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| 762 | Full and Partial Agonism of a Designed Enzyme Switch. | | |
| 761 | The benefits of atomic resolution. 1997 , 7, 681-8 | | 131 |
| 760 | Structure and mechanism of endo/exocellulase E4 from <i>Thermomonospora fusca</i> . <i>Nature Structural Biology</i> , 1997 , 4, 810-8 | | 309 |
| 759 | Crystal structure of the amphiphysin-2 SH3 domain and its role in the prevention of dynamin ring formation. 1998 , 17, 5273-85 | | 146 |
| 758 | Enzyme inactivation through sulfhydryl oxidation by physiologic NO-carriers. <i>Nature Structural Biology</i> , 1998 , 5, 267-71 | | 140 |
| 757 | Crystal structure of the RNA-binding domain from transcription termination factor rho. <i>Nature Structural Biology</i> , 1998 , 5, 352-6 | | 62 |
| 756 | Conformational changes on substrate binding to methylmalonyl CoA mutase and new insights into the free radical mechanism. 1998 , 6, 711-20 | | 181 |
| 755 | The crystal structure of human cytosolic serine hydroxymethyltransferase: a target for cancer chemotherapy. 1998 , 6, 1105-16 | | 145 |
| 754 | Crystal structures of two mutants that have implications for the folding of bovine pancreatic ribonuclease A. 1998 , 7, 1255-8 | | 36 |
| 753 | Two non-proline cis peptide bonds may be important for factor XIII function. 1998 , 423, 291-6 | | 114 |
| 752 | The structure of a trimeric archaeal adenylate kinase. 1998 , 282, 167-79 | | 60 |
| 751 | The 1.25 Å resolution refinement of the cholera toxin B-pentamer: evidence of peptide backbone strain at the receptor-binding site. 1998 , 282, 1043-59 | | 148 |
| 750 | A structural explanation for the recognition of tyrosine-based endocytotic signals. 1998 , 282, 1327-32 | | 467 |
| 749 | On the active site of Old Yellow Enzyme. Role of histidine 191 and asparagine 194. 1998 , 273, 32753-62 | | 105 |
| 748 | Functional changes in the structure of the SRP GTPase on binding GDP and Mg ²⁺ GDP. <i>Nature Structural Biology</i> , 1999 , 6, 793-801 | | 72 |
| 747 | A productive NADP ⁺ binding mode of ferredoxin-NADP ⁺ reductase revealed by protein engineering and crystallographic studies. <i>Nature Structural Biology</i> , 1999 , 6, 847-53 | | 158 |
| 746 | Structure and mechanism of the glycyl radical enzyme pyruvate formate-lyase. <i>Nature Structural Biology</i> , 1999 , 6, 969-75 | | 159 |

| | | |
|-----|--|-----|
| 745 | A structural explanation for the binding of multiple ligands by the alpha-adaptin appendage domain. 1999 , 97, 805-15 | 255 |
| 744 | Crystal structure of human ubiquitous mitochondrial creatine kinase. 2000 , 39, 216-25 | 59 |
| 743 | Crystal structure of MalK, the ATPase subunit of the trehalose/maltose ABC transporter of the archaeon <i>Thermococcus litoralis</i> . 2000 , 19, 5951-61 | 255 |
| 742 | The structural basis for the recognition of acetylated histone H4 by the bromodomain of histone acetyltransferase gcn5p. 2000 , 19, 6141-9 | 387 |
| 741 | Flt3 ligand structure and unexpected commonalities of helical bundles and cystine knots. <i>Nature Structural Biology</i> , 2000 , 7, 486-91 | 61 |
| 740 | The x-ray structure of D-amino acid oxidase at very high resolution identifies the chemical mechanism of flavin-dependent substrate dehydrogenation. 2000 , 97, 12463-8 | 165 |
| 739 | Inactive conformation of the serpin alpha(1)-antichymotrypsin indicates two-stage insertion of the reactive loop: implications for inhibitory function and conformational disease. 2000 , 97, 67-72 | 166 |
| 738 | Crystal structure of <i>Pseudomonas aeruginosa</i> PAK pilin suggests a main-chain-dominated mode of receptor binding. 2000 , 299, 1005-17 | 120 |
| 737 | Structure of bacteriophage T4 gene product 11, the interface between the baseplate and short tail fibers. 2000 , 301, 975-85 | 48 |
| 736 | The crystal structure of bacillus cereus phosphonoacetaldehyde hydrolase: insight into catalysis of phosphorus bond cleavage and catalytic diversification within the HAD enzyme superfamily. 2000 , 39, 10385-96 | 124 |
| 735 | Conformational change of elongation factor Tu (EF-Tu) induced by antibiotic binding. Crystal structure of the complex between EF-Tu.GDP and aurodox. 2001 , 276, 17149-55 | 95 |
| 734 | Crystal structure of chaperonin-60 from <i>Paracoccus denitrificans</i> . 2001 , 312, 501-9 | 15 |
| 733 | Crystal structure of the dimeric phosphoenolpyruvate carboxykinase (PEPCK) from <i>Trypanosoma cruzi</i> at 2 Å resolution. 2001 , 313, 1059-72 | 55 |
| 732 | X-ray crystal structure of MTH938 from <i>Methanobacterium thermoautotrophicum</i> at 2.2 Å resolution reveals a novel tertiary protein fold. 2001 , 45, 486-8 | 4 |
| 731 | Structure and mechanism of the RNA triphosphatase component of mammalian mRNA capping enzyme. 2001 , 20, 2575-86 | 74 |
| 730 | Structure of the electron transfer complex between ferredoxin and ferredoxin-NADP(+) reductase. <i>Nature Structural Biology</i> , 2001 , 8, 117-21 | 256 |
| 729 | The crystal structure of <i>E. coli</i> pantothenate synthetase confirms it as a member of the cytidyltransferase superfamily. 2001 , 9, 439-50 | 64 |
| 728 | Dynamic properties of the Ras switch I region and its importance for binding to effectors. 2001 , 98, 4944-9 | 245 |

| | | |
|-----|--|-----|
| 727 | A crystallographic map of the transition from B-DNA to A-DNA. 2001 , 98, 7265-70 | 99 |
| 726 | The effect of cytosine methylation on the structure and geometry of the Holliday junction: the structure of d(CCGGTACm5CGG) at 1.5 Å resolution. 2002 , 277, 21041-9 | 21 |
| 725 | X-ray structure of pyruvate formate-lyase in complex with pyruvate and CoA. How the enzyme uses the Cys-418 thiol radical for pyruvate cleavage. 2002 , 277, 40036-42 | 69 |
| 724 | The role of glutamine 114 in old yellow enzyme. 2002 , 277, 2138-45 | 38 |
| 723 | Crystal structure of the antioxidant enzyme glutathione reductase inactivated by peroxynitrite. 2002 , 277, 2779-84 | 102 |
| 722 | Crystal structure analysis of the exocytosis-sensitive phosphoprotein, pp63/parafusin (phosphoglucomutase), from <i>Paramecium</i> reveals significant conformational variability. 2002 , 315, 141-53 | 21 |
| 721 | Molecular architecture and functional model of the endocytic AP2 complex. 2002 , 109, 523-35 | 453 |
| 720 | X-ray structure of a dihydropyrimidinase from <i>Thermus</i> sp. at 1.3 Å resolution. 2002 , 320, 143-56 | 79 |
| 719 | Structural enzymology of Li(+)-sensitive/Mg(2+)-dependent phosphatases. 2002 , 320, 1087-94 | 30 |
| 718 | Yeast D-amino acid oxidase: structural basis of its catalytic properties. 2002 , 324, 535-46 | 98 |
| 717 | Structure of a Sir2 enzyme bound to an acetylated p53 peptide. 2002 , 10, 523-35 | 210 |
| 716 | Foreword. 2002 , xi-xiv | 7 |
| 715 | Preface. 2002 , xv-xviii | |
| 714 | INTRODUCTION. 2002 , 1-20 | |
| 713 | SCIENCE IN PERSPECTIVE. 2002 , 21-73 | |
| 712 | SCIENCE WARS. 2002 , 74-111 | |
| 711 | SCIENCE'S PRESUPPOSITIONS. 2002 , 112-155 | |
| 710 | DEDUCTIVE LOGIC. 2002 , 156-190 | |

709 INDUCTIVE LOGIC AND STATISTICS. **2002**, 217-268

708 PARSIMONY AND EFFICIENCY. **2002**, 269-326

1

707 CASE STUDIES. **2002**, 327-366

706 SCIENCE'S POWERS AND LIMITS. **2002**, 367-376

705 CONCLUSIONS. **2002**, 406-409

704 SCIENCE EDUCATION. **2002**, 377-405

703 PROBABILITY. **2002**, 191-216

702 References. **2002**, 410-430

701 Evidence of intradomain and interdomain flexibility in an OmpR/PhoB homolog from *Thermotoga maritima*. **2002**, 10, 153-64

95

700 Structural description of the active sites of mouse L-chain ferritin at 1.2 Å resolution. **2003**, 8, 105-11

55

699 Structure of *E. coli* ketopantoate hydroxymethyl transferase complexed with ketopantoate and Mg²⁺, solved by locating 160 selenomethionine sites. **2003**, 11, 985-96

42

698 Structure of a complex between *E. coli* DNA topoisomerase I and single-stranded DNA. **2003**, 11, 1349-58

37

697 Structural basis for binding of accessory proteins by the appendage domain of GGAs. **2003**, 10, 607-13

45

696 The 0.93Å crystal structure of spherocase: a calcium-loaded serine protease from *Bacillus sphaericus*. **2003**, 332, 1071-82

35

695 Crystal structure of *Salmonella typhimurium* 2-methylisocitrate lyase (PrpB) and its complex with pyruvate and Mg(2+). **2003**, 311, 193-201

14

694 Glutathione reductase of the malarial parasite *Plasmodium falciparum*: crystal structure and inhibitor development. **2003**, 328, 893-907

108

693 Expression, purification, crystallization, and preliminary X-ray analysis of recombinant human saposin B. **2003**, 27, 186-93

15

692 The structure of the GGA1-GAT domain reveals the molecular basis for ARF binding and membrane association of GGAs. **2003**, 4, 321-32

51

| | | |
|-----|---|-----|
| 691 | Homomeric ring assemblies of eukaryotic Sm proteins have affinity for both RNA and DNA. Crystal structure of an oligomeric complex of yeast SmF. 2003 , 278, 17291-8 | 23 |
| 690 | The structure of the periplasmic ligand-binding domain of the sensor kinase CitA reveals the first extracellular PAS domain. 2003 , 278, 39189-96 | 118 |
| 689 | Impact of N-terminal myristoylation on the Ca ²⁺ -dependent conformational transition in recoverin. 2003 , 278, 22972-9 | 40 |
| 688 | Binding partners for the COOH-terminal appendage domains of the GGAs and gamma-adaptin. 2003 , 14, 2385-98 | 66 |
| 687 | Structure of the active N-terminal domain of Ezrin. Conformational and mobility changes identify keystone interactions. 2003 , 278, 4949-56 | 85 |
| 686 | Cation-pi interactions as determinants for binding of the compatible solutes glycine betaine and proline betaine by the periplasmic ligand-binding protein ProX from Escherichia coli. 2004 , 279, 5588-96 | 97 |
| 685 | Structural basis for the binding of compatible solutes by ProX from the hyperthermophilic archaeon Archaeoglobus fulgidus. 2004 , 279, 48270-81 | 46 |
| 684 | Structure of adeno-associated virus type 2 Rep40-ADP complex: insight into nucleotide recognition and catalysis by superfamily 3 helicases. 2004 , 101, 12455-60 | 34 |
| 683 | Structural basis for the attachment of a paramyxoviral polymerase to its template. 2004 , 101, 8301-6 | 163 |
| 682 | Structure-function correlation in glycine oxidase from Bacillus subtilis. 2004 , 279, 29718-27 | 51 |
| 681 | Structure and assembly of the pseudopilin PulG. 2004 , 54, 647-64 | 89 |
| 680 | The structural basis for the interaction between nonsense-mediated mRNA decay factors UPF2 and UPF3. 2004 , 11, 330-7 | 145 |
| 679 | Sequence-specific DNA binding determined by contacts outside the helix-turn-helix motif of the ParB homolog KorB. 2004 , 11, 656-63 | 57 |
| 678 | Structural insights into the stability and flexibility of unusual erythroid spectrin repeats. 2004 , 12, 645-56 | 69 |
| 677 | Crystal structure of human vinculin. 2004 , 12, 1189-97 | 126 |
| 676 | X-Ray Structure of Rhodobacter Capsulatus Cytochrome bc (1): Comparison with its Mitochondrial and Chloroplast Counterparts. 2004 , 81, 251-75 | 174 |
| 675 | Crystal structure of a putative oxalate decarboxylase (TM1287) from Thermotoga maritima at 1.95 Å resolution. 2004 , 56, 392-5 | 16 |
| 674 | Crystal structure of PqqC from Klebsiella pneumoniae at 2.1 Å resolution. 2004 , 56, 401-3 | 10 |

| | | |
|-----|---|-----|
| 673 | Crystal structure of a novel manganese-containing cupin (TM1459) from <i>Thermotoga maritima</i> at 1.65 Å resolution. 2004 , 56, 611-4 | 22 |
| 672 | Crystal structure of a novel <i>Thermotoga maritima</i> enzyme (TM1112) from the cupin family at 1.83 Å resolution. 2004 , 56, 615-8 | 5 |
| 671 | Structural and functional studies of FkpA from <i>Escherichia coli</i> , a cis/trans peptidyl-prolyl isomerase with chaperone activity. 2004 , 335, 595-608 | 110 |
| 670 | Crystal structure and biochemical properties of the human mitochondrial ferritin and its mutant Ser144Ala. 2004 , 340, 277-93 | 107 |
| 669 | How small peptides block and reverse serpin polymerisation. 2004 , 342, 931-41 | 76 |
| 668 | Independent movement, dimerization and stability of tandem repeats of chicken brain alpha-spectrin. 2004 , 344, 495-511 | 94 |
| 667 | Synchrotron radiation in atomic-resolution studies of protein structure. 2004 , 362, 12-20 | 8 |
| 666 | Crystallographic analysis of AcrB. 2004 , 564, 333-9 | 31 |
| 665 | Crystallization, X-ray diffraction analysis and phasing of carboxylesterase PA3859 from <i>Pseudomonas aeruginosa</i> . 2005 , 1752, 197-201 | 12 |
| 664 | Crystal structure of <i>Yersinia enterocolitica</i> type III secretion chaperone SycT. 2005 , 14, 1993-2002 | 26 |
| 663 | Catalytically enhanced endocellulase cel5a from <i>Acidothermus cellulolyticus</i> . 2005 , 121, 0129-0148 | 42 |
| 662 | The crystal structure of human CD1d with and without alpha-galactosylceramide. 2005 , 6, 819-26 | 328 |
| 661 | Efficient use of synchrotron radiation for macromolecular diffraction data collection. 2005 , 89, 153-72 | 15 |
| 660 | Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of propionate kinase (TdcD) from <i>Salmonella typhimurium</i> . 2005 , 61, 52-5 | 3 |
| 659 | Crystallization and preliminary X-ray analysis of Mlc from <i>Escherichia coli</i> . 2005 , 61, 183-5 | 2 |
| 658 | Crystallization and preliminary X-ray analysis of immunophilin-like FKBP42 from <i>Arabidopsis thaliana</i> . 2005 , 61, 363-5 | 5 |
| 657 | Crystallization and preliminary X-ray diffraction data for the aconitase form of human iron-regulatory protein 1. 2005 , 61, 482-5 | 6 |
| 656 | Characterization of different crystal forms of the alpha-glucosidase MalA from <i>Sulfolobus solfataricus</i> . 2005 , 61, 1039-42 | 4 |

- 655 Biased mutagenesis in the N-terminal region by degenerate oligonucleotide gene shuffling enhances secretory expression of barley alpha-amylase 2 in yeast. **2005**, 18, 515-26 11
- 654 Crystal structure of a 92-residue C-terminal fragment of TonB from Escherichia coli reveals significant conformational changes compared to structures of smaller TonB fragments. **2005**, 280, 3022-8 54
- 653 Structure of Ptr ToxA: an RGD-containing host-selective toxin from Pyrenophora tritici-repentis. **2005**, 17, 3190-202 85
- 652 Crystal structure of baculovirus RNA triphosphatase complexed with phosphate. **2005**, 280, 17848-56 21
- 651 Competitive inhibitors of Mycobacterium tuberculosis ribose-5-phosphate isomerase B reveal new information about the reaction mechanism. **2005**, 280, 6416-22 32
- 650 The x-ray crystal structure of lysine-2,3-aminomutase from Clostridium subterminale. **2005**, 102, 13819-24 140
- 649 The crystal structure of Mlc, a global regulator of sugar metabolism in Escherichia coli. **2005**, 280, 29073-9 37
- 648 Crystallographic and spectroscopic evidence for high affinity binding of FeEDTA(H₂O)- to the periplasmic nickel transporter NikA. **2005**, 127, 10075-82 69
- 647 Structural dynamics of alpha-actinin-vinculin interactions. **2005**, 25, 6112-22 74
- 646 Crystal structure of a novel Plasmodium falciparum 1-Cys peroxiredoxin. **2005**, 346, 1021-34 81
- 645 The X-ray structure of the type II secretion system complex formed by the N-terminal domain of EpsE and the cytoplasmic domain of EpsL of Vibrio cholerae. **2005**, 348, 845-55 83
- 644 Molecular basis for the glyphosate-insensitivity of the reaction of 5-enolpyruvylshikimate 3-phosphate synthase with shikimate. **2005**, 579, 5773-80 11
- 643 Analysis of the link between enzymatic activity and oligomeric state in AhpC, a bacterial peroxiredoxin. **2005**, 44, 10583-92 174
- 642 A novel inhibitor that suspends the induced fit mechanism of UDP-N-acetylglucosamine enolpyruvyl transferase (MurA). **2005**, 280, 14070-5 54
- 641 Structural determinants of Torpedo californica acetylcholinesterase inhibition by the novel and orally active carbamate based anti-alzheimer drug ganstigmine (CHF-2819). *Journal of Medicinal Chemistry*, **2006**, 49, 5051-8 8.3 34
- 640 Structure of coenzyme A-disulfide reductase from Staphylococcus aureus at 1.54 Å resolution. **2006**, 45, 11278-89 35
- 639 Crystal structure of a plant immunophilin domain involved in regulation of MDR-type ABC transporters. **2006**, 580, 251-5 20
- 638 Crystal structure of a major fragment of the salt-tolerant glutaminase from Micrococcus luteus K-3. **2006**, 346, 1118-24 15

| | | |
|-----|--|-----|
| 637 | Structural basis for transcription-coupled repair: the N terminus of Mfd resembles UvrB with degenerate ATPase motifs. 2006 , 355, 675-83 | 28 |
| 636 | Barnase fusion as a tool to determine the crystal structure of the small disulfide-rich protein McoEeTl. 2006 , 356, 1-8 | 15 |
| 635 | Co-repressor induced order and biotin repressor dimerization: a case for divergent followed by convergent evolution. 2006 , 357, 509-23 | 72 |
| 634 | Structure of the regulatory subunit of acetohydroxyacid synthase isozyme III from <i>Escherichia coli</i> . 2006 , 357, 951-63 | 65 |
| 633 | Structure of the <i>Sulfolobus solfataricus</i> alpha-glucosidase: implications for domain conservation and substrate recognition in GH31. 2006 , 358, 1106-24 | 110 |
| 632 | NADP ⁺ expels both the co-factor and a substrate analog from the <i>Mycobacterium tuberculosis</i> ThyX active site: opportunities for anti-bacterial drug design. 2006 , 360, 1-6 | 17 |
| 631 | T-rich DNA single strands bind to a preformed site on the bacterial cold shock protein Bs-CspB. 2006 , 360, 702-14 | 53 |
| 630 | Purification, crystallization and preliminary X-ray analysis of the outer membrane complex HasA-HasR from <i>Serratia marcescens</i> . 2006 , 62, 56-60 | 7 |
| 629 | Structure of the synthetase domain of human CTP synthetase, a target for anticancer therapy. 2006 , 62, 613-7 | 27 |
| 628 | Expression, crystallization and preliminary X-ray analysis of the periplasmic stress sensory protein RseB from <i>Escherichia coli</i> . 2006 , 62, 895-8 | 1 |
| 627 | Crystallization and preliminary crystallographic analysis of two <i>Streptococcus agalactiae</i> proteins: the family II inorganic pyrophosphatase and the serine/threonine phosphatase. 2006 , 62, 891-4 | 3 |
| 626 | Crystallization and X-ray data analysis of the 10 kDa C-terminal lid subdomain from <i>Caenorhabditis elegans</i> Hsp70. 2006 , 62, 938-43 | 2 |
| 625 | The crystal structure of a Cys25 -> Ala mutant of human procathepsin S elucidates enzyme-prosequence interactions. 2006 , 15, 2619-29 | 18 |
| 624 | Insights into the sirtuin mechanism from ternary complexes containing NAD ⁺ and acetylated peptide. 2006 , 14, 1231-40 | 115 |
| 623 | Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. 2007 , 35, 495-505 | 40 |
| 622 | Experimental determination of the radiation dose limit for cryocooled protein crystals. 2006 , 103, 4912-7 | 332 |
| 621 | The crystal structure of <i>Arabidopsis thaliana</i> allene oxide cyclase: insights into the oxylipin cyclization reaction. 2006 , 18, 3201-17 | 79 |
| 620 | Crystal structure of the sugar binding domain of the archaeal transcriptional regulator TrmB. 2006 , 281, 10976-82 | 28 |

| | | |
|-----|--|----|
| 619 | Tuning of a neuronal calcium sensor. 2006 , 281, 37594-602 | 37 |
| 618 | Crystal structure of NblA from <i>Anabaena</i> sp. PCC 7120, a small protein playing a key role in phycobilisome degradation. 2006 , 281, 5216-23 | 41 |
| 617 | Crystal structure of a bacterial type IB DNA topoisomerase reveals a preassembled active site in the absence of DNA. 2006 , 281, 6030-7 | 21 |
| 616 | Structural basis for the regulation of N-acetylglutamate kinase by PII in <i>Arabidopsis thaliana</i> . 2007 , 282, 35733-40 | 49 |
| 615 | Structures of <i>Mycobacterium tuberculosis</i> 1-deoxy-D-xylulose-5-phosphate reductoisomerase provide new insights into catalysis. 2007 , 282, 19905-16 | 67 |
| 614 | Cross-reactivity studies of an anti- <i>Plasmodium vivax</i> apical membrane antigen 1 monoclonal antibody: binding and structural characterisation. 2007 , 366, 1523-37 | 56 |
| 613 | Structural studies of <i>E. coli</i> topoisomerase III-DNA complexes reveal a novel type IA topoisomerase-DNA conformational intermediate. 2007 , 368, 105-18 | 30 |
| 612 | The structure of a tandem pair of spectrin repeats of plectin reveals a modular organization of the plakin domain. 2007 , 368, 1379-91 | 46 |
| 611 | Optimized variants of the cold shock protein from in vitro selection: structural basis of their high thermostability. 2007 , 369, 1087-97 | 20 |
| 610 | Cyclin box structure of the P-TEFb subunit cyclin T1 derived from a fusion complex with EIAV tat. 2007 , 370, 826-36 | 35 |
| 609 | The structure of RseB: a sensor in periplasmic stress response of <i>E. coli</i> . 2007 , 372, 927-941 | 30 |
| 608 | A structural insight into the inhibition of human and <i>Leishmania donovani</i> ornithine decarboxylases by 1-amino-oxy-3-aminopropane. 2007 , 405, 261-8 | 43 |
| 607 | Structure of the <i>Streptococcus agalactiae</i> family II inorganic pyrophosphatase at 2.80 Å resolution. 2007 , 63, 738-43 | 18 |
| 606 | Preliminary time-of-flight neutron diffraction study on diisopropyl fluorophosphatase (DFPase) from <i>Loligo vulgaris</i> . 2007 , 63, 42-5 | 18 |
| 605 | Common mode of DNA binding to cold shock domains. Crystal structure of hexathymidine bound to the domain-swapped form of a major cold shock protein from <i>Bacillus caldolyticus</i> . 2007 , 274, 1265-79 | 43 |
| 604 | Structure of <i>Streptococcus agalactiae</i> serine/threonine phosphatase. The subdomain conformation is coupled to the binding of a third metal ion. 2007 , 274, 3128-37 | 47 |
| 603 | The crystal structure of the ligand-binding module of human TAG-1 suggests a new mode of homophilic interaction. 2007 , 16, 2174-83 | 37 |
| 602 | Structure-based design of robust glucose biosensors using a <i>Thermotoga maritima</i> periplasmic glucose-binding protein. 2007 , 16, 2240-50 | 33 |

| | | |
|-----|---|-----|
| 601 | Analysis of xenon binding to photosystem II by X-ray crystallography. 2008 , 98, 523-7 | 23 |
| 600 | Determining Rieske cluster reduction potentials. 2008 , 13, 1301-13 | 37 |
| 599 | Expression, purification and crystallization of a lyssavirus matrix (M) protein. 2008 , 64, 258-62 | 15 |
| 598 | Preliminary time-of-flight neutron diffraction study of human deoxyhemoglobin. 2008 , 64, 270-3 | 9 |
| 597 | Crystallization and preliminary characterization of a novel haem-binding protein of <i>Streptomyces reticuli</i> . 2008 , 64, 386-90 | 13 |
| 596 | Purification, crystallization and preliminary crystallographic analysis of biotin protein ligase from <i>Staphylococcus aureus</i> . 2008 , 64, 520-3 | 9 |
| 595 | Expression, crystallization and preliminary X-ray analysis of an outer membrane protein from <i>Thermus thermophilus</i> HB27. 2008 , 64, 533-6 | 4 |
| 594 | Expression, purification, crystallization and structure determination of two glutathione S-transferase-like proteins from <i>Shewanella oneidensis</i> . 2008 , 64, 548-53 | 5 |
| 593 | Effect of leucine-to-methionine substitutions on the diffraction quality of histone chaperone SET/TAF-1beta/INHAT crystals. 2008 , 64, 960-5 | 4 |
| 592 | Purification, crystallization and X-ray diffraction analysis of pavine N-methyltransferase from <i>Thalictrum flavum</i> . 2008 , 64, 1066-9 | 2 |
| 591 | Crystallization and preliminary X-ray diffraction analysis of arginyl-tRNA synthetase from <i>Escherichia coli</i> . 1997 , 6, 2636-8 | 4 |
| 590 | Crystal structure of brain-type creatine kinase at 1.41 Å resolution. 1999 , 8, 2258-69 | 75 |
| 589 | Protein crystallography for non-crystallographers, or how to get the best (but not more) from published macromolecular structures. 2008 , 275, 1-21 | 187 |
| 588 | Structural basis for LEAFY floral switch function and similarity with helix-turn-helix proteins. 2008 , 27, 2628-37 | 81 |
| 587 | Structure of the minor pseudopilin EpsH from the Type 2 secretion system of <i>Vibrio cholerae</i> . 2008 , 377, 91-103 | 40 |
| 586 | Structure of the <i>Yersinia enterocolitica</i> type III secretion translocator chaperone SycD. 2008 , 375, 997-1012 | 51 |
| 585 | Structure of the nucleocapsid-binding domain from the mumps virus polymerase; an example of protein folding induced by crystallization. 2008 , 379, 719-31 | 44 |
| 584 | Crystal structure of Ca ²⁺ -free S100A2 at 1.6-Å resolution. 2008 , 378, 933-42 | 25 |

| | | |
|-----|---|-----|
| 583 | Ligand binding mode of GABAA receptor-associated protein. 2008 , 381, 1320-31 | 38 |
| 582 | The interplay of ligand binding and quaternary structure in the diverse interactions of dynein light chain LC8. 2008 , 384, 954-66 | 33 |
| 581 | X-ray crystallography identifies two chloride binding sites in the oxygen evolving centre of Photosystem II. 2008 , 1, 161 | 107 |
| 580 | Cysteine pK(a) values for the bacterial peroxiredoxin AhpC. 2008 , 47, 12860-8 | 90 |
| 579 | A protein functional leap: how a single mutation reverses the function of the transcription regulator TetR. 2008 , 36, 4390-401 | 27 |
| 578 | Structure and evolution of a novel dimeric enzyme from a clinically important bacterial pathogen. 2008 , 283, 27598-27603 | 78 |
| 577 | Phycocerythrobilin synthase (PebS) of a marine virus. Crystal structures of the biliverdin complex and the substrate-free form. 2008 , 283, 27547-27554 | 37 |
| 576 | CD94-NKG2A recognition of human leukocyte antigen (HLA)-E bound to an HLA class I leader sequence. 2008 , 205, 725-35 | 145 |
| 575 | Multivalency in the assembly of intrinsically disordered Dynein intermediate chain. 2009 , 284, 33115-21 | 57 |
| 574 | Crystal structure and autoactivation pathway of the precursor form of human tripeptidyl-peptidase 1, the enzyme deficient in late infantile ceroid lipofuscinosis. 2009 , 284, 3985-97 | 41 |
| 573 | Crystal structure of the caseinolytic protease gene regulator, a transcriptional activator in actinomycetes. 2009 , 284, 5208-16 | 12 |
| 572 | Structure of signal-regulatory protein alpha: a link to antigen receptor evolution. 2009 , 284, 26613-9 | 24 |
| 571 | Crystal structure of KorA bound to operator DNA: insight into repressor cooperation in RP4 gene regulation. 2009 , 37, 1915-24 | 14 |
| 570 | Structural characterization of a viral NEIL1 ortholog unliganded and bound to abasic site-containing DNA. 2009 , 284, 26174-83 | 35 |
| 569 | 3D structure of a binary ROP-PRONE complex: the final intermediate for a complete set of molecular snapshots of the RopGEF reaction. 2009 , 390, 427-35 | 18 |
| 568 | Molecular shape and prominent role of beta-strand swapping in organization of dUTPase oligomers. 2009 , 583, 865-71 | 21 |
| 567 | Crystal structure of human eIF5A1: insight into functional similarity of human eIF5A1 and eIF5A2. 2009 , 75, 1040-5 | 42 |
| 566 | Crystal structures of Lys-63-linked tri- and di-ubiquitin reveal a highly extended chain architecture. 2009 , 77, 753-9 | 44 |

| | | |
|-----|--|--------|
| 565 | Involvement of a carboxylated lysine in UV damage endonuclease. 2009 , 18, 549-58 | 4 |
| 564 | Structure of ristocetin A in complex with a bacterial cell-wall mimetic. 2009 , 65, 832-8 | 14 |
| 563 | Crystallization and preliminary characterization of the <i>Thermus thermophilus</i> RNA helicase Hera C-terminal domain. 2009 , 65, 248-52 | 7 |
| 562 | A preliminary neutron crystallographic study of proteinase K at pD 6.5. 2009 , 65, 184-7 | 2 |
| 561 | Preliminary X-ray crystallographic studies of <i>Bacillus subtilis</i> SpeA protein. 2009 , 65, 282-4 | 2 |
| 560 | Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of YvoA from <i>Bacillus subtilis</i> . 2009 , 65, 410-4 | 4 |
| 559 | Preliminary joint neutron and X-ray crystallographic study of human carbonic anhydrase II. 2009 , 65, 495-8 | 12 |
| 558 | Isolation, crystallization and preliminary X-ray analysis of the transamidosome, a ribonucleoprotein involved in asparagine formation. 2009 , 65, 577-81 | 6 |
| 557 | Crystallization and preliminary X-ray diffraction studies of the tetramerization domain derived from the human potassium channel Kv1.3. 2009 , 65, 688-91 | 1 |
| 556 | Crystallization and preliminary X-ray crystallographic analysis of PhoK, an extracellular alkaline phosphatase from <i>Sphingomonas</i> sp. BSAR-1. 2009 , 65, 917-9 | 5 |
| 555 | Crystallization and preliminary X-ray analysis of mannosyl-3-phosphoglycerate synthase from <i>Thermus thermophilus</i> HB27. 2009 , 65, 1014-7 | 4 |
| 554 | Crystallization and preliminary crystallographic analysis of the global nitrogen regulator AmtR from <i>Corynebacterium glutamicum</i> . 2009 , 65, 1123-7 | 6 |
| 553 | The taming of small heat-shock proteins: crystallization of the alpha-crystallin domain from human Hsp27. 2009 , 65, 1277-81 | 11 |
| 552 | Development of a shutterless continuous rotation method using an X-ray CMOS detector for protein crystallography. <i>Journal of Applied Crystallography</i> , 2009 , 42, 1165-1175 | 3.8 17 |
| 551 | FpvA bound to non-cognate pyoverdines: molecular basis of siderophore recognition by an iron transporter. 2009 , 72, 1246-59 | 49 |
| 550 | High-resolution structure of the rotor ring of a proton-dependent ATP synthase. 2009 , 16, 1068-73 | 163 |
| 549 | X-ray crystal structures of <i>Phanerochaete chrysosporium</i> Laminarinase 16A in complex with products from lichenin and laminarin hydrolysis. 2009 , 276, 3858-69 | 25 |
| 548 | Structural and kinetic analysis of <i>Saccharomyces cerevisiae</i> thioredoxin Trx1: implications for the catalytic mechanism of GSSG reduced by the thioredoxin system. 2009 , 1794, 1218-23 | 18 |

| | | |
|-----|--|--------|
| 547 | Structure-based prediction of modifications in glutarylamidase to allow single-step enzymatic production of 7-aminocephalosporanic acid from cephalosporin C. 2002 , 11, 92-103 | 7 |
| 546 | Crystal Structure of A-amylose: A Revisit from Synchrotron Microdiffraction Analysis of Single Crystals. 2009 , 42, 1167-1174 | 103 |
| 545 | Crystal structure of a major outer membrane protein from <i>Thermus thermophilus</i> HB27. 2009 , 385, 1445-55 | 15 |
| 544 | The oligomeric assembly of the novel haem-degrading protein HbpS is essential for interaction with its cognate two-component sensor kinase. 2009 , 386, 1108-22 | 21 |
| 543 | Structure and function of the FeoB G-domain from <i>Methanococcus jannaschii</i> . 2009 , 392, 405-19 | 25 |
| 542 | Structural changes common to catalysis in the Tpx peroxiredoxin subfamily. 2009 , 393, 867-81 | 42 |
| 541 | The crystal structure of human pyrin b30.2 domain: implications for mutations associated with familial Mediterranean fever. 2009 , 394, 226-36 | 53 |
| 540 | Structural and thermodynamic characterization of pre- and postpolymerization states in the F4 fimbrial subunit FaeG. 2009 , 394, 957-67 | 14 |
| 539 | Occurrence of Uncommon Infinite Chains Consisting of Edge-Sharing Octahedra in a Porous Metal Organic Framework-Type Aluminum Pyromellitate Al ₄ (OH) ₈ [C ₁₀ O ₈ H ₂] (MIL-120): Synthesis, Structure, and Gas Sorption Properties. 2009 , 21, 5783-5791 | 90 |
| 538 | Structures of the spectrin-ankyrin interaction binding domains. 2009 , 113, 5385-93 | 72 |
| 537 | Structural basis for spectrin recognition by ankyrin. 2010 , 115, 4093-101 | 69 |
| 536 | Crystal structure and functional interpretation of the erythrocyte spectrin tetramerization domain complex. 2010 , 115, 4843-52 | 60 |
| 535 | Structure of D-AKAP2:PKA RI complex: insights into AKAP specificity and selectivity. 2010 , 18, 155-66 | 87 |
| 534 | Structural analysis of the RZZ complex reveals common ancestry with multisubunit vesicle tethering machinery. 2010 , 18, 616-26 | 63 |
| 533 | Structures of minimal catalytic fragments of topoisomerase V reveals conformational changes relevant for DNA binding. 2010 , 18, 829-38 | 8 |
| 532 | Crystal structure of a bacterial topoisomerase IB in complex with DNA reveals a secondary DNA binding site. 2010 , 18, 725-33 | 22 |
| 531 | Potential use of ultrasound to promote protein crystallization. <i>Journal of Applied Crystallography</i> , 2010 , 43, 1419-1425 | 3.8 35 |
| 530 | Feasibility of one-shot-per-crystal structure determination using Laue diffraction. 2010 , 66, 2-11 | 19 |

| | | |
|-----|--|-------|
| 529 | XDS. 2010 , 66, 125-32 | 10708 |
| 528 | Integration, scaling, space-group assignment and post-refinement. 2010 , 66, 133-44 | 1591 |
| 527 | Hemoglobin redux: combining neutron and X-ray diffraction with mass spectrometry to analyse the quaternary state of oxidized hemoglobins. 2010 , 66, 1249-56 | 1 |
| 526 | Structural study and thermodynamic characterization of inhibitor binding to lumazine synthase from <i>Bacillus anthracis</i> . 2010 , 66, 1001-11 | 16 |
| 525 | The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. 2010 , 66, 1174-81 | 7 |
| 524 | Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. 2010 , 66, 1205-10 | 2 |
| 523 | Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. 2010 , 66, 1245-53 | 8 |
| 522 | The structure of BVU2987 from <i>Bacteroides vulgatus</i> reveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. 2010 , 66, 1265-73 | 6 |
| 521 | Cloning, expression and crystallization of dihydrodipicolinate reductase from methicillin-resistant <i>Staphylococcus aureus</i> . 2010 , 66, 57-60 | 10 |
| 520 | The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. 2010 , 66, 1160-6 | 15 |
| 519 | Crystallization and X-ray diffraction studies of cellobiose phosphorylase from <i>Cellulomonas uda</i> . 2010 , 66, 346-51 | 18 |
| 518 | Expression, purification, crystallization and preliminary X-ray analysis of calmodulin in complex with the regulatory domain of the plasma-membrane Ca ²⁺ -ATPase ACA8. 2010 , 66, 361-3 | 6 |
| 517 | Crystallization and X-ray diffraction studies of inverting trehalose phosphorylase from <i>Thermoanaerobacter</i> sp. 2010 , 66, 442-7 | 5 |
| 516 | A conserved fold for fimbrial components revealed by the crystal structure of a putative fimbrial assembly protein (BT1062) from <i>Bacteroides thetaiotaomicron</i> at 2.2 Å resolution. 2010 , 66, 1281-6 | 8 |
| 515 | Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. 2010 , 66, 1167-73 | 3 |
| 514 | Preliminary neutron and X-ray crystallographic studies of equine cyanomethemoglobin. 2010 , 66, 474-7 | 4 |
| 513 | Crystallization of a 45 kDa peroxygenase/peroxidase from the mushroom <i>Agrocybe aegerita</i> and structure determination by SAD utilizing only the haem iron. 2010 , 66, 693-8 | 49 |
| 512 | The structure of PhaZ7 at atomic (1.2 Å) resolution reveals details of the active site and suggests a substrate-binding mode. 2010 , 66, 648-54 | 11 |

| | | |
|-----|---|--------|
| 511 | Purification, crystallization and preliminary X-ray analysis of human GIMAP2. 2010 , 66, 725-9 | 5 |
| 510 | Crystallization and preliminary X-ray analysis of L-azetidine-2-carboxylate hydrolase from <i>Pseudomonas</i> sp. strain A2C. 2010 , 66, 801-4 | 5 |
| 509 | Preliminary X-ray crystallographic analysis of the D-xylulose 5-phosphate phosphoketolase from <i>Lactococcus lactis</i> . 2010 , 66, 805-7 | 4 |
| 508 | Purification and crystallization of human Cu/Zn superoxide dismutase recombinantly produced in the protozoan <i>Leishmania tarentolae</i> . 2010 , 66, 871-7 | 19 |
| 507 | Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved β -core domain and an auxiliary C-terminal treble-clef zinc finger. 2010 , 66, 1335-46 | 7 |
| 506 | Expression, crystallization and preliminary X-ray diffraction analysis of the CMM2 region of the <i>Arabidopsis thaliana</i> Morpheus' molecule 1 protein. 2010 , 66, 916-8 | 2 |
| 505 | The structure of <i>Haemophilus influenzae</i> prephenate dehydrogenase suggests unique features of bifunctional TyrA enzymes. 2010 , 66, 1317-25 | 9 |
| 504 | Structure of a putative NTP pyrophosphohydrolase: YP_001813558.1 from <i>Exiguobacterium sibiricum</i> 255-15. 2010 , 66, 1237-44 | 2 |
| 503 | Expression, purification and crystallization of <i>Chaetomium thermophilum</i> Cu,Zn superoxide dismutase. 2010 , 66, 1089-92 | 2 |
| 502 | <i>Staphylococcus aureus</i> elongation factor G--structure and analysis of a target for fusidic acid. 2010 , 277, 3789-803 | 37 |
| 501 | An extracellular steric seeding mechanism for Eph-ephrin signaling platform assembly. 2010 , 17, 398-402 | 153 |
| 500 | Comparative structural analysis of human DEAD-box RNA helicases. <i>PLoS ONE</i> , 2010 , 5, e12791 | 3-7 72 |
| 499 | The crystal structure of dynein intermediate chain-light chain roadblock complex gives new insights into dynein assembly. 2010 , 285, 22566-75 | 36 |
| 498 | Crystal structure of the protealysin precursor: insights into propeptide function. 2010 , 285, 2003-13 | 24 |
| 497 | Neuroplastin-55 binds to and signals through the fibroblast growth factor receptor. 2010 , 24, 1139-50 | 42 |
| 496 | Insight into the induction mechanism of the GntR/HutC bacterial transcription regulator YvoA. 2010 , 38, 2485-97 | 35 |
| 495 | Structural insight into substrate differentiation of the sugar-metabolizing enzyme galactitol dehydrogenase from <i>Rhodobacter sphaeroides</i> D. 2010 , 285, 20006-14 | 16 |
| 494 | Structural analysis of <i>Thermus thermophilus</i> HB27 mannosyl-3-phosphoglycerate synthase provides evidence for a second catalytic metal ion and new insight into the retaining mechanism of glycosyltransferases. 2010 , 285, 17857-68 | 11 |

| | | |
|-----|---|-------|
| 493 | Structural basis of multivalent binding to wheat germ agglutinin. 2010 , 132, 8704-19 | 152 |
| 492 | The mechanism of prion inhibition by HET-S. 2010 , 38, 889-99 | 71 |
| 491 | Crystallographic analysis reveals a unique lidocaine binding site on human serum albumin. 2010 , 171, 353-60 | 75 |
| 490 | Crystal structures of an oligopeptide-binding protein from the biosynthetic pathway of the beta-lactamase inhibitor clavulanic acid. 2010 , 396, 332-44 | 9 |
| 489 | The three-dimensional structure of [NiFeSe] hydrogenase from <i>Desulfovibrio vulgaris</i> Hildenborough: a hydrogenase without a bridging ligand in the active site in its oxidised, "as-isolated" state. 2010 , 396, 893-907 | 103 |
| 488 | Structural evidence that peroxiredoxin catalytic power is based on transition-state stabilization. 2010 , 402, 194-209 | 136 |
| 487 | Crystallographic studies on the binding of selectively deuterated LLD- and LLL-substrate epimers by isopenicillin N synthase. 2010 , 398, 659-64 | 8 |
| 486 | Searching for novel crystal forms by in situ high-pressure crystallisation: the example of gabapentin heptahydrate. 2010 , 12, 2354 | 29 |
| 485 | Introduction to Macromolecular X-Ray Crystallography. 2010 , 51-89 | |
| 484 | Structure and function of the universal stress protein TeaD and its role in regulating the ectoine transporter TeaABC of <i>Halomonas elongata</i> DSM 2581(T). 2010 , 49, 2194-204 | 33 |
| 483 | Conformational flexibility in the allosteric regulation of human UDP-glucose 6-dehydrogenase. 2011 , 50, 9651-63 | 18 |
| 482 | Structure and mechanism of the trans-acting acyltransferase from the disorazole synthase. 2011 , 50, 6539-48 | 64 |
| 481 | Three-dimensional structure of mannosyl-3-phosphoglycerate phosphatase from <i>Thermus thermophilus</i> HB27: a new member of the haloalcanoic acid dehalogenase superfamily. 2011 , 50, 9551-67 | 8 |
| 480 | Structural and functional characterization of Rv2966c protein reveals an RsmD-like methyltransferase from <i>Mycobacterium tuberculosis</i> and the role of its N-terminal domain in target recognition. 2011 , 286, 19652-61 | 30 |
| 479 | The crystal structure of isopenicillin N synthase with E(L)-ε-amino adipoyl-(L)-cysteinyl-(D)-methionine reveals thioether coordination to iron. <i>Archives of Biochemistry and Biophysics</i> , 2011 , 516, 103-7 | 4.1 7 |
| 478 | Structural linkage between ligand discrimination and receptor activation by type I interferons. 2011 , 146, 621-32 | 253 |
| 477 | The molecular basis for the endocytosis of small R-SNAREs by the clathrin adaptor CALM. 2011 , 147, 1118-31 | 140 |
| 476 | The structure of the eukaryotic ribosome at 3.0 Å resolution. 2011 , 334, 1524-9 | 802 |

| | | |
|-----|--|-----|
| 475 | Structural and functional insights into a dodecameric molecular machine - the RuvBL1/RuvBL2 complex. 2011 , 176, 279-91 | 80 |
| 474 | Crystal structures exploring the origins of the broader specificity of escherichia coli heat-labile enterotoxin compared to cholera toxin. 2011 , 406, 387-402 | 23 |
| 473 | Symerythrin structures at atomic resolution and the origins of rubrerythrins and the ferritin-like superfamily. 2011 , 413, 177-94 | 16 |
| 472 | Two distinct ferritin-like molecules in <i>Pseudomonas aeruginosa</i> : the product of the <i>bfrA</i> gene is a bacterial ferritin (FtnA) and not a bacterioferritin (Bfr). 2011 , 50, 5236-48 | 37 |
| 471 | Structural study of the complex stereoselectivity of human butyrylcholinesterase for the neurotoxic V-agents. 2011 , 286, 16783-9 | 35 |
| 470 | Crystal structure of β tubulin complex protein GCP4 provides insight into microtubule nucleation. 2011 , 18, 915-9 | 70 |
| 469 | Sequence and structural convergence of broad and potent HIV antibodies that mimic CD4 binding. 2011 , 333, 1633-7 | 874 |
| 468 | Atypical DNA recognition mechanism used by the EspR virulence regulator of <i>Mycobacterium tuberculosis</i> . 2011 , 82, 251-64 | 20 |
| 467 | Atomic resolution structure of EhpR: phenazine resistance in <i>Enterobacter agglomerans</i> Eh1087 follows principles of bleomycin/mitomycin C resistance in other bacteria. 2011 , 11, 33 | 4 |
| 466 | An introduction to data reduction: space-group determination, scaling and intensity statistics. 2011 , 67, 282-92 | 946 |
| 465 | Multi-crystal anomalous diffraction for low-resolution macromolecular phasing. 2011 , 67, 45-59 | 61 |
| 464 | The design of macromolecular crystallography diffraction experiments. 2011 , 67, 261-70 | 35 |
| 463 | Simultaneous X-ray diffraction from multiple single crystals of macromolecules. 2011 , 67, 608-18 | 12 |
| 462 | Energy dependence of site-specific radiation damage in protein crystals. 2011 , 18, 338-45 | 14 |
| 461 | Structure of laccase from <i>Streptomyces coelicolor</i> after soaking with potassium hexacyanoferrate and at an improved resolution of 2.3 Å 2011 , 67, 27-32 | 9 |
| 460 | Crystallization and preliminary X-ray analysis of the human long myosin light-chain kinase 1-specific domain IgCAM3. 2011 , 67, 221-3 | 4 |
| 459 | Preliminary joint X-ray and neutron protein crystallographic studies of endoxylanase II from the fungus <i>Trichoderma longibrachiatum</i> . 2011 , 67, 283-6 | 5 |
| 458 | Crystallization and preliminary X-ray diffraction analysis of the wild-type haloalkane dehalogenase DhaA and its variant DhaA13 complexed with different ligands. 2011 , 67, 253-7 | 5 |

| | | |
|-----|---|----|
| 457 | Preliminary joint neutron time-of-flight and X-ray crystallographic study of human ABO(H) blood group A glycosyltransferase. 2011 , 67, 258-62 | 3 |
| 456 | Crystallization and preliminary X-ray analysis of mannosyl-3-phosphoglycerate phosphatase from <i>Thermus thermophilus</i> HB27. 2011 , 67, 390-6 | 1 |
| 455 | Time-of-flight neutron diffraction study of bovine Ecthyotrypsin at the Protein Crystallography Station. 2011 , 67, 587-90 | 1 |
| 454 | Superoxide reductase from <i>Nanoarchaeum equitans</i> : expression, purification, crystallization and preliminary X-ray crystallographic analysis. 2011 , 67, 591-5 | 2 |
| 453 | Structure of a Nudix hydrolase (MutT) in the Mg(2+)-bound state from <i>Bartonella henselae</i> , the bacterium responsible for cat scratch fever. 2011 , 67, 1078-83 | 4 |
| 452 | Crystallization and preliminary structural analysis of the <i>Listeria monocytogenes</i> Ca(2+)-ATPase LMCA1. 2011 , 67, 718-22 | 9 |
| 451 | Purification, crystallization and preliminary crystallographic studies of the TLDC domain of oxidation resistance protein 2 from zebrafish. 2011 , 67, 1253-6 | 4 |
| 450 | Crystallization and preliminary crystallographic analysis of an Ig-domain-encompassing fragment of the giant adhesion protein SiiE from <i>Salmonella enterica</i> . 2011 , 67, 1371-4 | 4 |
| 449 | Isopenicillin N synthase binds [L-ε-aminoadipoyl]-L-cysteinyl-D-thia-allo-isoleucine through both sulfur atoms. 2011 , 12, 1881-5 | 8 |
| 448 | Human DNA polymerase beta mutations allowing efficient abasic site bypass. 2011 , 286, 4011-20 | 9 |
| 447 | Structural basis for the oxidation of protein-bound sulfur by the sulfur cycle molybdohemo-enzyme sulfane dehydrogenase SoxCD. 2011 , 286, 8349-8360 | 31 |
| 446 | Structure-functional analyses of CRHSP-24 plasticity and dynamics in oxidative stress response. 2011 , 286, 9623-35 | 22 |
| 445 | Evidence for an allosteric mechanism of substrate release from membrane-transporter accessory binding proteins. 2011 , 108, E1285-92 | 21 |
| 444 | Structure of <i>Burkholderia cepacia</i> UDP-glucose dehydrogenase (UGD) BceC and role of Tyr10 in final hydrolysis of UGD thioester intermediate. 2011 , 193, 3978-87 | 21 |
| 443 | Structural and mechanistic insight into the ferredoxin-mediated two-electron reduction of bilins. 2011 , 439, 257-64 | 20 |
| 442 | The structure of the plakin domain of plectin reveals a non-canonical SH3 domain interacting with its fourth spectrin repeat. 2011 , 286, 12429-38 | 37 |
| 441 | Structure of human Na ⁺ /H ⁺ exchanger NHE1 regulatory region in complex with calmodulin and Ca ²⁺ . 2011 , 286, 40954-61 | 41 |
| 440 | Crystal structure of a Josephin-ubiquitin complex: evolutionary restraints on ataxin-3 deubiquitinating activity. 2011 , 286, 4555-65 | 34 |

| | | | |
|-----|---|-----|-----|
| 439 | Crystal structures of <i>T. b. rhodesiense</i> adenosine kinase complexed with inhibitor and activator: implications for catalysis and hyperactivation. 2011 , 5, e1164 | | 18 |
| 438 | DNA binding by the plant-specific NAC transcription factors in crystal and solution: a firm link to WRKY and GCM transcription factors. 2012 , 444, 395-404 | | 56 |
| 437 | Structural basis of transcriptional gene silencing mediated by Arabidopsis MOM1. <i>PLoS Genetics</i> , 2012 , 8, e1002484 | 6 | 17 |
| 436 | Functional consequence of covalent reaction of phosphoenolpyruvate with UDP-N-acetylglucosamine 1-carboxyvinyltransferase (MurA). 2012 , 287, 12657-67 | | 34 |
| 435 | Mouse Clr-g, a ligand for NK cell activation receptor NKR-P1F: crystal structure and biophysical properties. 2012 , 189, 4881-9 | | 18 |
| 434 | Structure/function relationships of adipose phospholipase A2 containing a cys-his-his catalytic triad. 2012 , 287, 35260-35274 | | 36 |
| 433 | Structural analysis reveals features of the spindle checkpoint kinase Bub1-kinetochore subunit Knl1 interaction. 2012 , 196, 451-67 | | 93 |
| 432 | <i>Pseudomonas aeruginosa</i> Cif defines a distinct class of epoxide hydrolases utilizing a His/Tyr ring-opening pair. 2012 , 19, 186-93 | | 17 |
| 431 | A molecular mechanism for direct sirtuin activation by resveratrol. <i>PLoS ONE</i> , 2012 , 7, e49761 | 3.7 | 188 |
| 430 | Structure of the <i>Archaeoglobus fulgidus</i> orphan ORF AF1382 determined by sulfur SAD from a moderately diffracting crystal. 2012 , 68, 1242-52 | | 5 |
| 429 | RNA single strands bind to a conserved surface of the major cold shock protein in crystals and solution. 2012 , 18, 65-76 | | 59 |
| 428 | X-ray structure of the <i>Yersinia pestis</i> heme transporter HmuUV. 2012 , 19, 1310-5 | | 74 |
| 427 | The crystal structure of samarosporin I at atomic resolution. 2012 , 18, 678-84 | | 9 |
| 426 | Structural and biochemical studies of a plant formamidopyrimidine-DNA glycosylase reveal why eukaryotic Fpg glycosylases do not excise 8-oxoguanine. 2012 , 11, 714-25 | | 35 |
| 425 | Cofactor binding triggers a molecular switch to allosterically activate human UDP-D-glucose 6-dehydrogenase. 2012 , 51, 9364-74 | | 12 |
| 424 | Implications of binding mode and active site flexibility for inhibitor potency against the salicylate synthase from <i>Mycobacterium tuberculosis</i> . 2012 , 51, 4868-79 | | 26 |
| 423 | A novel DNA binding mechanism for maf basic region-leucine zipper factors inferred from a MafA-DNA complex structure and binding specificities. 2012 , 51, 9706-17 | | 13 |
| 422 | Human UDP-D-xylose synthase and <i>Escherichia coli</i> ArnA conserve a conformational shunt that controls whether xylose or 4-keto-xylose is produced. 2012 , 51, 8844-55 | | 17 |

| | | | |
|-----|---|-----|-----|
| 421 | The structure of the BfrB-Bfd complex reveals protein-protein interactions enabling iron release from bacterioferritin. 2012 , 134, 13470-81 | | 49 |
| 420 | X-ray sources and high-throughput data collection methods. <i>Methods in Molecular Biology</i> , 2012 , 841, 93-141 | 1.4 | |
| 419 | Structurally similar but functionally diverse ZU5 domains in human erythrocyte ankyrin. 2012 , 417, 336-50 | | 14 |
| 418 | Structure and function of the transketolase from <i>Mycobacterium tuberculosis</i> and comparison with the human enzyme. 2012 , 2, 110026 | | 26 |
| 417 | A novel approach to the discovery of small-molecule ligands of CDK2. 2012 , 13, 2128-36 | | 54 |
| 416 | pH effects on binding between the anthrax protective antigen and the host cellular receptor CMG2. 2012 , 21, 1467-80 | | 9 |
| 415 | Serine is a natural ligand and allosteric activator of pyruvate kinase M2. 2012 , 491, 458-462 | | 394 |
| 414 | A new crystal form of MshB from <i>Mycobacterium tuberculosis</i> with glycerol and acetate in the active site suggests the catalytic mechanism. 2012 , 68, 1450-9 | | 11 |
| 413 | A monomeric TIM-barrel structure from <i>Pyrococcus furiosus</i> is optimized for extreme temperatures. 2012 , 68, 1479-87 | | 2 |
| 412 | High-resolution structure of AKR1a4 in the apo form and its interaction with ligands. 2012 , 68, 1271-4 | | 3 |
| 411 | Production and crystallization of a panel of structure-based mutants of the human myelin peripheral membrane protein P2. 2012 , 68, 1359-62 | | 10 |
| 410 | Structure of PA1221, a nonribosomal peptide synthetase containing adenylation and peptidyl carrier protein domains. 2012 , 51, 3252-63 | | 101 |
| 409 | Structure of a novel winged-helix like domain from human NFRKB protein. <i>PLoS ONE</i> , 2012 , 7, e43761 | 3.7 | 4 |
| 408 | Induced fit and the catalytic mechanism of isocitrate dehydrogenase. 2012 , 51, 7098-115 | | 23 |
| 407 | 1.8 Structure Validation and Analysis. 2012 , 116-135 | | 1 |
| 406 | Four complete turns of a curved 3 $\frac{1}{2}$ helix at atomic resolution: the crystal structure of the peptaibol trichovirin I-4A in a polar environment suggests a transition to $\frac{1}{2}$ helix for membrane function. 2012 , 68, 109-16 | | 15 |
| 405 | Expression, refolding and preliminary X-ray crystallographic analysis of equine MHC class I molecule complexed with an EIAV-Env CTL epitope. 2012 , 68, 20-3 | | 4 |
| 404 | Crystallization and preliminary X-ray crystallographic analysis of the membrane-binding haemprotein nitrophorin 7 from <i>Rhodnius prolixus</i> . 2012 , 68, 37-40 | | 5 |

| | | |
|-----|--|------|
| 403 | Purification, crystallization and preliminary crystallographic analysis of human dihydrodipicolinate synthase-like protein (DHDPSL). 2012 , 68, 59-62 | 6 |
| 402 | Purification, crystallization and preliminary X-ray diffraction analysis of the Hsp40 protein CPIP1 from <i>Nicotiana tabacum</i> . 2012 , 68, 236-9 | 1 |
| 401 | Formyl-coenzyme A (CoA):oxalate CoA-transferase from the acidophile <i>Acetobacter aceti</i> has a distinctive electrostatic surface and inherent acid stability. 2012 , 21, 686-96 | 14 |
| 400 | Functional and structural characterization of a thermostable acetyl esterase from <i>Thermotoga maritima</i> . 2012 , 80, 1545-59 | 36 |
| 399 | Linking crystallographic model and data quality. 2012 , 336, 1030-3 | 1329 |
| 398 | Biochemistry. Resolving some old problems in protein crystallography. 2012 , 336, 986-7 | 58 |
| 397 | Improving the accuracy of macromolecular structure refinement at 7 Å resolution. 2012 , 20, 957-66 | 36 |
| 396 | Biochemical and structural characterization of <i>Plasmodium falciparum</i> glutamate dehydrogenase 2. 2012 , 183, 52-62 | 19 |
| 395 | Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from <i>Corynebacterium glutamicum</i> . 2012 , 68, 391-403 | 24 |
| 394 | Low-resolution structure determination of Na(+)-translocating NADH:ubiquinone oxidoreductase from <i>Vibrio cholerae</i> by ab initio phasing and electron microscopy. 2012 , 68, 724-31 | 4 |
| 393 | Structure of a post-translationally processed heterodimeric double-headed Kunitz-type serine protease inhibitor from potato. 2012 , 68, 794-9 | 19 |
| 392 | Purification, crystallization and preliminary crystallographic studies of a Pacl homologue from <i>Listeria monocytogenes</i> . 2012 , 68, 424-7 | 4 |
| 391 | Detection and analysis of unusual features in the structural model and structure-factor data of a birch pollen allergen. 2012 , 68, 366-76 | 15 |
| 390 | Crystallization and preliminary characterization of chloromuconolactone dehalogenase from <i>Rhodococcus opacus</i> 1CP. 2012 , 68, 591-5 | 2 |
| 389 | Crystallization of an atypical short-chain dehydrogenase from <i>Vibrio vulnificus</i> lacking the conserved catalytic tetrad. 2012 , 68, 771-4 | 3 |
| 388 | Structural biology computing: Lessons for the biomedical research sciences. 2013 , 99, 809-16 | 6 |
| 387 | Crystal structure of the <i>Plasmodium falciparum</i> thioredoxin reductase-thioredoxin complex. 2013 , 425, 3446-60 | 23 |
| 386 | Structural and mechanistic studies of the orf12 gene product from the clavulanic acid biosynthesis pathway. 2013 , 69, 1567-79 | 6 |

| | | | |
|-----|---|-----|-----|
| 385 | The crystal structure of isopenicillin N synthase with a dipeptide substrate analogue. <i>Archives of Biochemistry and Biophysics</i> , 2013 , 530, 48-53 | 4.1 | 6 |
| 384 | 1.2 Å X-ray structure of the renal potassium channel Kv1.3 T1 domain. 2013 , 32, 533-42 | | 3 |
| 383 | Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. 2013 , 280, 5705-36 | | 73 |
| 382 | Crystal structure of the N-terminal domains of the surface cell antigen 4 of <i>Rickettsia</i> . 2013 , 22, 1425-31 | | 4 |
| 381 | Better models by discarding data?. 2013 , 69, 1215-22 | | 183 |
| 380 | Structure and assembly of an inner membrane platform for initiation of type IV pilus biogenesis. 2013 , 110, E4638-47 | | 46 |
| 379 | Structural investigation of a viral ortholog of human NEIL2/3 DNA glycosylases. 2013 , 12, 1062-71 | | 14 |
| 378 | A pipeline for comprehensive and automated processing of electron diffraction data in IPLT. 2013 , 182, 173-85 | | 8 |
| 377 | In human pseudouridine synthase 1 (hPus1), a C-terminal helical insert blocks tRNA from binding in the same orientation as in the Pus1 bacterial homologue TruA, consistent with their different target selectivities. 2013 , 425, 3875-87 | | 20 |
| 376 | The crystal structure of an isopenicillin N synthase complex with an ethereal substrate analogue reveals water in the oxygen binding site. 2013 , 587, 2705-9 | | 5 |
| 375 | Redox state-dependent changes in the crystal structure of [NiFeSe] hydrogenase from <i>Desulfovibrio vulgaris</i> Hildenborough. 2013 , 38, 8664-8682 | | 31 |
| 374 | X-ray Crystallography. 2013 , 217-255 | | 4 |
| 373 | The interaction of isopenicillin N synthase with homologated substrate analogues [L-(β -aminoadipoyl)-L-homocysteinyl-D-Xaa characterised by protein crystallography. 2013 , 14, 599-606 | | 5 |
| 372 | Structural and thermodynamic characterization of Nore1-SARAH: a small, helical module important in signal transduction networks. 2013 , 52, 1045-54 | | 30 |
| 371 | Structural basis of the binding of fatty acids to peptidoglycan recognition protein, PGRP-S through second binding site. <i>Archives of Biochemistry and Biophysics</i> , 2013 , 529, 1-10 | 4.1 | 5 |
| 370 | The N-terminal cytoplasmic region of NCBE displays features of an intrinsic disordered structure and represents a novel target for specific drug screening. 2013 , 4, 320 | | 2 |
| 369 | Structure and function of a novel LD-carboxypeptidase a involved in peptidoglycan recycling. 2013 , 195, 5555-66 | | 14 |
| 368 | Expression, purification, crystallization and preliminary X-ray diffraction analysis of a core fragment of FlgG, a bacterial flagellar rod protein. 2013 , 69, 547-50 | | 6 |

| | | |
|-----|---|------|
| 367 | Identification of one of the apurinic/apyrimidinic lyase active sites of topoisomerase V by structural and functional studies. 2013 , 41, 657-66 | 5 |
| 366 | Data Processing: How Good Are My Data Really?. 2013 , 59-68 | |
| 365 | How good are my data and what is the resolution?. 2013 , 69, 1204-14 | 2556 |
| 364 | Invariom refinement of a new monoclinic solvate of thiostrepton at 0.64 Å resolution. 2013 , 69, 1530-9 | 13 |
| 363 | Clustering procedures for the optimal selection of data sets from multiple crystals in macromolecular crystallography. 2013 , 69, 1617-32 | 167 |
| 362 | The N-terminal substrate-recognition domain of a LonC protease exhibits structural and functional similarity to cytosolic chaperones. 2013 , 69, 1789-97 | 4 |
| 361 | Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of AHP2, a signal transmitter protein from <i>Arabidopsis thaliana</i> . 2013 , 69, 158-61 | 6 |
| 360 | Expression, purification, crystallization and preliminary X-ray crystallographic studies of hepatitis B virus core fusion protein corresponding to octahedral particles. 2013 , 69, 165-9 | 2 |
| 359 | Differences in crystallization of two LinB variants from <i>Sphingobium japonicum</i> UT26. 2013 , 69, 284-7 | 4 |
| 358 | Structure of the <i>Yersinia pestis</i> tip protein LcrV refined to 1.65 Å resolution. 2013 , 69, 477-81 | 19 |
| 357 | Crystallographic analysis of new psychrophilic haloalkane dehalogenases: DpcA from <i>Psychrobacter cryohalolentis</i> K5 and DmxA from <i>Marinobacter</i> sp. ELB17. 2013 , 69, 683-8 | 7 |
| 356 | Protein expression, crystallization and preliminary X-ray crystallographic analysis of the isolated <i>Shigella flexneri</i> VapC toxin. 2013 , 69, 762-5 | 6 |
| 355 | The structure of substrate-free 1,5-anhydro-D-fructose reductase from <i>Sinorhizobium meliloti</i> 1021 reveals an open enzyme conformation. 2013 , 69, 844-9 | 7 |
| 354 | Expression, purification, crystallization and preliminary crystallographic analysis of hepatitis B virus core protein dimerized via a peptide linker containing an EGFP insertion. 2013 , 69, 942-5 | 4 |
| 353 | 12-Fold symmetry of the putative portal protein from the <i>Thermus thermophilus</i> bacteriophage G20C determined by X-ray analysis. 2013 , 69, 1239-41 | 4 |
| 352 | Recombinant production, crystallization and preliminary structural characterization of <i>Schistosoma japonicum</i> profilin. 2013 , 69, 1264-7 | |
| 351 | Cloning, expression, purification, crystallization and preliminary crystallographic analysis of the putative NlpC/P60 endopeptidase, TTHA0266, from <i>Thermus thermophilus</i> HB8. 2013 , 69, 1291-4 | 2 |
| 350 | Expression, purification and crystallization of the C-terminal LRR domain of <i>Streptococcus pyogenes</i> protein 0843. 2013 , 69, 559-61 | 1 |

| | | |
|-----|---|-------|
| 349 | A broad specificity nucleoside kinase from <i>Thermoplasma acidophilum</i> . 2013 , 81, 568-82 | 7 |
| 348 | Preliminary crystallographic analysis of the N-terminal PDZ-like domain of periaxin, an abundant peripheral nerve protein linked to human neuropathies. 2013 , 69, 804-8 | 2 |
| 347 | Bacterial microcompartment shells of diverse functional types possess pentameric vertex proteins. 2013 , 22, 660-5 | 57 |
| 346 | Structural basis for universal corrinoid recognition by the cobalamin transport protein haptocorrin. 2013 , 288, 25466-25476 | 34 |
| 345 | Structure and function of the DUF2233 domain in bacteria and in the human mannose 6-phosphate uncovering enzyme. 2013 , 288, 16789-16799 | 7 |
| 344 | The mechanism of the amidases: mutating the glutamate adjacent to the catalytic triad inactivates the enzyme due to substrate mispositioning. 2013 , 288, 28514-23 | 22 |
| 343 | The structure of human β ,6-sialyltransferase reveals the binding mode of complex glycans. 2013 , 69, 1826-38 | 60 |
| 342 | Crystallographic analysis of an RNA polymerase β subunit fragment complexed with -10 promoter element ssDNA: quadruplex formation as a possible tool for engineering crystal contacts in protein-ssDNA complexes. 2013 , 69, 950-5 | 2 |
| 341 | The Eps1p protein disulfide isomerase conserves classic thioredoxin superfamily amino acid motifs but not their functional geometries. <i>PLoS ONE</i> , 2014 , 9, e113431 | 3-7 5 |
| 340 | Structural and biochemical characterization of <i>Chlamydia trachomatis</i> hypothetical protein CT263 supports that menaquinone synthesis occurs through the futasolone pathway. 2014 , 289, 32214-32229 | 12 |
| 339 | The structure of Rv2372c identifies an RsmE-like methyltransferase from <i>Mycobacterium tuberculosis</i> . 2014 , 70, 821-32 | 8 |
| 338 | Atomic resolution structure of a lysine-specific endoprotease from <i>Lysobacter enzymogenes</i> suggests a hydroxyl group bound to the oxyanion hole. 2014 , 70, 1832-43 | 8 |
| 337 | Diamonds in the rough: a strong case for the inclusion of weak-intensity X-ray diffraction data. 2014 , 70, 1491-7 | 15 |
| 336 | Electrostatic transition state stabilization rather than reactant destabilization provides the chemical basis for efficient chorismate mutase catalysis. 2014 , 111, 17516-21 | 23 |
| 335 | A proton wire and water channel revealed in the crystal structure of isatin hydrolase. 2014 , 289, 21351-9 | 16 |
| 334 | Mapping the conformational space accessible to catechol-O-methyltransferase. 2014 , 70, 2163-74 | 24 |
| 333 | Use of massively multiple merged data for low-resolution S-SAD phasing and refinement of flavivirus NS1. 2014 , 70, 2719-29 | 30 |
| 332 | Structural differences explain diverse functions of <i>Plasmodium</i> actins. 2014 , 10, e1004091 | 50 |

| | | | | |
|-----|--|-----|-----|----|
| 331 | Signal to noise considerations for single crystal femtosecond time resolved crystallography of the Photoactive Yellow Protein. 2014 , 171, 439-55 | | | 14 |
| 330 | Unique subunit packing in mycobacterial nanoRNase leads to alternate substrate recognitions in DHH phosphodiesterases. 2014 , 42, 7894-910 | | | 21 |
| 329 | Solvent minimization induces preferential orientation and crystal clustering in serial micro-crystallography on micro-meshes, in situ plates and on a movable crystal conveyor belt. 2014 , 21, 1231-9 | | | 10 |
| 328 | Structure of a backtracked state reveals conformational changes similar to the state following nucleotide incorporation in human norovirus polymerase. 2014 , 70, 3099-109 | | | 9 |
| 327 | Gleaning unexpected fruits from hard-won synthetases: probing principles of permissivity in non-canonical amino acid-tRNA synthetases. 2014 , 15, 1810-9 | | | 25 |
| 326 | Structure of the monofunctional heme catalase DR1998 from <i>Deinococcus radiodurans</i> . 2014 , 281, 4138-50 | | | 10 |
| 325 | Determination of the phase diagram for the crystallization of L-asparaginase II by a turbidity technique - part II. -MPD and crystallography studies-. 2014 , 49, 393-399 | | | 3 |
| 324 | Crystal structure of a putative quorum sensing-regulated protein (PA3611) from the <i>Pseudomonas</i> -specific DUF4146 family. 2014 , 82, 1086-92 | | | 4 |
| 323 | Crystallization, room-temperature X-ray diffraction and preliminary analysis of Kaposi's sarcoma herpesvirus LANA bound to DNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1570-4 | 1.1 | | 4 |
| 322 | Hysteresis in human UDP-glucose dehydrogenase is due to a restrained hexameric structure that favors feedback inhibition. 2014 , 53, 8043-51 | | | 7 |
| 321 | Structure of a bacterial microcompartment shell protein bound to a cobalamin cofactor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1584-90 | 1.1 | | 17 |
| 320 | Structural genomics analysis of uncharacterized protein families overrepresented in human gut bacteria identifies a novel glycoside hydrolase. 2014 , 15, 112 | | | 10 |
| 319 | Protein crystal harvesting using the RodBot: a wireless mobile microrobot. <i>Journal of Applied Crystallography</i> , 2014 , 47, 692-700 | | 3.8 | 29 |
| 318 | Recombinant production, purification and crystallization of the <i>Toxoplasma gondii</i> coronin WD40 domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 517-21 | 1.1 | | 2 |
| 317 | Preliminary time-of-flight neutron diffraction studies of <i>Escherichia coli</i> ABC transport receptor phosphate-binding protein at the Protein Crystallography Station. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 819-22 | 1.1 | | 4 |
| 316 | Crystallization and preliminary X-ray crystallographic analysis of an artificial molten-globular-like triosephosphate isomerase protein of mixed phylogenetic origin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1521-5 | 1.1 | | 2 |
| 315 | The mechanism of pseudouridine synthases from a covalent complex with RNA, and alternate specificity for U2605 versus U2604 between close homologs. 2014 , 42, 2037-48 | | | 13 |
| 314 | Preliminary crystallographic analysis of the ankyrin-repeat domain of <i>Arabidopsis thaliana</i> AKT1: identification of the domain boundaries for protein crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 509-12 | 1.1 | | 2 |

| | | | |
|-----|--|-----|-----|
| 313 | Crystallization and preliminary X-ray diffraction analysis of proximal thread matrix protein 1 (PTMP1) from <i>Mytilus galloprovincialis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 769-72 | 1.1 | 5 |
| 312 | Purification, crystallization and phase determination of the DR1998 haem b catalase from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 659-62 | 1.1 | 1 |
| 311 | Protein expression, characterization, crystallization and preliminary X-ray crystallographic analysis of a Fic protein from <i>Clostridium difficile</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 827-31 | 1.1 | 4 |
| 310 | Engineering specificity in a dynamic protein complex with a single conserved mutation. 2014 , 281, 4892-905 | | 3 |
| 309 | Structural elucidation of the hormonal inhibition mechanism of the bile acid cholate on human carbonic anhydrase II. 2014 , 70, 1758-63 | | 15 |
| 308 | The structure of the cysteine protease and lectin-like domains of Cwp84, a surface layer-associated protein from <i>Clostridium difficile</i> . 2014 , 70, 1983-93 | | 13 |
| 307 | Structural insight into arginine methylation by the mouse protein arginine methyltransferase 7: a zinc finger freezes the mimic of the dimeric state into a single active site. 2014 , 70, 2401-12 | | 28 |
| 306 | New methods for indexing multi-lattice diffraction data. 2014 , 70, 2652-66 | | 51 |
| 305 | Structural analysis of arabinose-5-phosphate isomerase from <i>Bacteroides fragilis</i> and functional implications. 2014 , 70, 2640-51 | | |
| 304 | Effect of the L499M mutation of the ascomycetous <i>Botrytis aclada</i> laccase on redox potential and catalytic properties. 2014 , 70, 2913-23 | | 21 |
| 303 | 1.15 Å resolution structure of the proteasome-assembly chaperone Nas2 PDZ domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 418-23 | 1.1 | 7 |
| 302 | Purification, crystallization and preliminary X-ray data collection of the N-terminal domain of the 26S proteasome regulatory subunit p27 and its complex with the ATPase domain of Rpt5 from <i>Mus musculus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 611-5 | 1.1 | 1 |
| 301 | Expression, crystallization and preliminary X-ray crystallographic analysis of DNA-directed RNA polymerase subunit L from <i>Thermococcus onnurineus</i> NA1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 639-42 | 1.1 | |
| 300 | High-resolution crystal structures of two crystal forms of human cyclophilin D in complex with PEG 400 molecules. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 717-22 | 1.1 | 4 |
| 299 | Enhancing ubiquitin crystallization through surface-entropy reduction. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1434-42 | 1.1 | 4 |
| 298 | New mini-zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. 2014 , 15, 1 | | 225 |
| 297 | Structural Genomics and Drug Discovery. <i>Methods in Molecular Biology</i> , 2014 , | 1.4 | 3 |
| 296 | Weak data do not make a free lunch, only a cheap meal. 2014 , 70, 253-60 | | 17 |

| | | | |
|-----|--|-----|-----|
| 295 | Structure of crenactin, an archaeal actin homologue active at 90°C. 2014 , 70, 492-500 | | 20 |
| 294 | Structural basis of improved second-generation 3-nitro-tyrosine tRNA synthetases. 2014 , 53, 1916-24 | | 37 |
| 293 | Membrane and chaperone recognition by the major translocator protein PopB of the type III secretion system of <i>Pseudomonas aeruginosa</i> . 2014 , 289, 3591-601 | | 18 |
| 292 | <i>Chlamydia trachomatis</i> CT771 (nudH) is an asymmetric Ap4A hydrolase. 2014 , 53, 214-24 | | 1 |
| 291 | De novo protein crystal structure determination from X-ray free-electron laser data. 2014 , 505, 244-7 | | 226 |
| 290 | Structure of <i>Toxoplasma gondii</i> coronin, an actin-binding protein that relocalizes to the posterior pole of invasive parasites and contributes to invasion and egress. 2014 , 28, 4729-47 | | 38 |
| 289 | Crystal structures of <i>Entamoeba histolytica</i> lysyl-tRNA synthetase reveal conformational changes upon lysine binding and a specific helix bundle domain. 2014 , 588, 4478-86 | | 1 |
| 288 | Expression, purification and crystallization of MnSOD from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 669-72 | 1.1 | 4 |
| 287 | Crystallization and preliminary X-ray analysis of two variants of the <i>Escherichia coli</i> O157 ParE2-PaaA2 toxin-antitoxin complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1284-91 | 1.1 | 1 |
| 286 | Structure of <i>Rhodococcus equi</i> virulence-associated protein B (VapB) reveals an eight-stranded antiparallel β-barrel consisting of two Greek-key motifs. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 866-71 | 1.1 | 13 |
| 285 | Crystal structures of three representatives of a new Pfam family PF14869 (DUF4488) suggest they function in sugar binding/uptake. 2014 , 23, 1380-91 | | 1 |
| 284 | Structures of bacterial homologues of SWEET transporters in two distinct conformations. 2014 , 515, 448-452 | | 104 |
| 283 | Structural basis for organohalide respiration. 2014 , 346, 455-8 | | 170 |
| 282 | Crystal structure of <i>Escherichia coli</i> SsuE: defining a general catalytic cycle for FMN reductases of the flavodoxin-like superfamily. 2014 , 53, 3509-19 | | 21 |
| 281 | Signature motifs identify an <i>Acinetobacter</i> Cif virulence factor with epoxide hydrolase activity. 2014 , 289, 7460-9 | | 17 |
| 280 | (19)F nuclear magnetic resonance and crystallographic studies of 5-fluorotryptophan-labeled anthrax protective antigen and effects of the receptor on stability. 2014 , 53, 690-701 | | 9 |
| 279 | Replacing the axial ligand tyrosine 75 or its hydrogen bond partner histidine 83 minimally affects heme acquisition by the hemophore HasAp from <i>Pseudomonas aeruginosa</i> . 2014 , 53, 2112-25 | | 21 |
| 278 | Copper-transporting P-type ATPases use a unique ion-release pathway. 2014 , 21, 43-8 | | 77 |

| | | | |
|-----|---|-----|-----|
| 277 | Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. 2014 , 15, 75 | | 1 |
| 276 | Structure of the Elongator cofactor complex Kti11/Kti13 provides insight into the role of Kti13 in Elongator-dependent tRNA modification. 2015 , 282, 819-33 | | 19 |
| 275 | Structural Features of a Bacteroidetes-Affiliated Cellulase Linked with a Polysaccharide Utilization Locus. 2015 , 5, 11666 | | 18 |
| 274 | An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. 2015 , 5, 14017 | | 49 |
| 273 | The first crystal structure of the peptidase domain of the U32 peptidase family. 2015 , 71, 2505-12 | | 5 |
| 272 | A split-beam probe-pump-probe scheme for femtosecond time resolved protein X-ray crystallography. 2015 , 2, 014102 | | 13 |
| 271 | Crystallization behaviour of glyceraldehyde dehydrogenase from <i>Thermoplasma acidophilum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 1475-80 | 1.1 | |
| 270 | The catalytic mechanism and unique low pH optimum of <i>Caldicellulosiruptor bescii</i> family 3 pectate lyase. 2015 , 71, 1946-54 | | 8 |
| 269 | Cofactor-induced reversible folding of Flavodoxin-4 from <i>Lactobacillus acidophilus</i> . 2015 , 24, 1600-8 | | 2 |
| 268 | Empirical correction for resolution- and temperature-dependent errors caused by factors such as thermal diffuse scattering. <i>Journal of Applied Crystallography</i> , 2015 , 48, 1485-1497 | 3.8 | 16 |
| 267 | Hypothetical protein CT398 (CdsZ) interacts with σ^{54} (RpoN)-holoenzyme and the type III secretion export apparatus in <i>Chlamydia trachomatis</i> . 2015 , 24, 1617-32 | | 13 |
| 266 | Structural mapping of the ClpB ATPases of <i>Plasmodium falciparum</i> : Targeting protein folding and secretion for antimalarial drug design. 2015 , 24, 1508-20 | | 16 |
| 265 | Functional properties and structural characterization of rice δ^1 -pyrroline-5-carboxylate reductase. 2015 , 6, 565 | | 19 |
| 264 | The structure of <i>Medicago truncatula</i> δ^1 -pyrroline-5-carboxylate reductase provides new insights into regulation of proline biosynthesis in plants. 2015 , 6, 869 | | 26 |
| 263 | Structure of a bacterial RNA polymerase holoenzyme open promoter complex. <i>ELife</i> , 2015 , 4, | 8.9 | 130 |
| 262 | In meso in situ serial X-ray crystallography of soluble and membrane proteins. 2015 , 71, 1238-56 | | 88 |
| 261 | Evidence of Kinetic Cooperativity in Dimeric Ketopantoate Reductase from <i>Staphylococcus aureus</i> . 2015 , 54, 3360-3369 | | 10 |
| 260 | Structure-guided design and optimization of dipeptidyl inhibitors of norovirus 3CL protease. Structure-activity relationships and biochemical, X-ray crystallographic, cell-based, and in vivo studies. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 3144-55 | 8.3 | 40 |

| | | | |
|-----|---|-----|-----|
| 259 | Two independently folding units of Plasmodium profilin suggest evolution via gene fusion. 2015 , 72, 4193-203 | | 4 |
| 258 | Structural, functional, and genetic analyses of the actinobacterial transcription factor RbpA. 2015 , 112, 7171-6 | | 29 |
| 257 | Crystal Structure of the Human tRNA m(1)A58 Methyltransferase-tRNA(3)(Lys) Complex: Refolding of Substrate tRNA Allows Access to the Methylation Target. 2015 , 427, 3862-76 | | 30 |
| 256 | Chlamydia trachomatis protein CT009 is a structural and functional homolog to the key morphogenesis component RodZ and interacts with division septal plane localized MreB. 2015 , 95, 365-82 | | 18 |
| 255 | Concerted motions networking pores and distant ferroxidase centers enable bacterioferritin function and iron traffic. 2015 , 54, 1611-27 | | 13 |
| 254 | Man o' war mutation in UDP- β -xylose synthase favors the abortive catalytic cycle and uncovers a latent potential for hexamer formation. 2015 , 54, 807-19 | | 3 |
| 253 | Room-temperature serial crystallography at synchrotron X-ray sources using slowly flowing free-standing high-viscosity microstreams. 2015 , 71, 387-97 | | 149 |
| 252 | Protein structure. Structure and activity of tryptophan-rich TSPO proteins. 2015 , 347, 551-5 | | 124 |
| 251 | A guide to the crystallographic analysis of icosahedral viruses. <i>Crystallography Reviews</i> , 2015 , 21, 3-56 | 1.3 | 5 |
| 250 | Structures of aspartate aminotransferases from Trypanosoma brucei, Leishmania major and Giardia lamblia. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 566-71 | 1.1 | 3 |
| 249 | Crystallization and preliminary X-ray crystallographic analysis of the sclerostin-neutralizing Fab AbD09097. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 388-92 | 1.1 | 2 |
| 248 | Atomic Structure of GRK5 Reveals Distinct Structural Features Novel for G Protein-coupled Receptor Kinases. 2015 , 290, 20629-20647 | | 23 |
| 247 | Expression, purification, crystallization and preliminary X-ray crystallographic analysis of the histone-like HU protein from Spiroplasma melliferum KC3. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 24-7 | 1.1 | 21 |
| 246 | Recombinant production, crystallization and crystal structure determination of dihydroorotate dehydrogenase from Leishmania (Viannia) braziliensis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 547-52 | 1.1 | 4 |
| 245 | Assessing and maximizing data quality in macromolecular crystallography. 2015 , 34, 60-8 | | 142 |
| 244 | Structural Basis of Proline-Proline Peptide Bond Specificity of the Metalloprotease Zmp1 Implicated in Motility of Clostridium difficile. 2015 , 23, 1632-1642 | | 15 |
| 243 | Protein Crystallography and Drug Discovery. 2015 , 511-537 | | 3 |
| 242 | Four crystal structures of human LLT1, a ligand of human NKR-P1, in varied glycosylation and oligomerization states. 2015 , 71, 578-91 | | 16 |

| | | | |
|-----|---|-----|----|
| 241 | Expression, purification, crystallization and crystallographic study of the <i>Aspergillus terreus</i> aromatic prenyltransferase AtaPT. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 889-94 | 1.1 | 4 |
| 240 | ANS complex of St John's wort PR-10 protein with 28 copies in the asymmetric unit: a fiendish combination of pseudosymmetry with tetartohedral twinning. 2015 , 71, 829-43 | | 14 |
| 239 | Combination of X-ray crystallography, SAXS and DEER to obtain the structure of the FnIII-3,4 domains of integrin $\beta 4$. 2015 , 71, 969-85 | | 31 |
| 238 | Structural insights into the assembly of the histone deacetylase-associated Sin3L/Rpd3L corepressor complex. 2015 , 112, E3669-78 | | 23 |
| 237 | Expression, purification and crystallization of a family 55 β 1,3-glucanase from <i>Chaetomium thermophilum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 680-3 | 1.1 | 4 |
| 236 | Kinetic and structural characterization of an alternatively spliced variant of human mitochondrial 5'(3')-deoxyribonucleotidase. 2015 , 30, 63-8 | | |
| 235 | Structure-based discovery of NANOG variant with enhanced properties to promote self-renewal and reprogramming of pluripotent stem cells. 2015 , 112, 4666-71 | | 32 |
| 234 | Production, purification and crystallization of a trans-sialidase from <i>Trypanosoma vivax</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 577-85 | 1.1 | 2 |
| 233 | Elucidation of the crystal structure of <i>Coriolopsis caperata</i> laccase: restoration of the structure and activity of the native enzyme from the T2-depleted form by copper ions. 2015 , 71, 854-61 | | 18 |
| 232 | Structural and inhibitory effects of hinge loop mutagenesis in serpin-2 from the malaria vector <i>Anopheles gambiae</i> . 2015 , 290, 2946-56 | | 7 |
| 231 | Crystallization and preliminary X-ray analysis of four cysteine proteases from <i>Ficus carica</i> latex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 459-65 | 1.1 | 12 |
| 230 | Atomic-resolution structure of the β galactosyl binding <i>Lyophyllum decastes</i> lectin reveals a new protein family found in both fungi and plants. 2015 , 25, 492-501 | | 11 |
| 229 | Structure of a CutA1 divalent-cation tolerance protein from <i>Cryptosporidium parvum</i> , the protozoal parasite responsible for cryptosporidiosis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 522-30 | 1.1 | 0 |
| 228 | Structure of Serotype 1 Reovirus Attachment Protein σ in Complex with Junctional Adhesion Molecule A Reveals a Conserved Serotype-Independent Binding Epitope. 2015 , 89, 6136-40 | | 16 |
| 227 | Structure of Liver Receptor Homolog-1 (NR5A2) with PIP3 hormone bound in the ligand binding pocket. 2015 , 192, 342-348 | | 35 |
| 226 | Laminin α 4 domain structure resembles adhesion modules in ephrin receptor and other transmembrane glycoproteins. 2015 , 282, 2746-57 | | 9 |
| 225 | High-resolution crystal structure of cAMP-dependent protein kinase from <i>Cricetulus griseus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 1088-93 | 1.1 | 5 |
| 224 | Structures of Arg- and Gln-type bacterial cysteine dioxygenase homologs. 2015 , 24, 154-61 | | 20 |

| | | | |
|-----|--|-----|----|
| 223 | Crystal structure and solution characterization of the thioredoxin-2 from Plasmodium falciparum, a constituent of an essential parasitic protein export complex. 2015 , 456, 403-9 | | 15 |
| 222 | The structure and dynamics of secretory component and its interactions with polymeric immunoglobulins. <i>ELife</i> , 2016 , 5, | 8.9 | 50 |
| 221 | Functional and Structural Characterization of a Novel HLA-DRB1*04:01-Restricted β Enolase T Cell Epitope in Rheumatoid Arthritis. 2016 , 7, 494 | | 32 |
| 220 | pHluorin-assisted expression, purification, crystallization and X-ray diffraction data analysis of the C-terminal domain of the HsdR subunit of the Escherichia coli type I restriction-modification system EcoR124I. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 672-6 | 1.1 | 2 |
| 219 | An Unusual Member of the Papain Superfamily: Mapping the Catalytic Cleft of the Marasmius oreades agglutinin (MOA) with a Caspase Inhibitor. <i>PLoS ONE</i> , 2016 , 11, e0149407 | 3.7 | 5 |
| 218 | Comparison of human glutamate carboxypeptidases II and III reveals their divergent substrate specificities. 2016 , 283, 2528-45 | | 13 |
| 217 | 1.45 Å resolution structure of SRPN18 from the malaria vector Anopheles gambiae. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 853-862 | 1.1 | 2 |
| 216 | Quadruple space-group ambiguity owing to rotational and translational noncrystallographic symmetry in human liver fructose-1,6-bisphosphatase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 1212-1224 | 5.5 | 3 |
| 215 | Structural and functional characterization of a small chitin-active lytic polysaccharide monooxygenase domain of a multi-modular chitinase from Jonesia denitrificans. 2016 , 590, 34-42 | | 23 |
| 214 | Crystal structure of histone-like protein from Streptococcus mutans refined to 1.9 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 257-62 | 1.1 | 4 |
| 213 | Structural and Functional Analysis of a Lytic Polysaccharide Monooxygenase Important for Efficient Utilization of Chitin in Cellvibrio japonicus. 2016 , 291, 7300-12 | | 72 |
| 212 | Replacing Arginine 33 for Alanine in the Hemophore HasA from Pseudomonas aeruginosa Causes Closure of the H32 Loop in the Apo-Protein. 2016 , 55, 2622-31 | | 12 |
| 211 | Structural Studies of Medicago truncatula Histidinol Phosphate Phosphatase from Inositol Monophosphatase Superfamily Reveal Details of Penultimate Step of Histidine Biosynthesis in Plants. 2016 , 291, 9960-73 | | 13 |
| 210 | A Novel Fic (Filamentation Induced by cAMP) Protein from Clostridium difficile Reveals an Inhibitory Motif-independent Adenylation/AMPylation Mechanism. 2016 , 291, 13286-300 | | 10 |
| 209 | Structure-based design and synthesis of triazole-based macrocyclic inhibitors of norovirus protease: Structural, biochemical, spectroscopic, and antiviral studies. 2016 , 119, 300-18 | | 20 |
| 208 | Structural basis for integration of GluD receptors within synaptic organizer complexes. 2016 , 353, 295-9 | | 81 |
| 207 | The Structure of the Plakin Domain of Plectin Reveals an Extended Rod-like Shape. 2016 , 291, 18643-62 | | 19 |
| 206 | Structural and Functional Characterization of Plasmodium falciparum Nicotinic Acid Mononucleotide Adenylyltransferase. 2016 , 428, 4946-4961 | | 5 |

| | | | |
|-----|--|-----|-----|
| 205 | Crystal structure and MD simulation of mouse EndoV reveal wedge motif plasticity in this inosine-specific endonuclease. 2016 , 6, 24979 | | 8 |
| 204 | Crystal Structures of the Human Doublecortin C- and N-terminal Domains in Complex with Specific Antibodies. 2016 , 291, 16292-306 | | 10 |
| 203 | SAD phasing: History, current impact and future opportunities. <i>Archives of Biochemistry and Biophysics</i> , 2016 , 602, 80-94 | 4.1 | 14 |
| 202 | Insights into Lysine Deacetylation of Natively Folded Substrate Proteins by Sirtuins. 2016 , 291, 14677-94 | | 33 |
| 201 | Galectin-related protein: An integral member of the network of chicken galectins 1. From strong sequence conservation of the gene confined to vertebrates to biochemical characteristics of the chicken protein and its crystal structure. 2016 , 1860, 2285-97 | | 21 |
| 200 | Atomic resolution structure of a chimeric DNA-RNA Z-type duplex in complex with Ba(2+) ions: a case of complicated multi-domain twinning. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 211-23 | 5.5 | 7 |
| 199 | Crystal structure of Rv2258c from Mycobacterium tuberculosis H37Rv, an S-adenosyl-l-methionine-dependent methyltransferase. 2016 , 193, 172-180 | | 2 |
| 198 | First structure of archaeal branched-chain amino acid aminotransferase from Thermoproteus uzoniensis specific for L-amino acids and R-amines. 2016 , 20, 215-25 | | 23 |
| 197 | Visualizing the Mechanism of Epoxide Hydrolysis by the Bacterial Virulence Enzyme Cif. 2016 , 55, 788-97 | | 7 |
| 196 | Oxadiazole-Based Cell Permeable Macrocyclic Transition State Inhibitors of Norovirus 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 1899-913 | 8.3 | 17 |
| 195 | Dlx5 Homeodomain:DNA Complex: Structure, Binding and Effect of Mutations Related to Split Hand and Foot Malformation Syndrome. 2016 , 428, 1130-1141 | | 8 |
| 194 | Discovery of a new selective inhibitor of A Disintegrin And Metalloprotease 10 (ADAM-10) able to reduce the shedding of NKG2D ligands in Hodgkin's lymphoma cell models. 2016 , 111, 193-201 | | 32 |
| 193 | Crystal Structure and Activity Studies of the C11 Cysteine Peptidase from Parabacteroides merdae in the Human Gut Microbiome. 2016 , 291, 9482-91 | | 9 |
| 192 | Structural and Mechanistic Insights into the Regulation of the Fundamental Rho Regulator RhoGDI β by Lysine Acetylation. 2016 , 291, 5484-5499 | | 37 |
| 191 | Structure of an Actinobacterial-Type [NiFe]-Hydrogenase Reveals Insight into O ₂ -Tolerant H ₂ Oxidation. 2016 , 24, 285-92 | | 30 |
| 190 | Nucleic Acid Crystallography. <i>Methods in Molecular Biology</i> , 2016 , | 1.4 | 3 |
| 189 | Thienopyrimidinone Based Sirtuin-2 (SIRT2)-Selective Inhibitors Bind in the Ligand Induced Selectivity Pocket. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 1928-1945 | 8.3 | 39 |
| 188 | The cytotoxic PSM β reveals a cross- β amyloid-like fibril. 2017 , 355, 831-833 | | 154 |

| | | | |
|-----|---|-----|----|
| 187 | Status of the crystallography beamlines at synchrotron SOLEIL?. 2017 , 132, 1 | | 7 |
| 186 | A unique structural domain in ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) acts as a small subunit mimic. 2017 , 292, 6838-6850 | | 9 |
| 185 | Crystal structure and biological implications of a glycoside hydrolase family 55 β 1,3-glucanase from <i>Chaetomium thermophilum</i> . 2017 , 1865, 1030-1038 | | 6 |
| 184 | Design, synthesis, and evaluation of a novel series of macrocyclic inhibitors of norovirus 3CL protease. 2017 , 127, 41-61 | | 8 |
| 183 | Allostery and Hysteresis Are Coupled in Human UDP-Glucose Dehydrogenase. 2017 , 56, 202-211 | | 5 |
| 182 | Protein structure determination by electron diffraction using a single three-dimensional nanocrystal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 738-748 | 5.5 | 56 |
| 181 | Molecular architecture of the PBP2-MreC core bacterial cell wall synthesis complex. 2017 , 8, 776 | | 36 |
| 180 | Structural characterization of the Man5 glycoform of human IgG3 Fc. 2017 , 92, 28-37 | | 14 |
| 179 | Single-domain antibodies pinpoint potential targets within invasion plasmid antigen D of the needle tip complex for inhibition of type III secretion. 2017 , 292, 16677-16687 | | 10 |
| 178 | Experimental charge-density studies: data reduction and model quality: the more the better?. 2017 , 73, 531-543 | | 10 |
| 177 | Intermolecular base stacking mediates RNA-RNA interaction in a crystal structure of the RNA chaperone Hfq. 2017 , 7, 9903 | | 6 |
| 176 | Structural dissection of <i>Shewanella oneidensis</i> old yellow enzyme 4 bound to a Meisenheimer complex and (nitro)phenolic ligands. 2017 , 591, 3391-3401 | | 5 |
| 175 | Structures of <i>Medicago truncatula</i> L-Histidinol Dehydrogenase Show Rearrangements Required for NAD Binding and the Cofactor Positioned to Accept a Hydride. 2017 , 7, 10476 | | 7 |
| 174 | Autocatalytic association of proteins by covalent bond formation: a Bio Molecular Welding toolbox derived from a bacterial adhesin. 2017 , 7, 43564 | | 9 |
| 173 | The crystal structure of full-length Sizzled from yields insights into Wnt-antagonistic function of secreted Frizzled-related proteins. 2017 , 292, 16055-16069 | | 6 |
| 172 | Family of Papain-Like Fungal Chimerolectins with Distinct Ca-Dependent Activation Mechanism. 2017 , 56, 4689-4700 | | 2 |
| 171 | Structure-based exploration and exploitation of the S subsite of norovirus 3CL protease in the design of potent and permeable inhibitors. 2017 , 126, 502-516 | | 11 |
| 170 | <i>Desulfovibrio vulgaris</i> CbiK cobaltochelataase: evolution of a haem binding protein orchestrated by the incorporation of two histidine residues. 2017 , 19, 106-118 | | 5 |

| | | | |
|-----|--|-----|----|
| 169 | Structure and function of the mycobacterial transcription initiation complex with the essential regulator RbpA. <i>ELife</i> , 2017 , 6, | 8.9 | 67 |
| 168 | Using disruptive insertional mutagenesis to identify the in situ structure-function landscape of the <i>Shigella</i> translocator protein IpaB. 2018 , 27, 1392-1406 | | 9 |
| 167 | Structural insights into the RNA methyltransferase domain of METTL16. 2018 , 8, 5311 | | 57 |
| 166 | Structural insight into industrially relevant glucoamylases: flexible positions of starch-binding domains. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 463-470 | 5.5 | 7 |
| 165 | Structures of the Gasdermin D C-Terminal Domains Reveal Mechanisms of Autoinhibition. 2018 , 26, 778-784.e343 | | |
| 164 | Structure-guided design of potent and permeable inhibitors of MERS coronavirus 3CL protease that utilize a piperidine moiety as a novel design element. 2018 , 150, 334-346 | | 70 |
| 163 | Structural determinants of bacterial lytic polysaccharide monooxygenase functionality. 2018 , 293, 1397-1412 | | 58 |
| 162 | Structure-guided design, synthesis and evaluation of oxazolidinone-based inhibitors of norovirus 3CL protease. 2018 , 143, 881-890 | | 3 |
| 161 | Characterization at the Level of Individual Crystals: Single-Crystal MFI Type Zeolite Grains. 2018 , 24, 2384-2388 | | 13 |
| 160 | Crystal structure and catalytic characterization of the dehydrogenase/reductase SDR family member 4 (DHRS4) from <i>Caenorhabditis elegans</i> . 2018 , 285, 275-293 | | 7 |
| 159 | The entropic force generated by intrinsically disordered segments tunes protein function. 2018 , 563, 584-588 | | 66 |
| 158 | Operation and performance of the JUNGFR AU photon detector during first FEL and synchrotron experiments. 2018 , 13, C11006-C11006 | | 9 |
| 157 | Hysteresis and Allostery in Human UDP-Glucose Dehydrogenase Require a Flexible Protein Core. 2018 , 57, 6848-6859 | | 2 |
| 156 | Crystal structure of native β -D-rhamnosidase from <i>Aspergillus terreus</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 1078-1084 | 5.5 | 10 |
| 155 | Structural characterization of geranylgeranyl pyrophosphate synthase GACE1337 from the hyperthermophilic archaeon <i>Geoglobus acetivorans</i> . 2018 , 22, 877-888 | | 3 |
| 154 | Fast and accurate data collection for macromolecular crystallography using the JUNGFR AU detector. 2018 , 15, 799-804 | | 30 |
| 153 | Structural basis of latent TGF- β presentation and activation by GARP on human regulatory T cells. 2018 , 362, 952-956 | | 68 |
| 152 | Bfd, a New Class of [2Fe-2S] Protein That Functions in Bacterial Iron Homeostasis, Requires a Structural Anion Binding Site. 2018 , 57, 5533-5543 | | 3 |

| | | | |
|-----|---|-----|----|
| 151 | On avoiding negative electron density in Gram-Charlier refinements of anharmonic motion: the example of glutathione. <i>Zeitschrift Fur Kristallographie - Crystalline Materials</i> , 2018 , 233, 695-706 | 1 | 3 |
| 150 | Diaminopelargonic acid transaminase from <i>Psychrobacter cryohalolentis</i> is active towards (S)-(-)-1-phenylethylamine, aldehydes and β -diketones. 2018 , 102, 9621-9633 | | 4 |
| 149 | Extreme amyloid polymorphism in <i>Staphylococcus aureus</i> virulent PSM peptides. 2018 , 9, 3512 | | 47 |
| 148 | Memory T cells specific to citrullinated Enolase are enriched in the rheumatic joint. 2018 , 92, 47-56 | | 25 |
| 147 | Guarding the gateway to histidine biosynthesis in plants: ATP-phosphoribosyltransferase in relaxed and tense states. 2018 , 475, 2681-2697 | | 1 |
| 146 | Chloroplastic Serine Hydroxymethyltransferase From : A Structural Characterization. 2018 , 9, 584 | | 8 |
| 145 | Against Method: Table 1-Cui Bono?. 2018 , 26, 919-923 | | 6 |
| 144 | Structure-function study of two new middle-redox potential laccases from basidiomycetes <i>Antrodia faginea</i> and <i>Steccherinum murashkinskyi</i> . 2018 , 118, 406-418 | | 15 |
| 143 | Volumetric Segmentation Neural Networks Improves Neutron Crystallography Data Analysis. 2019 , 2019, 549-555 | | 2 |
| 142 | Crystal Growth in Gels from the Mechanisms of Crystal Growth to Control of Polymorphism: New Trends on Theoretical and Experimental Aspects. <i>Crystals</i> , 2019 , 9, 443 | 2,3 | 8 |
| 141 | Conservation of Atypical Allostery in UDP-Glucose Dehydrogenase. 2019 , 4, 16318-16329 | | 3 |
| 140 | Characterization of the pleiotropic LysR-type transcription regulator LeuO of <i>Escherichia coli</i> . 2019 , 47, 7363-7379 | | 5 |
| 139 | Crystal structure of a xylulose 5-phosphate phosphoketolase. Insights into the substrate specificity for xylulose 5-phosphate. 2019 , 207, 85-102 | | 2 |
| 138 | Molecular Fingerprints for a Novel Enzyme Family in with Glucosamine Kinase Activity. 2019 , 10, | | 2 |
| 137 | Structural basis for eIF2B inhibition in integrated stress response. 2019 , 364, 495-499 | | 44 |
| 136 | Functional characterization of PLP fold type IV transaminase with a mixed type of activity from <i>Haliangium ochraceum</i> . 2019 , 1867, 575-585 | | 9 |
| 135 | Putative structural rearrangements associated with the interaction of macrocyclic inhibitors with norovirus 3CL protease. 2019 , 87, 579-587 | | 1 |
| 134 | Thermostable Branched-Chain Amino Acid Transaminases From the Archaea and : Biochemical and Structural Characterization. 2019 , 7, 7 | | 12 |

| | | | |
|-----|---|-----|-----|
| 133 | Chemical Crystallography: when are [bad data] [good data]. <i>Crystallography Reviews</i> , 2019 , 25, 3-53 | 1.3 | 6 |
| 132 | Crystal Structure of VapBC-1 from Nontypeable Haemophilus influenzae and the Effect of PIN Domain Mutations on Survival during Infection. 2019 , 201, | | 4 |
| 131 | Crystal structures of the naturally fused CS and cytochrome b reductase (bR) domains of Ncb5or reveal an expanded CS fold, extensive CS-bR interactions and productive binding of the NAD(P) nicotinamide ring. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 628-638 | 5.5 | 2 |
| 130 | Structure and mechanism of piperideine-6-carboxylate dehydrogenase from Streptomyces clavuligerus. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 1107-1118 | 5.5 | 1 |
| 129 | Structure and reactivity of a siderophore-interacting protein from the marine bacterium reveals unanticipated functional versatility. 2019 , 294, 157-167 | | 9 |
| 128 | Analysis of a new flavodiiron core structural arrangement in Flv1-FlR protein from Synechocystis sp. PCC6803. 2019 , 205, 91-102 | | 8 |
| 127 | Structural and ligand binding analyses of the periplasmic sensor domain of RsbU in Chlamydia trachomatis support a role in TCA cycle regulation. 2020 , 113, 68-88 | | 4 |
| 126 | Crystal and solution structures of human oncoprotein Musashi-2 N-terminal RNA recognition motif 1. 2020 , 88, 573-583 | | 5 |
| 125 | Structural biology techniques: X-ray crystallography, cryo-electron microscopy, and small-angle X-ray scattering. 2020 , 375-416 | | 1 |
| 124 | The Resolution in X-ray Crystallography and Single-Particle Cryogenic Electron Microscopy. <i>Crystals</i> , 2020 , 10, 580 | 2.3 | 2 |
| 123 | Structure of the Diphtheria Toxin at Acidic pH: Implications for the Conformational Switching of the Translocation Domain. 2020 , 12, | | 3 |
| 122 | Characterizing human H1,6-fucosyltransferase (FUT8) substrate specificity and structural similarities with related fucosyltransferases. 2020 , 295, 17027-17045 | | 11 |
| 121 | Experimental Charge Densities from Multipole Modeling: Moving into the Twenty-First Century. 2020 , 145-182 | | 2 |
| 120 | The Human LL-37(17-29) antimicrobial peptide reveals a functional supramolecular structure. 2020 , 11, 3894 | | 27 |
| 119 | 3C-like protease inhibitors block coronavirus replication in vitro and improve survival in MERS-CoV-infected mice. 2020 , 12, | | 113 |
| 118 | Crystal structures of human PAICS reveal substrate and product binding of an emerging cancer target. 2020 , 295, 11656-11668 | | 6 |
| 117 | Structure-Guided Optimization of Dipeptidyl Inhibitors of Norovirus 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 11945-11963 | 8.3 | 3 |
| 116 | Exploring the gas access routes in a [NiFeSe] hydrogenase using crystals pressurized with krypton and oxygen. 2020 , 25, 863-874 | | 2 |

| | | |
|-----|---|-----|
| 115 | Crystal structure: How to use data quality Indicators to select a high resolution cutoff. 2020 , 783, 012005 | |
| 114 | The Structures of SctK and SctD from <i>Pseudomonas aeruginosa</i> Reveal the Interface of the Type III Secretion System Basal Body and Sorting Platform. 2020 , 432, 166693 | 5 |
| 113 | Methionine-Rich Loop of Multicopper Oxidase McoA Follows Open-to-Close Transitions with a Role in Enzyme Catalysis. 2020 , 10, 7162-7176 | 9 |
| 112 | Pterocarpan synthase (PTS) structures suggest a common quinone methide-stabilizing function in dirigent proteins and proteins with dirigent-like domains. 2020 , 295, 11584-11601 | 10 |
| 111 | Cryo-electron microscopic and X-ray crystallographic analysis of the light-driven proton pump proteorhodopsin reveals a pentameric assembly. 2020 , 4, 100024 | 3 |
| 110 | A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. 2020 , 13, | 7 |
| 109 | Computational backbone design enables soluble engineering of transferrin receptor apical domain. 2020 , 88, 1569-1577 | 1 |
| 108 | Design, synthesis, and bioevaluation of pyrazolo[1,5-a]pyrimidine derivatives as tubulin polymerization inhibitors targeting the colchicine binding site with potent anticancer activities. 2020 , 202, 112519 | 20 |
| 107 | Rutinosidase from <i>Aspergillus niger</i> : crystal structure and insight into the enzymatic activity. 2020 , 287, 3315-3327 | 8 |
| 106 | Assessment of Crystallographic Structure Quality and Protein-Ligand Complex Structure Validation. 2020 , 253-275 | 2 |
| 105 | Crystal structure of SARS-CoV-2 nucleocapsid protein RNA binding domain reveals potential unique drug targeting sites. 2020 , 10, 1228-1238 | 354 |
| 104 | Structural and functional analysis of the inhibition of equine glutathione transferase A3-3 by organotin endocrine disrupting pollutants. 2021 , 268, 115960 | 1 |
| 103 | High-resolution X-ray structure of three microtubule-stabilizing agents in complex with tubulin provide a rationale for drug design. 2021 , 534, 330-336 | 3 |
| 102 | Structural insight into the novel iron-coordination and domain interactions of transferrin-1 from a model insect, <i>Manduca sexta</i> . 2021 , 30, 408-422 | 4 |
| 101 | Comparison of human poly-N-acetyl-lactosamine synthase structure with GT-A fold glycosyltransferases supports a modular assembly of catalytic subsites. 2021 , 296, 100110 | 6 |
| 100 | The SARS-CoV-2 Conserved Macrodomain Is a Mono-ADP-Ribosylhydrolase. 2021 , 95, | 45 |
| 99 | Nucleoside selectivity of <i>Aspergillus fumigatus</i> nucleoside-diphosphate kinase. 2021 , 288, 2398-2417 | 2 |
| 98 | Structural Analysis of Strigolactone-Related Gene Products. <i>Methods in Molecular Biology</i> , 2021 , 2309, 245-257 | 1.4 |

| | | | |
|----|---|-----|----|
| 97 | Active site architecture reveals coordination sphere flexibility and specificity determinants in a group of closely related molybdoenzymes. 2021 , 296, 100672 | | 1 |
| 96 | Post-infection treatment with a protease inhibitor increases survival of mice with a fatal SARS-CoV-2 infection. | | 3 |
| 95 | Structural and functional study of Legionella pneumophila effector RavA. 2021 , 30, 940-955 | | 2 |
| 94 | Structural insights into the inhibition of glycine reuptake. 2021 , 591, 677-681 | | 18 |
| 93 | Fungal GH25 muramidases: New family members with applications in animal nutrition and a crystal structure at 0.78Å resolution. <i>PLoS ONE</i> , 2021 , 16, e0248190 | 3.7 | 0 |
| 92 | Structure and Dynamics of Mepri ⁿ In Complex with a Hydroxamate-Based Inhibitor. <i>International Journal of Molecular Sciences</i> , 2021 , 22, | 6.3 | 3 |
| 91 | Exchange catalysis by tapasin exploits conserved and allele-specific features of MHC-I molecules. 2021 , 12, 4236 | | 3 |
| 90 | Structure-Guided Design of Conformationally Constrained Cyclohexane Inhibitors of Severe Acute Respiratory Syndrome Coronavirus-2 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 10047-10058 | 8.3 | 8 |
| 89 | Structures of full-length VanR from Streptomyces coelicolor in both the inactive and activated states. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1027-1039 | 5.5 | 0 |
| 88 | Crystal Structure of a Cu,Zn Superoxide Dismutase From the Thermophilic Fungus Chaetomium thermophilum. 2021 , 28, 1043-1053 | | 0 |
| 87 | The crystal structure of MreC provides insights into polymer formation. 2021 , | | |
| 86 | Structural Insight Into the SARS-CoV-2 Nucleocapsid Protein C-Terminal Domain Reveals a Novel Recognition Mechanism for Viral Transcriptional Regulatory Sequences. 2020 , 8, 624765 | | 24 |
| 85 | Crystal structures of the EVE-HNH endonuclease VcaM4I in the presence and absence of DNA. 2021 , 49, 1708-1723 | | 1 |
| 84 | The amphibian antimicrobial peptide uperin 3.5 is a cross- β -chameleon functional amyloid. 2021 , 118, | | 11 |
| 83 | Crystallographic Data and Model Quality. <i>Methods in Molecular Biology</i> , 2016 , 1320, 147-73 | 1.4 | 9 |
| 82 | Serial Synchrotron X-Ray Crystallography (SSX). <i>Methods in Molecular Biology</i> , 2017 , 1607, 239-272 | 1.4 | 25 |
| 81 | Structure Refinement at Atomic Resolution. <i>Methods in Molecular Biology</i> , 2017 , 1607, 549-563 | 1.4 | 2 |
| 80 | Collection of X-Ray Diffraction Data from Macromolecular Crystals. <i>Methods in Molecular Biology</i> , 2017 , 1607, 165-184 | 1.4 | 14 |

| | | |
|----|--|-------|
| 79 | Catalytically Enhanced Endocellulase Cel5A from <i>Acidothermus cellulolyticus</i> . 2005 , 129-148 | 5 |
| 78 | High Resolution Macromolecular Crystallography. 2013 , 259-275 | 4 |
| 77 | Scientific Method in Practice. 2002 , | 33 |
| 76 | Structure of the electron transfer complex between ferredoxin and ferredoxin-NADP+ reductase. | 1 |
| 75 | A novel redox-active switch in Fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. | 0 |
| 74 | The Human LL-37(17-29) Antimicrobial Peptide Reveals a Functional Supramolecular Nanostructure. | 2 |
| 73 | The SARS-CoV-2 conserved macrodomain is a mono-ADP-ribosylhydrolase. 2020 , | 9 |
| 72 | Model Selection for Biological Crystallography. | 1 |
| 71 | A challenging interpretation of a hexagonally layered protein structure. 2014 , 70, 203-8 | 4 |
| 70 | Crystallization and preliminary X-ray crystallographic analysis of the amylomaltase from <i>Corynebacterium glutamicum</i> . 2013 , 69, 1004-6 | 7 |
| 69 | Crystallization and preliminary structural characterization of the two actin isoforms of the malaria parasite. 2013 , 69, 1171-6 | 5 |
| 68 | Structure of a 13-fold superhelix (almost) determined from first principles. 2015 , 2, 177-87 | 2 |
| 67 | Native SAD is maturing. 2015 , 2, 431-40 | 41 |
| 66 | Electron crystallography with the EIGER detector. 2018 , 5, 190-199 | 28 |
| 65 | The predictive power of data-processing statistics. 2020 , 7, 342-354 | 6 |
| 64 | Cloning, expression, purification and preliminary X-ray crystallographic analysis of mouse protein arginine methyltransferase 7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 80-6 | 1.1 7 |
| 63 | Cleavage of nicotinamide adenine dinucleotide by the ribosome-inactivating protein from <i>Momordica charantia</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 1152-5 | 1.1 1 |
| 62 | 1.65 Å resolution structure of the AraC-family transcriptional activator ToxT from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 726-31 | 1.1 8 |

| | | | |
|----|--|-----|----|
| 61 | Structural studies of a glycoside hydrolase family 3 β -glucosidase from the model fungus <i>Neurospora crassa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 787-796 ^{1,1} | | 1 |
| 60 | Structure of Rubisco from <i>Arabidopsis thaliana</i> in complex with 2-carboxyarabinitol-1,5-bisphosphate. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 1-9 | 5.5 | 9 |
| 59 | Domain swap in the C-terminal ubiquitin-like domain of human doublecortin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 450-462 | 5.5 | 6 |
| 58 | The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013 , 2, 154 | 3.6 | 2 |
| 57 | The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013 , 2, 154 | 3.6 | 3 |
| 56 | The Anti-sigma Factor RsiV Is a Bacterial Receptor for Lysozyme: Co-crystal Structure Determination and Demonstration That Binding of Lysozyme to RsiV Is Required for σ^70 Activation. <i>PLoS Genetics</i> , 2016 , 12, e1006287 | 6 | 26 |
| 55 | A glutathione transferase from <i>Agrobacterium tumefaciens</i> reveals a novel class of bacterial GST superfamily. <i>PLoS ONE</i> , 2012 , 7, e34263 | 3.7 | 21 |
| 54 | Cyanuric acid hydrolase from <i>Azorhizobium caulinodans</i> ORS 571: crystal structure and insights into a new class of Ser-Lys dyad proteins. <i>PLoS ONE</i> , 2014 , 9, e99349 | 3.7 | 8 |
| 53 | Structure-guided engineering of molinate hydrolase for the degradation of thiocarbamate pesticides. <i>PLoS ONE</i> , 2015 , 10, e0123430 | 3.7 | 2 |
| 52 | Structural Basis of the Heterodimer Formation between Cell Shape-Determining Proteins Csd1 and Csd2 from <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2016 , 11, e0164243 | 3.7 | 11 |
| 51 | Structural and Biochemical Studies Reveal a Putative FtsZ Recognition Site on the Z-ring Stabilizer ZapD. <i>Molecules and Cells</i> , 2016 , 39, 814-820 | 3.5 | 4 |
| 50 | Direct way to anomalous scatterers. <i>Zeitschrift Fur Kristallographie - Crystalline Materials</i> , 2002 , 217, 694-702 | | 1 |
| 49 | CarD uses a minor groove wedge mechanism to stabilize the RNA polymerase open promoter complex. <i>ELife</i> , 2015 , 4, | 8.9 | 43 |
| 48 | Structural insights into the light-driven auto-assembly process of the water-oxidizing MnCaO-cluster in photosystem II. <i>ELife</i> , 2017 , 6, | 8.9 | 46 |
| 47 | The Sec1/Munc18 protein Vps45 holds the Qa-SNARE Tlg2 in an open conformation. <i>ELife</i> , 2020 , 9, | 8.9 | 3 |
| 46 | The superior salinity tolerance of wheat cultivar Shanrong No. 3 cannot be attributed to elevated Ta-sro1 poly(ADP-ribose) polymerase activity. | | |
| 45 | Loops around the Heme Pocket Have a Critical Role in the Function and Stability of DyP from. <i>International Journal of Molecular Sciences</i> , 2021 , 22, | 6.3 | 1 |
| 44 | Machine learning applications in macromolecular X-ray crystallography. <i>Crystallography Reviews</i> , 1-48 | 1.3 | 1 |

- 43 Introduction to Macromolecular X-Ray Crystallography. **2010**, 312-343
- 42 Protein X-Ray Crystallography in Drug Discovery. 1
- 41 Data collection for crystallographic structure determination. *Methods in Molecular Biology*, **2014**, 1140, 211-37 1.4 1
- 40 Structure determination, refinement, and validation. *Methods in Molecular Biology*, **2014**, 1140, 239-49 1.4
- 39 Structural insights into the light-driven auto-assembly process of the water-oxidizing Mn₄CaO₅-cluster in photosystem II.
- 38 Cryptic genetic variation defines the adaptive evolutionary potential of enzymes.
- 37 Extreme Amyloid Polymorphism in Staphylococcus aureus Virulent PSM Peptides.
- 36 Integrin $\beta 4$ recognition of a linear motif of bullous pemphigoid antigen BP230 controls its recruitment to hemidesmosomes. 1
- 35 Molecular fingerprints for a novel glucosamine kinase family in Actinobacteria.
- 34 Single-crystal time-of-flight neutron Laue methods: application to manganese catalase from Thermus thermophilus HB27. *Journal of Applied Crystallography*, **2019**, 52, 972-983 3.8 2
- 33 Structure of a dominant negative mutant reveals a stalled intermediate state of anthrax protective antigen pore maturation. 0
- 32 The Amphibian Antimicrobial Peptide Uperin 3.5 is a Cross-Cross-Chameleon Functional Amyloid. 1
- 31 A synthetic synaptic organizer protein restores glutamatergic neuronal circuits.
- 30 The Sec1/Munc18 protein Vps45 holds the Qa-SNARE Tlg2 in an open conformation.
- 29 The Structures of SctK and SctD from Pseudomonas aeruginosa Reveal the Interface of the Type III Secretion System Basal Body and Sorting Platform.
- 28 The Crystal Structure of N ϵ -tosyl-lysyl Chloromethylketone-Bound Oligopeptidase B from Serratia Proteamaculans Revealed a New Type of Inhibitor Binding. *Crystals*, **2021**, 11, 1438 2.3 3
- 27 Structure and conservation of amyloid spines from the Candida albicans Als5 adhesin including similarity to human LARKS. 0
- 26 Multitasking in the gut: the X-ray structure of the multidomain BbgIII from Bifidobacterium bifidum offers possible explanations for its alternative functions. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 1564-1578 5.5

| | | | |
|----|--|-----|---|
| 25 | Two states of a light-sensitive membrane protein captured at room temperature using thin-film sample mounts.. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022 , 78, 52-58 | 5.5 | 0 |
| 24 | Improving the kinetic parameters of nicotine oxidizing enzymes by homologous structure comparison and rational design.. <i>Archives of Biochemistry and Biophysics</i> , 2022 , 109122 | 4.1 | 2 |
| 23 | Deciphering the structure of 5--pyruvyl-shikimate-3-phosphate synthase: An essential step toward the discovery of novel inhibitors to supersede glyphosate.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 1494-1505 | 6.8 | 0 |
| 22 | Structure-Guided Design of Potent Inhibitors of SARS-CoV-2 3CL Protease: Structural, Biochemical, and Cell-Based Studies. <i>Journal of Medicinal Chemistry</i> , 2021 , | 8.3 | 2 |
| 21 | Data_Sheet_1.PDF. 2019 , | | |
| 20 | Image_1.PDF. 2018 , | | |
| 19 | Structure-Guided Design of Potent Spirocyclic Inhibitors of Severe Acute Respiratory Syndrome Coronavirus-2 3C-like Protease. <i>Journal of Medicinal Chemistry</i> , | 8.3 | 2 |
| 18 | Repair of Iron Center Proteins in a Different Class of Hemerythrin-Like Proteins. <i>Molecules</i> , 2022 , 27, 4051 | 4.8 | 0 |
| 17 | Structure of a HIV-1 IN-Allosteric Inhibitor Complex at 2.93 Å Resolution: Routes to Inhibitor Optimization. | | |
| 16 | Structure and Conservation of Amyloid Spines From the <i>Candida albicans</i> Als5 Adhesin. <i>Frontiers in Molecular Biosciences</i> , 9, | 5.6 | 1 |
| 15 | Room-temperature serial synchrotron crystallography of <i>Drosophila</i> cryptochrome. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022 , 78, | 5.5 | 0 |
| 14 | Unveiling molecular details behind improved activity at neutral to alkaline pH of an engineered DyP-type peroxidase. 2022 , 20, 3899-3910 | | 0 |
| 13 | Crystallization and preliminary structural determination of the universal stress G4LZ13 protein from <i>Schistosoma mansoni</i> . 2022 , 32, 101057 | | 0 |
| 12 | Structural Analysis of the Complex of Human Transthyretin with 3,5-Dichlorophenylanthranilic Acid at 1.5 Å Resolution. 2022 , 27, 7206 | | 0 |
| 11 | X-ray structure of human aldo-keto reductase 1C3 in complex with a bile acid fused tetrazole inhibitor: experimental validation, molecular docking and structural analysis. | | 0 |
| 10 | Structure of Phosphorylated-like ClpXP Adaptor RssB Reveals an Interface Switch for Activation. | | 0 |
| 9 | Crystal polymorphism in fragment-based lead discovery of ligands of the catalytic domain of UGGT, the glycoprotein folding quality control checkpoint. 9, | | 0 |
| 8 | Structure of VanS from Vancomycin-Resistant Enterococci: A Sensor Kinase with Weak ATP Binding. | | 0 |

- 7 Broad-Spectrum Cyclopropane-Based Inhibitors of Coronavirus 3C-like Proteases: Biochemical, Structural, and Virological Studies. **2023**, 6, 181-194 ○
- 6 Conformation-dependent ligand hot spots in the spliceosomal RNA helicase BRR2. **2023**, 79, 304-317 ○
- 5 Structure-guided design of direct-acting antivirals that exploit the gem-dimethyl effect and potently inhibit 3CL proteases of severe acute respiratory syndrome Coronavirus-2 (SARS-CoV-2) and middle east respiratory syndrome coronavirus (MERS-CoV). **2023**, 254, 115376 ○
- 4 Structure of VanS from vancomycin-resistant enterococci: A Γ sensor kinase with weak ATP binding. **2023**, 299, 103001 ○
- 3 *Pseudomonas aeruginosa* Dps (PA0962) Functions in H₂O₂ Mediated Oxidative Stress Defense and Exhibits In Vitro DNA Cleaving Activity. **2023**, 24, 4669 ○
- 2 Biochemical Studies of Systemic Lupus Erythematosus-Associated Mutations in Nonreceptor Tyrosine Kinases Ack1 and Brk. **2023**, 62, 1124-1137 ○
- 1 Structure of a HIV-1 IN-Allosteric inhibitor complex at 2.93 Å resolution: Routes to inhibitor optimization. **2023**, 19, e1011097 ○