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PROFESSIONAL EXPERIENCE

- Associate Research Scientist, Bioinformatics, Digital Technology Center, University of Minnesota. (July 2003 - present)
- Assistant Research Scientist, Integrative Bioscience, San Diego Supercomputer Center, University of California, San Diego (UCSD). (April, 2001- June, 2003)
- Visiting Scientist, National Partnership for Advanced Computational Infrastructure - Integrative Bioscience, San Diego Supercomputer Center, University of California, San Diego. (1998-2001)
- Staff Scientist GrIV(3), Center for Cellular and Molecular Biology, Hyderabad, India. (1993-1998)
- Visiting Research Fellow, Berkbeck College, University of London, UK. (1991-1993)
- Staff Scientist GrIIV(2) Center for Cellular and Molecular Biology, Hyderabad, India. (1988-1993)
- Research Associate, Department of Zoology, University of Pune, India. (1987-1988)

EDUCATION

- Post Doc., Prof. Sir. Tom Blundell(F.R.S)'s Lab. Berkbeck College, University of London, UK. (1991-1993).
- Ph.D., Life Sciences, University of Hyderabad & Centre for Cellular and Molecular Biology, Hyderabad, India. (1988) Thesis Title: "*DNA sequence data analysis some structural and Biological Implications".*
- M.Sc., Life Sciences, Jawaharlal Nehru University, New Delhi, India. (1982)
- B.Sc. (Math, Physics, Chemistry), Osmania University, Hyderabad, India. (1980)

AWARDS & HONORS

- Indian National Science Academy – British Royal Society exchange award. (1997)
- Visiting Scientist, European Bioinformatics Institute, Hinxton, Cambridge, U.K. (August, 1997)
- Visiting Scientist, Department of Biochemistry, University of Cambridge, U.K. (July, 1997)
- European Economic Commission Bursary award. (1992-93)
- Department of Biotechnology, Govt. of India, Overseas Associate award. (1991-1992)
- Council of Scientific and Industrial Research National Merit Scholarship, Ph.D. (1982-1988)
- Merit Scholarship, Jawaharlal Nehru University, New Delhi, India, M.Sc. (1980-1982)

RESEARCH GRANTS

- **Boojala Reddy (PI)**, Yiannis Kaznessis (co-PI) National Science Foundation USA. "A systematic analysis of hyperthermophile, mesophile and psychrophile genomes to discover rationale for function at varied temperatures. (submitted in July, 2004)
- **Boojala Reddy (PI)**, Yiannis Kaznessis (co-PI) National Science Foundation USA. "Analysis of protein structural data to develop novel method(s) to improve protein core modeling. (submitted in July, 2004)
- Philip E. Bourne (PI), Mauricio S Montal (co-PI) & **Boojala V. B. Reddy (co-PI)** (DBI-0111709 Dated Sept. 13,2001: $240,001) Awarded by National Science Foundation USA. "Voltage-gated ion channel protein resource database".
- **Boojala V. B. Reddy (PI)** . (SP/SO/D-01/95 Dated: June 21,1996: INR 1,367,470) award by Department of Science and Technology, Ministry of Science and Technology, Govrnment of India. (1996-1999) "Analysis of Packing Relations of Secondary Structures in Proteins".

COMPUTATIONAL EXPERIENCE

- FORTRAN, C/C++ , PERL, JAVA extensively used for software development.
- Several Sequence and structural data analysis software tools (Modeler, Composer, Swiss-Model, PC_GENE, GCG, etc.)
- Accelrys Software InsightII, (Biopolymer, Discover, Dock, Homology, Ludi etc.) and FRODO.
- Computers: SGI, DEC-alpha, SUN, VAX, PDP-11, Evans & Sutherland, convex., PC.
- Operating systems: UNIX/IRIX, DOS, VMS, OSF, LINUX.

TEACHING / SUPERVISING

- DNA and Protein sequence data analysis tools to graduate researchers at CCMB.
- UCSD-Bioscience Extension Classes to Industry Professionals.
  - Protein Sequence and structural data analysis. (2000-01)
  - Comparative Protein Modeling Principles and Practice. (2001-02)
  - Advanced tools and Algorithms in Bioinformatics. (2001-02)
  - Principles of Protein Structure and Comparative Modeling. (2002-2003)

  U of MN Bioinformatics Workshop: “Perl for Bioinformatics”.
- Supervised 4 postgraduate researchers and 3 technical assistants, 3 summer interns

CONSULTING EXPERIENCE

- Senior Consultant for Identification of Peptidomimetics by Knowledge-based modeling for Reddy US therapeutics, GA (2002).
- Senior Consultant on the project for Identification of Peptidomimetics by Knowledge-based modeling for Angion Biomedica, NY. Lead products have been tested to be promising (2001).

MANUSCRIPT REVIEWER

- Bioinformatics
- Journal of Biosciences
- Biophysical Journal
- Genes
- Journal of Biomolecular Structure and Dynamics
- Proteins: structure, function and bioinformatics
- Indian Journal of Biochemistry & Biophysics
- Protein Engineering Design and Selection

MEMBERSHIP TO PROFESSIONAL SOCITIES

- Member American Association for Advancement of Science (AAAS)
- Elected Member American Chemical Society (ACS)
- Member International Society for Computational Biology (ISCB)
- Member Protein Society (PS)
- Life Member Indian Biophysical Society (IBS)
- Life Member Society of Biological Chemists, India (SBCI)

RESEARCH PUBLICATIONS (*Communicating author)

- **Reddy BVB**, Kaznessis Y (2004) Quantitative analysis of amino acid position conservation in interface regions of protein-protein hetrocomplexes. (submitted).
- Duan, Y. **Reddy BVB**, Kaznessis Y (2004) Physicochemical and residue conservation calculations to improve the ranking of protein-protein docking solutions. *Protein Science* (in press).
- Vicatos S, **Reddy BVB**, Kaznessis, Y. (2004) Prediction of distant residue contacts with the use of evolutionary information from PFAM database. *Proteins: Struct. Func. and Bioinfo* (in press).
- **Reddy BVB**, Li WW, Bourne P. (2002) Use of Conserved Key Amino Acid Positions to Morph Protein Folds. *Biopolymers*. 64: 139 – 145.
- Li WW, **Reddy BVB**, Tate J, Shindyal I, Bourne P (2002) CKAAPs: A Conserved Key Amino Acid Positions DataBase. *Nucleic Acids Research.* 30: 409 - 411.
- Li WW, **Reddy BVB**, Shindyal I, Bourne P (2001) CKAAPs: A Conserved Key Amino Acid Positions DataBase. *Nucleic Acids Research.* 29: 329-31.
- **Reddy BVB**, Li WW, Shindyal I, Bourne P (2001) Conserved Key amino acid Positions (CKAAPs) derived from analysis of common substructures in proteins. *Proteins: Struct.*

Func. and Genetics. 42: 148-63.

- Nagarajaram HA, **Reddy BVB**, Blundell TL (1999) Analysis and prediction of inter-strand packing distances between beta-sheets of globular proteins. *Protein Engng* 12(12): 1055-1062.
- Burke DF, Deane CM, Nagarajaram HA, Campillo N, Martinez MM, Mends J, Molina F, Perry J, **Reddy BVB**, Soares CM, Steward RE, Williams M, Carrondo MA, Blundell TL, Mizyguchi K (1999) An iterative structure-assisted approach to sequence alignment and comparative modelling. *Proteins: Struct. Func. and Genetics.* Supplement 3, 55-60.
- **Reddy BVB**, Nagarajaram HA, Blundell TL (1999) Analysis of interactive packing of secondary structural elements in a/b units. *Protein Science* 8, 573-586.
- Tiwari S, **Reddy BVB*** (1999) A statistical analytical approach to predict secondary structure of protein from amino acid sequence information. *Theoretical Chemistry Accounts* 101, 41-45.
- **Reddy BVB***, Datta S, Tiwari S (1998) Use of structural environment of amino acids to study effect of substitution mutations on protein stability. *Protein Engng.* 11, 1137-1145.
- **Reddy BVB***, Ramesh P, Tiwari S (1998) MICPS: substitution mutations to engineer intracellular protein stability. *Bioinformatics* 14, 225 - 226.
- **Reddy BVB**, Gopal V, Chatterji D (1997) Recognition of promoter DNA by subdomain 4.2 of *Escherichia coli* sigma-70: A knowledge based model of -35 hexamer interaction with 4.2 helix-turn-helix motif. *J. Biomol. Str. Dyn.* 14, 407 - 419.
- **Reddy BVB*** (1996) Structural distribution of di-peptides that are identified to be determinants of intracellular protein stability. *J. Biomol. Str. Dyn.* 14, 201 - 210.
- Kolaskar AS, Joshi B, **Reddy BVB** (1995) Contextual constraints in the choice of synonymous codons *Indian J. Biochem. Biophy.* 32, 417 - 423.
- **Reddy BVB***, Pandit MW (1995) A statistical analytical approach to decipher information from biological sequences: Application to murine splice-site analysis and prediction *J. Biomol. Str. Dyn.* 12, 785 - 801.
- Rajendrakumar CSV, **Reddy BVB**, Reddy AR (1994) Proline - protein interactions: Protection of structural and functional integrity of M4 lactate dehydrogenase. *Biochem. Biophy. Res. Com.* 201, 957 - 963.
- **Reddy BVB**, Blundell TL (1993) Packing of secondary structural elements in proteins: Analysis and prediction of inter-helix distances. *J. Mol. Biol.,* 233, 464-479.
- Guruprasad K, **Reddy BVB**, Pandit MW (1990) Correlation between Stability of a Protein and its Di-peptide Composition: A Novel Approach for Predicting in vivo Stability of a Protein from its Primary Sequence. *Protein Engng.* 4, 155-161.
- Kolaskar AS, **Reddy BVB** (1986) Contextual Constraints on Codon Pair Usage Structural and Biological Implications. *J. Biomol. Struc. Dyn.* 3, 725-738.
- Kolaskar AS, **Reddy BVB** (1985) Complementary DNA Sequence Data Analysis of Prokaryotic Systems. *J. Biosci.* 7, 45-59.
- Kolaskar AS, **Reddy BVB** (1985) A method to locate Protein Coding Sequences in DNA of prokaryotic systems. *Nucleic Acids Res.* 13, 185-194.

CHAPTERS IN BOOKS

- **Reddy BVB***, Bourne P. (2002) Chapter 12: Protein Structure Evolution and the SCOP database in *Structural Bioinformatics* – John Wiley & Sons Publication. (Edt. Phil E. Bourne, Helge Weissig) 239 – 248.
- **Reddy BVB*** (2002) Chapter 2: Secondary Structural packing in proteins in *Protein Folding Stability and Design* (Edt: Machael Gromiha , S. Seljaraj) 25 - 36.
- **Reddy BVB***, Deshpande M, Pandit MW (1991) “Computer Prediction of Splice Sites in Human Genome in *Computers in Bio-medicine* - Computational Mechanics Publications (Edt: K D Held, C A Brebbia and R D Ciskowski) 47 - 60.

PUBLISHED RESEARCH SUMMARIES/ABSTRACTS

- Duan, Y., **Reddy, BVB,** Breslauer, D, Kaznessis Y. (2004) An Efficient Docking Method to Study Protein Interactions. *Biophysical Journal* (Suppliment) 86(1): pp267a
- David A. Chalton, **Reddy, BVB.**, Murray-Rust, J (2002) Catalysis and regulation: Proteins - Web alert, *Current Opinion in Structural Biology.* 12: 693-694.

- Lakey JH, **Reddy BVB**, Murray-Rust, J (2001) Macromolecular assemblages Theory and simulation - Web alert. *Current Opinion in Structural Biology.* 11: 139-40.
- **Reddy, BVB.**, Nair,T M., Li, WW., Shindyalov, IN. and Bourne, PE. (2000) Conserved Amino Acid Positions (CKAAPs) in Proteins: Implications in Protein stability and structural integrity *Protein Science* l9(suppl.1),78
- **Reddy BVB**, Datta S (1997) Analysis of structural environment of amino acids that alter in vitro protein stability. *J. Biomol. Str. Dyn.* 14(6), pp772.
- **Reddy BVB**, Blundell TL (1993) Proximal distance between two interacting helices and a volume dependent parameter of the residues in packing interface - a useful correlation for protein modelling. *Protein Engineering.* 6 (Supplement), pp 123.
- **Reddy BVB** (1993) Correlation Between Stability of a Protein and its Di-peptide Composition: Studies on the Structural and Biological Implications. *Protein Eng.* 6 (Supplement), pp24.
- Nagarajaram HA, **Reddy BVB**, Blundell TL (1997) Packing of secondary structural elements in proteins - An analysis. *Protein Science.* 6: pp87.

INVITED TALKS (SELECTED)

- Department of Biotechnology, University de Montreal, Canada. “Conserved key amino acids: implications to protein folding, function and protein-protein interactions” (Dec, 2003).
- Department of Biology, University of Alaska, Fairbanks. “Use of Conserved Key Amino Acid Positions to morph protein folds” (July, 2003).
- Epimmune, San Diego, California. “Correlation between Stability of a Protein and its Di-peptide Composition: A Novel Approach for Predicting In vivo Stability of a Proteins from its Primary Sequence”. (2002)
- Keck Graduate Institute, Claremont, California. “Use of Conserved Key Amino Acid Positions (CKAAPs) for Fold Recognition in Protein Modeling”. (2000)
- The Burnham Institute, La Jolla, California. “Comparative Protein Modeling Principles and Practice”. (2000)
- EMBL Heidelberg, Germany. “Theoretical Studies on Protein Stability and its Di-peptide Composition”. (1992)
- First International Meeting, Young Perspectives in Molecular Biotechnology, at Maxplank's Institute, Gottingen, Germany. “Synonymous Codon Choice - Possible Relevance to Protein Folding”. (1992)

I HAVE OVER 30 PRESENTATIONS IN CONFERENCES AND MEETINGS

REFERENCES

- Prof. Phil E Bourne, Senior Principle Scientist, San Diego Supercomputer Center, University of California, 9500 Gilman Drive, La Jolla, San Diego CA 92093-0537. Email: bourne@sdsc.edu; Tel:858-534-8301; Fax: 858-822-0873
- Dr. Ilya N. Shindyalov, San Diego Supercomputer Center, University of California, 9500 Gilman Drive, La Jolla, San Diego CA 92093-0537. Email: shindyal@sdsc.edu; Tel:858-534-8322; Fax: 858-822-0873.
- Michael Gribskov, Ph.D., President, ISCB, Professor of Biological Sciences, Purdue University, Lilly Hall of Life Sciences, 915 W. State Street, West Lafayette, IN 47907-2054; Email: mgribsko@purdue.edu Tel: 765-494-6933, Fax: 765-494-0876
- Dr Ch. Mohan Rao, Deputy Director, Centre for Cellular and Molecular Biology , Uppal Road, Hyderabad - 500 007, India; mohan@ccmb.res.in; Tel: 91-40-27160222; FAX:91-40-27160591.
- Prof. Yiannis Kaznessis, 253 Amundson Hall, 421 Washington Ave SE, Chemical Engineering and Meterials Science, University of Minnesota, Minneapolis, MN 55455. Email: yiannis@cems.umn.edu, Tel: 612-624-4197; Fax: 612-626-7246.