. (Oct 2001- Mar 2002).
- ISMB/ISCB Partial Travel Fellowship Award to attend the 9th International Conference on Intelligent Systems for Molecular Biology (ISMB 2001), Copenhagen, Denmark, July 21 -25, 2001.
- Wellcome Trust Grant (2000-2001) for Research Assistant post under supervision of Dr.R.Sowdhamini, Computational Approaches to Protein Science, National Centre for Biological Sciences – TATA Institute for Fundamental Research (NCBS-TIFR), Bangalore, India.
- Junior Research Fellowship from National Centre for Biological Sciences – TATA Institute for Fundamental Research (NCBS-TIFR) under supervision of Dr.R.Sowdhamini, Computational Approaches to Protein Science, Bangalore, India.
- DBT fellowship for Post-M.Sc., Advanced Diploma course in Bioinformatics (1998 -1999) from Department of Bio-Technology, Government of India.

Extracurricular Activity

- Hobby photographer (self taught): <http://www.flickr.com/photos/kaaviyam>
- Volunteered as a photographer for:
 - Godzik's Lab's Retreat on 28th June 2007, at Misson Bay, San Diego.
 - <http://picasaweb.google.com/kaaviyam/GodzikLabRetreat62807732PM>
 - SDTS: San Diego Tamil Sangam (<http://sdts.org/>), Pongal Sirippu Nigazhchchi, 26, Jan, 2008.
 - <http://picasaweb.google.com/kaaviyam/SDTSPongalCelebrations?authkey=RTLxrWUr7A4>

Academic References

Prof. Adam Godzik, Bioinformatics and Systems Biology Program Director,

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<http://bioinformatics.burnham.org>

Prof. David Gilbert, Chair and Head of School of Information Systems, Computing and Mathematics,

St Johns - Room SJ023A, Interdisciplinary programme in Computational Systems and Synthetic Biology, School of Information Systems, Computing and Mathematics, Brunel University, Uxbridge, Middlesex UB8 3PH, UK

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<http://people.brunel.ac.uk/~csstdrg>

Prof. Angus Lamond, FRSE Wellcome Principal Research Fellow and Professor of Biochemistry,

Division of Gene Regulation and Expression, Wellcome Trust Biocentre, University of Dundee,

Dundee DD1 5EH. E-mail: a.i.lamond@lifesci.dundee.ac.uk, Ph: +44 (0)1382 385473.

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Dr. R. Sowdhamini, Faculty member and Group Leader of CAPS,

Computational approaches to protein sciences (CAPS), NCBS-TIFR, UAS-GKVK Campus, Bangalore-560065, Karnataka, India. E-mail: mini@ncbs.res.in, Ph: +91-(0)80-3636421/8 Ex: 4240.

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