



# **Form and Function of Biomolecules**

## **Macromolecular crystallography**

### **in India**

#### **A Historical Profile through Publications (1981-2015)**





## FOREWORD

Structural biology is concerned with the structures of and the structure-function relationship in biomolecules. Macromolecular crystallography is central to structural biology and indeed to modern biology as a whole. Although exploratory efforts in the field were initiated as early as in 1934 by J.D. Bernal and Dorothy Hodgkin (then Crowfoot), substantive results began to appear only by around 1960 with the structure solution of hemoglobin and myoglobin by the groups of Max Perutz and John Kendrew respectively. In an outstanding parallel computational/bioinformatics effort, G.N. Ramachandran and his colleagues at Madras developed what subsequently came to be known as the Ramachandran map which even now remains as the simplest descriptor and tool for validation of protein structures. However, initiation of macromolecular crystallographic studies in India had to wait two more decades.

A few Indians have been involved in the early macromolecular crystallography projects abroad. From among them, I was the first to return to India. When I rejoined the Indian Institute of Science, Bangalore in 1971 after participating in the structure solution of insulin in Dorothy Hodgkin's laboratory at Oxford, I would have liked nothing more than to straightway start macromolecular crystallography studies in the laboratory, but the resources available then were not even enough to carry out preliminary investigations in the area. I therefore concentrated on studies involving small molecules which are relevant to protein structure, and more so to chemical evolution and origin of life, while at the same time looking for opportunities to initiate macromolecular work. In the meantime, attempts to start macromolecular crystallography were initiated in the late seventies at the Bhabha Atomic Research Centre, Mumbai as well. The efforts truly took off the ground in the country after the Department of Science and Technology (DST) decided in 1983 to handsomely fund the Bangalore Centre under their Thurst Area Programme. The Bangalore laboratory also came to be recognized as a national nucleus for the development of the area in India. Since then, the DST (and now SERB) has continued to support the centres at Bangalore and elsewhere. Over the years, agencies such as the Department of Biotechnology (DBT), the Council of Scientific and Industrial Research (CSIR) and the Department of Atomic Energy (DAE) have also strongly supported the macromolecular crystallography efforts in the country in different ways. In spite of a slow start, work in the area has

rapidly expanded in recent years and is being pursued in nearly 40 institutions by about twice as many research groups.

Starting with a single modern in-house facility at Bangalore in the early 1990s for collection of intensity data from macromolecular crystals, dozens of such facilities now exist in different parts of the country. Indian workers now have assured access to the European Synchrotron Facility, thanks to the generous support of the DBT. A dedicated beam line, set up with the support of the DST at Elettra, is expected to be available soon. Happily, the macromolecular crystallography beamline of the second generation synchrotron INDUS-2 at RRCAT, Indore is now fully functional. Thus, although there is a need for setting up a state-of-the art synchrotron facility in India, reasonable arrangements exist for Indian macromolecular crystallographers for collection of diffraction data.

For historical reasons, a majority of macromolecular crystallography groups in the country are led by scientists trained at Bangalore and their descendents. However, over the years, scientists with widely different national and international backgrounds have also established strong groups in different institutions in India. Thus, macromolecular crystallographers in India today constitute a reasonably coherent, vibrant community consisting of a mosaic of backgrounds and expertise, with healthy interactions among themselves and with other concerned biologists. The evolution of the community is perhaps best followed through publications in the area emanating from the country. A historically organized compilation of such publications was first produced in 2005, followed by another in 2011. Much has happened since then and the time is ripe for another compilation. Hence this document which lists relevant papers published till the end of 2015.\*

-----  
\*The subject matter of the papers in the compilation is meant to be wholly or substantially crystallographic. Efforts have been made to enforce this criterion, probably not with complete success. It is also possible that some publications with substantial crystallographic content, have been eliminated in the process. I apologise to the concerned authors for such omissions, if any.

Macromolecular crystallographic studies in the country now encompass almost all areas of modern biology and also have in some cases medicinal implications. Concerted efforts pertaining to specific systems have also emerged. In some sense, macromolecular crystallography came of age in the country by the turn of the century and was by then equipped to address issues specific to developing countries like India. Even the by the end of 1990s, work had started on proteins from pathogenic microbes which cause infectious diseases. In the early years of this century, we orchestrated a national programme on the structural genomics of microbial pathogens, which provided additional impetus to these efforts. The pathogen that has received maximum attention is *Mycobacterium tuberculosis*, the causative agent of TB which is a major health issue in India. In a loosely coordinated effort, about a dozen laboratories in India are involved in structural studies on TB proteins. Consequently, we now have a robust Indian platform for structure-based inhibitor design which could lead to development of drugs against TB. The other pathogens, the structural biology of which is being pursued in India, include malarial parasites, *Salmonella typhimurium*, *Vibrio cholerae*, *Entamoeba histolytica*, *Staphylococcus aureus*, *Leishmania donovani*, HIV and rotavirus. Thus macromolecular crystallography efforts in India encompass engagement with fundamental biological issues as well as exploration of systems with application potential.

I thank my colleagues at Bangalore and elsewhere including K. Suguna, B. Gopal, K. Sekar, Aravind Penmatsa, Shankar Kanaujia, K.V. Abhinav and Amandeep Singh who helped me in putting together this compilation. I am deeply indebted to Pankaja, C. who played a central role in the effort.

M. Vijayan

Bangalore  
August, 2016



## THE BEGINNINGS 1981-1989

### Indian Institute of Science, Bangalore

Krishna Murthy, H.M., Vijayan, M. & Gurnani, S. (1981). X-ray studies on the binding of bromophenol red and bromophenol blue to lysozyme. *Acta Cryst.* **A37**, C-33.

Salunke, D.M., Islam Khan, M., Surolia, A. & Vijayan, M. (1982). Crystallization and preliminary X-ray studies of the anti-T lectin from peanut (*Arachis hypogaea*). *J. Mol. Biol.* **154**, 177-178.

Salunke, D.M., Islam Khan, M., Surolia, A. & Vijayan, M. (1983). Preparation and preliminary X-ray studies of three acidic pH crystal forms of the anti-T lectin from peanut (*Arachis hypogaea*). *FEBS Letts.* **156**, 127-129.

Salunke, D.M., Veerapandian, B. & Vijayan, M. (1984). Water-mediated structural transformation in a new crystal form of ribonuclease A and tetragonal lysozyme. *Curr. Sci.* **53**, 231-235.

Salunke, D.M., Kodandapani, R. & Vijayan, M. (1984). Environmental effects on water-mediated transformations in the crystals of ribonuclease A. *Acta Cryst.* **A40**, C-53.

Vijayan, M. & Salunke, D.M. (1984). Structural mobility and transformations in globular proteins. *J. Biosci.* **6**, 357-377.

Salunke, D.M., Veerapandian, B., Kodandapani, R. & Vijayan, M. (1985). Structural transformations in protein crystals caused by controlled dehydration. Proceedings of the International Symposium on Biomolecular Structure and Interactions. Supplement to *J. Biosci.* **8**, 37-44.

Veerapandian, B., Salunke, D.M. & Vijayan, M. (1985). X-ray characterisation of an additional binding site in lysozyme. *FEBS Letts.* **186**, 163-167.



Salunke, D.M., Veerapandian, B., Kodandapani, R. & Vijayan, M. (1985). Water mediated transformations in protein crystals. *Acta Cryst.* **B41**, 431-436.

Salunke, D.M., Swamy, M.J., Khan, M.I., Mande, S.C., Surolia, A. & Vijayan, M. (1985). Arrangement of subunits in Peanut Lectin. Rotation function and chemical cross linking studies. *J. Biol. Chem.* **260**, 13576-13579.

Vijayan, M. (1987). Anomalous scattering methods. In *Direct Methods, Macromolecular Crystallography and Crystallographic Statistics*. Edited by H. Schenk, A.J.C. Wilson & S. Parthasarathy, World Scientific, Singapore pp.121-140.

Vijayan, M. (1987). Structure, transformations and interaction of proteins: An X-ray study. *Curr. Sci.* **56**, 174-175.

Mande, S.C., Raghunathan, S., Islam Khan, M., Surolia, A. & Vijayan, M. (1987). Structural similarity between peanut lectin and concanavalin A. *Acta Cryst.* **A43**, C-21.

Murthy, M.R.N., Munshi, S.K., Hiremath, C.N., Suryanarayana, S. & Savithri, H.S. (1987). Structural studies on belladonna mottle virus. *Curr. Sci.* **56**, 168-169.

Munshi, S.K., Hiremath, C.N., Savithri, H.S. & Murthy, M.R.N. (1987). Symmetry of belladonna mottle virus, rotation function studies. *Acta Cryst.* **B43**, 376-382.

Munshi, S.K. & Murthy, M.R.N. (1987). Strategies for collecting screenless oscillation data. *J. Appl. Cryst.* **19**, 61-62.

Mande, S.C., Raghunathan, R., Salunke, D.M., Islam Khan, M., Swamy, M.J., Surolia, A. & Vijayan, M. (1988). Structural studies on peanut lectin. *Ind. J. Biochem. Biophys.* **25**, 166-171.

Dhanaraj, V., Patanjali, S.R., Surolia, A. & Vijayan, M. (1988). Preparation and preliminary X-ray studies of two crystal forms of the anti-T lectin from jackfruit (*Artocarpus integrifolia*). *J. Mol. Biol.* **203**, 1135-1136.

Mande, S.C. & Suguna, K. (1989). A fast algorithm for macromolecular packing calculation. *J. Appl. Cryst.* **22**, 627-629.

Savithri, H.S., Suryanarayana, S. & Murthy, M.R.N. (1989). Structure-function relationships of icosahedral plant viruses. *Arch. Virol.* **109**, 153-172.

### **Bhabha Atomic Research Centre, Mumbai**

Kannan, K.K. & Ramanadham, M. (1981). Structure, refinement and function of human carbonic anhydrase B. *Int. J. Quant. Chem.* **XX**, 199-209.

Kannan, K.K., Singh, S., Ramanadham, M. & Eaker, J. D. (1981). Structure of presynaptic toxins: Crystallization and preliminary X-ray diffraction data on Notechis II-5, a presynaptic toxin phospholipase. *J. Biosci.* **3**, 29-31.

Kannan, K.K. & Chidambaram, R. (1983). Macromolecular crystallography at Trombay. Proceedings of the Indian Academy of Sciences. *Chem. Sci.* **92**, 497-507.

Kannan, K.K., Ramanadham, M. & Jones, T.A. (1984). Structure, Refinement and Function of carbonic anhydrase isozymes: Refinement of Human Carbonic anhydrase I. *Ann. New York Academy of Sci.* **429**, 49-60.

Chakravarthy, S., Yadava, V.S., Kumar, V. & Kannan, K.K. (1985). Drug protein Interaction at the Molecular level : A study of sulphonamide carbonic anhydrase complexes. *J. Biosci. (Suppl.)* **8**, 491-498.

Kumar, V., Sankaran, K. & Kannan, K.K. (1986). Crystallization and preliminary data of Indian buffalo erythrocyte carbonic anhydrase. *J. Mol. Biol.* **190**, 129-131.

Kannan, K.K., Kumar, V., Sankaran, K., Sathyamurthy, P. & Chakravarthy, S. (1987). How Drugs affect enzyme function? A protein crystallographic approach. *Curr. Sci.* **56**, 173-174.

Kumar, V., Sathyamurthy, P. & Kannan, K.K. (1987). Human carbonic anhydrase I- Iodide complex: Structure and inhibition mechanism. *Acta Cryst.* **A43**, C-23-C24.

Kannan, K.K. (1987). Methods in macromolecular crystallography. In *Direct Methods, Macromolecular Crystallography and Crystallographic Statistics*. Edited by H. Schenk, A.J.C. Wilson & S. Parthasarathy, World Scientific, Singapore pp. 22-40.

Kumar, V., Kannan, K.K. & Chidambaram, R. (1989). Crystal structure of carbonic anhydrase II from Erythrocyte of Indian Buffalo (*Bubalus Bubalus*) *Curr. Sci.* **58**, 344-348.

## THE CONSOLIDATION 1990-1999

### Indian Institute of Science, Bangalore

Kodandapani, R., Suresh, C.G. & Vijayan, M. (1990). Crystal structure of the low humidity form of tetragonal lysozyme. *Acta Cryst.* **A46**, C-84.

Kodandapani, R., Suresh, C.G. & Vijayan, M. (1990). Crystal structure of Low Humidity Tetragonal Lysozyme at 2.1-Å Resolution. Variability in hydration shell and its structural consequences. *J. Biol. Chem.* **265**, 16126-16131.

Hiremath, C.N., Munshi, S.K. & Murthy, M.R.N. (1990). Structure of belladonna mottle virus: Cross rotation function studies with southern bean mosaic virus. *Acta Cryst.* **B46**, 562-567.

Murthy, M.R.N., Hiremath, C.N. & Savithri, H.S. (1991). Structure and assembly of viruses. In *Molecular Conformation and Biological structure*. Edited by P. Balaram & S. Ramaseshan, Indian Academy of Sciences, Bangalore pp. 687-702.

Madhusudan & Vijayan, M. (1991). Rigid and flexible regions in lysozyme and the invariant features in its hydration shell. *Curr. Sci.* **60**, 165-170.

Banerjee, R., Dhanaraj, V., Mahanta, S.K., Surolia, A. & Vijayan, M. (1991). Preparation and X-ray characterization of four new crystal forms of jacalin, a lectin from *Artocarpus integrifolia*. *J. Mol. Biol.* **221**, 773-776.

Vijayan, M. & Kodandapani, R. (1991). Variability in protein hydration and its structural consequences. A novel approach involving water-mediated transformations. In *Molecular Conformation and Biological Interactions*. Edited by P. Balaram & S. Ramaseshan, Indian Academy of Sciences, Bangalore pp.149-170.

Madhusudan & Vijayan, M. (1992). Additional binding sites in lysozyme. X-ray analysis of lysozyme complexes with bromophenol red and bromophenol blue. *Protein Eng.* **5**, 399-404.

Madhusudan, Kodandapani, R. & Vijayan, M. (1993). Protein hydration and water structure: X-ray analysis of a closely packed protein crystal with very low solvent content. *Acta Cryst.* **D49**, 234-245.

Sankaranarayanan, R., Puri, K.D., Ganesh, V., Banerjee, R., Surolia, A. & Vijayan, M. (1993). Crystallization and preliminary X-ray studies of the basic lectin from winged bean (*Psophocarpus tetragonolobus*). *J. Mol. Biol.* **229**, 558-560.

Vijayan, M. & Ramaseshan, S. (1993). Isomorphous replacement and anomalous scattering. In *International Tables for Crystallography*. Vol. B. Reciprocal Space. Edited by U. Shmueli, Kluwer Academic Publishers, Dordrecht pp. 264-279.

Banerjee, R., Mande, S.C., Ganesh, V., Das, K., Dhanaraj, V., Mahanta, S.K., Suguna, K., Surolia, A. & Vijayan, M. (1993). Crystal structure of peanut lectin, a protein with an open quaternary arrangement. *Acta Cryst.* **A49**, C-95.

Suguna, K. (1993). Laue Crystallography. *Curr. Sci.* **65**, 627-629.

Subramanya, H.S., Gopinath, K., Nayudu, M.V., Savithri, H.S. & Murthy, M.R.N. (1993). Structure of Sesbania mosaic virus at 4.7Å resolution and partial amino acid sequence of the coat protein. *J. Mol. Biol.* **229**, 20-25.

Viswamitra, M.A., Bhanumoorthy, P., Ramakumar, S., Manjula, M.V., Vithayathil, P.J., Murthy, S.K. & Naren, A.P. (1993). Crystallization and preliminary X-ray diffraction analysis of crystals of *Thermoascus aurantiacus* xylanase. *J. Mol. Biol.* **232**, 987-988.

Velankar, S. & Murthy, M.R.N. (1994). Studies on molecular evolution and structural features of double headed inhibitor of  $\alpha$ -amylase and trypsin in plants. *J. Genetics* **73**, 43-54.

Prakash, B., Murthy, M.R.N., Sreerama, Y.N., Rama Sarma, P.R. & Rajagopala Rao, D. (1994). Crystallization and preliminary X-ray diffraction studies on a Trypsin/Chymotrypsin double headed inhibitor from horse gram. *J. Mol. Biol.* **235**, 364-366.

Eswaramoorthy, S., Vithayathil, P.J. & Viswamitra, M.A. (1994). Crystallization and preliminary X-ray crystallographic studies of thermostable xylanase crystals isolated from *Paecilomyces varioti*. *J. Mol. Biol.* **243**, 806-808.

Banerjee, R., Mande, S.C., Ganesh, V., Das, K., Dhanaraj, V., Mahanta, S.K., Suguna, K., Surolia, A. & Vijayan, M. (1994). Crystal structure of peanut lectin, a protein with an unusual quaternary structure. *Proc. Natl. Acad. Sci. (U.S.A.)* **91**, 227-231.

Nagendra, H.G., Sudarsanakumar, C. & Vijayan, M. (1995). Characterization of lysozyme crystals with unusually low solvent content. *Acta Cryst.* **D51**, 390-392.

Radha Kishan, K.V., Chandra, N.R., Sudarsanakumar, C., Suguna, K. & Vijayan, M. (1995). Water-dependent domain motion and flexibility in Ribonuclease A and the invariant features in its hydration shell. An X-ray study of two low humidity crystal forms of the enzyme. *Acta Cryst.* **D51**, 703-710.

Bhuvaneshwari, M., Subramanya, H.S., Gopinath, K., Nayudu, M.V., Savithri, H.S. & Murthy, M.R.N. (1995). Structure of sesbania mosaic virus at 3.0 Å resolution. *Structure* **3**, 1021-1030.

Nagendra, H.G., Sudarsanakumar, C. & Vijayan, M. (1996). An X-ray analysis of native monoclinic lysozyme. A case study on the reliability of refined protein structures and a comparison with the low humidity form in relation to mobility and enzyme action. *Acta Cryst.* **D52**, 1067-1074.

Vijayan, M. (1996). Form and function. X-rays in structural biology. *Curr. Sci.* **70**, 889-898.

Banerjee, R., Das, K., Ravishankar, R., Suguna, K., Surolia, A. & Vijayan, M. (1996). Conformation, protein-carbohydrate interactions and a novel subunit association in the refined structure of peanut lectin-lactose complex. *J. Mol. Biol.* **259**, 281-296.

Ravishankar, R., Ravindra, M., Suguna, K., Surolia, A. & Vijayan, M. (1996). Crystal structure of peanut agglutinin-T-antigen complex. *Prog. Biophys. Mol. Biol.* **65**, Supplement 1, 33.

Sekar, K., Banerjee, R., Mahanta, S.K., Surolia, A., Sankaranarayanan, R. & Vijayan, M. (1996). A threefold symmetric  $\beta$ -prism fold without internal sequence homology in the two-chain lectin, jacalin. *Acta Cryst.* **A52**, C-174.

Sankaranarayanan, R., Sekar, K., Banerjee, R., Sharma, V., Surolia, A. & Vijayan, M. (1996). A novel mode of carbohydrate recognition in jacalin, a *Moraceae* plant lectin with a  $\beta$ -prism fold. *Nat. Struct. Biol.* **3**, 596-603.

Sharma, V., Vijayan, M. & Surolia, A. (1996). Imparting exquisite specificity to peanut agglutinin for tumor associated Thomsen-Friedenreich antigen by redesign of its combining site. *J. Biol. Chem.* **271**, 21209-21213.

Ravishankar, R., Ravindran, M., Suguna, K., Surolia, A. & Vijayan, M. (1997). Crystal structure of the peanut lectin-T-antigen complex. Carbohydrate specificity generated by water bridges. *Curr. Sci.* **72**, 855-861.

Suresh, S., A., Rani, P.G., Pratap, J.V., Sankaranarayanan, R., Surolia, A. & Vijayan, M. (1997). Homology between jacalin and artocarpin from jackfruit (*Artocarpus integrifolia*) seeds. Partial sequence and preliminary crystallographic studies of artocarpin. *Acta Cryst.* **D53**, 469-471.

Chandra, N.R., Dam, T.K., Surolia, A. & Vijayan, M. (1997). Crystallization and preliminary crystallographic studies on the mannose-specific lectin from garlic. *Acta Cryst.* **D53**, 787-788.

Vijayan, M. (1997). Quaternary structure of proteins. In Aspects of Crystallography in Molecular Biology. Edited by S. Parthasarathy & J.P. Glusker, New Age International Publishers, New Delhi pp. 225-238.

Bhuvanewari, M., Subramanya, H.S., Murthy, M.R.N., Gopinath, K. & Savithri, H.S. (1997). Architecture of small RNA viruses. *Prog. Crystal Growth and Charact.* **34**, 1-10.

Velankar, S.S., Ray, S.S., Gokhale, R.S., Suma, S., Balaram, H., Balaram, P. & Murthy, M.R.N. (1997). Triosephosphate isomerase from *Plasmodium falciparum*: the crystal structure provides insights into antimalarial drug design. *Structure* **5**, 751-761.

Murthy, M.R.N., Bhuvanewari, M., Subramanya, H.S., Gopinath, K. & Savithri, H.S. (1997). Sesbania mosaic virus structure at 3Å resolution. *Biophysical Chem.* **68**, 33-42.

Gopal, B., Prasanna, V., Parthasarathy, S., Santi, D.V., Balaram, P. & Murthy, M.R.N. (1997). Crystals of a thymidylate synthase mutant offer insights into crystal packing and plasticity of protein-protein contacts. *Curr. Sci.* **75**, 299-304.

Ratnaparkhi, G.S. & Varadarajan, R. (1997). Structural Studies of Protein Unfolding. *Curr. Sci.* **72**, 826-830.

Ratnaparkhi, G.S., Ramachandran, S., Udgaonkar, J.B. & Varadarajan, R. (1998). Discrepancies between the NMR and X-ray structures of uncomplexed Barstar: Analysis suggests that packing densities of protein structures determined by NMR are unreliable. *Biochemistry* **37**, 6958-6966.

Gopal, B., Suma, R., Swaminathan, C.P., Surolia, A., Murthy, M.R.N., Bhattacharya, A. & Bhattacharya, S. (1998). Crystallization and preliminary X-ray diffraction studies of a recombinant calcium binding protein from *Entamoeba histolytica*. *Acta Cryst.* **D54**, 1442-1445.



Murthy, M.R.N. & Savithri, H.S. (1998). Structural studies on isometric plant viruses. In *Topics in Tropical Virology*, 1. Edited by D.N.Black, D.D.Shukla & N.Rishi, Malhotra Publishing House, New Delhi pp. 59-75.

Prabu, M.M., Sankaranarayanan, R., Puri, K.D., Sharma, V., Surolia, A., Vijayan, M. & Suguna, K. (1998). Carbohydrate specificity and quaternary association in basic winged bean lectin: X-ray analysis of the lectin at 2.5 Å resolution. *J. Mol. Biol.* **276**, 787-796.

Nagendra, H.G., Sukumar, N. & Vijayan, M. (1998). Role of water in plasticity, stability and action of proteins. The crystal structures of lysozyme at very low levels of hydration. *Proteins* **32**, 229-240.

Sharma, V., Srinivas, V.R., Adhikari, P., Vijayan, M. & Surolia, A. (1998). Molecular basis of recognition by Gal/GalNac specific legume lectins: Influence of Glu 129 on the specificity of peanut agglutinin (PNA) towards C2-substituents of galactose. *Glycobiology* **10**, 1007-1012.

Ravishankar, R., Bidyasagar, M., Roy, S., Purnapatre, K., Handa, P., Varshney, U. & Vijayan, M. (1998). X-ray analysis of *Escherichia coli* uracil DNA glycosylase (EcUDG) with a proteinaceous inhibitor. The structure elucidation of a prokaryotic UDG. *Nucl. Acids Res.* **26**, 4880-4887.

Sadasivan, C., Nagendra, H.G. & Vijayan, M. (1998). Plasticity, hydration and accessibility in Ribonuclease A. The structure of a new crystal form and its low humidity variant. *Acta Cryst.* **D54**, 1343-1352.

Ravishankar, R., Surolia, A., Lim, S., Kishi, Y. & Vijayan, M. (1998). Preferred conformation of C-lactose at the free and peanut lectin bound states. *J. Am. Chem. Soc.* **120**, 11297-11303.

Nandi, A., Visweswariah, S., Suguna, K. & Surolia, A. (1998). Topological mimicry and epitope duplication in the guanylyl cyclase C receptor. *Protein Sci.* **7**, 2175-2183.

Bhandari, R., Suguna, K. & Visweswariah, S. (1999). Guanylyl cyclase C receptor: Regulation of catalytic activity by ATP. *Bioscience Reports* **19**, 179-188.

Ravishankar, R., Suguna, K., Surolia, A. & Vijayan, M. (1999). Structures of the complexes of peanut lectin with methyl-beta-galactose and N-acetyllactosamine and a comparative study of carbohydrate binding in Gal/GalNac specific legume lectins. *J. Biosci.* **24**, Supplement 1, 35.

Chandra, N.R., Ramachandraiah, G., Bachhawat, K., Dam, T.K., Surolia, A. & Vijayan, M. (1999). Crystal structure of a dimeric mannose specific agglutinin from garlic: Quaternary association and carbohydrate specificity. *J. Mol. Biol.* **285**, 1157-1168.

Prabu, M.M. Suguna, K. & Vijayan, M. (1999). Variability in quaternary association of proteins with the same tertiary fold. A case study and rationalisation involving legume lectins. *Proteins* **35**, 58-69.

Sukumar, N., Biswal, B.K. & Vijayan, M. (1999). Structures of orthorhombic lysozyme grown at basic pH and its low humidity variant. *Acta Cryst.* **D55**, 934-937.

Bidya Sagar, M., Ravishankar, R., Saikrishnan, K., Roy, S. Purnapatre, K., Handa, P., Varshney, U. & Vijayan, M. (1999). Structural analysis of wild type *E.coli* uracil DNA glycosylase (EcUDG) and new crystal forms of its complex with a proteinaceous inhibitor, Ugi. *J. Biosci.* **24**, Supplement 1, 36.

Biswal, B.K., Sukumar, N. & Vijayan, M. (1999). Plasticity and hydration of lysozyme. X-ray analysis of crystal form grown at near neutral pH and its low humidity variant and a comparative study of known crystal structures. *J. Biosci.* **24**, Supplement 1, 36.

Ravishankar, R., Suguna, K., Surolia, A. & Vijayan, M. (1999). The crystal structures of the complexes of peanut lectin with methyl-β-Galactose and N-acetyllactosamine and a comparative study of carbohydrate binding in Gal/GalNac specific legume lectins. *Acta Cryst.* **D55**, 1375-1382.

Suguna, K., Surolia, A. & Vijayan, M. (1999). Structural diversity and carbohydrate specificity of plant lectins. In *Perspectives in Structural Biology*. Edited by M.Vijayan, N. Yathindra & A.S. Kolaskar, Indian Academy of Sciences, Bangalore and University Press, Hyderabad pp. 367-379.

Vijayan, M. & Chandra, N.R. (1999). Lectins. *Curr. Opin. Stru. Biol.* **9**, 707-714.

Manoj, N., Srinivas, V.R., Surolia, A., Vijayan, M. & Suguna, K. (1999). Crystal structure of winged bean acidic lectin. *J. Biosci.* **24**, Supplement 1, 35.

Manoj, N., Srinivas, V.R. & Suguna, K. (1999). Structure of basic winged bean lectin and a comparison with its saccharide-bound form. *Acta Cryst.* **D55**, 794-800.

Manoj, N., Srinivas, V.R., Satish, B., Singha, N.C. & Suguna, K. (1999). Crystallization and preliminary crystallographic analysis of winged bean acidic lectin. *Acta Cryst.* **D55**, 564-565.

Sekar, K. & Sundaralingam, M. (1999). 1.5 Å resolution refinement of orthorhombic bovine pancreatic phospholipase A<sub>2</sub>. *J. Biosci.* **24**, Supplement 1, 40.

Gopal, B., Ray, S.S., Gokhale, R.S., Balaram, H., Murthy, M.R.N. & Balaram, P. (1999). Cavity creating mutation at dimer interface of *Plasmodium falciparum* and restoration of stability by disulfide cross linking of subunits. *Biochemistry* **38**, 478-486.

Prasanna, V., Gopal, B., Murthy, M.R.N., Santi, D.V. & Balaram, P. (1999). Effect of amino acid substitutions at the subunit interface on the stability and aggregation properties of a dimeric protein: role of Arg178 and Arg218 at the dimer interface of thymidylate synthase. *Proteins* **34**, 356-368.

Sri Krishna, S., Hiremath, C.N., Munshi, S.K., Sastri, M., Savithri, H.S. & Murthy, M.R.N. (1999). Three Dimensional Structure of Physalis mottle virus: Implications for the viral assembly. *J. Mol. Biol.* **289**, 919-934.

Velankar, S.S., Gokhale, R.S., Ray, S.S., Gopal, B., Santi, D.V., Balaram, P. & Murthy, M.R.N. (1999). Disulfide engineering at the dimer interface of *L. Casei* thymidylate synthase: Crystal structure of the T155C/E188C/C244T mutant. *Protein Sci.* **8**, 930-933.

Anu K. Moorthy, Gopal, B., Gopi Mohan, C. & Murthy, M.R.N. (1999). Temperature-dependent cell transformation in a calcium-binding protein from *Entamoeba histolytica*. *Curr. Sci.* **77**, 855-856.

Sri Krishna, S., Sastri, M., Savithri, H.S. & Murthy, M.R.N. (1999). Investigations on the structure and stability of physalis mottle tymovirus. *J. Biosci.* **24**, Supplement 1, 37.

Murthy, M.R.N., Sri Krishna, S., Sastri, M. & Savithri, H.S. (1999). Structure, stability and assembly of physalis mottle virus. In Perspectives in Structural Biology. Edited by M.Vijayan, N. Yathindra & A.S. Kolaskar, Indian Academy of Sciences, Bangalore and University Press, Hyderabad pp. 467-484.

Savitha, G. & Viswamitra, M.A. (1999). An A-DNA structure with two independent duplexes in the asymmetric unit. *Acta Cryst.* **D55**, 1136-1143.

Natesh, R., Bhanumoorthy, P., Vithayathil, P. J., Sekar, K., Ramakumar, S. & Viswamitra, M.A. (1999). Crystal structure at 1.8 Å resolution and proposed amino acid sequence of a thermostable xylanase from *Thermoascus aurantiacus*. *J. Mol. Biol.* **288**, 999-1012.

Viswamitra, M.A. (1999). Molecular recognition in relation to certain oligonucleotide and protein structures. *J. Biosci.* **24**, Supplement 1, 3.

Ratnaparkhi, G.S. & Varadarajan, R. (1999). X-ray crystallographic analysis of the denaturation of Ribonuclease S. *Proteins* **36**, 282-294 .

## **Bhabha Atomic Research Centre, Mumbai**

Ramanadham, M., Sieker, L.C. & Jensen, L.H. (1990). Refinement of triclinic lysozyme: II. The method of stereochemically restrained least squares. *Acta Cryst.* **B46**, 63-69.

Chakravarthy, S. & Kannan, K.K. (1990). Automatic evaluation of general spot profiles in oscillation photography. *J. Appl. Cryst.* **23**, 549-553.

Kannan, K.K. (1991). Structural Perspectives in the Function of Carbonic anhydrase. In *Molecular Conformation and Biological Interactions*. Edited by P. Balaram & S. Ramaseshan, Indian Academy of Sciences, Bangalore pp. 131-147.

Hosur, M.V., Sainis, J.K. & Kannan, K.K. (1993). Crystallization and X-ray analysis of a Multi-Enzyme Complex containing RUBISCO and RuBP. *J. Mol. Biol.* **234**, 1274-1278.

Hosur, M.V. & Kannan, K.K. (1993). Phase Perturbation as a means of Reducing Model Bias in Macromolecular Crystallography. *Acta Cryst.* **A49**, C-49.

Ramanadham, M. & Kannan, K.K. (1993). High Resolution X-ray Structure refinement of Human Carbonic Anhydrase I. *Acta Cryst.* **A49**, C-92.

Yadava, V.S. & Kannan, K.K. (1993). Crystal Structure of Human Carbonic Anhydrase I at pH6.0 and implication to function. *Acta Cryst.* **A49**, C-92.

Kumar, B. & Kannan, K.K. (1993). Structure of Human Carbonic Anhydrase I complexed with Gold Cyanide Inhibitor. *Acta Cryst.* **A49**, C-92.

Hosur, M.V. & Kannan, K.K. (1993). Crystallography of a Multi-Enzyme Complex Containing Rubisco. *Acta Cryst.* **A49**, C-115.

Kumar, V. & Kannan, K.K. (1993). Identification of Key Residues for Carbonic Anhydrase Isoenzymes: Use of Sequence and Crystallographic Data. *Acta Cryst.* **A49**, C-153.

Chakravarthy, S. & Kannan, K.K. (1993). Correlation of Inhibitory Power with Structure of Sulfonamide Drugs Complexed to Human Carbonic Anhydrase I Enzyme. *Acta Cryst.* **A49**, C-161.

Kumar, V. & Kannan, K.K. (1994). Enzyme-Substrate Interaction: Structure of Human Carbonic Anhydrase I complexed with Bicarbonate. *J. Mol. Biol.* **241**, 226-232.

Chakravarthy, S. & Kannan, K.K. (1994). Drug-Protein Interactions: Refined Structures of three Sulfonamide Drug Complexes of Human Carbonic Anhydrase I Enzyme. *J. Mol. Biol.* **243**, 298-309.

Kumar, V., Kannan, K.K. & Sathyamurthy, P. (1994). Differences in Anionic Inhibition of Human Carbonic Anhydrase I Revealed from the Structures of Iodide and Gold Cyanide Inhibitor Complexes. *Acta Cryst.* **D50**, 731-738.

Sathyamurthy, P., Hosur, M.V., Misquith, S., Surolia, A. & Kannan, K.K. (1994). Crystallization of a scRIP- Gelonin Isolated from plant seeds *Gelonium multiflorum*. *Proteins* **19**, 340-342.

Kannan, K.K. (1994). Insight into the Function of an Enzyme from the Molecular Architecture. INSA Diamond Jubilee Medal Lectures. Vol 2. 1302.

Kumar, V. & Kannan, K.K. (1994). Carbonic Anhydrase: An Efficient Enzyme and an Elusive Mechanism. *Ind. J. Biochem. Biophys.* **31**, 377-386.

Hosur, M.V., Nair, B., Sathyamurthy, P., Misquith, S., Surolia, A. & Kannan, K.K. (1995). X-ray Structure of Gelonin at 1.8 Å Resolution. *J. Mol. Biol.* **250**, 368-380.

Chidambaram, R., Hosur, M.V. & Hosur, R.V. (1996). 100 years of X-rays and 50 years of NMR. *Curr. Sci.* **72**, 878-888.

Mohanty, A.K., Satyamurthy, M.B., Joshi, V.R., Mahajan, S.K., Hosur, M.V. & Kannan, K.K. (1997). Cloning and crystallographic analysis of human carbonic anhydrase I. *Curr. Sci.* **73**, 267-272.

Hosur, M.V., Pillai, B., Kumar, M. & Kannan, K.K. (1999). X-ray Studies of Ribosome Inactivating Proteins. In Perspectives in Structural Biology, Edited by M. Vijayan, N. Yathindra & A. S. Kolaskar, Indian Academy of Sciences, Bangalore and University Press, Hyderabad pp. 117-127.

Kumar, M., Dattagupta, S., Kannan, K.K. & Hosur, M.V. (1999). Purification, Crystallization & Preliminary X-ray Diffraction Study of Ribosome Inactivating Protein: saporin. *Biochim. Biophys. Acta* **1429**, 506-511.

Pillai, B., Kannan, K.K. & Hosur, M.V. (1999). 1.9Å X-ray study reveals closed flaps in unliganded HIV-1 PR tethered dimer. *J. Biosci.* **24**, Supplement 1, 38.

Kumar, M., Patwardhan, S., Kannan, K.K. & Hosur, M.V. (1999). X-ray study of the ribosome inactivating protein saporin S-9. *J. Biosci.* **24**, Supplement 1, 38.

### **Saha Institute of Nuclear Physics, Kolkata**

Dattagupta, J.K., Chakrabarti, C., Podder, A., Dutta, S.K. & Singh, M. (1990). Crystallization and Preliminary X-ray Studies of Psophocarpin B<sub>1</sub>, a Chymotrypsin Inhibitor from Winged Bean Seeds. *J. Mol. Biol.* **216**, 229-231.

Dattagupta, J.K., Podder, A., Chakrabarti, C., Sen, U., Dutta, S.K. & Singh, M. (1996). Structure of a Kunitz-type chymotrypsin inhibitor from winged bean seeds at 2.95 Å resolution. *Acta. Cryst.* **D52**, 521-528.

Dattagupta, J.K., Podder, A., Chakrabarti, C., Sen, U., Dutta, S. & Singh, M. (1997). Crystal Structure of Psophocarpin B<sub>1</sub>: A chymotrypsin inhibitor from winged bean seeds. In Aspects of Crystallography in Molecular Biology. Edited by S. Parthasarathy & J.P. Glusker, New Age International Publishers, New Delhi pp. 287-291.

Dattagupta, J.K., Podder, A., Chakrabarti, C., Sen, U., Mukhopadhyay, D., Dutta, S.K. & Singh, M. (1999). Refined Crystal Structure (2.3 Å) of a Double-Headed Winged Bean  $\alpha$ -Chymotrypsin Inhibitor and Location of its Second Reactive Site. *Proteins* **35**, 321-331.

Chakrabarti, C., Biswas, S., Kundu, S., Sundd, M., Jagannadham, M.V. & Dattagupta, J.K. (1999). Crystallization and preliminary X-ray analysis of ervatamin B and C, two thiol proteases from *Ervatamia coronaria*. *Acta Cryst.* **D55**, 1074-1075.

Dasgupta, J., Ravichandran, S., Mukhopadhyay, D., Sen, U., Podder, A., Chakrabarti, C. & Dattagupta, J.K. (1999). A Serine Protease Inhibitor Protein : From X-ray Structure to Protein Engineering. In *Perspectives in Structural Biology*. Edited by M. Vijayan, N. Yathindra & A. S. Kolaskar, Indian Academy of Sciences, Bangalore and University Press, Hyderabad pp. 75-82.

Ravichandran, S., Sen, U., Chakrabarti, C. & Dattagupta, J.K. (1999). Cryocrystallography of a Kunitz-type serine protease inhibitor : The 90 K structure of winged bean chymotrypsin inhibitor (WCI) at 2.13 Å resolution. *Acta. Cryst.* **D55**, 1814-1821.

### **All India Institute of Medical Sciences, New Delhi**

Srinivasan, A., Raman, A. & Singh, T.P. (1991). Preliminary X-ray Crystallographic Investigations of a Bifunctional Inhibitor from Indian Finger Millet (Ragi). *J. Mol. Biol.* **222**, 1-3.

Raman, A., Bhatia, K.L., Singh, T.P., Srinivasan, A. & Betzel, C. (1992). Crystallization and X-ray Diffraction Studies of Lactotransferrin from Buffalo Colostrum. *Arch. Biochem. Biophys.* **294**, 319-326.

Betzel, C., Visanji, M., Eschenburg, S., Peter, K., Fittkau, S., Singh, T.P. & Genov, N. (1993). Crystallization and Preliminary X-ray Analysis of Subtilisin DY, a Natural Mutant of Subtilisin Carlsberg. *Arch. Biochem. Biophys.* **302**, 499-502.



Betzel, C., Singh, T.P., Visanji, M., Peters, K., Fittkau, S., Saenger, W. & Wilson, K.S. (1993). Structure of the Complex of Proteinase K with a Substrate - Analogue Hexapeptide Inhibitor at 2.20 Å Resolution. *J. Biol. Chem.* **268**, 15854-15861.

Srinivasan, A. & Singh, T.P. (1993). Stability and Kinetics of a Bifunctional Amylase/Trypsin Inhibitor. *Biochim. Biophys. Acta* **1203**, 77-84.

Betzel, C., Visanji, M., Genov, N., Manchova, I., Aleksiev, B. & Singh, T.P. (1993). Crystallization and Preliminary X-ray Analysis of the Complex Between a Toxic Phospholipase A2 and its Natural Polypeptide Inhibitor from the Venom of the Bulgarian Viper (*Vipera ammodytes ammodytes*, Serpents). *J. Mol. Biol.* **231**, 498-501.

Kumar, R., Bhatia, K.L. & Singh, T.P. (1995). Purification, Crystallization & Preliminary X-ray Crystallographic Analysis of Lactoperoxidase from Buffalo Milk. *Acta Cryst.* **D51**, 1094-1096.

Saenger, W., Muller, A., Wolf, W., Bajorath, J., Raghunathan, S., Singh, T.P. & Hinrichs, W. (1995). X-ray Structure of a Complex of Proteinase K with its Inhibitor Methoxysuccinyl-Ala-Ala-Pro-Ala-Chloromethyl-Ketone at 2.20Å Resolution. *Adv. Exp. Med. Biol.* **379**, 1-11.

Kaur, P., Sharma, A.K., Karthikeyan, S., Mitra, S.N. & Singh, T.P. (1996). Structure of Mare lactoferrin at 4.0Å Resolution. *Prog. Biophys. Mol. Biol.* **65**, Supplement 1, 29-30.

Saxena, A.K., Singh, T.P., Peters, K., Fittkau, S., Visanji, M., Wilson, K.S. & Betzel, C. (1996). Structure of a Ternary Complex of Proteinase K, Mercury and a Substrate-Analogue Hexapeptide at 2.2 Å Resolution. *Proteins* **25**, 195-201.

Saxena, A.K., Singh, T.P., Peters, K., Fittkau, S. & Betzel, C. (1996). Strategy to Design Peptide Inhibitors: Structure of a Complex of Proteinase K with a Designed Octapeptide Inhibitor N-Ac-Pro-Ala-Pro-Phe-DAla-Ala-Ala-Ala-NH<sub>2</sub>. *Protein Sci.* **5**, 2453-2458.

Sharma, A.K., Karthikeyan, S., Kaur, P., Singh, T.P. & Yadav, M.P. (1996). Purification, Crystallization and Preliminary Crystallographic Analysis of Mare Lactoferrin. *Acta Cryst.* **D52**, 1196-1201.

Betzel, C., Perbandt, M., Singh, T.P. & Genov, N. (1996). X-ray Structure of Vipoxin, A Complex Between a Toxic Phospholipase A2 and its Natural Inhibitor. *Acta Cryst.* **A52**, C-166.

Sharma, S., Singh, T.P. & Bhatia, K.L. (1997). Crystallization and Preliminary X-ray Diffraction Studies of the Proteolytically Engineered C-terminal half of Buffalo Lactoferrin in its Iron saturated form. *Acta Cryst.* **D53**, 116-119.

Sharma, A.K., Karthikeyan, S., Sharma, S., Yadav, S., Srinivasan, A. & Singh, T.P. (1997). Structures of Buffalo and Mare Lactoferrins: Similarities, Differences and Flexibility. *Adv. Exp. Med. Biol.* **380**, 15-21.

Perbandt, M., Wilson, J.C., Eschenburg, S., Mancheva, T., Aleksiev, B., Genov, N., Willingmann, P., Weber, W., Singh, T.P. & Betzel Ch. (1997). Crystal Structure of Vipoxin : An Example of Regulation of a Toxic Function Generated by Molecular Evolution. *FEBS Letts.* **412**, 573-577.

Sharma, S. & Singh, T.P. (1997). Structural Changes in Serine Proteinases in Ethanol. *Ind. J. Phys.* **72B**, 185-190.

Sharma A.K., Karthikeyan, S. Sharma, S., Yadav, S., Srinivasan, A. & Singh, T.P. (1997). Structures of buffalo and mare lactoferrins : similarities, differences and flexibility. *Adv. Exp. Med. Biol.* **443**, 15-41.

Sharma, S., Singh, T.P. & Bhatia, K.L. (1998). Preparation and Characterization of proteolytically engineered N and C monoferric functional halves of buffalo lactoferrin. *J. Dairy Res.* **66**, 81-90.

Sharma, S. & Singh, T.P. (1998). Enzyme structure in organic solvent. *Ind. J. Phys.* **72B**, 165-169.

Singh, T.P., Sharma, S., Karthikeyan, S., Betzel, C. & Bhatia, K.L. (1998). Crystal Structure of a complex formed between proteolytically generated lactoferrin fragment and proteinase K. *Proteins* **33**, 30-38.

Karthikeyan, S., Sharma, S., Sharma, A.K., Paramasivam, M., Yadav, S., Srinivasan, A. & Singh T.P. (1999). Structural variability and functional convergence in lactoferrins. *Curr. Sci.* **77**, 241-255.

Rajashankar, K.R., Genov, N., Aleksiev, B., Singh, T.P. & Betzel, Ch. (1999). X-ray structure of the heterodimeric postsynaptic neurotoxin vipoxin from the venom of the snake *Vipera ammodytes meridionalis*. In *Perspectives in Structural Biology*. Edited by M. Vijayan, N. Yathindra & A. S. Kolaskar, Indian Academy of Sciences, Bangalore and University Press, Hyderabad pp. 108-116.

Sharma, A.K. & Singh, T.P. (1999). Crystal structure of mare apolactoferrin demonstrates the closed conformations of N- and C- lobes. In *Perspectives in Structural Biology*. Edited by M. Vijayan, N. Yathindra & A. S. Kolaskar, Indian Academy of Sciences, Bangalore and University Press, Hyderabad pp. 99-107.

Gourinath, S., Srinivasan A. & Singh T.P. (1999). Crystal Structure of the bifunctional inhibitor of trypsin and  $\alpha$ -amylase from ragi seeds at 2.9Å Resolution. *Acta Cryst.* **D55**, 25-34.

Sharma, A.K., Kumar, S. & Singh, T.P. (1999). Three-dimensional Structure of a New Crystal form of Mare Lactoferrin at 3.8Å Resolution. *Ind. J. Biochem. Biophys.* **38**, 135-141.

Krauspenhaar, R., Eschenburg, S., Perbandt, M., Kornilov, V., Konareva, N., Mikailova, I., Stoeva, S., Wacker, R., Meier, T., Singh, T.P., Mikhailov, A., Voelter, W. & Betzel, C. (1999). Crystal Structure of Mistletoe Lectin I from *Viscum album*. *Biochem. Biophys. Res. Commun.* **257**, 418-424.

Sharma, S., Karthikeyan, S., Betzel, C. & Singh, T.P. (1999) Isolation, purification, crystallization and preliminary X-ray analysis of  $\beta$ 1-bungarotoxin from *Bungarus caeruleus* (Indian common krait). *Acta Cryst.* **D55**, 1093-1094.

Sharma, A.K. & Singh, T.P. (1999). Structure of oxalate-substituted diferric mare lactoferrin at 2.7 Å resolution. *Acta Cryst.* **D55**, 1792-1799.

Sharma, A.K. & Singh, T.P. (1999). Lactoferrin-metal interactions: first crystal structure of a complex of lactoferrin with a lanthanide ion (Sm<sup>3+</sup>) at 3.4 Å resolution. *Acta Cryst.* **D55**, 1799-1804.

Sharma, A.K., Paramasivam, M., Srinivasan, R., Rajashankar, K.R. & Singh, T.P. (1999). Three-dimensional structure of mare apolactoferrin reveals closed conformations of both N-and C-lobes. *Acta Cryst.* **D55**, 1152-1159.

Sharma, A.K., Paramasivam, M., Srinivasan, A., Yadav, M.P. & Singh, T.P. (1999). Three-dimensional structure of mare diferric lactoferrin at 2.6 Å resolution. *J. Mol. Biol.* **289**, 303-318.

Nagpal, A., Chandra, V., Kaur, P. & Singh, T.P. (1999). Purification, crystallization and preliminary crystallographic analysis of a natural complex of phospholipase A<sub>2</sub> from *Echis carinatus* (saw-scaled viper). *Acta Cryst.* **D55**, 1240-1242.

Karthikeyan, S., Paramasivam, M., Yadav, S., Srinivasan, A. & Singh, T.P. (1999). Structure of buffalo lactoferrin at 2.5 Å resolution using crystals grown at 303 K shows different orientations of the N and C lobes. *Acta Cryst.* **D55**, 1805-1812.

Chandra, V., Nagpal, A., Srinivasan, A. & Singh, T.P. (1999). Purification, crystallization and preliminary X-ray crystallographic analysis of a phospholipase A<sub>2</sub> from *Daboia russelli pulchella*. *Acta Cryst.* **D55**, 925-927.

Betzel, Ch., Genov, N. & Singh, T.P. (1999). Modulation of phospholipase A<sub>2</sub> activity generated by molecular evolution : a model for structure-based drug design. *Cell. Mol. Life. Sci.* **56**, 384-397.

Chandra, V., Kaur, P., Betzel, C. & Singh, T.P. (1999). Crystal structure-function relationship of neurotoxic phospholipase A<sub>2</sub> from *Daboia russelli pulchella* at 2.45Å. *J. Biosci.* **24**, Supplement 1, 39.

Karthikeyan, S., Sharma, S., Sharma, A.K., Paramasivam, M., Kumar, P., Khan, J.A., Yadav, S., Srinivasan, A. & Singh, T.P. (1999). Structural variability and functional convergence in lactoferrins. *J. Biosci.* **24**, Supplement 1, 39.

Gourinath S., Alam N., Srinivasan, A. & Singh, T.P. (1999). Structure of the bifunctional inhibitor of trypsin and  $\alpha$ -amylase from ragi seeds at 2.2Å resolution. *J. Biosci.* **24**, Supplement 1, 39.

### **National Institute of Immunology, New Delhi**

Raghunathan, V., Khurana, S., Gupta, V., Khurana, R., Udgaonkar, J.B. & Salunke, D.M. (1994). Crystallization and molecular packing analysis of barstar crystals. *J. Mol. Biol.* **243**, 533-536.

Khurana, S., Raghunathan, V. & Salunke, D.M. (1997). The variable domain glycosylation in a monoclonal antibody specific to GnRH modulates antigen binding. *Biochem. Biophys. Res. Commun.* **234**, 465-469.

Gupta, V., Muyldermans, S., Wyns, L. & Salunke, D.M. (1999). The crystal structure of recombinant rat pancreatic RNase A. *Proteins* **35**, 1-12.

### **University of Madras, Chennai**

Sadasivan, C., Karthe, P. & Gautham, N. (1994). Space-group degeneracy in the packing of non-selfcomplementary Z-DNA hexamer. *Acta Cryst.* **D50**, 192-196.

Sadasivan, C. & Gautham, N. (1995). Plasticity of Z-DNA as observed in the crystal structure of non-selfcomplementary hexanucleotides. *Curr. Sci.* **68**, 531-537.

Sadasivan, C. & Gautham, N. (1995). Sequence-dependent microheterogeneity of Z-DNA: the crystal and molecular structures of d(CACGCG).d(CGCGTG) and d(CGCACG).d(CGTGCG). *J. Mol. Biol.* **248**, 918-930.

Sadasivan, C. & Gautham, N. (1997). Perturbed and unperturbed DNA: the effect of A.T base pairs on the structure of Z-DNA. In *Aspects of Crystallography in Molecular Biology*. Edited by S. Parthasarathy & J.P. Glusker, New Age International Publishers, New Delhi pp. 353-367.

Johnson, A., Krishnasawamy, S., Sundaram, P.V. & Pattabhi, V. (1997). The first structure at 1.8 Å resolution of an active autolysate of porcine  $\alpha$ -trypsin. *Acta Cryst.* **D53**, 311-315.

Karthe, P. & Gautham, N. (1998). Structure of d(CACGCG).d(CGCGTG) in crystals grown in the presence of ruthenium hexammine chloride. *Acta Cryst.* **D54**, 501-509.

Johnson, A., Gautham, N. & Pattabhi, V. (1999). Crystal structure at 1.63 Å resolution of the native form of porcine  $\beta$  trypsin: revealing an acetate ion binding site and functional water net work. *Biochim. Biophys. Acta* **1435**, 7-21.

Johnson, A. & Pattabhi, V. (1999). Network of functional water molecules and acetate ion binding in crystal structures of  $\alpha$  and  $\beta$  porcine trypsin. In *Perspectives in Structural Biology*. Edited by M. Vijayan, N.Yathindra & A.S. Kolaskar, Indian Academy of Sciences, Bangalore and Universities Press, Hyderabad pp. 65-74.

Johnson, A. & Pattabhi, V. (1999). Interesting hydration patterns and their role in trypsin activity. *J. Biosci.* **24**, Supplement 1, 37.

Satheesh Kumar, P. & Gautham, N. (1999). Unusual ring-shaped oligonucleotide crystals. *Curr. Sci.* **77**, 1076-1078.

Gautham, N., Karthe, P. & Krishnaswamy, S. (1999). The effect of non-altering sequence on the structure of left-handed Z-DNA. In *Perspectives in Structural Biology*. Edited by M. Vijayan, N.Yathindra & A.S. Kolaskar, Indian Academy of Sciences, Bangalore and Universities Press, Hyderabad pp. 593-601.

### **National Chemical Laboratory, Pune**

Rao, K.N., Gurjar, M.M., Gaikwad, S.M., Khan, M.I. & Suresh, C.G. (1999). Crystallization and preliminary X-ray studies of the basic lectin from the seeds of *Artocarpus hirsuta*. *Acta Cryst.* **D55**, 1204-1205.

Rao, K.N., Hegde, S.S., Lewis, R.J. & Suresh, C.G. (1999). Crystallization and preliminary X-ray diffraction studies of a Bowman-Birk inhibitor from *Vigna unguiculata* seeds. *Acta Cryst.* **D55**, 1920-1922.

Suresh, C.G., Pundle, A.V., Rao, K.N., SivaRaman, H., Brannigan, J.A., McVey, C.E., Verma, C.S., Dauter, Z., Dodson, E.J. & Dodson, G.G. (1999). Penicillin V Acylase crystal structure reveals new Ntn-hydrolase family members. *Nature Struct. Mol. Biol.* **6**, 414-416.

### **Madurai Kamaraj University, Madurai**

Arockiasamy, A. & Krishnaswamy, S. (1999). Crystallization of the immunologically important outer membrane protein OmpC; the first protein crystals from the human pathogen *S. typhi*. *FEBS Letts.* **453**, 380-382.

### **Bose Institute, Kolkata**

Ghosh, S., Bera, A.K., Bhattacharya, S., Chakraborty, S., Pal, A.K., Mukhopadhyay, B.P., Dey, I., Haldar, U. & Banerjee, A. (1999). The structural view of nature's another 'Swiss Army Knife', calotropin DII, a thiol protease at 2.1 Å resolution. *J. Biosci.* **24**, Supplement 1, 40.

**THE GROWTH PHASE**  
**2000 – 2015**

**Indian Institute of Science, Bangalore**

Biswal, B.K., Sukumar, N. & Vijayan, M. (2000). Hydration, mobility and accessibility of lysozyme: structures of a pH 6.5 orthorhombic form and its low-humidity variant and a comparative study involving 20 crystallographically independent molecules. *Acta Cryst.* **D56**, 1110-1119.

Manoj, N., Srinivas, V.R., Surolia, A., Vijayan, M. & Suguna, K. (2000). Carbohydrate specificity and salt bridge mediated conformational change in acidic winged bean agglutinin. *J. Mol. Biol.* **302**, 1129-1137.

Datta, S., Prabu, M.M., Vaze, M.B., Ganesh, N., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2000). Crystal structure of *Mycobacterium tuberculosis* RecA and its complex with ADP-AIF<sub>4</sub>: implications for decreased ATPase activity and molecular aggregation. *Nucl. Acids Res.* **28**, 4964-4973.

Vijayachandra, K., Guruprasad, M., Rashna Bhandari, Manjunath, U. H., Somesh, B. P., Srinivasan, N., Suguna, K. & Visweswariah, S. S. (2000). Biochemical characterization of the intracellular domain of the human guanylyl cyclase C receptor provides evidence for a catalytically active homotrimer. *Biochemistry* **39**, 16075-16083.

Yu, B-Z., Poi, M.-J., Ramagopal, U.A., Jain, R., Ramakumar, S., Berg, O.G., Tsai, M.-D, Sekar, K. & Jain, M.K. (2000). Structural Basis of the Anionic Interface Preference and K<sub>cat</sub> Activation of Pancreatic Phospholipase A<sub>2</sub>. *Biochemistry* **39**, 12312-12323.

Kumar, P.R., Eswaramoorthy, S., Vithayathil, P.J. & Viswamitra, M.A. (2000). The tertiary structure at 1.59 Å resolution and the proposed amino acid sequence of a family-11 xylanase from the thermophilic fungus *Paecilomyces varioti* bainier. *J. Mol. Biol.* **295**, 581-593.



Ratnaparkhi, G.S., Awasthi, S.K., Rani, P., Balaram, P. & Varadarajan, R. (2000). Structural and thermodynamic consequences of introducing  $\alpha$ -aminoisobutyric acid in the S peptide of ribonuclease S. *Protein Eng.* **13**, 697-702.

Ravishankar, R., Thomas, C.J., Suguna, K., Surolia, A. & Vijayan, M. (2001). Crystal structures of the peanut lectin-lactose complex at acidic pH. Retention of unusual quaternary structure, empty and carbohydrate bound combining sites, molecular mimicry and crystal packing directed by interactions at the combining site. *Proteins* **43**, 260-270.

Manoj, N., Jeyaprakash, A.A., Pratap, J.V., Komath, S.S., Kenoth, R., Swamy, M.J. & Vijayan, M. (2001). Crystallization and preliminary X-ray studies of snake gourd lectin: Homology with Type II ribosome Inactivating Proteins. *Acta Cryst.* **D57**, 912-914.

Adhikari, P., Bacchawat-Sikder, K., Thomas, C.J., Ravishankar, R., Jeyaprakash, A.A., Sharma, V., Vijayan, M. & Surolia, A. (2001). Mutational analysis at N41 in peanut agglutinin (PNA): A residue critical for binding of the tumor-associated Thomsen-Friedenreich antigen. *J. Biol. Chem.* **276**, 40734-40739.

Pratap, J.V., Bradbrook, G.M., Reddy, G.B., Surolia, A., Raffery, J., Helliwell, J.R. & Vijayan, M. (2001). The combination of molecular dynamics with crystallography for elucidating protein-ligand interactions. A case study involving peanut lectin complexes with T-antigen and lactose. *Acta Cryst.* **D57**, 1584-1594.

Datta, S., Biswal, B.K. & Vijayan, M. (2001). The effect of stabilising additives on the structure and hydration of proteins. A study involving tetragonal lysozyme. *Acta Cryst.* **D57**, 1614-1620.

Biswal, B.K. & Vijayan, M. (2001). Structure of human methaemoglobin: The variation of a theme. *Curr. Sci.* **81**, 1100-1105.

Chandra, N.R., Prabu, M.M., Suguna, K. & Vijayan, M. (2001). Structural similarity and functional diversity in proteins containing the legume lectin fold. *Protein Eng.* **14**, 857-866.

- Bhandari, R., Srinivasan, N., Ghanekar, Y., Suguna, K. & Visweswariah, S. (2001). Functional inactivation of the human guanylyl cyclase C receptor. Modeling and mutation of the protein kinase-like domain. *Biochemistry* **40**, 9196-9206.
- Suguna, K., Surolia, A. & Surolia, N. (2001). Structural basis for triclosan and NAD binding to enoyl-ACP reductase of *Plasmodium falciparum*. *Biochem. Biophys. Res. Commun.* **283**, 224-228.
- Manoj, N. & Suguna, K. (2001). Signature of quaternary structure in the sequence of legume lectins. *Protein Eng.* **14**, 735-745.
- Padyana, A.K., Bhat, V.B., Madyastha, K.M., Rajashankar, K.R. & Ramakumar, S. (2001). Crystal structure of a light-harvesting protein C-phycoyanin from *Spirulina platensis*. *Biochem. Biophys. Res. Commun.* **282**, 893-898.
- Savitha, G., Leonidas, D., Acharya, K.R. & Viswamitra, M.A. (2001). Crystallization and preliminary investigations on a telomeric repeat sequence C4A2C4A2. *Acta Cryst.* **D57**, 873-875.
- Sri Krishna, S., Sastri, M., Savithri, H.S. & Murthy, M.R.N. (2001). Structural studies on the empty capsids of Physalis mottle virus. *J. Mol. Biol.* **307**, 1035-1047.
- Saikrishnan, K., Jeyakanthan, J., Venkatesh, J., Acharya, N., Purnapatre, K., Sekar, K., Varshney, U. & Vijayan, M. (2002). Crystallization and preliminary X-ray studies on the single-stranded DNA-binding protein from *Mycobacterium tuberculosis*. *Acta Cryst.* **D58**, 327-329.
- Ramachandraiah, G., Chandra, N.R., Surolia, A. & Vijayan, M. (2002). Refinement using re-processed data to improve the quality of the structure. A case study involving garlic lectin. *Acta Cryst.* **D58**, 414-420.
- Pratap, J.V., Jeyaprakash, A.A., Geetha Rani, P., Sekar, K., Surolia, A. & Vijayan, M. (2002). Crystal structure of artocarpin, a *Moraceae* lectin with mannose specificity and its complex with methyl- $\alpha$ -D-mannose. Implications to the generation of carbohydrate specificity. *J. Mol. Biol.* **317**, 237-247.

Saraswathi, N.T., Sankaranarayanan, R. & Vijayan, M. (2002). Effect of stabilizing additives on the structure and hydration of proteins. A study involving monoclinic lysozyme. *Acta Cryst.* **D58**, 1162-1167.

Biswal, B.K. & Vijayan, M. (2002). Crystal structures of human oxy and deoxyhemoglobin at different levels of humidity. Variability in the T state. *Acta Cryst.* **D58**, 1155-1161.

Saikrishnan, K., Bidya Sagar, M., Ravishankar, R., Roy, S., Purnapatre, K., Handa, P., Varshney, U. & Vijayan, M. (2002). Domain closure and action of uracil DNA glycosylase (UDG). Structures of new crystal forms containing the *Escherichia coli* enzyme and a comparative study of the known structures involving UDG. *Acta Cryst.* **D58**, 1269-1276.

Jeyaprakash, A.A., Geetha Rani, P., Banuprakash Reddy, G., Banumathi, S., Betzel, C., Sekar, K., Surolia, A. & Vijayan, M. (2002). Crystal structure of the jacalin-T-antigen complex and a comparative study of lectin-T-antigen complexes. *J. Mol. Biol.* **321**, 637-645.

Vijayan, M., Jeyakanthan, J., Venkatesh, J., Acharya, N., Sekar, K., Varshney, U. & Saikrishnan, K. (2002). The crystal structure of Single-stranded DNA-binding protein from *Mycobacterium tuberculosis*. *Acta Cryst.* **A58**, C-275.

Prasad, B.V.L.S. & Suguna, K. (2002). Role of water molecules in the structure and function of aspartic proteinases. *Acta Cryst.* **D58**, 250-258.

Rajakannan, V., Yogavel, M., Poi, M.-J., Jeyaprakash, A.A., Jeyakanthan, J., Velmurugan, D., Tsai, M-D. & Sekar, K. (2002). Observation of Additional Calcium Ion in the Crystal Structure of the Triple Mutant of Bovine Pancreatic Phospholipase A<sub>2</sub>. *J. Mol. Biol.* **324**, 755-762.

Rudresh, Jain, R., Dani, V., Mitra, S., Srivastava, S., Sarma, S.P., Varadarajan, R. & Ramakumar, S. (2002). Structural consequences of replacement of an  $\alpha$ -helical Pro residue in *Escherichia coli* thioredoxin. *Protein Eng.* **15**, 627-633.

Ramakumar, S., Natesh, R., Manikandan, K., Bhanumoorthy, P. & Viswamitra, M.A. (2002). Xylanase at ultra high 0.89 Å (100 K) and atomic 1.11 Å (293 K) resolutions: Evidence for salt bridge plasticity. *Acta Cryst.* **A58**, C-20.

Lokesh, G.L., Gowri, T.D.S., Satheshkumar, P.S., Murthy, M.R.N. & Savithri, H.S. (2002). A molecular switch in the capsid protein controls the particle polymorphism in an icosahedral virus. *Virology* **292**, 211-223.

Sangita, V., Parthasarathy, S., Toma, S., Lokesh, G.L., Gowri, T.D.S., Satheshkumar, P.S., Savithri, H.S. & Murthy, M.R.N. (2002). Determination of the structure of the recombinant T=1 capsid of sesbania mosaic virus. *Curr. Sci.* **82**, 1123-1131.

Parthasarathy, S., Balaram, H., Balaram, P. & Murthy, M.R.N. (2002). Structure of *Plasmodium falciparum* triosephosphate isomerase-phosphoglycolate complex in two crystal forms: characterization of catalytic loop in open and closed conformation in the ligand bound state. *Biochemistry* **41**, 13178-13188.

Parthasarathy, S., Balaram, H., Balaram, P. & Murthy, M.R.N. (2002). Structures of *Plasmodium falciparum* triosephosphate isomerase complexed to substrate analogues: observation of the catalytic loop in the open conformation in the ligand-bound state. *Acta Cryst.* **D58**, 1992-2000.

Simanshu, D.K., Satheshkumar, P.S., Parthasarathy, S., Savithri, H.S. & Murthy, M.R.N. (2002). Cloning, expression, purification and preliminary X-ray crystallographic studies of 2-methylisocitrate lyase from *Salmonella typhimurium*. *Acta Cryst.* **D58**, 2159-2161.

Murthy, M.R.N., Parthasarathy, S., Balaram, H. & Balaram, P. (2002). *Plasmodium falciparum* triosephosphate isomerase complexes: catalytic loop in the open and closed conformations. *Acta Cryst.* **A58**, C-109.

Datta, S., Ganesh, N., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2003). Structural studies on MtRecA-Nucleotide complexes: Insights into DNA and Nucleotide binding and the structural signature of NTP recognition. *Proteins* **50**, 474-485.

Datta, S., Krishna, R., Ganesh, N., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2003). Crystal Structures of *Mycobacterium smegmatis* RecA and its Nucleotide Complexes. *J. Bacteriology* **185**, 4280–4284.

Saikrishnan, K., Jeyakanthan, J., Venkatesh, J., Acharya, N., Sekar, K., Varshney, U. & Vijayan, M. (2003). Structure of *Mycobacterium tuberculosis* Single-stranded DNA-binding Protein. Variability in Quaternary Structure and its Implications. *J. Mol. Biol.* **331**, 385–393.

Jeyaprakash, A. A., Katiyar, S., Swaminathan, C.P., Sekar, K., Surolia, A. & Vijayan, M. (2003). Structural Basis of the Carbohydrate Specificities of Jacalin: An X-ray and Modeling Study. *J. Mol. Biol.* **332**, 217-228.

Ramachandraiah, G., Chandra, N.R., Surolia, A. & Vijayan, M. (2003). Computational analysis of multivalency of Lectins: Structures of garlic lectin-oligosachharide complexes and their aggregates. *Glycobiology* **13**, 765-775.

Roy, S., Gupta, S., Das, S., Sekar, K., Chatterjee, D. & Vijayan, M. (2003). Crystallization and preliminary X-ray diffraction analysis of *Mycobacterium smegmatis* Dps. *Acta Cryst.* **D59**, 2254-2256.

Vijayan, M. (2003). Structural Genomics of Microbial Pathogens – An Indian Programme. *Curr. Sci.* **85**, 878-885.

Acharya, N., Talawar, R.K., Saikrishnan, K., Vijayan, M. & Varshney, U. (2003). Substitutions at tyrosine 66 of *Escherichia coli* uracil DNA glycosylase lead to characterization of an efficient enzyme that is recalcitrant to product inhibition. *Nucl. Acids Res.* **31**, 7216-7226.

Prasad, B.V.L.S. & Suguna, K. (2003). Effect of pH on the structure of rhizopuspepsin. *Acta Cryst.* **D59**, 1755-1761.

Muralidharan, J., Suguna, K., Surolia, A. & Surolia, N. (2003). Exploring the interaction energies for the binding of hydroxydiphenyl ethers to enoyl-acyl carrier protein reductases. *J. Biomol. Struct. Dyn.* **20**, 589-594.

Sekar, K., Vaijayanthi Mala, S., Yogavel, M., Velmurugan, D., Poi, M.-J., Vishwanath, B.S., Gowda, T.V., Jeyaprakash, A.A. & Tsai, M.-D. (2003). Crystal Structures of the Free and Anisic Acid Bound Triple Mutant of Phospholipase. *J. Mol. Biol.* **333**, 367-376.

Natesh, R., Manikandan, K., Bhanumoorthy, P., Viswamitra, M.A. & Ramakumar, S. (2003). Thermostable xylanase from *Thermoascus aurantiacus* at ultrahigh resolution (0.89 Å) at 100 K and atomic resolution (1.11 Å) at 293 K refined anisotropically to small-molecule accuracy. *Acta Cryst.* **D59**, 105-117.

Rajaram, V., Rajaganapathi, J., Khan Farida, Savithri, H.S. & Murthy, M.R.N. (2003). Crystallization and Preliminary X-ray diffraction studies on recombinant diaminopropionate ammonia lyase from *Escherichia coli*. *Acta Cryst.* **D59**, 1668-1669.

Simanshu, D.K., Satheshkumar, P.S., Savithri, H.S. & Murthy, M.R.N. (2003). Crystal structure of *Salmonella typhimurium* 2-methylisocitrate lyase(PrpB) and its complex with pyruvate and Mg(2+). *Biochem. Biophys. Res. Commun.* **311**, 193-201.

Murthy, M.R.N. (2003). Interatomic contacts in virus crystals. *Curr. Sci.* **85**, 1071-1074.

Parthasarathy, S., Eaazhisai, K., Balaram, H., Balaram, P. & Murthy, M.R.N. (2003). Structure of *Plasmodium falciparum* TIM-2-phosphoglycerate complex at 1.1Å resolution. *J. Biol. Chem.* **278**, 52461-52470.

Muniyappa, K., Ganesh, N., Guhan, N., Singh Pawan, Manjunath, G.P., Datta, S., Chandra, N. R. & Vijayan, M. (2004). Homologous recombination in mycobacteria. *Curr. Sci.* **86**, 141-148.

Natchiar, S.K., Jeyaprakash, A. A., Ramya, T.N.C., Thomas, C.J., Suguna, K., Surolia, A. & Vijayan, M. (2004) . Structural plasticity of peanut lectin: an X-ray analysis involving variation in pH, ligand binding and crystal structure. *Acta Cryst.* **D60**, 211-219.

Saikrishnan, K., Kalapala, S.K., Bidya Sagar, M., Rao, A.R., Varshney., U. & Vijayan, M. (2004). Purification, crystallization and preliminary X-ray studies of *Mycobacterium tuberculosis* RRF. *Acta Cryst.* **D60**, 368-370.

Jeyaprakash, A.A., Srivastav, A., Surolia, A. & Vijayan, M. (2004). Structural basis for the carbohydrate specificities of artocarpin. Variation in the length of a loop as a strategy for generating ligand specificity. *J. Mol. Biol.* **338**, 757-770.

Kulkarni, K.A., Srivastav, A., Mitra, N., Sharon, N., Surolia, A., Vijayan, M. & Suguna, K. (2004). Effect of glycosylation on the structure of *Erythrina corallodendron* lectin. *Proteins* **56**, 821-827.

Roy, S., Gupta, S., Das, S., Sekar, K., Chatterji, D. & Vijayan, M. (2004). X-ray analysis of *Mycobacterium smegmatis* Dps and a comparative study involving other Dps and Dps-like molecules. *J. Mol. Biol.* **339**, 1103-1113.

Singh, D.D., Saikrishnan, K., Kumar Prashant, Dauter, Z., Sekar, K., Surolia, A. & Vijayan, M. (2004). Purification, crystallization and preliminary X-ray structure analysis of the banana lectin from *Musa paradisiaca*. *Acta Cryst.* **D60**, 2104-2106.

Deepa, R., Jagannath, M.R., Kesavulu, M.M., Durga Rao, C. & Suguna, K. (2004). Expression, purification, crystallization and preliminary crystallographic analysis of the diarrhoea-causing and virulence-determining region of rotaviral nonstructural protein NSP4. *Acta Cryst.* **D60**, 135-136.

Ketkar, A.D., Shenoy, A.R., Kesavulu, M.M., Visweswariah, S.S. & Suguna, K. (2004). Purification, crystallization and preliminary X-ray diffraction analysis of the catalytic domain of adenylyl cyclase Rv1625c from *Mycobacterium tuberculosis*. *Acta Cryst.* **D60**, 371-373.

Swarnamukhi, P.L., Kumar Sharma, S., Kapoor, M., Surolia, N., Surolia, A. & Suguna, K. (2004). Crystallization and preliminary crystallographic analysis of  $\beta$ -hydroxyacyl ACP dehydratase (FabZ) from *Plasmodium falciparum*. *Acta Cryst.* **D60**, 120-121.

- Kapoor, M., Swarnamukhi, P.L., Surolia, N., Suguna, K. & Surolia, A. (2004). Kinetic and structural analysis of the increased affinity of enoyl-ACP (acyl-carrier protein) reductase for triclosan in the presence of NAD<sup>+</sup>. *Biochem. J.* **381**, 725-733.
- Swarnamukhi, P.L., Kapoor, M., Surolia, N., Surolia, A. & Suguna, K. (2004). Structural basis for the variation in triclosan affinity to enoyl reductases. *J. Mol. Biol.* **343**, 147-155.
- Sekar, K., Rajakannan, V., Velmurugan, D., Yamane, T., Thirumurugan, R., Dauter, M. & Dauter, Z. (2004). A re-determination of the structure of the triple mutant (K53,56,120M) of phospholipase A2 at 1.6 Å resolution using Sulphur-SAS at 1.54 Å wavelength. *Acta Cryst.* **D60**, 1586-1590.
- Sangita, V., Lokesh, G.L., Satheshkumar, P.S., Vijay, C.S., Saravanan, V., Savithri, H.S. & Murthy, M.R.N. (2004). T=1 capsid structures of Sesbania mosaic virus coat protein mutants Determinants of T=3 and T=1 capsid assembly. *J. Mol. Biol.* **342**, 987-999.
- Eaazhisai, K., Jayalakshmi, R., Gayathri, P., Anand, R. P., Sumathy, K., Balam, H. & Murthy, M.R.N. (2004). Crystal Structure of fully ligated Adenylosuccinate synthetase from *Plasmodium falciparum*. *J. Mol. Biol.* **335**, 1251-1264.
- Das, S., Kumar, P., Bhor, B., Surolia, A. & Vijayan, M. (2005). Expression, purification, crystallization and preliminary X-ray crystallographic analysis of pantothenate kinase from *Mycobacterium tuberculosis*. *Acta Cryst.* **F61**, 65-67.
- Saikrishnan, K., Kalapala, S.K., Varshney, U. & Vijayan, M. (2005). X-ray structural studies of *Mycobacterium tuberculosis* RRF and a comparative study of RRFs of known structure. Molecular plasticity and biological implications. *J. Mol. Biol.* **345**, 29-38.
- Jeyaprakash, A.A., Jayashree, G., Mahanta, S.K., Swaminathan, C.P., Sekar, K., Surolia, A. & Vijayan, M. (2005). Structural basis for the energetics of jacalin-sugar interactions: Promiscuity *versus* specificity. *J. Mol. Biol.* **347**, 181-188.



Sankaranarayanan, R., Biswal, B.K. & Vijayan, M. (2005). A new relaxed state in Horse Methemoglobin characterized by crystallographic studies. *Proteins* **60**, 547–551.

Saikrishnan, K., Manjunath, G.P., Singh Pawan, Jeyakanthan, J., Dauter, Z., Sekar, K., Muniyappa, K. & Vijayan, M. (2005). Structure of *Mycobacterium smegmatis* single-stranded DNA-binding protein and a comparative study involving homologous SSBs: Biological implications of structural plasticity and variability in quaternary association. *Acta Cryst.* **D61**, 1140–1148.

Vijayan, M., Saikrishnan, K., Kumar, P., Dauter, Z., Sekar, K., Surolia, A. & Singh, D.D. (2005). Banana lectin, a  $\beta$ -prism I fold lectin with two carbohydrate binding sites. *Acta Cryst.* **A61**, C-232.

Kulkarni, K.A., Samiksha, K., Surolia, A., Vijayan, M. & Suguna, K. (2005). Structural basis for carbohydrate specificity of basic winged bean lectin. *Acta Cryst.* **A61**, C-265.

Singh, D.D., Saikrishnan, K., Kumar, P., Sekar, K., Surolia, A. & Vijayan, M. (2005). Unusual sugar specificity of banana lectin from *Musa paradisiaca* and its probable evolutionary origin. Crystallographic and modelling studies. *Glycobiology* **15**, 1025-1032.

Vijayan, M. (2005). Structural Biology of Mycobacterial Proteins: The Bangalore Effort. *Tuberculosis* **85**, 357-366

Kulkarni, K.A., Sinha, S., Katiyar, S., Surolia, A., Vijayan, M. & Suguna, K. (2005). Structural basis for the specificity of basic winged bean lectin for the Tn-antigen: A crystallographic, thermodynamic and modelling study. *FEBS Letts.* **579**, 6775-6780.

Kesavulu, M.M., Ramasubramanian, S. & Suguna, K. (2005). Effect of dimethyl sulphoxide on the crystal structure of porcine pepsin. *Biochem. Biophys. Res. Commun.* **331**, 1510-1514.

Sekar, K., Rajakannan, V., Gayathri, D., Velmurugan, D., Poi, M.-J., Dauter, M., Dauter, Z. & Tsai, M.-D. (2005). Atomic resolution (0.97Å) structure of the triple mutant (K53, 56, 121M) of bovine pancreatic phospholipase A<sub>2</sub>. *Acta Cryst.* **F61**, 3-7.

Manikandan, K., Bhardwaj, A., Ghosh, A., Reddy, V.S. & Ramakumar, S. (2005). Crystallization and preliminary X-ray study of a family 10 alkali-thermostable xylanase from alkalophilic *Bacillus sp.* Strain NG-27. *Acta Cryst.* **F61**, 747–749.

Simanshu, D.K. & Murthy, M.R.N. (2005). Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of propionate kinase (TdcD) from *Salmonella typhimurium*. *Acta Cryst.* **F61**, 52-55.

Simanshu, D.K., Savithri, H.S. & Murthy, M.R.N. (2005). Crystal structures of ADP and AMPPNP bound propionate kinase (TdcD) from *Salmonella typhimurium*: comparison with members of acetate and sugar kinase / heat shock cognate 70 / actin superfamily. *J. Mol. Biol.* **352**, 876-892.

Sangita, V., Lokesh, G.L., Satheshkumar, P.S., Saravanan, V., Vijay, C.S., Savithri, H.S. & Murthy, M.R.N. (2005). Structural studies on recombinant T=3 capsids of *Sesbania mosaic virus* coat protein mutants. *Acta Cryst.* **D61**, 1402-1405.

Sangita, V., Satheshkumar, P.S., Savithri, H.S. & Murthy, M.R.N. (2005). Structure of a mutant T=1 capsid of *Sesbania mosaic virus*: Role of water molecules in capsid architecture and integrity. *Acta Cryst.* **D61**, 1406-1412.

Satheshkumar, P.S., Lokesh, G.L., Murthy, M.R.N. & Savithri, H.S. (2005). The role of arginine-rich motif and β-annulus in the assembly and stability of *Sesbania mosaic virus*, *J. Mol. Biol.* **352**, 447-458.

Thakur, K.G. & Gopal, B. (2005). Crystallization and preliminary X-ray diffraction studies on the N- and C-terminal domains of the extra-cytoplasmic sigma factor SigC from *Mycobacterium tuberculosis*. *Acta Cryst.* **F61**, 779-781.

Girish, T.S. & Gopal, B. (2005). Crystallization and preliminary X-ray diffraction studies on the catalytic domain of the chick neurite inhibitory factor CRYP-2. *Acta Cryst.* **F61**, 381-383.

Gopal, B., Madan, L.L., Betz, S.F. & Kossiakoff, A.A. (2005). Crystal structure of quercetin 2,3 dioxygenase from *Bacillus subtilis* suggests modulation of enzyme activity by a change in the metal ion at the active site(s). *Biochemistry* **44**, 193-201.

Krishna, R., Manjunath, G.P., Kumar, P., Surolia, A., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2006). Crystallographic identification of an ordered C-terminal domain and a second nucleotide binding site in RecA. new insights into allostery. *Nucl. Acids Res.* **34**, 2186-2195.

Natchiar, S.K., Srinivas, O., Mitra, N., Dev, S., Jayaraman, N., Surolia, A. & Vijayan, M. Multivalency in lectins. (2006). A crystallographic, modelling and light scattering study involving peanut lectin and a bivalent ligand. *Curr. Sci.* **90**, 1230-1237.

Das, S., Kumar, P., Bhor, V., Surolia, A. & Vijayan, M. (2006). Invariance and variability in bacterial PanK: a study based on the crystal structure of *Mycobacterium tuberculosis* PanK. *Acta Cryst.* **D62**, 628–638.

Prabu, J.R., Thamocharan, S., Khanduja, J.S., Emily Zabala Alipio, Chang-Yub Kim, Geoffrey S. Waldo, Thomas C. Terwilliger, Brent Segelke, Tim Lakin, Dominique Toppani, Li-Wei Hung, Minmin Yu, Evan Bursey, K. Muniyappa, Chandra, N.R. & Vijayan, M. (2006). Structure of *Mycobacterium tuberculosis* RuvA, a protein involved in recombination. *Acta Cryst.* **F62**, 731–734.

Selvaraj, M., Singh, N.S., Roy, S., Sangeetha, R., Varshney, U. & Vijayan, M. (2006). Cloning, expression, purification, crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from *Mycobacterium tuberculosis*. *Acta Cryst.* **F62**, 913–915.

Kulkarni, K.A., Katiyar, S., Surolia, A., Vijayan, M. & Suguna, K. (2006). Structural basis for the carbohydrate-specificity of basic winged-bean lectin and its differential affinity for Gal and GalNac. *Acta Cryst.* **D62**, 1319-1324.

Natchiar, S.K., Srinivas, O., Mitra, N., Surolia, A., Jayaraman, N., & Vijayan, M. (2006). Structural studies on peanut lectin complexed with disaccharides involving different linkages: further insights into the structure and interactions of the lectin. *Acta Cryst.* **D62**, 1413-1421.

Kaushal, P.S., Talwar, R.K., Krishna, P.D.V., Varshney, U. & Vijayan, M. (2006). Overexpression, purification, crystallization and preliminary X-ray analysis of uracil *N*-glycosylase from *Mycobacterium tuberculosis* in complex with a proteinaceous inhibitor. *Acta Cryst.* **F62**, 1231-1234.

Ketkar, A.D., Shenoy, A.R., Ramagopal, U.A., Visweswariah, S.S. & Suguna, K. (2006). A structural basis for the role of nucleotide specifying residues in regulating the oligomerization of the Rv1625c Adenylyl Cyclase from *M. tuberculosis*. *J. Mol. Biol.* **356**, 904-916.

Swarnamukhi, P.L., Sharma, S.K., Bajaj, P., Surolia, N., Surolia, A. & Suguna, K. (2006). Crystal structure of dimeric FabZ of *Plasmodium falciparum* reveals conformational switching to active hexamers by peptide flips. *FEBS Letts.* **580**, 2653-2660.

Lavanya Latha, V., Kulkarni, K.A., Nagender Rao, R., Siva Kumar, N., Suguna, K. (2006). Crystallization and preliminary crystallographic analysis of a galactose specific lectin from *Dolichos lablab*. *Acta Cryst.* **F62**, 163-165.

Sekar, K., Yogavel, M., Gayathri, D., Velmurugan, D., Krishna, R., Poi, M.J., Dauter, Z., Dauter, M. & Tsai, M.D. (2006). Atomic resolution structure of the double mutant (K53,56M) of bovine pancreatic phospholipase A<sub>2</sub>. *Acta Cryst.* **F62**, 1-5.

Velmurugan, D., Rajakannan, V., Gayathri, D., Banumathi, S., Yamane, T., Dauter, Z., Dauter, M. & Sekar, K. (2006). *Ab initio* structure determination of the triple mutant (K53,56,121M) of bovine pancreatic phospholipase A<sub>2</sub> at atomic and high resolution using ACORN. *Curr. Sci.* **90(8)**, 1091-1099.

Sekar, K., Yogavel, M., Kanaujia, S.P., Sharma, A., Velmurugan, D., Poi, M.J., Dauter, Z. & Tsai, M.D. (2006). Suggestive evidence for the involvement of the second calcium and surface loop in interfacial binding: Monoclinic and trigonal crystal structures of a quadruple mutant of phospholipase A<sub>2</sub>. *Acta Cryst.* **D62**, 717-724.

Manikandan, K., Bhardwaj, A., Gupta, N., Lokanath, N.K., Ghosh, A., Reddy, V.S. & Ramakumar, S. (2006). Crystal structures of native and Xylosaccharide-bound alkali thermostable xylanase from an alkalophilic *Bacillus* sp. NG – 27: Structural insights into alkalophilicity and implications for adaptation to poly extreme conditions. *Protein Sci.* **15**,1951-1960.

Bagaria, A., Surendranath, K., Ramagopal, U.A., Ramakumar, S. & Karande, A.A. (2006). Structure-function analysis and insights into the reduced toxicity of *Abrus precatorius* agglutinin 1 in relation to Abrin. *J. Biol. Chem.* **281**, 34465-34474.

Manikandan, K., Jagtap, S., Rao, M. & Ramakumar, S. (2006). Crystallization and preliminary X ray characterization of a thermostable low-molecular weight 1,4 beta-D-glucan glucohydrolase from an alkalothermophilic *Thermomonospora* sp. *Acta Cryst.* **F62**, 385-387.

Gayathri, P., Satheshkumar, P.S., Prasad, K., Nair, S., Savithri, H.S. & Murthy, M.R.N. (2006). Crystal structure of the serine protease domain of *Sesbania mosaic virus* polyprotein and mutational analysis of residues forming the S1-binding pocket. *Virology* **346**, 440-451.

Rajaram, V., Prasad, K., Prasuna, P.R., Ramachandra, N., Bharat, S.R., Savithri, H.S. & Murthy, M.R.N. (2006). Cloning, purification, crystallization and preliminary X-ray crystallographic analysis of the N-acetylornithine aminotransferases from *Salmonella typhimurium* and *Escherichia coli*. *Acta Cryst.* **F62**, 980-983.

Simanshu, D.K., Savithri, H.S. & Murthy, M.R.N. (2006). Crystal structures of *Salmonella typhimurium* biodegradative threonine deaminase (TdcB) and its complex with CMP provide insights into ligand-induced oligomerization and enzyme activation. *J. Biol. Chem.* **281**, 39630-39641.

Simanshu, D.K., Chittori, S., Savithri, H.S. & Murthy, M.R.N. (2006). Crystallization and preliminary X-ray crystallographic analysis of biodegradative threonine deaminase (TdcB) from *Salmonella typhimurium*. *Acta Cryst.* **F62**, 275-278.

Rajavel, M., Warriar, T., & Gopal, B. (2006). Old fold in a new X-Ray diffraction dataset? Low-resolution molecular replacement using representative structural templates can provide phase information. *Proteins* **64**, 223-230.

Rajavel, M. & Gopal, B. (2006) Crystallization and preliminary X-Ray diffraction studies on the bicupin YwfC from *Bacillus subtilis* *Acta Cryst.* **F62**, 1259-1262.

Krishna, R., Prabu, J.R., Manjunath, G.P., Datta, S., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2007). Snapshots of RecA protein involving movement of the C-domain and different conformations of the DNA-binding loops: Crystallographic and comparative analysis of 11 structures of *Mycobacterium smegmatis* RecA. *J. Mol. Biol.* **367**, 1130-1144.

Kulkarni, K.A., Katiyar, S., Surolia, A., Vijayan, M., & Suguna, K. (2007). Generation of blood group specificity. New insights from structural studies on the complexes of A- and B- reactive saccharides with basic winged bean agglutinin. *Proteins* **68**, 762-769.

Natchiar, S.K., Suguna, K., Surolia, A., & Vijayan, M. (2007). Peanut agglutinin, a lectin with an unusual quaternary structure and interesting ligand binding properties. *Crystallographic Reviews* **13**, 1-26.

Sekar, K., Surolia, A. & Vijayan, M. (2007). Structure and carbohydrate specificity of  $\beta$ -prism I fold lectins. In *Glycobiology*. Edited by Sansom, C. & Markman, O., Scion Publishing Ltd., Bloxham (U.K.) pp. 150-159.

Roy, S., Saraswathi, Gupta, S., Sekar, K., Chatterji, D. & Vijayan, M. (2007). Role of N and C-terminal tails in DNA binding and assembly in Dps: Structural studies of *mycobacterium smegmatis* Dps deletion mutants *J. Mol. Biol.* **370**, 752-767.

Vijayan, M. (2007). Peanut lectin crystallography and macromolecular structural studies in India. *J. Biosci.* **32**, 1059–1066.

Sharma, A., Chandran, D., Singh, D.D & Vijayan, M. (2007). Multiplicity of carbohydrate binding sites in  $\beta$ -prism fold lectins: occurrence and possible evolutionary implications *J. Biosci.* **32**, 1089–1110.

Selvaraj, M., Roy, S., Singh, N.S., Sangeetha, R., Varshney, U. & Vijayan, M. (2007). Structural plasticity and enzyme action: Crystal structures of *Mycobacterium tuberculosis* peptidyl-tRNA hydrolase *J. Mol. Biol.* **372**, 186-193.

Vijayan, M. (2007). Macromolecular crystallography in India. A historical overview. *Journal of Indian Inst. Sci.* **87**, 261-277.

Sinha, S., Gupta, G., Vijayan, M. & Surolia, A. (2007). Subunit assembly of plant lectins. *Curr.Opin. Stru. Biol.* **17**, 498-505.

Deepa, R., Durga Rao, C. & Suguna, K. (2007). Structure of the extended diarrhea-inducing domain of rotavirus enterotoxigenic protein NSP4. *Arch. Virol.***152**, 847-859.

Swarnamukhi, P.L. , Sharma, S. K., Padala, P., Surolia, N., Surolia, A. & Suguna, K. (2007). Packing and loop-structure variations in non-isomorphous crystals of FabZ from *Plasmodium falciparum*. *Acta Cryst.* **D63**, 458-464.

Kanaujia, S.P., Ranjani, C.V., Jeyakanthan, J., Baba, S., Chen, L., Liu, Z.J., Wang, B.C., Nishida, M., Ebihara, A., Shinkai, A., Kuramitsu, S., Shiro, Y., Sekar, K. & Yokoyama S. (2007). Crystallization and preliminary crystallographic analysis of molybdenum cofactor biosynthesis protein C from *Thermus thermophilus*. *Acta Cryst.* **F63**, 27-29.

Kanaujia, S.P., Ranjani, C.V., Jeyakanthan, J., Baba, S., Kuroishi, C., Ebihara, A., Shinkai, A., Kuramitsu, S., Shiro, Y., Sekar, K. & Yokoyama, S. (2007). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of DHNA synthetase from *Geobacillus kaustophilus*. *Acta Cryst.* **F63**, 103-105.

Kanaujia, S.P., Ranjani, C.V., Jeyakanthan, J., Ohmori, M., Agari, K., Kitamura, Y., Baba, S., Ebihara, A., Shinkai, A., Kuramitsu, S., Shiro, Y., Sekar, K. & Yokoyama, S. (2007). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of molybdopterin synthase from *Thermus thermophilus* HB8. *Acta Cryst.* **F63**, 324-326.

Kanaujia, S.P., Ranjani, C.V., Jeyakanthan, J., Nishida, M., Kitamura, Y., Baba, S., Ebihara, A., Shimizu, N., Nakagawa, N., Shinkai, A., Yamamoto, M., Kuramitsu, S., Shiro, Y., Sekar, K. & Yokoyama, S. (2007). Preliminary X-ray crystallographic study of glucose dehydrogenase from *Thermus thermophilus* HB8. *Acta Cryst.* **F63**, 446-448.

Chittori, S., Simanshu, D.K., Savithri, H.S. & Murthy, M.R.N. (2007). Structure of the putative mutarotase YeaD from *Salmonella typhimurium*: structural comparison with galactose mutarotase, *Acta Cryst.* **D63**, 197-205.

Gayathri, P., Banerjee, M., Vijayalakshmi, A., Azeez, S., Balaram, H., Balaram, P. & Murthy, M.R.N. (2007). Structure of triosephosphate isomerase (TIM) from *Methanocaldococcus jannaschii*. *Acta Cryst.* **D63**, 206-220.

Simanshu, D.K., Chittori, S., Savithri, H.S. & Murthy, M.R.N. (2007). Structure and function of enzymes involved in the anaerobic degradation of L-threonine to propionate. *J. Biosci.* **32**, 1195-1206.

Rajaram, V., Bhavani, B.S., Kaul, P., Prakash, V., Rao, N.A., Savithri, H.S. & Murthy, M.R.N. (2007). Structure determination and biochemical studies on *Bacillus stearothermophilus* E53Q serine hydroxymethyltransferase and its complexes provide insights on function and enzyme memory. *FEBS Journal* **274**, 4148-4160.

Sagurthi, S.R., Panigrahi, R.R., Gowda G., Savithri, H.S. & Murthy, M.R.N. (2007). Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of universal stress protein F (YnaF) from *Salmonella typhimurium*. *Acta Cryst.* **F63**, 957-960.



Murthy, M.R.N. (2007). A personal account of virus structure determination at the Indian Institute of Science, Bangalore. *Journal of Indian. Inst. Sci.* **87**, 279-299.

Simanshu, D.K., Savithri, H.S. & Murthy, M.R.N. (2007). Crystal structures of *Salmonella typhimurium* biodegradative threonine deaminase (TdcB) and its complex with CMP provide insights into ligand-induced oligomerization and enzyme activation. *J. Biol. Chem.* **281**, 39630-39641.

Gayathri, P., Balaram, H. & Murthy, M.R.N. (2007). Structural biology of Plasmodial proteins. *Curr. Opin. Stru. Biol.* **17**, 744-754.

Girish, T.S. & Gopal, B. (2007). The crystal structure of the catalytic domain of the chick retinal neurite inhibitor- Receptor Protein Tyrosine Phosphatase CRYP-2 / cPTPRO. *Proteins* **65**, 1011-1015.

Thakur, K.G., Joshi, A.M. & Gopal, B. (2007). Structural and biophysical studies on two promoter recognition domains of the extra-cytoplasmic function  $\sigma$  factor  $\sigma^C$  from *Mycobacterium tuberculosis*. *J. Biol. Chem.* **282**, 4711-4718.

Roy, S., Saraswathi, R., Chatterji, D. & Vijayan, M. (2008). Structural studies on the second *Mycobacterium smegmatis* Dps: Invariant and variable features of structure, assembly and function. *J. Mol. Biol.* **375**, 948-959.

Vijayalakshmi, L., Krishna, R., Sankaranarayanan, R. & Vijayan, M. (2008). An asymmetric dimer of  $\beta$ -lactoglobulin in a low humidity crystal form-Structural changes that accompany partial dehydration and protein action. *Proteins* **71**, 241-249.

Kaushal, P.S., Talwar, R.K., Krishna, P.D.V., Varshney, U. & Vijayan, M. (2008). Unique features of the structure and interactions of mycobacterial uracil-DNA glycosylase: structure of a complex of the *Mycobacterium tuberculosis* enzyme in comparison with those from other sources. *Acta Cryst.* **D64**, 551-560.

Kaushal, P.S., Sankaranarayanan, R. & Vijayan, M. (2008). Water-mediated variability in the structure of relaxed state hemoglobin. *Acta Cryst.* **F64**, 463-467.

Kulkarni, K.A., Katiyar, S., Surolia, A., Vijayan, M. & Suguna, K. (2008). Structure and sugar specificity of basic winged bean lectin. Crystal structures of new disaccharide complexes and a comparative study with other known disaccharide complexes of the lectin. *Acta Cryst.* **D64**, 730-737.

Prabu, J.R. , Manjunath, G.P., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2008). Functionally important movements in RecA molecules and filaments: studies involving mutation and environmental changes. *Acta Cryst.* **D64**, 1146-1157.

Sawarkar, R., Roy, N., Rao, S., Raman, S., Venketesh, S., Suguna, K. & Tatu, U. (2008). Heat shock protein 90 regulates development in *Dictyostelium discoideum*. *J. Mol. Biol.* **383**, 24-35.

Rangarajan, S., Jeyakanthan, J., Mridula, P., Sakamoto, K., Kitamura, Y., Agari, Y., Shinkai, A., Ebihara, A., Kuramitsu, S., Yokoyama, S. & Sekar, K. (2008). Crystallization and preliminary crystallographic studies of L30e, a ribosomal protein from *Methanocaldococcus jannaschii* (MJ1044). *Acta Cryst.* **F64**, 102-104.

Kanaujia, S.P. & Sekar, K. (2008). Structures and molecular-dynamics studies of three active site mutants of bovine pancreatic phospholipase A<sub>2</sub>. *Acta Cryst.* **D64**, 1003-1011.

Jeyakanthan, J., Rangarajan, S., Mridula, P., Kanaujia, S.P., Shiro, Y., Kuramitsu, S., Yokoyama, S. & Sekar, K. (2008). Observation of a calcium-binding site in the gamma-class carbonic anhydrase from *Pyrococcus Horikoshii*. *Acta Cryst.* **D64**, 1012-1019.

Ramakumar, S., Bhowmick, T., Ghosh, S., Ramagopal, U.A. & Valakunja, N. (2008). Crystal structure and structure based drug design of HU(Histone like DNA binding protein) from *Mycobacterium tuberculosis*. *Acta Cryst.* **A64**, C342

Gowda, G., Sangurti, S.R., Savithri, H.S. & Murthy, M.R.N. (2008). Cloning, expression, purification and preliminary X-ray crystallographic analysis of mannose 6-phosphate isomerase from *Salmonella typhimutium*. *Acta Cryst.* **F64**, 81-84.

Bhavani, B.S., Rajaram, V., Bisht, S., Kaul, P., Prakash, V., Murthy, M.R.N., Rao, N.A. & Savithri, H.S. (2008). Importance of tyrosine residues of *Bacillus stearothermophilus* serine hydroxymethyltransferase in cofactor binding and L-allo-Thr cleavage: crystal structure and biochemical studies. *FEBS Journal* **275**, 4606-4619.

Pappachan, A., Subashchandrabose, C., Satheskumar, P.S., Savithri, H.S. & Murthy, M.R.N. (2008). Structure of recombinant capsids formed by the beta-annulus deletion mutant - rCP (Delta48-59) of *Sesbania mosaic virus*. *Virology* **375**, 190-196.

Rajaram, V., Ratna, P.P., Savithri, H.S. & Murthy, M.R.N. (2008). Structure of biosynthetic N-acetylornithine aminotransferase from *Salmonella typhimurium*: studies on substrate specificity and inhibitor binding. *Proteins* **70**, 429-441.

Simanshu, D.K., Savithri, H.S. & Murthy M.R.N. (2008). Crystal structures of *Salmonella typhimurium* propionate kinase and its complex with Ap4A: Evidence for a novel Ap4A synthetic activity. *Proteins* **70**, 1379-1388.

Gayathri, P., Subbayya, I.N., Ashok, C.S., Selvi, T.S., Balam, H. & Murthy, M.R.N. (2008). Crystal structure of a chimera of human and *Plasmodium falciparum* hypoxanthine guanine phosphoribosyltransferases provides insights into oligomerization. *Proteins* **73**, 1010-1020

Pappachan A., Savithri, H.S. & Murthy, M.R.N. (2008). Structural and functional studies on a mesophilic stationary phase survival protein (SurE) from *Salmonella typhimurium*. *FEBS Journal* **275**, 5855-5564.

Mizutani, H., Saraboji, K., Malathy, S.S.M., Ponnuswamy, M.N., Kumarevel, T., Krishna Swamy, B.S., Simanshu, D.K., Murthy, M.R.N. & Kunishima, N. (2008). Systematic study on crystal-contact engineering of diphthine synthase: influence of mutations at crystal-packing regions on X-ray diffraction quality. *Acta Cryst.* **D64**, 1020-1033.

Nair, S., Gayathri, P., Murthy, M.R.N. & Savithri, H.S. (2008). Stacking interactions of W271 and H275 of SeMV serine protease with W43 of natively unfolded VPg confer catalytic activity to protease. *Virology* **382**, 83-90.

Rajavel, M., Kulkarni, N.N. & Gopal, B. (2008). Conformational studies suggest that the double stranded  $\beta$  helix scaffold provides an optimal balance between protein stability and function. *Prot. Pept. Letts.* **15**, 244-249.

Girish, T.S., Sharma, E. & Gopal, B. (2008). Structural basis for the regulation of Dihydrodipicolinate Synthase (DHDPS) activity from *Staphylococcus aureus*. *FEBS Letts.* **582**, 2923-2930.

Chetnani, B., Das, S., Kumar, P., Surolia, A. & Vijayan, M. (2009). *Mycobacterium tuberculosis* pantothenate kinase: possible changes in location of ligands during enzyme action. *Acta Cryst.* **D65**, 312–325.

Prabu, J.R., Thamotharan, S., Khanduja, J.S., Chandra, N.R., Muniyappa, K. & Vijayan, M. (2009). Crystallographic and modelling studies on *Mycobacterium tuberculosis* RuvA Additional role of RuvB-binding domain and inter species variability. *Biochim. Biophys. Acta* **1794**, 1001–1009.

Sharma, S., Sekar, K. & Vijayan, M. (2009). Structure, dynamics, and interactions of jacalin. Insights from molecular dynamics simulations examined in conjunction with results of X-ray studies *Proteins* **77**, 760–777.

Vijayan, M. (2009). Back to Basics: Molecular Interactions and Aggregation, Hydration. *Proc. Ind. Nat. Sci. Acad.* **75**, 93-105.

Swarnamukhi, P.L., Maity, K., Ramaswamy, K., Surolia, N. & Suguna, K. (2009). Analysis of proteins with the 'Hot dog' fold: Prediction of function and identification of catalytic residues of hypothetical proteins. *BMC Struct. Biol.* **9**, 37.

Kanaujia, S.P. & Sekar, K. (2009). Structural and functional role of water molecules in bovine pancreatic phospholipase A<sub>2</sub>: A data-mining approach. *Acta Cryst.* **D65**, 74-84.

Bairagya, H.R., Mukhopadhyay, B.P. & Sekar, K. (2009). An insight to the dynamics of conserved water molecular triad in IMPDH II (Human): Recognition of cofactor and substrate to catalytic Arg 322. *J. Biomol. Struct. Dyn.* **27**, 149-158.

Sagurthi, S.R., Gowda, G., Savithri, H.S. & Murthy, M.R.N. (2009). Structures of mannose-6-phosphate isomerase from *Salmonella typhimurium* bound to metal atoms and substrate: implications for catalytic mechanism. *Acta Cryst.* **D65**, 724-732.

Pai, V.R., Rajaram, V., Bisht, S., Bhavani, B.S., Rao, N.A., Murthy, M.R.N. & Savithri, H.S. (2009). Structural and functional studies of *Bacillus stearothermophilus* serine hydroxymethyltransferase: the role of Asn(341), Tyr(60) and Phe(351) in tetrahydrofolate binding. *Biochem. J.* **418**, 635-642.

Rajavel, M., Mitra, A. & Gopal, B. (2009) Structural basis for the role of *Bacillus subtilis* BacB in the synthesis of the antibiotic bacilysin. *J. Biol. Chem.* **284**, 31882-31892.

Gayathri, P., Banerjee, M., Vijayalakshmi, A., Balaram, H., Balaram, P. & Murthy, M.R.N. (2009). Biochemical and structural characterization of residue 96 mutants of *Plasmodium falciparum* triosephosphate isomerase: active-site loop conformation, hydration and identification of a dimer-interface ligand-binding site. *Acta Cryst.* **D65**, 847-857.

Pappachan, A., Chinnathambi, S., Satheshkumar, P.S., Savithri, H.S. & Murthy, M.R.N. (2009). A single point mutation disrupts the capsid assembly in *Sesbania Mosaic Virus* resulting in a stable isolated dimer. *Virology* **392**, 215-221.

Chetnani, B., Kumar, P., Surolia, A. & Vijayan, M. (2010). *M. tuberculosis* Pantothenate Kinase: Dual Substrate Specificity and Unusual Changes in Ligand Locations. *J. Mol. Biol.* **400**, 171-185.

Kaushal, P.S., Talawar, R.K., Varshney, U. & Vijayan, M. (2010). Structure of uracil-DNA glycosylase from *Mycobacterium tuberculosis*: insights into interactions with ligands *Acta Cryst.* **F66**, 887-892.

Chandran, T., Sharma, A. & Vijayan, M. (2010). Crystallization and preliminary X-ray studies of a galactose-specific lectin from the seeds of bitter gourd (*Momordica charantia*). *Acta Cryst.* **F66**, 1037-1040.

Chandran, A.V., Prabu, J.R., Manjunath, G.P., Patil, N.K., Muniyappa, K. & Vijayan, M. (2010). Crystallization and preliminary X-ray studies of the C-terminal domain of *Mycobacterium tuberculosis* LexA. *Acta Cryst.* **F66**, 1093-1095.

Kaushal, P.S., Singh, P., Sharma, A., Muniyappa, K. & M. Vijayan, M. (2010). X-ray and molecular-dynamics studies on *Mycobacterium leprae* single-stranded DNA-binding protein and comparison with other eubacterial SSB structures. *Acta Cryst.* **D66**, 1048-1058.

Patra, D., Srikalaivani, R., Misra, A., Singh, D.D., Selvaraj, M. & Vijayan, M. (2010). Cloning, expression, purification, crystallization and preliminary X-ray studies of a secreted lectin (Rv1419) from *Mycobacterium tuberculosis*. *Acta Cryst.* **F66**, 1662–1665.

Maity, K., Bhargav, S.P., Sankaran, B., Surolia, N., Surolia, A. & Suguna, K. (2010). X-ray crystallographic analysis of the complexes of enoyl acyl carrier protein reductase of *Plasmodium falciparum* with triclosan variants to elucidate the importance of different functional groups in enzyme inhibition. *IUBMB Life* **62**, 467-476.

Suguna, K. & Durga Rao, C. (2010). Rotavirus nonstructural proteins: A structural perspective. *Curr. Sci.* **98**, 352-359.

Jeyakanthan, J., Kanaujia, S.P., Nishida, Y., Nakagawa, N., Praveen, S., Shinkai, A., Kuramitsu, S., Yokoyama, S. & Sekar, K. (2010). Free and ATP-bound structures of Ap<sub>4</sub>A hydrolase from *Aquifex aeolicus* V5. *Acta Cryst.* **D66**, 116-124.

Manjunath, K., Jeyakanthan, J., Nakagawa, N., Shinkai, A., Yoshimura, M., Kuramitsu, S., Yokoyama, S. & Sekar, K. (2010). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of the putative SAICAR synthetase (PH0239) from *Pyrococcus horikoshii* OT3. *Acta Cryst.* **F66**, 180-183.

Kanaujia, S.P., Jeyakanthan, J., Nakagawa, N., Balasubramaniam, S., Shinkai, A., Kuramitsu, S., Yokoyama, S. & Sekar, K. (2010). Crystal structures of apo and GTP-bound molybdenum cofactor biosynthesis protein MoaC from *Thermus thermophilus* HB8. *Acta Cryst.* **D66**, 821-833.

Savithri, H.S. & Murthy, M.R.N. (2010). Structure and assembly of *Sesbania mosaic virus*. *Curr. Sci.* **98**, 346-352.

Lokesh, B., Rashmi, P.R., Amruta, B.S., Srisathiyarayanan, D., Murthy, M.R.N. & Savithri H.S. (2010). NSs encoded by groundnut bud necrosis virus is a bifunctional enzyme. *PLoS One* **5**, e9757. Erratum in: *PLoS One* (2010) **5**(4).

Chittori, S., Simanshu, D.K., Savithri, H.S. & Murthy, M.R.N. (2010). Preliminary X-ray crystallographic analysis of 2-methylcitrate synthase from *Salmonella typhimurium*, *Acta Cryst.* **F66**, 467-470.

Thakur, K.G., Praveena, T. & Gopal, B. (2010). *Mycobacterium tuberculosis* Rv2704 is a member of YjgF/YER057c/UK114 family. *Proteins* **78**, 773-778.

Navratna, V., Nadig, S., Sood, V., Prasad, K., Arakere, G. & Gopal, B. (2010). Molecular Basis for the role of Penicillin Binding Protein 4 in the interplay of  $\beta$ -lactam antibiotics and antimicrobial resistance in *Staphylococcus aureus*. *J. Bacteriology* **192**, 134-144.

Chakrabarty, K., Thakur, G., Gopal, B. & Sarma, S. (2010). X-ray crystallographic and NMR studies of pantothenate synthetase provide insights into the mechanism of homotropic inhibition by pantoate. *FEBS Journal* **277**, 697-712.

Rajavel, M. & Gopal, B. (2010). Analysis of multiple crystal forms of *Bacillus subtilis* BacB suggests a role for a metal ion as a nucleant for crystallization. *Acta Cryst.* **D66**, 635-639.

Thakur, K.G., Praveena, T. & Gopal, B. (2010). Structural and biochemical basis for the redox sensitivity of *Mycobacterium tuberculosis* RslA. *J. Mol. Biol.* **397**, 1199-1208.

Jaiswal, R.K., Manjeera, G. & Gopal, B. (2010). Role of a PAS sensor domain in the *Mycobacterium tuberculosis* transcription regulator Rv1364c. *Biochem. Biophys. Res. Commun.* **398**, 342-349.

Girish, T.S. & Gopal, B. (2010). The crystal structure of *Staphylococcus aureus* metallopeptidase (Sapep) reveals large domain motions between the manganese bound and apo states. *J. Biol. Chem.* **285**, 29406-29415.

Madan, L.L., Veeranna, S., Shameer, K., Reddy, C.C.S., Sowdhamini, R. & Gopal, B. (2011). Modulation of catalytic activity in multi-domain protein tyrosine phosphatases. *Plos One* **6**, e24766.

Girish, T.S., Navratna, V. & Gopal, B. (2011). Structure and nucleotide specificity of *Staphylococcus aureus* dihydrodipicolinate reductase (DapB). *FEBS Letts.* **585**, 2561-2567.

Srivastava, S.K., Rajasree, K. & Gopal, B. (2011). Conformational basis for substrate recognition and regulation of catalytic activity in *Staphylococcus aureus* nucleoside di-phosphate kinase. *Biochim. Biophys. Acta* **1814**, 1349-1357.

Srivastava, S.K., Rajasree, K. & Gopal, B. (2011). in *Staphylococcus aureus: Biology and infections* edited By D Raghunath and G Arekere. Challenges and strategies for the design of novel *Staphylococcus* inhibitors. *Macmillan Advanced research series*.

Sharma, A. & Vijayan, M. (2011). Influence of glycosidic linkage on the nature of carbohydrate binding in  $\beta$ -prism I fold lectins. An X-ray and molecular dynamics investigation on banana lectin – carbohydrate complexes. *Glycobiology* **21**, 23-33.

Patra, D., Sharma, A., Chandran, D. & Vijayan, M. (2011). Cloning, expression, purification, crystallization and preliminary X-ray studies of the mannose-binding lectin domain of MSMEG\_3662 from *Mycobacterium smegmatis*. *Acta Cryst.* **F67**, 596-599.



Chetnani, B., Kumar, P., Abhinav, K.V., Chibbar, M., Surolia, A. & Vijayan, M. (2011). Location and conformation of pantothenate and its derivatives in *Mycobacterium tuberculosis* pantothenate kinase: insights into enzyme action. *Acta Cryst.* **D67**, 774-783.

Sharma, A. & Vijayan, M. (2011). Quaternary association in  $\beta$ -prism I fold plant lectins: Insights from X-ray crystallography, modelling and molecular dynamics. *J. Biosci.* **36**, 793-808.

Sugadev, R., Ponnuswamy, M.N. & Sekar, K. (2011). Structural analysis of NADPH depleted bovine liver catalase and its inhibitor complexes. *Int. J. Biochem. Mol. Biol.* **2**, 67-77.

Kanaujia, S.P., Jeyakanthan, J., Shinkai, A., Kuramitsu, S., Yokoyama, S. & Sekar K. (2011). Crystal structures, dynamics and functional implications of molybdenum cofactor biosynthesis protein MogA from two thermophilic organisms. *Acta Cryst.* **F67**, 2-16.

Misra, A., Biswas, T., Das, S., Marathe, U., Sehgal, D., Roy, R.P. & Ramakumar, S. (2011). Crystallisation and preliminary X-ray diffraction studies of Sortase A from *Streptococcus pneumoniae*. *Acta Cryst.* **F67**, 1195-1198.

Thamotharan, S., Karthikeyan, T., Kulkarni, K.A., Shetty, K.N., Surolia, A., Vijayan, M. & Suguna, K. (2011). Modification of the sugar specificity of a plant lectin: structural studies on a point mutant of *Erythrina corallodendron* lectin. *Acta Cryst.* **D67**, 218-227.

Chacko, A.R., Arifullah, M., Sastri, N.P., Jeyakanthan, J., Ueno, G., Sekar, K., Read, R.J., Dodson, E.J., Rao, D.C. & Suguna, K. (2011). Novel pentameric structure of the diarrhea-inducing region of the rotavirus enterotoxigenic protein NSP4. *J. Virol.* **85**, 12721-12732.

Maity, K., Venkata, B.S., Kapoor, N., Surolia, N., Surolia, A. & Suguna, K. (2011). Structural basis for the functional and inhibitory mechanisms of  $\beta$ -hydroxyacyl-acyl carrier protein dehydratase (FabZ) of *Plasmodium falciparum*. *J. Struct. Biol.* **176**, 238-249.

Maity, K., Banerjee, T., Prabakaran, N., Surolia, N., Surolia, A. & Suguna, K. (2011). Effect of substrate binding loop mutations on the structure, kinetics, and inhibition of enoyl acyl carrier protein reductase from *Plasmodium falciparum*. *IUBMB Life* **63**, 30-41.

Sastri, N.P., Pamidimukkala, K., Marathahalli, J.R., Suguna, K. & Rao, C.D. (2011). Conformational differences unfold a wide range of enterotoxigenic abilities exhibited by rNSP4 peptides from different rotavirus strains. *Open Virol. J.* **5**, 124-135.

Janardan, N., Paul, A., Harijan, R.K., Wierenga, R.K. & Murthy, M.R.N. (2011). Cloning, expression, purification and preliminary X-ray diffraction studies of a putative *Mycobacterium smegmatis* thiolase. *Acta Cryst.* **F67**, 817-820.

Bharath, S.R., Bisht, S., Savithri, H.S. & Murthy, M.R.N. (2011). Crystal structures of open and closed forms of d-serine deaminase from *Salmonella typhimurium* – implications on substrate specificity and catalysis. *FEBS J.* **278**, 2879-2891.

Samanta, M., Banerjee, M., Murthy, M.R.N., Balaram, H. & Balaram, P. (2011). Probing the role of the fully conserved Cys126 in triosephosphate isomerase by site-specific mutagenesis – distal effects on dimer stability. *FEBS J.* **278**, 1932-1943.

Samanta, M., Murthy, M.R.N., Balaram, H. & Balaram, P. (2011). Revisiting the mechanism of the triosephosphate isomerase reaction: The role of the fully conserved glutamic acid 97 residue. *Chem. Bio. Chem.* **12**, 1-12.

Chittori, S., Savithri, H.S. & Murthy, M.R.N. (2011). Crystal structure of *Salmonella typhimurium* 2-methylcitrate synthase: Insights on domain movement and substrate specificity. *J. Struct. Biol.* **174**, 58-68.

Srivastava, S.K., Gayathri, S., Manjasetty, B. & Gopal, B. (2012). Analysis of conformational variation in macromolecular structural models. *Plos One* **7**, e39993.

Madan, L.L. & Gopal, B. (2012). Conformational basis for substrate recruitment in Protein Tyrosine Phosphatase 10D. *Biochemistry* **50**, 10114-10125.

Madan, L.L., Goutam, P. & Gopal, B. (2012). Inter-domain interactions influence the stability and catalytic activity of the bi-domain protein tyrosine phosphatase PTP99A. *Biochim. Biophys. Acta* **1824**, 983-990.

Girish, T.S. & Gopal, B. (2012). Metallopeptidase (Sapep) *Staphylococcus aureus* in The Encyclopedia of Inorganic and Bioinorganic Chemistry edited by Albrecht Messerschmidt. Wiley-Blackwell Press. DOI: 10.1002 /9781119951438.eibc2058.

Selvaraj, M., Rais, A., Varshney, U. & Vijayan, M. (2012). Structures of new crystal forms of *Mycobacterium tuberculosis* peptidyl-tRNA hydrolase and functionally important plasticity of the molecule. *Acta Cryst.* **F68**, 124-128.

Arif, S.M. & Vijayan, M. (2012). Structural diversity based on variability in quaternary association A case study involving eubacterial and related SSBs. *In Single-Stranded DNA Binding Proteins (Methods in Molecular Biology)* Edited by James L Keck, Humana Press, Springer, pp 23-35.

Arif, S.M., Patil, A.G., Varshney, U. & Vijayan, M. (2012). Crystallization and preliminary X-ray studies of MutT1 (MSMEG\_2390) from *Mycobacterium smegmatis*. *Acta Cryst.* **F68**, 1214-1216.

Selvaraj, M., Rais, A., Varshney, U. & Vijayan, M. (2012). Crowding, molecular volume and plasticity An assessment involving crystallography, NMR and simulations. *J. Biosci.* **37**, 953-963.

Chacko, A.R., Zwart, P.H., Read, R.J., Dodson, E.J., Rao, C.D. & Suguna, K. (2012). Severe diffraction anisotropy, rotational pseudosymmetry and twinning complicate the refinement of a pentameric coiled-coil structure of NSP4 of rotavirus. *Acta Cryst.* **D68**, 1541-1548.

Maity, K., Bajaj, P., Surolia, N., Surolia, A. & Suguna, K. (2012). Insights into the substrate specificity of a thioesterase Rv0098 of *Mycobacterium tuberculosis* through X-ray crystallographic and molecular dynamics studies. *J. Biomol. Struct. Dyn.* **29**, 973-983.

Shetty, K.N., Bhat, G.G., Inamdar, S.R., Swamy, B.M. & Suguna, K. (2012). Crystal structure of a  $\beta$ -prism II lectin from *Remusatia vivipara*. *Glycobiology* **22**, 56-69.

Chacko, A.R., Jeyakanthan, J., Ueno, G., Sekar, K., Rao, C.D., Dodson, E.J., Suguna, K. & Read, R.J. (2012). A new pentameric structure of rotavirus NSP4 revealed by molecular replacement. *Acta Cryst.* **D68**, 57-61.

Bhardwaj, A., Mahanta, P., Ramakumar, S., Ghosh, A., Leelavathi, S. & Reddy, V.S. (2012). Emerging role of N- and C- terminal interactions in stabilizing (beta/alpha)<sub>8</sub> fold with special emphasis on family 10 xylanases. *Comput. Struct. Biotechnol. J.* **2**, e201209014.

Nair, S., Murthy, M.R.N. & Savithri, H.S. (2012). Intrinsically disordered domains of sesbania mosaic virus encoded proteins in "Flexible viruses", eds. V.N. Uverky and S. Longhi, John Wiley & Sons, Inc. pp 257-276.

Bisht, S., Rajaram, V., Bharath, S.R., Kalyani, J.N., Khan, F., Rao, A.N., Savithri, H.S. & Murthy, M.R.N. (2012). Crystal structure of *Escherichia coli* diaminopropionate ammonia-lyase reveals mechanism of enzyme activation and catalysis. *J. Biol. Chem.* **287**, 20369-20381.

Bharath, S.R., Bisht, S., Harijan, R.K., Savithri, H.S. & Murthy, M.R.N. (2012). Structural and mutational studies on substrate specificity and catalysis of *Salmonella typhimurium* D-cysteine desulphydrase. *Plos One* e36267.

Navratna, V. & Gopal, B. (2013). Crystallization and preliminary X-Ray diffraction studies of *Staphylococcus aureus* homoserine dehydrogenase. *Acta Cryst.* **F69**, 1216-1219.

Jaiswal, R.K., Suryaprabha, T., Manjeera, G. & Gopal, B. (2013). *Mycobacterium tuberculosis* RsdA provides a conformational rationale for selective regulation of  $\sigma$  factor activity by proteolysis. *Nucl. Acids Res.* **41**, 3414-3423.

Girish, T.S., Vivek, B., Colaco, M., Misquith, S. & Gopal, B. (2013). The crystal structure of an amidohydrolase SACOL0085 from methicillin resistant *Staphylococcus aureus* COL. *Acta Cryst.* **F69**, 103-108.

Rajavel, M., Kumar, P. & Gopal, B. (2013). Structural insights into the role of *Bacillus subtilis* YwfH (BacG) in tetrahydrotyrosine synthesis. *Acta Cryst.* **D69**, 324-332.

Joshi, A., Shukla, J.K., Jaiswal, R.K., Goutam, K. & Gopal, B. (2013). Conformational features of sigma factor/ anti-sigma factor complexes. in Biomolecular forms and functions edited by Manju Bansal and N Srinivasan. Singapore: IISc-WSPC publication. pp. 385-397.

Shukla, J.K. & Gopal, B. (2013). Peptidase V in The Handbook of Proteolytic Enzymes edited by Neil D Rawlings and Guy Salvesen. Elsevier Press. ISBN: 9780123822192.

Chandran, A.V. & Vijayan, M. (2013). Allosteric movements in eubacterial RecA. *Biophys. Rev.* **5**, 249-258.

Chandran, T., Sharma, A. & Vijayan, M. (2013). Generation of ligand specificity and modes of oligomerisation in  $\beta$ -Prism I fold lectins. *Advances in Proteins Chemistry and Structural Biology* Edited by Tatyana Karabencheva-Christova **92**, 135-178.

Sharma, A., Pohlentz, G., Bobbili, K.B., Jeyaprakash, A.A., Chandran, T., Mormann, M., Swamy, M.J. & Vijayan, M. (2013). The sequence and structure of snake gourd (*Trichosanthes anguina*) seed lectin, a three chain homologues of type II RIPs. *Acta Cryst.* **D69**, 1493-1503.

Paul, A., Mishra, A., Surolia, A. & Vijayan, M. (2013). Cloning, expression, purification, crystallization and preliminary X-ray studies of argininosuccinate lyase from *M. tuberculosis*. *Acta Cryst.* **F69**, 1422-1424.

Vijayan M. (2013). Form and function of proteins. Historical background and the Indian effort in macromolecular crystallography. *Natl. Acad. Sci. Lett.* **36**, 645-652.

Selvaraj, M., Govindan, A., Seshadri, A., Dubey, B., Varshney, U. & Vijayan, M. (2013). Molecular flexibility of *Mycobacterium tuberculosis* ribosome recycling factor and its functional consequences: An exploration involving mutants. *J. Biosci.* **38**, 845-855.

Barathy, D.V. & Suguna, K. (2013). Crystal structure of a putative aspartic proteinase domain of the *Mycobacterium tuberculosis* cell surface antigen PE\_PGRS16. *FEBS Open Bio.* **3**, 256-262.

Shetty, K.N., Latha, V.L., Rao, R.N., Nadimpalli, S.K. & Suguna, K. (2013). Affinity of a galactose-specific legume lectin from *Dolichos lablab* to adenine revealed by X-ray crystallography. *IUBMB Life* **65**, 633-644.

Kavyashree, M. & Sekar, K. (2013). Molecular dynamics perspective on the protein thermal stability: A case study using SAICAR synthetase. *J. Chem. Info. Model.* **53**, 2448-2461.

Chaudhary, S.K., Jeyakanthan, J. & Sekar, K. (2013). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of thymidylatekinase (TTHA1607) from *Thermus thermophilus* HB8. *Acta Cryst.* **F69**, 118-121.

Kavyashree, M., Kanaujia, S.P., Surekha, K., Jeyakanthan, J. & Sekar, K. (2013). Structure of SAICAR synthetase from *Pyrococcus horikoshii* OT3: Insights into thermal stability. *Int. J. Biol. Macromol.* **53**, 7-19.

Shaik, N.M., Misra, A., Singh, S., Fatangare, A.B., Ramakumar, S., Rawal, S.K. & Khan, B.M. (2013). Functional Characterisation, homology modeling and docking studies of beta-glucosidase responsible for bioactivation of cyanogenichydroxynitrileglucosides from *Leucaenaleucocephala* (subabul). *Mol. Biol. Rep.* **40**, 1351-1363.

Harijan, R.K., Kiema, T.R., Karjalainen, M.P., Janardan, N., Murthy, M.R.N., Weiss, M.S., Michels, P.A. & Wierenga, R.K. (2013). Crystal structures of SCP2-thiolases of Trypanosomatidae, human pathogens causing widespread tropical diseases: the importance for catalysis of the cysteine of the unique HDCF loop. *Biochem. J.* **455**, 119-130.

Kalyani, J.N., Bisht, S., Lakshmikanth, M., Murthy, M.R.N. & Savithri, H.S. (2013). Identification of key amino acid residues in the catalytic mechanism of diaminopropionate ammonialyase (DAPAL) from *S. typhimurium*. *FEBS J.* **280**, 5039-5051.

Chittori, S., Simanshu, D.K., Banerjee, S., Ambika, M.V., Mathivanan, S., Savithri, H.S. & Murthy, M.R.N. (2013). Mechanistic features of *Salmonella typhimurium* propionate kinase 2 (TdcD): Insights from kinetic and crystallographic studies. *Biochim. Biophys. Acta* **834**, 2036-2044.

Mathiharan, Y.K., Pappachan, A., Savithri, H.S. & Murthy, M.R.N. (2013). Dramatic structural changes resulting from the loss of a crucial hydrogen bond in the hinge region involved in C-terminal helix swapping in SurE: a survival protein from *Salmonella typhimurium*. *Plos One* **8**, e55978.

Govind, K., Murthy, M.R.N. & Savithri, H.S. (2013). Sobemovirus Peptidase. In Rawlings, ND and Salvesen, GS, Chapter 692 Eds: Handbook of Proteolytic Enzymes, 3<sup>rd</sup> Edition, pp 3141-3148.

Srivastava, S.K., Rajasree, K., Fasim, A., Arakere, G. & Gopal, B. (2014). Influence of the AgrC-AgrA complex in the response time of *Staphylococcus aureus* quorum sensing. *J. Bacteriology* **196**, 2876-2888.

Shukla, J.K., Gupta, R., Thakur, K.G., Gokhale, R.S. & Gopal, B. (2014). Structural basis for the redox sensitivity of the *Mycobacterium tuberculosis* SigK/RskA sigma/antisigma complex. *Acta Cryst.* **D70**, 1026-1036.

Ahuja, L.G. & Gopal, B. (2014). Bi-domain protein tyrosine Phosphatases reveal an evolutionary adaptation to optimize signal transduction. *Antiox. Redox Signal.* **20**, 2141-2159.

Guru Row, T.N. & Gopal, B. (2014). Crystals and Crystallography from Koh-i-Noor to IYCr. *J. Ind. Inst. Sci.* **94**, No 1. IISc Press. ISSN:0970-4140.

Arif, S.M., Sang, P.B., Varshney, U. & Vijayan, M. (2014). Crystallization and preliminary X-ray characterization of MutT2, MSMEG\_5148 from *Mycobacterium smegmatis*. *Acta Cryst.* **F70**, 190-192.

Williams, S.M., Chandran, A.V., Vijayabaskar, M.S., Roy, S., Balaram, H., Vishveshwara, S., Vijayan, M. & Chatterji, D. (2014). A histidine aspartate ionic lock gates the iron passage in miniferritins from *Mycobacterium smegmatis*. *J. Biol. Chem.* **289**, 11042-11058.

Patra, D., Mishra, P., Surolia, A. & Vijayan, M. (2014). Structure, interactions and evolutionary implications of a domain-swapped lectin dimer from *Mycobacterium smegmatis*. *Glycobiology* **24**, 956-965.

Abhinav, K.V. & Vijayan, M. (2014). Structural diversity and ligand specificity of lectins The Bangalore effort. *Pure & Appl. Chem.* **86**, 1335-1355.

Barathy, D., Mattoo, R., Visweswariah, S. & Suguna, K. (2014). New structural forms of a mycobacterial adenylyl cyclase Rv1625c. *IUCr Journal* **1**, 338-348.

Mir, M.A., Armugam, M., Mondal, S., Rajeswari, H.S., Ramakumar, S. & Ajitkumar, P. (2014). *Mycobacterium tuberculosis* cell division protein FtsE is an ATPase in dimeric form. *Protein J.* **34**, 35-47.



Bhowmick, T., Ghosh, S., Dixit, K., Ganesan, V., Ramagopal, U.A., Dey, D., Sarma, S.P., Ramakumar, S. & Nagaraja, V. (2014). Targeting *Mycobacterium tuberculosis* nucleoid-associated protein HU with structure-based inhibitors. *Nat. Commun.* **5**, 4124.

Verdaguer, N., Ferrero, D. & Murthy, M.R.N. (2014). Viruses and viral proteins. *IUCr Journal* **1**, 492-504.

Deka, G., Kalyani, J.N., Benazir, J.F., Savithri, H.S. & Murthy, M.R.N. (2014). Successful data recovery from oscillation photographs containing strong polycrystalline diffraction rings from an unknown small-molecule contaminant: preliminary structure solution of *Salmonella typhimurium* pyridoxal kinase (PdxK). *Acta Cryst.* **F70**, 526-529.

Banerjee, S., Agrawal, M.J., Mishra, D., Sharan, S., Balaram, H., Savithri, H.S. & Murthy, M.R.N. (2014). Structural and kinetic studies on Adenylosuccinate Lyase from *Mycobacterium smegmatis* and *Mycobacterium tuberculosis* provide new insights on the catalytic residues of the enzyme. *FEBS J.* **281**, 1642-1658.

Goutam, K., Gupta, A.K. & Gopal, B. (2015). Crystallization and preliminary X-ray diffraction studies of *Mycobacterium tuberculosis*  $\sigma^J$ . *Acta Cryst.* **F71**, 946-950.

Navratna, V., Reddy, G. & Gopal, B. (2015). Structural basis for the catalytic mechanism of homoserine dehydrogenase. *Acta Cryst.* **D71**, 1216-1225.

Abhinav, K.V., Kaushal, P.S., Swaminathan, C.P., Surolia, A. & Vijayan, M. (2015). Jacalin-carbohydrate interactions. Distortion of the ligand molecule as a determinant of affinity. *Acta Cryst.* **D71**, 324-331.

Chandran, A.V., Prabu, J.R., Nautiyal, A., Patil, K.N., Muniyappa, K. & Vijayan, M. (2015). Structural studies on *Mycobacterium tuberculosis* RecA: Molecular plasticity and interspecies variability. *J. Biosci.* **40**, 13-30.

Arif, S.M., Geethanandan, K., Mishra, P., Surolia, A., Varshney, U. & Vijayan, M. (2015). Structural plasticity in *Mycobacterium tuberculosis* uracil-DNA glycosylase (MtUng) and its functional implications. *Acta Cryst.* **D71**, 1514-1527.

Chandran, T., Sharma, A. & Vijayan, M. (2015). Structural studies on a non-toxic homologue of type II RIPs from bitter melon. Molecular basis of non-toxicity, conformational selection and glycan structure. *J. Biosci.* **40**, 929-941.

Raman, S., Singh, M., Tatu, U. & Suguna, K. (2015). First structural view of a peptide interacting with the nucleotide binding domain of heat shock protein 90. *Sci. Rep.* **5**, 17015.

Mani, N., Ramakrishna, K. & Suguna, K. (2015). Characterization of rice small heat shock proteins targeted to different cellular organelles. *Cell Stress Chaperones* **20**, 451-460.

Barathy, D.V., Bharambe, N.G., Syed, W., Zaveri, A., Visweswariah, S.S., Colaço, M., Misquith, S. & Suguna, K. (2015). Autoinhibitory mechanism and activity-related structural changes in a mycobacterial adenylyl cyclase. *J. Struct. Biol.* **190**, 304-313.

Raman, S. & Suguna, K. (2015). Functional characterization of heat-shock protein 90 from *Oryza sativa* and crystal structure of its N-terminal domain. *Acta Cryst.* **F71**, 688-696.

Kavyashree, M., Jeyakanthan, J. & Sekar, K. (2015). Catalytic pathway, substrate binding and stability in SAICAR synthetase: A Structure and molecular dynamics study. *J. Struct. Biol.* **191**, 22-31.

Mahanta, P., Bhardwaj, A., Kumar, K., Reddy, V.S. & Ramakumar, S. (2015). Structural insights into N-terminal to C-terminal interactions and implications for thermostability of a ( $\beta/\alpha$ ) 8-triosephosphate isomerase barrel enzyme. *FEBS J.* **282**, 3543-3555.

Bangera, M., Panigrahi, R., Sagurthi, S.R., Savithri, H.S. & Murthy, M.R.N. (2015). Structural and functional analysis of two universal stress proteins YdaA and YnaF from *Salmonella typhimurium*: Possible roles in microbial stress tolerance. *J. Struct. Biol.* **189**, 238-250.

## **Bhabha Atomic Research Centre, Mumbai**

Panchal, S.C., Pillai, B., Hosur, M.V. & Hosur, R.V. (2000). HIV-1 protease tethered heterodimer-pepstatinA complex. *Curr. Sci.* **79**, 1684-1695.

Kumar, V., Makde, R.D. & Mahajan, S.K. (2000). Structural Genomics: A perspective. *Solid State Physics (India)* **43**, 45-48.

Pillai, B., Kannan, K.K. & Hosur, M.V. (2001). 1.9 Å X-ray Study Shows Closed Flap Conformation in Crystals of Tethered HIV-1 Protease. *Proteins* **43**, 57-64.

Kumar, M., Kannan, K.K., Hosur, M.V., Neel, S., Bhavesh, N.S., Chatterjee, A., Mittal, R. & Hosur, R.V. (2002). Effects of remote mutation on the autolysis of HIV-1 PR: X-ray & NMR investigations. *Biochem. Biophys. Res. Commun.* **294**, 395-401.

Hosur, M.V., Kannan, K.K. & Kumar, M. (2002). Changes in active-site geometry through non-active-site C95A mutation in tethered HIV-1 protease heterodimer. *Acta Cryst.* **A58**, C-188.

Bagga, S., Hosur, M.V. & Batra, J.K. (2003). Cytotoxicity of ribosome-inactivating protein saporin is not mediated through  $\alpha$ 2-macroglobulin receptor. *FEBS Letts.* **541**, 16-20.

Kumar, M. & Hosur, M.V. (2003). Adaptability and flexibility of HIV-1 protease. *Eur. J. Biochem.* **270**, 1231-1239.

Makde, R.D., Kumar, V., Gupta, G.D., Jasti, J., Singh, T.P. & Mahajan, S.K. (2003). Expression, purification, crystallization and preliminary X-ray diffraction studies of recombinant class B non-specific acid phosphatase of *Salmonella typhimurium*. *Acta Cryst.* **D59**, 1849-1852.

- Makde, R.D., Kumar, V., Rao, A.S., Yadava, V.S. & Mahajan, S.K. (2003). Purification, crystallization and preliminary X-ray diffraction studies of recombinant class A non-specific acid phosphatase of *Salmonella typhimurium*. *Acta Cryst.* **D59**, 515-518.
- Pillai, B., Kannan, K.K., Bhat, S.V. & Hosur, M.V. (2004). Rapid screening for HIV-1 protease inhibitor-leads through X-ray diffraction. *Acta Cryst.* **D60**, 594-596.
- Prashar, V. & Hosur, M.V. (2004). 1.8 Å X-ray structure of C95M/C1095F double mutant of tethered HIV-1 protease dimer complexed with acetyl pepstatin. *Biochem. Biophys. Res. Commun.* **323**, 1229-1235.
- Kumar, M., Prashar, V., Mahale, S. & Hosur, M.V. (2005). Observation of a tetrahedral reaction intermediate in the structure of HIV-1 protease substrate complex. *Biochem. J.* **389**, 365–371.
- Das, A., Prashar, V., Mahale, S., Serre, L., Ferrer, J.L. & Hosur, M.V. (2006). X-ray structure of HIV-1 protease in situ product complex and observation of a low-barrier hydrogen bond between catalytic aspartates. *Proc. Natl. Acad. Sci. (USA)* **103**, 18464-18469.
- Das, A., Rao, D.R. & Hosur, M.V. (2007). X-ray Structure of HIV-1 Protease Tethered Dimer complexed to Ritonavir. *Prot. Pept. Letts.* **14**, 565 – 568.
- Makde, R.D., Gupta G.D., Mahajan, S.K. & Kumar, V. (2007). Structural and mutational analyses reveal the functional role of active-site Lys-154 and Asp-173 of *Salmonella typhimurium* AphA protein. *Arch. Biochem. Biophys.* **464**, 70-79.
- Makde, R.D., Mahajan, S.K. & Kumar, V. (2007). Structure and mutational analysis of the PhoN protein of *Salmonella typhimurium* provide insight into mechanistic details. *Biochemistry* **46**, 2079-2090.
- Gupta, G.D., Makde, R.D., Rao, B.J. & Kumar, V. (2008). Crystal structures of *Drosophila* mutant translin and characterization of translin variants reveal the structural plasticity of translin proteins. *FEBS Journal* **275**, 4235-4249.

Bihani, S., Das, A., Prashar, V., Ferrer, J.-L. & Hosur, M.V. (2008). X-ray structure of HIV-1 protease in situ product complex. *Proteins* **74**, 594-602.

Hosur, M.V. & Prashar, V. (2008). HIV-1 PR Crystallography at BARC. *Journal of Indian Inst. Sci.* **88**, 95-105.

Nilgiriwala, K.S., Bihani, S.C., Das, A., Prashar, V., Kumar, M., Ferrer, J.L., Apte, S.K. & Hosur, M.V. (2009). Crystallization and preliminary X-ray crystallographic analysis of PhoK, an extracellular alkaline phosphatase from *Sphingomonas* sp. BSAR-1 *Acta Cryst.* **F65**, 917-919.

Kumar, M., Dhanashree D. Jagtap, Mahale, S.D., Prashar, V., Kumar, A., Das, A., Bihani, S.C., Ferrer, J.-L., Hosur, M.V. & Ramanadham, M. (2009) Crystallization and preliminary X-ray diffraction analysis of human seminal plasma protein PSP9. *Acta Cryst.* **F65**, 389-391.

Bihani, S.C., Das, A., Prashar, V., Ferrer, J.-L. & Hosur, M.V. (2009). Resistance Mechanism revealed by Crystal Structures of unliganded nelfinavir-resistant HIV-1 protease non-active site mutants N88D and N88S. *Biochem. Biophys. Res. Commun.* **389**, 295–300.

Prashar, V., Das, A., Bihani, S., Ferrer, J.-L. & Hosur, M.V. (2009). Catalytic Water Co-Existing with a Product Peptide in the Active Site of HIV-1 Protease revealed by X-Ray Structure Analysis; *PLoS One* **4**, e7860. doi:10.1371/journal.pone.0007860.

Prashar, V., Bihani, S.C., Das, A., Rao, D.R. & Hosur, M.V. (2010). Insights into the mechanism of drug resistance: X-ray structure analysis of G48V/C95F tethered HIV-1 protease dimer/saquinavir complex. *Biochem. Biophys. Res. Commun.* **396**, 1018–1023.

Das, A., Mahale, S., Prashar, V., Bihani, S., Ferrer, J.-L. & Hosur, M.V. (2010) X-ray Snapshot of HIV-1 Protease in Action: Observation of Tetrahedral Intermediate and Short Ionic Hydrogen Bond SIHB with Catalytic Aspartate. *J. Am. Chem. Soc.* **132**, 6366–6373.

Hosur M.V. (2010). Combating HIV/AIDS: Contributions from Crystallography. Lead Article *Natl. Acad. Sci. (I) Lett.* **33**, 193 – 203.

Kumar, A., Jagtap, D.D., Mahale, S.D. & Kumar, M. (2010). Crystal structure of prostate secretory protein PSP94 shows an edge-to-edge association of two monomers to form a homodimer. *J. Mol. Biol.* **397**, 947-56.

Bihani, S.C., Das, A., Nilgiriwala, K.S., Prashar, V., Ferrer, J-L., Apte, S.K. & Hosur, M.V. (2011). X-ray structure reveals a new class and provides insight into evolution of alkaline phosphatases. *Plos One* **6**, e22767.

Das, A., Ferrer, J.-L. & Hosur, M.V. (2011). X-Ray snapshots of HIV-1 protease catalysis and substrate recognition. *Acta Cryst.* **A67**, C425.

Kumar, V. & Gupta, G.D. (2012). Low-resolution structure of drosophila translin. *FEBS Open Bio.* **2**, 37-46.

Hosur, M.V., Das, A., Hegde, S., Chitra, R., Chaudhary, R.R. & Hosur, R.V. (2013). Low Barrier Hydrogen Bonds in Proteins. *Cryst. Reviews* **19**, 2-50.

Bihani, S.C., Chakravarty, D. & Ballal, A. (2013). Purification, crystallization, and preliminary crystallographic analysis of KatB, a manganese catalase from *Anabaena* PCC7120. *Acta Cryst.* **F69**, 1299-1302.

Singh, P., Makde, R.D., Ghosh, S., Asthana, J., Kumar, V. & Panda, D. (2013). Assembly of *Bacillus subtilis* FtsA: effects of pH, ionic strength and nucleotides on FtsA assembly. *Int. J. Biol. Macromol.* **52**, 170-176.

Panicker, L., Misra, H.S. & Bihani, S.C. (2014). Purification, crystallization, and preliminary crystallographic investigation of FrnE, a disulfide oxidoreductase from *Deinococcus radiodurans*. *Acta Cryst.* **F70**, 1540-1542.

Kumar, A., Are, V.N. Ghosh, B., Agrawal, U., Jamdar, S.N., Makde, R.D. & Sharma, S.M. (2014). Crystallization and preliminary X-ray diffraction analysis of Xaa-Pro dipeptidase from *Xanthomonas campestris*. *Acta Cryst.* **F70**, 1268-1271.

Are, V.N., Ghosh, B., Kumar, A. Yadav, P., Bhatnagar, D., Jamdar, S.N. & Makde, R.D. (2014). Expression, purification, crystallization and preliminary X-ray diffraction analysis of acylpeptide hydrolase from *Deinococcus radiodurans*. *Acta Cryst.* **F70**, 1292-1295.

Goyal, V.D., Yadav, P., Kumar, A., Ghosh, B. & Makde R.D. (2014). Crystallization and preliminary X-ray crystallographic analysis of an artificial molten-globular-like triosephosphate isomerase protein of mixed phylogenetic origin. *Acta Cryst.* **F70**, 1521-1525.

Prashar, V., Bihani, S.C., Ferrer, J.-L. & Hosur, M.V. (2015). Structural Basis of Why Nelfinavir-Resistant D30N mutant of HIV-1 protease remains susceptible to saquinavir. *Chemical Biology & Drug Design* **86**, 302-308.

Raskar, T., Das, A. & Hosur, M. V. (2015). Drug resistance: Crystallography of drug-resistant HIV-1 protease mutant. *J. Biomol. Struct. Dyn.* **33**, 124.

Sonani, R.R., Gupta, G.D., Madamwar, D. & Kumar V. (2015). Crystal structure of allophycocyanin from marine cyanobacterium *Phormidium* sp. A09DM. *Plos One* **10**, e0124580.

Sonani, R.R., Sharma, M., Gupta, G.D., Kumar, V. & Madamwar, D. (2015). Phormidium phycoerythrin forms hexamers in crystals: a preliminary crystallographic study. *Acta Cryst.* **F71**, 998-1004.

Jamdar, S.N., Are, V.N., Navamani, M., Kumar, S., Nagar, V. & Makde. R.D. (2015). The members of M20D peptidase subfamily from *Burkholderia cepacia*, *Deinococcus radiodurans* and *Staphylococcus aureus* (HmrA) are carboxydipeptidases, primarily specific for Met-X dipeptides. *Arch Biochem. Biophys.* **587**, 18-30.

## Saha Institute of Nuclear Physics, Kolkata

Mukhopadhyay, D. (2000). The Molecular Evolutionary History of a Winged Bean  $\alpha$ -Chymotrypsin Inhibitor and Modeling of its Mutations Through Structural Analyses. *J. Mol. Evol.* **50**, 214-233.

Ravichandran, S., Dasgupta, J., Chakrabarti, C., Ghosh, S., Singh, M. & Dattagupta, J.K. (2001). The role of Asn 14 in the stability and conformation of the reactive-site loop of winged bean chymotrypsin inhibitor : Crystal structures of two point mutants Asn14 $\rightarrow$  Lys and Asn14  $\rightarrow$  Asp. *Protein Eng.* **14**, 349-357.

Choudhury, D., Guha Thakurta, P., Dasgupta, R., Sen, U., Biswas, S., Chakrabarti, C. & Dattagupta, J.K. (2002). Purification and Preliminary X-ray Studies on Hen Serrotransferrin in Apo- and Holo- form. *Biochem. Biophys. Res. Commun.* **295**, 125-128.

Dattagupta, J.K. (2002). Structure and function of a few plant proteins. *Acta Cryst.* **A58**, C-98.

Banerjee, R., Dutta, M., Sen, M. & Datta, A.K. (2002). Crystallization and preliminary X-ray analysis of cyclophilin from *Leishmania donovani*. *Acta Cryst.* **D58**, 1846-1847.

Biswas, S., Chakrabarti, C., Kundu, S., Jagannadham, M.V. & Dattagupta, J.K. (2003). Proposed Amino Acid Sequence and the 1.63 Å X-ray Crystal Structure of a Plant Cysteine Protease, Ervatamin B : Some Insights into the Structural Basis of its Stability and Substrate Specificity. *Proteins* **51**, 489-497.

Dasgupta, J., Sen, U., Choudhury, D., Datta, P., Chakrabarti, A., Basu Chakrabarty, S., Chakrabarty, A. & Dattagupta, J.K. (2003). Crystallization and preliminary X-ray structural studies of Hemoglobin A2 and Hemoglobin E, isolated from the blood samples of Beta-thalassemic patients. *Biochem. Biophys. Res. Commun.* **303**, 619-623.



Guha Thakurta, P., Choudhury, D., Dasgupta, R. & Dattagupta, J.K. (2003). Structure of diferric hen serum transferrin at 2.8 Å resolution. *Acta. Cryst.* **D59**, 1773-1781.

Guha Thakurta, P., Biswas, S., Chakrabarti, C., Sundd, M., Jagannadham, M.V. & Dattagupta, J.K. (2004) Structural basis of the unusual stability and substrate specificity of ervatamin C, a plant cysteine protease from *Ervatamia coronaria*. *Biochemistry* **43**,1532-1540.

Guha Thakurta, P., Choudhury, D., Dasgupta, R. & Dattagupta, J.K. (2004). Tertiary structural changes associated with iron binding and release in hen serum transferrin: a crystallographic and spectroscopic study. *Biochem. Biophys. Res. Commun.* **316**, 1124-1131.

Sen, U., Dasgupta, J., Choudhury, D., Datta, P., Chakrabarti, A., Basu Chakrabarty, S., Chakrabarty, A. & Dattagupta, J.K. (2004). Crystal structures of HbA<sub>2</sub> and HbE and modeling of Hb δ<sub>4</sub>: interpretations of the thermal stability and the antisickling effect of HbA<sub>2</sub>. *Biochemistry* **43**, 12477-12488.

Banerjee, R., Datta, M., Sen, M. & Datta, A.K. (2004). Crystal structure of cyclophilin from *Leishmania donovani* at 3.5 Å resolution. *Curr. Sci.* **86**, 319-322.

Ghosh, R. & Chakrabarti, C. (2005). Crystallization and X-ray diffraction studies of NP24-I, an isoform of the Thaumatin-like protein from ripe tomato fruits. *Acta Cryst.* **F61**, 806-807.

Dattagupta, J.K., Sen, U., Dasgupta, J. & Khamrui, S. (2005). Role of a scaffold in the inhibitory process of a serine protease inhibitor. *Acta Cryst.* **A61**, C-226.

Khamrui, S., Dasgupta, J., Dattagupta, J.K. & Sen, U. (2005). Single mutation at P1 of a chymotrypsin inhibitor changes it to a trypsin inhibitor: X-ray structural (2.15Å) and biochemical basis. *Biochim. Biophys. Acta – Proteins & Proteomics.* **1752**, 65-72.

Sen, U., Biswas, S., Chakrabarti, C. & Dattagupta, J.K. (2005). Structure-function of a few plant proteins using X-ray crystallography. *Ind. J. Phys.* **6**, 50-66.

Chakraborty, S., Biswas, S., Chakrabarti, C. & Dattagupta, J.K. (2005). Crystallization and preliminary X-ray diffraction studies of a cysteine protease Ervatamin A from *Ervatamia coronaria*. *Acta Cryst.* **F61**, 562-564.

Dasgupta, J., Khamrui, S., Dattagupta, J.K. & Sen, U. (2006). Spacer Asn determines the fate of Kunitz (STI) inhibitors, as revealed by the structural and biochemical studies on WCI mutants. *Biochemistry* **45**, 6783-92.

Choudhury, R., Subhasree, Gomes, A., Gomes, A., Dattagupta, J.K. & Sen, U. (2006). Purification, crystallization and preliminary X-ray structural studies of a 7.2 kDa cytotoxin, isolated from the venom of *Daboia russelli russelli* of Viperidae family. *Acta Cryst.* **F62**, 292-294.

Banerjee, M., Majumder, P., Bhattacharyya, N.P., Dattagupta, J.K. & Sen, U. (2006). Cloning, expression, purification, crystallization and preliminary crystallographic analysis of pseudo death-effector domain of HIPPI, a molecular partner of Huntingtin-interacting protein HIP-1. *Acta Cryst.* **F62**, 1247-1250.

Ghosh, R., Dattagupta, J.K. & Biswas, S. (2007). A thermostable cysteine protease precursor from a tropical plant contains an unusual C-terminal propeptide: cDNA cloning, sequence comparison and molecular modeling studies. *Biochem. Biophys. Res. Commun.* **362**, 965-970.

Venugopal, V., Sen, B., Datta, A.K. & Banerjee, R. (2007) Structure of cyclophilin from *Leishmania donovani* at 1.97 Å resolution. *Acta Cryst.* **F63**, 60 - 64.

Sen, B., Venugopal, V., Chakrabarty, A., Datta, R., Dolai, S., Banerjee, R. & Datta, A.K. (2007) Amino acid residues of *Leishmania donovani* cyclophilin key to interaction with its adenosine kinase : biological implications. *Biochemistry* **46**, 7832 - 43.

Ghosh, R., Chakraborty, S., Chakrabarti, C., Dattagupta, J.K., Biswas, S. (2008). Structural insight into the substrate specificity and activity of Ervatamins: the papain-like cysteine proteases from a tropical plant *Ervatamia coronaria*. *FEBS Journal* **275**, 421-434.

Ghosh, R. & Chakrabarti, C. (2008). Crystal structure analysis of NP24-I: a thaumatin-like protein. *Planta* **228**, 883-890.

Venugopal, V., Datta, A., Bhattacharya, D., Dasgupta, D. & Banerjee, R. (2009) Structure of cyclophilin from *Leishmania donovani* bound to cyclosporin at 2.6 Å resolution: correlation between structure and thermodynamic data. *Acta Cryst.* **D65**, 1187-1195.

Choudhury, D., Biswas, S., Roy, S. & Dattagupta, J.K. (2010). Improving thermostability of Papain through structure-based protein engineering. *Protein Eng. Des. Sel.* **23**, 457-467.

Khamrui, S., Biswas, M., Sen, U. & Dasgupta, J. (2010). Cloning, overexpression, purification, crystallization and preliminary X-ray analysis of CheY3, a response regulator that directly interacts with the flagellar 'switch complex' in *Vibrio cholerae*. *Acta Cryst.* **F66**, 944-947.

Khamrui, S., Ranjan, A., Pani, B., Sen, R. & Sen, U. (2010). Crystallization and Preliminary X-ray Analysis of Psi, an inhibitor of bacterial transcription terminator, Rho. *Acta Cryst.* **F66**, 204-206.

Khamrui, S., Majumder, S., Dasgupta, J., Dattagupta, J.K. & Sen, U. (2010). Identification of a novel set of scaffolding residues that are instrumental for the inhibitory property of Kunitz (STI) inhibitors. *Protein Sci.* **19**, 593-602.

Roy, S., Choudhury, D., Chakrabarti, C., Biswas, S. & Dattagupta, J.K. (2011). Crystallization and preliminary X-ray diffraction studies of the precursor protein of a thermostable variant of papain. *Acta Cryst.* **F67**, 634–636.

Dutta, S., Choudhury, D., Dattagupta, J.K. & Biswas, S. (2011). C-terminal extension of a plant cysteine protease modulates proteolytic activity through a partial inhibitory mechanism. *FEBS Journal* **278**, 3012–3024.

Das, S., Dey, S., Roy, T. & Sen, U. (2011). Cloning, expression, purification, crystallization and preliminary X-ray analysis of the 31 kDa *Vibrio cholerae* heat-shock protein VcHsp31. *Acta Cryst.* **F67**, 1382-1385.

Das, S., Raychaudhuri, M., Sen, U. & Mukhopadhyay, D. (2011). Functional implications of the conformational switch in AICD peptide upon binding to Grb2-SH2 domain. *J. Mol. Biol.* **414**, 217-230.

Roy, S., Choudhury, D., Aich, P., Dattagupta, J.K. & Biswas, S. (2012). The structure of a thermostable mutant of pro-papain reveals its activation mechanism. *Acta Cryst.* **D68**, 1591-1603.

Basu, S., Bhattacharyya, D. & Banerjee, R. (2012). Self – complementarity within proteins : bridging the gap between binding and folding. *Biophys. J.* **102**, 2605-2614.

Paul, R., Nath, S. & Sen, U. (2012). Cloning, expression, purification, crystallization and preliminary X-ray analysis of a fructokinase from *Vibrio cholerae* O395. *Acta Cryst.* **F68**, 1564-1567.

Banerjee, R., Nath, S., Ranjan, A., Khamrui, S., Pani, B., Sen, R. & Sen, U. (2012). The first structure of polarity suppression protein, psu from enterobacteria phage p4, reveals a novel fold and a knotted dimer. *J. Biol. Chem.* **287**, 44667-44675.

Nath, S., Banerjee, R., Khamrui, S. & Sen, U. (2012). Cloning, purification, crystallization and preliminary X-ray analysis of two low-molecular-weight protein tyrosinephosphatases from *Vibrio cholerae*. *Acta Cryst.* **F68**, 1204-1208.

Das, S., Ghosh, S., Dasgupta, D., Sen, U. & Mukhopadhyay, D. (2012). Biophysical studies with AICD-47 reveals unique binding behavior characteristic of an unfolded domain. *Biochem. Biophys. Res. Commun.* **425**, 201-206.

Majumder, S., Khamrui, S., Dasgupta, J., Dattagupta, J.K. & Sen, U. (2012). Role of remote scaffolding residues in the inhibitory loop pre-organization, flexibility, rigidification and enzyme inhibition of serine protease inhibitors. *Biochim Biophys Acta.* **1824**, 882-890.

Mitra, P., Banerjee, M., Biswas, S., & Basu, S. (2013). Protein interactions of Merocyanine 540: spectroscopic and crystallographic studies with lysozyme as a model protein. *J. Photochem. Photobiol.* **121**, 46–56.

Dutta, S., Dattagupta, J.K. & Biswas, S. (2013). Enhancement of proteolytic activity of a thermostable papain-like protease by structure-based rational design. *Plos One* **8**, e62619.

Ranjan, A., Banerjee, R., Pani, B., Sen, U. & Sen R. (2013 ). The moonlighting function of bacteriophage P4 capsid protein, Psu, as a transcription antiterminator. *Bacteriophage* **3**, e25657.

Ranjan, A., Sharma, S., Banerjee, R., Sen, U. & Sen, R. (2013). Structural and mechanistic basis of anti-termination of Rho-dependent transcription termination by bacteriophage P4 capsid protein Psu. *Nucl. Acids Res.* **41**, 6839-6856.

Koley Seth, B., Ray A., Biswas, S. & Basu, S. (2014). Ni<sup>II</sup> - Schiff base complex as enzyme inhibitor of hen egg white lysozyme: a crystallographic and spectroscopic study. *Metallomics* **6**, 1737-1747.

Basu, S., Bhattacharyya, D. & Banerjee, R. (2014). Applications of complementarity plot in error detection and structure validation of proteins. *Indian J. of Biochem. Biophys.* **51**, 188-200.

Paul, R., Patra, D.M., Banerjee, R. & Sen, U. (2014). Crystallization and preliminary X-ray analysis of a ribokinase from *Vibrio cholerae* O395. *Acta Cryst.* **F70**, 1098-1102.

Nath, S., Banerjee, R. & Sen, U. (2014). Atomic resolution crystal structure of VcLMWPTP-1 from *Vibrio cholerae* O395: insights into a novel mode of dimerization in the low molecular weight protein tyrosine phosphatase family. *Biochem. Biophys. Res. Commun.* **450**, 390-395.

Nath, S., Banerjee, R. & Sen, U. (2014). A Novel 8-nm protein cage formed by *Vibrio cholerae* Acylphosphatase. *J. Mol. Biol.* **426**, 36-38.

Majumder, S., Khamrui, S., Banerjee, R., Bhowmik, P. & Sen, U. (2015). A conserved tryptophan (W91) at the barrel-lid junction modulates the packing and stability of Kunitz (STI) family of inhibitors. *Biochim. Biophys. Acta.* **1854**, 55-64.

Paul, R., Patra, M.D. & Sen, U. (2015). Crystal structure of apo and ligand bound *Vibrio cholerae* ribokinase (Vc-RK): role of monovalent cation induced activation and structural flexibility in sugar phosphorylation. *Adv. Exp. Med. Biol.* **842**, 293-307.

### **All India Institute of Medical Sciences, New Delhi**

Saxena, A.K., Betzel, C. & Singh, T.P. (2000). Structure of a ternary complex of proteinase K, mercury and a substrate analogue heptapeptide amide Ac-Pro-Ala-Pro-Phe-Ala-Ala-Ala-NH<sub>2</sub> at 2.3Å resolution. *Ind. J. Phys.* **74B**, 445-456.

Kumar, S., Sharma, A.K. & Singh, T.P. (2000). Metal substitution in lactoferrins: the crystal structure of manganese lactoferrin at 3.4Å resolution. *Ind. J. Phys.* **74B**, 103-108.

Karthikeyan, S., Yadav, S., Paramasivam, M., Srinivasan, A. & Singh, T.P. (2000). Structure of buffalo lactoferrin at 3.3Å resolution at 277K. *Acta Cryst.* **D56**, 684-689.

Gourinath, S., Alam, N., Srinivasan, A., Betzel, C. & Singh, T.P. (2000). Structure of the bifunctional inhibitor of trypsin and  $\alpha$ -amylase from ragi seeds at 2.2 Å resolution. *Acta Cryst.* **D56**, 287-293.

Chandra, V., Kaur, P., Srinivasan, A. & Singh, T.P. (2000). Three-dimensional structure of a presynaptic neurotoxic phospholipase A<sub>2</sub> from *daboia russelli* pulchella at 2.4 Å resolution. *J. Mol. Biol.* **296**, 1117-1126.

Sharma, S., Kumar, P., Betzel, C. & Singh, T.P. (2001). Structure and Function of proteins involved in milk allergies. *J. Chromatogr.* **B756**, 183-187.

Singh, R.K., Gourinath, S., Sharma, S., Roy I., Gupta, M.N. & Singh, T.P. (2001). Enhancement of enzyme activity through three-phase partitioning : crystal structure of a modified serine proteinase at 1.5Å resolution. *Protein Eng.* **14**, 307-313.

Sharma, S., Tyagi, R., Gupta, M.N. & Singh, T.P. (2001). Enhancement of catalytic activity of enzymes by heating them in anhydrous organic solvents : three-dimensional structure of a modified serine proteinase at high resolution. *Ind. J. Biochem. Biophys.* **38**, 34-41.

Singh, G., Gourinath, S., Sharma, S., Paramasivam, M., Srinivasan, A. & Singh, T.P. (2001). Structure of a basic phospholipase A2 from *Bangarus Caeruleus* (Common krait:KPLA2) at 2.4Å resolution: identification and characterization of its pharmacological sites. *J. Mol. Biol.* **307**, 1049-1059.

Noetzel, C., Chandra, V., Rajashankar, K.R., Genov, N., Betzel, C. & Singh, T.P. (2001). Enzyme activity and inhibition of the neurotoxic complex vipoxin from the venom of *Vipera ammodytes meridionalis*. *Toxicon* **45**, 229-236.

Sharma, A.K., Kumar, S., Sharma, V., Nagpal, A., Singh, N., Tamboli, I., Mani, I., Raman, G. & Singh, T.P. (2001). Lactoferrin-melanin interaction and its possible implications in melanin polymerization: Crystal structure of the complex formed between mare lactoferrin and melanin monomers at 2.7Å resolution. *Proteins* **45**, 229-236.

Gourinath, S., Degenhardt, M., Eschenburg, S., Moore, K., Delucas, L.J., Betzel, C. & Singh, T.P. (2001). Mercury induced modifications in the stereochemistry of the active site through Cys-73 in a serine protease: crystal structure of the complex of a partially modified proteinase K with mercury at 1.8Å resolution. *Ind. J. Biochem. Biophys.* **38**, 298-302.

Alam, S., Gourinath, S., Dey, S., Srinivasan, A. & Singh, T.P. (2001). Substrate-inhibitor interactions in the kinetics of  $\alpha$ -amylase inhibition by ragi  $\alpha$ -amylase-trypsin inhibitor (RATI) and its various N-terminal fragments. *Biochemistry* **40**, 4299-4233.

Tomar, S., Yadav, S., Chandra, V., Kumar, P. & Singh, T.P. (2001). Purification, crystallization and preliminary crystallographic studies of distintegrin (schistatin) from saw-scaled venom (*Echis carinatus*). *Acta Cryst.* **D57**, 1669–1670.

Sharma, S., Jabeen, T., Singh, R.K., Bredehorst, R., Vogel, C.W., Betzel, C. & Singh, T.P. (2001). Structural studies of the cobra venom factor : isolation, purification, crystallization and preliminary crystallographic analysis. *Acta Cryst.* **D57**, 596-598.

Kumar, P., Yadav, S., Srinivasan, A., Bhatia, K.L. & Singh, T.P. (2001). A novel 40 kDa protein from goat mammary secretions : purification, crystallization and preliminary X-ray diffraction studies. *Acta Cryst.* **D57**, 1332-1333.

Kumar, S., Sharma, A.K., Paramsivam, M., Srinivasan, A. & Singh, T.P. (2001). Three-dimensional structure of a new form of mare lactoferrin in 70% PEG400 at 3.8Å resolution. *Ind. J. Biochem. Biophys.* **38**, 135-141.

Betzel, C., Gourinath, S., Kumar, P., Kaur, P., Perbandt, M., Eschenburg, S. & Singh, T.P. (2001). Structure of a serine protease proteinase K from *Tritirachium album* Limber at 0.98Å resolution. *Biochemistry* **40**, 3080-3088.

Khan, J.A., Kumar, P., Paramsivam, M., Yadav, R.S., Sahni, M.S., Sharma, S., Srinivasan, A. & Singh, T.P. (2001). Camel lactoferrin-A transferrin-cum-lactoferrin: crystal structure of camel apolactoferrin at 2.6Å resolution and structural basis of its dual role. *J. Mol. Biol.* **309**, 751-782.

Bhanumathi, S., Rajashankar, K.R., Noetzel, C., Aleksiev, B., Singh, T.P., Genov, N. & Betzel, Ch. (2001). Crystal structure of the neurotoxic complex vipoxin at 1.4Å resolution. *Acta Cryst.* **D57**, 1552-1559.

Chandra, V., Kaur, P., Jasti, J., Betzel, Ch. & Singh, T.P. (2001). Regulation of catalytic function by molecular association: Crystal structure of phospholipase A<sub>2</sub> from *Daboia russelli pulchella* at 1.9Å resolution. *Acta Cryst.* **D57**, 1793-1798.



Khan, J.A., Kumar, P., Srinivasan, A. & Singh, T.P. (2001). Formation of a protein intermediate and its trapping by the simultaneous crystallization process: Crystal structure of an iron-saturated tetrahedral intermediate in the  $\text{Fe}^{3+}$  binding pathway of camel lactoferrin at 2.7Å resolution. *J. Biol. Chem.* **276**, 36817-36823.

Khan, J.A., Kumar, P., Sharma, S., Mohanty, A.K., Jabeen, T., Paramasivam, M., Yadav, S., Srinivasan, A. & Singh, T.P. (2002). Mechanisms of iron-update and iron-release in lactoferrins. *Proc. Ind. Nat. Sci. Acad.* **B68**, 217-234.

Kumar, P., Khan, J.A., Yadav, S. & Singh, T.P. (2002). Crystal structure of equine apolactoferrin at 30°C provides further evidence of closed conformations of N- and C- lobes. *Acta Cryst.* **D58**, 225-232.

Kumar, P., Yadav, S. & Singh, T.P. (2002) Crystallization and structure determination of goat lactoferrin at 4.0 Å resolution : A new form of packing in lactoferrins with a high solvent content in crystals. *Ind. J. Biochem. Biophys.* **39**, 16-21.

Chandra, V., Jasti, J., Kaur, P., Betzel, Ch., Srinivasan, A. & Singh, T.P. (2002). First structural evidence of a specific inhibition of phospholipase  $A_2$  by  $\alpha$ -tocopherol (vitamin E) and its implications in inflammation: Crystal structure of russells viper-Phospholipase  $A_2$  in a complex with vitamin E at 1.7Å resolution. *J. Mol. Biol.* **320**, 215-222.

Chandra, V., Jasti, J., Kaur, P., Srinivasan, A., Betzel, Ch. & Singh, T.P. (2002). Structural basis of the mechanism of inhibitor for the synthesis of prostaglandins by a plant alkaloid aristolochic acid: Crystal structure of the complex formed between  $PLA_2$  and aristolochic acid at 1.7Å resolution. *Biochemistry* **41**, 10914-10919.

Chandra, V., Jasti, J., Kaur, P., Dey, S, Srinivasan, A., Betzel, Ch. & Singh, T.P. (2002). Design of specific peptide inhibitors of phospholipase  $A_2$ : Structure of a complex formed between Russell's viper phospholipase  $A_2$  and a designed peptide Leu-Ala-Ile-Tyr-Ser (LAIYS). *Acta Cryst.* **D58**, 1813-1819.

Chandra, V., Jasti, J., Kaur, P., Dey, S. Srinivasan, A., Betzel, Ch. & Singh, T.P. (2002). Design of specific peptides as inhibitors of phospholipase A<sub>2</sub>: Crystal structure of a complex formed between phospholipase A<sub>2</sub> and designed peptide Phe-Leu-Ser-Tyr-Lys at 1.8Å resolution. *J. Biol. Chem.* **277**, 18641-18647.

Paramasivam, M., Sarvanan, K., Uma, K., Sharma, S., Singh, T.P. & Srinivasan, A. (2002). Expression, purification and characterization of equine lactoferrin in *Pichia pastoris*. *J. Protein Exp. Purification* **26**, 28-34.

Noetzel, C., Chandra, V., Perbandt, M., Rajashankar, K.R., Singh, T.P., Aleksiev, B., Kalkura, N., Genov, N. & Betzel, Ch. (2002). Enzymatic activity and inhibitor of the neurotoxic complex vipoxin from the venom of *Vipera ammodytes meridionalis*. *Z. Naturforsch.* **57C**, 1078-1083.

Bhushan, A., Mishra, V., Verma, A.K., Yadav, S., Sharma, R.S., Babu, C.R. & Singh, T.P. (2002). Crystal structure of a ribosome inactivating viscumin from Indian viscumin album at 2.8 Å resolution. *Acta Cryst.* **A58**, C-288.

Mohanty, A.K., Singh, G., Paramasivam, M., Sharma, S., Yadav, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2002). Structure of novel glycoprotein (BP-39) from goat mammary gland expressed during non-lactating period. *Acta Cryst.* **A58**, C-307.

Kumar, J., Weber, W., Muendchau, S., Yadav, S., Bhaskar, S., Saravanan, K., Paramasivam, M., Sharma, S., Kaur, P., Bhushan, A., Srinivasan, A., Betzel, Ch. & Singh, T.P. (2003). Crystal Structure of human seminal diferric lactoferrin at 3.4Å resolution. *Ind. J. Biochem. Biophys.* **40**, 14-21.

Mohanty, A.K., Singh, G., Paramasivam, M., Sarvanan, K., Jabeen, T., Sharma, S., Yadav, S., Kaur, P., Kumar, P., Srinivasan, A. & Singh, T.P. (2003). Crystal structure of a new regulatory 40kDa mammary gland protein (MGP-40) involved in the metastases of patients with recurrent breast cancer. *J. Biol. Chem.* **278**, 14451-14460.

Sharma, S., Jasti, J., Kumar, J., Mohanty, A.K. & Singh, T.P. (2003). Crystal structure of a proteolytically generated functional monoferric C-lobe of bovine lactoferrin at 1.9Å resolution. *J. Mol. Biol.* **321**, 1286-1296.

Perbandt, M., Tsai, I-H., Fuchs, A., Bhanumathi, S., Rajashankar, K.R., Georgieva, D., Kalkura, N., Singh, T.P., Genov, N. & Betzel, Ch. (2003). Crystal structure of the heterodimeric neurotoxic complex viperatoxin F (RV-4/RV-7) from the venom of *vipera russelli formosensis* at 1.9 Å resolution. *Acta Cryst.* **D59**, 1679-1687.

Singh, R.K., Vikram, P., Makker, J., Jabeen, T., Sharma, S., Dey, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2003). Structure-based design of potent and selective inhibitors of phospholipase A<sub>2</sub>: Crystal Structure of the complex formed between phospholipase A<sub>2</sub> from *Naja naja sagittifera* and a designed peptide inhibitor at 1.9 Å resolution. *Biochemistry* **42**, 11701-11706.

Bilgrami, S., Tomar, S., Yadav, S., Kaur, P., Kumar, J., Jabeen, T., Sharma, S. & Singh, T.P. (2004). Crystal structure of Schistatin, a Disintegrin Homodimer from saw-scaled Viper (*Echis carinatus*) at 2.5 Å resolution. *J. Mol. Biol.* **341**, 829-837.

Singh, N., Jabeen, T., Sharma, S. & Singh, T.P. (2004). Crystal structure of the complex formed between Russell's viper PLA<sub>2</sub> and an anti-inflammatory agent oxyphenbutazone at 1.6 Å resolution. *Biochemistry* **43**, 14577-14583.

Jasti, J., Paramasivam, M., Srinivasan, A. & Singh, T.P. (2004). Structure of an acidic phospholipase A<sub>2</sub> from Indian saw-scaled viper (*Echis carinatus*) at 2.6 Å resolution reveals a novel intermolecular interaction. *Acta Cryst.* **D60**, 66-72.

Jasti, J., Paramasivam, M., Srinivasan, A. & Singh, T. P. (2004). Crystal structure of echicetin from *Echis carinatus* (Indian saw-scaled viper) at 2.4 Å resolution. *J. Mol. Biol.* **335**, 167-176.

Mishra, V., Sharma, R.S., Yadav, S., Babu, C.R. & Singh, T.P. (2004). Purification and characterization of four isoforms of Himalayan mistletoe ribosome inactivating protein from *Viscum album* having unique sugar affinities. *Arch. Biochem. Biophys.* **432**, 288-301.

Mishra, V., Ethayathullah, A.S., Sharma, R.S., Yadav, S., Krauspanhaar, R., Betzel, Ch., Babu, C.R. & Singh, T.P. (2004). Crystal structure of a novel ribosome inactivating protein from a semi-parasitic plant inhabiting north-western Himalayas. *Acta Cryst.* **D60**, 2295-2304.

Betzel, Ch., Singh, T.P. & Genov, N. (2004). Phospholipase A<sub>2</sub>: *Handbook of Metalloproteins*, Editors: A.Messerschmidt, W. Bode & M. Cygler, Vol. **3** pp. 677-691.

Jabeen, T., Singh, R.K., Sharma, S. & Singh, T.P. (2005). Structural studies on cobra venom factor(CVF), a complement activating protein:a new protocol for purification and crystallization and preliminary characterization of CVF. *Ind. J. Phys.* **6**, 67–76.

Singh, G., Gourinath, S., Sarvanan, K., Sharma, S., Bhanumathi, S., Betzel, Ch., Yadav, S., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of a carbohydrate induced homodimer of phospholipase A<sub>2</sub> from *Bangarus Caeruleus* at 2.1Å resolution. *J. Struc. Biol.* **149**, 264-276.

Singh, G., Gourinath, S., Sarvanan, K, Sharma, S., Bhanumathi, S., Betzel, Ch., Srinivasan, A. & Singh, T.P. (2005). Sequence-induced trimerization of phospholipase A<sub>2</sub>: structure of a trimeric isoform of PLA<sub>2</sub> from common krait (*Bangarus caeruleus*) at 2.5Å resolution. *Acta Cryst.* **F61**, 8–13.

Singh, G., Jasti, J., Sarvanan, K., Sharma, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of the complex formed between a group I phospholipase A<sub>2</sub> and a naturally occurring fatty acid at 2.7 Å resolution. *Protein Sci.* **14**, 395-400.

Singh, N., Jabeen, T., Sharma, S., Roy, I., Gupta, M.N., Bilgrami, S., Somvanshi, R.K., Dey, S., Perbandt, M., Betzel, Ch., Srinivasan, A. & Singh, T.P. (2005). Detection of native peptides as inhibitors of enzymes: Crystal structure of the complex formed between treated bovine α-chymotrypsin and an autocatalytically produced fragment, Ile-Val-Asn-Gly-Glu-Glu-Ala-Val-Pro-Gly-Ser-Trp-Pro-Trp, at 2.2 Å resolution. *FEBS Journal* **272**, 562-572.

Jabeen, T., Sharma, S., Singh, N., Singh, R.K., Verma, A.K., Paramasivam, M., Srinivasan, A. & Singh, T.P. (2005). Structure of the zinc-induced heterodimer of two calcium-free isoforms of phospholipase A2 from *Naja naja sagittifera* at 2.7 Å resolution. *Acta Cryst.* **D61**, 302-308.

Mikeska, R., Wacker, R., Arni, R., Singh, T.P., Mikhailov, A., Habdoulkhakov, A.G., Voelter, W. & Betzel, C. (2005). Mistletoe lectin I in complex with galactose and lactose reveals distinct sugar – binding properties. *Acta Cryst.* **F61**, 17–25.

Jabeen, T., Sharma, S., Singh, N., Singh, R.K., Verma, A.K., Paramasivam, M., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of a calcium – induced dimer of two isoforms of cobra phospholipase A2 at 1.6Å resolution. *Proteins* **59**, 856 – 863.

Kaur, P., Bilgrami, S., Yadav, S., Ethayathulla, A.S., Kumar, P., Sharma, S., Perbandt, M., Betzel, Ch. & Singh, T.P. (2005). Crystal structure of a disintegrin heterodimer from *Echis carinatus* at 1.9 Å resolution. *Acta Cryst.* **A61**, C-245.

Sharma, M., Kumar, S., Karthikeyan, S., Paramashivam, M., Sharma, S., Yadav, S., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of an acidic and highly potent neurotoxin from scorpion *Buthus tamulus* (red scorpion) at 2.2 Å resolution. *J. Struct. Biol.* **153**, 246-257.

Mishra, V., Bilgrami, S., Sharma, R.S., Kaur, P., Yadav, S., Krauspanhaar, R., Betzel, Ch., Voelter, W., Babu, C.R. & Singh, T.P. (2005). Crystal structure of the Himalayan mistletoe ribosome inactivating protein reveals the presence of a natural inhibitor and a new functionally active sugar-binding site. *J. Biol. Chem.* **280**, 20712-20721.

Jabeen, T., Sharma, S., Singh, N., Bhushan, A. & Singh, T.P. (2005). Structure of the zinc-saturated C- terminal half of bovine lactoferrin at 2.0 Å resolution. *Acta Cryst.* **D61**, 1107 – 1115.

Singh, R.K., Ethayathulla, A.S., Jabeen, T., Sharma, S., Kaur, P. & Singh, T.P. (2005). Aspirin induces its anti-inflammatory effects through its specific binding to phospholipase A2 : Crystal structure of the complex formed between phospholipase A2 and aspirin at 1.9 Å resolution. *J. Drug Target* **13**, 113–119.

Singh, R.K., Jabeen, T., Sharma, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of a novel phospholipase A2 from *Naja naja sagittifera* at 1.5 Å resolution. *Ind. J. Biochem. Biophys.* **42**, 1241 – 1248.

Balasubramanya, R., Chandra, V., Kaur, P. & Singh, T.P. (2005). Crystal structure of the complex of the secretory phospholipase A2 with a natural indole derivative, 2-carbamoylmethyl-5-propyl-octahydro-indol-7-yl-acetic acid at 1.8Å resolution. *Biochim. Biophys. Acta – Proteins & Proteomics* **1752**, 177-185.

Bilgrami, S., Kaur, P., Yadav, S., Sharma, S., Perbandt, M., Betzel Ch. & Singh, T.P. (2005). Crystal structure of the disintegrin heterodimer from saw-scaled viper (*Echis carinatus*) at 1.9 Å resolution. *Biochemistry* **44**, 11058-11066.

Srivastava, D.B., Kumar, J., Srivastava, P., Mandal, A., Jain, R., Jabeen, T., Singh, N., Sharma, S., Srinivasan, A. & Singh, T.P. (2005). Clinical proteomics: characterization and structural studies of new proteins from human body fluids and tissues. *Eur. Biophys. J.* **34**, 773.

Jabeen, T., Singh, N., Singh, R.K., Sharma, S., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of a novel phospholipase A2 from *Naja naja sagittifera* with a strong anticoagulant activity. *Toxicon* **46**, 865-875.

Jabeen, T., Singh, N., Singh, R.K., Sharma, S., Somvanshi, R.K., Dey, S. & Singh, T.P. (2005). Non-steroidal anti-inflammatory drugs as potent inhibitors of phospholipase A2: Crystal structure of the complex of phospholipase A2 with niflumic acid at 2.5 Å resolution. *Acta Cryst.* **D61**, 1579-1586.

Singh, R.K., Jabeen, T., Sharma, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2005). Crystal structure of a novel phospholipase A2 from *Naja naja sagittifera* at 1.5 Å resolution. *Ind. J. Biochem. Biophys.* **42**, 279-286.

Singh, R.K., Singh, N., Jabeen, T., Sharma, S., Dey, S., & Singh, T.P. (2005). Crystal structure of the complex of group I PLA2 with a group II - specific peptide Leu - Ala - Ile - Tyr - Ser (LAIYS) at 2.6 Å resolution. *J. Drug Target* **13**, 367-374.

Singh, N., Sarvanan, K., Paramasivam, M., Sharma, S., Singh, T.P. & Srinivasan, A. (2005). Purification and partial characterization of neurotoxins from red scorpion venom and cloning of toxin cDNAs. *Ind. J. Phys.* **6**, 77-86.

Singh, N., Jabeen, T., Sharma, S. & Singh, T.P. (2006). Specific binding of non-steroidal anti-inflammatory drugs (NSAIDs) to phospholipase A2: Crystal structure of the complex formed between phospholipase A2 and diclofenac at 2.7 Å resolution. *Acta Cryst.* **D62**, 410-416.

Jabeen, T., Singh N., Singh, R.K., Jasti, J., Sharma, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2006). Crystal structure of a heterodimer of phospholipase A2 from *Naja naja sagittifera* at 2.3 Å resolution reveals the presence of a new PLA2-like protein with a novel Cys32 – Cys49 disulfide bridge. *Proteins* **62**, 329-337.

Kumar, J., Ethayathulla, A.S., Srivastava, D.B., Singh, N., Sharma, S., Singh, S.B., Srinivasan, A., Yadav, M.P. & Singh, T.P. (2006). Crystal structure of a secretory signaling glycoprotein from bovine (SPC-40) at 2.1 Å resolution. *Acta Cryst.* **D62**, 953-963.

Singh, N., Jabeen, T., Pal, A., Sharma, S., Perbandt, M., Betzel, Ch. & Singh, T.P. (2006). Crystal structures of the complexes of a group IIA phospholipase A2 with two natural anti-inflammatory agents, anisic acid and atropine reveal their modes of binding. *Proteins* **63**, 386-395.

Sharma, M., Ethayathulla, A.S., Jabeen, T., Singh, N., Saravanan, K., Sharma, S., Yadav, S., Srinivasan, A. & Singh T.P. (2006). Crystal structure of an acidic and highly potent neurotoxin from scorpion *Buthus tamulus* (red scorpion) at 2.2 Å resolution. *J. Struct. Biol.* **155**, 52-62.

Srivastava, D.B., Ethayathulla, A.S., Kumar, J., Singh, N., Sharma, S., Das, U., Srinivasan, A. & Singh, T.P. (2006). Crystal structure of a secretory signalling glycoprotein from sheep at 2.0 Å resolution. *J. Struct. Biol.* **156**, 505-516.

Sherawat, M., Kaur, P., Perbandt, M., Betzel, Ch., Slusarchyk, W.A., Bisacchi, G.S., Chang, C., Jacobson, B.L., Einspahr, H.M. & Singh, T.P. (2007). Structure of the complex of trypsin with a highly potent synthetic inhibitor at 0.97 Å resolution. *Acta Cryst.* **D63**, 500-507.

Srivastava, D.B., Ethayathulla, A.S., Kumar, J., Somvanshi, R.K., Sharma, S., Dey, S. & Singh, T.P. (2007). Carbohydrate binding properties and carbohydrate induced conformational switch in sheep secretory glycoprotein (SPS-40): Crystal structures of four complexes of SPS-40 with chitin-like oligosaccharides. *J. Struct. Biol.* **158**, 255-268.

Kumar, J., Ethayathulla, A.S., Srivastava, D.B., Somvanshi, R.K., Singh, N., Bhushan, A., Sharma, S., Dey, S. & Singh, T.P. (2007). Carbohydrate-binding properties of goat secretory glycoprotein (SPG-40) and its functional implications: Crystal structures of the native glycoprotein and its four complexes with chitin-like oligosaccharides. *Acta Cryst.* **D63**, 437-446.

Ethayathulla, A.S., Srivastava, D.B., Kumar, J., Sarvanan, K., Bilgrami, S., Sharma, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2007). Structure of the buffalo secretory signaling glycoprotein at 2.8Å resolution. *Acta Cryst.* **F63**, 258-265.

Shee, C., Singh, T.P., Kumar, P. & Sharma, A.K. (2007). Crystallization and preliminary X-ray diffraction studies of *Murraya koenigii* trypsin inhibitor. *Acta Cryst.* **F63**, 318-319.

Meyer, A., Rypniewski, W., Celewicz, L., Erdmann, V.A., Voelter, W., Singh, T.P., Genov, N., Barciszewski, J. & Betzel, C. (2007). The mistletoe lectin I-phloretamide structure reveals a new function of plant lectins. *Biochem. Biophys. Res. Commun.* **364**, 195-200.

Ethayathulla, A.S., Bessho, Y., Shinkai, A., Padmanabhan, B., Singh, T.P., Kaur, P. & Yokoyama, S. (2008). Purification, crystallization and preliminary X-ray diffraction analysis of the putative ABC transporter ATP-binding protein from *Thermotoga maritima*. *Acta Cryst.* **F64**, 498-500.



Singh, A.K., Singh, N., Sharma, S., Singh, S.B., Kaur, P., Bhushan, A., Srinivasan, A. & Singh, T.P. (2008). Crystal structure of lactoperoxidase at 2.4 Å resolution. *J. Mol. Biol.* **376**, 1060-1075.

Hassan, M.I., Bilgrami, S., Kumar, V., Singh, N., Yadav, S., Kaur, P. & Singh, T.P. (2008). Crystal structure of the novel complex formed between zinc alpha2-glycoprotein (ZAG) and prolactin-inducible protein (PIP) from human seminal plasma. *J. Mol. Biol.* **384**, 663-762.

Sharma, P., Singh, N., Sinha, M., Sharma, S., Perbandt, M., Betzel, C., Kaur, P., Srinivasan, A. & Singh, T.P. (2008). Crystal structure of the peptidoglycan recognition protein at 1.8 Å resolution reveals dual strategy to combat infection through two independent functional homodimers. *J. Mol. Biol.* **378**, 921-930.

Sharma, P., Singh, N., Sinha, M., Sharma, S., Perbandt, M., Betzel, C., Kaur, P., Srinivasan, A. & Singh, T.P. (2009). Tryptophan as a three way switch in regulating the function of the secretory signaling glycoprotein (SPS-40) from mammary glands: Structure of SPS-40 complexed with 2-methylpentane-2,4-diol at 1.6 Å. *Acta Cryst.* **D65**, 375-378.

Mishra, P., Kumar, P., Ethayathullah, A.S., Singh, N., Sharma, S., Perbandt, M., Betzel, C., Kaur, P., Srinivasan, A., Bhakuni, V. & Singh, T.P. (2009). Hot spots in the polysaccharide binding site in hyaluronate lyase: Crystal structures of native phage-encoded hyaluronate lyase and its complexes with ascorbic acid and lactose. *FEBS Journal* **276**, 3392-3402.

Singh, N., Kumar, P., Kumar, S., Sharma, S., Mir, R., Kaur, P., Srinivasan, A. & Singh, T.P. (2009). Simultaneous inhibition of anti-coagulation and inflammation: crystal structure of phospholipase A2 complexed with indomethacin at 1.4 Å resolution reveals the presence of the new common ligand binding site. *J. Mol. Recognit.* **22**, 437-445.

Kumar, V., Roske, Y., Singh, N., Henemann, U., Singh, T.P. & Yadav, S. (2009). Purification and preliminary X-ray crystallographic studies of beta-microseminoprotein from human seminal plasma. *Acta Cryst.* **F65**, 518-521.

Kumar, S., Singh, N., Sinha, M., Sharma, S., Kaur, P., Srinivasan, A. & Singh, T.P. (2009). Isolation, purification, crystallization and preliminary crystallographic studies of amaryllin, a plant pathogenesis-related protein from *Amaryllis belladonna*. *Acta Cryst.* **F65**, 635-637.

Singh, A.K., Singh, N., Sharma, S., Shin, K., Takase, M., Kaur, P., Srinivasan, A. & Singh, T.P. (2009). Inhibition of lactoperoxidase by its own catalytic product: Crystal structure of the hypothiocyanate-inhibited bovine lactoperoxidase at 2.3 Å resolution. *Biophys. J.* **96**, 646-654.

Sheikh, I.A., Singh, A.K., Singh, N., Sinha, M., Singh, S.B., Bhushan, A., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2009). Structural evidence of substrate specificity in mammalian peroxidases: Structure of the thiocyanate complex with lactoperoxidase and its interactions at 2.4 Å resolution. *J. Biol. Chem.* **284**, 14849-14856.

Singh, A.K., Singh, N., Sinha, M., Bhushan, A., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2009). Binding modes of aromatic ligands to mammalian heme peroxidases with associated functional implications: Crystal structures of lactoperoxidase complexes with acetylsalicylic acid, salicylhydroxamic acid and benzylhydroxamic acid. *J. Biol. Chem.* **284**, 20311-20318.

Mir, R., Singh, N., Vikram, G., Kumar, R.P., Sinha, M., Bhushan, A., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2009). Structural basis of the prevention of NSAID-induced damage of the gastrointestinal tract by C-terminal half (C-lobe) of bovine colostrums protein lactoferrin: Binding and structural studies of the C-lobe complexes with indomethacin, diclofenac, aspirin and ibuprofen. *Biophys. J.* **97**, 3178-3186.

Singh, A.K., Kumar, R.P., Pandey, N., Singh, N., Sinha, M., Bhushan, A., Kaur, P., Sharma, S. & Singh, T.P. (2009). Mode of binding of the tuberculosis prodrug isoniazid to peroxidases: Crystal structure of bovine lactoperoxidase with isoniazid at 2.7 Å resolution. *J. Biol. Chem.* **285**, 1569-1576.

Kumar, S., Singh, N., Sinha, M., Singh, S.B., Bhushan, A., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2010). Crystal structure determination and inhibition studies of a novel xylanase and alpha-amylase inhibitor protein (XAIP) from *Scadoxus multiflorus*. *FEBS Journal* **277**, 2868-2882.

Singh, A.K., Singh, N., Tiwari, A., Sinha, M., Kushwaha, G.S., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2010). First structural evidence of mode of diffusion of aromatic ligands and ligand induced closure of hydrophobic channel in heme peroxidases. *J. Biol. Inorg. Chem.* **15**, 1099-1107.

Mir, R., Kumar, R.P., Singh, N., Vikram, G., Sinha, M., Bhushan, A., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2010). Specific interactions of C-terminal half (C-lobe) of lactoferrin protein with edible sugars: Binding and structural studies with implications on diabetes. *Int. J. Biol. Macromol.* **47**, 50-59.

Soni, B.R., Hasan, M.I., Parmar, A., Ethayathulla, A.S., Kumar, R.P., Singh, N.K., Sinha, M., Kaur, P., Yadav, S., Sharma, S. & Singh, T.P. (2010). Structure of the 14kDa fragment of alpha-subunit of phycoerythrin from the starving cyanobacterium *Phormidium tenue*. *J. Struct. Biol.* **171**, 247-255.

Mir, R., Singh, N., Vikram, G., Sinha, M., Bhushan, A., Kaur, P., Srinivasan, A., Sharma, S. & Singh, T.P. (2010). Structural and binding studies of C-terminal half (C-lobe) of lactoferrin protein with COX-2-specific non-steroidal anti-inflammatory Drugs (NSAIDs). *Arch. Biochem. Biophys.* **500**, 196-202.

Kumar, S., Singh, N., Mishra, B., Dube, D., Sinha, M., Dey, S., Kaur, P., Sharma, S. & Singh, T.P. (2010). Modulation of inhibitory activity of xylanase – alpha-amylase inhibitor protein (XAIP): Binding studies and crystal structure determination of XAIP-II from *Scadoxus multiflorus* at 1.2 Å resolution. *BMC Struct. Biol.* **10**, 41-51.

Sharma, P., Dube, D., Singh, A., Mishra, B., Singh, N., Sinha, M., Dey, S., Kaur, P., Mitra, D.K., Sharma, S. & Singh, T.P. (2011). Structural basis of recognition of pathogen-associated molecular patterns and inhibition of proinflammatory cytokines by camel peptidoglycan recognition protein. *J. Biol. Chem.* **286**, 16208-16217.

Singh, A.K., Pandey, N., Sinha, M., Kaur, P., Sharma, S. & Singh, T.P. (2011). Structural evidence for the order of preference of inorganic substrates in mammalian heme peroxidases: crystal structure of the complex of lactoperoxidase with four inorganic substrates, SCN, I, Br and Cl. *Int. J. Biochem. Mol. Biol.* **2**, 328-339.

Sharma, P., Dube, D., Sinha, M., Mishra, B., Dey, S., Mal, G., Pathak, K.M., Kaur, P., Sharma, S. & Singh, T.P. (2011). Multiligand specificity of pathogen-associated molecular pattern-binding site in peptidoglycan recognition protein. *J. Biol. Chem.* **286**, 31723-31730.

Kaur, N., Gautam, A., Kumar, S., Singh, A., Singh, N., Sharma, S., Tiwari, R. & Singh, T.P. (2011). Biochemical studies and crystal structure determination of Dihydrodipicolinate synthase from *Pseudomonas aeruginosa*. *Int. J. Biol. Macromol.* **48**, 779-787.

Sharma, P., Dube, D., Sinha, M., Kaur, P., Sharma, S. & Singh, T.P. (2011). Structural basis of recognition of pathogen-associated molecular patterns by CPGRP-S. *Acta Cryst.* **A67**, C546.

Anand, V., Gautam, A., Sareen, D., Singh, T.P. & Tiwari, R. (2011). Molecular cloning, biochemical and biophysical studies of dihydrodipicolinate reductase of *Pseudomonas aeruginosa* PAO1. *Int. J. Integr. Biol.* **11**, 1450-1452.

Hariprasad, G., Kumar, M., Srinivasan, A., Kaur, P., Sharma, S. Singh, T.P. Jithesh, O. (2011). Structural analysis of a group III Glu-62 phospholipase A2 from the scorpion *Mesobuthus tumulus*: Targetting and reversible inhibition by native peptides. *Int. J. Biol. Macromol.* **48**, 423-431.

Das, S., Mishra, B., Gill, K., Ashraf, M.S., Singh, A.K., Sinha, M., Sharma, S., Xess, I., Dalal, K., Singh, T.P. & Dey, S. (2011). Isolation and characterization of novel protein with anti-fungal and anti-inflammatory properties from Aloe vera leaf gel. *Int. J. Biol. Macramol.* **48**, 38-43.

Chandra, D.N., Prasanth, G.K., Singh, N., Kumar, S., Jithesh, O., Sadasivan, C., Sharma, S., Singh, T.P. & Haridas, M. (2011). Identification of a novel and potent inhibitor of phospholipase A2 in a medicinal plant: Crystal structure at 1.93Å and surface Plasmon resonance analysis of phospholipase A2 complexed with berberine. *Biochim. Biophys. Acta* **1814**, 657-663.

Kaur, P., Pandey, N., Singh, A.K., Sinha, M., Sharma, S. & Singh T.P. (2011). First structural evidence for the order of preference of inorganic substrates by lactoperoxidase. *Acta Cryst.* **A67**, C768-C769.

Kang, T.S., Geogieva, D., Genov, N., Murakami, M., Sinha, M., Kumar, R.P., Kaur, P., Kumar, S., Dey, S., Sharma, S., Vrieling, A., Betzel, Ch., Takeda, S., Arni, R.K., Singh, T.P. & Kini, R.M. (2011). Enzymatic toxins from snake venom: Structural characterization and mechanism of catalysis. *FEBS Journal* **278**, 4544-4576.

Kumar, A., Singh, N., Yadav, R., Kumar, R.P., Sharma, S., Arora, A. & Singh, T.P. (2012). Crystal structure of peptidyl -tRNA hydrolase from *Mycobacterium smegmatis* reveals novel features related to enzyme dynamics. *Int. J. Biochem. Mol. Biol.* **3**, 58-69.

Kushwaha, G.S., Pandey, N., Sinha, M., Singh, S.B., Kaur, P., Sharma, S. & Singh, T.P. (2012). Crystal structures of a type-1 ribosome inactivating protein from *Momordica balsamina* in the bound and unbound states. *Biochim. Biophys. Acta* **1824**, 679-691.

Hariprasad, G., Kaur, P., Srinivasan, A., Singh, T.P. & Kumar, M. (2012). Structural analysis of secretory phospholipase A2 from *Clonorchis sinensis*: therapeutic implications for hepatic fibrosis. *J. Mol. Model.* **18**, 3139-3145.

Kumar, S., Tomar, A.K., Singh, S., Saraswat, M., Singh, S., Singh, T.P. & Yadav, S. (2012). Human serum albumin as a new interacting partner of prolactin inducible protein in human seminal plasma. *Int. J. Biol. Macromol.* **50**, 317-322.

Sharma, P., Yamini, S., Dube, D., Singh, A., Sinha, M., Dey, S., Mitra, D.K., Kaur, P., Sharma, S. & Singh, T.P. (2012). Structural studies on the molecular interactions between camel peptidoglycan recognition protein, CPGRP-S and peptidoglycan moieties, N-acetylglucosamine and N-acetylmuramic acid. *J. Biol. Chem.* **287**, 22153-22164.

Singh, A.K., Smith, M.L., Yamini, S., Ohlsson, P-I., Sinha, M., Kaur, P., Sharma, S., Paul, J.A.K., Singh, T.P. & Paul, K.G. (2012). Bovine carbonyl lactoperoxidase crystal structure at 2.0 Å resolution and infrared spectra as a function of pH. *Protein J.* **31**, 598-608.

Sharma, P., Dube, D., Sinha, M., Dey, S., Kaur, P., Sharma, S. & Singh, T.P. (2012). Structural basis of heparin binding to camel peptidoglycan recognition protein-S. *Int. J. Biochem. Mol. Biol.* **3**, 86-94.

Sharma, P., Dube, D., Sinha, M., Yadav, S., Kaur, P., Sharma, S. & Singh, T.P. (2013). Structural insights into the dual strategy of recognition by peptidoglycan recognition protein, PGRP-S: Structure of the ternary complex of PGRP-S with lipopolysaccharide and stearic acid: *Plos One* **8**, e53756.

Kushwaha, G.S., Yamini, S., Kumar, M., Sinha, M., Kaur, P., Sharma, S. & Singh, T.P. (2013). First structural evidence of the sequestration of mRNA cap structure by type 1 ribosome inactivating protein from *Momordica balsamina*. *Proteins* **81**, 896-905.

Sharma, P., Yamini, S., Dube, D., Singh, A., Mal, G., Pandey, N., Sinha, M., Singh, A.K., Dey, S., Kaur, P., Mitra, D.K., Sharma, S. & Singh, T.P. (2013). Structural basis of the binding of fatty acids peptidoglycan recognition protein PGRP-S. *Arch Biochem Biophys.* **529**, 1-10.

Kaushik, S., Singh, A., Sinha, M., Kaur, P., Sharma, S. & Singh, T.P. (2013). Cloning, expression, crystallization and preliminary crystallographic studies of dihydrodipicolinate reductase from *Acinetobacter baumannii*. *Acta Cryst.* **F69**, 653-656.

Kaur, P., Sharma, P., Yamini, S., Dube, D., Pandey, N., Sinha, M., Sharma, S. & Singh T.P. (2013). Molecular Basis of ligand recognition by mammalian peptidoglycan recognition protein. *Biophys. J.* **529**, 1-10.

Mir, R., Jallu, S. & Singh, T.P. (2013). The shikimate pathway: review of amino acid sequence, function and three-dimensional structures of the enzymes. *Crit. Rev. Microbiol.* **41**, 172-189.

Madhuprakash, J., Singh, A., Kumar, S., Sinha, S., Kaur, P., Sharma, S., Podile, A.R. & Singh, T.P. (2013). Structure of chitinase D from *Serratia proteamaculans* revealed the presence of a novel platform for hydrolysis and transglycosylation of chitin oligomers. *Int. J. Biochem. Mol. Biol.* **4**, 166-178.

Sharma, P., Dube, D., Sinha, M., Dey, S., Kaur, P., Sharma, S. & Singh, T.P. (2013). Structural basis of heparin binding to camel peptidoglycan recognition protein, PGRP-S. *Int. J. Biochem. Mol. Biol.* **4**, 215-216.

Sharma, S., Singh, A.K., Kaushik, S., Sinha, M., Singh, R.P., Sharma, P., Sirohi, S., Kaur, P. & Singh, T.P. (2013). Lactoperoxidase: Structural insights into the function, ligand binding and inhibition. *Int. J. Biochem. Mol. Biol.* **4**, 108-128.

Das, U., Pogenberg, V., Subhramanyam, U.K., Wilmanns, M., Gourinath, S. & Srinivasan A. (2014). Crystal structure of the VapBC-15 complex from *Mycobacterium tuberculosis* reveals a two-metal ion dependent PIN-domain ribonuclease and a variable mode of toxin-antitoxin assembly. *J. Struct. Biol.* **188**, 249-258.

Sharma, P., Dube, D., Yadav, S.P., Sinha, M., Kaur, P., Sharma, S. & Singh, T.P. (2014). Structural and functional studies of mammalian peptidoglycan recognition Protein. *J. Ind. Inst. Sc.* **94**, 109-117.

Rastogi, R., Singh, A., Pandey, S., Sinha, M., Bhushan, A., Kaur, P., Sharma, S. & Singh, T.P. (2014). Structure of the iron-free true C-terminal half of bovine lactoferrin produced by tryptic digestion and its functional significance in the gut. *FEBS Journal* **281**, 2871-2882.

Kaur, P., Yamini, S., Kushwaha, G.S., Sinha, M., Sharma, S. & Singh, T.P. (2014). Stacking interactions mediate recognition in ribosome inactivating proteins. *Acta Cryst.* **A70**, C1654.

Sharma, S., Kaushik, S., Sinha, M., Kushwaha, G.S., Singh, A., Sikarwar, J., Chaudhary, A., Gupta, A., Kaur, P., & Singh, T.P. (2014). Structural and functional insights into Pertidyl-tRNA hydrolase. *Biochim. Biophys. Acta* **1844**, 1279-1288.

Singh, R.P., Singh, A., Kushwaha, G.S., Singh, A.K., Kaur, P., Sharma, S. & Singh, T.P. (2015). Mode of binding of antithyroid drug propylthiouracil to mammalian heme peroxidase. *Acta Cryst.* **F71**, 304-310.

Shukla, P.K., Gautam, L., Sinha, M., Kaur, P., Sharma, S. & Singh, T.P. (2015). Structures and binding studies of the complexes of Phospholipase A2 with five potent inhibitors. *Biochim. Biophys. Acta - Prot & Proteom.* **1854**, 269-277.

Yamini, S., Pandey, S., Kaur, P., Sharma, S. & Singh, T.P. (2015). Binding and structural studies of type 1 ribosome inactivating protein from *Momodica balsamina* with cytosine, cytidine and cytidine diphosphate. *Biochem. Biophys. Rep.* **4**, 134-140.

Kumar, M., Mukherjee, J., Sinha, M., Kaur, P., Sharma, S., Gupta, M.N. & Singh, T.P. (2015). Enhancement of stability of a lipase by subjecting to three phase portioning (TPP): Structures of native and TPP-treated lipase from *Thermomyces lanuginose*. *Sustain. Chem Process.* **3**, 14.

Kumar, S., Singh, A., Yamini, S., Dey, S. & Singh, T.P. (2015). Crystal structure of Mg<sup>2+</sup> containing hemopexin-fold protein from Kabuli Chana (Chickpea-White, CW-25) at 2.45 Å resolution reveals its metal ion transport property. *Protein J.* **34**, 284-290.



Madhuprakash, J., Bobbili, K.B., El Gueddari, N.E., Moerschbacher, B.M., Singh, T.P., Swamy, M.J. & Podile, A.P. (2015). Substrate binding cleft orchestrates multiple activities of chitinase D from *Serratia proteamaculans*. *Nature Scientific Reports* **5**, 15657.

### **National Institute of Immunology, New Delhi**

Jain, D., Kaur, K.J., Sundaravadivel, B. & Salunke, D.M. (2000). Structural and functional consequences of peptide-carbohydrate mimicry: crystal structure of a carbohydrate mimicking peptide bound to concanavalin A. *J. Biol. Chem.* **275**, 16098-16102.

Nair, D.T., Singh, K., Sahu, N., Rao, K.V.S. & Salunke, D.M. (2000). Crystal structure of an antibody bound to an immunodominant peptide epitope: Novel features in peptide-antibody recognition. *J. Immunol.* **165**, 6949-6955.

Jain, D., Kaur, K.J. & Salunke, D.M. (2001). Plasticity in protein-peptide recognition: crystal structures of two different peptides bound to concanavalin A. *Biophys. J.* **80**, 2912-2921.

Jain, D., Kaur, K.J. & Salunke, D.M. (2001). Enhanced binding of a peptide ligand of concanavalin A arises from improved geometrical complementarity. *Biochemistry* **40**, 12059-12066.

Goel, M., Jain, D., Kaur, K., Kenoth, R., Maiya, B.G., Swamy, M.J. & Salunke, D.M. (2001). Functional equality in the absence of structural similarity: an added dimension to molecular mimicry. *J. Biol. Chem.* **276**, 39277-39281.

Jain, D., Nair, D.T., Swaminathan, G.J., Abraham, E.G., Nagaraju, J. & Salunke, D.M. (2001). Structure of the induced antibacterial protein from Tasar silkworm, *antheraea mylitta*: Implications to molecular evolution. *J. Biol. Chem.* **276**, 41377-41382.

Nair, D.T., Singh, K., Siddiqui, Z., Nayak, B.P., Rao, K.V.S. & Salunke, D.M. (2002). Epitope recognition by diverse antibodies suggests conformational convergence in an antibody response. *J. Immunol.* **168**, 2371-2382.

Goel, M., Anuradha, P., Kaur, K.J., Maiya, B.G., Swamy, M.J. & Salunke, D.M. (2004). Porphyrin binding to jacalin is facilitated by the inherent plasticity of the carbohydrate binding site: Novel mode of lectin-ligand interaction. *Acta Cryst.* **D60**, 281-288.

Chanana, V., Kaur, K.J. & Salunke, D.M. (2004). Purification, identification and preliminary crystallographic characterization of a novel seed protein from *Vigna unguiculata*. *Acta Cryst.* **D60**, 2100-2103.

Goel, M., Damai, R.S., Sethi, D.K., Kaur, K.J., Maiya, B.G., Swamy, M.J. & Salunke, D.M. (2005). Crystal Structures of PNA-Porphyrin Complex in the Presence and Absence of Lactose: Mapping the Conformational Changes on Lactose Binding, Interacting Surfaces and Supramolecular Aggregations. *Biochemistry* **44**, 5588-5596.

Qureshi, I.A., Sethi, D.K. & Salunke, D.M. (2006). Purification, identification and preliminary crystallographic studies on an allergenic protein from *Lathyrus sativus* *Acta Cryst.* **F62**, 869-872.

Sethi, D.K., Agarwal, A., Manivel, V., Rao, K.V.S. & Salunke, D.M. (2006). Differential epitope positioning within the germline antibody paratope enhances promiscuity in the primary immune response. *Immunity* **24**, 429-438.

Krishnan, L., Sahni, G., Kaur, K.J. & Salunke, D.M. (2008). Role of antibody paratope conformational flexibility in the manifestation of molecular mimicry. *Biophys J.* **94**, 1367-1376.

Gupta, P., Gaur, V. & Salunke, D.M. (2008) Purification, identification and preliminary crystallographic characterization of a 2S albumin seed protein from *Lens culinaris*. *Acta Cryst.* **F64**, 733-736.

Gaur, V., Sethi, D.K. & Salunke, D.M. (2008). Purification, identification and preliminary crystallographic studies of Pru du amandin, an allergenic protein from *Prunus dulcis*. *Acta Cryst.* **F64**, 32-35.

Lomash, S., Nagpal, S. & Salunke, D.M. (2010). An antibody as surrogate receptor reveals determinants of activity of an innate immune peptide antibiotic. *J. Biol. Chem.* **285**, 35750-35758.

Gaur, V., Qureshi, I.A., Singh, A., Chanana, V. & Salunke, D.M. (2010). Crystal structure and functional insights of hemopexin fold protein from *Lathyrus sativus*. *Plant Physiol.* **152**, 1842-1850.

Bhushan, J., Vyas, R., Sharma, T., Sehgal, D. & Biswal, B.K. (2011). Cloning, overexpression, purification, crystallization, and preliminary X-ray studies of SP\_0149, the substrate binding protein of an ABC transporter from *Streptococcus pneumoniae*. *Acta Cryst.* **F67**, 797-799.

Ahangar, M.S., Khandokar, Y., Nasir, N., Vyas, R. & Biswal, B.K. (2011). HisB from *Mycobacterium tuberculosis*: cloning, overexpression in *Mycobacterium smegmatis*, purification, crystallization and preliminary X-ray crystallographic analysis. *Acta Cryst.* **F67**, 1451-1456.

Nasir, N., Vyas, R., Chugh, C., Ahangar, M.S. & Biswal, B.K. (2012). Molecular cloning, overexpression, purification, crystallization and preliminary X-ray diffraction studies of histidinol phosphate aminotransferase (HisC2) from *Mycobacterium tuberculosis*. *Acta Cryst.* **F68**, 32-36.

Nasir, N., Vyas, R. & Biswal, B.K. (2013). Sample preparation, crystallization, and structure solution of HisC from *Mycobacterium tuberculosis*. *Acta Cryst.* **F69**, 445-448.

Ahangar, M.S., Vyas, R., Nasir, N. & Biswal, B.K. (2013). Structures of native, substrate-bound and inhibited forms of *Mycobacterium tuberculosis* imidazoleglycerol-phosphate dehydratase. *Acta Cryst.* **D69**, 2461-2467.

Saroj, D.C., Singh, K.H., Anant, A. & Biswal, B.K. (2014). Overexpression, purification, crystallization and structure determination of AspB, a putative aspartate aminotransferase from *Mycobacterium tuberculosis*. *Acta Cryst.* **F70**, 928-932.

### **University of Madras, Chennai**

Deepthi, S., Johnson, A., Sathish, R. & Pattabhi, V. (2000). Purification, crystallization and preliminary X-ray study of Hemoglobin from *Crocodilis palustins* and *Crocodilis porosus*. *Biochim.Biophys. Acta* **1480**, 384-387.

Johnson, A., Damodharan, L. & Pattabhi, V. (2001). Specificity pocket water network and its role in the activity of proteolytic enzymes: revealed by crystal structures of trypsin. *J. Biochem. Mol. Biol. Biophys.* **5**, 559-565.

Deepthi, S., Johnson, A. & Pattabhi, V. (2001). Structures of porcine  $\square$ -trypsin-detergent complexes: the stabilisation of proteins through hydrophilic binding of polydocanol. *Acta Cryst.* **D57**, 1506-1512.

Thiyagarajan, S., Satheesh Kumar, P., Rajan, S.S. & Gautham, N. (2002). The structure of d(TpGpCpGpCpA)<sub>2</sub> at 293K: Comparison of the effects of sequence and temperature. *Acta Cryst.* **D58**, 1381-1384.

Balasundaresan, D., Sugadev, R. & Ponnuswamy, M.N. (2002). Purification and Crystallization of coconut globulin Cocosin from *Cocous nucifera*. *Biophysica Biochemica Acta- Protein and proteomics* **1601**, 121-122.

Swarnalatha, V., Deepthi, S., Pattabhi, V. & Manoharan, P.T. (2003). Crystal structure of nickel reconstituted hemoglobin - A case for permanent T state hemoglobin. *Curr. Sci.* **84**, 179-187.

Syed Ibrahim, B. & Pattabhi, V. (2003). Crystal structure of trypsin-turkey egg white inhibitor complex. *Biochem. Biophys. Res. Commun.* **313**, 8-16.

Syed Ibrahim, B., Shamaladevi, N. & Pattabhi, V. (2004). Trypsin activity reduced by an autocatalytically produced nonapeptide. *J. Biomol. Struct. Dyn.* **21**, 737-744.

Thiyagarajan, S., Rajan, S.S. & Gautham, N. (2004). Cobalt hexammine induced tautomeric shift in Z-DNA: the structure of d(CGCGCA).d(TGCGCG) in two crystal forms. *Nucl. Acids Res.* **32**, 5945-5953.

Rajakannan, V., Yamane, T., Shirai, T., Kobayashi, T., Ito, S. & Velmurugan, D. (2004). Applications of ACORN to data at 1.45 Å resolution. *J. Synchrotron Rad.* **11**, 64-67.

Rajakannan, V., Selvanayagam, S., Yamane, T., Shirai, T., Kobayashi, T., Ito, S. & Velmurugan, D. (2004). The use of ACORN in solving 39.5 kDa macromolecule with 1.9 Å resolution laboratory source data. *J. Synchrotron Rad.* **11**, 358-362.

Balasundaresan, D., Saraboji, K. & Ponnuswamy, M.N. (2004). Purification and Crystallization of Haemoglobin from Donkey (*equus asinus*). *Biochem. Biophys. Res. Commun.* **313**, 466-467.

Kumarevel, T. S., Gopinath, S. C. B., Hilda, A., Gautham, N. & Ponnuswamy, M.N. (2005). Purification of lipase from *Cunninghamella verticillata* by stepwise precipitation and optimized conditions for crystallization. *W. J. Microbiol. Biotech.* **21**, 23-26.

Thiyagarajan, S., Rajan, S.S. & Gautham, N. (2005). Structure of d(TGCGCG).d(CGCGCA) in two crystal forms: effect of sequence and crystal packing in Z-DNA. *Acta Cryst.* **D61**, 1125–1131.

Thiyagarajan, S. & Gautham, N. (2005). Sequence-dependent Structural Effects in Left-handed DNA. *Crystallographic Reviews* **11**, 337-355.

Shamaladevi, N. & Pattabhi, V. (2005). Secondary binding site of trypsin: revealed by crystal structure of trypsin-peptide complex. *J. Biomol. Struct. Dyn.* **22**, 635-642.

Syed Ibrahim, B. & Pattabhi, V. (2005). Trypsin inhibition by a peptide hormone: Crystal structure of trypsin-vasopressin complex. *J. Mol. Biol.* **348**, 1191-1198.

- Bharanidharan, D. & Gautham, N. (2006). Principal Component Analysis (PCA) of DNA Oligonucleotide Structural Data. *Biophys. Biochem. Res. Commun.* **340**, 1229-1237.
- Gaiser, O.J., Piotukh, K., Ponnuswamy, M.N., Planas, A., Borriss, R. & Heinemann, U. (2006). Structural Basis for the Substrate Specificity of a Bacillus 1,3-1,4- $\beta$ -Glucanase. *J. Mol. Biol.* **357**, 1211-1225.
- Balasundaresan, D., Saraboji, K. & Ponnuswamy, M.N. (2006). Crystal structure of haemoglobin from donkey (*Equus asinus*) at 3Å resolution. *Biochimie.* **88**, 719-23.
- Neelagandan, K., Moorthy, P.S., Balasubramanian, M. & Ponnuswamy, M.N. (2007). Crystallization of sheep (*Ovis aries*) and goat (*Capra hircus*) haemoglobins under unbuffered low-salt conditions. *Acta Cryst.* **F63**, 887-9.
- Liu, Q., Karthe, P., Xu, Y., Ganesh, V.K., Sillanpää, J., Murray, B.E., Narayana, S.V. & Höök, M. (2007). The Enterococcus faecalis MSCRAMM ACE binds its ligand by the Collagen Hug model. *J. Biol. Chem.* **282**, 19629-19637.
- Bharanidharan, D., Thiyagarajan, S. & Gautham, N. (2007). Hexammineruthenium(III) ion interactions with Z-DNA. *Acta Cryst.* **F63**, 1008-1013.
- Arunachalam, J. & Gautham, N. (2008). Hydrophobic Clusters in Protein Structures. *Proteins* **71**, 2012–2025.
- Mandal, P.K., Venkadesh, S. & Gautham, N. (2008). Structural Variations in Z DNA. *Journal of Indian. Inst. Sci.* **88**, 73-93.
- Bowden, M.G., Heuck, A.P., Karthe, P., Kolosova, E., Damon Choe, Gurusiddappa, S., Narayana, S.V.L., Johnson, A.E. & Höök, M. (2008). Evidence for the “Dock, Lock and Latch” ligand Binding Mechanism of the Staphylococcal MSCRAMM SDRG. *J. Biol. Chem.* **283**, 638-647.

Anuradha, B. & Karthe, P. (2008). Purification, crystallization and preliminary X-ray analysis of urease from pigeon pea (*Cajanus cajan*). *Acta Cryst.* **F64**, 662-664.

Ragunathan, P., Kumarevel, T., Agari, Y., Shinkai, A., Kuramitsu, S., Yokoyama, S. & Karthe, P. (2008). Crystal structure of ST2348, a CBS domain protein, from hyperthermophilic archaeon *Sulfolobus tokodai*. *Biochem. Biophys. Res. Commun.* **375**, 124-128.

Sundaresan, S., Charles, P., Neelagandan, K. & Ponnuswamy, M.N. (2008). Purification, crystallization and preliminary analysis of hemoglobin from rabbit (*Oryctolagus cuniculus*). *Prot. Pept. Letts.* **15**, 318-9.

Charles, P., Devanathan, V., Anbu, P., Ponnuswamy, M.N., Kalaichelvan, P.T. & Hur, B.K. (2008). Purification, characterization and crystallization of an extracellular alkaline protease from *Aspergillus nidulans* HA-10. *J. Basic Microbiol.* **48**, 347-52.

Mizutani, H., Saraboji, K., Malathy Sony, S.M., Ponnuswamy, M.N., Kumarevel, T., Krishna Swamy, B.S., Simanshu, D.K., Murthy, M.R. & Kunishima, N. (2008). Systematic study on crystal-contact engineering of diphthine synthase: influence of mutations at crystal-packing regions on X-ray diffraction quality. *Acta Cryst.* **D64**, 1020-33.

Venkadesh, S., Mandal, P.K. & Gautham, N. (2009). The Structure of d(CACACG)-d(CGTGTG). *Acta Cryst.* **F65**, 8-13.

Balasubramanian, M., Moorthy, P.S., Neelagandan, K. & Ponnuswamy, M.N. (2009). Purification, crystallization and preliminary crystallographic study of haemoglobin from camel (*Camelus dromedarius*): a high oxygen-affinity lowland species. *Acta Cryst.* **F65**, 773-775.

Sundaresan, S.S., Ramesh, P., Sivakumar, K., Ponnuswamy, M.N. (2009). Purification, crystallization and preliminary X-ray analysis of haemoglobin from ostrich (*Struthio camelus*). *Acta Cryst.* **F65**, 681-683.

Moorthy, P.S., Neelagandan, K., Balasubramanian, M. & Ponnuswamy, M.N. (2009). Purification, crystallization and preliminary X-ray diffraction studies on goat (*Capra hircus*) hemoglobin - a low oxygen affinity species. *Prot. Pept. Letts.* **16**, 454-456.

Balasubramanian, M., Moorthy, P.S., Neelagandan, K. & Ponnuswamy, M.N. (2009). Purification, crystallization and preliminary crystallographic study of low oxygen-affinity haemoglobin from cat (*Felis silvestris catus*) in two different crystal forms. *Acta Cryst.* **F65**, 313-316.

Balasubramanian, M., Moorthy, P.S., Neelagandan, K. & Ponnuswamy, M.N. (2009). Preliminary Crystallographic Study of Hemoglobin from Buffalo (*Bubalus bubalis*): A Low Oxygen Affinity Species. *Prot. Pept. Letts.* **16**, 213-215.

Sathya Moorthy, P., Neelagandan, K., Balasubramanian, M. & Ponnuswamy, M.N. (2009). Purification, crystallization and preliminary X-ray diffraction studies on avian haemoglobin from pigeon (*Columba livia*). *Acta Cryst.* **F65**, 120-122.

Ragunathan, P., Spellerberg, B. & Karthe, P. (2009). Expression, purification, crystallization and preliminary crystallographic analysis of laminin-binding protein (Lmb) from *Streptococcus agalactiae*. *Acta Cryst.* **F65**, 492-494.

Balasubramanian, A. & Karthe, P. (2009). Purification, crystallization and preliminary X-ray analysis of urease from jack bean (*Canavalia ensiformis*). *Acta Cryst.* **F65**, 949-951.

Ragunathan, P., Spellerberg, B. & Karthe, P. (2009). Crystal structure of laminin-binding adhesin (Lmb) of *Streptococcus agalactiae*. *Acta Cryst.* **D65**, 1262-1269.

Devi, A.S., Ogawa, Y., Shimoji, Y. & Karthe, P. (2010). Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of the collagen - binding region of RspB from *Erysipelothrix rhusiopathiae*. *Acta Cryst.* **F66**, 156-159.



Anuradha, B. & Karthe, P. (2010). Crystal structure of the first plant urease from jack bean: 83 years of journey from its first crystal to molecular structure. *J. Mol. Biol.* **400**, 274-283.

Devi, A.S. & Karthe, P. (2010). Cloning, expression, purification and ligand binding studies of novel fibrinogen-binding protein FbsB of *Streptococcus agalactiae*. *Protein Expr. Purif.* **74**, 148-55.

Jeyakanthan, J., Drevland, R.M., Gayathri, D., Velmurugan, D., Kuramitsu, S., Shinkai, A., Yokoyama, S. & Graham, D.E. (2010). Substrate specificity determinants of the methanogen homoacetylase enzyme: structure and function of small subunit residues. *Biochemistry* **49**, 2687-2696.

Venkadesh, S., Mandal, P.K. & Gautham, N. (2011). The structure of a full turn of an A-DNA duplex d(CGCGGGTACCCGCG)<sub>2</sub>. *Biochem. Biophys. Res. Commun.* **407**, 307-312.

Venkadesh, S., Mandal, P.K. & Gautham, N. (2011). The sequence d(CGCGGGCCGC) self-assembles into a two dimensional rhombic DNA lattice. *Biochem. Biophys. Res. Commun.* **407**, 548-551.

Mandal, P.K., Venkadesh, S. & Gautham, N. (2011). Structure of d(CGCGGTACCCG)<sub>4</sub> as a four-way Holliday junction. *Acta Cryst.* **F67**, 1506-1510.

Ragunathan, P. & Karthe, P. (2011). Expression, purification and structural analysis of a fibrinogen receptor FbsA from *Streptococcus agalactiae*. *Protein J.* **30**, 159-166.

Sundaresan, R., Samen, U. & Karthe, P. (2011). Expression, purification, crystallization and preliminary X-ray diffraction studies of the human keratin 4-binding domain of serine-rich repeat protein 1 from *Streptococcus agalactiae*. *Acta Cryst.* **F67**, 1582-1585.

Vennila, K.N. & Velmurugan, D. (2011). In-house SAD phasing with surface-bound cerium ions. *Acta Cryst.* **F67**, 1662-1665.

Veluraja, K., Vennila, K.N., Umamakeshvari, K., Jasmine, A. & Velmurugan, D. (2011). Structural investigation of porcine stomach mucin by X-ray fiber diffraction and homology modeling. *Biochem. Biophys. Res. Commun.* **406**, 570-573.

Dhanasekaran, V. & Velmurugan, D. (2011). SAD phasing with in-house Cu K $\alpha$  radiation using barium as anomalous scatterer. *Ind. J. of Biochem. Biophys.* **48**, 399-405.

Venkadesh, S., Mandal, P.K. & Gautham, N. (2012). Crystallographic and spectroscopic studies of d(CCGGTACCGG). *Nucleos. Nucleot. Nucl.* **31**, 184-196.

Mandal, P.K., Venkadesh, S. & Gautham, N. (2012). Structure of the tetradecanucleotided(CCCCGGTACCGGG)<sub>2</sub> as an A-DNA duplex. *Acta Cryst.* **F68**, 393-399.

Chakraborty, A., Mandal, P.K. & Gautham, N. (2012). Structure of d(CCGGGACCGG)<sub>4</sub> as a four-way junction at 1.6 Å resolution: new insights into solvent interactions. *Acta Cryst.* **F68**, 1169-1174.

Mandal, P.K., Venkadesh, S. & Gautham, N. (2012). Interactions of Mn<sup>2+</sup> with a non-self-complementary Z-type DNA duplex. *Acta Cryst.* **F68**, 1420-1426.

Sundaresan, R., Rangunathan, P., Kuramitsu, S., Yokoyama, S., Kumarevel, T. & Karthe, P. (2012). The structure of putative N-acetyl glutamate kinase from *Thermus thermophilus* reveals an intermediate active site conformation of the enzyme. *Biochem. Biophys. Res. Commun.* **420**, 692-627.

Devi, A.S., Ogawa, Y., Shimoji, Y., Balakumar, S. & Karthe, P. (2012). Collagen adhesin-nanoparticle interaction impairs adhesin's ligand binding mechanism. *Biochim. Biophys. Acta* **1820**, 819-828.

Rangunathan, P., Raghunath, G., Kuramitsu, S., Yokoyama, S., Kumarevel, T. & Karthe, P. (2013). Crystallization, characterization and preliminary X-ray crystallographic analysis of GK2848, a putative carbonic anhydrase of *Geobacillus kaustophilus*. *Acta Cryst.* **F69**, 162-164.

Devi, A.S., Ebihara, A., Kuramitsu, S., Yokoyama, S., Kumarevel, T. & Karthe, P. (2013). Crystal structure of type I 3-Dehydroquinase dehydratase of *Aquifex aeolicus* suggests closing of active site flap is not essential for enzyme action. *Biochem. Biophys. Res. Commun.* **432**, 350–354.

Nagarajan, R., Hendrickx, A.P.A. & Karthe, P. (2013). Cloning, expression, purification, crystallization and preliminary crystallographic analysis of the N-terminal domain of Serine glutamate repeat A (SgrA) protein from *Enterococcus faecium*. *Acta Cryst.* **F69**, 441-444.

Balasubramanian, A., Durairajpandian, V., Elumalai, S., Mathivanan, N., Munirajan, A.K. & Karthe P. (2013). Structural and functional studies on urease from pigeon pea (*Cajanus cajan*). *Int. J. Biol. Macromol.* **58**, 301-309.

Ragunathan, P., Sridaran, D., Weigel, A., Shabayek, S., Spellerberg, B. & Karthe, P. (2013). Metal binding is critical for the folding and function of laminin binding protein, Lmb of *Streptococcus agalactiae*. *Plos One* **8**, e67517.

Vijayakumar, B. & Velmurugan, D. (2013). Use of europium ions for SAD phasing of lysozyme at the Cu K $\alpha$  wavelength. *Acta Cryst.* **F69**, 20-24.

Vijayakumar, B. & Velmurugan, D. (2013). Insight of Endo-1, 4-Xylanase II from *Trichoderma reesei*: conserved water-mediated H-Bond and Ion pairs interactions. *Protein J.* **32**, 649-656.

Dhanasekaran, V., Velmurugan, D., Kanaujia, S.P. & Sekar, K. (2013). Role of invariant water molecules and water-mediated ionic interactions in D-xylose isomerase from *Streptomyces rubiginosus*. *J. Biomol. Struct. Dyn.* **31**, 376-384.

Narayanan, S. & Velmurugan, D. (2013). Lab source anomalous scattering using Cr K $\alpha$  radiation. *Crystal Structure Theory and Applications* **2**, 57-64.

Narayanan, S., & Velmurugan, D. (2013). Ce-SAD Phasing of glucose isomerase and thermolysin using Cu K $\alpha$  radiation. *Crystal Structure Theory and Applications* **2**, 93-99.

Ramesh, P., Sundaresan, S.S., Sathya Moorthy, P., Balasubramanian, M. & Ponnuswamy, M.N. (2013). Structural studies of haemoglobin from pisces species shortfin mako shark (*Isurus oxyrinchus*) at 1.9 Å resolution. *J. Synchrotron Rad.* **20**, 843-847.

Mohamed Abubakkar, M., Saraboji, K. & Ponnuswamy, M.N. (2013). Purification, crystallization and preliminary crystallographic studies of haemoglobin from mongoose (*Helogale parvula*) in two different crystal forms induced by pH variation. *Acta Cryst.* **F69**, 126-129.

Purushothaman, M., Varghese, A., Mandal, P.K. & Gautham, N. (2014). Structure of d(CCCCGGTACCGGG)<sub>2</sub> at 1.65 Å resolution. *Acta Cryst.* **F70**, 860-865.

Beulin, D.S., Yamaguchi, M., Kawabata, S. & Karthe, P. (2014). Crystal structure of PfbA, a surface adhesin of *Streptococcus pneumoniae*, provides hints into its interaction with fibronectin. *Int. J. Biol. Macromol.* **64**, 168-173.

Sridharan, U., Ebihara, A., Kuramitsu, S., Yokoyama, S., Kumarevel, T. & Karthe, P. (2014). Crystal structure and *in silico* studies of dihydrodipicolinate synthase (DHDPS) from *Aquifex aeolicus*. *Extremophiles.* **18**, 973-985.

Nagarajan, R. & Karthe, P. (2014). Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of glyceraldehyde-3-phosphate dehydrogenase from *Streptococcus agalactiae* NEM316. *Acta Cryst.* **F70**, 938-941.

Ramakrishnan, C., Joshi, V., Joseph, J.M., Vishwanath, B.S & Velmurugan, D. (2014). Identification of novel inhibitors of *Daboia russelli* Phospholipase A2 using the combined pharmacophore modeling approach. *Chem. Biol. & Drug Des.* **84**, 379-392.

Thiruselvam, V., Sivaraman, P., Kumarevel, T. & Ponnuswamy, M.N. (2014). Revelation of endogenously bound Fe<sup>2+</sup> ions in the crystal structure of ferritin from *Escherichia coli*. *Biochem. Biophys. Res. Commun.* **453**, 636-641.

Mohamed Abubakkar, M.H., Saraboji, K. & Ponnuswamy, M.N. (2014). The crystal structure of oxy hemoglobin from high oxygen affinity bird emu (*Dromaius novaehollandiae*). *Gen. Physiol. Biophys.* **33**, 373-382.

Balasubramanian, M., Sathya Moorthy, P., Neelagandan, K., Ramadoss, R., Kolatkar, P.R. & Ponnuswamy, M.N. (2014). Structure of liganded T-state haemoglobin from cat (*Felis silvestris catus*), a low oxygen-affinity species, in two different crystal forms. *Acta Cryst.* **D70**, 1898-1906.

Ramesh, P., Sundaresan, S.S., Sathya Moorthy, P., Balasubramanian, M. & Ponnuswamy, M.N. (2014). Response to comments on structural studies of haemoglobin from pisces species shortfin mako shark (*Isurus oxyrinchus*) at 1.9 Å resolution. *J. Synchrotron Rad.* **21**, 834.

Kamariah, N., Ponnuraj, S.M., Moovarkumudalvan, B. & Ponnuswamy, M.N. (2014). Structural studies on a low oxygen affinity hemoglobin from mammalian species: sheep (*Ovis aries*). *Biochem. Biophys. Res. Commun.* **450**, 36-41.

Thiruselvam, V., Sivaraman, P., Kumarevel, T. & Ponnuswamy, M.N. (2014). Crystal structure of the single-stranded RNA binding protein HutP from *Geobacillus thermodenitrificans*. *Biochem. Biophys. Res. Commun.* **446**, 945-51.

Thirugnanasambandam, A., Karthik, S., Mandal, P.K. & Gautham, N. (2015). The novel double-folded structure of d(GCATGCATGC) : a possible model for triplet-repeat sequences. *Acta Cryst.* **D71**, 2119-2126.

Sundaresan, R., Samen, U. & Karthe, P. (2015). Structure of KRT4 binding domain of Srr-1 from *Streptococcus agalactiae* reveals a novel  $\beta$ -sheet complementation. *Int. J. Biol. Macromol.* **75**, 97-105.

Sundaresan, R., Ebihara, A., Kuramitsu, S., Yokoyama, S., Kumarevel, T. & Karthe, P. (2015). Crystal structure analysis of Ornithine Transcarbamylase from *Thermus thermophilus*-HB8 provides insights on the plasticity of the active site. *Biochem. Biophys. Res. Commun.* **465**, 174-179.

Ponnuvel, S., Subramanian, B. & Karthe, P. (2015). Conformational change results in loss of enzymatic activity of Jack bean urease on its interaction with silver nanoparticle. *Protein J.* **34**, 329-337.

Devi, S.K., Chichili, V.P.R., Jeyakanthan, J., Velmurugan, D. & Sivaraman, J. (2015). Structural basis for the hydrolysis of ATP by a nucleotide binding subunit of an amino acid ABC transporter from *Thermus thermophilus*. *J. Struct. Biol.* **190**, 367-372.

### **National Chemical Laboratory, Pune**

Rao, K.N., Suresh, C.G., Katre, U.V., Gaikwad, S.M. & Khan, M.I. (2004). Two orthorhombic crystal structures of a galactose specific lectin from *Artocarpus hirsuta* in complex with methyl-  $\alpha$ - D-galactose. *Acta Cryst.* **D60**, 1404-1412.

Kumar, R.S., Brannigan, J.A., Pundle, A.V., Prabhune, A., Dodson, G.G. & Suresh, C.G. (2004). Expression, purification, crystallization and preliminary X-ray diffraction analysis of conjugated bile salt hydrolase from *Bifidobacterium longum*. *Acta Cryst.* **D60**, 1665-1667.

Manish Chandra, P., Brannigan, J.A., Prabhune, A.A., Pundle, A.V., Turkenburg, J. P., Dodson, G.G. & Suresh, C.G. (2005). Cloning, preparation and preliminary crystallographic studies of penicillin V acylase autoproteolytic processing mutants. *Acta Cryst.* **F61**, 124-127.

Priya, R., Pundle, A.V., Prabhune, A.A., SivaRaman, H., Brannigan, J.A., Dodson, G.G. & Suresh, C.G. (2005). Cloning, purification, crystallization and preliminary structural studies of penicillin V acylase from *Bacillus subtilis*. *Acta Cryst.* **F61**, 680-683.

Katre, U.V., Gaikwad, S.M., Bhagyawant, S.S., Deshpande, U.D., Khan, M.I. & Suresh, C.G. (2005). Crystallization and preliminary X-ray characterization of a lectin from *Cicer arietinum* (chickpea). *Acta Cryst.* **F61**, 141-143.

Satyanarayana, L., Suresh, C.G., Patel, Mishra, S. & Ghosh, P.K. (2005). X-ray crystallographic studies on C-phycoyanins from cyanobacteria from different habitats: marine and freshwater. *Acta Cryst.* **F61**, 844-847.

Balakrishnan, H., Satyanarayana, L., Gaikwad, S.M. & Suresh, C.G. (2006). Structural and active site modification studies implicate Glu, Trp and Arg in the activity of xylanase from alkalophilic *Bacillus* sp. (NCL 87-6-10). *Enzyme Microb. Technol.* **39**, 67-73.

Dharkar, P.D., Anuradha, P., Gaikwad, S.M. & Suresh, C.G. (2006). Crystallization and preliminary characterization of a highly thermostable lectin from *Trichosanthes dioica* and comparison with other *Trichosanthes* lectins. *Acta Cryst.* **F62**, 205-209.

Suresh Kumar, R., Brannigan, J.A., Prabhune, A A., Pundle, A.V., Dodson, G.G., Dodson E.J. & Suresh, C.G. (2006). Structural and functional analysis of a conjugated bile salt hydrolase from *Bifidobacterium longum* reveals evolutionary relationship with penicillin V acylase. *J. Biol. Chem.* **281**, 32516-32525.

Rao, K.N. & Suresh, C.G. (2007). Bowman-Birk protease inhibitor from the seeds of *Vigna unguiculata* forms a highly stable dimeric structure. *Biochim. Biophys. Acta* **1774**, 1264-1273.

Katre, U.V. & Suresh, C.G. (2009). Features of homotetrameric molecular association in protein crystals. *Acta Cryst.* **D65**, 1-10.

Urvashi, S. & Suresh, C.G. (2011). Purification, crystallization and X-ray characterization of a Kunitz-type trypsin inhibitor protein from the seeds of chickpea (*Cicer arietinum*). *Acta Cryst.* **F67**, 714-717.

Varshney, N.K, Suresh Kumar, R., Ignatova, Z., Prabhune, A.A., Pundle, A.V., Dodson, E.J., & Suresh, C.G. (2012). Crystallization and X-ray crystal structure analysis of a thermostable penicillin G acylase from *Alcaligenes faecalis*. *Acta Cryst.* **F68**, 273-277.

Satyanarayana, L., Gaikwad, S.M., Balakrishnan, H. & Suresh, C.G. (2013). Crystal structure and fluorescence analysis of alkaline thermostable xylanase from *Bacillus* sp. (NCL 87-6-10). *Prot. Pept. Letts.* **20**, 125-132.

Varshney, N.K., Suresh Kumar, R., Brannigan, J. A., Wilkinson, A.J. & Suresh, C.G. (2013). Cloning, overexpression, crystallization and preliminary X-ray crystallographic analysis of a slow-processing mutant of penicillin G acylase from *Kluyvera citrophila*, *Acta Cryst.* **F69**, 925-929.

Urvashi, S., Katre, U.V. & Suresh, C.G. (2015). Crystal Structure of a plant albumin from *Cicer arietinum* (chickpea) possessing hemopexin fold and hemagglutination activity. *Planta* **241**, 1061-1073.

Chand, D., Varshney, N.K., Suresh Kumar, R., Panigrahi, P., Brannigan, J.A., Wilkinson, A.J. & Suresh, C.G. (2015). Structure mediation in substrate binding and post-translational processing of penicillin acylases: Information from mutant structures of *Kluyvera citrophila* penicillin G acylase. *Protein Sci.* **24**, 1660-1670.

Avinash, V.S., Panigrahi, P., Pundle, A.V., Suresh, C.G. & Suresh Kumar, R., (2015). Structural analysis of a penicillin V acylase from *Pectobacterium atrosepticum* confirms the importance of a Trp residue for activity and specificity. *J. Struct. Biol.* **193**, 85-94.

### **Madurai Kamaraj University, Madurai**

Baalaji, S., Acharya, R.K., Singh, T.P. & Krishnaswamy, S. (2005). High-resolution diffraction from crystals of a membrane protein complex: bacterial Outer Membrane Protein, OmpC with antibacterial eukaryotic protein, Lactoferrin. *Acta Cryst.* **F61**, 773-775.

Mancika, S., Peleg, Y., Unger, T., Albeck, S., Dym, O., Greenblatt, H.M., Bourenkov, G., Lamzin, V., Krishnaswamy, S. & Sussman, J.L. (2008). Crystal structure of YagE, a putative DHDPS-like protein from *Escherichia coli* K12. *Proteins* **71**, 2102-2108.



Santha, S., Eswari, P.J.P., Rosen, B.P. & Thiyagarajan, S. (2011). Purification, crystallization and preliminary X-ray diffraction studies of an arsenic repressor ArsR from *Corynebacterium glutamicum*. *Acta Cryst.* **F67**, 1616-1618.

Bhaskar, V., Kumar, M., Manicka, S., Tripathi, S., Venkatraman, A. & Krishnaswamy, S. (2011). Identification of biochemical and putative biological role of a xenolog from *Escherichia coli* using structural analysis. *Proteins* **79**, 1132–1142.

Balasubramaniam, D., Arockiasamy, A., Kumar, P.D., Sharma, A. & Krishnaswamy, S. (2012). Asymmetric pore occupancy in crystal structure of OmpF porin from *Salmonella typhi*. *J. Struct. Biol.* **178**, 233-244.

### **Bose Institute, Kolkata**

Datta, A.B., Chakrabarti, P., Subramanya, H.S. & Parrack, P. (2001). Purification and crystallization of CII: an unstable transcription activator from phage  $\lambda$ . *Biochem. Biophys. Res. Commun.* **288**, 997-1000.

Datta, A. B., Panjekar, S., Weiss, M.S., Chakrabarti, P. & Parrack, P. (2005). Structure of  $\lambda$  CII: implications for recognition of direct-repeat DNA by an unusual tetrameric organization. *Proc. Natl. Acad. Sci. (USA)* **102**, 11242-11247.

Chongdar, N., Dasgupta, S., Dutta, A.B. & Basu, G. (2014). Preliminary X-ray crystallographic analysis of an engineered glutamyl-tRNA synthetase from *Escherichia coli*. *Acta Cryst.* **F70**, 922-927.

Mukherjee, D., Datta, A.B. & Chakrabarti, P. (2014). Crystal structure of HlyU, the hemolysin gene transcription activator, from *Vibrio cholerae* N16961 and functional implications. *Biochim. Biophys. Acta* **1844**, 2346-2354.

Mondal, A., Chattopadhyaya, R., Datta, A.B. & Parrack, P. (2015). Crystallization and X-ray analysis of the transcription-activator protein C1 of bacteriophage P22 in complex with the PRE promoter element. *Acta Cryst.* **F71**, 1286–1291.

Chatterjee, T., Mukherjee, D., Banerjee, M., Chatterjee, B.K. & Chakrabarti, P. (2015). Crystal structure and activity of protein L-isoaspartyl-O-methyltransferase from *Vibrio cholerae*, and the effect of AdoHcy binding. *Arch. Biochem. Biophys.* **583**, 140-149.

### **Institute of Microbial Technology, Chandigarh**

Mande, S.C. & Sophia, M.E. (2000). Structural characterization of protein denaturant interactions: crystal structures of hen egg white lysozyme in complex with guanidinium chloride and DMSO. *Protein Eng.* **13**, 133-141.

Taneja, B. & Mande, S.C. (2001). Three-dimensional structure of *Mycobacterium tuberculosis* chaperonin-10 reveals a partially stable conformation of its mobile loop. *Curr. Sci.* **81**, 87-91.

Kishan, K.V.R., Newcomer, M.E., Rhodes, T.H. & S.D. Guillot, S.D. (2001). Effect of pH and salt bridges on structural assembly: molecular structures of the monomer and intertwined dimer of the Eps8 SH3 domain, *Protein Sci.* **10**, 1046-1055.

Agrawal, V., Sharma, R., Vohra, R.M. & Kishan, K.V.R. (2002). Crystallization and preliminary X-ray diffraction analysis of a thermostable D-hydantoinase from the mesophilic bacteria *Bacillus* sp. AR9. *Acta Cryst.* **D58**, 2175-2176.

Taneja, B. & Mande, S.C. (2002). Structure of *Mycobacterium tuberculosis* chaperonin-10 at 3.5 Å resolution. *Acta Cryst.* **D58**, 260-266.

Goulding, C.W., Apostol, M., Anderson, D.H., Gill, H.S., Smith, C.V., Kuo, M.R., Yang, J.K., Waldo, G.S., Suh, S.W., Chauhan, R., Kale, A., Bachhawat, N., Mande, S.C., Johnston, J.M., Lott, J.S., Baker, E.N., Arcus, V.L., Leys, D., McLean, K.J., Munro, A.W., Berendzen, J., Sharma, V., Park, M.S., Eisenberg, D., Sacchettini, J., Alber, T., Rupp, B., Jacobs, W., Jr. & Terwilliger, T.C. (2002). The TB Structural genomics consortium: providing a structural foundation for drug discovery. *Curr. Drug Targets- Infect. Dis.* **2**, 121- 141.

Kishan, K.V.R., Vohra, R.M., Ganesan, K., Agrawal, V., Sharma, V.M. & Sharma, R. (2005). Molecular structure of D-Hydantoinase from *Bacillus* sp. AR9: Evidence for Mercury inhibition. *J. Mol. Biol.* **347**, 95-105.

Vyas, R., Kumar, V., Panjekar, S., Karthikeyan, S., Kishan, K.V.R., Tewari, R. & Weiss, M. S. (2008). Purification, crystallization and preliminary X-ray diffraction analysis of aspartate semialdehyde dehydrogenase (Rv3708c) from *Mycobacterium tuberculosis*. *Acta Cryst.* **F64**, 167–170.

Kapoor, D., Kumar, V., Chandrayan, S. K., Ahmed, S., Sharma, S., Datt, M., Singh, B., Karthikeyan, S. & Guptasarma, P. (2008). Replacement of the active surface of a thermophile protein by that of a homologous mesophile protein through structure-guided ‘protein surface grafting’. *Biochim. Biophys. Acta* **1784**, 1771-1776.

Chauhan, A., Islam, Z., Jain, R.K. & Karthikeyan, S. (2009). Expression, purification, crystallization and preliminary X-ray analysis of maleylacetate reductase from *Burkholderia* sp. strain SJ98. *Acta Cryst.* **F65**, 1313–1316.

Kumar, P., Singh, M., Gautam, R. & Karthikeyan, S. (2010). Potential anti-bacterial drug target: Structural characterization of 3,4-dihydroxy-2-butanone-4-phosphate synthase from *Salmonella typhimurium* LT2. *Proteins* **78**, 3292-3303.

Kumar, P., Singh, M. & Karthikeyan, S. (2011). Crystal structure analysis of icosahedral lumazine synthase from *Salmonella typhimurium*, an antibacterial drug target. *Acta Cryst.* **D67**, 131-139.

Singh, M., Kumar, P. & Karthikeyan, S. (2011). Structural basis for pH dependent monomer-dimer transition of 3, 4-dihydroxy 2-butanone-4-phosphate synthase domain from *M. tuberculosis*. *J. Struc. Biol.* **174**, 374-384.

Vyas, R., Tewari, R., Weiss, M.S. & Karthikeyan, S. (2012). Structures of ternary complexes of aspartate semialdehyde dehydrogenase (Rv3708c) from *Mycobacterium tuberculosis* H37Rv. *Acta Cryst.* **D68**, 671-679.

Singh, M., Kumar, P., Yadav, S., Gautam, R., Sharma, N. & Karthikeyan, S. (2013). The crystal structure reveals the molecular mechanism of bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (Rv1415) from *Mycobacterium tuberculosis*. *Acta Cryst.* **D69**, 1633-1644.

Kaur, G., Dutta, D. & Thakur, K.G. (2014). Crystal structure of *Mycobacterium tuberculosis* CarD, an essential RNA polymerase binding protein, reveals a quasidomain-swapped dimeric structural architecture. *Proteins* **82**, 879-884.

Ravala, S.K., Singh, S., Yadav, G.S., Kumar, S., Karthikeyan, S. & Chakraborti, P.K. (2015). Evidence that phosphorylation of threonine in GT motif triggers activation of PknA, a eukaryotic-type Serine/Threonine kinase from *Mycobacterium tuberculosis*. *FEBS Journal* **282**, 1419-1431.

Islam, Z., Kumar, A., Singh, S., Salmon, L. & Karthikeyan, S. (2015). Structural Basis for Competitive Inhibition of 3,4-Dihydroxy-2-butanone-4-phosphate Synthase from *Vibrio cholera*. *J. Biol. Chem.* **290**, 11293-11308.

Yadav, S. & Karthikeyan, S. (2015). Structural and biochemical characterization of GTP cyclohydrolase II from *Helicobacter pylori* reveals its redox dependent catalytic activity. *J. Struct. Biol.* **192**, 100-115.

Singh, P.K., Solanki, V., Sharma, S., Thakur, K.G., Krishnan, B. & Korpole, S. (2015). The intramolecular disulfide-stapled structure of laterosporulin, a class IId bacteriocin, conceals a human defensin-like structural module. *FEBS Journal* **282**, 203-214.

### **Central Drug Research Institute, Lucknow**

Gupta, A., Kumar, P.H., Dineshkumar, T.K., Varshney, U. & Subramanya, H.S. (2001). Crystal structure of Rv2118c: an AdoMet dependent methyltransferase from *Mycobacterium tuberculosis* H37Rv. *J. Mol. Biol.* **312**, 381-391.

Trivedi, V., Gupta, A., Jala, V.R., Saravanan, P., Rao, J.G.S., Rao, A.N., Savithri, H.S. & Subramanya, H.S. (2002). Crystal structures of Binary and Ternary Complexes of Serine hydroxymethyltransferases from *Bacillus stearothermophilus*. *J. Biol. Chem.* **277**, 17161-17169.

Tripti, S., Sandeep, K. & Ravishankar, R. (2004). Cloning, expression, purification and crystallization of a transcriptional regulatory protein (rv3291c) from *Mycobacterium tuberculosis* H37rv. *Acta Cryst.* **D60**, 1874-1876.

Srivastava, S.K., Tripathi, R.P. & Ravishankar, R. (2005). NAD<sup>+</sup> -dependent DNA ligase (rv3014c) from *M. tuberculosis*: Crystal structure of the adenylation domain and identification of novel inhibitors. *J. Biol. Chem.* **280**, 30273-30281.

Tripathi, S.M. & Ravishankar, R. (2006). Over-expression, purification and crystallization of Lysine  $\epsilon$ -aminotransferase (Rv3290c) from *Mycobacterium tuberculosis* H37Rv. *Acta Cryst.* **F62**, 572-575.

Tripathi, S.M. & Ravishankar, R. (2006). Direct evidence for a glutamate switch necessary for substrate recognition: Crystal structures of Lysine  $\epsilon$ -aminotransferase (Rv3290c) from *Mycobacterium tuberculosis* H37Rv. *J. Mol. Biol.* **362**, 877-886.

Tripti, S. & Ravishankar, R. (2007). Mechanistic insights from the crystal structures of a feast/famine regulatory protein from *Mycobacterium tuberculosis* H37Rv. *Nucl. Acids Res.* **35**, 7324-7335.

Misra, G., Aggarwal, A., Mittal, S., Singh, Y. & Ravishankar, R. (2007). Purification, crystallization and preliminary structural analysis of nucleoside diphosphate kinase from *Bacillus anthracis* *Acta. Cryst.* **F63**, 1084-1086.

Tripathi, S.M. & Ravishankar, R. (2008). Over-expression, purification, crystallization and preliminary X-ray analysis of Rv2780 from *Mycobacterium tuberculosis* H37Rv *Acta. Cryst.* **F64**, 367-370.

Tripathi, S.M. & Ravishankar, R. (2008). Crystal structures of the *Mycobacterium tuberculosis* secretory antigen Alanine dehydrogenase (Rv2780) in *apo* and ternary complex forms captures 'open' and 'closed' enzyme conformations *Proteins* **72**, 1089-1095.

Misra, G., Aggarwal, A., Dube, D., Zaman, M.S., Singh, Y. & Ravishankar, R. (2009). Crystal structure of the Bacillus anthracis nucleoside diphosphate kinase and its characterization reveals an enzyme adapted to perform under stress conditions *Proteins* **76**, 496-506.

Shrivastava, T., Dey, A. & Ravishankar, R. (2009). Ligand induced structural transitions, mutational analysis and 'open' quaternary structure of the *M. tuberculosis* Feast/famine regulatory protein (Rv3291c) *J. Mol. Biol.* **392**, 1007-1019.

Singh, P., Yadav, G.P., Gupta, S., Tripathi, A.K., Ramachandran, R. & Tripathi, R.P. (2011). A novel dimer-tetramer transition captured by the crystal structure of HIV-1 Nef. *Plos One* **6**, e26629.

Kukshal, V., Khanam, T., Chopra, D., Singh, N., Sanyal, S. & Ramachandran, R. (2012). *M. tuberculosis* sliding  $\beta$ -Clamp does not interact directly with the NAD<sup>+</sup> - dependent DNA ligase. *Plos One* **7**, e35702.

Macwan, A.S., Kukshal, V., Srivastava, N., Javed, S., Kumar, A. & Ramachandran, R. (2012). Crystal structure of the Hexachlorocyclohexane dehydrochlorinase (LinA-type2): mutational analysis, thermostability & enantioselectivity. *Plos One* **7**, e50373.

Srivastava, S., Srivastava, V.K., Arora, A. & Pratap, J.V. (2012). Overexpression, purification, crystallization and preliminary X-ray analysis of putative molybdenum cofactor biosynthesis protein C (MoaC2) from *Mycobacterium tuberculosis* H37Rv. *Acta Cryst.* **F68**, 687-691.

Srivastava, V.K., Srivastava, S., Arora, A. & Pratap, J.V. (2013). Structural insights into putative molybdenum cofactor biosynthesis protein C (MoaC2) from *Mycobacterium tuberculosis* H37Rv. *Plos One* **8**, e58333.

Srivastava, V.K., Rana, A.K., Sahasrabudde, A.A., Gupta, C.M. & Pratap, J.V. (2013) Cloning, overexpression, purification and crystallization of the CRN12 coiled-coil domain from *Leishmania donovani*. *Acta Cryst.* **F69**, 535-539.

Dey, A. & Ramachandran, R. (2014). Cloning, overexpression, purification and preliminary X-ray analysis of a Feast/famine regulatory protein (Rv2779c) from *Mycobacterium tuberculosis* H37Rv. *Acta Cryst.* **F70**, 97-100.

Tripathi, S.M., Agarwal, A. & Ramachandran, R. (2015). Mutational analysis of *Mycobacterium tuberculosis* lysine  $\epsilon$ -aminotransferase and inhibitor co-crystal structures, reveals distinct binding modes. *Biochem. Biophys. Res. Commun.* **463**, 154-160.

### **International Centre for Genetic Engineering and Biotechnology, New Delhi**

Singh, S.K., Prasad Sati, S., Kongkasuriyachai, D., Kumar, N. & Sharma, A. (2002). Expression, purification, crystallization and preliminary X-ray analysis of the sexual stage-specific protein Pfg27 from *Plasmodium falciparum*. *Acta Cryst.* **D58**, 1868-1870.

Chopra, S., Singh, S.K., Sati, S.P., Ranganathan, A. & Sharma, A. (2002). Expression, purification, crystallization and preliminary X-ray analysis of the acyl carrier protein synthase (acpS) from *Mycobacterium tuberculosis*. *Acta Cryst.* **D58**, 179-181.

Sharma, A., Sharma, I., Kogkasuriyachai, D. & Kumar, N. (2003). Structure of a gametocyte protein essential for sexual development in *Plasmodium falciparum*. *Nat. Struct. Biol.* **10**, 197-203.

Singh, S., Hora, R., Belrhali, H., Chitnis, C., & Sharma, A. (2006). Structural basis for recognition of Duffy receptor by malaria parasite Duffy-binding-like domain. *Nature* **439**, 741-744.

Chandra, B.R., Yogavel, M. & Sharma, A. (2007). Structural Analysis of ABC-family Periplasmic Zinc Binding Protein Provides New Insights Into Mechanism of Ligand Uptake and Release. *J. Mol. Biol.* **367**, 970-982.

Yogavel, M., Gill, J., Mishra, P.C. & Sharma, A. (2007). SAD phasing of a structure based on co-crystallized iodides using in-house Cu  $K\alpha$  X-ray source: effects of data redundancy, completeness, resolution on structure solution. *Acta Cryst.* **D63**, 931-934.

Akhouri, R.R., Sharma, A., Malhotra, P. & Sharma, A. (2008). Role of *Plasmodium falciparum* thrombospondin-related anonymous protein in host-cell interactions. *Malaria Journal* **7**, 63-70.

Yogavel, M., Mishra P.C., Gill, J., Bhardwaj, P.K., Dutt, S., Kumar, S., Ahuja, P.S., & Sharma, A. (2008). Structure of a superoxide dismutase and implications for copper-ion chelation. *Acta Cryst.* **D64**, 892-901.

Sharma, A., Yogavel, M., Akhouri, R.R., Gill, J. & Sharma, A. (2008). Crystal structure of soluble domain of malaria sporozoite protein UIS3 in complex with lipid. *J. Biol. Chem.* **283**, 24077-24088.

Yogavel, M., Mishra, P.C., Gill, J., Bhardwaj, P.K., Dutt, S., Kumar, S., Ahuja, P.S. & Sharma, A. (2008). Structure of a superoxide dismutase and implications for copper-ion chelation. *Acta Cryst.* **D64**, 892-901.

Yogavel, M., Gill, J. & Sharma A. (2009). Iodide-SAD, SIR and SIRAS phasing for structure solution of a nucleosome assembly protein. *Acta Cryst.* **D65**, 618-622.

Gill, J., Chitnis, C.E. & Sharma, A. (2009). Structural insights into chondroitin sulphate A binding Duffy-binding-like domains from *Plasmodium falciparum*: implications for intervention strategies against placental malaria. *Malaria Journal* **8**, 67-73.



Gill, J., Yogavel, M., Kumar, A., Belrhali, H., Jain, S.K., Rug, M., Brown, M., Maier, A.G. & Sharma, A. (2009). Crystal structure of malaria parasite nucleosome assembly protein: distinct modes of protein localization and histone recognition. *J. Biol. Chem.* **284**, 10076-10087.

Yogavel, M., Khan, S., Bhat, T.K. & Sharma, A. (2010). Structure of D-tyrosyl-tRNA<sup>Tyr</sup> deacylase using home source Cu K $\alpha$  and moderate quality iodide-SAD data: structural polymorphism and HEPES bound enzyme states. *Acta Cryst.* **D66**, 584-592.

Bhatt, T.K., Yogavel, M., Wydau, S., Berwal, R. & Sharma, A. (2010). Ligand-bound structures Provide Atomic Snapshots for the Catalytic Mechanism of D-Amino Acid Deacylase. *J. Biol. Chem.* **285**, 5917-5930.

Yogavel, M., Nithya, N., Suzuki, A., Sugiyama, Y., Yamane, T., Velmurugan, D. & Sharma, A. (2010). Structural analysis of actinidin and a comparison of cadmium and sulfur anomalous signals from actinidin crystals measured using in-house copper and chromium-anode X-ray sources. *Acta Cryst.* **D66**, 1323-1333.

Bhatt, T.K., Khan, S., Dwivedi, V.P., Banday, M.M., Sharma, A., Chandele, A., Camacho, N., de Pouplana, L.R., Wu, Y., Craig, A.G., Mikkonen, A.T., Maier, A.G., Yogavel, M. & Sharma, A. (2011). Malaria parasite tyrosyl-tRNA synthetase secretion triggers pro-inflammatory responses. *Nat. Commun.* **2**, 530.

Sharma, A., Sharma, A., Dixit, S. & Sharma, A. (2011). Structural insights into thioredoxin-2: a component of malaria parasite protein secretion machinery. *Sci. Rep.* **1**, 179.

Sharma, A. & Sharma, A. (2011). Fatty acid induced remodeling within the Human liver fatty acid binding protein. *J. Biol. Chem.* **286**, 31924-31928.

Kumar, A., Kashyap, M., Bhavesh, N.S., Yogavel, M. & Sharma, A. (2012). Structural delineation of histone post-translation modifications in histone-nucleosome assembly protein complex. *J. Struct. Biol.* **180**, 1-9.

Sharma, A. Yogavel, M. & Sharma, A. (2012). Utility of anion and cation combinations for phasing of protein structures. *J. Struct.Funct. Genomics* **3**,135-143.

Khan, S., Garg, A., Sharma, A., Camacho, N., Picchioni, D., Saint-Léger, A., Ribas de Pouplana, L., Yogavel, M. & Sharma, A. (2013). An appended domain results in an unusual architecture for malaria parasite tryptophanyl-tRNA synthetase. *Plos One* **6**, e66224.

Khan, S., Garg, A., Camacho, N., Rooyen, V.J., Kumar, A.P., Belrhali, H., Ribas de Pouplana, L., Sharma, V. & Sharma, A. (2013). Structural analysis of malaria parasite lysyl-tRNA synthetase provides platform for drug development. *Acta Cryst.* **D69**, 785-95.

Pihlajamaa, T., Kajander, T., Knuuti, J., Horkka, K., Sharma, A. & Permi, P. (2013). Structure of *Plasmodium falciparum* thrombospondin-related anonymous protein (TRAP) A domain highlights distinct features in apicomplexan von willebrand factor A homologues. *Biochem. J.* **450**, 469-76.

Yogavel, M., Tripathi, T., Gupta, A., Banday, M.M., Rahlfs, S., Becker, K., Belrhali, H. & Sharma, A. (2014). Atomic resolution crystal structure of glutaredoxin 1 from *Plasmodium falciparum* and comparison with other glutaredoxins. *Acta Cryst.* **D70**, 91-100.

van Rooven, J.M., Murat, J.B., Hammoudi, P.M., Kieffer-Jaquinod, S., Coute, Y., Sharma, A., Pelloux, H., Belrhali, H. & Hakimi, M.A. (2014). Assembly of the novel five-component apicomplexan multi-aminoacyl-tRNA synthetase complex is driven by the hybrid scaffold protein Tg-p43. *Plos One* **9**, e89487.

Khan, S., Sharma, A., Belrhali, H., Yogavel, M. & Sharma, A. (2014). Structural basis of malaria parasite lysyl-tRNA synthetase inhibition by cladosporin. *J. Struct. Funct. Genomics* **15**, 63-71.

Jain, V., Kikuchi, H., Oshima, Y., Sharma, A. & Yogavel, M. (2014). Structural and functional analysis of the anti-malarial drug target prolyl-tRNA synthetase. *J. Struct. Funct. Genomics* **15**, 181-190.

Datt, M. & Sharma, A. (2014). Evolutionary and structural annotation of disease-associated mutations in human aminoacyl-tRNA synthetases. *MC Genomics* **15**, 1063.

Datt, M. & Sharma, A. (2014). Novel and unique domains in aminoacyl-tRNA synthetases from human fungal pathogens *Aspergillus niger*, *Candida albicans* and *Cryptococcus neoformans*. *MC Genomics* **15**, 1069.

Jain, V., Yogavel, M., Oshima, Y., Kikuchi, H., Touquet, B., Hakimi, M.A. & Sharma A. (2015). Structure of prolyl-tRNA synthetase-halofuginone complex provides basis for development of drugs against malaria and toxoplasmosis. *Structure* **23**, 819-829.

### **Centre for DNA Fingerprinting and Diagnostics, Hyderabad**

Terwilliger, T.C., Park, M.S., Waldo, G.S., Berendzen, J., Hung, L.-W., Kim, C.-Y., Smith, C.V., Sacchettini, J.C., Bellinzoni, M., Bossi, R., De Rossi, E., Mattevi, A., Milano, A., Riccardi, G., Rizzi, M., Roberts, M.M., Coker, A.R., Tormay, P., Fossati, G., Mascagni, P., Coates, A.R.M., Wood, S.P., Goulding, C.W., Apostol, M., Anderson, D. H., Gill, H.S., Eisenberg, D.S., Taneja, B., Mande, S., Pohl, E., Lamzin, V., Tucker, P., Wilmanns, M., Colovos, C., Meyer-Klaucke, W., Munro, A.W., McLean, K.J., Marshall, K.R., Leys, D., Yang, J.K., Yoon, H.-J., Lee, B.I., Lee, M.G., Kwak, J.E., Han, B.W., Lee, J.Y., Baek, S.-H., Suh, S.W., Komen, M.M., Arcus, V.M.L., Baker, E.N., Lott, J.S., Jacobs □ □ Jr., W., Alber, T. & Rupp, B. (2003). The TB Structural Genomics Consortium: A Resource for TB Biology. *Tuberculosis* **83**, 223- 249.

Akif, Mohd., Chauhan, R. & Mande, S.C. (2004). Expression, purification, crystallization and preliminary X-ray crystallographic studies of *Mycobacterium tuberculosis* thioredoxin reductase. *Acta Cryst.* **D60**, 777-779.

- Qamra, R. & Mande, S.C. (2004). Crystal Structure of the 65 kDa Heat Shock Protein, Chaperonin 60.2 of *Mycobacterium tuberculosis*. *J. Bacteriology* **186**, 8105-8113.
- Qamra, R., Prakash, P., Aruna, B., Hasnain, S.E. & S.C. Mande (2005). Crystallization and preliminary X-ray crystallographic studies of *Mycobacterium tuberculosis* chorismate mutase. *Acta cryst.* **F61**, 473-475.
- Qamra, R., Mande, S.C., Coates, A.R.M. & Henderson, B. (2005). The unusual chaperonins of *Mycobacterium tuberculosis*. *Tuberculosis* **85**, 385-94.
- Deshpande, A., Nimsadkar, S. & Mande, S.C. (2005). Effect of alcohols on protein hydration: Crystallographic analysis of hen egg white lysozyme in presence of alcohols. *Acta Cryst.* **D61**, 1005-1008.
- Akif, Mohd., Suhre, K., Verma, C. & Mande, S.C. (2005). Conformational flexibility of *M. tuberculosis* Thioredoxin reductase: Crystal Structure and Normal Mode Analysis. *Acta cryst.* **D61**, 1603- 1611.
- Vijaykrishnan, S., Qamra, R., Verma, C., Sen, R. & Mande, S.C. (2006). Cation mediated interplay of loops in Chaperonin-10. *J. Biomol. Struct. Dyn.* **23**, 365-376.
- Qamra, R., Prakash, P., Aruna, B., Hasnain, S.E. & Mande, S.C. (2006). The 2.15Å crystal structure of *M. tuberculosis* chorismate mutase reveals unexpected gene duplication, and suggests a role in host-pathogen interactions. *Biochemistry* **45**, 6997- 7005.
- Akif, Mohd., Akhter, Y., Hasnain, S.E. & Mande, S.C. (2006). Crystallization and preliminary X-ray crystallographic studies of *Mycobacterium tuberculosis* CRP/FNR family transcription regulator. *Acta cryst.* **F62**, 873-875.
- Kumar, P., Issac, B., Dodson, E.J., Turkenburg, J.P. & Mande, S.C. (2008). Crystal structure of *Mycobacterium tuberculosis* YefM antitoxin reveals that it is not an intrinsically unstructured protein. *J. Mol. Biol.* **383**, 482-493.

Kumar, P., Joshi, D.C., Akif, Mohd, Akhter, Y., Hasnain, S.E. & Mande, S.C. (2010). Mapping conformational transitions in the cyclic-AMP receptor protein: Crystal structure and Normal Mode Analysis of *M. tuberculosis* apo-cAMP receptor protein. *Biophys. J.* **98**, 305-314.

### **Centre for Cellular and Molecular Biology, Hyderabad**

Rajakumara, E., Acharya, P., Ahmad, S., Shanmugam, V.M., Rao, N.M. & Sankaranarayanan, R. (2004). Crystallization and preliminary X-ray crystallographic investigations on several thermostable forms of a *Bacillus subtilis* lipase. *Acta Cryst.* **D60**, 160-162.

Rukmini, R., Shanmugam, V. M., Saxena, P., Gokhale, R.S. & Sankaranarayanan, R. (2004). Crystallization and preliminary X-ray crystallographic investigations of an unusual type III polyketide synthase PKS18 from *Mycobacterium tuberculosis*. *Acta Cryst.* **D60**, 749-751.

Sankaranarayanan, R., Saxena, P., Marathe, U., Gokhale, R.S., Shanmugam, V.M. & Rukmini, R. (2004). A novel tunnel in mycobacterial type III polyketide synthase reveals the structural basis for generating diverse metabolites. *Nature Struct. Mol. Biol.* **11**, 894-900.

Acharya, P., Rajakumara, E., Sankaranarayanan, R. & Rao, N.M. (2004). Structural basis for selection and enhanced thermostability of laboratory evolved *Bacillus subtilis* lipase. *J. Mol. Biol.* **341**, 1271-1281.

Dwivedi, S., Kruparani, S.P. & Sankaranarayanan, R. (2004). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic investigations on a unique editing domain from Archaeobacteria. *Acta Cryst.* **D60**, 1662-1664.

Dwivedi, S., Kruparani, S.P. & Sankaranarayanan, R. (2005). A D-amino acid editing module coupled to the translational apparatus in archaea. *Nature Struct. Mol. Biol.* **12**, 556-557.

Aravind, P., Rajini, B., Sharma, Y. & Sankaranarayanan, R. (2006). Crystallization and preliminary X-ray crystallographic investigations on a  $\beta\gamma$ -Crystallin domain of Absent In Melanoma 1 (AIM1), a protein from *Homo sapiens*. *Acta Cryst.* **F62**, 282-284.

Goyal, A., Yousuf, M., Rajakumara, E., Arora, P., Gokhale, R.S. & Sankaranarayanan, R. (2006). Crystallization and preliminary X-ray crystallographic studies of the N-terminal domain of FadD28, a fatty acyl AMP ligase from *Mycobacterium tuberculosis*. *Acta Cryst.* **F62**, 350-352.

Hussain, T., Kruparani, S.P., Pal, B., Dock-Bregeon, A-C., Dwivedi, S., Shekar, M.R., Sureshbabu, K. & Sankaranarayanan, R. (2006). Posttransfer editing mechanism of a D-aminoacyl-tRNA deacylase-like domain in threonyl-tRNA synthetase from archaea. *EMBO J.* **25**, 4152-4162.

Aparna, G., Chatterjee, A., Jha, G., Sonti, R.V. & Sankaranarayanan, R. (2007). Crystallization and preliminary crystallographic studies of LipA, a secretory lipase/esterase from *Xanthomonas oryzae pv. oryzae*. *Acta Cryst.* **F63**, 708-710.

Rajakumara, E., Acharya, P., Ahmad, S., Sankaranarayanan, R. & Rao, N.M. (2008). Structural basis for the remarkable stability of *Bacillus subtilis* lipase at low pH. *Biochim. Biophys. Acta* **1784**, 302-311.

Goyal, A., Saxena, P., Rahman, A., Singh, P., Kasbekar, D., Gokhale, R.S. & Sankaranarayanan, R. (2008). Structural insights into biosynthesis of resorcinolic lipids by a type III polyketide synthase in *Neurospora crassa*. *J. Struct. Biol.* **162**, 411-421.

Aravind, P., Wistow, G., Sharma, Y. & Sankaranarayanan, R. (2008). Exploring the limits of sequence and structure in a variant betagamma-crystallin domain of the protein absent in melanoma-1 (AIM1). *J. Mol. Biol.* **381**, 509-518.

Ahmad, S., Kamal, M.Z., Sankaranarayanan, R. & Rao, N.M. (2008). Thermostable *Bacillus subtilis* lipases: in vitro evolution and structural insight. *J. Mol. Biol.* **381**, 324-340.

Aravind, P., Mishra, A., Suman, S.K., Sharma, Y. & Sankaranarayanan, R. (2008). Betagamma-crystallins: A universal calcium-binding superfamily. *Protein Sci.* **17**, 173.

Aravind, P., Suman, S.K., Mishra, A., Sharma, Y. & Sankaranarayanan, R. (2009). Three-Dimensional domain swapping in Nitrollin, a single-domain  $\beta\gamma$ -Crystallin from *Nitrosospira multiformis*, controls protein conformation and stability but not dimerization. *J. Mol. Biol.* **385**, 163-177.

Arora, P., Goyal, A., Natarajan, V.T., Rajakumara, E., Verma, P., Gupta, R., Yousuf, M., Trivedi, O.A., Mohanty, D., Tyagi, A., Sankaranarayanan, R. & Gokhale, R.S. (2009). Mechanistic and functional insights into fatty acid activation in *Mycobacterium tuberculosis*. *Nature Chem. Biol.* **5**, 166-173.

Aparna, G., Chatterjee, A., Sonti, R.V. & Sankaranarayanan, R. (2009). A cell wall degrading esterase of *Xanthomonas oryzae* requires a unique substrate recognition module for pathogenesis on rice. *Plant Cell* **21**, 1860-1873.

Aravind, P., Mishra, A., Suman, S.K., Jobby, M.K., Sankaranarayanan, R. & Sharma, Y. (2009). betagamma-Crystallin superfamily contains a universal motif for binding calcium. *Biochemistry* **48**, 12180-12190.

Dubey, V.P., Pal, B., Srikantan, S., Pottabathini, S., De, P.K. & Sankaranarayanan, R. (2010). Cloning, overexpression, purification, crystallization and preliminary X-ray analysis of a female-specific lipocalin (FLP) expressed in the lacrimal glands of Syrian hamsters. *Acta Cryst.* **F66**, 509-512.

Hussain, T., Kamarthapu, V., Kruparani, S.P., Deshmukh, M.V. & Sankaranarayanan, R. (2010). Mechanistic insights into cognate substrate discrimination during proofreading in translation. *Proc. Natl. Acad. Sci. (USA)* **107**, 22117-22121.

Kamal, M.Z., Ahmad, S., Molugu, T.R., Vijayalakshmi, A., Deshmukh, M.V., Sankaranarayanan, R. & Rao, N.M. (2011). In vitro evolved and non-aggregating and thermostable lipase: Structural and thermodynamic investigation. *J. Mol. Biol.* **413**, 726-741.

Mishra, A., Suman, A.K., Srivastava, S.S., Sankaranarayanan, R. & Sharma, Y. (2012). Decoding the molecular design principles underlying Ca(2+) binding to  $\beta\gamma$ -crystallin motifs. *J. Mol. Biol.* **415**, 75-91.

Goyal, A., Verma, P. Anandhakrishnan, M., Gokhale, R.S. & Sankaranarayanan R. (2012). Molecular basis of the functional divergence of fatty acyl-AMP ligase biosynthetic enzymes of *Mycobacterium tuberculosis*. *J. Mol. Biol.* **416**, 221-238.

Chhabra, A., Haque, A. S., Pal, R.K., Goyal, A., Rai, R., Joshi, S., Panjekar, S., Pasha, S., Sankaranarayanan, R. & Gokhale, R.S. (2012). Nonprocessive [2+2] $e^-$  off-loading reductase domains from mycobacterial nonribosomal peptide synthetases. *Proc. Natl. Acad. Sci. (USA)* **109**, 5681-5686.

Kumar, S., Haque, A.S., Jha, G., Sonti, R.V. & Sankaranarayanan, R. (2012). Crystallization and preliminary crystallographic studies of CbsA, a secretory exoglucanase from *Xanthomonas oryzae* pv. *oryzae*. *Acta Cryst.* **F68**, 1191-1194.

Rajanikanth, V., Srivastava, S.S., Singh, A.K., Rajyalakshmi, M., Chandra, K., Aravind, P., Sankaranarayanan, R. & Sharma, Y. (2012). Aggregation prone near-native intermediate formation during unfolding of a structurally similar nonlenticular  $\beta\gamma$  crystallin domain. *Biochemistry* **51**, 8502-8513.

Ahmad, S., Sravankumar, A.S., Kruparani, S.P. & Sankaranarayanan, R. (2012). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analyses of threonyl-tRNA synthetase editing domain from *Aeropyrum pernix*. *Acta Cryst.* **F68**, 1390-1393.

Ahmad, S., Routh, S.B., Kamarthapu, V., Chalissery, J., Muthukumar, S., Hussain, T., Kruparani, S.P., Deshmukh, M.V. & Sankaranarayanan, R. (2013). Mechanism of chiral proofreading during translation of the genetic code. *eLife* **2**, e01519.



Ahmad, S., Muthukumar, S., Kuncha, S.K., Routh, S.B., Yerabham, A.S.K., Hussain, T., Kamarthapu, V., Kruparani, S.P. & Sankaranarayanan, R. (2015). Specificity and catalysis hardwired at the RNA-protein interface in a translational proofreading enzyme. *Nature Commun.* **6**, 7552.

### **Indian Institute of Technology, Kharagpur**

Chaithanya, M., Rajakumara, E., Mazumdar, P., Saha, B., Mitra, D., Wiker, H. G., Sankaranarayanan, R. & Das, A.K. (2005). Crystal Structure of Low Molecular-Weight Protein Tyrosine Phosphatase from *Mycobacterium tuberculosis* at 1.9-Å Resolution. *J. Bacteriology* **187**, 2175-2181.

Roy, S., Aravind, P., Chaithanya, M., Ghosh, A.K., Sankaranarayanan, R. & Das, A.K., (2006). Crystallization and preliminary X-ray diffraction analysis of a protease inhibitor from the haemolymph of the Indian tasar silkworm *Antheraea mylitta*. *Acta Cryst.* **F62**, 669-671.

Mazumdar, P.A., Kumaran, D., Swaminathan, S. & Das, A.K. (2008). A novel acetate-bound complex of human carbonic anhydrase II. *Acta Cryst.* **F64**, 163-166.

Mukherjee, S., Dutta, D., Saha, B. & Das, A.K. (2008). Expression, purification, crystallization and preliminary X-ray diffraction studies of glyceraldehyde-3-phosphate dehydrogenase 1 from methicillin-resistant *Staphylococcus aureus* (MRSA252). *Acta Cryst.* **F64**, 929-932.

Roy, S., Aravind, P., Chaithanya, M., Ghosh, A.K., Sankaranarayanan, R. & Das, A.K. (2009). Crystal structure of a fungal protease inhibitor from *Antheraea mylitta*. *J. Struct. Biol.* **166**, 79-87.

Saha, B., Mukherjee, S., Dutta, D. & Das, A.K. (2009). Expression, purification, crystallization and preliminary X-ray diffraction analysis of transcriptional repressor SirR from *Mycobacterium tuberculosis* H37Rv. *Acta Cryst.* **F65**, 154-158.

Mukherjee, S., Dutta, D., Saha, B. & Das, A.K. (2009). Expression, purification, crystallization and preliminary X-ray diffraction studies of triosephosphate isomerase from methicillin-resistant *Staphylococcus aureus* (MRSA252). *Acta Cryst.* **F65**, 398-401.

Mukherjee, S., Maity, S., Roy, S., Ghorai, S., Chakrabarti, M., Agarwal, R., Dutta, D., Ghosh, A.K. & Das A.K. (2009). Cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of Glyceraldehyde-3-phosphate dehydrogenase from *Antheraea mylitta*. *Acta Cryst.* **F65**, 937-940.

Bhattacharyya, S., Dutta, D., Ghosh, A.K. & Das, A.K. (2009). Cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of an atypical two-cysteine peroxiredoxin (SAOUHSC\_01822) from *Staphylococcus aureus* NCTC 8325. *Acta Cryst.* **F65**, 1113-1115.

Mukherjee, S., Saha, B., Dutta, D. & Das, A.K., (2010). Purification, crystallization and preliminary X-ray analysis of apo glyceraldehyde-3-phosphate dehydrogenase 1 (GAP1) from methicillin-resistant *Staphylococcus aureus* (MRSA252). *Acta Cryst.* **F66**, 506-508.

Mukherjee, S., Dutta, D., Saha, B. & Das, A.K. (2010). Crystal structure of glyceraldehyde-3-phosphate dehydrogenase 1 from methicillin-resistant *Staphylococcus aureus* MRSA252 provides novel insights into substrate binding and catalytic mechanism. *J Mol Biol.* **401**, 949-968.

Dutta, D., Bhattacharyya, S., Mukherjee, S., Saha B. & Das A.K. (2010). Crystal structure of FabG4 from *Mycobacterium tuberculosis* reveals the importance of C-terminal residues in ketoreductase activity. *J. Struct. Biol.* **174**, 147-155.

Bhattacharyya, S., Dutta, D., Ghosh A.K. & Das A.K. (2011). Cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of an inositol monophosphatase family protein (SAS2203) from *Staphylococcus aureus* MSSA476. *Acta Cryst.* **F67**, 471-474.

Roychowdhury, A., Mukherjee, S., Das, A.K. (2011). Expression, purification, crystallization and preliminary X-ray diffraction studies of phosphoglycerate kinase from methicillin resistant *Staphylococcus aureus* MRSA252. *Acta Cryst.* **F67**, 668-671.

Bhattacharyya, S., Dutta, D., Saha, B., Ghosh, A.K. & Das A.K. (2012). Crystal structure of Staphylococcal dual specific inositol monophosphatase/NADP(H) phosphatase (SAS2203) delineates the molecular basis of substrate specificity. *Biochimie* **94**, 879-890.

Dutta, D., Bhattacharyya, S. & Das, A.K. (2012). Crystal structure and fluorescence studies reveal the role of helical dimeric interface of staphylococcal FabG1 in positive cooperativity for NADPH. *Proteins* **80**, 1250-1257.

Dutta, D., Bhattacharyya, S. & Das, A.K. (2012). Crystallization and preliminary X-ray diffraction analysis of the high molecular weight ketoacyl reductase FabG4 complexed with NADH. *Acta Cryst.* **F68**, 786-789.

Mukherjee, S., Roychowdhury, A., Dutta, D. & Das, A.K. (2012). Crystal structures of triosephosphatisomerase from methicillin resistant *Staphylococcus aureus* MRSA252 provide structural insights into novel modes of ligand binding and unique conformations of catalytic loop. *Biochimie* **94**, 2532-2544.

Dutta, D., Bhattacharyya, S., Roychowdhury, A., Biswas, R. & Das A.K. (2013). Crystal structure of Hexanoyl-CoA bound to  $\beta$ -ketoacyl reductase FabG4 of *Mycobacterium tuberculosis*. *Biochem. J.* **450**, 127-139.

Biswas, R., Dutta, D. & Das, A.K. (2013). Cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of Rv0241c (HtdX) from *Mycobacterium tuberculosis* H37Rv. *Acta Cryst.* **F69**, 1110-1113.

Roychowdhury, A., Kundu, A., Gujar, A., Bose, M. & Das, A.K. (2014). Expression, purification, crystallization and preliminary X-ray diffraction studies of phosphoglycerate mutase from *Staphylococcus aureus* NCTC8325. *Acta Cryst.* **F70**, 53-56.

Dutta, D., Dutta, A., Bhattacharjee, A., Basak, A. & Das, A.K. (2014). Cloning, expression, crystallization and preliminary X-ray diffraction studies of Staphylococcal superantigen-like protein 1. *Acta Cryst.* **F70**, 600-603.

Dutta, A., Bhattacharyya, S., Dutta, D. & Das, A.K. (2014). Structural elucidation of the binding site and mode of inhibition of  $\text{Li}^+$  and  $\text{Mg}^{2+}$  in inositol monophosphatase. *FEBS J.* **281**, 5309–5324.

Biswas, R., Dutta, A., Dutta, D., Hazra, D., Banerjee, D.R., Basak, A. & Das, A.K. (2015). Crystal structure of dehydratase component HadAB complex of mycobacterial FAS-II pathway. *Biochem. Biophys. Res. Commun.* **458**, 369-374.

Roychowdhury, A., Kundu, A., Bose, M., Gujar, A. & Das A.K. (2015). The complete catalytic cycle of cofactor-independent phosphoglycerate mutase involves a spring-loaded mechanism. *FEBS Journal* **282**, 1097-1110.

### **Jawaharlal Nehru University, New Delhi**

Gourinath, S., Padhan, N., Alam, N. & Bhattacharya, A. (2005). Crystallization and preliminary crystallographic analysis of calcium-binding protein-2 from *Entamoeba histolytica* and its complexes with strontium and the IQ1 motif of myosin V. *Acta Cryst.* **F61**, 417-420.

Yuting, Y., Gourinath, S., Kovács M., Nyitray, L., Reutzel, R., Himmel, D.M., O'Neill-Hennessey E., Reshetnikova, L., Szent-Györgyi, A.G., Brown, J.H. & Cohen, C. (2007). Rigor-like states in muscle myosins reveal key mechanical elements in the transduction pathways of this allosteric motor. *Structure* **15**, 553 – 564.

Krishna, C., Jain, R., Kashav, T., Wadhwa, D., Alam, N., & Gourinath S. (2007). Crystallization and preliminary crystallographic analysis of cysteine synthase from *Entamoeba histolytica*. *Acta. Cryst.* **F63**, 512-515.

Kumar, S., Pradhan, N., Alam, N., & Gourinath, S. (2007). Crystal structure of Calcium binding protein-1 from *Entamoeba histolytica* : novel arrangement of EF hand motifs. *Proteins* **68**, 990-998.

Brown, J.H., Yuting, Y., Reshetnikova L., Gourinath, S., Suveges, D., Kardos, J., Hobor, F., Reutzler, R., Nyitray L. & Cohen, C. (2008). An Unstable Head–Rod Junction May Promote Folding into the Compact Off-State Conformation of Regulated Myosins. *J. Mol. Biol.* **325**, 1434-1443.

Krishna, H., Kumar, M., Kumar, S., Jain, S., Alam, N. & Gourinath, S. (2008). Crystal structure of native O-acetyl-serine sulfhydrylase from *Entamoeba histolytica* and its complex with cysteine: Structural evidence for cysteine binding and lack of interactions with Serine acetyl transferase. *Proteins* **72** ,1222-1232 .

Jain, R., Kumar, S., Gourinath, S., Bhattacharya, S. & Bhattacharya, A. (2009). N- and C-terminal domains of the calcium binding protein EhCaBP1 of the parasite entamoeba histolytica display distinct functions. *PLoS One* **4**, e5269.

Kashav, T., Nitharwal, R., Abdulrehman, S.A., Gabdoulkhakov, A., Saenger, W., Dhar, S.K. & Gourinath, S. (2009). Three-dimensional structure of N-terminal domain of DnaB Helicase and Helicase-Primase interactions in *Helicobacter pylori*. *PLoS One* **10**, e7515.

Manford, A., Xia, T., Saxena, A.K., Stefan, C., Hu, F., Emr, S.D. & Mao, Y. (2010). Crystal structure of the yeast Sac1: implications for its phosphoinositidephosphatase function (PDB-3LWT). *EMBO J.* **29**,1489-1498. (Erratum in *EMBO J.* **29**, 2472)

Kumar, S., Ahmad, E., Mansuri, M.d., Kumar, S., Jain, R., Khan, R.H. & Gourinath, S. (2010). Crystal structure and trimer-monomer transition of N-terminal domain of EhCaBP1 from *Entamoeba histolytica*. *Biophys. J.* **98**, 2933-2942.

Kumar, S., Raj, I., Nagpal, I., Subbarao, N. & Gourinath, S. (2011). Structural and biochemical studies of Serine Acetyltransferase reveal why the parasite *Entamoebahistolytica* cannot form Cysteine Synthase complex. *J. Biol. Chem.* **286**, 12533-12541.

Gangwar, S.P., Meena, S.R. & Saxena, A.K. (2011). Cloning, purification, crystallization and preliminary x-ray analysis of EspR: a secreted transcription factor from *M. tuberculosis*. *Acta Cryst.* **F67**, 83-86.

Kumar, S., Zaidi, R. & Gourinath, S. (2012). Cloning, purification, crystallization and preliminary crystallographic study of calcium-binding protein 5 from *Entamoeba histolytica*. *Acta Cryst.* **F68**, 1542-1544.

Kumar, S., Ahmad, E., Kumar, S., Khan, R.H. & Gourinath, S. (2012). Flexibility of EF-hand motifs: structural and thermodynamic studies of calcium binding protein-1 from *Entamoeba histolytica* with  $Pb^{2+}$ ,  $Ba^{2+}$ , and  $Sr^{2+}$ . *BMC Biophys.* **5**, 15.

Raj, I., Kumar, S. & Gourinath, S. (2012). The narrow active site cleft of O-acetyl serine sulfhydrylase from *Leishmania donovani* allows complex formation with serine acetyl transferases having a range of C-terminal sequences. *Acta Cryst.* **D68**, 909-919.

Saxena, A.K. (2012). Structure of Fab fragment of malaria transmission-blocking antibody 2A8 against *P. vivax* P25 protein. (PDB-3S62). *Int. J. Biol. Macromol.* **50**, 153-156.

Meena, S.R., Gangwar, S.P. & Saxena, A.K. (2012). Purification, crystallization and preliminary x-ray crystallographic analysis of ATPase domain of TAPin nucleotide free, ADP, vanadate and azide inhibited form. *Acta Cryst.* **F68**, 655-658.

Gangwar, S.P., Meena, S.R. & Saxena, A.K. (2012). Purification, crystallization and preliminary X-ray crystallographic analysis ETS domain of Ergp55 in complex with cfo promoter DNA sequence. *Acta Cryst.* **F68**, 1333-1336.

Das, U., Kumar, N., Gourinath, S. & Srinivasan, A. (2013). Preliminary crystallographic analysis of recombinant VapBC-15 toxin-antitoxin complex from *Mycobacterium tuberculosis*. *Acta Cryst.* **F69**, 1242-1245.

Raj, I., Mazumder, M. & Gourinath, S. (2013). Molecular basis of ligand recognition by OASS from *E. histolytica*: Insights from structural and molecular dynamics simulation studies. *Biochim. Biophys. Acta* **1830**, 4573-4583.

Rehman, S.A.A., Verma, A., Mazumder, M., Dhar, S.K., & Gourinath, S. (2013). Crystal structure and mode of helicase binding of the C-terminal domain of primase from *Helicobacter pylori*. *J. Bacteriology* **195**, 2826-2838.

Kumar, S., Mazumder, M. & Gourinath, S. (2013). Single residue mutation in EhSAT3 active site assists in partial regaining of feedback inhibition by cysteine. *Plos One* **8**, e55932.

Kumar, S., Aslam, S., Mazumder, M, Dahiya, P., Murmu, A., Manjasetty, B.A., Zaidi, R., Bhattacharya, A. & Gourinath, S. (2014). Crystal Structure of Calcium Binding Protein-5 from *Entamoebahistolytica* and its involvement in initiation of phagocytosis of human erythrocytes. *PLoS Pathogens* **10**, e1004532.

Tarique, K.F., Rehman, S.A.A., Betzel, Ch. & Gourinath, S. (2014). Structure-based identification of inositol polyphosphate 1 - phosphatase from *Entamoeba histolytica*. *Acta Cryst.* **D70**, 3023-3033.

Singh, R.K., Raj, I., Pujari, R. & Gourinath, S. (2014). Crystal Structures and Kinetics of Type III 3-phosphoglycerate dehydrogenase reveal Catalysis by Lysine. *FEBS Journal* **281**, 5498-5512 .

Kumar, N., Somlata, Mazumder, M., Dutta, P., Maiti, S., & Gourinath, S. (2014). EhCoactosin stabilizes actin filaments in the protist parasite *Entamoeba histolytica*. *PLoS Pathogens*. **10**, e1004362.

Tarique, F.A., Abdulrehman, S.A, & Gourinath, S. (2014). Structural elucidation of a dual active PAP Phosphatase1 of *Entamoeba histolytica*: capable of hydrolysing both 3'adenosine5'-phosphate and inositol 1,4-bisphosphate. *Acta Cryst.* **D70**, 2019-2031.

Kumar, S., Kumar, N., Alam, N. & Gourinath, S. (2014). Crystal structure of serine acetyl transferase from *Brucella abortus* and its complex with coenzyme A. *Biochim Biophys Acta* **1844**, 1741-1748.

Singh, N.K., Hasan S.S., Kumar, J., Raj, I., Pathan, A.A., Parmar, A., Shakil, S., Gourinath, S. & Madamwar, D. (2014). Crystal structure and interaction of phycocyanin with  $\beta$ -Secretase: A putative therapy for Alzheimer's disease. *CNS Neurol. Disord. Drug Targets* **13**, 691-698.

Gangwar, S.P., Meena, S.R. & Saxena, A.K. (2014). Comparison of different crystal forms of ESX-1 secreted protein regulator *EspR* from *M. tuberculosis* and its implication for protein regulator activity (PDB-4NDW). *Acta Cryst.* **F70**, 433-437.

Gangwar, S.P., Meena, S.R. & Saxena, A.K. (2014). Crystal structure of carboxy-terminal domain of *M. tuberculosis* *CarD* protein: an essential rRNA transcriptional regulator (PDB-4KMC). *Acta Cryst.* **F70**, 160-165.

### **Indian Institute of Technology, Roorkee**

Shee, C., Singh, T.P., Kumar, P. & Sharma, A.K. (2007). Crystallization and preliminary X-ray diffraction studies of *Murraya koenigii* trypsin inhibitor. *Acta Cryst.* **F63**, 318-319.

Chaudhary, N.S., Shee, C., Islam, A., Ahmad, F., Yernool, D., Kumar, P. & Sharma, A.K. (2008). Purification and characterization of a trypsin inhibitor from *Putranjiva roxburghii* seeds. *Phytochemistry* **69**, 2120-2126.

Patil, D.N., Preeti, Chaudhry, A., Sharma, A.K., Tomar, S., Kumar, P. (2009). Purification, crystallization and preliminary crystallographic studies of a Kunitz-type proteinase inhibitor from tamarind (*Tamarindus indica*) seeds. *Acta Cryst.* **F65**, 736-738.



Patil, D.N., Datta, M., Chaudhary, A., Tomar, S., Sharma, A.K. & Kumar, P. (2009). Isolation, purification, crystallization and preliminary crystallographic studies of chitinase from tamarind (*Tamarindus indica*) seeds. *Acta Cryst.* **F65**, 343-345.

Tomar, S., Patil, D.N., Datta, M., Tapas, S., Preeti, Chaudhary, A., Sharma, A.K., Tomar, S. & Kumar, P. (2009). Crystallization and preliminary X-ray diffraction analysis of the complex of Kunitz-type tamarind trypsin inhibitor and porcine pancreatic trypsin. *Acta Cryst.* **F65**, 1179-1181.

Gahloth, D., Selvakumar, P., Shee, C., Kumar, P., Sharma, A.K. (2010). Cloning, sequence analysis and crystal structure determination of a miraculin-like protein from *Murraya koenigii*. *Arch. Biochem. Biophys.* **494**, 15-22.

Sakshi, Patil, D.N., Tomar, S., Sylvestre, M. & Kumar, P. (2010). Expression, purification, crystallization and preliminary crystallographic studies of cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase from *Pandoraea pnomenusa* B-356. *Acta Cryst.* **F66**, 1517-1520.

Aggarwal, M., Dhindwal, S., Pratap, S., Kuhn, R.J., Kumar P., & Tomar, S. (2011). Crystallization, high-resolution data collection and preliminary crystallographic analysis of Aura virus capsid protease and its complex with dioxane. *Acta Cryst.* **F67**, 1394-1398.

Dhindwal, S., Patil, D.N., Mohammadi, M., Sylvestre, M., Tomar, S. & Kumar, P. (2011). Biochemical studies and ligand bound structures of biphenyl dehydrogenase from *Pandoraea pnomenusa* strain B-356 reveal a basis for broad specificity of the enzyme. *J. Biol. Chem.* **286**, 37011-37022.

Mohammadi, M., Viger, J.F., Kumar, P., Barriault, D., Bolin, J.T. & Sylvestre, M. (2011). Fine tuning Rieske - type oxygenases reactive atoms to expand their substrate range. *J. Biol. Chem.* **286**, 27612-27621.

Kumar, P., Gómez-Gil, L., Mohammadi, M., Sylvestre, M., Eltis, L.D. & Bolin, J.T. (2011). Anaerobic crystallization and initial X-ray diffraction data of biphenyl 2,3-dioxygenase from *Burkholderia xenovorans* LB400: addition of agarose improved the quality of the crystals. *Acta Cryst.* **F67**, 59-62.

Kumar, P., Mohammadi, M., Viger, J.F., Barriault, D., Gomez-Gil, L., Eltis, L.D., Bolin, J.T. & Sylvestre, M. (2011). Structural Insight into the Expanded PCB-Degrading Abilities of a Biphenyl Dioxygenase Obtained by Directed Evolution. *J. Mol. Biol.* **405**, 531-547.

Narayanan, A., Paul, L.N., Tomar, S., Patil, D.N., Kumar, P. & Yernool, D.A. (2012). Structure-function studies of DNA binding domain of response regulator KdpE reveals equal affinity interactions at DNA half-sites. *Plos One* **7**, e30102.

Patil, D.N., Chaudhry, A., Sharma, A.K., Tomar, S., Kumar, P. (2012). Structural basis for dual inhibitory role of tamarind Kunitz inhibitor (TKI) against factor Xa and trypsin *FEBS J.* **279**, 4547-4564.

Kumar, P., Mohammadi, M., Dhindwal, S., Bolin, J.T. & Sylvestre, M. (2012). Structural insights into the metabolism of 2-chlorodibenzofuran by an evolved biphenyl dioxygenase. *Biochem. Biophys. Res. Commun.* **421**, 757-762.

Aggarwal, M., Tapas, S., Preeti, Siwach, A., Kumar, P., Kuhn, R.J., Tomar, S. (2012). Crystal structure of aura virus capsid protease and its complex with dioxane: new insights into capsid-glycoprotein molecular contacts. *Plos One* **7**, e51288.

Patil, D.N., Datta, M., Dev, A., Dhindwal, S., Singh, N., Dasauni, P., Kundu, S., Sharma, A.K., Tomar, S., & Kumar, P. (2013). Structural investigation of a novel N-Acetyl glucosamine binding Chi-Lectin which reveals evolutionary relationship with class III chitinases. *Plos One* **8**, e63779.

Preeti, Tapas, S., Kumar, P., Madhubala, R. & Tomar, S. (2013). Structural insight into DFMO resistant ornithine decarboxylase from *Entamoeba histolytica*: an inkling to adaptive evolution. *Plos One* **8**, e53397.

Colbert, C.L., Agar, N.Y., Kumar, P., Chakko, M.N., Sinha, S.C., Powlowski, J.B., Eltis, L.D. & Bolin, J.T. (2013). Structural characterization of *Pandoraea pnomenusa* B-356 biphenyl dioxygenase reveals features of potent polychlorinated biphenyl-degrading enzymes. *Plos One* **8**, e52550.

Aggarwal, M., Dhindhwal, S., Kumar, P., Kuhn, R.J. & Tomar, S. (2014). Trans-protease activity and structural insights into the active form of the alphavirus capsid protease. *J. Virol.* **88**, 12242-12253.

Selvakumar, P., Sharma, N., Tomar, P.P.S., Kumar, P. & Sharma, A.K. (2014). Structural insights into the aggregation behavior of *Murraya koenigii* miraculin-like protein below pH 7.5. *Proteins* **82**, 830-840.

Pratap, S., Katiki, M., Gill, P., Kumar, P. & Golemi-Kotra, D. (2015). Active-Site plasticity is essential to carbapenem hydrolysis by OXA-58 class D  $\beta$ -Lactamase of *Acinetobacter baumannii*. *Antimicrob Agents Chemother.* **60**, 75-86.

Dhindwal, S., Priyadarshini, P., Patil, D.N., Tapas, S., Kumar, P., Tomar, S. & Kumar, P. (2015). Ligand-bound structures of 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase from *Moraxella catarrhalis* reveal a water channel connecting to the active site for the second step of catalysis. *Acta Cryst.* **D71**, 239-255.

Sharma, N., Selvakumar, P., Bhose, S., Ghosh, D.K., Kumar, P. & Sharma, A.K. (2015). Crystal structure of a periplasmic solute binding protein in metal-free, intermediate and metal-bound states from *Candidatus Liberibacter asiaticus*. *J. Struct. Biol.* **189**, 184-194.

## **Delhi University**

Gupta, V., Gupta, R.K., Khare, G., Surolia, A., Salunke, D.M. & Tyagi, A.K. (2008). crystallization and preliminary X-ray diffraction analysis of biotin acetyl-CoA carboxylase ligase (BirA) from *Mycobacterium tuberculosis*. *Acta Cryst.* **F64**, 524-527.

Gupta, V., Gupta, R.K., Khare, G., Salunke, D.M. & Tyagi, A.K. (2008). Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analysis of bacterioferritin A from *Mycobacterium tuberculosis*. *Acta Cryst.* **F64**, 398-401.

Gupta, V., Gupta R.K., Khare, G., Salunke, D.M. & Tyagi, A.K. (2009). Crystal structure of Bfr A from *Mycobacterium tuberculosis*: incorporation of selenomethionine results in cleavage and demetallation of haem. *PLoS One* **4**, e8028.

Gupta, V., Gupta R.K., Khare, G., Salunke, D.M., Surolia, A. & Tyagi, A.K. (2010). Structural ordering of disordered ligand binding loops of biotin protein ligase into active conformation as a consequence of dehydration. *PLoS One* **5**, e9222.

Khare, G., Gupta, V., Nangpal, P., Gupta, R.K., Sauter, N.K., & Tyagi, A.K. (2011). Ferritin structure from *Mycobacterium tuberculosis*: Comparative study with homologues identifies extended C-terminus involved in ferroxidase activity. *Plos One* **6**, e18570.

Mukhi, N., Dhindwal, S., Uppal, S., Kumar, P., Kaur, J. & Kundu, S. (2013). X-Ray crystallographic structural characteristics of *Arabidopsis* hemoglobin I and their functional implications. *Biochim. Biophys. Acta* **1834**, 1944-1956.

### **Indian Institute of Technology, Kanpur**

Verma, S.K., Jaiswal, M., Kumar, N., Parikh, A., Nandicoori, V.K. & Prakash, B. (2009). Crystal structure of N-acetylglucosamine-1-phosphate uridyltransferase (GlmU) from *Mycobacterium tuberculosis* in a cubic space group. *Acta Cryst.* **F65**, 435–439.

Parikh, A., Verma, S.K., Khan, S., Prakash, B. & Nandicoori V.K. (2009). PknB mediated phosphorylation of a novel substrate, N-acetylglucosamine-1-phosphate uridyltransferase (GlmU), modulates its acetyltransferase activity. *J. Mol. Biol.* **386**, 451-64.

Tomar, S.K., Kumar, P. & Prakash, B. (2011). Deciphering the catalytic machinery in a universally conserved ribosome binding ATPase YchF. *Biochem. Biophys. Res. Commun.* **408**, 459–464.

Jagtap, P.K., Soni, V., Vithani, N., Jhingan, G.D., Bais, V.S., Nandicoori, V.K. & Prakash, B. (2012). Substrate bound crystal structures reveal features unique to *Mycobacterium tuberculosis* N-acetyl-glucosamine-1-phosphate uridyltransferase and a catalytic mechanism for acetyltransfer. *J. Biol. Chem.* **287**, 39524-39537.

Rafay, A., Majumdar, S. & Prakash, B. (2012). Exploring potassium-dependent GTP hydrolysis in TEES family GTPases. *FEBS Open Bio.* **2**, 173-177.

Tomar, S.K., Kumar, P., Majumdar, S., Bhaskar, V., Dutta P., & Prakash, B. (2012). Extended C-terminus and length of the linker connecting the G-domains are species-specific variations in the EngA family of GTPases. *FEBS Open Bio.* **2**, 191–195.

Jagtap, P.K., Verma, S.K., Vithani, N., Bais, V. & Prakash, B. (2013). Crystal structures identify an atypical two-metal ion mechanism for uridyl transfer in GlmU: Its significance to sugar nucleotidyltransferases. *J. Mol. Biol.* **425**, 1745 - 1759.

Jain, N., Vithani, N., Rafay, A. & Prakash, B. (2013). Identification and characterization of a hitherto unknown nucleotide binding domain and an intricate inter-domain regulation in HflX, a ribosome binding GTPase. *Nucl. Acids Res.* **41**, 9557-9569.

Baskaran, A., Majumdar, S. & Prakash, B. (2013). The structural basis unifying diverse GTP hydrolysis mechanisms. *Biochemistry* **52**, 1122-1130.

Vithani, N., Bais, V. & Prakash, B. (2014). GlmU (N-acetylglucosamine-1-phosphate uridyltransferase) bound to three magnesium ions and ATP at the active site. *Acta Cryst.* **F70**, 703-708.

Vithani N. & Prakash, B. (2015). GlnU from *Mycobacterium tuberculosis* – Structure, function and the role of metal ions in catalysis. *Encyclopedia of Inorganic and Bioinorganic Chemistry* doi/10.1002/9781119951438.

### **National Centre for Biological Sciences, Bangalore**

Namadurai, S., Jain, D., Kulkarni, D.S., Tabib, C.R., Friedhoff, P., Rao, D.N. & Nair, D.T. (2010). The C-terminal domain of the MutL homolog from *Neisseria gonorrhoeae* forms an inverted homodimer. *PLoS One* **5**, e13726.

Sharma A. & Nair, D.T. (2011). Cloning, expression, purification, crystallization and preliminary crystallographic analysis of MsDpo4: a Y-family DNA polymerase from *Mycobacterium smegmatis*. *Acta Cryst.* **F67**, 812-816.

Sharma, A., Subramanian, V. & Nair, D.T. (2012). The PAD region in the mycobacterial dinB homolog MsPollV exhibits positional heterogeneity. *Acta Cryst.* **D68**, 960-967.

Jain, D. & Nair, D.T (2013) Spacing between core recognition motifs determines relative orientation of AraR monomers on bipartite operators. *Nucl. Acids Res.* **41**, 639-647.

Sharma, A., Kottur, J., Narayanan, N. & Nair, D.T. (2013). A strategically located serine residue is critical for the mutator activity of DNA Polymerase IV from *Escherichia coli*. *Nucl. Acids Res.* **41**, 5104-5114.

Surana, P., Vijaya, S. & Nair, D.T. (2014). RNA-dependent RNA polymerase of *Japanese Encephalitis Virus* binds the initiator nucleotide GTP to form a mechanistically important pre-initiation state. *Nucl. Acids Res.* **42**, 2758-2773.

## Regional Centre for Biotechnology, Faridabad

Gaur, V., Chanana, V., Jain, A. & Salunke, D.M. (2011). The structure of a haemopexin-fold protein from cow pea (*Vigna unguiculata*) suggests functional diversity of haemopexins in plants. *Acta Cryst.* **F67**, 193-200.

Khan, T. & Salunke, D.M. (2012). Structural elucidation of the mechanistic basis of degeneracy in the primary humoral response. *J. Immunol.* **188**, 1819-1827.

Tomar, D., Khan, T., Singh, R.R., Mishra, S., Gupta, S., Surolia, A. & Salunke, D.M. (2012). Crystallographic study of novel transthyretin ligands exhibiting negative-cooperativity between two thyroxine binding sites. *Plos One* **7**, e43522.

Tapryal, S., Gaur, V., Kaur, K.J. & Salunke, D.M. (2013). Structural evaluation of a mimicry recognizing paratope: plasticity in antigen–antibody interactions manifests in molecular mimicry. *J. Immunol.* **191**, 456-463.

Vengadesan, K., Dwivedi, P., Kim, B.J., Samal, A., Macon, K., Ma, X., Mishra, A., Doran K.S., Ton-That H. & Narayana, S.V. (2013). Structure of *Streptococcus agalactiae* tip pilin GBS104: a model for GBS pili assembly and host interactions. *Acta Cryst.* **D69**, 1073-1089.

Vengadesan, K., Macon, K., Sugumoto, S., Mizunoe, Y., Iwase, T. & Narayana, S.V. (2013). Purification, crystallization and preliminary X-ray diffraction analysis of the *Staphylococcus epidermidis* extracellular serine protease Esp. *Acta Cryst.* **F69**, 49-52.

Singh, D., Von Ossowski, I., Palva, A. & Vengadesan, K. (2013). Purification, crystallization and preliminary crystallographic analysis of the SpaA backbone-pilin subunit from probiotic *Lactobacillus rhamnosus* GG. *Acta Cryst.* **F69**, 1182-1185.

Khan, T. & Salunke, D.M. (2014). Adjustable locks and flexible keys: plasticity of epitope-paratope interactions in germline antibodies. *J. Immunol.* **192**, 5398-5405.

Weinert, T., Olieric, V., Waltersperger, S., Panepucci, E., Chen, L., Zhang, H., Zhou, D., Rose, J., Ebihara, A., Kuramitsu, S., Li, D., Howe, N., Schnapp, G., Pautsch, A., Bargsten, K., Protá, A.E., Surana, P., Kottur, J., Nair, D.T., Basilico, F., Cecatiello, V., Pasqualato, S., Boland, A., Weichenrieder, O., Wang, B.C., Steinmetz, M.O., Caffrey, M. & Wang, M. (2014). Fast native-SAD phasing for routine macromolecular structure determination. *Nat. Methods* **12**, 131-133.

Kottur, J., Sharma, A., Gore, K.R., Narayanan, N., Samanta, B., Pradeepkumar, P.I. & Nair, D.T. (2014). Unique Structural Features in DNA Polymerase IV enable efficient bypass of the N<sup>2</sup>-Adduct induced by the Nitrofurazone antibiotic. *Structure* **23**, 56-67.

Nair, D.T., Kottur, J. & Sharma, R. (2015) A rescue act: Translesion DNA synthesis past N(2)-deoxyguanosine adducts. *IUBMB Life* **67**, 564-574.

Jain, A. & Salunke, D.M. (2015). Purification, identification and preliminary crystallographic studies of an allergenic protein from *Solanum melongena*. *Acta Cryst.* **F71**, 221-225.

Jain, D., Narayanan, N. & Nair, D.T. (2015). Plasticity in repressor-DNA interactions neutralizes loss of symmetry in bipartite operators. *J. Biol. Chem.* **291**, 1235-1242.

Jain D. (2015). Allosteric control of transcription in GntR family of transcription regulators: A structural overview. *IUBMB Life* **67**, 556-563.

Chaurasia, P., von Ossowski, I., Palva, A. & Krishnan, V. (2015). Purification, crystallization and preliminary X-ray diffraction analysis of SpaD, a backbone-pilin subunit encoded by the fimbrial spaFED operon in *Lactobacillus rhamnosus* GG. *Acta Cryst.* **F71**, 103-106.

Krishnan, V. (2015). Pilins in gram-positive bacteria: A structural perspective. *IUBMB Life* **67**, 533-543.



## **Kannur University, Kannur**

Geethanandan, K., Abhilash, J., Bharath, S.R., Sadasivan, C. & Haridas M. (2011). X-ray structure of a galactose-specific lectin from *Spatholobous parviflorous*. *Int. J. Biol. Macromol.* **49**, 992-998.

Dileep, K.V., Tintu, I., Mandal, P.K., Karthe, P., Haridas, M. & Sdasivan, C. (2011). Crystal structure of porcine pancreatic phospholipase A<sub>2</sub> in complex with 2-methoxycyclohexa-2-5diene-1,4-dione. *Frontiers in Life Science* **5**, 135-139.

Geethanandan, K., Abhilash, J., Bharath, S.R., Sadasivan, C. & Haridas M. (2011). Crystallization and preliminary X-ray studies of a galactose-specific lectin from the seeds of *Spatholobus parviflorus*. *Acta Cryst.* **67**, 700-702.

Abhilash, J., Geethanandan, K., Bharath, S.R., Sadasivan, C. & Haridas, M. (2011). Crystallization and preliminary X-ray diffraction analysis of a galactose specific lectin from the seeds of *Butea monosperma*. *Acta Cryst.* **67**, 524-526.

Chandra, D.N., Prasanth, G.K., Singh, N., Kumar, S., Jithesh, O., Sadasivan, C., Sharma, S., Singh, T.P. & Haridas, M. (2011). Identification of a novel and potent inhibitor of Phospholipase A<sub>2</sub> in a medicinal plant: Crystal structure at 1.93 Å and surface plasmon resonance analysis of Phospholipase A<sub>2</sub> complexed with berberine. *Biochim. Biophys. Acta* **1814**, 657-663.

Aparna, V., Dileep, K.V., Mandal, P.K., Karthe, P., Sadasivan, C. & Haridas, M. (2012). Anti-inflammatory property of n-hexadecanoic acid: Structural evidence and Kinetic assessment. *Chem. Biol. Drug Des.* **80**, 434-439.

Naveen, C.D., Abhilash, J., Prasanth, G.K., Sabu, A., Sadasivan, C. & Haridas M. (2012). Inverted binding due to a minor structural change in berberine enhances its phospholipase A<sub>2</sub> inhibitory effect. *Intl. J. Biol. Macromol.* **50**, 578-585.

Dileep, K.V., Tintu, I., Mandal, P.K., Karthe, P., Haridas, M. & Sdasivan, C. (2012). Binding to PLA<sub>2</sub> may contribute to the Anti-Inflammatory activity of catechol. *Chem. Biol. Drug Des.* **79**, 143-147.

Abhilash, J., Geethanandan, K., Bharath, S.R., Sadasivan, C. & Haridas, M. (2014). The crystal structure of a lectin from *Butea monosperma* insight into its glycosylation and binding of ligands. *Int. J. Biol. Macromol.* **72**, 1376-1383.

### **Institute of Genomics and Integrative Biology, Delhi**

Kumar, A., Saigal, K., Malhotra, K., Sinha, K.M. & Taneja, B. (2011). Structural and functional characterization of Rv2966c protein reveals an RsmD-like Methyltransferase from *Mycobacterium tuberculosis* and the role of its N-terminal domain in target recognition. *J. Biol. Chem.* **286**, 19652-19661.

Kumar, A., Kumar, S., Kumar, D., Mishra, A., Dewangan, R.P., Shrivastava, P., Ramachandran, S. & Taneja, B. (2013). Crystal structure of Rv3717 reveals a novel amidase from *Mycobacterium tuberculosis*. *Acta Cryst.* **D69**, 2543-2554.

Srivastav, R., Kumar, D., Grover, A., Singh, A., Manjasetty, B., Sharma, R. & Taneja, B. (2014). Unique subunit packing in mycobacterial nanoRNase leads to alternate substrate recognitions in DHH phosphodiesterases. *Nucl. Acids Res.* **42**, 7894-7910.

Kumar, A., Kumar, S. & Taneja, B. (2014). Crystal structure of Rv2372c identifies a RsmE-like methyltransferase from *M. tuberculosis*. *Acta Cryst.* **D70**, 821-832.

### **National Centre for Cell Science, Pune**

Arora, A., Chandra, N.R., Das, A., Gopal, B., Mande, S.C., Prakash, B., Ramachandran R., Sankaranarayanan, R., Sekar, K., Suguna, K., Tyagi, A.K. & Vijayan M. (2011). Structural Biology of Mycobacterium tuberculosis proteins: the Indian Efforts. *Tuberculosis* **91**, 456-458.

Phulera, S. & Mande, S.C. (2013). Crystal structure of *M. tuberculosis* NrdH at 0.87 Å resolution suggests a possible mode of its activity. *Biochemistry* **52**, 4056- 4065.

## Indian Institute of Chemical Technology, Hyderabad

Gumpena, R., Kishor, C., Ganji, R.J. & Addlagatta, A. (2011). Discovery of  $\alpha,\beta$ - and  $\alpha,\gamma$ -diamino acid scaffolds for the inhibition of M1 family aminopeptidases. *Chem. Med. Chem.* **6**, 1971-1976.

Gumpena, R., Kishor, C., Ganji, R. J, Jain, N. & Addlagatta, A. (2012). Glu121-Lys319 salt-bridge between catalytic and N-terminal domains is pivotal for the activity and stability of *E. coli* aminopeptidase N. *Prot. Sci.* **21**, 727-736.

Kishor, C., Gumpena, R., & Reddi, R. & Addlagatta, A. (2012). Structural studies of *Enterococcus faecalis* methionine aminopeptidase and design of microbe specific 2,2'-bipyridine based inhibitors. *Med. Chem.Comm.* **3**, 1406-1412.

Kishor, C., Arya, T., Reddi, R., Chen, X., Saddanapu, V. Marapaka, A.K., Gumpena, R., Ma, D., Liu, J.O. & Addlagatta, A. (2013). Identification, biochemical and structural evaluation of species-specific inhibitors against Type I methionine aminopeptidases. *J. Med. Chem.* **56**, 5295–5305.

Arya, T., Kishor, C., Saddanapu, V., Reddi, R. & Addlagatta, A. (2013). Discovery of a new genetic variant of Methionine Aminopeptidase from Streptococci with possible post-translational modifications: Biochemical and structural characterization. *Plos One* **8**, e75207.

Reddi, R., Arya, T., Kishor, C., Gumpena, R., Ganji, R.J., Bhukya, S. & Addlagatta, A. (2014). Selective targeting of the conserved active site cysteine of *Mycobacterium tuberculosis* methionine aminopeptidase with electrophilic reagents. *FEBS Journal* **281**, 4240-4248.

Ganji, R.J., Reddi, R., Gumpena, R., Marapaka, A.K., Arya, T., Sankuju, P., Bhukya, S. & Addlagatta, A. (2015). Structural basis for the inhibition of M1 family aminopeptidases by the natural product actinonin: Crystal structure in complex with *E. coli* Aminopeptidase N. *Prot. Sci.* **24**, 823-831.

Arya, T., Reddi, R., Kishor, C., Ganji, R.J., Bhukya, S., Gumpena, R., McGowan, S., Drag, M. & Addlagatta, A. (2015). Identification of the molecular basis of inhibitor selectivity between the human and Streptococcal Type I methionine aminopeptidases. *J. Med. Chem.* **12**, 2350-2357.

### **St. Xavier's College, Kolkata**

Biswas, M., Khamrui, S., Sen, U. & Dasgupta, J. (2011). Overexpression, purification, crystallization and preliminary X-ray analysis of CheY4 from *Vibrio cholerae* O395. *Acta Cryst.* **F67**, 1645-1648.

Dey, S. & Dasgupta, J. (2013). Purification, crystallization and preliminary X-ray analysis of the AAA+  $\sigma 54$  activator domain of FlrC from *Vibrio cholerae*. *Acta Cryst.* **F69**, 800-803.

Biswas, M., Dey, S., Khamrui, S., Sen, U. & Dasgupta, J. (2013). Conformational barrier of CheY3 and inability of CheY4 to bind FlhM control the flagellar motor action in *Vibrio cholerae*. *Plos One* **16**, e73923.

Agarwal, S., Biswas, M. & Dasgupta, J. (2015). Purification, crystallization and preliminary X-ray analysis of the periplasmic haem-binding protein HutB from *Vibrio cholerae*. *Acta Cryst.* **F71**, 401-404.

Dey, S., Biswas, M., Sen, U. & Dasgupta, J. (2015). Unique ATPase site architecture triggers cis-mediated synchronized ATP binding in heptameric AAA+-ATPase domain of flagellar regulatory protein FlrC. *J. Biol. Chem.* **290**, 8734-8747.

### **Alagappa University, Karaikudi**

Manimekalai, M.S., Kumar, A., Jeyakanthan, J. & Grüber, G. (2011). The Transition-like State and P<sub>i</sub> Entrance into the Catalytic A Subunit of the Biological Engine A-ATP synthase. *J. Mol. Biol.* **408**, 736-754.

## Indian Institute of Advanced Research, Gandhinagar

Nair, D., Suresh, C.G. & Singh, D.D. (2011). Purification, crystallization and preliminary X-ray characterization of an haemagglutinin from the seeds of *Jatropha curcas*. *Acta Cryst.* **F67**, 1534-1536.

## Institute for Stem Cell Biology and Regenerative Medicine (InStem), Bangalore

Plapp, B.V. & Ramaswamy, S. (2012). Atomic-resolution structures of horse liver alcohol dehydrogenase with NAD<sup>+</sup> and fluoroalcohols define strained michaelis complexes. *Biochemistry* **51**, 4035-4048.

Gangi Setty, T., Cho, C., Govindappa, S., Apicella, M.A. & Ramaswamy, S. (2014). Bacterial periplasmic sialic acid-binding proteins exhibit a conserved binding site. *Acta Cryst.* **D70**, 1801-1811.

Singh, D., Kumari, A., Ramaswamy, S. & Ramanathan, G. (2014). Expression, purification and substrate specificities of 3-nitrotoluene dioxygenase from *Diaphorobacter* sp. strain DS2. *Biochem. Biophys. Res. Commun.* **445**, 36-42.

Gallat, F.-X., Matsugaki, N., Coussens, N.P., Yagi, K.J., Boudes, M., Higashi, T., Tsuji, D., Tatano, Y., Suzuki, M., Mizohata, E., Tono, K., Joti, Y., Kameshima, T., Park, J., Song, C., Hatsui, T., Yabashi, M., Nango, E., Itoh, K., Coulibaly, F., Tobe, S., Ramaswamy, S., Stay, B., Iwata, S. & Chavas, L.M. (2014). In vivo crystallography at X-ray free-electron lasers: the next generation of structural biology? *Philos. Trans. R. Soc. Lond. B. Biol. Sci.* **369** (1647), 20130497.

Ver Heul, A.M., Gakhar, L., Piper, R.C. & Subramanian, R. (2014). Crystal structure of a complex of NOD1 CARD and ubiquitin. *Plos One* **9**, e104017.

## Indian Institute of Technology, Bombay

Tanwar, A.S., Morar, M., Panjikar, S. & Anand, R. (2012). Formylglycinamide ribonucleotide amidotransferase from *Salmonella typhimurium*: role of ATP complexation and the glutaminase domain in catalytic coupling. *Acta Cryst.* **D68**, 627-636.

Bitra, A., Hussain, B., Tanwar, A.S. & Anand, R. (2013). Identification of function and mechanistic insights of guanine deaminase from *Nitrosomonas europaea*: Role of the C-terminal loop in catalysis. *Biochemistry* **52**, 3512-3522.

Bitra, A., Biswas, A. & Anand, R. (2013). Structural basis of the substrate specificity of cytidine deaminase superfamily Guanine deaminase. *Biochemistry* **52**, 8106-8114.

Tanwar, A.S., Goyal, V.D., Choudhary, D., Panjikar, S. & Anand, R. (2013) Importance of hydrophobic cavities in allosteric regulation of formylglycinamide synthetase: insight from xenon trapping and statistical coupling analysis. *Plos One* **8**, e77781.

Bhukya, H., Bhujbalrao, R., Bitra, A. & Anand, R. (2014). Structural and functional basis of transcriptional regulation by TetR family protein CprB from *S. coelicolor* A3(2). *Nucl. Acids Res.* **42**, 10122-10133.

Prakash, P., Walvekar, A.S., Puneekar, N.S. & Bhaumik, P. (2014). Purification, crystallization and preliminary X-ray diffraction analysis of NADP-dependent glutamate dehydrogenase from *Aspergillus niger*. *Acta Cryst.* **F70**, 1508-1512.

Tanwar, A.S, Sindhikara, D.J, Hirata, F. & Anand, R. (2015). Determination of the formylglycinamide ribonucleotide amidotransferase ammonia pathway by combining 3D-RISM theory with experiment. *ACS Chem. Biol.* **10**, 698-704.

Pandey, S., Modak, A., Phale, P.S. & Bhaumik, P. (2015). Cloning, purification, crystallization and preliminary X-ray diffraction studies of periplasmic glucose binding protein of *Pseudomonas putida* CSV86. *Adv. Biosci. Biotechnol.* **6**, 164-171.

**National Institute of Mental Health and Neuro Sciences (NIMHANS),  
Bangalore**

Padmanabhan, B., Nakamura, Y., Antonyuk, S.V., Strange, R.W., Hasnain, S.S., Yokoyama, S. & Bessho, Y. (2013). Structure of the hypothetical DUF1811-family protein GK0453 from *Geobacillus kaustophilus* HTA426. *Acta Cryst.* **F69**, 342-345.

Padmanabhan, B., Yokoyama, S. & Bessho, Y. (2013). Crystal structure of putative CbiT from *Methanocaldococcus jannaschii*: an intermediate enzyme activity in cobalamin (vitamin B12) biosynthesis. *BMC Struct. Biol.* **13**, 10.

Padmanabhan, B., Prashant, D., Yokoyama, S. & Bessho Y. (2015). Crystal structure of the MazG-related nucleoside triphosphate pyrophosphohydrolase from *Thermatoga maritima* MSB8. *J. Struc. Func. Genomics* **16**, 81-89.

**Indian Institute of Technology, Madras**

Aggarwal, N., Mandal, P.K., Gautham, N. & Chadha, A. (2013). Expression, purification, crystallization and preliminary X-ray diffraction analysis of carbonyl reductase from *Candida parapsilosis* ATCC 7330. *Acta Cryst.* **F69**, 313-315.

**Advanced Centre for Treatment, Research and Education in Cancer, Navi  
Mumbai**

Badgujar, D.C., Sawant, U., Vikrant, Yadav, L., Hosur, M.V. & Varma, A.K. (2013). Preliminary crystallographic studies of BRCA1 BRCT-ABRAXAS complex. *Acta Cryst.* **F69**, 1401-1404.

### **Jubilant Biosys Ltd., Bangalore**

Lukacs, C., Belunis, C., Crowther, R., Danho, W., Gao, L., Goggin, B., Janson, C.A., Li, S., Remiszewski, S., Schutt, A., Thakur, M.K., Singh, S.K., Swaminathan, S., Pandey, R., Tyagi, R., Gosu, R., Kamath, A.V. & Kuglstatter, A. (2013). The structure of XIAP BIR2: understanding the selectivity of the BIR domains. *Acta Cryst.* **D69**, 1717-1725.

### **Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore**

Srinivasan B, Forouhar F, Shukla A, Sampangi C, Kulkarni S, Abashidze M, Seetharaman J, Lew S, Mao L, Acton TB, Xiao R, Everett JK, Montelione GT, Tong L, Balaram H. Allosteric regulation and substrate activation in cytosolic nucleotidase II from *Legionella pneumophila*. *FEBS J.* 2014 281:1613-28.

### **Indian Institute of Science Education and Research, Bhopal**

Srivastava, K.V., Chandra, M. & Datta, S. (2014). Crystallization and preliminary X-ray analysis of RabX3, a tandem GTPase from *Entamoeba histolytica*. *Acta Cryst.* **F70**, 933-937.

### **Indian Institute of Chemical Biology, Kolkata**

Dey, S. & Datta S. (2014). Interfacial residues of SpcS chaperone affects binding of effector toxin ExoT in *Pseudomonas aeruginosa*: novel insights from structural and computational studies. *FEBS Journal* **28**, 1267-1280.

### **Central Food Technological Research Institute, Mysuru**

Kumar, V., Murugeson, S., Vithani, N., Prakash, B. & Gowda, L.R. (2015). A salt-bridge stabilized C-terminal hook is critical for the dimerization of a Bowman Birk inhibitor. *Arch. Biochem. Biophys.* **566**, 15-25.



**Indian Institute of Science Education and Research, Pune**

Chand, M.K., Nirwan, N., Diffin, F., van Aelst, K., Kulkarni, M., Pernstich, C., Szczelkun, M.D. & Saikrishnan, K. (2015). Translocation-coupled nucleolytic DNA shredding by the ATP-dependent Type ISP restriction-modification enzymes. *Nature Chem. Biol.* **11**, 870-877.