

- [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  $\gamma$ -crystallin based on  $\beta$  and  $\gamma$ -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 HGFI/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 Helveticae.*, **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)  $\alpha$ -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  $G\alpha$  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  $G\alpha$  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 $\alpha$  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  $\beta$ -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.Garrod, 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 glycylic 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.
- [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.
- [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<sub>Delhi</sub>. *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) Analcys: 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  $\gamma$ 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  $\gamma$ -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. Chattapadhyay, 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 $\alpha$  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. *Bioinformatics*, **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.Kangueane) 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. *Nature 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 $\alpha$  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] R.M. Bhaskara, A.G. de Brevern, N. Srinivasan (2012) Understanding the role of domain-domain linkers in the spatial orientation of domains in multi-domain proteins. *J. Biomol. Str. Dyn.* (in press)
- [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. *Nature Sci. Rep.* **2**, 334.

[201] 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.

[202] 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)

[203] 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)

[204] 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).

---

[205] 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)

[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* (in press).

[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* (in press).

- [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 (in press).
- [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] S. Léonard, A.P. Joseph, N. Srinivasan, J.-C. Gelly & A.G. de Brevern (2013) mulPBA : an efficient multiple protein structure alignment method based on a structural alphabet. *J. Biomol. Str. Dyn.* (in press).
- [215] S. Mahajan, A.G. de Brevern, B. Offmann & N. Srinivasan (2013) Correlation between local structural dynamics of proteins inferred from NMR ensembles and evolutionary dynamics of homologues of known structure. *J. Biomol. Str. Dyn.* (in press).
- [216] A.-M.Hansen, R.Chaerkady, J.Sharma, J.J. Díaz-Mejía, N.Tyagi, S.Renuse, H.K.C. Jacob, S.M. Pinto, N.A Sahasrabuddhe, 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.
- [217] S.Mahajan, G.Agarwal, M.Iftekhar, B.Offmann, A.G.de Brevern & N.Srinivasan (2013) DoSA: Database of Structural Alignments. *Database* (in press).
- [218] 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
- [219] 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. (in press).
- [220] R. Rakshambikai, N. Srinivasan & R.A. Gadkari (2013) Repertoire of protein kinases encoded in the genome of zebrafish shows remarkably large population of PIM kinases. *J. Bioinf. Comp. Biol.* (in press).
- [221] R. Rakshambikai, N. Srinivasan & K.T. Nishant (2013) Structural insights into *Saccharomyces cerevisiae* MSH4-MSH5 complex function using homology modeling. *PLoS ONE* **8**, e78753.
- [222] B. Lakshmi, C. Ramakrishnan, G. Archunan, R. Sowdhamini & N. Srinivasan (2013) Investigations of Ramachandran disallowed conformations in protein domain families. *Int. J. Biol. Macromol.* (in press).

- [223] 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* (in press).
- [224] L.S. Swapna, G. Sudha, R. Rakesh & N. Srinivasan (2014) Current trends in structural bioinformatics of protein-protein interactions. *Proc. AP Acad. Sci.* (in press).
- [225] 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.* (in press).
- [226] R.M. Bhaskara, P. Mehrotra, R. Rakshambikai, M. Gnanavel, J. Martin & N. Srinivasan (2014) Critical assessment of an approach to classification of full length proteins. *Mol. Biosyst.* (in press).

### **Edited book**

M. Bansal & N. Srinivasan (2013) Biomolecular forms and functions. World Scientific Press. & IISc Press.