

LIST OF PUBLICATIONS : 2007 to 2015 (as of 19th October 2015)

BM14 Publications

Year	2016	2015	2014	2013	2012	2011	2010	2009	2008	2007
Publications	33*	63	74	67	58	60	63	61	70	58

*as of 1 September 2016

1. Abhinav KV, Sharma K, Swaminathan CP, Surolia A, Vijayan M: **Jacalin–carbohydrate interactions: distortion of the ligand molecule as a determinant of affinity.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:324–331.
2. Arif SM, Geethanandan K, Mishra P, Surolia A, Varshney U, Vijayan M: **Structural plasticity in *Mycobacterium tuberculosis* uracil-DNA glycosylase (*Mt* Ung) and its functional implications.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:1514–1527.
3. Bandyopadhyay D, Murthy MRN, Balaram H, Balaram P: **Probing the role of highly conserved residues in triosephosphate isomerase – analysis of site specific mutants at positions 64 and 75 in the Plasmodial enzyme.** *FEBS J* 2015, **282**:3863–3882.
4. Bangera M, Panigrahi R, Sagurthi SR, Savithri HS, Murthy MRN: **Structural and functional analysis of two universal stress proteins YdaA and YnaF from *Salmonella typhimurium*: possible roles in microbial stress tolerance.** *Journal of Structural Biology* 2015, **189**:238–250.
5. Barathy DV, Bharambe NG, Syed W, Zaveri A, Visweswariah SS, Colaço M, Misquith S, Suguna K: **Autoinhibitory mechanism and activity-related structural changes in a mycobacterial adenylyl cyclase.** *Journal of Structural Biology* 2015, **190**:304–313.
6. Blažek Bregović V, Halasz I, Basarić N, Mlinarić-Majerski K: **Anthracene adamantylbisurea receptors: switching of anion binding by photocyclization.** *Tetrahedron* 2015, **71**:9321–9327.
7. Bowler MW, Mueller U, Weiss MS, Sanchez-Weatherby J, Sorensen TL-M, Thunnissen MMGM, Ursby T, Gobbo A, Russi S, Bowler MG, et al.: **Automation and Experience of Controlled Crystal Dehydration: Results from the European Synchrotron HC1 Collaboration.** *Crystal Growth & Design* 2015, **15**:1043–1054.
8. Caillat C, Macheboeuf P, Wu Y, McCarthy AA, Boeri-Erba E, Effantin G, Göttlinger HG, Weissenhorn W, Renesto P: **Asymmetric ring structure of Vps4 required for ESCRT-III disassembly.** *Nature Communications* 2015, **6**:8781.
9. Chand MK, Nirwan N, Diffin FM, van Aelst K, Kulkarni M, Pernstich C, Szczelkun MD, Saikrishnan K: **Translocation-coupled DNA cleavage by the Type ISP restriction-modification enzymes [Internet].** *Nat Chem Biol* 2015, advance online publication.
10. Chandran AV, Prabu JR, Nautiyal A, Patil KN, Muniyappa K, Vijayan M: **Structural studies on *Mycobacterium tuberculosis* RecA: Molecular plasticity and interspecies variability.** *J Biosci* 2015, **40**:13–30.
11. Chandran T, Sharma A, Vijayan M: **Structural studies on a non-toxic homologue of type II RIPs from bitter gourd: Molecular basis of non-toxicity, conformational selection and glycan structure.** *J Biosci* 2015, **40**:929–941.
12. Cohen-Dvashi H, Cohen N, Israeli H, Diskin R: **Molecular Mechanism for LAMP1 Recognition by Lassa Virus.** *J. Virol.* 2015, **89**:7584–7592.
13. De Henau S, Tillemans L, Vanghele M, Luyckx E, Trashin S, Pauwels M, Germani F, Vlaeminck C, Vanfleteren JR, Bert W, et al.: **A redox signalling globin is essential for reproduction in *Caenorhabditis elegans*.** *Nature Communications* 2015, **6**:8782.

14. Delaforge E, Milles S, Bouvignies G, Bouvier D, Boivin S, Salvi N, Maurin D, Martel A, Round A, Lemke EA, et al.: **Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin α .** *J. Am. Chem. Soc.* 2015, **137**:15122–15134.
15. Delo CF, Heisler FF, Kuper J, Sander B, Kneussel M, Schindelin H: **The LisH Motif of Muskelin Is Crucial for Oligomerization and Governs Intracellular Localization.** *Structure* 2015, **23**:364–373.
16. Dey S, Biswas M, Sen U, Dasgupta J: **Unique ATPase Site Architecture Triggers cis-Mediated Synchronized ATP Binding in Heptameric AAA+-ATPase Domain of Flagellar Regulatory Protein FlrC.** *J. Biol. Chem.* 2015, **290**:8734–8747.
17. Dror A, Kanteev M, Kagan I, Gihaz S, Shahar A, Fishman A: **Structural insights into methanol-stable variants of lipase T6 from *Geobacillus stearothermophilus*.** *Appl Microbiol Biotechnol* 2015, **99**:9449–9461.
18. Eerde A van, Grahn EM, Winter HC, Goldstein IJ, Krengel U: **Atomic-resolution structure of the α -galactosyl binding Lyophyllum decastes lectin reveals a new protein family found in both fungi and plants.** *Glycobiology* 2015, **25**:492–501.
19. Fichou Y, Schirò G, Gallat F-X, Laguri C, Moulin M, Combet J, Zamponi M, Härtlein M, Picart C, Mossou E, et al.: **Hydration water mobility is enhanced around tau amyloid fibers.** *PNAS* 2015, **112**:6365–6370.
20. Gadd MS, Bulatov E, Ciulli A: **Serendipitous SAD Solution for DMSO-Soaked SOCS2-ElonginC-ElonginB Crystals Using Covalently Incorporated Dimethylarsenic: Insights into Substrate Receptor Conformational Flexibility in Cullin RING Ligases.** *PLoS ONE* 2015, **10**:e0131218.
21. Gourlay LJ, Thomas RJ, Peri C, Conchillo-Solé O, Ferrer-Navarro M, Nithichanon A, Vila J, Daura X, Lertmemongkolchai G, Titball R, et al.: **From crystal structure to *in silico* epitope discovery in the *Burkholderia pseudomallei* flagellar hook-associated protein FlgK.** *FEBS J* 2015, **282**:1319–1333.
22. Goutam K, Gupta AK, Gopal B: **Crystallographic studies of the extracytoplasmic function σ factor σ^J from *Mycobacterium tuberculosis*.** *Acta Crystallographica Section F Structural Biology Communications* 2015, **71**:946–950.
23. Islam Z, Kumar A, Singh S, Salmon L, Karthikeyan S: **Structural Basis for Competitive Inhibition of 3,4-Dihydroxy-2-butanone-4-phosphate Synthase from *Vibrio cholerae*.** *J. Biol. Chem.* 2015, **290**:11293–11308.
24. Jain A, Salunke DM: **Purification, identification and preliminary crystallographic studies of an allergenic protein from *Solanum melongena*.** *Acta Crystallographica Section F Structural Biology Communications* 2015, **71**:221–225.
25. Jamwal A, Round AR, Bannwarth L, Venien-Bryan C, Belrhali H, Yogavel M, Sharma A: **Structural and Functional Highlights of Vacuolar Soluble Protein 1 from Pathogen *Trypanosoma brucei brucei*.** *J. Biol. Chem.* 2015, **290**:30498–30513.
26. Janardan N, Harijan RK, Kiema T-R, Wierenga RK, Murthy MRN: **Structural characterization of a mitochondrial 3-ketoacyl-CoA (T1)-like thiolase from *Mycobacterium smegmatis*.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:2479–2493.
27. Kanteev M, Bregman-Cohen A, Deri B, Shahar A, Adir N, Fishman A: **A crystal structure of 2-hydroxybiphenyl 3-monooxygenase with bound substrate provides insights into the enzymatic mechanism.** *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics* 2015, **1854**:1906–1913.
28. Kottur J, Sharma A, Gore KR, Narayanan N, Samanta B, Pradeepkumar PI, Nair DT: **Unique Structural Features in DNA Polymerase IV Enable Efficient Bypass of the N2 Adduct Induced by the Nitrofurazone Antibiotic.** *Structure* 2015, **23**:56–67.

29. Kumar M, Mukherjee J, Sinha M, Kaur P, Sharma S, Gupta MN, Singh TP: **Enhancement of stability of a lipase by subjecting to three phase partitioning (TPP): structures of native and TPP-treated lipase from *Thermomyces lanuginosa*** [Internet]. *Sustainable Chemical Processes* 2015, **3**.
30. Kumar S, Singh A, Yamini S, Dey S, Singh TP: **Crystal Structure of Mg²⁺ Containing Hemopexin-Fold Protein from Kabuli Chana (Chickpea-White, CW-25) at 2.45 Å Resolution Reveals Its Metal Ion Transport Property.** *Protein J* 2015, **34**:284–290.
31. Labourel A, Jam M, Legentil L, Sylla B, Hehemann J-H, Ferrières V, Czjzek M, Michel G: **Structural and biochemical characterization of the laminarinase Zg LamC_{GH16} from *Zobellia galactanivorans* suggests preferred recognition of branched laminarin.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:173–184.
32. Mahanta P, Bhardwaj A, Kumar K, Reddy VS, Ramakumar S: **Structural insights into N-terminal to C-terminal interactions and implications for thermostability of a (β/α)8-triosephosphate isomerase barrel enzyme.** *FEBS J* 2015, **282**:3543–3555.
33. Majumder S, Khamrui S, Banerjee R, Bhowmik P, Sen U: **A conserved tryptophan (W91) at the barrel-lid junction modulates the packing and stability of Kunitz (STI) family of inhibitors.** *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics* 2015, **1854**:55–64.
34. Mathiharan YK, Savithri HS, Murthy MRN: **Insights into stabilizing interactions in the distorted domain-swapped dimer of *Salmonella typhimurium* survival protein.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:1812–1823.
35. McGovern RE, Snarr BD, Lyons JA, McFarlane J, Whiting AL, Paci I, Hof F, Crowley PB: **Structural study of a small molecule receptor bound to dimethyllysine in lysozyme.** *Chem. Sci.* 2014, **6**:442–449.
36. Mueller-Dieckmann C, Bowler MW, Carpentier P, Flot D, McCarthy AA, Nanao MH, Nurizzo D, Pernot P, Popov A, Round A, et al.: **The status of the macromolecular crystallography beamlines at the European Synchrotron Radiation Facility.** *Eur. Phys. J. Plus* 2015, **130**:1–11.
37. Navratna V, Reddy G, Gopal B: **Structural basis for the catalytic mechanism of homoserine dehydrogenase.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:1216–1225.
38. Normand BV-L, Faber BW, Saul FA, Eijk M van der, Thomas AW, Singh B, Kocken CHM, Bentley GA: **Crystal Structure of Plasmodium knowlesi Apical Membrane Antigen 1 and Its Complex with an Invasion-Inhibitory Monoclonal Antibody.** *PLOS ONE* 2015, **10**:e0123567.
39. Pakharukova N, Garnett JA, Tuittila M, Paavilainen S, Diallo M, Xu Y, Matthews SJ, Zavialov AV: **Structural Insight into Archaic and Alternative Chaperone-Usher Pathways Reveals a Novel Mechanism of Pilus Biogenesis.** *PLOS Pathog* 2015, **11**:e1005269.
40. Pakharukova N, Tuittila M, Paavilainen S, Zavialov A: **Crystallization and preliminary X-ray diffraction analysis of the Cs_u pili Cs_uC–Cs_uA/B chaperone–major subunit pre-assembly complex from *Acinetobacter baumannii*.** *Acta Crystallographica Section F Structural Biology Communications* 2015, **71**:770–774.
41. Paul R, Patra MD, Sen U: **Crystal Structure of Apo and Ligand Bound *Vibrio cholerae* Ribokinase (Vc-RK): Role of Monovalent Cation Induced Activation and Structural Flexibility in Sugar Phosphorylation** [Internet]. In *Biochemical Roles of Eukaryotic Cell Surface Macromolecules*. Edited by Chakrabarti A, Surolia A. Springer International Publishing; 2015:293–307.
42. Poyraz Ö, Brunner K, Lohkamp B, Axelsson H, Hammarström LGJ, Schnell R, Schneider G: **Crystal Structures of the Kinase Domain of the Sulfate-Activating Complex in *Mycobacterium tuberculosis*.** *PLoS ONE* 2015, **10**:e0121494.
43. Pozzi C, Di Pisa F, Lalli D, Rosa C, Theil E, Turano P, Mangani S: **Time-lapse anomalous X-ray diffraction shows how Fe²⁺ substrate ions move through ferritin protein nanocages to oxidoreductase sites.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:941–953.

44. Raman S, Singh M, Tatu U, Suguna K: **First Structural View of a Peptide Interacting with the Nucleotide Binding Domain of Heat Shock Protein 90.** *Scientific Reports* 2015, **5**:17015.
45. Raman S, Suguna K: **Functional characterization of heat-shock protein 90 from *Oryza sativa* and crystal structure of its N-terminal domain.** *Acta Crystallographica Section F Structural Biology Communications* 2015, **71**:688–696.
46. Roy SP: **Structure and host-receptor recognition studies of Gram-negative bacterial fimbriae assembled via the chaperone/usher pathway [Internet].** 2015, [no volume].
47. Schaefer CM, Lu R, Nesbitt NM, Schiebel J, Sampson NS, Kisker C: **FadA5 a Thiolase from *Mycobacterium tuberculosis*: A Steroid-Binding Pocket Reveals the Potential for Drug Development against Tuberculosis.** *Structure* 2015, **23**:21–33.
48. Shaik MM, Lombardi C, Trindade DM, Fenel D, Schoehn G, Guilmi AMD, Dessen A: **A Structural Snapshot of Type II Pilus Formation in *Streptococcus pneumoniae*.** *J. Biol. Chem.* 2015, **290**:22581–22592.
49. Shukla PK, Gautam L, Sinha M, Kaur P, Sharma S, Singh TP: **Structures and binding studies of the complexes of phospholipase A2 with five inhibitors.** *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics* 2015, **1854**:269–277.
50. Singh AK, Manjasetty B, GL B, Koul S, Kaushik A, Ekka MK, Singh V, Kumaran S: **Crystal Structure of Fad35R from *Mycobacterium tuberculosis* H37Rv in the Apo-State.** *PLoS ONE* 2015, **10**:e0124333.
51. Singh RP, Singh A, Kushwaha GS, Singh AK, Kaur P, Sharma S, Singh TP: **Mode of binding of the antithyroid drug propylthiouracil to mammalian haem peroxidases.** *Acta Crystallographica Section F Structural Biology Communications* 2015, **71**:304–310.
52. Srivastava M, Duan G, Kershaw NJ, Athanasopoulos V, Yeo JHC, Ose T, Hu D, Brown SHJ, Jergic S, Patel HR, et al.: **Roquin binds microRNA-146a and Argonaute2 to regulate microRNA homeostasis [Internet].** *Nat Commun* 2015, **6**.
53. Srivastava S, Chaudhary S, Thukral L, Shi C, Gupta RD, Gupta R, Priyadarshan K, Vats A, Haque AS, Sankaranarayanan R, et al.: **Unsaturated Lipid Assimilation by Mycobacteria Requires Auxiliary cis-trans Enoyl CoA Isomerase.** *Chemistry & Biology* 2015, **22**:1577–1587.
54. Srivastava V kumar, Chandra M, Saito-Nakano Y, Nozaki T, Datta S: **Crystal Structure Analysis of Wild Type and Fast Hydrolyzing Mutant of EhRabX3, a Tandem Ras Superfamily GTPase from Entamoeba histolytica.** *Journal of Molecular Biology* 2016, **428**:41–51.
55. Sulzenbacher G, Roig-Zamboni V, Peumans WJ, Henrissat B, van Damme EJM, Bourne Y: **Structural basis for carbohydrate binding properties of a plant chitinase-like agglutinin with conserved catalytic machinery.** *Journal of Structural Biology* 2015, **190**:115–121.
56. Swier LJYM, Monjas L, Guskov A, de Voogd AR, Erkens GB, Slotboom DJ, Hirsch AKH: **Structure-Based Design of Potent Small-Molecule Binders to the S-Component of the ECF Transporter for Thiamine.** *ChemBioChem* 2015, **16**:819–826.
57. Thirugnanasambandam A, Karthik S, Mandal PK, Gautham N: **The novel double-folded structure of d(GCATGCATGC): a possible model for triplet-repeat sequences.** *Acta Crystallographica Section D Biological Crystallography* 2015, **71**:2119–2126.
58. Trubitsyna M, Grey H, Houston DR, Finnegan DJ, Richardson JM: **Structural Basis for the Inverted Repeat Preferences of mariner Transposases.** *J. Biol. Chem.* 2015, **290**:13531–13540.
59. Vallese F, Percudani R, Fischer W, Zanotti G: **The crystal structure of Helicobacter pylori HP1029 highlights the functional diversity of the sialic acid-related DUF386 family.** *FEBS J* 2015, **282**:3311–3322.

60. van Rooyen JM, Hakimi M-A, Belrhali H: **Recombinant expression, purification, and crystallization of the glutaminyl-tRNA synthetase from *Toxoplasma gondii*.** *Protein Expression and Purification* 2015, **110**:115–121.
61. Venditto I, Bule P, Thompson A, Sanchez-Weatherby J, Sandy J, Ferreira LMA, Fontes CMGA, Najmudin S: **Expression, purification, crystallization and preliminary X-ray analysis of CttA, a putative cellulose-binding protein from *Ruminococcus flavefaciens*.** *Acta Crystallographica Section F Structural Biology Communications* 2015, **71**:784–789.
62. Yamini S, Pandey SN, Kaur P, Sharma S, Singh TP: **Binding and structural studies of the complexes of type 1 ribosome inactivating protein from *Momordica balsamina* with cytosine, cytidine, and cytidine diphosphate.** *Biochemistry and Biophysics Reports* 2015, **4**:134–140.
63. Zou T, Risso VA, Gavira JA, Sanchez-Ruiz JM, Ozkan SB: **Evolution of Conformational Dynamics Determines the Conversion of a Promiscuous Generalist into a Specialist Enzyme.** *Mol Biol Evol* 2015, **32**:132–143.

2014

1. Abraini JH, Marassio G, David HN, Vallone B, Prangé T, Colloc'h N: **Crystallographic Studies with Xenon and Nitrous Oxide Provide Evidence for Protein-dependent Processes in the Mechanisms of General Anesthesia:** *Anesthesiology* 2014, **121**:1018–1027.
2. Arif SM, Sang PB, Varshney U, Vijayan M: **Crystallization and preliminary X-ray characterization of MutT2, MSMEG_5148 from *Mycobacterium smegmatis*.** *Acta Cryst F, Acta Cryst Sect F, Acta Crystallogr F, Acta Crystallogr Sect F, Acta Cryst F Struct Biol Cryst Commun, Acta Cryst Sect F Struct Biol Cryst Commun, Acta Crystallogr Sect F Struct Biol Cryst Commun* 2014, **70**:190–192.
3. Azim N, Deery E, Warren MJ, Wolfenden BAA, Erskine P, Cooper JB, Coker A, Wood SP, Akhtar M: **Structural evidence for the partially oxidized dipyrromethene and dipyrromethanone forms of the cofactor of porphobilinogen deaminase: structures of the *Bacillus megaterium* enzyme at near-atomic resolution.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:744–751.
4. Banerjee S, Agrawal MJ, Mishra D, Sharan S, Balaram H, Savithri HS, Murthy MRN: **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* 2014, **281**:1642–1658.
5. Barak R, Lahmi R, Gevorkyan-Airapetov L, Levy E, Tzur A, Opatowsky Y: **Crystal structure of the extracellular juxtamembrane region of Robo1.** *Journal of Structural Biology* 2014, **186**:283–291.
6. Barathy D, Mattoo R, Visweswariah S, Suguna K: **New structural forms of a mycobacterial adenylyl cyclase Rv1625c.** *IUCrJ* 2014, **1**:338–348.
7. Beaven G, Bowyer A, Erskine P, Wood SP, McCoy A, Coates L, Keegan R, Lebedev A, Hopper DJ, Kaderbhai MA, et al.: **Crystallization and preliminary X-ray characterization of the 2,4'-dihydroxyacetophenone dioxygenase from *Alcaligenes* sp. 4HAP.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:823–826.
8. Bezerra GA, Viertlmayr R, Moura TR, Delatorre P, Rocha BAM, do Nascimento KS, Figueiredo JG, Bezerra IG, Teixeira CS, Simões RC, et al.: **Structural Studies of an Anti-Inflammatory Lectin from *Canavalia boliviiana* Seeds in Complex with Dimannosides.** *PLoS ONE* 2014, **9**:e97015.
9. Bhukya H, Bhujbalrao R, Bitra A, Anand R: **Structural and functional basis of transcriptional regulation by TetR family protein CprB from *S. coelicolor* A3(2).** *Nucl. Acids Res.* 2014, **42**:10122–10133.

10. Breugel M van, Wilcken R, McLaughlin SH, Rutherford TJ, Johnson CM: **Structure of the SAS-6 cartwheel hub from Leishmania major**. *eLife Sciences* 2014, **3**:e01812.
11. Buch M, Wine Y, Dror Y, Rosenheck S, Lebendiker M, Giordano R, Leal RMF, Popov AN, Freeman A, Frolow F: **Protein products obtained by site-preferred partial crosslinking in protein crystals and “liberated” by redissolution**. *Biotechnol. Bioeng.* 2014, **111**:1296–1303.
12. Buschmann S, Richers S, Ermler U, Michel H: **A decade of crystallization drops: Crystallization of the cbb3 cytochrome c oxidase from Pseudomonas stutzeri**. *Protein Science* 2014, **23**:411–422.
13. Clerici M, Deniaud A, Boehm V, Gehring NH, Schaffitzel C, Cusack S: **Structural and functional analysis of the three MIF4G domains of nonsense-mediated decay factor UPF2**. *Nucl. Acids Res.* 2014, **42**:2673–2686.
14. Colloc'h N, Prangé T: **Functional relevance of the internal hydrophobic cavity of urate oxidase**. *FEBS Letters* 2014, **588**:1715–1719.
15. Dann R, Lansky S, Lavid N, Zehavi A, Belakhov V, Baasov T, Dvir H, Manjasetty B, Belrhali H, Shoham Y, et al.: **Preliminary crystallographic analysis of Xyn52B2, a GH52 β- D -xylosidase from Geobacillus stearothermophilus T6**. *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:1675–1682.
16. Das U, Pogenberg V, Subramanyam UKT, Wilmanns M, Gourinath S, Srinivasan A: **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**. *Journal of Structural Biology* 2014, **188**:249–258.
17. de Rosa M, Bemporad F, Pellegrino S, Chiti F, Bolognesi M, Ricagno S: **Edge strand engineering prevents native-like aggregation in Sulfolobus solfataricus acylphosphatase**. *FEBS J* 2014, **281**:4072–4084.
18. Dias J, Nguyen NV, Georgiev P, Gaub A, Brettschneider J, Cusack S, Kadlec J, Akhtar A: **Structural analysis of the KANSL1/WDR5/KANSL2 complex reveals that WDR5 is required for efficient assembly and chromatin targeting of the NSL complex**. *Genes Dev.* 2014, **28**:929–942.
19. Discola KF, Förster A, Boulay F, Simorre J-P, Attree I, Dessen A, Job V: **Membrane and Chaperone Recognition by the Major Translocator Protein PopB of the Type III Secretion System of Pseudomonas aeruginosa**. *J. Biol. Chem.* 2014, **289**:3591–3601.
20. Faisal Tarique K, Arif Abdul Rehman S, Betzel C, Gourinath S: **Structure-based identification of inositol polyphosphate 1-phosphatase from Entamoeba histolytica**. *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:3023–3033.
21. Gabison L, Colloc'h N, Prangé T: **Azide inhibition of urate oxidase**. *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:896–902.
22. Galdeano C, Gadd MS, Soares P, Scaffidi S, Van Molle I, Birced I, Hewitt S, Dias DM, Ciulli A: **Structure-Guided Design and Optimization of Small Molecules Targeting the Protein–Protein Interaction between the von Hippel–Lindau (VHL) E3 Ubiquitin Ligase and the Hypoxia Inducible Factor (HIF) Alpha Subunit with in Vitro Nanomolar Affinities**. *J. Med. Chem.* 2014, **57**:8657–8663.
23. Gangwar SP, Meena SR, Saxena AK: **Comparison of four different crystal forms of the Mycobacterium tuberculosis ESX-1 secreted protein regulator EspR**. *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:433–437.
24. Gangwar SP, Meena SR, Saxena AK: **Structure of the carboxy-terminal domain of Mycobacterium tuberculosis CarD protein: an essential rRNA transcriptional regulator**. *Acta Cryst F, Acta Cryst Sect F, Acta Crystallogr F, Acta Crystallogr Sect F, Acta Cryst F Struct Biol Cryst Commun, Acta Cryst Sect F Struct Biol Cryst Commun, Acta Crystallogr Sect F Struct Biol Cryst Commun* 2014, **70**:160–165.

25. Guilligay D, Kadlec J, Crépin T, Lunardi T, Bouvier D, Kochs G, Ruigrok RWH, Cusack S: **Comparative Structural and Functional Analysis of Orthomyxovirus Polymerase Cap-Snatching Domains.** *PLoS ONE* 2014, **9**:e84973.
26. Halabelian L, Ricagno S, Giorgetti S, Santambrogio C, Barbiroli A, Pellegrino S, Achour A, Grandori R, Marchese L, Raimondi S, et al.: **Class I Major Histocompatibility Complex, the Trojan Horse for Secretion of Amyloidogenic β 2-Microglobulin.** *J. Biol. Chem.* 2014, **289**:3318–3327.
27. Hofbauer S, Gysel K, Bellei M, Hagemüller A, Schaffner I, Mlynek G, Kostan J, Pirker KF, Daims H, Furtmüller PG, et al.: **Manipulating Conserved Heme Cavity Residues of Chlorite Dismutase: Effect on Structure, Redox Chemistry, and Reactivity.** *Biochemistry* 2014, **53**:77–89.
28. Karkehabadi S, Helmich KE, Kaper T, Hansson H, Mikkelsen N-E, Gudmundsson M, Piens K, Fujdala M, Banerjee G, Scott-Craig JS, et al.: **Biochemical Characterization and Crystal Structures of a Fungal Family 3 β -Glucosidase, Cel3A from Hypocrea jecorina.** *J. Biol. Chem.* 2014, **289**:31624–31637.
29. Keegan R, Lebedev A, Erskine P, Guo J, Wood SP, Hopper DJ, Rigby SEJ, Cooper JB: **Structure of the 2,4'-dihydroxyacetophenone dioxygenase from *Alcaligenes* sp. 4HAP.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:2444–2454.
30. Khan S, Sharma A, Belrhali H, Yogavel M, Sharma A: **Structural basis of malaria parasite lysyl-tRNA synthetase inhibition by cladosporin.** *J Struct Funct Genomics* 2014, **15**:63–71.
31. Klejnot M, Falnikar A, Ulaganathan V, Cross RA, Baas PW, Kozielski F: **The crystal structure and biochemical characterization of Kif15: a bifunctional molecular motor involved in bipolar spindle formation and neuronal development.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:123–133.
32. Kolstoe SE, Jenvey MC, Purvis A, Light ME, Thompson D, Hughes P, Pepys MB, Wood SP: **Interaction of serum amyloid P component with hexanoyl bis(D -proline) (CPHPC).** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:2232–2240.
33. Kumar A, Kumar S, Taneja B: **The structure of Rv2372c identifies an RsmE-like methyltransferase from Mycobacterium tuberculosis.** *Acta Cryst D, Acta Cryst Sect D, Acta Crystallogr D, Acta Crystallogr Sect D, Acta Crystallogr D Biol Crystallogr, Acta Crystallogr Sect D Biol Crystallogr* 2014, **70**:821–832.
34. Kumar N, Somlata, Mazumder M, Dutta P, Maiti S, Gourinath S: **EhCoactosin Stabilizes Actin Filaments in the Protist Parasite Entamoeba histolytica.** *PLoS Pathog* 2014, **10**:e1004362.
35. Kumar S, Aslam S, Mazumder M, Dahiya P, Murmu A, Manjasetty BA, Zaidi R, Bhattacharya A, Gourinath S: **Crystal Structure of Calcium Binding Protein-5 from Entamoeba histolytica and Its Involvement in Initiation of Phagocytosis of Human Erythrocytes.** *PLoS Pathog* 2014, **10**:e1004532.
36. Kumar S, Kumar N, Alam N, Gourinath S: **Crystal structure of serine acetyl transferase from Brucella abortus and its complex with coenzyme A.** *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics* 2014, **1844**:1741–1748.
37. Kumar Srivastava V, Chandra M, Datta S: **Crystallization and preliminary X-ray analysis of RabX3, a tandem GTPase from Entamoeba histolytica.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:933–937.
38. Kyrieleis OJP, Chang J, de la Peña M, Shuman S, Cusack S: **Crystal Structure of Vaccinia Virus mRNA Capping Enzyme Provides Insights into the Mechanism and Evolution of the Capping Apparatus.** *Structure* 2014, **22**:452–465.
39. Lallement P-A, Meux E, Gualberto JM, Prosper P, Didierjean C, Saul F, Haouz A, Rouhier N, Hecker A: **Structural and enzymatic insights into Lambda glutathione transferases from Populus trichocarpa, monomeric enzymes constituting an early divergent class specific to terrestrial plants.** *Biochemical Journal* 2014, **462**:39–52.

40. Lansky S, Alalouf O, Salama R, Dvir H, Shoham Y, Shoham G: **Preliminary crystallographic analysis of a double mutant of the acetyl xylo-oligosaccharide esterase Axe2 in its dimeric form.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:476–481.
41. Lansky S, Alalouf O, Solomon HV, Alhassid A, Govada L, Chayen NE, Belrhali H, Shoham Y, Shoham G: **A unique octameric structure of Axe2, an intracellular acetyl-xylooligosaccharide esterase from *Geobacillus stearothermophilus*.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:261–278.
42. Lansky S, Salama R, Dann R, Shner I, Manjasetty BA, Belrhali H, Shoham Y, Shoham G: **Cloning, purification and preliminary crystallographic analysis of Ara127N, a GH127 β -L-arabinofuranosidase from *Geobacillus stearothermophilus* T6.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:1038–1045.
43. Lansky S, Salama R, Solomon HV, Feinberg H, Belrhali H, Shoham Y, Shoham G: **Structure–specificity relationships in Abp, a GH27 β -L-arabinopyranosidase from *Geobacillus stearothermophilus* T6.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:2994–3012.
44. Lansky S, Zehavi A, Dann R, Dvir H, Belrhali H, Shoham Y, Shoham G: **Purification, crystallization and preliminary crystallographic analysis of Gan1D, a GH1 6-phospho- β -galactosidase from *Geobacillus stearothermophilus* T1.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:225–231.
45. Lassaux P, Conchillo-Solé O, Manjasetty BA, Yero D, Perletti L, Belrhali H, Daura X, Gourlay LJ, Bolognesi M: **Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PilO2Bp S-SAD Crystal Structure.** *PLoS ONE* 2014, **9**:e94981.
46. Lebreton A, Job V, Ragon M, Monnier AL, Dessen A, Cossart P, Bierne H: **Structural Basis for the Inhibition of the Chromatin Repressor BAH1 by the Bacterial Nucleomodulin LntA.** *mBio* 2014, **5**:e00775–13.
47. Manhas R, Tripathi P, Khan S, Lakshmi BS, Lal SK, Gowri VS, Sharma A, Madhubala R: **Identification and Functional Characterization of a Novel Bacterial Type Asparagine Synthetase A A tRNA SYNTHETASE PARALOG FROM LEISHMANIA DONOVANI.** *J. Biol. Chem.* 2014, **289**:12096–12108.
48. Möller S, Alfieri A, Bertinetti D, Aquila M, Schwede F, Lolicato M, Rehmann H, Moroni A, Herberg FW: **Cyclic Nucleotide Mapping of Hyperpolarization-Activated Cyclic Nucleotide-Gated (HCN) Channels.** *ACS Chem. Biol.* 2014, **9**:1128–1137.
49. Neznansky A, Blus-Kadosh I, Yerushalmi G, Banin E, Opatowsky Y: **The *Pseudomonas aeruginosa* phosphate transport protein PstS plays a phosphate-independent role in biofilm formation.** *FASEB J* 2014, **28**:5223–5233.
50. Neznansky A, Opatowsky Y: **Expression, purification and crystallization of the phosphate-binding PstS protein from *Pseudomonas aeruginosa*.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:906–910.
51. Otrelo-Cardoso AR, da Silva Correia MA, Schwuchow V, Svergun DI, Romão MJ, Leimkühler S, Santos-Silva T: **Structural Data on the Periplasmic Aldehyde Oxidoreductase PaoABC from *Escherichia coli*: SAXS and Preliminary X-ray Crystallography Analysis.** *International Journal of Molecular Sciences* 2014, **15**:2223–2236.
52. Paul R, Dandopath Patra M, Banerjee R, Sen U: **Crystallization and preliminary X-ray analysis of a ribokinase from *Vibrio cholerae* O395.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:1098–1102.
53. Poulsen C, Panjikar S, Holton SJ, Wilmanns M, Song Y-H: **WXG100 Protein Superfamily Consists of Three Subfamilies and Exhibits an α -Helical C-Terminal Conserved Residue Pattern.** *PLoS ONE* 2014, **9**:e89313.

54. Purushothaman M, Varghese A, Mandal PK, Gautham N: **Structure of d(CCCCGGTACCGGGG) ₂ at 1.65 Å resolution.** *Acta Crystallographica Section F Structural Biology Communications* 2014, **70**:860–865.
55. Quarantini S, Cendron L, Zanotti G: **Crystal structure of the secreted protein HP1454 from the human pathogen Helicobacter pylori.** *Proteins* 2014, **82**:2868–2873.
56. Rastogi N, Singh A, Pandey SN, Sinha M, Bhushan A, Kaur P, Sharma S, Singh TP: **Structure of the iron-free true C-terminal half of bovine lactoferrin produced by tryptic digestion and its functional significance in the gut.** *FEBS J* 2014, **281**:2871–2882.
57. Renko M, Taler-Verčič A, Mihelič M, Žerovnik E, Turk D: **Partial rotational lattice order-disorder in stefin B crystals.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:1015–1025.
58. Risso VA, Gavira JA, Gaucher EA, Sanchez-Ruiz JM: **Phenotypic comparisons of consensus variants versus laboratory resurrections of Precambrian proteins.** *Proteins* 2014, **82**:887–896.
59. Sachyani D, Dvir M, Strulovich R, Tria G, Tobelaim W, Peretz A, Pongs O, Svergun D, Attali B, Hirsch JA: **Structural Basis of a Kv7.1 Potassium Channel Gating Module: Studies of the Intracellular C-Terminal Domain in Complex with Calmodulin.** *Structure* 2014, **22**:1582–1594.
60. Shaik MM, Cendron L, Salamina M, Ruzzene M, Zanotti G: **Helicobacter pylori periplasmic receptor CeuE (HP1561) modulates its nickel affinity via organic metallophores.** *Molecular Microbiology* 2014, **91**:724–735.
61. Singh AK, Menéndez-Conejero R, San Martín C, van Raaij MJ: **Crystal Structure of the Fibre Head Domain of the Atadenovirus Snake Adenovirus 1.** *PLoS ONE* 2014, **9**:e114373.
62. Singh A, Gautam L, Sinha M, Bhushan A, Kaur P, Sharma S, Singh TP: **Crystal structure of peptidyl-tRNA hydrolase from a Gram-positive bacterium, Streptococcus pyogenes at 2.19 Å resolution shows the closed structure of the substrate-binding cleft.** *FEBS Open Bio* 2014, **4**:915–922.
63. Singh A, Kumar A, Gautam L, Sharma P, Sinha M, Bhushan A, Kaur P, Sharma S, Arora A, Singh TP: **Structural and binding studies of peptidyl-tRNA hydrolase from Pseudomonas aeruginosa provide a platform for the structure-based inhibitor design against peptidyl-tRNA hydrolase.** *Biochemical Journal* 2014, **463**:329–337.
64. Singh RK, Raj I, Pujari R, Gourinath S: **Crystal structures and kinetics of Type III 3-phosphoglycerate dehydrogenase reveal catalysis by lysine.** *FEBS J* 2014, **281**:5498–5512.
65. Squeglia F, Ruggiero A, Romano M, Vitagliano L, Berisio R: **Mutational and structural study of RipA, a key enzyme in *Mycobacterium tuberculosis* cell division: evidence for the L -to- D inversion of configuration of the catalytic cysteine.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:2295–2300.
66. Srivastav R, Kumar D, Grover A, Singh A, Manjasetty BA, Sharma R, Taneja B: **Unique subunit packing in mycobacterial nanoRNase leads to alternate substrate recognitions in DHH phosphodiesterases.** *Nucl. Acids Res.* 2014, doi:10.1093/nar/gku425.
67. Srivastava SK, Rajasree K, Fasim A, Arakere G, Gopal B: **Influence of the AgrC-AgrA Complex on the Response Time of *Staphylococcus aureus* Quorum Sensing.** *J. Bacteriol.* 2014, **196**:2876–2888.
68. Steinkellner G, Gruber CC, Pavkov-Keller T, Binter A, Steiner K, Winkler C, Łyskowski A, Schwamberger O, Oberer M, Schwab H, et al.: **Identification of promiscuous ene-reductase activity by mining structural databases using active site constellations [Internet].** *Nat Commun* 2014, **5**.
69. Surana P, Satchidanandam V, Nair DT: **RNA-dependent RNA polymerase of Japanese encephalitis virus binds the initiator nucleotide GTP to form a mechanistically important pre-initiation state.** *Nucl. Acids Res.* 2014, **42**:2758–2773.

70. Tamir S, Eisenberg-Domovich Y, Conlan AR, Stofleth JT, Lipper CH, Paddock ML, Mittler R, Jennings PA, Livnah O, Nechushtai R: **A point mutation in the [2Fe–2S] cluster binding region of the NAF-1 protein (H114C) dramatically hinders the cluster donor properties.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:1572–1578.
71. Temmerman K, de Diego I, Poggenberg V, Simon B, Jonko W, Li X, Wilmanns M: **A PEF/Y Substrate Recognition and Signature Motif Plays a Critical Role in DAPK-Related Kinase Activity.** *Chemistry & Biology* 2014, **21**:264–273.
72. Yogavel M, Tripathi T, Gupta A, Banday MM, Rahlf S, Becker K, Belrhali H, Sharma A: **Atomic resolution crystal structure of glutaredoxin 1 from *Plasmodium falciparum* and comparison with other glutaredoxins.** *Acta Crystallographica Section D Biological Crystallography* 2014, **70**:91–100.
73. Zimmerman E, Bashan A, Yonath A: **Antibiotics at the Ribosomal Exit Tunnel—Selected Structural Aspects [Internet].** In *Antibiotics*. Edited by Gualerzi CO, Brandi L, Fabbretti A, Pon CL. Wiley-VCH Verlag GmbH & Co. KGaA; 2013:509–524.
74. Žurga S, Pohleven J, Renko M, Bleuler-Martinez S, Sosnowski P, Turk D, Künzler M, Kos J, Sabotić J: **A novel β-trefoil lectin from the parasol mushroom (*Macrolepiota procera*) is nematotoxic.** *FEBS J* 2014, **281**:3489–3506.

2013

1. Ahangar MS, Vyas R, Nasir N, Biswal BK: **Structures of native, substrate-bound and inhibited forms of *Mycobacterium tuberculosis* imidazoleglycerol-phosphate dehydratase.** *Acta Crystallographica Section D Biological Crystallography* 2013, **69**:2461–2467.
2. Badgjar DC, Sawant U, Vikrant, Yadav L, Hosur MV, Varma AK: **Preliminary crystallographic studies of BRCA1 BRCT-ABRAXAS complex.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:1401–1404.
3. Barak R, Opatowsky Y: **Expression, derivatization, crystallization and experimental phasing of an extracellular segment of the human Robo1 receptor.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:771–775.
4. Barathy DV, Suguna K: **Crystal structure of a putative aspartic proteinase domain of the *Mycobacterium tuberculosis* cell surface antigen PE_PGRS16.** *FEBS Open Bio* 2013, **3**:256–262.
5. Benini S, Chechik M, Ortiz Lombardía M, Polier S, Leech A, Shevtsov MB, Alonso JC: **The 1.58 Å resolution structure of the DNA-binding domain of bacteriophage SF6 small terminase provides new hints on DNA binding.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:376–381.
6. Bertolacci L, Romeo E, Veronesi M, Magotti P, Albani C, Dionisi M, Lambruschini C, Scarpelli R, Cavalli A, De Vivo M, et al.: **A binding site for nonsteroidal anti-inflammatory drugs in fatty acid amide hydrolase.** *J. Am. Chem. Soc.* 2013, **135**:22–25.
7. Bitra A, Biswas A, Anand R: **Structural Basis of the Substrate Specificity of Cytidine Deaminase Superfamily Guanine Deaminase.** *Biochemistry* 2013, **52**:8106–8114.
8. Bitra A, Hussain B, Tanwar AS, Anand R: **Identification of Function and Mechanistic Insights of Guanine Deaminase from *Nitrosomonas europaea*: Role of the C-Terminal Loop in Catalysis.** *Biochemistry* 2013, **52**:3512–3522.
9. Blažek V, Molčanov K, Mlinarić-Majerski K, Kojić-Prodić B, Basarić N: **Adamantane bisurea derivatives: anion binding in the solution and in the solid state.** *Tetrahedron* 2013, **69**:517–526.

10. Chowdhury R, Candela-Lena JI, Chan MC, Greenald DJ, Yeoh KK, Tian Y-M, McDonough MA, Tumber A, Rose NR, Conejo-Garcia A, et al.: **Selective Small Molecule Probes for the Hypoxia Inducible Factor (HIF) Prolyl Hydroxylases.** *ACS Chem. Biol.* 2013, **8**:1488–1496.
11. Correale S, Ruggiero A, Capparelli R, Pedone E, Berisio R: **Structures of free and inhibited forms of the L₊D-transpeptidase Ldt_{Mt1} from *Mycobacterium tuberculosis*.** *Acta Crystallographica Section D Biological Crystallography* 2013, **69**:1697–1706.
12. Correale S, Ruggiero A, Pedone E, Berisio R: **Expression, purification, crystallization and preliminary X-ray crystallographic analysis of the L₊D-transpeptidase Ldt_{Mt1} from *Mycobacterium tuberculosis*.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:253–256.
13. Das U, Kumar N, Gourinath S, Srinivasan A: **Preliminary crystallographic analysis of recombinant VapBC-15 toxin-antitoxin complex from *Mycobacterium tuberculosis*.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:1242–1245.
14. Dey S, Dasgupta J: **Purification, crystallization and preliminary X-ray analysis of the AAA⁺ σ⁵⁴ activator domain of FlrC from *Vibrio cholerae*.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:800–803.
15. Eulenburg G, Higman VA, Diehl A, Wilmanns M, Holton SJ: **Structural and biochemical characterization of Rv2140c, a phosphatidylethanolamine-binding protein from *Mycobacterium tuberculosis*.** *FEBS Letters* 2013, **587**:2936–2942.
16. Gaboriaud C, Gupta RK, Martin L, Lacroix M, Serre L, Teillet F, Arlaud GJ, Rossi V, Thielens NM: **The Serine Protease Domain of MASP-3: Enzymatic Properties and Crystal Structure in Complex with Ecotin.** *PLoS ONE* 2013, **8**:e67962.
17. Gallego del Sol F, Marina A: **Structural Basis of Rap Phosphatase Inhibition by Phr Peptides.** *PLoS Biol* 2013, **11**:e1001511.
18. Girish TS, B V, Colaco M, Misquith S, Gopal B: **Structure of an amidohydrolase, SACOL0085, from methicillin-resistant *Staphylococcus aureus* COL.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2013, **69**:103–108.
19. Green V, Curtis FA, Sedelnikova S, Rafferty JB, Sharples GJ: **Mutants of phage bIL67 RuvC with enhanced Holliday junction binding selectivity and resolution symmetry.** *Molecular Microbiology* 2013, **89**:1240–1258.
20. Hrast M, Turk S, Sosič I, Knez D, Randall CP, Barreteau H, Contreras-Martel C, Dessen A, O'Neill AJ, Mengin-Lecreux D, et al.: **Structure-activity relationships of new cyanothiophene inhibitors of the essential peptidoglycan biosynthesis enzyme MurF.** *European Journal of Medicinal Chemistry* 2013, **66**:32–45.
21. Jacewicz A, Izumi A, Brunner K, Schnell R, Schneider G: **Structural Insights into the UbiD Protein Family from the Crystal Structure of PA0254 from *Pseudomonas aeruginosa*.** *PLoS ONE* 2013, **8**:e63161.
22. Jacobson F, Karkehabadi S, Hansson H, Goedegebuur F, Wallace L, Mitchinson C, Piens K, Stals I, Sandgren M: **The Crystal Structure of the Core Domain of a Cellulose Induced Protein (Cip1) from Hypocrea jecorina, at 1.5 Å Resolution.** *PLoS ONE* 2013, **8**:e70562.
23. Jain D, Nair DT: **Spacing between core recognition motifs determines relative orientation of AraR monomers on bipartite operators.** *Nucleic Acids Res.* 2013, **41**:639–647.
24. Jaiswal RK, Prabha TS, Manjeera G, Gopal B: **Mycobacterium tuberculosis RsdA provides a conformational rationale for selective regulation of σ-factor activity by proteolysis.** *Nucleic Acids Res.* 2013, **41**:3414–3423.

25. Jank T, Bogdanović X, Wirth C, Haaf E, Spoerner M, Böhmer KE, Steinemann M, Orth JHC, Kalbitzer HR, Warscheid B, et al.: **A bacterial toxin catalyzing tyrosine glycosylation of Rho and deamidation of Gq and Gi proteins.** *Nat Struct Mol Biol* 2013, **20**:1273–1280.
26. Kellosalo J, Kajander T, Honkanen R, Goldman A: **Crystallization and preliminary X-ray analysis of membrane-bound pyrophosphatases.** *Molecular Membrane Biology* 2013, **30**:64–74.
27. Khan S, Garg A, Camacho N, Van Rooyen J, Kumar Pole A, Belrhali H, Ribas de Pouplana L, Sharma V, Sharma A: **Structural analysis of malaria-parasite lysyl-tRNA synthetase provides a platform for drug development.** *Acta Crystallographica Section D Biological Crystallography* 2013, **69**:785–795.
28. Khan S, Garg A, Sharma A, Camacho N, Picchioni D, Saint-Léger A, de Pouplana LR, Yogavel M, Sharma A: **An Appended Domain Results in an Unusual Architecture for Malaria Parasite Tryptophanyl-tRNA Synthetase.** *PLoS ONE* 2013, **8**:e66224.
29. Kumar A, Kumar S, Kumar D, Mishra A, Dewangan RP, Shrivastava P, Ramachandran S, Taneja B: **The structure of Rv3717 reveals a novel amidase from *Mycobacterium tuberculosis*.** *Acta Crystallographica Section D Biological Crystallography* 2013, **69**:2543–2554.
30. Kushwaha GS, Yamini S, Kumar M, Sinha M, Kaur P, Sharma S, Singh TP: **First structural evidence of sequestration of mRNA cap structures by type 1 ribosome inactivating protein from *Momordica balsamina*.** *Proteins: Structure, Function, and Bioinformatics* 2013, **81**:896–905.
31. Lahiri SD, Mangani S, Durand-Reville T, Benvenuti M, Luca FD, Sanyal G, Docquier J-D: **Structural Insight into Potent Broad-Spectrum Inhibition with Reversible Recyclization Mechanism: Avibactam in Complex with CTX-M-15 and *Pseudomonas aeruginosa* AmpC β-Lactamases.** *Antimicrob. Agents Chemother.* 2013, **57**:2496–2505.
32. Lansky S, Alalouf O, Solomon V, Alhassid A, Govada L, Chayan NE, Belrhali H, Shoham Y, Shoham G: **Crystallization and preliminary crystallographic analysis of Axe2, an acetylxytan esterase from *Geobacillus stearothermophilus*.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:430–434.
33. Lansky S, Salama R, Solomon VH, Belrhali H, Shoham Y, Shoham G: **Crystallization and preliminary crystallographic analysis of Abp, a GH27 β- L -arabinopyranosidase from *Geobacillus stearothermophilus*.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:695–699.
34. Liu C, Sanders JM, Pascal JM, Hou Y-M: **Adaptation to tRNA acceptor stem structure by flexible adjustment in the catalytic domain of class I tRNA synthetases.** *RNA* 2012, **18**:213–221.
35. Madhuprakash J, Singh A, Kumar S, Sinha M, Kaur P, Sharma S, Podile AR, Singh TP: **Structure of chitinase D from *Serratia proteamaculans* reveals the structural basis of its dual action of hydrolysis and transglycosylation.** *Int J Biochem Mol Biol* 2013, **4**:166–178.
36. Marlow VA, Rea D, Najmudin S, Wills M, Fülop V: **Structure and Mechanism of Acetolactate Decarboxylase.** *ACS Chem. Biol.* 2013, **8**:2339–2344.
37. Mathiharan YK, Pappachan A, Savithri HS, Murthy MRN: **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* 2013, **8**:e55978.
38. Menyhárd DK, Kiss-Szemán A, Tichy-Rács É, Hornung B, Rádi K, Szeltner Z, Domokos K, Szamosi I, Náray-Szabó G, Polgár L, et al.: **A Self-compartmentalizing Hexamer Serine Protease from Pyrococcus Horikoshii SUBSTRATE SELECTION ACHIEVED THROUGH MULTIMERIZATION.** *J. Biol. Chem.* 2013, **288**:17884–17894.
39. Mocibob M, Ivic N, Luic M, Weygand-Durasevic I: **Adaptation of Aminoacyl-tRNA Synthetase Catalytic Core to Carrier Protein Aminoacylation.** *Structure* 2013, **21**:614–626.

40. Moynie L, Schnell R, McMahon SA, Sandalova T, Boulkerou WA, Schmidberger JW, Alphey M, Cukier C, Duthie F, Kopec J, et al.: **The AEROPATH project targeting *Pseudomonas aeruginosa*: crystallographic studies for assessment of potential targets in early-stage drug discovery.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2012, **69**:25–34.
41. Navratna V, Gopal B: **Crystallization and preliminary X-ray diffraction studies of *Staphylococcus aureus* homoserine dehydrogenase.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:1216–1219.
42. Nichols CE, Lamb HK, Thompson P, Omari KE, Lockyer M, Charles I, Hawkins AR, Stammers DK: **Crystal structure of the dimer of two essential *Salmonella typhimurium* proteins, YgjD & YeaZ and calorimetric evidence for the formation of a ternary YgjD-YeaZ-YjeE complex.** *Protein Sci.* 2013, doi:10.1002/pro.2247.
43. Oja T, Niiranen L, Sandalova T, Klika KD, Niemi J, Mäntsälä P, Schneider G, Metsä-Ketelä M: **Structural basis for C-ribosylation in the alnumycin A biosynthetic pathway.** *Proc. Natl. Acad. Sci. U.S.A.* 2013, **110**:1291–1296.
44. Oliete R, Pous J, Rodríguez-Puente S, Abad-Zapatero C, Guasch A: **Elastic and inelastic diffraction changes upon variation of the relative humidity environment of PurE crystals.** *Acta Crystallographica Section D Biological Crystallography* 2013, **69**:194–212.
45. Oyen D, Wechselberger R, Srinivasan V, Steyaert J, Barlow JN: **Mechanistic analysis of allosteric and non-allosteric effects arising from nanobody binding to two epitopes of the dihydrofolate reductase of *Escherichia coli*.** *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics* 2013, **1834**:2147–2157.
46. Pakharukova N, Tuittila M, Zavialov A: **Crystallization and sulfur SAD phasing of AggA, the major subunit of aggregative adherence fimbriae type I from the *Escherichia coli* strain that caused an outbreak of haemolytic-uraemic syndrome in Germany.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:1389–1392.
47. Paradzik T, Ivic N, Filic Z, Manjasetty BA, Herron P, Luic M, Vujaklija D: **Structure-function relationships of two paralogous single-stranded DNA-binding proteins from *Streptomyces coelicolor*: implication of SsbB in chromosome segregation during sporulation.** *Nucleic Acids Res.* 2013, doi:10.1093/nar/gkt050.
48. Paul A, Mishra A, Surolia A, Vijayan M: **Cloning, expression, purification, crystallization and preliminary X-ray studies of argininosuccinate lyase (Rv1659) from *Mycobacterium tuberculosis*.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:1422–1424.
49. Paulus JK, Schlieper D, Groth G: **Greater efficiency of photosynthetic carbon fixation due to single amino-acid substitution.** *Nat Commun* 2013, **4**:1518.
50. Phulera S, Mande SC: **The Crystal Structure of *Mycobacterium tuberculosis* NrdH at 0.87 Å Suggests a Possible Mode of Its Activity.** *Biochemistry* 2013, **52**:4056–4065.
51. Rajavel M, Perinbam K, Gopal B: **Structural insights into the role of *Bacillus subtilis* YwfH (BacG) in tetrahydroxyproline synthesis.** *Acta Crystallographica Section D Biological Crystallography* 2013, **69**:324–332.
52. Rehman SAA, Verma V, Mazumder M, Dhar SK, Gourinath S: **Crystal Structure and Mode of Helicase Binding of the C-Terminal Domain of Primase from *Helicobacter pylori*.** *J. Bacteriol.* 2013, **195**:2826–2838.
53. Rodrigue J, Ganne G, Blanchard B, Saucier C, Giguère D, Shiao TC, Varrot A, Imbert A, Roy R: **Aromatic thioglycoside inhibitors against the virulence factor LecA from *Pseudomonas aeruginosa*.** *Org. Biomol. Chem.* 2013, **11**:6906–6918.

54. Roversi P, Ryffel B, Togbe D, Maillet I, Teixeira M, Ahmat N, Paesen GC, Lissina O, Boland W, Ploss K, et al.: **Bifunctional Lipocalin Ameliorates Murine Immune Complex-induced Acute Lung Injury.** *J. Biol. Chem.* 2013, **288**:18789–18802.
55. Salama-Alber O, Jobby MK, Chitayat S, Smith SP, White BA, Shimon LJW, Lamed R, Frolow F, Bayer EA: **Atypical Cohesin-Dockerin Complex Responsible for Cell Surface Attachment of Cellulosomal Components BINDING FIDELITY, PROMISCUITY, AND STRUCTURAL BUTTRESSES.** *J. Biol. Chem.* 2013, **288**:16827–16838.
56. Sharma A, Kottur J, Narayanan N, Nair DT: **A strategically located serine residue is critical for the mutator activity of DNA polymerase IV from Escherichia coli.** *Nucl. Acids Res.* 2013, **41**:5104–5114.
57. Sharma P, Dube D, Sinha M, Yadav S, Kaur P, Sharma S, Singh TP: **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* 2013, **8**:e53756.
58. Sharma P, Yamini S, Dube D, Singh A, Mal G, Pandey N, Sinha M, Singh AK, Dey S, Kaur P, et al.: **Structural basis of the binding of fatty acids to peptidoglycan recognition protein, PGRP-S through second binding site.** *Archives of Biochemistry and Biophysics* 2013, **529**:1–10.
59. Shetty KN, Latha VL, Rao RN, Nadimpalli SK, Suguna K: **Affinity of a galactose-specific legume lectin from Dolichos lablab to adenine revealed by X-ray crystallography.** *IUBMB Life* 2013, **65**:633–644.
60. Singh D, von Ossowski I, Palva A, Krishnan V: **Purification, crystallization and preliminary crystallographic analysis of the SpaA backbone-pilin subunit from probiotic *Lactobacillus rhamnosus* GG.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:1182–1185.
61. Squeglia F, Romano M, Ruggiero A, Vitagliano L, De Simone A, Berisio R: **Carbohydrate Recognition by RpfB from Mycobacterium tuberculosis Unveiled by Crystallographic and Molecular Dynamics Analyses.** *Biophysical Journal* 2013, **104**:2530–2539.
62. Srivastava VK, Rana AK, Sahasrabuddhe AA, Gupta CM, Pratap JV: **Cloning, overexpression, purification and crystallization of the CRN12 coiled-coil domain from Leishmania donovani.** *Acta Crystallographica Section F Structural Biology and Crystallization Communications* 2013, **69**:535–539.
63. Srivastava VK, Srivastava S, Arora A, Pratap JV: **Structural Insights into Putative Molybdenum Cofactor Biosynthesis Protein C (MoaC2) from Mycobacterium tuberculosis H37Rv.** *PLoS ONE* 2013, **8**:e58333.
64. Tanwar AS, Goyal VD, Choudhary D, Panjikar S, Anand R: **Importance of Hydrophobic Cavities in Allosteric Regulation of Formylglycinamide Synthetase: Insight from Xenon Trapping and Statistical Coupling Analysis.** *PLoS ONE* 2013, **8**:e77781.
65. Taylor NMI, Glatt S, Hennrich ML, Scheven G von, Grötsch H, Fernández-Tornero C, Rybin V, Gavin A-C, Kolb P, Müller CW: **Structural and Functional Characterization of a Phosphatase Domain within Yeast General Transcription Factor IIIC.** *J. Biol. Chem.* 2013, **288**:15110–15120.
66. Theveneau P, Baker R, Barrett R, Beteva A, Bowler MW, Carpentier P, Caserotto H, Sanctis D de, Dobias F, Flot D, et al.: **The Upgrade Programme for the Structural Biology beamlines at the European Synchrotron Radiation Facility – High throughput sample evaluation and automation.** *J. Phys.: Conf. Ser.* 2013, **425**:012001.
67. Weber BW, Kimani SW, Varsani A, Cowan DA, Hunter R, Venter GA, Gumbart JC, Sewell BT: **The Mechanism of the Amidases MUTATING THE GLUTAMATE ADJACENT TO THE CATALYTIC TRIAD INACTIVATES THE ENZYME DUE TO SUBSTRATE MISPOSITIONING.** *J. Biol. Chem.* 2013, **288**:28514–28523.

2012

1. Almagor L, Chomsky-Hecht O, Ben-Mocha A, Hedin-Barak D, Dascal N, Hirsch JA: **The Role of a Voltage-Dependent Ca₂₊ Channel Intracellular Linker: A Structure-Function Analysis.** *J. Neurosci.* 2012, **32**:7602–7613.
2. Balasubramaniam D, Arockiasamy A, Kumar PD, Sharma A, Krishnaswamy S: **Asymmetric pore occupancy in crystal structure of OmpF porin from *Salmonella typhi*.** *J. Struct. Biol.* 2012, **178**:233–244.
3. Bharath SR, Bisht S, Harijan RK, Savithri HS, Murthy MRN: **Structural and Mutational Studies on Substrate Specificity and Catalysis of *Salmonella typhimurium* D-Cysteine Desulphydrase.** *PLoS ONE* 2012, **7**:e36267.
4. Bisht S, Rajaram V, Bharath SR, Kalyani JN, Khan F, Rao AN, Savithri HS, Murthy MRN: **Crystal Structure of *Escherichia coli* Diaminopropionate Ammonia-lyase Reveals Mechanism of Enzyme Activation and Catalysis.** *J. Biol. Chem.* 2012, **287**:20369–20381.
5. Boix E, Pulido D, Moussaoui M, Nogués MV, Russi S: **The sulfate-binding site structure of the human eosinophil cationic protein as revealed by a new crystal form.** *J. Struct. Biol.* 2012, **179**:1–9.
6. Broadley SG, Gumbart JC, Weber BW, Marakalala MJ, Steenkamp DJ, Sewell BT: **A new crystal form of MshB from *Mycobacterium tuberculosis* with glycerol and acetate in the active site suggests the catalytic mechanism.** *Acta Crystallogr. D Biol. Crystallogr.* 2012, **68**:1450–1459.
7. Büttner CR, Chechik M, Ortiz-Lombardía M, Smits C, Ebong I-O, Chechik V, Jeschke G, Dykeman E, Benini S, Robinson CV, et al.: **Structural Basis for DNA Recognition and Loading into a Viral Packaging Motor [Internet].** *PNAS* 2011, doi:10.1073/pnas.1110270109.
8. Cendron L, Mičetić I, Polverino de Laureto P, Paoli M: **Structural analysis of trimeric phospholipase A2 neurotoxin from the Australian taipan snake venom.** *FEBS J.* 2012, **279**:3121–3135.
9. Chittori S, Savithri HS, Murthy MRN: **Structural and mechanistic investigations on *Salmonella typhimurium* acetate kinase (AckA): identification of a putative ligand binding pocket at the dimeric interface.** *BMC Struct. Biol.* 2012, **12**:24.
10. Collins R, Johansson A-L, Karlberg T, Markova N, Van den Berg S, Olesen K, Hammarström M, Flores A, Schüler H, Schiavone LH, et al.: **Biochemical discrimination between selenium and sulfur 1: a single residue provides selenium specificity to human selenocysteine lyase.** *PLoS ONE* 2012, **7**:e30581.
11. De Colibus L, Sonnen AF-P, Morris KJ, Siebert CA, Abrusci P, Plitzko J, Hodnik V, Leippe M, Volpi E, Anderluh G, et al.: **Structures of lysenin reveal a shared evolutionary origin for pore-forming proteins and its mode of sphingomyelin recognition.** *Structure* 2012, **20**:1498–1507.
12. Deery E, Schroeder S, Lawrence AD, Taylor SL, Seyedarabi A, Waterman J, Wilson KS, Brown D, Geeves MA, Howard MJ, et al.: **An enzyme-trap approach allows isolation of intermediates in cobalamin biosynthesis.** *Nat. Chem. Biol.* 2012, **8**:933–940.
13. Fibriansah G, Gliubich FI, Thunissen A-MWH: **On the mechanism of peptidoglycan binding and cleavage by the endo-specific lytic transglycosylase MltE from *Escherichia coli*.** *Biochemistry* 2012, **51**:9164–9177.
14. Fodor K, Wolf J, Erdmann R, Schliebs W, Wilmanns M: **Molecular requirements for peroxisomal targeting of alanine-glyoxylate aminotransferase as an essential determinant in primary hyperoxaluria type 1.** *PLoS Biol.* 2012, **10**:e1001309.
15. Gangwar SP, Meena SR, Saxena AK: **Purification, crystallization and preliminary X-ray crystallographic analysis of the ETS domain of human Ergp55 in complex with the c-fos promoter DNA sequence.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:1333–1336.

16. Garcia-Doval C, Raaij MJV: **Structure of the Receptor-Binding Carboxy-Terminal Domain of Bacteriophage T7 Tail Fibers** [Internet]. *PNAS* 2012, doi:10.1073/pnas.1119719109.
17. Hissa DC, Bezerra GA, Obrist B, Birner-Grünberger R, Melo VMM, Gruber K: **Crystallization and preliminary X-ray diffraction of the surfactant protein Lv-ranaspumin from the frog Leptodactylus vastus**. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:321–323.
18. Izumi A, Schnell R, Schneider G: **Crystal structure of NirD, the small subunit of the nitrite reductase NirbD from Mycobacterium tuberculosis at 2.0 Å resolution**. *Proteins* 2012, **80**:2799–2803.
19. Jagtap PKA, Soni V, Vithani N, Jhingan GD, Bais VS, Nandicoori VK, Prakash B: **Substrate-bound crystal structures reveal features unique to Mycobacterium tuberculosis N-acetyl-glucosamine 1-phosphate uridyltransferase and a catalytic mechanism for acetyl transfer**. *J. Biol. Chem.* 2012, **287**:39524–39537.
20. Janardan N, Harijan RK, Wierenga RK, Murthy MRN: **Crystal structure of a monomeric thiolase-like protein type 1 (TLP1) from Mycobacterium smegmatis**. *PLoS ONE* 2012, **7**:e41894.
21. Khan T, Salunke DM: **Structural elucidation of the mechanistic basis of degeneracy in the primary humoral response**. *J. Immunol.* 2012, **188**:1819–1827.
22. Korczynska JE, Turkenburg JP, Taylor EJ: **The structural characterization of a prophage-encoded extracellular DNase from Streptococcus pyogenes**. *Nucleic Acids Res* 2012, **40**:928–938.
23. Kumar S, Zaidi R, Gourinath S: **Cloning, purification, crystallization and preliminary crystallographic study of calcium-binding protein 5 from Entamoeba histolytica**. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:1542–1544.
24. Kumar V, Gupta GD: **Low-resolution structure of Drosophila translin**. *FEBS Open Bio* 2012, **2**:37–46.
25. Kuper J, Wolski SC, Michels G, Kisker C: **Functional and structural studies of the nucleotide excision repair helicase XPD suggest a polarity for DNA translocation**. *EMBO J.* 2012, **31**:494–502.
26. Kushwaha GS, Pandey N, Sinha M, Singh SB, Kaur P, Sharma S, Singh TP: **Crystal structures of a type-1 ribosome inactivating protein from Momordica balsamina in the bound and unbound states**. *Biochim. Biophys. Acta* 2012, **1824**:679–691.
27. Maity K, Venkata BS, Kapoor N, Surolia N, Surolia A, Suguna K: **Structural basis for the functional and inhibitory mechanisms of β-hydroxyacyl-acyl carrier protein dehydratase (FabZ) of Plasmodium falciparum**. *J. Struct. Biol.* 2011, **176**:238–249.
28. Manjasetty B, Büssow K, Panjikar S, Turnbull A: **Current methods in structural proteomics and its applications in biological sciences**. *3 Biotech* 2012, **2**:89–113.
29. Manjasetty BA, Yu X-H, Panjikar S, Taguchi G, Chance MR, Liu C-J: **Structural basis for modification of flavonol and naphthol glucoconjugates by Nicotiana tabacum malonyltransferase (NtMaT1)** [Internet]. *Planta* 2012, doi:10.1007/s00425-012-1660-8.
30. Martínez-Júlez M, Rojas AL, Olekhovich I, Espinosa Angarica V, Hoffman PS, Sancho J: **Structure of RdxA--an oxygen-insensitive nitroreductase essential for metronidazole activation in Helicobacter pylori**. *FEBS J.* 2012, **279**:4306–4317.
31. Mastrangelo E, Pezzullo M, Tarantino D, Petazzi R, Germani F, Kramer D, Robel I, Rohayem J, Bolognesi M, Milani M: **Structure-Based Inhibition of Norovirus RNA-Dependent RNA Polymerases**. *J. Mol. Biol.* 2012, **419**:198–210.
32. McGovern RE, Fernandes H, Khan AR, Power NP, Crowley PB: **Protein camouflage in cytochrome c-calixarene complexes**. *Nat Chem* 2012, **4**:527–533.

33. Oliveira T, Panjikar S, Carrigan JB, Hamza M, Sharkey MA, Engel PC, Khan AR: **Crystal structure of NAD⁺-dependent *Peptoniphilus asaccharolyticus* glutamate dehydrogenase reveals determinants of cofactor specificity.** *J Struct Biol* 2012, **177**:543–52.
34. Papale D, Bruckmann C, Gazur B, Miles CS, Mowat CG, Daff S: **Oxygen activation in neuronal NO synthase: resolving the consecutive mono-oxygenation steps.** *Biochem. J.* 2012, **443**:505–514.
35. Pinotsis N, Chatziefthimiou SD, Berkemeier F, Beuron F, Mavridis IM, Konarev PV, Svergun DI, Morris E, Rief M, Wilmanns M: **Superhelical architecture of the myosin filament-linking protein myomesin with unusual elastic properties.** *PLoS Biol.* 2012, **10**:e1001261.
36. Raj I, Kumar S, Gourinath S: **The narrow active-site cleft of O-acetylserine sulfhydrylase from *Leishmania donovani* allows complex formation with serine acetyltransferases with a range of C-terminal sequences.** *Acta Crystallogr. D Biol. Crystallogr.* 2012, **68**:909–919.
37. Roszak AW, Moulisová V, Reksodipuro ADP, Gardiner AT, Fujii R, Hashimoto H, Isaacs NW, Cogdell RJ: **New insights into the structure of the reaction centre from *Blastochloris viridis*: evolution in the laboratory.** *Biochem. J.* 2012, **442**:27–37.
38. Roy SP, Rahman MM, Yu XD, Tuittila M, Knight SD, Zavialov AV: **Crystal structure of enterotoxigenic *Escherichia coli* colonization factor CS6 reveals a novel type of functional assembly.** *Mol. Microbiol.* 2012, **86**:1100–1115.
39. Sainsbury S, Ren J, Saunders NJ, Stuart DI, Owens RJ: **Structure of the regulatory domain of the LysR family regulator NMB2055 (MetR-like protein) from *Neisseria meningitidis*.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:730–737.
40. Salama-Alber O, Gat Y, Lamed R, Shimon LJW, Bayer EA, Frolov F: **Crystallization and preliminary X-ray characterization of a type III cohesin-dockerin complex from the cellulosome system of *Ruminococcus flavefaciens*.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:1116–1119.
41. Sarin LP, Wright S, Chen Q, Degerth LH, Stuart DI, Grimes JM, Bamford DH, Poranen MM: **The C-terminal priming domain is strongly associated with the main body of bacteriophage φ6 RNA-dependent RNA polymerase.** *Virology* 2012, **432**:184–193.
42. Schimpl M, Rush CL, Betou M, Eggleston IM, Recklies AD, Van Aalten DMF: **Human YKL-39 is a pseudo-chitinase with retained chitooligosaccharide-binding properties.** *Biochem. J.* 2012, **446**:149–157.
43. Shaik MM, Zanotti G, Cendron L: **The crystal structure of ADP-L-glycero-D-manno-heptose-6-epimerase (HP0859) from *Helicobacter pylori*.** *Biochim. Biophys. Acta* 2011, **1814**:1641–1647.
44. Sharma A, Subramanian V, Nair DT: **The PAD region in the mycobacterial DinB homologue MsPolIV exhibits positional heterogeneity.** *Acta Crystallogr. D Biol. Crystallogr.* 2012, **68**:960–967.
45. Sharma P, Yamini S, Dube D, Singh A, Sinha M, Dey S, Mitra DK, Kaur P, Sharma S, Singh TP: **Structural studies on molecular interactions between camel peptidoglycan recognition protein, CPGRP-S, and peptidoglycan moieties N-acetylglicosamine and N-acetylmuramic acid.** *J. Biol. Chem.* 2012, **287**:22153–22164.
46. Shetty KN, Bhat GG, Inamdar SR, Swamy BM, Suguna K: **Crystal structure of a β-prism II lectin from *Remusatia vivipara*.** *Glycobiology* 2012, **22**:56–69.
47. Srivastava SK, Gayathri S, Manjasetty BA, Gopal B: **Analysis of conformational variation in macromolecular structural models.** *PLoS ONE* 2012, **7**:e39993.
48. Štefanić Z, Narczyk M, Mikleušević G, Wielgus-Kutrowska B, Bzowska A, Luić M: **New phosphate binding sites in the crystal structure of *Escherichia coli* purine nucleoside phosphorylase complexed with phosphate and formycin A.** *FEBS Lett.* 2012, **586**:967–971.

49. Tanwar AS, Morar M, Panjikar S, Anand R: **Formylglycinamide ribonucleotide amidotransferase from *Salmonella typhimurium* : role of ATP complexation and the glutaminase domain in catalytic coupling.** *Acta Crystallographica Section D Biological Crystallography* 2012, **68**:627–636.
50. Tars K, Kotelovica S, Lipowsky G, Bauer M, Beerli RR, Bachmann MF, Maurer P: **Different binding modes of free and carrier-protein-coupled nicotine in a human monoclonal antibody.** *J. Mol. Biol.* 2012, **415**:118–127.
51. Venkadesh S, Mandal PK, Gautham N: **Crystallographic and spectroscopic studies of d(CCGGTACCGG).** *Nucleosides Nucleotides Nucleic Acids* 2012, **31**:184–196.
52. Vyas R, Tewari R, Weiss MS, Karthikeyan S: **Structures of ternary complexes of aspartate-semialdehyde dehydrogenase (Rv3708c) from Mycobacterium tuberculosis H37Rv.** *Acta Crystallographica Section D Biological Crystallography* 2012, **68**:671–679.
53. Westfall CS, Zubietta C, Herrmann J, Kapp U, Nanao MH, Jez JM: **Structural basis for prereceptor modulation of plant hormones by GH3 proteins.** *Science* 2012, **336**:1708–1711.
54. Wojtas MN, Abrescia NGA: **Soaking of DNA into crystals of archaeal RNA polymerase achieved by desalting in droplets.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:1134–1138.
55. Wojtas MN, Mogni M, Millet O, Bell SD, Abrescia NGA: **Structural and functional analyses of the interaction of archaeal RNA polymerase with DNA.** *Nucleic Acids Res.* 2012, **40**:9941–9952.
56. Wong E, Vaaje-Kolstad G, Ghosh A, Hurtado-Guerrero R, Konarev PV, Ibrahim AFM, Svergun DI, Eijssink VGH, Chatterjee NS, Van Aalten DMF: **The Vibrio cholerae Colonization Factor GbpA Possesses a Modular Structure that Governs Binding to Different Host Surfaces.** *PLoS Pathog* 2012, **8**:e1002373.
57. Wrenger C, Müller IB, Butzloff S, Jordanova R, Lunev S, Groves MR: **Crystallization and preliminary X-ray diffraction of malate dehydrogenase from Plasmodium falciparum.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:659–662.
58. Yaniv O, Halfon Y, Shimon LJW, Bayer EA, Lamed R, Frolov F: **Structure of CBM3b of the major cellulosomal scaffoldin subunit ScaA from Acetivibrio cellulolyticus.** *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.* 2012, **68**:8–13.

Gorlani A. –

Development of llama single-domain antibodies as ingredient for an HIV -1 entry-inhibitor microbicide
Utrecht University, The Netherlands (PhD Thesis), 2012

2011

Abad-Zapatero C./Oliete R./Rodriguez-Puente S./Pous J./Martinelli L./Johnson M.E./Guasch A. - Humidity control can compensate for the damage induced in protein crystals by alien solutions
Acta Crystallographica F **67**, 1300-1308 (2011)

Abrescia N.G.A./Grimes J.M./Oksanen H.M./Bamford J.K.H./Bamford D.H./Stuart D.I. - The use of low-resolution phasing followed by phase extension from 7.6 to 2.5 Å resolution with noncrystallographic symmetry to solve the structure of a bacteriophage capsid protein
Acta Crystallographica D **67**, 228-232 (2011)

Bellinzoni M./Bastard K./Perret A./Zaparucha A./Perchat N./Vergne C./Wagner T./de Melo-Minardi R.C./Artiguenave F./Cohen G.N./Weissenbach J./Salanoubat M./Alzari P.M. - 3-Keto-5-aminohexanoate cleavage enzyme: A common fold for an uncommon claisen-type condensation
Journal of Biological Chemistry **286**, 27399-27405 (2011)

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

Bhaskar V./Kumar M./Manicka S./Tripathi S./Venkatraman A./Krishnaswamy S. - Identification of biochemical and putative biological role of a xenolog from *Escherichia coli* using structural analysis
Proteins: Structure, Function and Bioinformatics **79**, 1132-1142 (2011)

Brotsudarmo T.H.P./Collins A.M./Gall A./Roszak A.W./Gardiner A.T./Blankenship R.E./Cogdell R.J. - The light intensity under which cells are grown controls the type of peripheral light-harvesting complexes that are assembled in a purple photosynthetic bacterium
Biochemical Journal **440**, 51-61 (2011)

Carrasco-López C./Rojas-Altuve A./Zhang W./Hesek D./Lee M./Barbe S./André I./Ferrer P./Silva-Martin N./Castro G.R./Martínez-Ripoll M./Mobashery S./Hermoso J.A. - Crystal structures of bacterial peptidoglycan amidase AmpD and an unprecedented activation mechanism
Journal of Biological Chemistry **286**, 31714-31722 (2011)

Chittori S./Savithri H.S./Murthy M.R.N. - Preliminary X-ray crystallographic studies on acetate kinase (AckA) from *Salmonella typhimurium* in two crystal forms
Acta Crystallographica F **67**, 1658-1661 (2011)

Coles C.H./Shen Y./Tenney A.P./Siebold C./Sutton G.C./Lu W./Gallagher J.T./Jones E.Y./Flanagan J.G./Aricescu A.R. - Proteoglycan-specific molecular switch for RPTP⁺ clustering and neuronal extension
Science **332**, 484-488 (2011)

Dhindwal S./Patil D.N./Mohammadi M./Sylvestre M./Tomar S./Kumar P. - Biochemical studies and ligand-bound structures of biphenyl dehydrogenase from *Pandoraea pnomenusa* strain B-356 reveal a basis for broad specificity of the enzyme
Journal of Biological Chemistry **286**, 37011-37022 (2011)

Dorfmueller H.C./Borodkin V.S./Blair D.E./Pathak S./Navrátilová I./van Aalten D.M.F. - Substrate and product analogues as human O-GlcNAc transferase inhibitors
Amino Acids **40**, 781-792 (2011)

Due A.V./Kuper J./Geerlof A./von Kries J.P./Wilmanns M. - Bisubstrate specificity in histidine/tryptophan biosynthesis isomerase from *Mycobacterium tuberculosis* by active site metamorphosis
Proceedings of the National Academy of Sciences of the USA **108**, 3554-3559 (2011)

El Omari K./Dhaliwal B./Ren J./Abrescia N.G.A./Lockyer M./Powell K.L./Hawkins A.R./Stammers D.K. - Structures of respiratory syncytial virus nucleocapsid protein from two crystal forms: Details of potential packing interactions in the native helical form
Acta Crystallographica F **67**, 1179-1183 (2011)

El Omari K./Hoosdally S.J./Tuladhar K./Karia D./Vyas P./Patient R./Porcher C./Mancini E.J. - Structure of the leukemia oncogene LMO2: Implications for the assembly of a hematopoietic transcription factor complex
Blood **117**, 2146-2156 (2011)

Elovaara H./Kidron H./Parkash V./Nymalm Y./Bligt E./Ollikka P./Smith D.J./Pihlavisto M./Salmi M./Jalkanen S./Salminen T.A. - Identification of two imidazole binding sites and key residues for substrate specificity in human primary amine oxidase AOC3
Biochemistry **50**, 5507-5520 (2011)

Gangwar S.P./Meena S.R./Saxena A.K. - Cloning, purification, crystallization and preliminary X-ray analysis of ESX-1-secreted protein regulator (EspR) from *Mycobacterium tuberculosis*
Acta Crystallographica F **67**, 83-86 (2011)

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

Gut H./Xu G./Taylor G.L./Walsh M.A. - Structural basis for Streptococcus pneumoniae NanA inhibition by influenza antivirals zanamivir and oseltamivir carboxylate
Journal of Molecular Biology **409**, 496-503 (2011)

Hemsworth G.R./Moroz O.V./Fogg M.J./Scott B./Bosch-Navarrete C./González-Pacanowska D./Wilson K.S. - The crystal structure of the Leishmania major deoxyuridine triphosphate nucleotidohydrolase in complex with nucleotide analogues, dUMP, and deoxyuridine
Journal of Biological Chemistry **286**, 16470-16481 (2011)

Kajander T./Kuja-Panula J./Rauvala H./Goldman A. - Crystal structure and role of glycans and dimerization in folding of neuronal leucine-rich repeat protein AMIGO-1
Journal of Molecular Biology **413**, 1001-1015 (2011)

Kilmartin J.R./Maher M.J./Krusong K./Noble C.J./Hanson G.R./Bernhardt P.V./Riley M.J./Kappler U. - Insights into structure and function of the active site of SoxAX cytochromes
Journal of Biological Chemistry **286**, 24872-24881 (2011)

Knijnenburg A.D./Kapoerchan V.V./Grotenbreg G.M./Spalburg E./de Neeling A.J./Mars-Groenendijk R.H./Noort D./Otero J.M./Llamas-Saiz A.L./van Raaij M.J./Ravensbergen B./Nibbering P.H./van der Marel G.A./Overkleeft H.S./Overhand M. - Synthesis and evaluation of strand and turn modified ring-extended gramicidin S derivatives
Bioorganic & Medicinal Chemistry **19**, 3402-3409 (2011)

Kumar A./Saigal K./Malhotra K./Sinha K.M./Taneja B. - 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
Journal of Biological Chemistry **286**, 19652-19661 (2011)

Kumar S./Raj I./Nagpal I./Subbarao N./Gourinath S. - Structural and biochemical studies of serine acetyltransferase reveal why the parasite Entamoeba histolytica cannot form a cysteine synthase complex
Journal of Biological Chemistry **286**, 12533-12541 (2011)

Lagarde A./Spinelli S./Qiao H./Tegoni M./Pelosi P./Cambillau C. - Crystal structure of a novel type of odorant-binding protein from Anopheles gambiae, belonging to the C-plus class
Biochemical Journal **437**, 423-430 (2011)

Lagarde A./Spinelli S./Tegoni M./He X./Field L./Zhou J.J./Cambillau C. - The crystal structure of odorant binding protein 7 from Anopheles gambiae exhibits an outstanding adaptability of its binding site
Journal of Molecular Biology **414**, 401-412 (2011)

Lamb D./Schüttelkopf A.W./van Aalten D.M.F./Brighty D.W. - Charge-surrounded pockets and electrostatic interactions with small ions modulate the activity of retroviral fusion proteins
PLoS Pathogens **7**, e1001268-1-e1001268-12 (2011)

Leo J.C./Lyskowski A./Hattula K./Hartmann M.D./Schwarz H./Butcher S.J./Linke D./Lupas A.N./Goldman A. - The structure of *E. coli* IgG-binding protein D suggests a general model for bending and binding in trimeric autotransporter adhesins
Structure **19**, 1021-1030 (2011)

Madan L.L./Gopal B. - Conformational basis for substrate recruitment in protein tyrosine phosphatase 10D
Biochemistry **50**, 10114-10125 (2011)

Maiti K./Venkata B.S./Kapoor N./Surolia N./Surolia A./Suguna K. - Structural basis for the functional and inhibitory mechanisms of 2-hydroxyacyl-acyl carrier protein dehydratase (FabZ) of Plasmodium falciparum
Journal of Structural Biology **176**, 238-249 (2011)

Malinauskas T./Aricescu A.R./Lu W./Siebold C./Jones E.Y. - Modular mechanism of Wnt signaling inhibition by Wnt inhibitory factor 1
Nature Structural & Molecular Biology **18**, 886-893 (2011)

Marassio G./Prangé T./David H.N./Sopkova-de Oliveira Santos J./Gabison L./Delcroix N./Abraini J.H./Colloc'h N. - Pressure-response analysis of anesthetic gases xenon and nitrous oxide on urate oxidase: A crystallographic study
FASEB Journal **25**, 2266-2275 (2011)

Mikleusevic G./Stefanic Z./Narczyk M./Wielgus-Kutrowska B./Bzowska A./Luic M. - Validation of the catalytic mechanism of Escherichia coli purine nucleoside phosphorylase by structural and kinetic studies
Biochimie **93**, 1610-1622 (2011)

Milic D./Demidkina T.V./Faleev N.G./Phillips R.S./Matkovic-Calogovic D./Antson A.A. - Crystallographic snapshots of tyrosine phenol-lyase show that substrate strain plays a role in C-C bond cleavage
Journal of the American Chemical Society **133**, 16468-16476 (2011)

Moor N./Klipcan L./Safro M.G. - Bacterial and eukaryotic phenylalanyl-tRNA synthetases catalyze misaminoacylation of tRNAPhe with 3,4-dihydroxy-L-phenylalanine
Chemistry & Biology **18**, 1221-1229 (2011)

Nel A.J.M./Tuffin I.M./Sewell B.T./Cowan D.A. - Unique aliphatic amidase from a psychrotrophic and haloalkaliphilic Nesterenkonia isolate
Applied and Environmental Microbiology **77**, 3696-3702 (2011)

Romão C.V./Ladakis D./Lobo S.A.L./Carrondo M.A./Brindley A.A./Deery E./Matias P.M./Pickersgill R.W./Saraiva L.M./Warren M.J. - Evolution in a family of chelatases facilitated by the introduction of active site asymmetry and protein oligomerization
Proceedings of the National Academy of Sciences of the USA **108**, 97-102 (2011)

Rossi F./Khanduja J.S./Bortoluzzi A./Houghton J./Sander P./Güthlein C./Davis E.O./Springer B./Böttger E.C./Relini A./Penco A./Muniyappa K./Rizzi M. - The biological and structural characterization of Mycobacterium tuberculosis UvrA provides novel insights into its mechanism of action
Nucleic Acids Research **39**, 7316-7328 (2011)

Roy S./Choudhury D./Chakrabarti C./Biswas S./Dattagupta J.K. - Crystallization and preliminary X-ray diffraction studies of the precursor protein of a thermostable variant of papain
Acta Crystallographica F **67**, 634-636 (2011)

Ruggiero A./Squeglia F./Pirone L./Correale S./Berisio R. - Expression, purification, crystallization and preliminary X-ray crystallographic analysis of a major fragment of the resuscitation-promoting factor RpfB from Mycobacterium tuberculosis
Acta Crystallographica F **67**, 164-168 (2011)

Russi S./Juers D.H./Sanchez-Weatherby J./Pellegrini E./Mossou E./Forsyth V.T./Huet J./Gobbo A./Felisaz F./Moya R./McSweeney S.M./Cusack S./Cipriani F./Bowler M.W. - Inducing phase changes in crystals of macromolecules: Status and perspectives for controlled crystal dehydration
Journal of Structural Biology **175**, 236-243 (2011)

Salgado P.S./Yan R./Rowan F./Cota E. - Expression, crystallization and preliminary X-ray data analysis of NT-Als9-2, a fungal adhesin from Candida albicans
Acta Crystallographica F **67**, 467-470 (2011)

Salgado P.S./Yan R./Taylor J.D./Burchell L./Jones R./Hoyer L.L./Matthews S.J./Simpson P.J./Cota E. - Structural basis for the broad specificity to host-cell ligands by the pathogenic fungus Candida albicans
Proceedings of the National Academy of Sciences of the USA **108**, 15775-15779 (2011)

Schroeder K.T./Daldrop P./Lilley D.M.J. - RNA tertiary interactions in a riboswitch stabilize the structure of a kink turn
Structure **19**, 1233-1240 (2011)

Schüttelkopf A.W./Andersen O.A./Rao F.V./Allwood M./Rush C.L./Eggleston I.M./van Aalten D.M.F. - Bisdionin C-A rationally designed, submicromolar inhibitor of family 18 chitinases

ACS Medicinal Chemistry Letters **2**, 428-432 (2011)

Shaik M.M./Zanotti G./Cendron L. - The crystal structure of ADP-L-glycero-D-manno-heptose-6-epimerase (HP0859) from Helicobacter pylori
Biochimica et Biophysica Acta **1814**, 1641-1647 (2011)

Sharma As./Nair D.T. - Cloning, expression, purification, crystallization and preliminary crystallographic analysis of MsDpo4: A Y-family DNA polymerase from Mycobacterium smegmatis
Acta Crystallographica F **67**, 812-816 (2011)

Sharma As./Sharma Ar./Dixit S./Sharma Am. - Structural insights into thioredoxin-2: A component of malaria parasite protein secretion machinery
Scientific Reports **1**, 179-1-179-9 (2011)

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

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

Sharma U./Suresh C.G. - Purification, crystallization and X-ray characterization of a Kunitz-type trypsin inhibitor protein from the seeds of chickpea (*Cicer arietinum*)
Acta Crystallographica F **67**, 714-717 (2011)

Singh M./Kumar P./Karthikeyan S. - Structural basis for pH dependent monomer-dimer transition of 3,4-dihydroxy 2-butanone-4-phosphate synthase domain from *Mycobacterium tuberculosis*
Journal of Structural Biology **174**, 374-384 (2011)

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

Su J./Schlicker C./Forchhammer K. - A third metal is required for catalytic activity of the signal-transducing protein phosphatase M tPphA
Journal of Biological Chemistry **286**, 13481-13488 (2011)

Sultana A./Jin Y./Dregger C./Franklin E./Weisman L.S./Khan A.R. - The activation cycle of Rab GTPase Ypt32 reveals structural determinants of effector recruitment and GDI binding
FEBS Letters **585**, 3520-3527 (2011)

van Rooyen J.M./Abratt V.R./Belrhali H./Sewell B.T. - Crystal structure of Type III glutamine synthetase: surprising reversal of the inter-ring interface.
Structure, 19(4), 471-83 (2011)

Tosi T./Nickerson N.N./Mollica L./Jensen M.R./Blackledge M./Baron B./England P./Pugsley A.P./Dessen A. - Pilotin-secretin recognition in the type II secretion system of *Klebsiella oxytoca*
Molecular Microbiology **82**, 1422-1432 (2011)

van Breugel M./Hirono M./Andreeva A./Yanagisawa H.A./Yamaguchi S./Nakazawa Y./Morgner N./Petrovich M./Ebong I.O./Robinson C.V./Johnson C.M./Veprintsev D./Zuber B. - Structures of SAS-6 suggest its organization in centrioles
Science **331**, 1196-1199 (2011)

van Rooyen J./Belrhali H./Abratt V./Sewell B.T. - Proteolysis of the type III glutamine synthetase from *Bacteroides fragilis* causes expedient crystal-packing rearrangements
Acta Crystallographica F **67**, 358-363 (2011)

Venkadesh S./Mandal P.K./Gautham N. - The sequence d(CGGCGGCCGC) self-assembles into a two dimensional rhombic DNA lattice
Biochemical and Biophysical Research Communications **407**, 548-551 (2011)

2010

Albesa-Jové D./Bertrand T./Carpenter E.P./Swain G.V./Lim J./Zhang J./Haire L.F./Vasisht N./Braun V./Lange A./von Eichel-Streiber C./Svergun D.I./Fairweather N.F./Brown K.A. - Four distinct structural domains in Clostridium difficile toxin B visualized using SAXS
Journal of Molecular Biology **396**, 1260-1270 (2010)

Ash M.R./Faelber K./Kosslick D./Albert G.I./Roske Y./Kofler M./Schuemann M./Krause E./Freund C. - Conserved beta-hairpin recognition by the GYF domains of Smy2 and GIGYF2 in mRNA surveillance and vesicular transport complexes
Structure **18**, 944-954 (2010)

Bandeiras T.M./Romão C.V./Rodrigues J.V./Teixeira M./Matias P.M. - Purification, crystallization and X-ray crystallographic analysis of Archaeoglobus fulgidus neelaredoxin
Acta Crystallographica F **66**, 316-319 (2010)

Bhatt T.K./Yogavel M./Wydau S./Berwal R./Sharma As. - Ligand-bound structures provide atomic snapshots for the catalytic mechanism of D-amino acid deacylase
Journal of Biological Chemistry **285**, 5917-5930 (2010)

Bird L.E./Ren J./Nettleship J.E./Folkers G.E./Owens R.J./Stammers D.K. - Novel structural features in two ZHX homeodomains derived from a systematic study of single and multiple domains
BMC Structural Biology **10**, 13-1-13-15 (2010)

Cafasso J, Manjasetty BA, Karr EA, Sandman K, Chance MR, Reeve JN. - Preliminary crystallography confirms that the archaeal DNA-binding and tryptophan-sensing regulator TrpY is a dimer.
Acta Crystallographica F **66**, 1493-1495 (2010).

Dawson A./Chen M./Fyfe P.K./Guo Z./Hunter W.N. - Structure and reactivity of *Bacillus subtilis* MenD catalyzing the first committed step in menaquinone biosynthesis
Journal of Molecular Biology **401**, 253-264 (2010)

de Diego I./Kuper J./Bakalova N./Kursula P./Wilmanns M. - Molecular basis of the death-associated protein kinase-calcium/calmodulin regulator complex
Science Signaling **3**, ra6-1-ra6-9 (2010)

De Luchi D./Usón I./Wright G./Gouyette C./Subirana J.A. - Structure of a stacked anthraquinone-DNA complex
Acta Crystallographica F **66**, 1019-1022 (2010)

Dorfmueller H.C./Borodkin V.S./Schimpl M./Zheng X./Kime R./Read K.D./van Aalten D.M.F. - Cell-penetrant, nanomolar O-GlcNAcase inhibitors selective against lysosomal hexosaminidases
Chemistry & Biology **17**, 1250-1255 (2010)

El Omari K./Porcher C./Mancini E.J. - Purification, crystallization and preliminary X-ray analysis of a fusion of the LIM domains of LMO2 and the LID domain of Ldb1
Acta Crystallographica F **66**, 1466-1469 (2010)

Fernández I.S./Cuevas P./Angulo J./López-Navajas P./Canales-Mayordomo A./González-Corrochano R./Lozano R.M./Valverde S./Jiménez-Barbero J./Romero A./Giménez-Gallego G. - Gentisic acid, a compound associated with plant defense and a metabolite of aspirin, heads a new class of in vivo fibroblast growth factor inhibitors
Journal of Biological Chemistry **285**, 11714-11729 (2010)

Fry E.E./Tuthill T.J./Harlos K./Walter T.S./Rowlands D.J./Stuart D.I. - Crystal structure of equine rhinitis A virus in complex with its sialic acid receptor
Journal of General Virology **91**, 1971-1977 (2010)

Gabison L./Chiadmi M./El Hajji M./Castro B./Colloc'h N./Prangé T. - Near-atomic resolution structures of urate oxidase complexed with its substrate and analogues: The protonation state of the ligand
Acta Crystallographica D **66**, 714-724 (2010)

Garces F./Fernández F.J./Montellà C./Penya-Soler E./Prohens R./Aguilar J./Baldomà L./Coll M./Badía J./Vega M.C. - Molecular architecture of the Mn²⁺-dependent lactonase UlaG reveals an RNase-like metallo-β-lactamase fold and a novel quaternary structure
Journal of Molecular Biology **398**, 715-729 (2010)

Gill J./Kumar A./Yogavel M./Belrhali H./Jain S.K./Rug M./Brown M./Maier A.G./Sharma As. - Structure, localization and histone binding properties of nuclear-associated nucleosome assembly protein from Plasmodium falciparum
Malaria Journal **9**, 90-1-90-15 (2010)

Hinz A./Hulsić D.L./Forsman A./Koh W.W.L./Belrhali H./Gorlani A./de Haard H./Weiss R.A./Verrips T./Weissenhorn W. - Crystal structure of the neutralizing Llama V(HH) D7 and its mode of HIV-1 gp120 interaction
PloS One **5**, e10482-1-e10482-7 (2010)

Hurtado-Guerrero R./Zusman T./Pathak S./Ibrahim A.F.M./Shepherd S./Prescott A./Segal G./van Aalten D.M.F. - Molecular mechanism of elongation factor 1A inhibition by a Legionella pneumophila glycosyltransferase
Biochemical Journal **426**, 281-292 (2010)

Ivanov I./Crépin T./Jamin M./Ruigrok R.W.H. - Structure of the dimerization domain of the rabies virus phosphoprotein
Journal of Virology **84**, 3707-3710 (2010)

Jaiswal R.K./Manjeera G./Gopal B. - Role of a PAS sensor domain in the Mycobacterium tuberculosis transcription regulator Rv1364c
Biochemical and Biophysical Research Communications **398**, 342-349 (2010)

Khersonsky O./Röthlisberger D./Dym O./Albeck S./Jackson C.J./Baker D./Tawfik D.S. - Evolutionary optimization of computationally designed enzymes: Kemp eliminases of the KE07 series
Journal of Molecular Biology **396**, 1025-1042 (2010)

Kowatz T./Morrison J.P./Tanner M.E./Naismith J.H. - The crystal structure of the Y140F mutant of ADP-L-glycero-D-manno-heptose 6-epimerase bound to ADP-?-D-mannose suggests a one base mechanism
Protein Science **19**, 1337-1343 (2010)

Kumar P./Singh M./Gautam R./Karthikeyan S. - Potential anti-bacterial drug target: Structural characterization of 3,4-dihydroxy-2-butanone-4-phosphate synthase from *Salmonella typhimurium* LT2
Proteins: Structure, Function and Bioinformatics **78**, 3292-3303 (2010)

Kümmel D./Walter J./Heck M./Heinemann U./Veit M. - Characterization of the self-palmitoylation activity of the transport protein particle component Bet3
Cellular and Molecular Life Sciences **67**, 2653-2664 (2010)

Liu C./Walter T.S./Huang P./Zhang S./Zhu X./Wu Y./Wedderburn L.R./Tang P./Owens R.J./Stuart D.I./Ren J./Gao B. - Structural and functional insights of RANKL-RANK interaction and signaling
Journal of Immunology **184**, 6910-6919 (2010)

Manjasetty B., Turnbull A., Panjikar S. - The impact of structural proteomics on biotechnology.
Biotechnol Genet Eng Rev, **26**, 353-370 (2010)

McLuskey K./Paterson N.G./Bland N.D./Isaacs N.W./Mottram J.C. - Crystal structure of Leishmania major oligopeptidase B gives insight into the enzymatic properties of a trypanosomatid virulence factor
Journal of Biological Chemistry **285**, 39249-39259 (2010)

Milic D. - Structural basis for the enzymatic activity of tyrosine phenol-lyase
Zagreb University, Croatia (PhD Thesis), 2010

Morgan H.P./McNae I.W./Nowicki M.W./Hannaert V./Michels P.A.M./Fothergill-Gilmore L.A./Walkinshaw M.D. - Allosteric mechanism of pyruvate kinase from Leishmania mexicana uses a rock and lock model
Journal of Biological Chemistry **285**, 12892-12898 (2010)

Mourão A./Varrot A./Mackereth C.D./Cusack S./Sattler M. - Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX
RNA **16**, 1205-1216 (2010)

Namadurai S./Jain D./Kulkarni D.S./Tabib C.R./Friedhoff P./Rao D.N./Nair D.T. - The C-terminal domain of the MutL homolog from Neisseria gonorrhoeae forms an inverted homodimer
PloS One **5**, e13726-1-e13726-17 (2010)

Navratna V./Nadig S./Sood V./Prasad K./Arakere G./Gopal B. - Molecular basis for the role of Staphylococcus aureus penicillin binding protein 4 in antimicrobial resistance
Journal of Bacteriology **192**, 134-144 (2010)

Ng C.L./Waterman D.G./Antson A.A./Ortíz-Lombardía M. - Structure of the Methanothermobacter thermautrophicus exosome RNase PH ring
Acta Crystallographica D **66**, 522-528 (2010)

Nüss D./Goettig P./Magler I./Denk U./Breitenbach M./Schneider P.B./Brandstetter H./Simon-Nobbe B. - Crystal structure of the NADP-dependent mannitol dehydrogenase from Cladosporium herbarum: Implications for oligomerisation and catalysis
Biochimie **92**, 985-993 (2010)

Oke M./Carter L.G./Johnson K.A./Liu H./McMahon S.A./Yan X./Kerou M./Weikart N.D./Kadi N./Sheikh M.A./Schmelz S./Dorward M./Zawadzki M./Cozens C./Falconer H./Powers H./Overton I.M./van Niekerk C.A.J./Peng X./Patel P./Garrett R.A./Prangishvili D./Botting C.H./Coote P.J./Dryden D.T.F./Barton G.J./Schwarz-Linek U./Challis G.L./Taylor G.L./White M.F./Naismith J.H. - The Scottish Structural Proteomics Facility: Targets, methods and outputs
Journal of Structural and Functional Genomics **11**, 167-180 (2010)

Oliveira T.F./Carrigan J.B./Hamza M.A./Sharkey M.A./Engel P.C./Khan A.R. - Crystallization and preliminary structural analyses of glutamate dehydrogenase from Peptoniphilus asaccharolyticus
Acta Crystallographica F **66**, 523-526 (2010)

Opperman D.J./Sewell B.T./Litthauer D./Isupov M.N./Littlechild J.A./van Heerden E. - Crystal structure of a thermostable Old Yellow Enzyme from Thermus scotoductus SA-01
Biochemical and Biophysical Research Communications **393**, 426-431 (2010)

Patterson A./Price N.C./Nairn J. - Unliganded structure of human bisphosphoglycerate mutase reveals side-chain movements induced by ligand binding
Acta Crystallographica F **66**, 1415-1420 (2010)

Persson B.D./Schmitz N.B./Santiago C./Zocher G./Larvie M./Scheu U./Casasnovas J.M./Stehle T. - Structure of the extracellular portion of CD46 provides insights into its interactions with complement proteins and pathogens
PLoS Pathogens **6**, e1001122-1-e1001122-12 (2010)

Pointon J.A./Smith W.D./Saalbach G./Crow A./Kehoe M.A./Banfield M.J. - A highly unusual thioester bond in a pilus adhesin is required for efficient host cell interaction
Journal of Biological Chemistry **285**, 33858-33866 (2010)

Raman M.C.C./Johnson K.A./Clarke D.J./Naismith J.H./Campopiano D.J. - The serine palmitoyltransferase from *Sphingomonas wittichii* RW1: An interesting link to an unusual acyl carrier protein
Biopolymers **93**, 811-822 (2010)

Ren J./Sainsbury S./Nettleship J.E./Saunders N.J./Owens R.J. - The crystal structure of NGO0477 from *Neisseria gonorrhoeae* reveals a novel protein fold incorporating a helix-turn-helix motif
Proteins: Structure, Function and Bioinformatics **78**, 1798-1802 (2010)

Ruggiero A./Marasco D./Squeglia F./Soldini S./Pedone E./Pedone C./Berisio R. - Structure and functional regulation of RipA, a mycobacterial enzyme essential for daughter cell separation
Structure **18**, 1184-1190 (2010)

Sainsbury S./Ren J./Nettleship J.E./Saunders N.J./Stuart D.I./Owens R.J. - The structure of a reduced form of OxyR from *Neisseria meningitidis*
BMC Structural Biology **10**, 10-1-10-10 (2010)

Schimpel M./Schüttelkopf A.W./Borodkin V.S./van Aalten D.M.F. - Human OGA binds substrates in a conserved peptide recognition groove
Biochemical Journal **432**, 1-7 (2010)

Seiradake E./Harlos K./Sutton G./Aricescu A.R./Jones E.Y. - An extracellular steric seeding mechanism for Eph-ephrin signaling platform assembly
Nature Structural & Molecular Biology **17**, 398-402 (2010)

Shevtsov M.B./Chen Y./Isupov M.N./Leech A./Gollnick P./Antson A.A. - *Bacillus licheniformis* Anti-TRAP can assemble into two types of dodecameric particles with the same symmetry but inverted orientation of trimers
Journal of Structural Biology **170**, 127-133 (2010)

Smith M.A./Pirrat P./Pearson A.R./Kurtis C.R.P./Trinh C.H./Gaule T.G./Knowles P.F./Phillips S.E.V./McPherson M.J. - Exploring the roles of the metal ions in *Escherichia coli* copper amine oxidase
Biochemistry **49**, 1268-1280 (2010)

Spencer J./Murphy L.M./Conners R./Sessions R.B./Gamblin S.J. - Crystal structure of the LasA virulence factor from *Pseudomonas aeruginosa*: Substrate specificity and mechanism of M23 metallopeptidases
Journal of Molecular Biology **396**, 908-923 (2010)

Tars K./Rumnieks J./Zeltins A./Kazaks A./Kotelovica S./Leonciks A./Sharipo J./Viksna A./Kuka J./Liepinsh E./Dambrova M. - Crystal structure of human gamma-butyrobetaine hydroxylase
Biochemical and Biophysical Research Communications **398**, 634-639 (2010)

Taylor I.A./Goldstone D.C./Pala P./Haire L.F./Smerdon S.J. - Structure of the amino-terminal domain from the cell-cycle regulator Swi6
Proteins: Structure, Function and Bioinformatics **78**, 2861-2865 (2010)

Thakur K.G./Praveena T./Gopal B. - Structural and biochemical bases for the redox sensitivity of *Mycobacterium tuberculosis* RslA
Journal of Molecular Biology **397**, 1199-1208 (2010)

Tulloch L.B./Martini V.P./Iulek J./Huggan J.K./Lee J.H./Gibson C.L./Smith T.K./Suckling C.J./Hunter W.N. - Structure-based design of pteridine reductase inhibitors targeting African sleeping sickness and the leishmaniases
Journal of Medicinal Chemistry **53**, 221-229 (2010)

Tuominen H./Salminen A./Oksanen E./Jämsen J./Heikkilä O./Lehtio L./Magretova N.N./Goldman A./Baykov A.A./Lahti R. - Crystal structures of the CBS and DRTGG domains of the regulatory region of *Clostridium perfringens* pyrophosphatase complexed with the inhibitor, AMP, and activator, diadenosine tetraphosphate
Journal of Molecular Biology **398**, 400-413 (2010)

Unger T./Dym O./Albeck S./Jacobovitch Y./Bernehim R./Marom D./Pisanty O./Breiman A. - Crystal structure of the three FK506 binding protein domains of wheat FKBP73: Evidence for a unique wFK73_2 domain

Journal of Structural and Functional Genomics **11**, 113-123 (2010)

van Rooyen J.M./Abratt V.R./Belrhali H./Sewell B.T. - Crystallization of recombinant *Bacteroides fragilis* glutamine synthetase (GlnN) isolated using a novel and rapid purification protocol
Protein Expression and Purification **74**, 211-216 (2010)

Veesler D./Blangy S./Lichièvre J./Ortíz-Lombardía M./Tavares P./Campanacci V./Cambillau C. - Crystal structure of *Bacillus subtilis* SPP1 phage gp23.1, a putative chaperone
Protein Science **19**, 1812-1816 (2010)

Veesler D./Blangy S./Spinelli S./Tavares P./Campanacci V./Cambillau C. - Crystal structure of *Bacillus subtilis* SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP
Protein Science **19**, 1439-1443 (2010)

Veesler D./Robin G./Lichièvre J./Auzat I./Tavares P./Bron P./Campanacci V./Cambillau C. - Crystal structure of bacteriophage SPP1 distal tail protein (gp19.1). A baseplate hub paradigm in gram-positive infecting phages
Journal of Biological Chemistry **285**, 36666-36673 (2010)

Watermeyer J.M./Kröger W.L./O'Neill H.G./Sewell B.T./Sturrock E.D. - Characterization of domain-selective inhibitor binding in angiotensin-converting enzyme using a novel derivative of lisinopril
Biochemical Journal **428**, 67-74 (2010)

Watson A.A./O'Callaghan C.A. - Crystallization and X-ray diffraction analysis of human CLEC5A (MDL-1), a dengue virus receptor
Acta Crystallographica F **66**, 29-31 (2010)

Wigren E./Bourhis J.M./Kursula I./Guy J.E./Lindqvist Y. - Crystal structure of the LMAN1-CRD/MCFD2 transport receptor complex provides insight into combined deficiency of factor V and factor VIII
FEBS Letters **584**, 878-882 (2010)

2009

Andersson C.S./Högblom M. - A *Mycobacterium tuberculosis* ligand-binding Mn/Fe protein reveals a new cofactor in a remodeled R2-protein scaffold
Proceedings of the National Academy of Sciences of the USA **106**, 5633-5638 (2009)

Boer D.R./Ruiz-Masó J.A./López-Blanco J.R./Blanco A.G./Vives-Llacer M./Chacón P./Usón I./Gomis-Rüth F.X./Espinosa M./Llorca O./del Solar G./Coll M. - Plasmid replication initiator RepB forms a hexamer reminiscent of ring helicases and has mobile nuclease domains
EMBO Journal **28**, 1666-1678 (2009)

Bowden T.A./Aricescu A.R./Nettleship J.E./Siebold C./Rahman-Huq N./Owens R.J./Stuart D.I./Jones E.Y. - Structural plasticity of Eph receptor A4 facilitates cross-class ephrin signaling
Structure **17**, 1386-1397 (2009)

Bowden T.A./Crispin M./Graham S.C./Harvey D.J./Grimes J.M./Jones E.Y./Stuart D.I. - Unusual molecular architecture of the Machupo virus attachment glycoprotein
Journal of Virology **83**, 8259-8265 (2009)

Cendron L./Couturier M./Angelini A./Barison N./Stein M./Zanotti G. - The *Helicobacter pylori* CagD (HP0545, Cag24) protein is essential for CagA translocation and maximal induction of interleukin-8 secretion
Journal of Molecular Biology **386**, 204-217 (2009)

Chauhan A./Islam Z./Jain R.K./Karthikeyan S. - Expression, purification, crystallization and preliminary X-ray analysis of maleylacetate reductase from *Burkholderia* sp. strain SJ98
Acta Crystallographica F **65**, 1313-1316 (2009)

Clayton A./Siebold C./Gilbert R.J.C./Sutton G.C./Harlos K./McIlhinney R.A.J./Jones E.Y./Aricescu A.R. - Crystal structure of the GluR2 amino-terminal domain provides insights into the architecture and assembly of ionotropic glutamate receptors
Journal of Molecular Biology **392**, 1125-1132 (2009)

Connaris H./Crocker P.R./Taylor G.L. - Enhancing the receptor affinity of the sialic acid-binding domain of *Vibrio Cholerae* sialidase through multivalency
Journal of Biological Chemistry **284**, 7339-7351 (2009)

Coquière D./de la Lande A./Marti S./Parisel O./Prangé T./Reinaud O. - Multipoint molecular recognition within a calix[6]arene funnel complex
Proceedings of the National Academy of Sciences of the USA **106**, 10449-10454 (2009)

Crispin M./Bowden T.A./Coles C.H./Harlos K./Aricescu A.R./Harvey D.J./Stuart D.I./Jones E.Y. - Carbohydrate and domain architecture of an immature antibody glycoform exhibiting enhanced effector functions
Journal of Molecular Biology **387**, 1061-1066 (2009)

Davies K.M./Lowe E.D./Vénien-Bryan C./Johnson L.N. - The HupR receiver domain crystal structure in its nonphospho and inhibitory phospho states
Journal of Molecular Biology **385**, 51-64 (2009)

Davies M./Heikkilä T./McConkey G.A./Fishwick C.W.G./Parsons M.R./Johnson A.P. - Structure-based design, synthesis, and characterization of inhibitors of human and *Plasmodium falciparum* dihydroorotate dehydrogenases
Journal of Medicinal Chemistry **52**, 2683-2693 (2009)

de Geus D.C./van Roon A.M.M./Thomassen E.A.J./Hokke C.H./Deelder A.M./Abrahams J.P. - Characterization of a diagnostic Fab fragment binding trimeric Lewis X
Proteins: Structure, Function and Bioinformatics **76**, 439-447 (2009)

Deng D.M./Urch J.E./ten Cate J.M./Rao V.A./van Aalten D.M.F./Crielaard W. - *Streptococcus mutans* SMU.623c codes for a functional, metal-dependent polysaccharide deacetylase that modulates interactions with salivary agglutinin
Journal of Bacteriology **191**, 394-402 (2009)

Dusková J./Dohnálek J./Skálová T./Østergaard L.H./Fuglsang C.C./Kolenko P./Stepánková A./Hasek J. - Crystallization of carbohydrate oxidase from *Microdochium nivale*
Acta Crystallographica F **65**, 638-640 (2009)

Emami K./Topakas E./Nagy T./Henshaw J./Jackson K.A./Nelson K.E./Mongodin E.F./Murray J.W./Lewis R.J./Gilbert H.J. - Regulation of the xylan-degrading apparatus of *Cellvibrio japonicus* by a novel two-component system
Journal of Biological Chemistry **284**, 1086-1096 (2009)

Finarov I./Moor N./Kessler N./Safro M. - Crystallization and X-ray analysis of human cytoplasmic phenylalanyl-tRNA synthetase
Acta Crystallographica F **65**, 93-97 (2009)

Frayne J./Taylor A./Cameron G./Hadfield A.T. - Structure of insoluble rat sperm glyceraldehyde-3-phosphate dehydrogenase (GAPDH) via heterotetramer formation with *Escherichia coli* GAPDH reveals target for contraceptive design
Journal of Biological Chemistry **284**, 22703-22712 (2009)

Garnett J.A./Liu Y./Leon E./Allman S.A./Friedrich N./Saouros S./Curry S./Soldati-Favre D./Davis B.G./Feizi T./Matthews S. - Detailed insights from microarray and crystallographic studies into carbohydrate recognition by microneme protein 1 (MIC1) of *Toxoplasma gondii*
Protein Science **18**, 1935-1947 (2009)

Gill R./Kolstoe S.E./Mohammed F./Al D-Bass A./Moseley J.E./Sarwar M./Cooper J.B./Wood S.P./Shoolingin-Jordan P.M. - Structure of human porphobilinogen deaminase at 2.8 °C: The molecular basis of acute intermittent porphyria
Biochemical Journal **420**, 17-25 (2009)

Guy J.E./Ståhl U./Lindqvist Y. - Crystal structure of a class XIB phospholipase A2 (PLA2). Rice (*Oryza sativa*) isoform-2 PLA2 and an octanoate complex
Journal of Biological Chemistry **284**, 19371-19379 (2009)

Hare S./Shun M.C./Gupta S.S./Valkov E./Engelman A./Cherepanov P. - A novel Co-crystal structure affords the design of gain-of-function lentiviral integrase mutants in the presence of modified PSIP1/LEDGF/p75
PLoS Pathogens **5**, e1000259-1-e1000259-12 (2009)

Hänelmann P./Dahl J.U./Kuper J./Urban A./Müller-Theissen U./Leimkühler S./Schindelin H. - Crystal structure of YnjE from *Escherichia coli*, a sulfurtransferase with three rhodanese domains
Protein Science **18**, 2480-2491 (2009)

Hearnshaw S./West C./Singleton C./Zhou L./Kihlken M.A./Strange R.W./Le Brun N.E./Hemmings A.M. - A tetrานuclear Cu(I) cluster in the metallochaperone protein CopZ
Biochemistry **48**, 9324-9326 (2009)

Herman M.D./Moche M./Flodin S./Welin M./Trésaugues L./Johansson I./Nilsson M./Nordlund P./Nyman T. - Structures of BIR domains from human NAIP and cIAP2
Acta Crystallographica F **65**, 1091-1096 (2009)

Hernández A./Maté M.J./Sánchez-Díaz P.C./Romero A./Rojo F./Martínez J.L. - Structural and functional analysis of SmeT, the repressor of the *Stenotrophomonas maltophilia* multidrug efflux pump SmeDEF
Journal of Biological Chemistry **284**, 14428-14438 (2009)

Hothorn M./Neumann H./Lenherr E.D./Wehner M./Rybin V./Hassa P.O./Uttenweiler A./Reinhardt M./Schmidt A./Seiler J./Ladurner A.G./Hermann C./Scheffzek K./Mayer A. - Catalytic core of a membrane-associated eukaryotic polyphosphate polymerase
Science **324**, 513-516 (2009)

Khunrae P./Philip J.M.D./Bull D.R./Higgins M.K. - Structural comparison of two CSPG-binding DBL domains from the VAR2CSA protein important in Malaria during pregnancy
Journal of Molecular Biology **393**, 202-213 (2009)

Klipcan L./Moor N./Kessler N./Safro M.G. - Eukaryotic cytosolic and mitochondrial phenylalanyl-tRNA synthetases catalyze the charging of tRNA with the meta-tyrosine
Proceedings of the National Academy of Sciences of the USA **106**, 11045-11048 (2009)

Lehtiö L./Jemth A.S./Collins R./Loseva O./Johansson A./Markova N./Hammarström M./Flores A./Holmberg-Schiavone L./Weigelt J./Helleday T./Schüler H./Karlberg T. - Structural basis for inhibitor specificity in human poly(ADP-ribose) polymerase-3
Journal of Medicinal Chemistry **52**, 3108-3111 (2009)

Loh P.G./Yang H.S./Walsh M.A./Wang Q./Wang X./Cheng Z./Liu D.G./Song H. - Structural basis for translational inhibition by the tumour suppressor Pcd4
EMBO Journal **28**, 274-285 (2009)

López-Lucendo M.F./Solís D./Sáiz J.L./Kaltner H./Russwurm R./André S./Gabius H.J./Romero A. - Homodimeric chicken galectin CG-1B (C-14): Crystal structure and detection of unique redox-dependent shape changes involving inter- and intrasubunit disulfide bridges by gel filtration, ultracentrifugation, site-directed mutagenesis, and peptide mass fingerprinting
Journal of Molecular Biology **386**, 366-378 (2009)

MacKenzie D.A./Tailford L.E./Hemmings A.M./Juge N. - Crystal structure of a mucus-binding protein repeat reveals an unexpected functional immunoglobulin binding activity
Journal of Biological Chemistry **284**, 32444-32453 (2009)

McRobbie A.M./Carter L.G./Kerou M./Liu H./McMahon S.A./Johnson K.A./Oke M./Naismith J.H./White M.F. - Structural and functional characterisation of a conserved archaeal RadA paralog with antirecombinase activity
Journal of Molecular Biology **389**, 661-673 (2009)

Moroz O.V./Blagova E.V./Wilkinson A.J./Wilson K.S./Bronstein I.B. - The crystal structures of human S100A12 in apo form and in complex with zinc: New insights into S100A12 oligomerisation
Journal of Molecular Biology **391**, 536-551 (2009)

Ng C.L./Watermann D.G./Koonin E.V./Walters A.D./Chong J.P.J./Isupov M.N./Lebedev A.A./Bunka D.H.J./Stockley P.G./Ortíz-Lombardía M./Antson A.A. - Conformational flexibility and molecular interactions of an archaeal homologue of the Shwachman-Bodian-Diamond syndrome protein
BMC Structural Biology **9**, 32-1-32-15 (2009)

Nichols C.E./Sainsbury S./Ren J./Walter T.S./Verma A./Stammers D.K./Saunders N.J./Owens R.J. - The structure of NMB1585, a MarR-family regulator from Neisseria meningitidis
Acta Crystallographica F **65**, 204-209 (2009)

Oda S.I./Schröder M./Khan A.R. - Structural basis for targeting of human RNA helicase DDX3 by poxvirus protein K7
Structure **17**, 1528-1537 (2009)

Parkash V./Linholm P./Peränen J./Kalkkinen N./Oksanen E./Saarma M./Leppänen V.M./Goldman A. - The structure of the conserved neurotrophic factors MANF and CDNF explains why they are bifunctional
Protein Engineering, Design and Selection **22**, 233-241 (2009)

Ramakrishnan V./Wimberly B.T./Brodersen D.E./Carter A.P./Clemons Jr W.M. - Crystal structure of the 30s ribosome and its use.
, ()

Raman M.C.C./Johnson K.A./Yard B.A./Lowther J./Carter L.G./Naismith J.H./Campopiano D.J. - The external aldimine form of serine palmitoyltransferase. Structural, kinetic, and spectroscopic analysis of the wild-type enzyme and HSAN1 mutant mimics
Journal of Biological Chemistry **284**, 17328-17339 (2009)

Ranaivoson F.M./Neiers F./Kauffmann B./Boschi-Muller S./Branlant G./Favier F. - Methionine sulfoxide reductase B displays a high level of flexibility
Journal of Molecular Biology **394**, 83-93 (2009)

Recacha R./Boulet A./Jollivet F./Monier S./Houdusse A./Goud B./Khan A.R. - Structural basis for recruitment of Rab6-interacting protein 1 to Golgi via a RUN domain
Structure **17**, 21-30 (2009)

Ren B./Kühn J./Meslet-Cladière L./Briffaut J./Norais C./Lavigne R./Flament D./Ladenstein R./Myllykallio H. - Structure and function of a novel endonuclease acting on branched DNA substrates
EMBO Journal **28**, 2479-2489 (2009)

Richardson J.M./Colloms S.D./Finnegan D.J./Walkinshaw M.D. - Molecular architecture of the Mos1 paired-end complex: The structural basis of DNA transposition in a eukaryote
Cell **138**, 1096-1108 (2009)

Richardson J.M./Morrison L.S./Bland N.D./Bruce S./Coombs G.H./Mottram J.C./Walkinshaw M.D. - Structures of Leishmania major orthologues of macrophage migration inhibitory factor
Biochemical and Biophysical Research Communications **380**, 442-448 (2009)

Ruggiero A./Tizzano B./Pedone E./Pedone C./Wilmanns M./Berisio R. - Crystal structure of the resuscitation-promoting factor deltaDUFRpfB from M. tuberculosis
Journal of Molecular Biology **385**, 153-162 (2009)

Sabbadin F./Jackson R./Haider K./Tampi G./Turkenburg J.P./Hart S./Bruce N.C./Grogan G. - The 1.5-Å structure of XplA-heme, an unusual cytochrome P450 heme domain that catalyzes reductive biotransformation of royal demolition explosive
Journal of Biological Chemistry **284**, 28467-28475 (2009)

Sainsbury S./Lane L.A./Ren J./Gilbert R.J./Saunders N.J./Robinson C.V./Stuart D.I./Owens R.J. - The structure of CrgA from *Neisseria meningitidis* reveals a new octameric assembly state for LysR transcriptional regulators
Nucleic Acids Research **37**, 4545-4558 (2009)

Sanchez-Weatherby J./Bowler M.W./Huet J./Gobbo A./Felisaz F./Lavault B./Moya R./Kadlec J./Ravelli R.B.G./Cipriani F. - Improving diffraction by humidity control: A novel device compatible with X-ray beamlines
Acta Crystallographica D **65**, 1237-1246 (2009)

Schmelz S./Kadi N./McMahon S.A./Song L./Oves-Costales D./Oke M./Liu H./Johnson K.A./Carter L.G./Botting C.H./White M.F./Challis G.L./Naismith J.H. - AcsD catalyzes enantioselective citrate desymmetrization in siderophore biosynthesis
Nature Chemical Biology **5**, 174-182 (2009)

Schneider M.C./Prosser B.E./Caesar J.J.E./Kugelberg E./Li S./Zhang Q./Quoraishi S./Lovett J.E./Deane J.E./Sim R.B./Roversi P./Johnson S./Tang C.M./Lea S.M. - *Neisseria meningitidis* recruits factor H using protein mimicry of host carbohydrates
Nature **458**, 890-893 (2009)

Skálová T./Dohnálek J./Østergaard L.H./Østergaard P.R./Kolenko P./Dusková J./Stepánková A./Hasek J. - The structure of the small laccase from *Streptomyces coelicolor* reveals a link between laccases and nitrite reductases
Journal of Molecular Biology **385**, 1165-1178 (2009)

Smits C./Chechik M./Kovalevskiy O.V./Shevtsov M.B./Foster A.W./Alonso J.C./Antson A.A. - Structural basis for the nuclelease activity of a bacteriophage large terminase
EMBO Reports **10**, 592-598 (2009)

Tron C.M./McNae I.W./Nutley M./Clarke D.J./Cooper A./Walkinshaw M.D./Baxter R.L./Campopiano D.J. - Structural and functional studies of the biotin protein ligase from *Aquifex aeolicus* reveal a critical role for a conserved residue in target specificity
Journal of Molecular Biology **387**, 129-146 (2009)

Tuthill T.J./Harlos K./Walter T.S./Knowles N.J./Groppelli E./Rowlands D.J./Stuart D.I./Fry E.E. - Equine rhinitis A virus and its low pH empty particle: Clues towards an aphthovirus entry mechanism?
PLoS Pathogens **5**, e1000620-1-e1000620-11 (2009)

Ulens C./Akdemir A./Jongejan A./van Elk R./Bertrand S./Perrakis A./Leurs R./Smit A.B./Sixma T.K./Bertrand D./Esch I.J.P. - Use of acetylcholine binding protein in the search for novel ?7 nicotinic receptor ligands. In silico docking, pharmacological screening, and X-ray analysis
Journal of Medicinal Chemistry **52**, 2372-2383 (2009)

Valkov E./Gupta S.S./Hare S./Helander A./Roversi P./McClure M./Cherepanov P. - Functional and structural characterization of the integrase from the prototype foamy virus
Nucleic Acids Research **37**, 243-255 (2009)

Wagener N./Pierik A.J./Ibdah A./Hille R./Dobbek H. - The Mo-Se active site of nicotinate dehydrogenase
Proceedings of the National Academy of Sciences of the USA **106**, 11055-11060 (2009)

Walter T.S./Liu C./Huang S./Wedderburn L.R./Gao B./Owens R.J./Stuart D.I./Tang P./Ren J. - Crystallization and preliminary X-ray analysis of mouse RANK and its complex with RANKL
Acta Crystallographica F **65**, 597-600 (2009)

Willand N./Dirié B./Carette X./Bifani P./Singhal A./Desroses M./Leroux F./Willery E./Mathys V./Déprez-Poulain R./Delcroix G./Frénois F./Aumercier M./Locht C./Villeret V./Déprez B./Baulard A.R. - Synthetic EthR inhibitors boost antituberculous activity of ethionamide
Nature Medicine **15**, 537-544 (2009)

2008

Alfieri A./Malito E./Orru R./Fraaije M.W./Mattevi A. - Revealing the moonlighting role of NADP in the structure of a flavin-containing monooxygenase
Proceedings of the National Academy of Sciences of the USA **105**, 6572-6577 (2008)

Aricescu A.R./Siebold C./Jones Y./Jones E.Y. - Receptor protein tyrosine phosphatase μ : Measuring where to stick
Biochemical Society Transactions **36**, 167-172 (2008)

Assenberg R./Delmas O./Graham S.C./Verma A./Berrow N./Stuart D.I./Owens R.J./Bourhy H./Grimes J.M. - Expression, purification and crystallization of a lyssavirus matrix (M) protein
Acta Crystallographica F **64**, 258-262 (2008)

Au K./Ren J./Walter T.S./Harlos K./Nettleship J.E./Owens R.J./Stuart D.I./Esnouf R.M. - Structures of an alanine racemase from *Bacillus anthracis* (BA0252) in the presence and absence of (R)-1-aminoethylphosphonic acid (L-Ala-P)
Acta Crystallographica F **64**, 327-333 (2008)

Bagnérés C./Ageichik A.V./Cronin N./Wallace B./Collins M./Boshoff C./Waksman G./Barrett T. - Crystal structure of a vFlip-IKKgamma complex: Insights into viral activation of the IKK signalosome
Molecular Cell **30**, 620-631 (2008)

Bahar M.W./Kenyon J.C./Putz M.M./Abrescia N.G.A./Pease J.E./Wise E.L./Stuart D.I./Smith G.L./Grimes J.M. - Structure and function of A41, a vaccinia virus chemokine binding protein
PLoS Pathogens **4**, e5-0055-e5-0068 (2008)

Brown J./Delaine C./Zaccheo O.J./Siebold C./Gilbert R.J./van Boxel G./Denley A./Wallace J.C./Hassan A.B./Forbes B.E./Jones E.Y. - Structure and functional analysis of the IGF-II/IGF2R interaction
EMBO Journal **27**, 265-276 (2008)

Colloc'h N./Gabison L./Monard G./Altarsha M./Chiadmi M./Marassio G./Sopkova-de Oliveira Santos J./El Hajji M./Castro B./Abraim J.H./Prangé T. - Oxygen pressurized X-ray crystallography: Probing the dioxygen binding site in cofactorless urate oxidase and implications for its catalytic mechanism
Biophysical Journal **95**, 2415-2422 (2008)

Connors R./Hill D.J./Borodina E./Agnew C./Daniell S.J./Burton N.M./Sessions R.B./Clarke A.R./Catto L.E./Lammie D./Wess T./Brady R.L./Virji M. - The *Moraxella* adhesin UspA1 binds to its human CEACAM1 receptor by a deformable trimeric coiled-coil
EMBO Journal **27**, 1779-1789 (2008)

Cordle J./Johnson S./Zi Yan Tay J./Roversi P./Wilkin M.B./Hernández de Madrid B./Shimizu H./Jensen S./Whiteman P./Jin B./Redfield C./Baron M./Lea S.M./Handford P.A. - A conserved face of the Jagged/Serrate DSL domain is involved in Notch trans-activation and cis-inhibition
Nature Structural & Molecular Biology **15**, 849-857 (2008)

Dawson A./Fyfe P.K./Hunter W.N. - Specificity and reactivity in menaquinone biosynthesis: The structure of *Escherichia coli* MenD (2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexadiene-1-carboxylate synthase)
Journal of Molecular Biology **384**, 1353-1368 (2008)

De Sanctis D./Bento I./Inácio J.M./Custódio S./de Sá-Nogueira I./Carrondo M.A. - Overproduction, crystallization and preliminary X-ray characterization of Abn2, an endo-1,5-alpha-arabinanase from *Bacillus subtilis*
Acta Crystallographica F **64**, 636-638 (2008)

Eckhard U./Nüss D./Ducka P./Schönauer E./Brandstetter H. - Crystallization and preliminary X-ray characterization of the catalytic domain of collagenase G from *Clostridium histolyticum*
Acta Crystallographica F **64**, 419-421 (2008)

El Omari K./Scott K./Dhaliwal B./Ren J./Abrescia N.G.A./Budworth J./Lockyer M./Powell K.L./Hawkins A.R./Stammers D.K. - Crystallization and preliminary X-ray analysis of the human respiratory syncytial virus nucleocapsid protein
Acta Crystallographica F **64**, 1019-1023 (2008)

Fyfe P.K./Oza S.L./Fairlamb A.H./Hunter W.N. - Leishmania trypanothione synthetase-amidase structure reveals a basis for regulation of conflicting synthetic and hydrolytic activities
Journal of Biological Chemistry **283**, 17672-17680 (2008)

Gabison L./Prangé T./Colloc'h N./El Hajji M./Castro B./Chiadmi M. - Structural analysis of urate oxidase in complex with its natural substrate inhibited by cyanide: Mechanistic implications
BMC Structural Biology **8**, 32-1-32-8 (2008)

Garcia-Saez I./Docquier J.D./Rossolini G.M./Dideberg O. - The three-dimensional structure of VIM-2, a Zn-beta-lactamase from *Pseudomonas aeruginosa* in its reduced and oxidised form
Journal of Molecular Biology **375**, 604-611 (2008)

Graham S.C./Bahar M.W./Cooray S./Chen R.A.J./Whalen D.M./Abrescia N.G.A./Alderton D./Owens R.J./Stuart D.I./Smith G.L./Grimes J.M. - Vaccinia virus proteins A52 and B14 share a Bcl-2-like fold but have evolved to inhibit NF-kappaB rather than apoptosis
PLoS Pathogens **4**, e1000128-1-e1000128-12 (2008)

Grininger M./Nöll G./Trawöger S./Sinner E.K./Oesterhelt D. - Electrochemical switching of the flavoprotein dodecin at gold surfaces modified by flavin-DNA hybrid linkers
Biointerphases **3**, 51-58 (2008)

Guilligay D./Tarendau F./Resa-Infante P./Coloma R./Crépin T./Sehr P./Lewis J./Ruigrok R.W.H./Ortin J./Hart D.J./Cusack S. - The structural basis for cap binding by influenza virus polymerase subunit PB2
Nature Structural & Molecular Biology **15**, 500-506 (2008)

Gut H./King S.J./Walsh M.A. - Structural and functional studies of *Streptococcus pneumoniae* neuraminidase B: An intramolecular trans-sialidase
FEBS Letters **582**, 3348-3352 (2008)

Hatherley D./Graham S.C./Turner J./Harlos K./Stuart D.I./Barclay A.N. - Paired receptor specificity explained by structures of signal regulatory proteins alone and complexed with CD47
Molecular Cell **31**, 266-277 (2008)

Herman M.D./Nyman T./Welin M./Lehtiö L./Flodin S./Trésaugues L./Kotenyova T./Flores A./Nordlund P. - Completing the family portrait of the anti-apoptotic Bcl-2 proteins: Crystal structure of human Bfl-1 in complex with Bim
FEBS Letters **582**, 3590-3594 (2008)

Hewitson K.S./Holmes S.L./Ehrismann D./Hardy A.P./Chowdhury R./Schofield C.J./McDonough M.A. - Evidence that two enzyme-derived histidine ligands are sufficient for iron binding and catalysis by factor inhibiting HIF (FIH)
Journal of Biological Chemistry **283**, 25971-25978 (2008)

Hirsch A.K.H./Alphey M.S./Lauw S./Seet M./Barandun L./Eisenreich W./Rohdich F./Hunter W.N./Bacher A./Diederich F. - Inhibitors of the kinase IspE: Structure-activity relationships and co-crystal structure analysis
Organic & Biomolecular Chemistry **6**, 2719-2730 (2008)

Hu N.J./Yusof A.M./Winter A./Osman A./Reeve A.K./Hofmann A. - The crystal structure of calcium-bound annexin Gh1 from *Gossypium hirsutum* and its implications for membrane binding mechanisms of plant annexins
Journal of Biological Chemistry **283**, 18314-18322 (2008)

Hurtado-Guerrero R./Raimi O.G./Min J./Zeng H./Vallius L./Shepherd S./Ibrahim A.F.M./Wu H./Plotnikov A.N./van Aalten D.M.F. - Structural and kinetic differences between human and *Aspergillus fumigatus* D-glucosamine-6-phosphate N-acetyltransferase

Biochemical Journal **415**, 217-223 (2008)

Jain A./Ziegler J./Liscombe D.K./Facchini P.J./Tucker P.A./Panjikar S. - Purification, crystallization and X-ray diffraction analysis of pavine N-methyltransferase from Thalictrum flavum
Acta Crystallographica F **64**, 1066-1069 (2008)

Janowski R./Auerbach-Nevo T./Weiss M.S. - Bacterioferritin from Mycobacterium smegmatis contains zinc in its di-nuclear site
Protein Science **17**, 1138-1150 (2008)

Kadlec J./Loureiro S./Abrescia N.G.A./Stuart D.I./Jones I.M. - The postfusion structure of baculovirus gp64 supports a unified view of viral fusion machines
Nature Structural & Molecular Biology **15**, 1024-1030 (2008)

Kainov D.E./Mancini E.J./Telenius J./Lísal J./Grimes J.M./Bamford D.H./Stuart D.I./Tuma R. - Structural basis of mechanochemical coupling in a hexameric molecular motor
Journal of Biological Chemistry **283**, 3607-3617 (2008)

Karkehabadi S./Hansson H./Kim S./Piens K./Mitchinson C./Sandgren M. - The first structure of a glycoside hydrolase family 61 member, Cel61B from Hypocrea jecorina, at 1.6 Å resolution
Journal of Molecular Biology **383**, 144-154 (2008)

Korndörfer I.P./Kanitz A./Danzer J./Zimmer M./Loessner M.J./Skerra A. - Structural analysis of the L-alanoyl-D-glutamate endopeptidase domain of Listeria bacteriophage endolysin Ply500 reveals a new member of the LAS peptidase family
Acta Crystallographica D **64**, 644-650 (2008)

Kotaka M./Johnson C./Lamb H.K./Hawkins A.R./Ren J./Stammers D.K. - Structural analysis of the recognition of the negative regulator NmrA and DNA by the zinc finger from the GATA-type transcription factor AreA
Journal of Molecular Biology **381**, 373-382 (2008)

Kouwen T.R.H.M./Andréll J./Schrijver R./Dubois J.Y.F./Maher M.J./Iwata S./Carpenter E.P./van Dijl J.M. - Thioredoxin A active-site mutants form mixed disulfide dimers that resemble enzyme-substrate reaction intermediates
Journal of Molecular Biology **379**, 520-534 (2008)

Lebars I./Legrand P./Aimé A./Pinaud N./Fribourg S./Di Primo C. - Exploring TAR-RNA aptamer loop-loop interaction by X-ray crystallography, UV spectroscopy and surface plasmon resonance
Nucleic Acids Research **36**, 7146-7156 (2008)

Lberman N./Dym O./Unger T./Albeck S./Peleg Y./Jacobovitch Y./Branzburg A./Eisenstein M./Marash L./Kimchi A. - The crystal structure of the C-terminal DAP5/p97 domain sheds light on the molecular basis for its processing by caspase cleavage
Journal of Molecular Biology **383**, 539-548 (2008)

Ling S.H.M./Decker C.J./Walsh M.A./She M./Parker R./Song H. - Crystal structure of human Edc3 and its functional implications
Molecular and Cellular Biology **28**, 5965-5976 (2008)

Liu H./Rudolf J./Johnson K.A./McMahon S.A./Oke M./Carter L./McRobbie A.M./Brown S.E./Naismith J.H./White M.F. - Structure of the DNA repair helicase XPD
Cell **133**, 801-812 (2008)

Liu W./Pucci B./Rossi M./Pisani F.M./Ladenstein R. - Structural analysis of the Sulfolobus solfataricus MCM protein N-terminal domain
Nucleic Acids Research **36**, 3235-3243 (2008)

Marsh M./Shoemark D.K./Jacob A./Robinson C./Cahill B./Zhou N.Y./Williams P.A./Hadfield A.T. - Structure of bacterial glutathione-S-transferase maleyl pyruvate isomerase and implications for mechanism of isomerisation

Journal of Molecular Biology **384**, 165-177 (2008)

McMahon S.A./Oke M./Liu H./Johnson K.A./Carter L./Kadi N./White M.F./Challis G.L./Naismith J.H. - Purification, crystallization and data collection of *Pectobacterium chrysanthemi* AcsD, a type A siderophore synthetase
Acta Crystallographica F **64**, 1052-1055 (2008)

Meier C./Carter L.G./Sainsbury S./Mancini E.J./Owens R.J./Stuart D.I./Esnouf R.M. - The crystal structure of UMP kinase from *Bacillus anthracis* (BA1797) reveals an allosteric nucleotide-binding site
Journal of Molecular Biology **381**, 1098-1105 (2008)

Merckx A./Echalier A./Langford K./Sicard A./Langsley G./Jooore J./Doerig C./Noble M./Endicott J. - Structures of *P. falciparum* protein kinase 7 identify an activation motif and leads for inhibitor design
Structure **16**, 228-238 (2008)

Milic D./Demidkina T.V./Faleev N.G./Matkovic-Calogovic D./Antson A.A. - Insights into the catalytic mechanism of tyrosine phenol-lyase from X-ray structures of quinonoid intermediates
Journal of Biological Chemistry **283**, 29206-29214 (2008)

Minoprio P./Alzari P./Buschiazzo A./Degrave W./Gregoire C./Chamond N./Berneman A. - Crystallographic structure of TcPRACA and uses therefor
()

Monné M./Han L./Schwend T./Burendahl S./Jovine L. - Crystal structure of the ZP-N domain of ZP3 reveals the core fold of animal egg coats
Nature **456**, 653-657 (2008)

Nagano C.S./Calvette J.J./Barettino D./Pérez A./Cavada B.S./Sanz L. - Insights into the structural basis of the pH-dependent dimer-tetramer equilibrium through crystallographic analysis of recombinant Diocleinae lectins
Biochemical Journal **409**, 417-428 (2008)

Nettleship J.E./Ren J./Rahman N./Berrow N.S./Hatherley D./Barclay A.N./Owens R.J. - A pipeline for the production of antibody fragments for structural studies using transient expression in HEK 293T cells
Protein Expression and Purification **62**, 83-89 (2008)

Oke M./Ching R.T.Y./Carter L.G./Johnson K.A./Liu H./McMahon S.A./White M.F./Bloch Jr C./Botting C.H./Walsh M.A./Latiff A.A./Kennedy M.W./Cooper A./Naismith J.H. - Unusual chromophore and cross-links in ranasmurfin: A blue protein from the foam nests of a tropical frog
Angewandte Chemie International Edition **47**, 7853-7856 (2008)

Paës G./Skov L.K./O'Donohue M.J./Rémond C./Kastrup J.S./Gajhede M./Mirza O. - The structure of the complex between a branched pentasaccharide and *Thermobacillus xylanilyticus* GH-51 arabinofuranosidase reveals xylan-binding determinants and induced fit
Biochemistry **47**, 7441-7451 (2008)

Ranaivoson F.M./Antoine M./Kauffmann B./Boschi-Muller S./Aubry A./Brantl G./Favier F. - A structural analysis of the catalytic mechanism of methionine sulfoxide reductase A from *Neisseria meningitidis*
Journal of Molecular Biology **377**, 268-280 (2008)

Ren J./Nettleship J.E./Sainsbury S./Saunders N.J./Owens R.J. - Structure of the cold-shock domain protein from *Neisseria meningitidis* reveals a strand-exchanged dimer
Acta Crystallographica F **64**, 247-251 (2008)

Richards J.D./Johnson K.A./Liu H./McRobbie A.M./McMahon S./Oke M./Carter L./Naismith J.H./White M.F. - Structure of the DNA repair helicase Hel308 reveals DNA binding and autoinhibitory domains
Journal of Biological Chemistry **283**, 5118-5126 (2008)

Roces L./Knowles P.P./Fox G./Juanhuix J./Scaplehorn N./Way M./McDonald N.Q. - Crystallization and preliminary X-ray diffraction analysis of vaccinia virus H1L phosphatase
Acta Crystallographica F **64**, 190-192 (2008)

Roos A.K./Mariano S./Kowalinski E./Salmon L./Mowbray S.L. - D-ribose 5-phosphate isomerase B from Escherichia coli is also a functional D-allos-6-phosphate isomerase, while the Mycobacterium tuberculosis enzyme is not

Journal of Molecular Biology **382**, 667-679 (2008)

Rossi F./Garavaglia S./Montalbano V./Walsh M.A./Rizzi M. - Crystal structure of human kynurenone aminotransferase II, a drug target for the treatment of schizophrenia
Journal of Biological Chemistry **283**, 3559-3566 (2008)

Sainsbury S./Ren J./Saunders N.J./Stuart D.I./Owens R.J. - Crystallization and preliminary X-ray analysis of CrgA, a LysR-type transcriptional regulator from pathogenic Neisseria meningitidis MC58
Acta Crystallographica F **64**, 797-801 (2008)

Sharma As./Yogavel M./Akhouri R.R./Gill J./Sharma Am. - Crystal structure of soluble domain of malaria sporozoite protein UIS3 in complex with lipid
Journal of Biological Chemistry **283**, 24077-24088 (2008)

Tarendeau F./Crépin T./Guilligay D./Ruigrok R.W.H./Cusack S./Hart D.J. - Host determinant residue lysine 627 lies on the surface of a discrete, folded domain of influenza virus polymerase PB2 subunit
PLoS Pathogens **4**, e1000136-1-e1000136-8 (2008)

Tottey S./Waldron K.J./Firbank S.J./Reale B./Bessant C./Sato K./Cheek T.R./Gray J./Banfield M.J./Dennison C./Robinson N.J. - Protein-folding location can regulate manganese-binding versus copper- or zinc-binding
Nature **455**, 1138-1142 (2008)

Vicente J.B./Carrodo M.A./Teixeira M./Frazão C. - Structural studies on flavodiiron proteins
Methods in Enzymology **437**, 3-19 (2008)

Villa F./Deak M./Alessi D.R./van Aalten D.M.F. - Structure of the OSR1 kinase, a hypertension drug target
Proteins: Structure, Function and Bioinformatics **73**, 1082-1087 (2008)

Vitu E./Gross E./Greenblatt H.M./Sevier C.S./Kaiser C.A./Fass D. - Yeast Mpd1p reveals the structural diversity of the protein disulfide isomerase family
Journal of Molecular Biology **384**, 631-640 (2008)

Vyas R./Kumar V./Panjikar S./Karthikeyan S./Kishan K.V.R./Tewari R./Weiss M.S. - Purification, crystallization and preliminary X-ray diffraction analysis of aspartate semialdehyde dehydrogenase (Rv3708c) from Mycobacterium tuberculosis
Acta Crystallographica F **64**, 167-170 (2008)

Walter T.S./Mancini E.J./Kadlec J./Graham S.C./Assenberg R./Ren J./Sainsbury S./Owens R.J./Stuart D.I./Grimes J.M./Harlos K. - Semi-automated microseeding of nanolitre crystallization experiments
Acta Crystallographica F **64**, 14-18 (2008)

Watermeyer J.M./Kröger W.L./O'Neill H.G./Sewell B.T./Sturrock E.D. - Probing the basis of domain-dependent inhibition using novel ketone inhibitors of angiotensin-converting enzyme
Biochemistry **47**, 5942-5950 (2008)

Wolski S.C./Kuper J./Hänelmann P./Truglio J.J./Croteau D.L./Van Houten B./Kisker C. - Crystal structure of the FeS cluster-containing nucleotide excision repair helicase XPD
PLoS Biology **6**, e149-1332-e149-1342 (2008)

Wright H./Noda-García L./Ochoa-Leyva A./Hodgson D.A./Fülöp V./Barona-Gómez F. - The structure/function relationship of a dual-substrate (beta alpha)8-isomerase
Biochemical and Biophysical Research Communications **635**, 16-21 (2008)

Zhang Y./Illarionov B./Morgunova E./Jin G./Bacher A./Fischer M./Ladenstein R./Cushman M. - A new series of N-[2,4-dioxo-6-D-ribitylamino-1,2,3,4-tetrahydropyrimidin-5-yl]oxalamic acid derivatives as inhibitors of

lumazine synthase and riboflavin synthase: Design, synthesis, biochemical evaluation, crystallography, and mechanistic implications
Journal of Organic Chemistry **73**, 2715-2724 (2008)

2007

Abbott R.J.M./Spendlove I./Roversi P./Fitzgibbon H./Knott V./Teriete P./McDonnell J.M./Handford P.A./Lea S.M. - Structural and functional characterization of a novel T cell receptor co-regulatory protein complex, CD97-CD55
Journal of Biological Chemistry **282**, 22023-22032 (2007)

Ahn S./Moniot S./Elias M./Chabrière E./Kim D./Scott K. - Structure-function relationships in a bacterial DING protein
FEBS Letters **581**, 3455-3460 (2007)

Assenberg R./Ren J./Verma A./Walter T.S./Alderton D./Hurrelbrink R.J./Fuller S.D./Bressanelli S./Owens R.J./Stuart D.I./Grimes J.M. - Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues
Journal of General Virology **88**, 2228-2236 (2007)

Brumshtain B./Greenblatt H.M./Butters T.D./Shaaltiel Y./Aviezer D./Silman I./Futerman A.H./Sussman J.L. - Crystal structures of complexes of N-butyl- and N-nonyl-deoxynojirimycin bound to acid beta-glucosidase. Insights into the mechanism of chemical chaperone action in Gaucher disease
Journal of Biological Chemistry **282**, 29052-29058 (2007)

Chaudhuri I. - Evolution der beta-propeller-proteine
Technische Universität München (PhD thesis), 2007

Clantin B./Delattre A.S./Rucktooa P./Saint N./Méli A.C./Locht C./Jacob-Dubuisson F./Villeret V. - Structure of the membrane protein FhaC: A member of the Omp85/TpsB transporter superfamily
Science **317**, 957-961 (2007)

Colloc'h N./Sopkova-de Oliveira Santos J./Retailleau P./Vivarès D./Bonneté F./Langlois d'Estainto B./Gallois B./Brisson A./Risso J.J./Lemaire M./Prangé T./Abraïni J.H. - Protein crystallography under xenon and nitrous oxide pressure: Comparison with in vivo pharmacology studies and implications for the mechanism of inhaled anesthetic action
Biophysical Journal **92**, 217-224 (2007)

Cooray S./Bahar M.W./Abrescia N.G.A./McVey C.E./Bartlett N.W./Chen R.A.J./Stuart D.I./Grimes J.M./Smith G.L. - Functional and structural studies of the vaccinia virus virulence factor N1 reveal a Bcl-2-like anti-apoptotic protein
Journal of General Virology **88**, 1656-1666 (2007)

Coquelle N./Fioravanti E./Weik M./Vellieux F./Madern D. - Activity, stability and structural studies of lactate dehydrogenases adapted to extreme thermal environments
Journal of Molecular Biology **374**, 547-562 (2007)

Corradi H.R./Chitapi I./Sewell B.T./Georgiadis D./Dive V./Sturrock E.D./Acharya K.R. - The structure of testis angiotensin-converting enzyme in complex with the C domain-specific inhibitor RXPA380
Biochemistry **46**, 5473-5478 (2007)

Deshpande A./Wang S./Walsh M.A./Dokland T. - Structure of the equine arteritis virus nucleocapsid protein reveals a dimer-dimer arrangement
Acta Crystallographica D **63**, 581-586 (2007)

Fabrichny I.P./Lehtiö L./Tammenkoski M./Zyryanov A.B./Oksanen E./Baykov A.A./Lahti R./Goldman A. - A trimetal site and substrate distortion in a family II inorganic pyrophosphatase
Journal of Biological Chemistry **282**, 1422-1431 (2007)

Forouhar F./Ross Anderson J.L./Mowat C.G./Vorobiev S.M./Hussain A./Abashidze M./Bruckmann C./Thackray S.J./Seetharaman J./Tucker T./Xiao R./Ma L.C./Zhao L./Acton T.B./Montelione G.T./Chapman S.K./Tong L. - Molecular insights into substrate recognition and catalysis by tryptophan 2,3-dioxygenase
Proceedings of the National Academy of Sciences of the USA **104**, 473-478 (2007)

Graham S.C./Bahar M.W./Abrescia N.G.A./Smith G.L./Stuart D.I./Grimes J.M. - Structure of CrmE, a virus-encoded tumour necrosis factor receptor
Journal of Molecular Biology **372**, 660-671 (2007)

Hardwick S.W./Pané-Farré J./Delumeau O./Marles-Wright J./Murray J.W./Hecker M./Lewis R.J. - Structural and functional characterization of partner switching regulating the environmental stress response in *Bacillus subtilis*
Journal of Biological Chemistry **282**, 11562-11572 (2007)

Hartlieb B./Muñoz T./Weissenhorn W./Becker S. - Crystal structure of the C-terminal domain of Ebola virus VP30 reveals a role in transcription and nucleocapsid association
Proceedings of the National Academy of Sciences of the USA **104**, 624-629 (2007)

Hatherley D./Harlos K./Dunlop D.C./Stuart D.I./Barclay A.N. - The structure of the macrophage signal regulatory protein {alpha} (SIRP{alpha}) inhibitory receptor reveals a binding face reminiscent of that used by T cell receptors
Journal of Biological Chemistry **282**, 14567-14575 (2007)

Hulsken R./Mery A./Thomassen E.A./Ranieri A./Solà M./Verbeet M.P./Kohzuma T./Ubbink M. - Protonation of a histidine copper ligand in fern plastocyanin
Journal of the American Chemical Society **129**, 4423-4429 (2007)

Hurtado-Guerrero R./Raimi O./Shepherd S./van Aalten D.M.F. - Glucose-6-phosphate as a probe for the glucosamine-6-phosphate N-acetyltransferase Michaelis complex
FEBS Letters **581**, 5597-5600 (2007)

Koch M./Camp S./Collen T./Avila D./Salomonsen J./Wallny H.J./van Hateren A./Hunt L./Jacob J.P./Johnston F./Marston D.A./Shaw I./Dunbar P.R./Cerundolo V./Jones E.Y./Kaufman J. - Structures of an MHC class I molecule from B21 chickens illustrate promiscuous peptide binding
Immunity **27**, 885-899 (2007)

Kovalevskiy O.V./Lebedev A.A./Surin A.K./Solonin A.S./Antson A.A. - Crystal structure of *Bacillus cereus* HlyIIR, a transcriptional regulator of the gene for pore-forming toxin hemolysin II
Journal of Molecular Biology **365**, 825-834 (2007)

Lascombe M.B./Retailleau P./Ponchet M./Industri B./Blein J.P./Prangé T. - Structure of sylvaticin, a new alpha-elicitin-like protein from *Pythium sylvaticum*
Acta Crystallographica D **63**, 1102-1108 (2007)

Legrand P./Pinaud N./Minvielle-Sébastia L./Fribourg S. - The structure of the CstF-77 homodimer provides insights into CstF assembly
Nucleic Acids Research **35**, 4515-4522 (2007)

Leppänen V.M./Tossavainen H./Permi P./Lehtiö L./Rönnholm G./Goldman A./Kilpeläinen I./Pihlajamaa T. - Crystal structure of the N-terminal NC4 domain of collagen IX, a unique binding member of the laminin-neurexin-sex hormone binding globulin (LNS) domain family
Journal of Biological Chemistry **282**, 23219-23230 (2007)

Liu H./Woznicka K./Catton G./Crawford A./Botting N./Naismith J.H. - Structural and kinetic characterization of quinolinate phosphoribosyltransferase (hQPRTase) from *Homo sapiens*
Journal of Molecular Biology **373**, 755-763 (2007)

MacKenzie A.K./Kershaw N.J./Hernandez H./Robinson C.V./Schofield C.J./Andersson I. - Clavulanic acid dehydrogenase: Structural and biochemical analysis of the final step in the biosynthesis of the beta-lactamase inhibitor clavulanic acid

Biochemistry **46**, 1523-1533 (2007)

Malet H./Egloff M.P./Selisko B./Butcher R.E./Wright P.J./Roberts M./Gruez A./Sulzenbacher G./Vonrhein C./Bricogne G./Mackenzie J.M./Khromykh A.A./Davidson A.D./Canard B. - Crystal structure of the RNA polymerase domain of the west nile virus non-structural protein 5
Journal of Biological Chemistry **282**, 10678-10689 (2007)

Moniot S./Elias M./Kim D./Scott K./Chabrière E. - Crystallization, diffraction data collection and preliminary crystallographic analysis of DING protein from *Pseudomonas fluorescens*
Acta Crystallographica F **63**, 590-592 (2007)

Nichols C.E./Lamb H.K./Lockyer M./Charles I.G./Pyne S./Hawkins A.R./Stammers D.K. - Characterization of *Salmonella typhimurium* YegS, a putative lipid kinase homologous to eukaryotic sphingosine and diacylglycerol kinases
Proteins: Structure, Function and Bioinformatics **68**, 13-25 (2007)

Paesen G.C./Siebold C./Harlos K./Peacey M.F./Nuttall P.A./Stuart D.I. - A tick protein with a modified Kunitz fold inhibits human tryptase
Journal of Molecular Biology **368**, 1172-1186 (2007)

Paspaleva K./Thomassen E./Pannu N.S./Iwai S./Moolenaar G.F./Goosen N./Abrahams J.P. - Crystal structure of the DNA repair enzyme ultraviolet damage endonuclease
Structure **15**, 1316-1324 (2007)

Rea D./Fülop V./Bugg T.D.H./Roper D.I. - Structure and mechanism of HpcH: A metal ion dependent class II aldolase from the homoprotocatechuate degradation pathway of *Escherichia coli*
Journal of Molecular Biology **373**, 866-876 (2007)

Ren J./Sainsbury S./Combs S.E./Capper R.G./Jordan P.W./Berrow N.S./Stammers D.K./Saunders N.J./Owens R.J. - The structure and transcriptional analysis of a global regulator from *Neisseria meningitidis*
Journal of Biological Chemistry **282**, 14655-14664 (2007)

Richardson J.M./Finnegan D.J./Walkinshaw M.D. - Crystallization of a Mos1 transposase-inverted-repeat DNA complex: Biochemical and preliminary crystallographic analyses
Acta Crystallographica F **63**, 434-437 (2007)

Roszak A.W./Gardiner A.T./Isaacs N.W./Cogdell R.J. - Brominated lipids identify lipid binding sites on the surface of the reaction center from *Rhodobacter sphaeroides*
Biochemistry **46**, 2909-2916 (2007)

Roversi P./Lissina O./Johnson S./Ahmat N./Paesen G.C./Ploss K./Boland W./Nunn M.A./Lea S.M. - The structure of OMCI, a novel lipocalin inhibitor of the complement system
Journal of Molecular Biology **369**, 784-793 (2007)

Röben A. - Röntgenstrukturanalyse eines Aktin-Homologen Ta0583 aus *Thermoplasma acidophilum* und der UDP-Glukose Pyrophosphorylase aus *Saccharomyces cerevisiae*
Universität München (PhD thesis), 2007

Rudiño-Piñera E./Ravelli R.B.G./Sheldrick G.M./Nanao M.H./Korostelev V.V./Werner J.M./Schwarz-Linek U./Potts J.R./Garman E.F. - The solution and crystal structures of a module pair from the *Staphylococcus aureus*-binding site of human fibronectin—A tale with a twist
Journal of Molecular Biology **368**, 833-844 (2007)

Ruggiero A./Tizzano B./Geerlof A./Pedone E./Pedone C./Wilmanns M./Berisio R. - Expression, purification, crystallization and preliminary X-ray crystallographic analysis of a resuscitation-promoting factor from *Mycobacterium tuberculosis*
Acta Crystallographica F **63**, 870-873 (2007)

Sanders C.M./Kovalevskiy O.V./Sizov D./Lebedev A.A./Isupov M.N./Antson A.A. - Papillomavirus E1 helicase assembly maintains an asymmetric state in the absence of DNA and nucleotide cofactors

Nucleic Acids Research **35**, 6451-6457 (2007)

Sanders C.M./Sizov D./Seavers P.R./Ortíz-Lombardía M./Antson A.A. - Transcription activator structure reveals redox control of a replication initiation reaction
Nucleic Acids Research **35**, 3504-3515 (2007)

Saschenbrecker S. - Folding and assembly of RuBisCO : Structural and functional characterization of the RuBisCO assembly chaperone RbcX
Universität München (PhD thesis), 2007

Saschenbrecker S./Bracher A./Rao K.V./Rao B.V./Hartl F.U./Hayer-Hartl M. - Structure and function of RbcX, an assembly chaperone for hexadecameric rubisco
Cell **129**, 1189-1200 (2007)

Sauvé V./Bruno S./Berks B.C./Hemmings A.M. - The SoxYZ complex carries sulfur cycle intermediates on a peptide swinging arm
Journal of Biological Chemistry **282**, 23194-23204 (2007)

Shenoy A.R./Capuder M./Draskovic P./Lamba D./Visweswariah S.S./Podobnik M. - Structural and biochemical analysis of the Rv0805 cyclic nucleotide phosphodiesterase from Mycobacterium tuberculosis
Journal of Molecular Biology **365**, 211-225 (2007)

Sonnenberg A./Rojas A.M./de Pereda J.M. - The structure of a tandem pair of spectrin repeats of plectin reveals a modular organization of the plakin domain
Journal of Molecular Biology **368**, 1379-1391 (2007)

Splingard A./Ménétrey J./Perderiset M./Cicolari J./Regazzoni K./Hamoudi F./Cabanié L./El Marjou A./Wells A./Houdusse A./de Gunzburg J. - Biochemical and structural characterization of the gem GTPase
Journal of Biological Chemistry **282**, 1905-1915 (2007)

Sutton G./Grimes J.M./Stuart D.I./Roy P. - Bluetongue virus VP4 is an RNA-capping assembly line
Nature Structural & Molecular Biology **14**, 449-451 (2007)

Tan W.S./McNae I.W./Ho K.L./Walkinshaw M.D. - Crystallization and X-ray analysis of the T = 4 particle of hepatitis B capsid protein with an N-terminal extension
Acta Crystallographica F **63**, 642-647 (2007)

Tatur J./Hagen W.R./Matias P.M. - Crystal structure of the ferritin from the hyperthermophilic archaeal anaerobe Pyrococcus furiosus
Journal of Biological Inorganic Chemistry **12**, 615-630 (2007)

Textor L.C./Wilmanns M./Holton S.J. - Expression, purification, crystallization and preliminary crystallographic analysis of the mouse transcription factor MafB in complex with its DNA-recognition motif Cmare
Acta Crystallographica F **63**, 657-661 (2007)

Thapper A./Boer D.R./Brondino C.D./Moura J.J.G./Romão M.J. - Correlating EPR and X-ray structural analysis of arsenite-inhibited forms of aldehyde oxidoreductase
Journal of Biological Inorganic Chemistry **12**, 353-366 (2007)

Verger D./Carr P.D./Kwok T./Ollis D.L. - Crystal structure of the N-terminal domain of the TyrR transcription factor responsible for gene regulation of aromatic amino acid biosynthesis and transport in Escherichia coli K12
Journal of Molecular Biology **367**, 102-112 (2007)

Villa F./Goebel J./Rafiqi F.H./Deak M./Thastrup J./Alessi D.R./van Aalten D.M.F. - Structural insights into the recognition of substrates and activators by the OSR1 kinase
EMBO Reports **8**, 839-845 (2007)

Worrall L.J./Walkinshaw M.D. - Crystal structure of the C-terminal three-helix bundle subdomain of C. elegans Hsp70
Biochemical and Biophysical Research Communications **357**, 105-110 (2007)

Yang J./Roe S.M./Prickett T.D./Brautigan D.L./Barford D. - The structure of Tap42/alpha4 reveals a tetratricopeptide repeat-like fold and provides insights into PP2A regulation
Biochemistry **46**, 8807-8815 (2007)

Yard B.A./Carter L.G./Johnson K.A./Overton I.M./Dorward M./Liu H./McMahon S.A./Oke M./Puech D./Barton G.J./Naismith J.H./Campopiano D.J. - The structure of serine palmitoyltransferase; gateway to sphingolipid biosynthesis
Journal of Molecular Biology **370**, 870-886 (2007)

Zaccaj N.R./May A.P./Robinson R.C./Burtnick L.D./Crocker P.R./Brossmer R./Kelm S./Jones E.Y. - Crystallographic and in silico analysis of the sialoside-binding characteristics of the Siglec sialoadhesin
Journal of Molecular Biology **365**, 1469-1479 (2007)

Zahn K.E./Belrhali H./Wallace S.S./Doublie S. - Caught bending the A-rule: Crystal structures of translesion DNA synthesis with a non-natural nucleotide
Biochemistry **46**, 10551-10561 (2007)