

Curriculum Vitae of N. Srinivasan
(dated 24 May 2015)

Personal Details:

Name (with expanded initials)	Narayanaswamy Srinivasan
Date of Birth:	1 April 1962
Sex:	Male
Place of Birth:	Madras (Chennai), India
Nationality:	Indian
Address for correspondence:	Molecular Biophysics Unit Indian Institute of Science Bangalore 560 012 India
Telephone:	+91-80-2293 2837
Fax:	+91-80-2360 0535
E-mail:	ns@mbu.iisc.ernet.in
Lab URL:	http://nslab.mbu.iisc.ernet.in

Research Interests:

Computational genomics, bioinformatics and structural biology involving relationship between protein structure, function and interactions. Cellular signal transduction. Protein-protein interactions, biological pathways.

Educational Qualifications:

1991	Ph.D Molecular Biophysics Unit, Indian Institute of Science, Bangalore. Thesis: <i>Conformational studies on globular proteins: Data analysis.</i>
1984	First class M.Sc in Biophysics at Dept. of Crystallography and Biophysics, University of Madras, India.
1982	First class B.Sc in Physics, University of Madras, India.

Positions:

Post	Funded by	Dates	Educational establishment
Professor	DBT, DST, CSIR New Delhi; Indo-French and Indo-UK collaborative grants	June '10 – Till date	Molecular Biophysics Unit, IISc, Bangalore. India
Associate Professor	DBT and CSIR, New Delhi; Indo-French and Indo-UK collaborative grants	June '04 – June '10	Molecular Biophysics Unit, IISc, Bangalore. India
Assistant Professor & International Senior Fellow of the Wellcome Trust.	The Wellcome Trust, London	June '98-June '04	Molecular Biophysics Unit, IISc, Bangalore. India
Visiting Professor	Reunion University, Reunion islands, France	Yearly visits since May '04	Biochemistry department, Reunion University, Reunion islands, France
Senior Fellow	Manchester University, UK	March 08 onwards	Biological Sciences, Manchester University,
Honourary Research Fellow	Honourary position	Sep. '98 – Sep. 2000	Dept. Cryst. Birkbeck College, London, U.K.
Postdoctoral – Computing	Wellcome Trust, to Prof. Blundell	Oct '96-May '98	Dept. of Biochem., Univ. Cambridge, U.K.
Postdoctoral - crystallography & computing *	Ludwig Institute for Cancer Res., London, to Prof. Waterfield	Aug '94- Sep '96	Ludwig Institute for Cancer Res., University College, London, U.K.
Postdoctoral - Computing	A grant by Tripos Inc., St. Louis, to Prof. Blundell	Nov '91-July '94	Dept. Cryst. Birkbeck College, London, U.K.
Senior Research Fellow	Dept. of Sci. & Tech. India, to Prof. Balaram	Jan '91-Oct '91	Mol. Biophys. Unit, Indian Inst. of Sci., Bangalore.

* Honourary visiting research fellow in the laboratory of Prof. Blundell, Birkbeck college, London.

Research group:

Srinivasan's group has an average population of 18 members in the last 6 years with roughly half the number corresponding to PhD students and the other half corresponding to postdoctorals and technicians. So far, 14 of his students have obtained their PhD under his guidance. Several students have done their Masters project with him. He is currently guiding 6 direct students towards their PhDs and he is a joint-guide to another 4 students from Mathematical Biology Programme.

Honours and Awards:

International Senior Fellow of the Wellcome Trust, UK

National Bioscience Award of DBT, Government of India.

Shanti Swarup Bhatnagar Prize awarded by the Council of Scientific and Industrial Research, Government of India – Highest Science prize in India

J. C. Bose National Fellowship, Department of Science & Technology, Government of India

Membership / affiliations in professional bodies

Elected Fellow of the Indian Academy of Sciences, Bangalore (Since 2007)

Elected Fellow of the National Academy of Sciences, India, Allahabad.

Member of the committee on Affiliates and Special Interests Group, International Society of Computational Biology (ISCB), USA

Visiting Professor of Bioinformatics to Reunion university, France since 2004 involving annual visits.

Visiting Professor of Bioinformatics to University of Nantes, France during July 2012

Senior Fellow of the Manchester University, UK

Other professional activities:

A faculty member in the *Faculty of 1000 in Biology* in the section *Structural Biology – Structural Genomics*.

Member of the Editorial Board of the journals

1. *Bioinformatics*
2. *PLoS ONE*
3. *F1000 Research*
4. *International Journal of Bioinformatics Research and Applications*
5. *Research & Reviews in Biosciences*
6. *Resonance*

7. *In Silico Biology*
8. *The Scientific World Journal - Structural Biology*
9. *Biology Direct*
10. *Scientific Reports (Nature Publishing Group)*

Associate Editor of

1. *International Journal of Knowledge Discovery in Bioinformatics*
2. *Bioinformation*.

Acted as a Guest Editor for

1. *PLoS Computational Biology*.
2. *Journal of Biosciences*
3. *Progress in Biophysics & Molecular Biology*
4. *Current Opinions in Structural Biology - Theory and Simulation section* (ongoing).

Member of the programme committee of PRIB 2007 (Pattern Recognition In Biology), an International conference held in Singapore in October 2007.

A speaker in the *Keystone symposium* held in Cambridge, UK in 2006 on *Multi-protein complexes*.

Invited keynote speaker in Asia-Pacific Bioinformatics Conference 2012, Melbourne, Australia

Refereed manuscripts for publication in: *PNAS, J. Mol. Biol., Proteins: Str. Fn. Gen., Prot. Engng., Prot. Sci., Bioinformatics, BMC Bioinformatics, BMC Structural Biology, J. Biomol. Str. Dyn., J. Biosci., Curr. Sci., Trends Biotech., PEDS, Prog. Biophys. Mol. Biol., BMC Genomics, BMC Microbiology, Amer. J. Pharmacogenomics, Nucl. Acids Res., FEBS Letters., PLoS Comp. Biol. J. Struct. Biol., Int. J. Biol. Macromol., J. Bact., Resonance, FEBS Journal, PLoS ONE, IJBRA, Plant Systematics and Evolution, DNA Research, Theory in Biosciences, BBA, Computers in Biology & Medicine, J Mol Recogn*

Refereed grant applications for Department of Biotechnology, New Delhi, Career Development program of the Wellcome Trust, London, HFSP, France, Wellcome Trust's review of progress made by Sanger Centre, UK, Council of Scientific and Industrial Research and Department of Science and Technology, New Delhi, Department of Information Technology, Delhi. Acted as a member of the committee for the promotion of scientists working in CSIR institutions and various awards.

Acted as PhD thesis examiner of thesis submitted from Panjab university, University of Kerala, Central University – Hyderabad, Delhi University, Madurai-Kamaraj University, Jadhavpur university, Anna University, Reunion university, SASTRA and Bharathidasan University, Vellore Institute of Technology, Kuvempu University, Reunion university (France), Macquarie University, Sydney, Australia. J.N. University, Delhi.

Acted as a referee for the promotion of a faculty member of Brigham Young University, USA, for a member of faculty in a South African University and for a faculty member in University of Manchester, UK.

Served as a coordinator of the Integrated PhD programme in Biological Sciences and a member of the core committee on Integrated PhD programmes, Indian Institute of Science.

Coordinator of BS Programme in Biology

Member of the Scientific Advisory Board of Jubilant Biosys.

Patents:

Complete application filed for Novel AAV vectors-

1. INDIA 1714/CHE/2012
2. USA 13/886,241
3. EUROPEAN UNION EP13166332.0

Inventors: G.R. Jayandharan, Dwaipayana Sen, Sangeetha Hareendran, Nishanth Gabriel, Ruchita Selot, Akshaya, K, Balaji B, Alok Srivastava [CMC, Vellore], Sudha Govindarajan, Rupali Gadkari, N Srinivasan [IISc, Bengaluru]

General publications

[1] C.Ramakrishnan, N.Srinivasan & D.Prashanth (1987) Conformation of glycyI residues in globular proteins. *Int. J. Pept. Prot. Res.*, **29**, 629-637.

[2] R.Sowdhamini, N.Srinivasan, B.Shoichet, D.V.Santi, C.Ramakrishnan & P.Balaram (1989) Stereochemical modeling of disulfide bridges: Criteria for introduction into proteins by site-directed mutagenesis. *Prot. Engng.*, **3**, 95-103.

[3] C.Ramakrishnan & N.Srinivasan (1990) Glycyl residues in proteins and peptides - An analysis. *Curr. Sci.*, **59**, 851-861.

[4] N.Srinivasan, R.Sowdhamini, C.Ramakrishnan & P.Balaram (1990) Conformations of disulfide bridges in proteins. *Int. J. Pept. Prot. Res.*, **36**, 147-155.

[5] N.Srinivasan, R.Sowdhamini, C.Ramakrishnan & P.Balaram (1991) Analysis of short loops connecting secondary structural elements in proteins. In *Molecular conformation and biological Interactions*, (Eds. P.Balaram & S.Ramaseshan) Indian Academy of Sciences, Bangalore. pp 59-73.

[6] R.Sowdhamini, N.Srinivasan, C.Ramakrishnan & P.Balaram (1992) Orthogonal $\beta\beta$ motifs in proteins. *J. Mol. Biol.*, **223**, 845-851.

[7] C.Ramakrishnan & N.Srinivasan (1992) Conformational preference of glycyI residues in proteins. A further confirmation. *Proc. Ind. Natl. Acad. Sci.*, **B59**, 45-54.

- [8] N.Srinivasan (1993) Conformational studies on globular proteins: Data analysis. (A paper on the Ph.D thesis work). *J. Ind. Inst. Sci.*, **73**, 114-120.
- [9] N.Srinivasan & T.L.Blundell (1993) An evaluation of the performance of an automated procedure for comparative modelling of protein tertiary structure. *Prot. Engng.*, **6**, 501-512.
- [10] M.S.Johnson, N.Srinivasan, R.Sowdhamini & T.L.Blundell (1994) Knowledge-based protein modelling. *CRC Crit. Rev. Biochem. Mol. Biol.*, **29**, 1-68.
- [11] J.Emsley, H.E.White, B.P.O'Hara, G.Oliva, N.Srinivasan, I.J.Tickle, T.L.Blundell, M.B.Pepys & S.P.Wood (1994) Structure of pentameric human serum amyloid P component. *Nature*, **367**, 338-345.
- [12] A.C.W.May, M.S.Johnson, S.D.Rufino, H.Wako, Z.-Y.Zhu, R.Sowdhamini, N.Srinivasan, M.A.Rodionov & T.L.Blundell (1994) The recognition of protein structure and function from sequence: adding value to genome data. *Phil. Trans. Roy. Soc. (London)* **344**, 373-381.
- [13] C.M.Topham, N.Srinivasan, C.J.Thorpe, J.P.Overington & N.A.Kalsheker (1994) Comparative modelling of major dust mite allergen *Der p I*. Structure validation using an extended environmental amino acid propensity table. *Prot. Engng.* **7**, 869-894.
- [14] N.Srinivasan, V.S.Anuradha, C.Ramakrishnan, R.Sowdhamini & P.Balaram (1994) Conformational characteristics of asparaginy residues in proteins. *Int. J. Pept. Prot. Res.* **44**, 112-122.
- [15] S.Zarina, C.Slingsby, R.Jaenicke, Z.H.Zaidi, H.Driessen & N.Srinivasan (1994) Three dimensional model and quaternary structure of the human eye lens protein γ -s crystallin based on β and γ -crystallin X-ray coordinates and ultracentrifugation. *Prot. Sci.* **3**, 1840-1846.
- [16] N.Srinivasan, H.E.White, J.Emsley, S.P.Wood, M.B.Pepys & T.L.Blundell (1994) Comparative analyses of pentraxins: implications for protomer assembly and ligand binding. *Structure.* **2**, 1017-1027.
- [17] L.E.Donate, E.Gherardi, N.Srinivasan, R.Sowdhamini, S.Aparicio & T.L.Blundell (1994) Molecular evolution and domain structure of plasminogen-related growth factors (HGF/SF and HGF1/MSP). *Prot. Sci.* **3**, 2378-2394.
- [18] R.Sowdhamini, N.Srinivasan, K.Guruprasad, S.D.Rufino, V.Dhanaraj, S.P.Wood, J.Emsley, H.E.White & T.L.Blundell (1995) Protein three-dimensional structure and molecular recognition: A story of soft locks and keys. *Pharmaceutica Acta Helvetiae.*, **69**, 185-192.
- [19] S.D.Rufino, N.Srinivasan, R.Sowdhamini, J.Murray-Rust, L.E.Donate, A.C.W.May, K.Guruprasad, V.Dhanaraj, B.L.Sibanda & T.L.Blundell (1995) Structure-based design of proteins. Learning from evolution by comparative analyses

of protein families. In Proceedings of the Annual Symposium on Protein Engineering, September 1994, Oxford, U.K. pp. 1-8.

[20] D.V.Nataraj, N.Srinivasan, R.Sowdhamini & C.Ramakrishnan (1995) α -turns in protein structures. *Curr. Sci.*, **69**, 434-447.

[21] N.Srinivasan, M.D.Waterfield & T.L.Blundell (1995) Regions binding $\beta\gamma$ subunits in G α and PH domains have common structural motifs. *Proceedings of the International conference on Molecular Structural Biology*, 17-20 Sep. 1995, Vienna. (Eds. A.J.Kungl, P.J.Andrew & H.Schreiber) pp. 27-39.

[22] M.Introna, V.V.Alles, M.Castellano, G.Picardi, L.De Gioia, B.Bottazzi, G.Peri, F.Breviario, M.Salmona, L.De Gregorio, T.A.Dragani, N.Srinivasan, T.L.Blundell, T.A.Hamilton & A.Mantovani (1996) Cloning of mouse ptx3, a new member of the pentraxin gene family expressed in extrahepatic sites. *Blood*, **87**, 1862-1872.

[23] N.Srinivasan, M.D.Waterfield & T.L.Blundell (1996) Comparative analysis of the regions binding $\beta\gamma$ -subunits in G α and PH domains. *Biochem. Biophys. Res. Commn.*, **220**, 697-702.

[24] N.Srinivasan, S.D.Rufino, M.B.Pepys, S.P.Wood & T.L.Blundell (1996) A superfamily of proteins with the lectin fold. *Chemtracts Biochem. Mol. Biol.*, **6**, 149-164.

[25] N.Srinivasan, K.Guruprasad & T.L.Blundell (1996) Comparative modelling of proteins. In *Protein structure prediction - A practical approach*. (Ed. M.J.E.Sternberg) Oxford University Press, Oxford. pp. 111-140.

[26] N.Srinivasan, B.Bax, T.L.Blundell & P.J.Parker (1996) Structural aspects of the functional modules in human protein kinase C α deduced from comparative analyses. *Proteins Str. Fn. Gen.*, **26**, 217-235.

[27] T.L.Blundell & N.Srinivasan (1996) Symmetry, stability and dynamics of multidomain and multicomponent protein systems. *Proc. Natl. Acad. Sci. (USA)*, **93**, 14243-14248.

[28] C.Ramakrishnan, N.Srinivasan & D.V.Nataraj (1996) Motifs and conformational analysis of aminoacid residues adjoining β -turns in proteins. *Int. J. Pept. Prot. Res.*, **48**, 420-428.

[29] N.Srinivasan & T.L.Blundell (1996) Insights on the structures of functional modules in protein kinase C family. In *Molecular Biology Intelligence Unit - Protein kinase C*. (eds. P.J.Parker & L.V.Dekker). R.G.Landes company, Texas. pp. 11-24.

[30] C.M.Topham, N.Srinivasan & T.L.Blundell (1997) Prediction of protein mutant stability based on three-dimensional structure dependent aminoacid substitution and propensity tables. *Prot. Engng.*, **10**, 7-21.

- [31] C.Robinson, N.A.Kalsheker, N.Srinivasan, C.M.King, D.R.Garrood, P.J.Thompson & G.A.Stewart (1997) On the potential significance of the enzymatic activity of mite allergens to immunogenicity. Clues to structure and function revealed by molecular characterization. *Clin. Exp. Allergy* **27**, 10-21.
- [32] E.Gherardi, G.Hartmann, J.Hepple, D.Chirgadze, N.Srinivasan & T.Blundell (1997) Domain structure of hepatocyte growth factor / scatter factor (HGF/SF). *CIBA Foundation symposia*, **212**. 84-98.
- [33] A.Albert, T.L.Blundell, V.Dhanaraj, L.E.Donate, M.Groves, K.Guruprasad, P.G.Nugent, P.Orprayoon, J.E.Pitts, S.Rufino, N.Srinivasan, M.Williams & J.Wilsher (1998) Protein engineering of aspartic proteinases: Site-directed mutagenesis, biochemical characterisation and X-ray analysis of chymosins with substituted single aminoacid substitutions and loop replacements. *Adv. Exp. Med. Biol.*, **436**, 169-177.
- [34] R.Sowdhamini, D.F.Burke, , J.-F.Huang, K.Mizuguchi, H.A.Nagarajaram, N.Srinivasan, R.E.Stewart & T.L.Blundell (1998) CAMPASS: A database of structurally aligned protein superfamilies. *Structure* **6**, 1087-1094.
- [35] R.Sowdhamini, D.F.Burke, C.M.Deane, J.-F.Huang, K.Mizuguchi, H.A.Nagarajaram, J.P.Overington, S.D.Rufino, N.Srinivasan, R.E.Stewart & T.L.Blundell (1998) Protein 3D structural databases: domains, structurally aligned homologues and superfamilies. *Acta Cryst. D* , **54**, 1168-1177.
- [36] N.Srinivasan, M.Antonelli, G.Jacob, I.Korn, F.Romero, A.Jedlicki, V.Dhanaraj, M.-F.Sayed, T.L.Blundell, C.C.Allende & J.E.Allende (1999) Structural interpretation of site-directed mutagenesis and specificity of the catalytic subunit of protein kinase CK2 using comparative modelling. *Prot. Engng.*, **12**, 119-127.
- [37] I.Korn, S.Gutkind, N.Srinivasan, T.L.Blundell, C.C.Allende & J.E.Allende (1999) Interactions of protein kinase CK2 subunits. *Mol. Cell. Biochem.*, **191**, 75-83.
- [38] A.R.Walker, P.A.Davison, C.Agnese, B-.Winfield, C.M.James, N.Srinivasan, T.L.Blundell, J.J.Esch, M.D.Marks & J.C.Gray (1999) The TTG1 (*Transparent Testa, Glabra1*) locus which regulates trichome differentiation and anthocyanin biosynthesis in Arabidopsis encodes a WD40-repeat protein. *Plant Cell* **11**, 1337-1349.
- [39] N.Srinivasan & V.S.R.Rao (1999) Structural features of protein – carbohydrate interactions in galactose and mannose binding proteins complexes. (in *Perspectives in Structural Biology*. Eds. M.Vijayan, N.Yathindra & A.S.Kolaskar) Indian Academy of Sciences. pp. 355-366.
- [40] L.A.Lindsey-Boltz, G.Chawla, N.Srinivasan, U.Vijayraghavan & M.A.Garcia-Blanco (2000) The Carboxy Terminal WD Domain of the pre-mRNA splicing Factor Prp17p is Critical for Function. *RNA* **6**, 1289-1305.
- [41] K. Vijayachandra, M. Guruprasad, R. Bhandari, U.H. Manjunath, B.P. Somesh, N. Srinivasan, K. Suguna and S.S. Visweswariah (2000) Biochemical characterization

of the intracellular domain of the human guanylyl cyclase C receptor provides evidence for a catalytically active homotrimer. *Biochemistry* **36**, 16075-16083.

[42] S.Deam, N.Srinivasan, J.Westby, E.H.Horn & G.Dolan (2001) Factor X Nottingham and factor X Taunton: Two novel mutations in factor X resulting in loss of functional activity and an interpretation using molecular modelling. *Thrombosis and Haemostasis* **85**, 265-269.

[43] S. Balaji, S. Sujatha, S. Sai Chetan Kumar & N. Srinivasan (2001) PALI - A database of Phylogeny and ALignment of homologous protein structures. *Nucleic Acids Res.* **29**, 61-65.

[44] S. Sujatha, S. Balaji & N. Srinivasan (2001) PALI - Web-interfaced access to a database of alignments and phylogeny of homologous protein structures. *Bioinformatics*, **17**, 375-376.

[45] R.J.Newbold, E.C.Raux, C.E.Walker, S.E.Wilkie, N.Srinivasan, D.M.Hunt, S.S.Bhattacharya & M.J.Warren (2001) A cone-rod dystrophy caused by the destabilisation of human GCAP1 by a proline to leucine mutation. *Human Mol. Gen.* **10**, 47-54.

[46] S. Balaji & N. Srinivasan (2001) Use of a database of structural alignments and phylogenetic trees in investigating the relationship between sequence and structural variability among homologous proteins. *Prot. Engng.*, **14**, 219-226.

[47] R.Bhandari, N. Srinivasan, Mahaboobi, K. Suguna & S.S.Visweswariah (2001) Functional inactivation of the human guanylyl cyclase C receptor: Modelling and mutation of the protein kinase -like domain. *Biochemistry*, **40**, 9196-9206.

[48] S.B. Pandit, D. Gosar, S. Abhiman, S. Sujatha, S.S. Dixit, N.S. Mhatre, R. Sowdhamini & N. Srinivasan (2002) SUPFAM - A database of potential protein superfamily relationships derived by comparing sequence-based and structure-based families: Implications for structural genomics and function annotation in genomes. *Nucleic Acids Res.* **30**, 289-293.

[49] S. Balaji, S. Sujatha, S. Aruna, N.S. Mhatre & N. Srinivasan (2002) PALI (Release 1.3) *Nucleic Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> -on-line publication.

[50] A. Krupa & N. Srinivasan (2002) Lipopolysaccharide phosphorylating enzymes encoded in the genomes of Gram-negative bacteria are related to the eukaryotic protein kinases. *Prot. Sci.* **11**, 1580-1584.

[51] S.Gupta, S.B. Pandit, N. Srinivasan & D. Chatterji (2002) Proteomics analysis of carbon starved *Mycobacterium smegmatis*: Induction of Dps like protein. *Prot. Engng.* **15**, 503-511.

[52] A.R. Shenoy, N. Srinivasan & S. S. Visweswariah (2002) The ascent of nucleotide cyclases: conservation and evolution of a theme. *J. Biosci.* **27**, 85-91.

[53] N.Eswar, H.A.Nagarajaram, C.Ramakrishnan & N.Srinivasan (2002) Influence of solvent molecules on the stereochemical code of glyceryl residues in proteins. *Proteins Str. Fn. Gen.*, **49**, 326-334.

[54] S. Sehrawat, N. Srinivasan & K.P.Gopinathan (2002) Functional characterization and structural modeling of late gene expression factor 4 from *Bombyx mori* nucleopolyhedrovirus. *Biochem. J.* **368**, 159-169.

[55] A. Krupa & N. Srinivasan (2002) Repertoire of protein kinases encoded in the draft version of the human genome: Atypical variations and uncommon domain combinations. *Genome Biology* **3**, 66.1-66.14.

See *Nature News India* (March 2003 issue, pp.12) for a news item on this work.

[56] V.S. Gowri, S.B. Pandit, P.S. Karthik, N. Srinivasan & S. Balaji (2003) Integration of related sequences with protein three-dimensional structural families in an updated version of PALI database *Nucleic Acids Res.* **31**, 486-488.

[57] S.B. Pandit, S. Balaji, V.S. Gowri, K.R. Abhinandan, R. Vaishnavi & N. Srinivasan (2003) SUPFAM - Release 1.2. *Nucleic Acids Res.*
<http://www3.oup.co.uk/nar/database/summary/219> -On-line publication.

[58] A. Krupa, K. Sandhya, N. Srinivasan & S. Jonnalagadda (2003) A conserved domain in the prokaryotic bifunctional FAD synthetases can potentially catalyze nucleotide transfer *Trends Biochem. Sci.* **28**, 10-13.

[59] A. Rahaman, N. Srinivasan, N. Shamala & M.S. Shaila (2003) Fusion Core Complex of Peste des Petits Ruminants Virus is a Six-Helix Bundle Assembly. *Biochemistry*, **42**, 922-931.

[60] R. Pudi, S. Abhiman, N. Srinivasan & S. Das (2003) Hepatitis C virus Internal Ribosome Entry Site-mediated translation is stimulated by specific interaction of independent regions of human La autoantigen. *J. Biol. Chem.* **278**, 12231-12240.

[61] S.B. Pandit & N. Srinivasan (2003) Survey for G-proteins in the prokaryotic genomes: Prediction of functional roles based on classification. *Proteins Str. Fn. Gen.* **52**, 585-597.

The paper mentioned above is listed in Faculty of 1000

[62] S. Sopory, S. Balaji, N. Srinivasan & S.S. Visweswariah (2003) Modeling and mutational analysis of the GAF domain of the cGMP-binding, cGMP-specific phosphodiesterase PDE5. *FEBS Letters.* **539**, 161-166.

[63] N. Eswar, C. Ramakrishnan & N. Srinivasan (2003) Stranded in isolation: Structural role of isolated extended-strands in proteins. *Prot. Engng.* **16**, 331-339.

- [64] N. Rekha & N. Srinivasan (2003) Structural basis of regulation and substrate specificity of protein kinase CK2 deduced from the modeling of protein-protein interactions. *BMC Strl. Biol.* **3**, 4.1-4.13
- [65] A.R. Shenoy, N. Srinivasan, M. Subramaniam & S.S. Visweswariah (2003) Mutational analysis of Mycobacterium tuberculosis Rv1625c adenylyl cyclase: Residues that confer nucleotide specificity contribute to dimerization. *FEBS Letters* **545**, 253-259.
- [66] S. Balaji, S. Aruna & N. Srinivasan (2003) Tolerance to the substitution of buried apolar residues by charged residues in the homologous protein structures. *Proteins Str. Fn. Gen.* **53**, 783-791.
- [67] S. Sandhya, S. Kishore, R. Sowdhamini & N. Srinivasan (2003) Effective detection of remote homologues by searching in sequence dataset of a protein domain fold. *FEBS Letters*, **552**, 225-230.
- [68] V. Sampath, N. Rekha, N. Srinivasan & P.P. Sadhale (2003) The conserved and non-conserved regions of Rpb4 are involved in multiple phenotypes in *Saccharomyces cerevisiae*. *J. Biol. Chem.* **278**, 51566-51576.
- [69] M. Praseeda, K.K. Pradeep, A. Krupa, S. Sri Krishna, S. Leena, R. Rajeev Kumar, J. Cheriyan, M. Mayadevi, N. Srinivasan & R.V. Omkumar (2003) Influence of a mutation in the ATP-binding region of Calcium/Calmodulin dependent protein kinase II on its interaction with peptide substrates. *Biochem. J.* **378**, 391-397.
- [70] A. Shenoy, K. Sivakumar, A. Krupa, N. Srinivasan & S.S. Visweswariah. (2003) A survey of nucleotide cyclases in Actinobacteria: unique domain organization and expansion of the class III cyclase family in Mycobacterium tuberculosis. *Comp. Fnl. Genomics* **5**, 17-38.
- [71] A. Krupa, K.R. Abhinandan & N. Srinivasan (2004) KinG: A database of protein Kinases IN Genomes. *Nucl. Acids Res.* **32**, 153-155.
- [72] V.S. Gowri, S.B. Pandit., B. Anand., N. Srinivasan & S. Balaji (2004) PALI. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (on-line publication).
- [73] S.B. Pandit, R. Bhadra, V.S. Gowri, S. Balaji, B. Anand & N.Srinivasan (2004) SUPFAM. *Nucl. Acids Res.*, <http://www3.oup.co.uk/nar/database/summary/219> (on-line publication).
- [74] S. Singh, N. Rekha, B. Pillai, V. Singh, A. Naorem, V. Sampath, N. Srinivasan & P.P. Sadhale (2004) Domainal Organization Of The Lower Eukaryotic Homologs Of The Yeast RNA Polymerase II Core Subunit Rpb7 Reflects Functional Conservation. *Nucl. Acids Res.* **32**, 201-210.

- [75] A. Rahaman, N. Srinivasan, N. Shamala & M.S. Shaila (2004) Phosphoprotein of Rinderpest virus forms a tetramer through coiled-coil region important for biological function: A structural insight. *J. Biol. Chem.*, **279**, 23606-23614.
- [76] B. Anand, S. Namboori, S. Sandhya & N. Srinivasan (2004) Influence of protein structural similarities in adding value to genome data. *Ind. J. Biotech.* **3**, 473-485.
- [77] S.B. Pandit, R. Bhadra, V.S. Gowri, S. Balaji, B. Anand & N. Srinivasan (2004) SUPFAM: A database of sequence superfamilies of protein domains. *BMC Bioinformatics*, **5**, 28.1-28.5.
- [78] A. Krupa, G. Preethi & N. Srinivasan (2004) Structural modes of stabilization of permissive phosphorylation sites in protein kinases: Distinct strategies in Ser/Thr and Tyr kinases. *J. Mol. Biol.*, **339**, 1025-1039.
- [79] A. Mahajan, A. Sharma, S. Chavali, M. Kabra, M.R. Chowdhury, N. Srinivasan & D. Bharadwaj (2004) Novel missense mutation in the coagulation factor IX catalytic domain associated with severe hemophilia B factor IX_{Delhi}. *Haemophilia*, **10**, 550-552.
- [80] S. Namboori, N. Mhatre, S. Sujatha, N. Srinivasan & S.B. Pandit (2004) Enhanced functional and structural domain assignments using remote similarity detection procedures for proteins encoded in the genome of Mycobacterium tuberculosis H37Rv. *J. Biosci.*, **29**, 245-259.
- [81] S. Namboori, N. Srinivasan & S.B. Pandit (2004) Recognition of remotely related structural homologues using sequence profiles of aligned homologous protein structures. *In Silico Biol.*, **4**, 445-460.
- [82] S.B. Pandit, S. Balaji & N. Srinivasan (2004) Structural and functional characterization of gene products encoded in the human genome by homology detection. *IUBMB Life*, **56**, 317-331.
- [83] S.B. Pandit & N. Srinivasan (2004) Identification and analysis of a new family of bacterial serine proteinases. *In Silico Biol.*, **4**, 563-572.
- [84] V.S. Gowri, S. Balaji, O. Krishnadev, S.B. Pandit. & N. Srinivasan (2005) PALI. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (on-line publication).
- [85] O. Krishnadev, V.S. Gowri, S. Balaji, N.Srinivasan & S.B. Pandit (2005) SUPFAM. *Nucl. Acids Res.*, <http://www3.oup.co.uk/nar/database/summary/219> (on-line publication).
- [86] A. Krupa, K.R. Abhinandan, Anamika & N.Srinivasan (2005) KinG. *Nucl. Acids Res.*, <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).

- [87] Anamika, N. Srinivasan & A. Krupa (2005) A genomic perspective of protein kinases in *Plasmodium falciparum*. *Proteins Str. Fn. Bioinf.*, **58**, 180-189.
- [88] N. Rekha, S.M. Machado, C. Narayanan, A. Krupa & N. Srinivasan (2005) Interaction interfaces of protein domains are not topologically equivalent across families within superfamilies: Implications for metabolic and signalling pathways. *Proteins Str. Fn. Bioinf.*, **58**, 339-353.
- [89] R. Gadkari, S. Roy, G.S. Murthy, N. Rekha, N. Srinivasan & R.R. Dighe (2005) Identification Of A Heterodimer-Specific Epitope Present In Human Chorionic Gonadotropin (hCG) Using A Monoclonal Antibody That Can Distinguish Between hCG and Human Luteinizing Hormone. *J. Mol. Endocrin.* **34**, 879-884.
- [90] B. Anand, V.S. Gowri & N. Srinivasan (2005) Use of multiple profiles corresponding to a sequence alignment enables effective detection of remote homologues. *Bioinformatics* **21**, 2821-2826.
- [91] O. Krishnadev, N. Rekha, S.B. Pandit, S. Abhiman, S. Mohanty, L.S. Swapna, S. Gore & N. Srinivasan (2005) PRODOC resource for comparison of tethered protein domain architectures with in-built information on distantly related domain families. *Nucl. Acids Res.* **33**, W126-129.
- [92] R. Bhadra, N. Srinivasan & S.B. Pandit (2005) A new domain family in the superfamily of alkaline phosphatases. *In Silico Biol.* **5**, 0034.
- [93] S. Sandhya, C. Jayadev, S. Chakrabarti, K.R. Abhinandan, R. Sowdhamini & N. Srinivasan (2005) Relating protein families in sequence space through multiple intermediates. In *Mathematical Biology* edited by P.Chandra & B.V.R.Kumar, Anamaya Publishers, New Delhi pp. 173-180.
- [94] S. Sandhya, S. Chakrabarti, K.R. Abhinandan, R. Sowdhamini & N. Srinivasan (2005) Assessment of a rigorous transitive profile based search method to detect remotely similar proteins. *J. Biomol. Str. Dyn.* **23**, 283-298..
- [95] S. De, O. Krishnadev, N. Srinivasan & N. Rekha (2005) Interaction preferences across protein-protein interfaces of obligatory and non-obligatory components are different. *BMC Strl. Biol.* **5**, 15.
- [96] A. Krupa & N. Srinivasan (2005) Diversity in domain architectures of Ser/Thr kinases and their homologues in prokaryotes. *BMC Genomics* . **6**, 129.
- [97] P.K. Padmanabhan, A. Mukherjee, S. Singh, S. Chattopadhyaya, V.S. Gowri, P.J Myler, N. Srinivasan & M. Rentala (2005) Glyoxalase I from *Leishmania donovani*: A potential target for anti-parasite drug. *Biochem. Biophys. Res. Commn.* **337**, 1237-1248.
- [98] H.G. Mahesha, S.A., Singh, N. Srinivasan & A.G.A. Rao (2006) A spectroscopic study of the interactions of isoflavones with human serum albumin. *FEBS Journal* **273**, 451-467.

- [99] V.S. Gowri, O. Krishnadev, C.S. Swamy & N. Srinivasan (2006) MulPSSM: A database of multiple position specific scoring matrices of protein domain families. *Nucl. Acids Res.* **34**, D243-246.
- [100] N. Srinivasan (2006) Computational Biology and Bioinformatics: A tinge of Indian spice. *Bioinformatics*, **1**, 105-109.
Reproduced with permission in *Biobytes* by the editors of *Biobytes*.
- [101] O. Krishnadev, V.S. Gowri, C.S. Swamy & N.Srinivasan (2006) SUPFAM - Grouping of sequence families into superfamilies *Nucl. Acids Res.*, <http://www3.oup.co.uk/nar/database/summary/219> (on-line publication).
- [102] C.S. Swamy, O. Krishnadev, N. Srinivasan & V.S. Gowri (2006) PALI – Phylogeny and alignment of homologous protein structures. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (on-line publication).
- [103] Anamika, A. Krupa & N. Srinivasan (2006) KinG –Kinases in Genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [104] L.S.Swapna, B. Offmann & N. Srinivasan (2006) Evolutionary dynamics of protein-protein interactions: A case study using the DJ-1/PfpI family of enzymes. In *Knowledge Discovery in Bioinformatics: Techniques, Methods and Application* edited by Yi Pan and Tony Hu. Wiley publishers. Pp.209-231.
- [105] R. Bhadra, S. Sandhya, K.R. Abhinandan, S. Chakrabarti, R. Sowdhamini & N. Srinivasan (2006) Cascade PSI-BLAST Web server: A remote homology search tool for relating protein domains. *Nucl. Acids Res.* **34**, W143-146.
- [106] M. Tyagi, P. Sharma, S. Swamy, F. Cadet, N. Srinivasan, A. de Brevern & B. Offmann (2006) Protein Block Expert (PBE): A web-based protein structure analysis server using a structural alphabet. *Nucl. Acids Res.* **34**, W119-223.
- [107] G. Pugalenti, K. Shameer, N. Srinivasan & R. Sowdhamini.(2006) HARMONY: a web-server for the assessment of protein structures. *Nucl. Acids Res.* **34**, W231-234.
- [108] A. Krupa, Anamika & N. Srinivasan (2006) Genome wide comparative analyses of domain organisation of repertoires of protein kinases of *Arabidopsis thaliana* and *Oryza sativa*. *Gene* **318**, 1-13.
- [109] M. Tyagi, V.S. Gowri, N. Srinivasan, A.G. de Brevern & B. Offmann (2006) A substitution matrix for structural alphabet based on structural alignment of homologous proteins and its applications. *Proteins Str. Fn. Bioinf.*, **65**, 32-39.
- [110] K. Sharma, M. Gupta, A. Krupa, N. Srinivasan & Y. Singh (2006) EmbR, a regulatory protein with ATPase activity, is a substrate of multiple serine/threonine kinases and phosphatase in *Mycobacterium tuberculosis*. *FEBS J.* **273**, 2711-2721.

- [111] V.S. Gowri, Tina K. Graceline, O. Krishnadev and N. Srinivasan (2007) Strategies for the effective identification of remotely related sequences in multiple PSSM search approach. *Proteins Str. Fn. Bioinf.*, **67**, 789-794.
- [112] R.R. Thangudu, P. Sharma, N. Srinivasan & B. Offmann (2006) Analycys: a database for conservation and conformation of disulphide bonds in homologous proteins. *Proteins Str. Fn. Bioinf.*, **67**, 255-261.
- [113] V. Talla, C. Narayanan, N. Srinivasan & D. Balasubramanian (2006) Mutations causing self-aggregation in human γ C crystalline leads to congenital cataract. *Investigative Ophthalmology & Visual Science*. **47**, 5212-5217.
- [114] N.Srinivasan as one of the members of the NMITLI BioSuite team. (2007) BioSuite: A comprehensive bioinformatics software package (A unique industry-academia collaboration). *Curr. Sci.*, **92**, 29-38.
- [115] O. Krishnadev, L.S., Swapna, V.S. Gowri, G. Agarwal, S.B. Pandit & N.Srinivasan (2007) SUPFAM - Grouping of sequence families into superfamilies *Nucl. Acids Res.*, <http://www3.oup.co.uk/nar/database/summary/219> (on-line publication).
- [116] G. Agarwal, O. Krishnadev, A. Sebastian, N. Srinivasan, S. Balaji & V.S. Gowri (2007) PALI – Phylogeny and alignment of homologous protein structures. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (on-line publication).
- [117] Anamika, A. Krupa, K.R. Abhinandan & N. Srinivasan (2007) KinG –Kinases in Genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [118] S. Mohanty, L.S. Swapna, V.S., Gowri, G. Agarwal, N. Srinivasan & O. Krishnadev (2007) MulPSSM – A database of multiple profiles of protein domain families. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/844> (on-line publication).
- [119] N. Srinivasan, R. Sowdhamini & A. Bhattacharya (2007) Computational Biology: More than just a set of techniques. *J. Biosci.*, **32**, 1-2.
- [120] S. Balaji & N. Srinivasan (2007) Comparison of sequence-based and structure-based phylogenetic trees of homologous proteins: Inferences on protein evolution. *J. Biosci.* **32**, 83-96.
- [121] K.G. Tina, R. Bhadra & N. Srinivasan (2007) PIC: Protein Interactions Calculator. *Nucl. Acids Res.* **35**, W473-476.
- [122] K. Anamika & N. Srinivasan (2007) Comparative kinomics of Plasmodium organisms: Unity in diversity. *Pept. Prot. Letts.* **14**, 509-517.

- [123] V.S. Gowri, K. Anamika, S. Gore & N. Srinivasan (2007) Analysis of sliding helices and strands in protein structural comparisons: A case study with protein kinases. *J. Biosci.*, **32**, 921-928.
- [124] M. Tyagi, N. Srinivasan, A.G. de Brevern & B. Offmann (2007) Protein structure mining using a structural alphabet. *Proteins* **71**, 720-737
- [125] C. Ramakrishnan, B. Lakshmi, A. Kurien, D. Devipriya & N. Srinivasan (2007) Structural compromise of disallowed conformations in peptide and protein structures. *Pept. Prot. Letts.* **14**, 672-682.
- [126] K. Anamika, A. Bhattacharya & N. Srinivasan (2007) Analysis of the kinome of *Entamoeba histolytica*. *Proteins* **71**, 995-1006.
- [127] G. Agarwal, O. Krishnadev O., V.S. Gowri N. Srinivasan & S. Balaji S.(2008) PALI- Phylogeny and alignment of homologous protein structures. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (online publication)
- [128] O. Krishnadev, L.S. Swapna, V.S. Gowri, G. Agarwal, N. Srinivasan & S.B. Pandit (2008) SUPFAM- Grouping of sequence families into superfamilies. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/219> (online publication)
- [129] S. Mohanty, L.S. Swapna, V.S. Gowri, G. Agarwal, N. Srinivasan & O. Krishnadev (2008) MulPSSM- A database of multiple profiles of protein domain families. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/844> (online publication)
- [130] Anamika, K., Martin, J., Krupa, A, Abhinandan, K.R., Srinivasan, N. (2008) KinG –Kinases in Genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [131] A. Jhingran, P.K. Padmanabhan, S. Singh, K. Anamika, A. A. Bakre, S. Bhattacharya, A. Bhattacharya, N. Srinivasan and R. Madhubala (2008) Characterization of the *Entamoeba histolytica* Ornithine decarboxylase-like enzyme. *PLoS NTD* **2**, e115.
- [132] V.S. Gowri, D. Venkatasubramanian, K.S. Raghavendran, C.S. Swamy & N. Srinivasan (2008) Stretching the limits of comparative modeling of proteins: Modeling on the basis of remote relationships. In *Recent Advances in Structural Bioinformatics* , Research Signpost. pp. 299-312.
- [133] A. Krupa & N. Srinivasan (2008) Evolution of FAD synthetases and associated functional domains. In *Recent Advances in Structural Bioinformatics*, Research Signpost. pp. 313-329.
- [134] D.V. Pantakani, L.S. Swapna, N. Srinivasan & A.U. Mannan (2008) Spastin oligomerizes into a hexamer and the mutant spastin (E442Q) redistribute the wild-type spastin into filamentous microtubule. *J. Neurochem.*, **106**, 613-624..

- [135] V. Talla, N. Srinivasan & D. Balasubramanian (2008) Visualization of *in situ* intracellular aggregation of two cataract-associated human γ -Crystallin mutants: Lose a tail, lose transparency. *Invest Ophthalmol Vis Sci.* **49**, 3483-3490.
- [136] S. Sandhya, B. Pankaj, M.K. Govind, B. Offmann, N. Srinivasan & R. Sowdhamini (2008) CUSP: an algorithm to distinguish structurally conserved and unconserved regions in protein domain alignments and its application in the study of large length variations. *BMC Strl. Biol.*, **8**, 28.
- [137] O. Krishnadev & N. Srinivasan (2008) A data integration approach to predict host - pathogen protein-protein interactions: application to recognize protein interactions between human and a malarial parasite. *In Silico Biol.*, **8**, 20.
- [138] D. Varughese & N. Srinivasan (2008) New resources for remote homology detection of proteins. *BioBytes*, **2**, 14-16.
- [139] A. Roy, N. Srinivasan & V.S. Gowri (2008) Molecular and structural basis of drift in the functions of closely-related homologous enzyme domains: Implications for function annotation based on homology searches and structural genomics. *In Silico Biol.*, **9**, S41-55.
- [140] R Thangudu, M. Manoharan, N. Srinivasan, F. Cadet, R. Sowdhamini & B. Offmann (2008) Analysis on conservation of disulphide bonds and their structural features in homologous protein domain families. *BMC Strl. Biol.* **8**, 55
- [141] K. Anamika, J. Martin & N. Srinivasan (2008) Comparative kinomics of human and chimpanzee reveals unique kinship and functional diversity generated by new domain combinations. *BMC Genomics*, **9**, 625.
- [142] G. Agarwal, O. Krishnadev O., V.S. Gowri N. Srinivasan & S. Balaji S.(2009) PALI- Phylogeny and alignment of homologous protein structures. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (online publication)
- [143] O. Krishnadev, R.M. Bhaskara, G. Agarwal, & N. Srinivasan (2009) SUPFAM- Grouping of sequence families into superfamilies. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/219> (online publication)
- [144] O. Krishnadev, R.M. Bhaskara, G. Agarwal & N. Srinivasan (2009) MulPSSM- Multiple PSSMs of protein domain families. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/844> (online publication)
- [145] K. Anamika, N. Tyagi, J. Martin, A. Krupa, K.R. Abhinandan, Srinivasan, N. (2009) KinG –Ser/Thr/Tyr-specific protein kinases encoded in complete genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [146] J. Rath, V.S. Gowri, S. Chattapathyay, P.K. Padmanabhan, N. Srinivasan & M. Rentala (2009) A glutathione-specific aldose reductase of *Leishmania donovani* and its potential implications for methylglyoxal detoxification pathway. *Gene*, **429**, 1-9.

- [147] A. Kumar, S. Reddy, N. Srinivasan & D. Nandi (2009) Interaction between two residues in the inter-domain interface of Escherichia coli peptidase N modulates catalytic activity. *Prot. Pept. Lett.*, **16**, 415-422.
- [148] S. Mohanty & N. Srinivasan (2009) Identification of “missing” metabolic proteins of *Plasmodium falciparum*: A bioinformatics approach. *Prot. Pept. Lett.* **16**, 961-968.
- [149] S. Mohanty, S.B. Pandit & N. Srinivasan (2009) Dynamics of protein-protein interaction network in *Plasmodium falciparum* in “Biological Data Mining in Protein Interaction Networks” (Editors: Xiao-Li Li & See-Kiong Ng). IGI Global Press. pp. 257-285.
- [150] R. Gadkari, D. Varughese & N. Srinivasan (2009) Recognition of interaction interface residues in low-resolution structures of protein assemblies solely from the positions of C α atoms. *PLoS ONE*, **4**, e4476.
- [151] A.J. Kandathil, A.P. Joseph, R. Kannangai, N. Srinivasan, O.C. Abraham, S.A. Pulimood & G. Sridharam (2009) Structural basis of drug resistance by genetic variants of HIV-1 clade C protease from India. *AIDS Res. Human Reteroviruses*, **25**, 511-519.
- [152] S. Sandhya, S.S. Rani, B. Pankaj, M.K. Govind, B. Offmann, N. Srinivasan & R. Sowdhamini (2009) Length variations amongst protein domain superfamilies and consequences on structure and function. *PLoS ONE*, **4**, e4981.
- [153] N. Tyagi, L.S. Swapna, S. Mohanty, G. Agarwal, V.S. Gowri, K. Anamika, M.L. Priya, O. Krishnadev & N. Srinivasan (2009) Evolutionary divergence of *Plasmodium falciparum*: Sequences, protein-protein interactions, pathways and processes. *Infectious Disorders-Drug Targets* **9**, 257-271.
- [154] G. Agarwal, M. Rajavel, B. Gopal & N. Srinivasan (2009) Structure-based phylogeny as a diagnostic for functional characterization of proteins with a cupin fold. *PLoS ONE*, **4**, e5736.
- [155] A. Kumar, M. Bhosale, S. Reddy, N. Srinivasan & D. Nandi (2009) Importance of non-conserved distal carboxyl terminal amino acids in two peptidases belonging to the M1 family: *Thermoplasma acidophilum* Tricorn interacting factor F2 and Escherichia coli Peptidase N. *Biochimie*, **91**, 1145-1155.
- [156] N. Tyagi, O. Krishnadev & N. Srinivasan (2009) Prediction of Protein-Protein Interactions between *Helicobacter Pylori* and human. *Mol. Bio. Sys.* **5**, 1630-1635.
- [157] A.J. Kandathil, A.P. Joseph, R. Kannangai, N. Srinivasan, O.C. Abraham, S.A. Pulimood & G. Sridharan (2009) HIV reverse transcriptase: Structural interpretation of drug resistant genetic variants from India. *Bioinformation*, **4**, 36-45.

- [158] S. Mohanty & N. Srinivasan (2009) How effective is the data on co-occurrence of domains in multi-domain proteins in prediction of protein-protein interactions? In IEEE proceedings on *Genomic Signal Processing and Statistics, 2009*. (GENSIPS 2009.). 1-4.
- [159] K. Anamika, K.R. Abhinandan, K. Deshmukh & N. Srinivasan (2009) Classification of Non-enzymatic Homologues of Protein Kinases. *Comp. Fnl. Genomics*. e365637.
- [160] K. Anamika, N. Garnier & N. Srinivasan (2009) Functional diversity of human protein kinase splice variants marks significant expansion of human kinome.. *BMC Genomics*, **10**, 622.
- [161] B. Chawla, A. Jhingran, S. Singh, N. Tyagi, M.H. Park, N Srinivasan, S.C. Roberts & R. Madhubala (2010) Identification and characterization of a novel Deoxyhypusine synthase in *Leishmania donovani*. *J. Biol. Chem.* **285**, 453-463.
- [162] G. Agarwal, D.C. Dinesh, N. Srinivasan & A.G. de Brevern (2010) Characterization of conformational patterns in active and inactive forms of kinases using protein blocks approach. In "*Computational Intelligence and Pattern Analysis in Biological Informatics*" edited by U. Maulik, S. Bandyopadhyay & J. T. L. Wang. John Wiley Press, pp. 169-188.
- [163] K. Deshmukh, K. Anamika & N. Srinivasan (2010) Evolution of domain combinations in protein kinases and its implications for functional diversity. *Prog. Biophys. Mol. Biol.* **102**, 1-15.
- [164] O. Krishnadev, S. Bisht & N. Srinivasan (2010) Prediction of protein-protein interactions between human host and two mycobacterial organisms. *Int. J. Knowledge Discovery Bioinf.* **1**, 1-13.
- [165] V. Malshetty, K. Kurthkoti, A. China, B. Mullick, S. Yamunadevi, P.B. Sang, N. Srinivasan, V. Nagaraja & U. Varshney (2010) Novel insertion and deletion mutants of RpoB which render *Mycobacterium smegmatis* RNA polymerase recalcitrant to rifampicin mediated inhibition of transcription. *Microbiology* **156**, 1565-1573.
- [166] R.M. Bhaskara , S. Mohanty, O. Krishnadev, N.Srinivasan, S. Balaji , V.S. Gowri & G. Agarwal (2010) PALI- Phylogeny and alignment of homologous protein structures. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (online publication)
- [167] O. Krishnadev & N. Srinivasan (2010) SUPFAM- Grouping of sequence families into superfamilies. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/219> (online publication)
- [168] S. Mohanty, R. Mudgal, O. Krishnadev & N. Srinivasan (2010) MulPSSM- Multiple PSSMs of protein domain families. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/844> (online publication)

- [169] N. Garnier, N. Tyagi, R. Rakshambikai, D.C. Dinesh, K. Anamika, J. Martin, A. Krupa, K.R. Abhinandan & N.Srinivasan (2010) KinG –Ser/Thr/Tyr-specific protein kinases encoded in complete genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [170] P. Aggarwal, M.D. Gupta, A.P. Joseph, N. Chatterjee, N. Srinivasan & U. Nath (2010) Identification of specific DNA-binding residues in the TCP family of transcription factors. *Plant Cell* **22**, 1174-1189.
- [171] R. Gadkari & N. Srinivasan (2010) Prediction of Protein-protein Interactions in Dengue Virus Coat Proteins Guided by Low Resolution cryoEM Structures. *BMC Strl. Biol.*, **10**, 17.
- [172] N. Tyagi, K. Anamika & N. Srinivasan (2010) A Framework for Classification of Prokaryotic Protein Kinases. *PLoS ONE*, **5**, e10608.
- [173] A.P. Joseph, G. Agarwal, S. Mahajan, J.-C. Gelly, L.S. Swapna, B. Offmann, F. Cadet, A. Bornot, M. Tyagi, H. Valadié, B. Schneider, C. Etchebest, N. Srinivasan, A.G. de Brevern (2010) A short survey on protein blocks. *Biophys. Rev.*, **2**, 137-145.
- [174] L.S. Swapna, B. Offmann & N. Srinivasan (2010) Evolutionary dynamics at protein-protein interfaces of legume lectins. In *Protein-protein interactions*. (Ed. P. Kanguane) Nova publishers, New York. pp 293-310.
- [175] J. Martin, K. Anamika & N. Srinivasan (2010) Classification of protein kinases on the basis of both kinase and non-kinase regions *PLoS ONE* **5**, e12460.
- [176] O. Krishnadev & N. Srinivasan (2011) Prediction of protein - protein interactions between human host and a pathogen and its application to three pathogenic bacteria. *Int. J. Biol. Macromol.* **48**, 613-619.
- [177] G. Agarwal, S. Mahajan, N. Srinivasan & A.G. de Brevern (2011) Identification of local conformational similarity in structurally variable regions of homologous proteins using protein blocks. *PLoS ONE*, **6**, e17826.
- [178] N. Srinivasan, G. Agarwal, R.M. Bhaskara, R. Gadkari, O. Krishnadev, B. Lakshmi, S. Mahajan, S. Mohanty, R. Mudgal, R. Rakshambikai, S. Sankaran, G. Sudha, L.S. Swapna & N. Tyagi (2011) Influence of genomic and other biological data sets in the understanding of protein structures, functions and interactions. *Int. J. Knowledge Discovery Bioinf.*, **2**, 24-44.
- [179] A.P. Joseph, N. Srinivasan & A.G. de Brevern (2011) Improvement of protein structure comparison using a structural alphabet. *Biochimie*, **93**, 1434-1445.
- [180] J.C. Gelly, A.P. Joseph, N. Srinivasan & A.G. de Brevern (2011) iPBA: a tool for protein structure comparison using sequence alignment strategies. *Nucl. Acids Res.*, **39**, W18-23.
- [181] O. Krishnadev & N. Srinivasan (2011) AlignHUSH : Alignment of HMMs Using Structure and Hydrophobicity information. *BMC Bioinformatics*, **12**, 275.

- [182] R.M. Bhaskara & N. Srinivasan (2011) Stability of domain structures in multi-domain proteins. *Sci. Rep.*, **1**, 40.
- [183] R.M. Bhaskara, S. Mohanty, S. Mahajan, G. Agarwal, S. Balaji, V.S. Gowri & N. Srinivasan (2012) PALI- Phylogeny and alignment of homologous protein structures. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (online publication)
- [184] R. Mudgal, O. Krishnadev, S. Mukherjee & N. Srinivasan (2012) SUPFAM-Grouping of sequence families into superfamilies. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/219> (online publication)
- [185] R. Rakshambikai, N. Tyagi, N. Garnier, D.C. Dinesh, K. Anamika, J. Martin, A. Krupa, K.R. Abhinandan & N. Srinivasan (2012) KinG –Ser/Thr/Tyr-specific protein kinases encoded in complete genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [186] R. Gayatri, S. Mohanty, R. Mudgal, O. Krishnadev & N. Srinivasan (2012) MulPSSM- Multiple PSSMs of protein domain families. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/844> (online publication).
-
- [187] L.S. Swapna, N. Rekha & N. Srinivasan (2012) Accommodation of profound sequence differences at the interfaces of eubacterial RNA polymerase multi-protein assembly. *Bioinformatics*, **8**, 6-12.
- [188] A.P. Joseph, N. Srinivasan & A.G. de Brevern (2012) *Cis - trans* peptide inter-conversions in structurally similar proteins. *Amino Acids*, **43**, 1369-1381.
- [189] S. Amarnath, T. Kawli, S. Mohanty, N. Srinivasan & V. Nanjundiah (2012) Pleiotropic Roles of a Ribosomal Protein in *Dictyostelium discoideum*. *PLoS ONE*, **7**, e30644.
- [190] R.A. Gadkari & N. Srinivasan (2012) Protein-protein interactions in clathrin vesicular assembly: Radial distribution of evolutionary constraints in interfaces. *PLoS ONE*, **7**, e31445.
- [191] B. Chawla, R.R. Kumar, N. Tyagi, G. Subramanian, N. Srinivasan, M.H. Park & R. Madhubala (2012) Unique Modification of the Eukaryotic Initiation Factor 5A shows the Presence of the Complete Hypusine Pathway in *Leishmania donovani*. *PLoS ONE*, **7**, e33138.
- [192] R. Rakshambikai, S. Yamunadevi, K. Anamika, N. Tyagi & N. Srinivasan (2012) Repertoire of protein kinases encoded in the genome of *Takifugu rubripes*. *Comp. Fnl. Genomics*, **2012**, 258284.
- [193] L.S. Swapna, S. Mahajan, A. G. de Brevern & N. Srinivasan (2012) Comparison of tertiary structures of proteins in protein-protein complexes with

unbound forms suggests prevalence of allostery in signalling proteins. *BMC Strl. Biol.*, **12**, 6.

[194] L.S. Swapna, K. Srikeerthana & N. Srinivasan (2012) Extent of structural asymmetry in homodimeric proteins: prevalence and relevance. *PLoS ONE*, **7**, e36688.

[195] S. Sandhya, R. Mudgal, C. Jayadev, K.R. Abhinandan, R. Sowdhamini & N. Srinivasan (2012) Cascaded walks in protein sequence space: Use of artificial sequences in remote homology detection between natural proteins. *Mol. Biosyst.*, **8**, 2076-2084.

[196] A.P. Joseph, H. Valadie, N. Srinivasan & A.G. de Brevern (2012) Local structural differences in homologous proteins: Specificities in different SCOP classes. *PLoS ONE*, **7**, e38805.

[197] G. Sudha, S. Yamunadevi, N. Tyagi, S. Das & N. Srinivasan (2012) Structural and molecular basis of interaction of HCV non-structural protein 5A with human casein kinase 1 α and PKR. *BMC Strl. Biol.* **12**, 28.

[198] A.P. Joseph, N. Srinivasan & A.G. de Brevern (2012) Progressive structure-based alignment of homologous proteins: Adopting sequence comparison strategies, *Biochimie*, **94**, 2025-2034.

[199] L.S. Swapna, N. Srinivasan, D.L. Robertson & S.C. Lovell (2012) The origins of evolutionary signals used to predict protein-protein interactions. *BMC Evol. Biol.*, **12**, 238.

[200] L.S. Swapna, R.M. Bhaskara, J. Sharma & N. Srinivasan (2012) Roles of residues in the interface of transient protein-protein complexes in their unbound forms. *Sci. Rep.* **2**, 334.

[201] R. Rakesh, R. Mudgal, R.M. Bhaskara & N. Srinivasan (2013) PALI-Phylogeny and alignment of homologous protein structures. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/274> (online publication)

[202] R. Mudgal, O. Krishnadev & N. Srinivasan (2013) SUPFAM- Grouping of sequence families into superfamilies. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/219> (online publication)

[203] M. Gnanavel, R. Rakshambikai & N. Srinivasan (2013) KinG –Ser/Thr/Tyr-specific protein kinases encoded in complete genomes. *Nucl. Acids Res.* <http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).

[204] G. Ramakrishnan, R. Mudgal, S. Mohanty, O. Krishnadev & N. Srinivasan (2013) MulPSSM- Multiple PSSMs of protein domain families. *Nucl Acids Res.* <http://www3.oup.co.uk/nar/database/summary/844> (online publication)

- [205] R.M. Bhaskara, A.G. de Brevern, N. Srinivasan (2013) Understanding the role of domain-domain linkers in the spatial orientation of domains in multi-domain proteins. *J. Biomol. Str. Dyn.*, **31**, 1467-1480
- [206] B. Lakshmi, G. Archunan & N. Srinivasan (2013) Propensities of amino acid residues in proteins for different regions of the Ramachandran map. In *Biomolecular Forms and Functions* (Eds. Manju Bansal & N. Srinivasan), World Scientific Press. pp.128-135.
- [207] U. Ray, C. L. Roy, A. Kumar, P. Mani, A.P. Joseph, G.Sudha, D. P. Sarkar, N. Srinivasan & S. Das (2013) Inhibition of the interaction between NS3 protease and HCV IRES with a small peptide: A novel therapeutic strategy. *Mol. Therapy* **21**, 57-67.
- [208] N. Tyagi & N. Srinivasan (2013) Recognition of Nontrivial Remote Homology Relationships Involving Proteins of Helicobacter pylori: Implications for Function Recognition. *Methods Mol. Biol.*, **993**, 155-175.
- [209] S. Gabriel, S. Hareendran, D. Sen, R.A. Gadkari, G. Sudha, R. Selot, M. Hussain, R. Dakshamoorthy, R. Samuel, N. Srinivasan, A. Srivastava & G.R. Jayandharan (2013) Bio-engineering of AAV-2 capsid at specific serine, threonine or lysine residues improves its transduction efficiency *in vitro* and *in vivo*. *Hum. Mol. Therapy Methods*, **24**, 80-93.
- [210] S. Kaushik, E. Mutt, A. Chellappan, S. Sankaran, N. Srinivasan & R. Sowdhamini (2013) Improved detection of remote homologues using Cascade PSI_BLAST: Influence of neighboring protein families on sequence coverage. *PLoS ONE* **8**, e56449.
- [211] D. Sen, R. A Gadkari, G. Sudha, N. Gabriel, Y. Kumar, R. Selot, R. Samuel, N. Srinivasan, A. Srivastava, G.R Jayandharan (2013) Targeted modifications in adeno-associated virus serotype (AAV)-8 capsid improves its hepatic gene transfer efficiency *in vivo*. *Hum. Mol. Therapy Methods*, **24**, 104-116.
- [212] G. Ramakrishnan, V.S. Gowri, R. Mudgal, N.R. Chandra & N. Srinivasan (2013) Mining the sequence databases for homology detection: Application to recognition of functions of *Trypanosoma brucei brucei* proteins and drug targets. In *Biological Data Mining and its Applications in Healthcare* (Editors: X.-L. Li, S.-K. Ng & J.T.L. Wang), World Scientific, Singapore. pp. 3-31.
- [213] S. Mohanty, M. Purwar, N. Srinivasan & N. Rekha (2013) Tethering preferences of domain families co-occurring in multi-domain proteins. *Mol. BioSyst.* **9**, 1708-1725.
- [214] A.-M.Hansen, R.Charkady, J.Sharma, J.J. Díaz-Mejía, N.Tyagi, S.Renuse, H.K.C. Jacob, S.M. Pinto, N.A Sahasrabudhe, M.-K.Kim, B.Delanghe, N. Srinivasan, A.Emili, J.B.Kaper & A. Pandey (2013) The *Escherichia coli* phosphotyrosine proteome relates to core pathways and virulence. *PLoS Pathogens* **9**, e1003403.

- [215] S.Mahajan, G.Agarwal, M.Iftekhar, B.Offmann, A.G.de Brevern & N.Srinivasan (2013) DoSA: Database of Structural Alignments. *Database* bat048, doi:10.1093/database/bat04
- [216] V.P.R. Vendra, G. Agarwal, V. Talla, N. Srinivasan & D. Balasubramanian (2013) Structural integrity of the Greek Key motif in $\beta\gamma$ -crystallins is Vital for Central Eye Lens Transparency. *PLoS ONE* **8**, e70336
- [217] S. Mohanty, G. Ramakrishnan, P. Dave & N. Srinivasan (2013) Analysis of Sequence Divergence in Metabolic Proteins of *Plasmodium falciparum*: Implications for Remote Homology Detection. In "Frontiers in Protein and Peptide Sciences" (Ed. B. Dunn), Bentham Science Publishers. pp. 226-272.
- [218] R. Rakshambikai, N. Srinivasan & K.T. Nishant (2013) Structural insights into *Saccharomyces cerevisiae* MSH4-MSH5 complex function using homology modeling. *PLoS ONE* **8**, e78753.
- [219] R.M. Bhaskara, A. Padhi & N. Srinivasan (2013) Accurate prediction of interfacial residues in two-domain proteins using evolutionary information: Implications for 3-D modelling. *Proteins* **82**, 1219-1234.
- [220] L.S. Swapna, G. Sudha, R. Rakesh & N. Srinivasan (2013) Current trends in structural bioinformatics of protein-protein interactions. *Proc. AP Acad. Sci.*, **15**, 69-79.
- [221] R. Rakesh, R.M. Bhaskara & N. Srinivasan (2014) PALI- Phylogeny and alignment of homologous protein structures. *Nucl Acids Res.*
<http://www3.oup.co.uk/nar/database/summary/274> (online publication)
- [222] R. Mudgal, O. Krishnadev & N. Srinivasan (2014) SUPFAM- Grouping of sequence families into superfamilies. *Nucl Acids Res.*
<http://www3.oup.co.uk/nar/database/summary/219> (online publication)
- [223] M. Gnanavel, R. Rakshambikai & N. Srinivasan (2014) KinG –Ser/Thr/Tyr-specific protein kinases encoded in complete genomes. *Nucl. Acids Res.*
<http://www3.oup.co.uk/nar/database/summary/518> (on-line publication).
- [224] G. Ramakrishnan, S. Mohanty, O. Krishnadev & N. Srinivasan (2014) MulPSSM- Multiple PSSMs of protein domain families. *Nucl Acids Res.*
<http://www3.oup.co.uk/nar/database/summary/844> (online publication)
- [225] S. Léonard, A.P. Joseph, N. Srinivasan, J.-C. Gelly & A.G. de Brevern (2014) mulPBA : an efficient multiple protein structure alignment method based on a structural alphabet. *J. Biomol. Str. Dyn.*, **32**, 661-668
- [226] R. Rakshambikai, N. Srinivasan & R.A. Gadkari (2014) Repertoire of protein kinases encoded in the genome of zebrafish shows remarkably large population of PIM kinases. *J. Bioinf. Comp. Biol.*, **12**, 1350014

- [227] B. Lakshmi, C. Ramakrishnan, G. Archunan, R. Sowdhamini & N. Srinivasan (2014) Investigations of Ramachandran disallowed conformations in protein domain families. *Int. J. Biol. Macromol.*, **63**, 119-125.
- [228] S. Mahajan, A.G. de Brevern, B. Offmann & N. Srinivasan (2014) Correlation between local structural dynamics of proteins inferred from NMR ensembles and evolutionary dynamics of homologues of known structure. *J. Biomol. Str. Dyn.*, **32**, 751-758
- [229] R. Mudgal, R. Sowdhamini, N. Chandra, N. Srinivasan & S. Sandhya (2014) Filling in void and sparse regions in protein sequence space by protein-like artificial sequences enables remarkable enhancement in remote homology detection capability. *J. Mol. Biol.* **426**, 962-979.
- [230] R.M. Bhaskara, P. Mehrotra, R. Rakshambikai, M. Gnanavel, J. Martin & N. Srinivasan (2014) The relationship between classification of multi-domain proteins using an alignment-free approach and their functions: A case study with immunoglobulins. *Mol. Biosyst.*, **10**, 1082-1093
- [231] B. Lakshmi, C. Sinduja, G. Archunan & N. Srinivasan (2014) Ramachandran analysis of conserved glyceryl residues in homologous proteins of known structure. *Prot. Sci.* **23**, 843-850.
- [232] A.P. Joseph, P. Bhat, S. Das & N. Srinivasan (2014) Re-analysis of cryoEM data on HCV IRES bound to 40S subunit of human ribosome integrated with recent structural information suggests new contact regions between ribosomal proteins and HCV RNA. *RNA Biol.* **11**, 891-905.
- [233] U.B. Reddy, R. Mullick, A. Kumar, G. Sudha, N. Srinivasan & S. Das (2014) Small molecule inhibitors of HCV replication from Pomegranate. *Sci. Rep.* **4**, 5411
- [234] G. Sudha, R. Nussinov & N. Srinivasan (2014) An overview of recent advances in structural bioinformatics of protein-protein interactions and a guide to their principles. *Prog. Biophys. Mol. Biol.*, **116**, 141-150.
- [235] S. Vishwanath & N. Srinivasan (2014) Chemical specificity and conformational flexibility in proteinase - inhibitor interaction: Scaffolds for promiscuous binding. *Prog. Biophys. Mol. Biol.* **116**, 151-157.
- [236] R. Rakshambikai, M. Gnanavel & N. Srinivasan (2014) Hybrid and rogue kinases encoded in the genomes of model eukaryotes. *PLoS ONE*, **9**, e107956.
- [237] M. Gnanavel, P. Mehrotra, R. Rakshambikai, J. Martin, N. Srinivasan & R.M. Bhaskara, (2014) CLAP: A web server for automatic classification of proteins with special reference to multi-domain proteins. *BMC Bioinformatics* **15**, 343.

- [238] S. Mahajan, A. G. de Brevern, Y. -H. Sanejouand, N. Srinivasan & B. Offmann (2014) Use of a structural alphabet to find compatible folds for amino acid sequences. *Prot. Sci.*, **24**, 145-153.
- [239] G. Ramakrishnan, B. Ochoa-Montano, U.S. Raghavender, R. Mudgal, A.G. Joshi, N.R. Chandra, R. Sowdhamini, T.L. Blundell & N. Srinivasan (2014) Enriching the annotation of *Mycobacterium tuberculosis* proteome using remote homology detection approaches: Insights into structure and function. *Tuberculosis*, **95**, 14-25.
- [240] G. Ramakrishnan, N.R. Chandra & N. Srinivasan (2014) From workstations to workbenches: Towards predicting physicochemically viable protein-protein interactions across a host and a pathogen. *IUBMB Life*, **66**, 759-774.
- [241] M. Manoharan, P. Sharma, Ch. Janaki, S. Shekhar, N. Srinivasan & R. Rakshambikai (2015) KinG – Kinases in genomes. *Nucl. Acids Res.* http://www.oxfordjournals.org/our_journals/nar/database/summary/518 (online publication)
- [242] R. Mudgal, S. Sandhya, G. Kumar, R. Sowdhamini, N. R. Chandra & N. Srinivasan (2015) NrichD Database: Sequence databases enriched with computationally designed protein-like sequences aid in remote homology detection. *Nucl. Acids Res.*, **43**, 300-305.
- [243] R. Kalaivani & N. Srinivasan (2015) A Gaussian network model study suggests that structural fluctuations are higher for inactive than active states of protein kinases. *Mol. Biosyst.*, **11**, 1079-1095.
- [244] P. Bhat, S. Shwetha, D. Sharma, A.P. Joseph, N. Srinivasan & S. Das (2015) The beta hairpin structure within ribosomal protein S5 mediates interplay between domain II and IV and regulates HCV-IRES function. *Nucl. Acids Res.* **43**, 2888-2901.
- [245] R. Rakshambikai, M. Manoharan, M. Gnanavel & N. Srinivasan (2015) Typical and atypical domain combinations of human protein kinases: Functions, disease causing mutations and conservation in other primates *RSC Advances*, **5**, 25132-25148.
- [246] G.L. Holliday, A. Bairoch, P.G. Bagos, A. Chatonnet, D.J. Craik, R.D. Flinn, B. Henrissat, D. Landsman, G. Manning, N. Nagano, C.O'Donovan, K.D. Pruitt, N.D. Rawlings, M. Saier, R. Sowdhamini, M. Spedding, N. Srinivasan, G. Vriend, P.C. Babbitt & A. Bateman (2015) Key challenges for the creation and maintenance of specialist protein resources. *Proteins* (in press).
- [247] P. Craveur, A.P Joseph, J. Esque, T.J. Narwani, F. Noel, N. Shinada, M. Goguet, L. Sylvain, P. Poulain, O. Bertrand, G. Faure, J. Rebehmed, A. Ghozlane, L.S. Swapna, R.M. Bhaskara, J. Barnoud, S. Téletchéa, V. Jallu, J. Cerny, B. Schneider, C. Etchebest, N. Srinivasan, J.-C. Gelly & A.G. de Brevern (2015) Protein flexibility in the light of structural alphabets. *Frontiers in Mol. Biosci.* (in press).
- [248] P.C. Babbitt, P. G. Bagos, A. Bairoch, A. Bateman, A. Chatonnet, M. J. Chen, D. Craik, R. Finn, D. Gloriam, D. Haft, B. Henrissat, G. L. Holliday, V. Isberg, Q.

Kaas, D. Landsman, N. Lenfant, G. Manning, N. Nagano, N. Srinivasan, C. O'Donovan, K. D. Pruitt, R. Sowdhamini, N. D. Rawlings, M. Saier. Jr, J. L. Sharman, M. Spedding, K. D. Tsirigos, A. Vastermark & G. Vriend (2015) Creating a Specialist Protein Resource Network: A meeting report for the Protein Bioinformatics and Community Resources Retreat. *DATABASE* (in press).

[249] G. Sudha, N. Naveenkumar & N. Srinivasan (2015) Evolutionary and structural analyses of heterodimeric proteins composed of subunits with same fold. *Proteins* (under revision).

[250] B. Lakshmi, M. Mishra, N. Srinivasan & G. Archunan (2015) Structure-based phylogenetic analysis on superfamily of lipocalins. *PLoS ONE* (under revision).

[251] R. Metri, S. Hariharaputran, G. Ramakrishnan, P. Anand, U. S. Raghavender, B. Ochoa-Montano, A. P. Higuero, R. Sowdhamini, N. R. Chandra, T. L. Blundell & N. Srinivasan (2015) SInCRE - Structural Interactome Computational Resource for *Mycobacterium tuberculosis*. *DATABASE* (under revision).

[252] R. Mudgal, S. Sandhya, N. Chandra & N. Srinivasan (2015) De-DUFing the DUFs: Deciphering distant evolutionary relationships of Domains of Unknown Function using sensitive remote homology detection methods. *Biology Direct* (under revision).

[253] G. Sudha, P. Singh, L.S. Swapna & N. Srinivasan (2015) Weak conservation of structural features in the interfaces of homologous transient protein-protein complexes. *Prot. Sci.* (under revision).

Edited book

M. Bansal & N. Srinivasan (2012) Biomolecular forms and functions. World Scientific Press. & IISc Press.