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## Overview of the CCP4 suite and current developments

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2148	Crystallization and preliminary X-ray diffraction analysis of mouse prostaglandin F2 synthase, AKR1B3. <b>2011, 67, 1630-2</b>	
2147	Preliminary neutron crystallographic study of human transthyretin. <b>2011, 67, 1428-31</b>	4
2146	Preliminary X-ray analysis of twinned crystals of the Q88Y25_Lacpl esterase from <i>Lactobacillus plantarum</i> WCFS1. <b>2011, 67, 1436-9</b>	3
2145	Crystallization and preliminary X-ray data collection of the L27(PATJ)-(L27N,L27C)(Pals1)-L27(MALS) tripartite complex. <b>2011, 67, 1443-7</b>	0
2144	HisB from <i>Mycobacterium tuberculosis</i> : cloning, overexpression in <i>Mycobacterium smegmatis</i> , purification, crystallization and preliminary X-ray crystallographic analysis. <b>2011, 67, 1451-6</b>	5
2143	Crystallization and preliminary X-ray diffraction crystallographic study of tRNA m(1)A58 methyltransferase from <i>Saccharomyces cerevisiae</i> . <b>2011, 67, 1448-50</b>	2
2142	Crystallization and X-ray diffraction analysis of the C-terminal domain of the flax rust effector protein AvrM. <b>2011, 67, 1603-7</b>	4
2141	Expression, crystallization and preliminary X-ray crystallographic analysis of glucose-6-phosphate dehydrogenase from the human pathogen <i>Trypanosoma cruzi</i> in complex with substrate. <b>2011, 67, 1457-61</b>	7
2140	Thermostable multicopper oxidase from <i>Thermus thermophilus</i> HB27: crystallization and preliminary X-ray diffraction analysis of apo and holo forms. <b>2011, 67, 1595-8</b>	15
2139	Crystallization of <i>Chlorella</i> deoxyuridine triphosphatase. <b>2011, 67, 1599-602</b>	3
2138	Crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from <i>Escherichia coli</i> in complex with the acceptor-T $\psi$ C domain of tRNA. <b>2011, 67, 1566-9</b>	9
2137	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the grapevine <i>Vitis vinifera</i> . <b>2011, 67, 1537-41</b>	10
2136	Crystallization and preliminary crystallographic analysis of dextranase from <i>Streptococcus mutans</i> . <b>2011, 67, 1542-4</b>	5
2135	A 1.5 Å resolution X-ray structure of the catalytic module of <i>Caldicellulosiruptor bescii</i> family 3 pectate lyase. <b>2011, 67, 1498-500</b>	13

2134	Purification, crystallization and preliminary crystallographic analysis of peroxidase from the palm tree <i>Chamaerops excelsa</i> . <b>2011</b> , 67, 1641-4	1
2133	Crystallization and X-ray data collection of HP0902 from <i>Helicobacter pylori</i> 26695. <b>2011</b> , 67, 1619-22	2
2132	Engineered tryptophan in the adenine-binding pocket of catalytic subunit A of A-ATP synthase demonstrates the importance of aromatic residues in adenine binding, forming a tool for steady-state and time-resolved fluorescence spectroscopy. <b>2011</b> , 67, 1485-91	
2131	Expression, purification, crystallization and preliminary X-ray diffraction crystallographic study of PurH from <i>Escherichia coli</i> . <b>2011</b> , 67, 1590-4	4
2130	Therapeutic target-site variability in $\beta$ -antitrypsin characterized at high resolution. <b>2011</b> , 67, 1492-7	31
2129	Expression, purification, crystallization and preliminary X-ray diffraction studies of the human keratin 4-binding domain of serine-rich repeat protein 1 from <i>Streptococcus agalactiae</i> . <b>2011</b> , 67, 1582-5	6
2128	Improved X-ray diffraction from <i>Bacillus megaterium</i> penicillin G acylase crystals through long cryosoaking dehydration. <b>2011</b> , 67, 1570-4	4
2127	Crystallization and preliminary crystallographic analysis of a C2 protein from <i>Arabidopsis thaliana</i> . <b>2011</b> , 67, 1575-8	1
2126	Crystallization and preliminary crystallographic analysis of a putative glucokinase/hexokinase from <i>Thermus thermophilus</i> . <b>2011</b> , 67, 1559-62	1
2125	Overexpression, crystallization and preliminary X-ray crystallographic analysis of shikimate dehydrogenase from <i>Archaeoglobus fulgidus</i> . <b>2011</b> , 67, 1556-8	1
2124	Overexpression, purification, crystallization and preliminary X-ray analysis of CheY4 from <i>Vibrio cholerae</i> O395. <b>2011</b> , 67, 1645-8	1
2123	Seleno-detergent MAD phasing of leukotriene C4 synthase in complex with dodecyl- $\beta$ -D-selenomaltoside. <b>2011</b> , 67, 1666-73	6
2122	The structure of LsrB from <i>Yersinia pestis</i> complexed with autoinducer-2. <b>2011</b> , 67, 1501-5	16
2121	The structure of an N11A mutant of the G-protein domain of FeoB. <b>2011</b> , 67, 1511-5	8
2120	Crystallization of a 79 kDa fragment of the hook protein FlgE from <i>Campylobacter jejuni</i> . <b>2011</b> , 67, 1653-7	4
2119	Preliminary X-ray crystallographic studies on acetate kinase (AckA) from <i>Salmonella typhimurium</i> in two crystal forms. <b>2011</b> , 67, 1658-61	5
2118	Structure of the H107R variant of the extracellular domain of mouse NKR-P1A at 2.3 Å resolution. <b>2011</b> , 67, 1519-23	6
2117	Structure of d(CGGGTACCCG) <sub>4</sub> as a four-way Holliday junction. <b>2011</b> , 67, 1506-10	4

2116	Crystal structure of New Delhi metallo-β-lactamase reveals molecular basis for antibiotic resistance. <b>2011</b> , 20, 1484-91	135
2115	Design, synthesis, and evaluation of 5'-diphenyl nucleoside analogues as inhibitors of the Plasmodium falciparum dUTPase. <b>2011</b> , 6, 1816-31	25
2114	How the binding of human transferrin primes the transferrin receptor potentiating iron release at endosomal pH. <b>2011</b> , 108, 13089-94	110
2113	Osh4p exchanges sterols for phosphatidylinositol 4-phosphate between lipid bilayers. <b>2011</b> , 195, 965-78	290
2112	The crystal structure of an oligo(U):pre-mRNA duplex from a trypanosome RNA editing substrate. <b>2011</b> , 17, 1870-83	18
2111	The transition from closed to open conformation of Treponema pallidum outer membrane-associated lipoprotein TP0453 involves membrane sensing and integration by two amphipathic helices. <b>2011</b> , 286, 41656-41668	20
2110	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <b>2011</b> , 480, 336-43	682
2109	Remote control of regioselectivity in acyl-acyl carrier protein-desaturases. <b>2011</b> , 108, 16594-9	51
2108	New N-acetyltransferase fold in the structure and mechanism of the phosphonate biosynthetic enzyme FrbF. <b>2011</b> , 286, 36132-36141	8
2107	The cystic fibrosis transmembrane conductance regulator (CFTR): three-dimensional structure and localization of a channel gate. <b>2011</b> , 286, 42647-42654	58
2106	Mechanism of ubiquitylation by dimeric RING ligase RNF4. <b>2011</b> , 18, 1052-9	123
2105	Membrane remodeling by the double-barrel scaffolding protein of poxvirus. <b>2011</b> , 7, e1002239	33
2104	Crystal structure of novel metallopeptidase inhibitor from marine mollusk Nerita versicolor in complex with human carboxypeptidase A4. <b>2012</b> , 287, 9250-8	20
2103	Specificity of linear motifs that bind to a common mitogen-activated protein kinase docking groove. <b>2012</b> , 5, ra74	106
2102	The NC2 domain of type IX collagen determines the chain register of the triple helix. <b>2012</b> , 287, 44536-45	15
2101	Design and evaluation of meningococcal vaccines through structure-based modification of host and pathogen molecules. <b>2012</b> , 8, e1002981	48
2100	Structural and functional insights into the malaria parasite moving junction complex. <b>2012</b> , 8, e1002755	96
2099	Specialized peptidoglycan hydrolases sculpt the intra-bacterial niche of predatory Bdellovibrio and increase population fitness. <b>2012</b> , 8, e1002524	48

2098	Novel <i>Clostridium thermocellum</i> type I cohesin-dockerin complexes reveal a single binding mode. <b>2012</b> , 287, 44394-405	25
2097	Identification of the HIV-1 NC binding interface in Alix Bro1 reveals a role for RNA. <b>2012</b> , 86, 11608-15	25
2096	The crystal structure of a coxsackievirus B3-RD variant and a refined 9-angstrom cryo-electron microscopy reconstruction of the virus complexed with decay-accelerating factor (DAF) provide a new footprint of DAF on the virus surface. <b>2012</b> , 86, 12571-81	39
2095	Ni(II) coordination to mixed sites modulates DNA binding of HpNikR via a long-range effect. <b>2012</b> , 109, 5633-8	31
2094	Functional and structural characterization of $\alpha$ (1 $\rightarrow$ 2) branching sucrose derived from DSR-E glucansucrase. <b>2012</b> , 287, 7915-24	70
2093	Structural and functional insights into (S)-ureidoglycine aminohydrolase, key enzyme of purine catabolism in <i>Arabidopsis thaliana</i> . <b>2012</b> , 287, 18796-805	12
2092	Structural enzymology of <i>Cellvibrio japonicus</i> Agd31B protein reveals $\beta$ transglucosylase activity in glycoside hydrolase family 31. <b>2012</b> , 287, 43288-99	30
2091	Crystal structure of urea carboxylase provides insights into the carboxyltransfer reaction. <b>2012</b> , 287, 9389-98	27
2090	Characterization of a <i>Phanerochaete chrysosporium</i> glutathione transferase reveals a novel structural and functional class with ligandin properties. <b>2012</b> , 287, 39001-11	29
2089	Structural and functional basis for substrate specificity and catalysis of levan fructotransferase. <b>2012</b> , 287, 31233-41	21
2088	Structure of the pentameric ligand-gated ion channel ELIC cocrystallized with its competitive antagonist acetylcholine. <b>2012</b> , 3, 714	85
2087	The crystal structure of the lipid II-degrading bacteriocin syringacin M suggests unexpected evolutionary relationships between colicin M-like bacteriocins. <b>2012</b> , 287, 38876-88	28
2086	Substitution of asparagine 76 by a tyrosine residue induces domain swapping in <i>Helicobacter pylori</i> phosphopantetheine adenylyltransferase. <b>2012</b> , 30, 488-502	
2085	Structural insight into how <i>Pseudomonas aeruginosa</i> peptidoglycanhydrolase Tse1 and its immunity protein Tsi1 function. <b>2012</b> , 448, 201-11	19
2084	The binding of Varp to VAMP7 traps VAMP7 in a closed, fusogenically inactive conformation. <b>2012</b> , 19, 1300-9	56
2083	Data management challenges in three-dimensional EM. <b>2012</b> , 19, 1203-7	34
2082	Structure of RPE65 isomerase in a lipidic matrix reveals roles for phospholipids and iron in catalysis. <b>2012</b> , 109, E2747-56	51
2081	Trapping and structure determination of an intermediate in the allosteric transition of aspartate transcarbamoylase. <b>2012</b> , 109, 7741-6	6

2080	The molecular mechanism of thermostable $\beta$ -galactosidases AgaA and AgaB explained by x-ray crystallography and mutational studies. <b>2012</b> , 287, 39642-52	34
2079	Structural and biochemical characterization of glycoside hydrolase family 79 $\beta$ -glucuronidase from <i>Acidobacterium capsulatum</i> . <b>2012</b> , 287, 14069-77	29
2078	Mechanisms of monomeric and dimeric glycogenin autoglucosylation. <b>2012</b> , 287, 1955-61	10
2077	Precursor of ether phospholipids is synthesized by a flavoenzyme through covalent catalysis. <b>2012</b> , 109, 18791-6	14
2076	Structural and functional analysis of phosphorylation-specific binders of the kinase ERK from designed ankyrin repeat protein libraries. <b>2012</b> , 109, E2248-57	70
2075	Structural basis for WDR5 interaction (Win) motif recognition in human SET1 family histone methyltransferases. <b>2012</b> , 287, 27275-89	69
2074	The novel structure of a cytosolic M14 metalloprotease (CCP) from <i>Pseudomonas aeruginosa</i> : a model for mammalian CCPs. <b>2012</b> , 26, 3754-64	12
2073	Diversity in the C3b [corrected] contact residues and tertiary structures of the staphylococcal complement inhibitor (SCIN) protein family. <b>2012</b> , 287, 628-640	20
2072	Crystal structures of N-acetylmannosamine kinase provide insights into enzyme activity and inhibition. <b>2012</b> , 287, 13656-65	24
2071	The structure of the yeast NADH dehydrogenase (Ndi1) reveals overlapping binding sites for water- and lipid-soluble substrates. <b>2012</b> , 109, 15247-52	78
2070	Sequence, structure, and evolution of cellulases in glycoside hydrolase family 48. <b>2012</b> , 287, 41068-77	28
2069	Structural mechanism of <i>Staphylococcus aureus</i> Hfq binding to an RNA A-tract. <b>2012</b> , 40, 11023-35	32
2068	Crystal structure of IgE bound to its B-cell receptor CD23 reveals a mechanism of reciprocal allosteric inhibition with high affinity receptor Fc $\epsilon$ R1. <b>2012</b> , 109, 12686-91	71
2067	Structural elucidation of dextran degradation mechanism by streptococcus mutans dextranase belonging to glycoside hydrolase family 66. <b>2012</b> , 287, 19916-26	22
2066	Structure-based analyses reveal distinct binding sites for Atg2 and phosphoinositides in Atg18. <b>2012</b> , 287, 31681-90	93
2065	RIBER/DIBER: a software suite for crystal content analysis in the studies of protein-nucleic acid complexes. <b>2012</b> , 28, 880-1	5
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2063	Emergent decarboxylase activity and attenuation of $\beta$ -hydroxylase activity during the evolution of methylketone biosynthesis in tomato. <b>2012</b> , 24, 1596-607	18

2062	Interactions of Mn <sup>2+</sup> with a non-self-complementary Z-type DNA duplex. <b>2012</b> , 68, 1420-6	6
2061	Crystal structure of the human ecto-5'-nucleotidase (CD73): insights into the regulation of purinergic signaling. <b>2012</b> , 20, 2161-73	119
2060	Low-density crystal packing of human protein kinase CK2 catalytic subunit in complex with resorufin or other ligands: a tool to study the unique hinge-region plasticity of the enzyme without packing bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 883-92	16
2059	Crystallographic analysis of the conserved C-terminal domain of transcription factor Cdc73 from <i>Saccharomyces cerevisiae</i> reveals a GTPase-like fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 953-9	11
2058	The PAD region in the mycobacterial DinB homologue MsPolIV exhibits positional heterogeneity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 960-7	4
2057	The promiscuous binding of the Fyn SH3 domain to a peptide from the NS5A protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1030-40	19
2056	Structural features of the single-stranded DNA-binding protein MoSub1 from <i>Magnaporthe oryzae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1071-6	8
2055	X-ray structure of p38 $\beta$ bound to TAK-715: comparison with three classic inhibitors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1041-50	22
2054	Dimerization properties of the RpBphP2 chromophore-binding domain crystallized by homologue-directed mutagenesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1058-66	30
2053	High-resolution structure of <i>Bombyx mori</i> lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1140-51	13
2052	Structure of a tetrameric galectin from <i>Cinachyrella</i> sp. (ball sponge). <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1163-74	11
2051	Segmenting data sets for RIP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1152-62	12
2050	Structural analysis of the Asn152Gly mutant of P99 cephalosporinase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1189-93	4
2049	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogen <i>Giardia lamblia</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1194-200	8
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2047	Induced-fit motion of a lid loop involved in catalysis in alginate lyase A1-III. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1207-16	24
2046	Structure determination of enterovirus 71. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1217-22	12
2045	The structure of <i>Enterococcus faecalis</i> thymidylate synthase provides clues about folate bacterial metabolism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1232-41	22

2044	The structures of T6, T3R3 and R6 bovine insulin: combining X-ray diffraction and absorption spectroscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1259-71	13
2043	Contamination from an affinity column: an encounter with a new villain in the world of membrane-protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1272-7	5
2042	The structure of the ternary Eg5-ADP-ispinesib complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1311-9	35
2041	Structural insight into the ISC domain of VibB from <i>Vibrio cholerae</i> at atomic resolution: a snapshot just before the enzymatic reaction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1329-38	5
2040	Structural characterization and comparison of three acyl-carrier-protein synthases from pathogenic bacteria. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1359-70	5
2039	Crystallization, dehydration and experimental phasing of WbdD, a bifunctional kinase and methyltransferase from <i>Escherichia coli</i> O9a. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1371-9	5
2038	Structure of a thermophilic cyanobacterial b6f-type Rieske protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1400-8	11
2037	Structure of the CFA/III major pilin subunit CofA from human enterotoxigenic <i>Escherichia coli</i> determined at 0.90 Å resolution by sulfur-SAD phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1418-29	10
2036	Crystallization and preliminary X-ray studies of ferric uptake regulator from <i>Magnetospirillum gryphiswaldense</i> . <b>2012</b> , 68, 902-5	1
2035	Crystallization and preliminary crystallographic analysis of the C-terminal domain of MamM, a magnetosome-associated protein from <i>Magnetospirillum gryphiswaldense</i> MSR-1. <b>2012</b> , 68, 927-30	13
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2033	Crystallization and preliminary X-ray analysis of the receiver domain of a putative response regulator, BPSL0128, from <i>Burkholderia pseudomallei</i> . <b>2012</b> , 68, 917-22	
2032	Purification, crystallization and preliminary crystallographic analysis of banyan peroxidase. <b>2012</b> , 68, 931-4	1
2031	Structural characterization of recombinant crustacyanin subunits from the lobster <i>Homarus americanus</i> . <b>2012</b> , 68, 846-53	10
2030	Purification, crystallization and preliminary X-ray analysis of the IgV domain of human nectin-4. <b>2012</b> , 68, 942-5	1
2029	Cloning, purification, crystallization and preliminary X-ray diffraction studies of <i>Escherichia coli</i> PapD-like protein (EcpD). <b>2012</b> , 68, 954-7	2
2028	Structure of human Rack1 protein at a resolution of 2.45 Å <b>2012</b> , 68, 867-72	28
2027	Binding of the unreactive substrate analog L-2-amino-3-guanidinopropionic acid (dinor-L-arginine) to human arginase I. <b>2012</b> , 68, 889-93	2

2026	Characterization of crystals of an antibody-recognition fragment of the cancer differentiation antigen mesothelin in complex with the therapeutic antibody MORAb-009. <b>2012</b> , 68, 950-3	7
2025	Anomalous dispersion analysis of inhibitor flexibility: a case study of the kinase inhibitor H-89. <b>2012</b> , 68, 873-7	8
2024	Structure of a fluorescent protein from <i>Aequorea victoria</i> bearing the obligate-monomer mutation A206K. <b>2012</b> , 68, 878-82	46
2023	Preliminary crystallographic analysis of glyceraldehyde-3-phosphate dehydrogenase 3 from <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 68, 978-80	5
2022	Crystallization and preliminary X-ray analysis of Pac17 from the pacidamycin-biosynthetic cluster of <i>Streptomyces coeruleorubidus</i> . <b>2012</b> , 68, 971-4	
2021	Expression, purification and preliminary crystallographic analysis of <i>Drosophila melanogaster</i> lysosomal $\beta$ -mannosidase. <b>2012</b> , 68, 965-70	3
2020	A new crystal form of human histidine triad nucleotide-binding protein 1 (hHINT1) in complex with adenosine 5'-monophosphate at 1.38 Å resolution. <b>2012</b> , 68, 883-8	10
2019	Purification, crystallization and preliminary X-ray analysis of uracil-DNA glycosylase from <i>Sulfolobus tokodaii</i> strain 7. <b>2012</b> , 68, 1102-5	2
2018	Crystallization and preliminary X-ray diffraction analysis of tau protein microtubule-binding motifs in complex with Tau5 and DC25 antibody Fab fragments. <b>2012</b> , 68, 1181-5	6
2017	Macrophage migration inhibitory factor covalently complexed with phenethyl isothiocyanate. <b>2012</b> , 68, 999-1002	10
2016	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of succinyl-diaminopimelate desuccinylase (Rv1202, DapE) from <i>Mycobacterium tuberculosis</i> . <b>2012</b> , 68, 1089-93	2
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2014	Crystallization and preliminary crystallographic analysis of the NheA component of the Nhe toxin from <i>Bacillus cereus</i> . <b>2012</b> , 68, 1073-6	6
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2011	Crystallographic study of the interaction of the anti-HIV lectin actinohivin with the $\beta$ (1-2)mannobiose moiety of gp120 HMTG. <b>2012</b> , 68, 1060-3	5
2010	Use of a repetitive seeding protocol to obtain diffraction-quality crystals of a putative human D-xylulokinase. <b>2012</b> , 68, 1259-62	4
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2008	The role of active-site Phe87 in modulating the organic co-solvent tolerance of cytochrome P450 BM3 monooxygenase. <b>2012</b> , 68, 1013-7	21
2007	Purification, crystallization and preliminary X-ray characterization of the <i>Acetivibrio cellulolyticus</i> type I cohesin ScaC in complex with the ScaB dockerin. <b>2012</b> , 68, 1030-3	3
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2003	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from <i>Agrobacterium tumefaciens</i> . <b>2012</b> , 68, 1040-7	8
2002	Structural insights into ChpT, an essential dimeric histidine phosphotransferase regulating the cell cycle in <i>Caulobacter crescentus</i> . <b>2012</b> , 68, 1025-9	9
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1999	High-resolution structures of <i>Thermus thermophilus</i> enoyl-acyl carrier protein reductase in the apo form, in complex with NAD <sup>+</sup> and in complex with NAD <sup>+</sup> and triclosan. <b>2012</b> , 68, 1139-48	2
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1997	Structure of d(CCGGGACCGG) <sub>4</sub> as a four-way junction at 1.6 Å resolution: new insights into solvent interactions. <b>2012</b> , 68, 1169-74	
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1995	Purification, crystallization and preliminary crystallographic analysis of the CBS-domain pair of cyclin M2 (CNNM2). <b>2012</b> , 68, 1198-203	11
1994	Crystallization and preliminary X-ray studies of MutT1 (MSMEG_2390) from <i>Mycobacterium smegmatis</i> . <b>2012</b> , 68, 1214-6	3
1993	Structure of the [NiFe]-hydrogenase maturation protein HypF from <i>Thermococcus kodakarensis</i> KOD1. <b>2012</b> , 68, 1153-7	11
1992	Expression, purification and crystallization of the outer membrane lipoprotein GumB from <i>Xanthomonas campestris</i> . <b>2012</b> , 68, 1255-8	7
1991	Structure of $\beta$ -1,4-mannanase from the common sea hare <i>Aplysia kurodai</i> at 1.05 Å resolution. <b>2012</b> , 68, 1164-8	9

1990	Purification, crystallization and preliminary X-ray diffraction analysis of the RNA-dependent RNA polymerase from <i>Thomovirus</i> virus. <b>2012</b> , 68, 1263-6	3
1989	Recombinant portal protein from <i>Staphylococcus epidermidis</i> bacteriophage CNPH82 is a 13-subunit oligomer. <b>2012</b> , 68, 1267-70	2
1988	Crystal structure of the glycosyltransferase SnogD from the biosynthetic pathway of nogalamycin in <i>Streptomyces nogalater</i> . <b>2012</b> , 279, 3251-63	15
1987	Structure and mechanism of a bacterial sodium-dependent dicarboxylate transporter. <b>2012</b> , 491, 622-6	118
1986	Toward a hepatitis C virus vaccine: the structural basis of hepatitis C virus neutralization by AP33, a broadly neutralizing antibody. <b>2012</b> , 86, 12923-32	72
1985	Noncanonical recognition and UBL loading of distinct E2s by autophagy-essential Atg7. <b>2012</b> , 19, 1250-6	42
1984	A subnanomolar fluorescent probe for protein kinase CK2 interaction studies. <b>2012</b> , 10, 8645-53	29
1983	Structure of a RING E3 ligase and ubiquitin-loaded E2 primed for catalysis. <b>2012</b> , 489, 115-20	339
1982	Design and characterization of modular scaffolds for tubulin assembly. <b>2012</b> , 287, 31085-94	19
1981	Crystal structure of the HLA-DM-HLA-DR1 complex defines mechanisms for rapid peptide selection. <b>2012</b> , 151, 1557-68	123
1980	Structure and catalytic mechanism of 3-ketosteroid-Delta4-(5)-dehydrogenase from <i>Rhodococcus jostii</i> RHA1 genome. <b>2012</b> , 287, 30975-83	21
1979	Binding mechanism of metal-NTP substrates and stringent-response alarmones to bacterial DnaG-type primases. <b>2012</b> , 20, 1478-89	58
1978	Crystallization and preliminary crystallographic studies of the W2 domain of <i>Drosophila melanogaster</i> eukaryotic translation initiation factor 5C domain-containing protein. <b>2012</b> , 68, 1315-7	
1977	Crystal structure of the human two-pore domain potassium channel K2P1. <b>2012</b> , 335, 432-6	232
1976	Engineering of dual-functional hybrid glucanases. <b>2012</b> , 25, 771-80	8
1975	Identification and characterization of a multifunctional dye peroxidase from a lignin-reactive bacterium. <b>2012</b> , 7, 2074-81	160
1974	Crystallization of uridine phosphorylase from <i>Shewanella oneidensis</i> MR-1 in the laboratory and under microgravity and preliminary X-ray diffraction analysis. <b>2012</b> , 68, 1387-9	11
1973	Crystallization and preliminary X-ray diffraction analysis of <i>Bacillus subtilis</i> YwfE, an L-amino-acid ligase. <b>2012</b> , 68, 203-6	4

1972	The crystal structure of samarosporin I at atomic resolution. <b>2012</b> , 18, 678-84	9
1971	Crystal structures of rice ( <i>Oryza sativa</i> ) glyceraldehyde-3-phosphate dehydrogenase complexes with NAD and sulfate suggest involvement of Phe37 in NAD binding for catalysis. <b>2012</b> , 80, 389-403	10
1970	Engineering a naturally inactive isoform of type III antifreeze protein into one that can stop the growth of ice. <b>2012</b> , 586, 3876-81	23
1969	Crystal structure of the globular domain of C1QTNF5: Implications for late-onset retinal macular degeneration. <b>2012</b> , 180, 439-46	28
1968	Novel structural features of xylanase A1 from <i>Paenibacillus</i> sp. JDR-2. <b>2012</b> , 180, 303-11	9
1967	<i>Escherichia coli</i> expression, purification, crystallization, and structure determination of bacterial cohesin-dockerin complexes. <b>2012</b> , 510, 395-415	4
1966	Interdomain disulfide bridge in the rice granule bound starch synthase I catalytic domain as elucidated by X-ray structure analysis. <b>2012</b> , 76, 1591-5	41
1965	A structural element that facilitates proton-coupled electron transfer in oxalate decarboxylase. <b>2012</b> , 51, 2911-20	20
1964	Molecular structure of human GM-CSF in complex with a disease-associated anti-human GM-CSF autoantibody and its potential biological implications. <b>2012</b> , 447, 205-15	13
1963	Kinetics of <i>Torpedo californica</i> acetylcholinesterase inhibition by bisnorcymserine and crystal structure of the complex with its leaving group. <b>2012</b> , 444, 269-77	20
1962	Exploring the structural basis of substrate preferences in Baeyer-Villiger monooxygenases: insight from steroid monooxygenase. <b>2012</b> , 287, 22626-34	39
1961	Two translation products of <i>Yersinia</i> yscQ assemble to form a complex essential to type III secretion. <b>2012</b> , 51, 1669-77	40
1960	Identification of the dimer interface of a bacterial Ca(2+)/H(+) antiporter. <b>2012</b> , 51, 9603-11	3
1959	Side chain independent recognition of aminoacyl adenylates by the Hint1 transcription suppressor. <b>2012</b> , 116, 6798-805	17
1958	Structure of STING bound to cyclic di-GMP reveals the mechanism of cyclic dinucleotide recognition by the immune system. <b>2012</b> , 19, 722-4	186
1957	Structure and mechanism of the UvrA-UvrB DNA damage sensor. <b>2012</b> , 19, 291-8	56
1956	<i>Leishmania major</i> peroxidase is a cytochrome c peroxidase. <b>2012</b> , 51, 2453-60	18
1955	Atomic-resolution structures of horse liver alcohol dehydrogenase with NAD(+) and fluoroalcohols define strained Michaelis complexes. <b>2012</b> , 51, 4035-48	33

1954	Structural basis for the role of tyrosine 257 of homoprotocatechuate 2,3-dioxygenase in substrate and oxygen activation. <b>2012</b> , 51, 8755-63	26
1953	Crystal structure of a preacylation complex of the $\beta$ -lactamase inhibitor sulbactam bound to a sulfenamide bond-containing thiol- $\beta$ -lactamase. <b>2012</b> , 134, 16798-804	22
1952	Correction to "Structural evidence of a productive active site architecture for an evolved quorum-quenching GKL lactonase". <b>2012</b> , 51, 10120	3
1951	Structure and glycolipid binding properties of the nematocidal protein Cry5B. <b>2012</b> , 51, 9911-21	48
1950	Evidence in support of lysine 77 and histidine 96 as acid-base catalytic residues in saccharopine dehydrogenase from <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 51, 857-66	8
1949	A dodecameric CcmK2 structure suggests $\beta$ -carboxysomal shell facets have a double-layered organization. <b>2012</b> , 20, 1353-62	44
1948	Structure of a bacteriophytochrome and light-stimulated protomer swapping with a gene repressor. <b>2012</b> , 20, 1436-46	76
1947	Type II natural killer T cells use features of both innate-like and conventional T cells to recognize sulfatide self antigens. <b>2012</b> , 13, 851-6	102
1946	Crystallization and preliminary X-ray crystallographic analysis of Aquifex aeolicus Sela, a bacterial selenocysteine synthase. <b>2012</b> , 68, 1128-33	3
1945	Structures of bovine, equine and leporine serum albumin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1278-89	444
1944	Flexibility of the P-loop of Pim-1 kinase: observation of a novel conformation induced by interaction with an inhibitor. <b>2012</b> , 68, 860-6	13
1943	Superbinder SH2 domains act as antagonists of cell signaling. <b>2012</b> , 5, ra68	78
1942	GFP-like phototransformation mechanisms in the cytotoxic fluorescent protein KillerRed unraveled by structural and spectroscopic investigations. <b>2012</b> , 134, 18015-21	18
1941	Binding of N-acetylglucosamine (GlcNAc) $\beta$ 1-6-branched oligosaccharide acceptors to $\beta$ 4-galactosyltransferase I reveals a new ligand binding mode. <b>2012</b> , 287, 28666-74	13
1940	Crystallographic Analysis of Rotavirus NSP2-RNA Complex Reveals Specific Recognition of 5' GG Sequence for RTPase Activity. <b>2012</b> , 86, 10547-57	22
1939	Structural reorganization of the bacterial cell-division protein FtsZ from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1175-88	123
1938	Molecular basis for the activation of a catalytic asparagine residue in a self-cleaving bacterial autotransporter. <b>2012</b> , 415, 128-42	34
1937	Crystal structure of p44, a constitutively active splice variant of visual arrestin. <b>2012</b> , 416, 611-8	47

1936	Structural basis for the slow dark recovery of a full-length LOV protein from <i>Pseudomonas putida</i> . <b>2012</b> , 417, 362-74	42
1935	Crystal structure of bifunctional aldose-2-ulose dehydratase/isomerase from <i>Phanerochaete chrysosporium</i> with the reaction intermediate ascopyrone M. <b>2012</b> , 417, 279-93	3
1934	<i>Plasmodium falciparum</i> SSB tetramer wraps single-stranded DNA with similar topology but opposite polarity to <i>E. coli</i> SSB. <b>2012</b> , 420, 269-83	31
1933	Interaction of mammalian end binding proteins with CAP-Gly domains of CLIP-170 and p150(glued). <b>2012</b> , 177, 160-7	32
1932	Crystal structure of the Rasputin NTF2-like domain from <i>Drosophila melanogaster</i> . <b>2012</b> , 420, 188-92	10
1931	Crystal structure of <i>Plasmodium falciparum</i> thioredoxin reductase, a validated drug target. <b>2012</b> , 425, 806-11	19
1930	Intersubunit bridge formation governs agonist efficacy at nicotinic acetylcholine $\alpha 7$ receptors: unique role of halogen bonding revealed. <b>2012</b> , 287, 4248-59	40
1929	The 1.2 Å resolution crystal structure of TcpG, the <i>Vibrio cholerae</i> DsbA disulfide-forming protein required for pilus and cholera-toxin production. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1290-302	18
1928	Towards a new tuberculosis drug: pyridomycin - nature's isoniazid. <b>2012</b> , 4, 1032-42	149
1927	Structural characterization of S100A15 reveals a novel zinc coordination site among S100 proteins and altered surface chemistry with functional implications for receptor binding. <b>2012</b> , 12, 16	19
1926	Crystal structure of a new benzoic acid inhibitor of influenza neuraminidase bound with a new tilt induced by overpacking subsite C6. <b>2012</b> , 12, 7	8
1925	Structural insights into the function of the nicotinate mononucleotide:phenol/p-cresol phosphoribosyltransferase (ArsAB) enzyme from <i>Sporomusa ovata</i> . <b>2012</b> , 51, 8571-82	12
1924	High-throughput counter-diffusion capillary crystallization and in situ diffraction using high-pressure freezing in protein crystallography. <b>2012</b> , 45, 999-1008	8
1923	Comparative structural and functional analysis of two octaheme nitrite reductases from closely related <i>Thioalkalivibrio</i> species. <b>2012</b> , 279, 4052-61	21
1922	Structural basis for benzothiazinone-mediated killing of <i>Mycobacterium tuberculosis</i> . <b>2012</b> , 4, 150ra121	123
1921	Extracellular assembly and activation principles of oncogenic class III receptor tyrosine kinases. <b>2012</b> , 12, 753-66	61
1920	Utilizing the GAAA tetraloop/receptor to facilitate crystal packing and determination of the structure of a CUG RNA helix. <b>2012</b> , 51, 8330-7	31
1919	Structures of haemoglobin from woolly mammoth in liganded and unliganded states. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1441-9	7

1918	Endo- $\beta$ -D-1,4-mannanase from <i>Chrysonilia sitophila</i> displays a novel loop arrangement for substrate selectivity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1468-78	18
1917	Structural insights into the broadened substrate profile of the extended-spectrum $\beta$ -lactamase OXY-1-1 from <i>Klebsiella oxytoca</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1460-7	2
1916	A monomeric TIM-barrel structure from <i>Pyrococcus furiosus</i> is optimized for extreme temperatures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1479-87	2
1915	Structural studies on the folded domain of the human prion protein bound to the Fab fragment of the antibody POM1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1501-12	19
1914	Alteration of fluorescent protein spectroscopic properties upon cryoprotection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1578-83	5
1913	The structure of L-amino-acid ligase from <i>Bacillus licheniformis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1535-40	10
1912	Severe diffraction anisotropy, rotational pseudosymmetry and twinning complicate the refinement of a pentameric coiled-coil structure of NSP4 of rotavirus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1541-8	5
1911	Structure of the corrinoid:coenzyme M methyltransferase MtaA from <i>Methanosarcina mazei</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1549-57	4
1910	The structure of a thermostable mutant of pro-papain reveals its activation mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1591-603	16
1909	Structure-activity correlations of variant forms of the B pentamer of <i>Escherichia coli</i> type II heat-labile enterotoxin LT-IIb with Toll-like receptor 2 binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1604-12	7
1908	Structure of the catalytic domain of the <i>Salmonella</i> virulence factor Ssel. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1613-21	13
1907	AMPLE: a cluster-and-truncate approach to solve the crystal structures of small proteins using rapidly computed ab initio models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1622-31	89
1906	Substrate channels revealed in the trimeric <i>Lactobacillus reuteri</i> bacterial microcompartment shell protein PduB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1642-52	47
1905	Structural insights into the specific anti-HIV property of actinohivin: structure of its complex with the $\beta$ (1-2)mannobiose moiety of gp120. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1671-9	8
1904	In situ X-ray data collection from highly sensitive crystals of <i>Pseudomonas putida</i> PtxS in complex with DNA. <b>2012</b> , 68, 1307-10	6
1903	Crystallization and preliminary X-ray analysis of the FliH-FliI complex responsible for bacterial flagellar type III protein export. <b>2012</b> , 68, 1311-4	2
1902	High-resolution structure of AKR1a4 in the apo form and its interaction with ligands. <b>2012</b> , 68, 1271-4	3
1901	Purification, crystallization and preliminary crystallographic analysis of human cystathionine $\beta$ -synthase. <b>2012</b> , 68, 1318-22	5

1900	Influence of intermolecular contacts on the structure of recombinant prolidase from <i>Thermococcus sibiricus</i> . <b>2012</b> , 68, 1275-8	5
1899	Purification, crystallization and preliminary crystallographic analysis of the full-length cystathionine $\beta$ -synthase from <i>Apis mellifera</i> . <b>2012</b> , 68, 1323-8	3
1898	Purification, crystallization and preliminary X-ray crystallographic analysis of the ETS domain of human Ergp55 in complex with the cfos promoter DNA sequence. <b>2012</b> , 68, 1333-6	1
1897	Crystallization and preliminary crystallographic analysis of 2-aminophenol 1,6-dioxygenase complexed with substrate and with an inhibitor. <b>2012</b> , 68, 1337-40	3
1896	Cloning, purification and preliminary X-ray data analysis of the human ID2 homodimer. <b>2012</b> , 68, 1354-8	3
1895	Structure of the recombinant BPTI/Kunitz-type inhibitor rShPI-1A from the marine invertebrate <i>Stichodactyla helianthus</i> . <b>2012</b> , 68, 1289-93	7
1894	Purification, crystallization, preliminary X-ray diffraction and molecular-replacement studies of catfish ( <i>Clarias magur</i> ) haemoglobin. <b>2012</b> , 68, 1371-3	
1893	Crystallization, optimization and preliminary X-ray characterization of a metal-dependent PI-PLC from <i>Streptomyces antibioticus</i> . <b>2012</b> , 68, 1378-86	1
1892	Expression, purification, crystallization and preliminary X-ray structure analysis of <i>Vibrio cholerae</i> uridine phosphorylase in complex with thymidine. <b>2012</b> , 68, 1394-7	6
1891	Structure of <i>Escherichia coli</i> RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the rut operon. <b>2012</b> , 68, 1294-9	12
1890	Crystallization and first data collection of the putative transfer protein TraN from the Gram-positive conjugative plasmid pIP501. <b>2012</b> , 68, 1402-5	5
1889	Crystallization and preliminary X-ray characterization of the tetrapyrrole-biosynthetic enzyme porphobilinogen deaminase from <i>Arabidopsis thaliana</i> . <b>2012</b> , 68, 1491-3	2
1888	Cloning, expression, purification and crystallization of an endotoxin-biosynthesis enzyme from <i>Neisseria meningitidis</i> . <b>2012</b> , 68, 1494-7	5
1887	Crystallization and preliminary X-ray crystallographic analysis of the oxysterol-binding protein Osh3 from <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 68, 1498-502	4
1886	Purification, crystallization and preliminary X-ray analysis of two hydrogen sulfide-producing enzymes from <i>Fusobacterium nucleatum</i> . <b>2012</b> , 68, 1507-10	3
1885	Purification, crystallization and X-ray diffraction analysis of <i>Trypanosoma congolense</i> insect-stage surface antigen (TcCISSA). <b>2012</b> , 68, 1503-6	2
1884	Crystallization and preliminary X-ray crystallographic analysis of human Apaf-1-interacting protein. <b>2012</b> , 68, 1518-20	3
1883	ATP-dependent DNA ligase from <i>Thermococcus</i> sp. 1519 displays a new arrangement of the OB-fold domain. <b>2012</b> , 68, 1440-7	14

1882	Molecular cloning, expression, purification and crystallographic analysis of zebrafish THEM2. <b>2012</b> , 68, 1525-8	
1881	Structure of the $\beta$ 1,6/ $\beta$ 1,4-specific glucanase GTFA from <i>Lactobacillus reuteri</i> 121. <b>2012</b> , 68, 1448-54	47
1880	Crystallization and preliminary X-ray diffraction analysis of the invertase from <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 68, 1538-41	4
1879	Structure of the Rho-specific guanine nucleotide-exchange factor Xpln. <b>2012</b> , 68, 1455-9	2
1878	Crystallization and preliminary X-ray analysis of the open form of human ecto-5'-nucleotidase (CD73). <b>2012</b> , 68, 1545-9	2
1877	Complex of myoglobin with phenol bound in a proximal cavity. <b>2012</b> , 68, 1465-71	3
1876	Production, purification, crystallization and structure determination of H-1 Parvovirus. <b>2012</b> , 68, 1571-6	10
1875	Structure determination of LpxA from the lipopolysaccharide-synthesis pathway of <i>Acinetobacter baumannii</i> . <b>2012</b> , 68, 1477-81	12
1874	Preliminary crystallographic analysis of the Megavirus superoxide dismutase. <b>2012</b> , 68, 1557-9	2
1873	Crystallization and preliminary X-ray diffraction analysis of mevalonate kinase from <i>Methanosarcina mazei</i> . <b>2012</b> , 68, 1560-3	2
1872	Cloning, expression, purification, crystallization and preliminary X-ray analysis of a fructokinase from <i>Vibrio cholerae</i> O395. <b>2012</b> , 68, 1564-7	3
1871	Crystal structures of arginine kinase in complex with ADP, nitrate, and various phosphagen analogs. <b>2012</b> , 427, 212-7	10
1870	Structure of the pentameric ligand-gated ion channel GLIC bound with anesthetic ketamine. <b>2012</b> , 20, 1463-9	75
1869	Structures of the Phactr1 RPEL domain and RPEL motif complexes with G-actin reveal the molecular basis for actin binding cooperativity. <b>2012</b> , 20, 1960-70	25
1868	Ego3 functions as a homodimer to mediate the interaction between Gtr1-Gtr2 and Ego1 in the ego complex to activate TORC1. <b>2012</b> , 20, 2151-60	51
1867	The structure of DNA-bound human topoisomerase II alpha: conformational mechanisms for coordinating inter-subunit interactions with DNA cleavage. <b>2012</b> , 424, 109-24	138
1866	Analysis of structure-function relationships in the colibactin-maturing enzyme ClbP. <b>2012</b> , 424, 203-14	51
1865	Structure of PA1221, a nonribosomal peptide synthetase containing adenylation and peptidyl carrier protein domains. <b>2012</b> , 51, 3252-63	101

1864	Broad and potent neutralization of HIV-1 by a gp41-specific human antibody. <b>2012</b> , 491, 406-12	624
1863	Structural basis of DNA ligase IV-Artemis interaction in nonhomologous end-joining. <b>2012</b> , 2, 1505-12	29
1862	Induced fit and the catalytic mechanism of isocitrate dehydrogenase. <b>2012</b> , 51, 7098-115	23
1861	Ligand migration in myoglobin: a combined study of computer simulation and x-ray crystallography. <b>2012</b> , 136, 165101	7
1860	Molecular Insights into Human Monoamine Oxidase B Inhibition by the Glitazone Anti-Diabetes Drugs. <b>2011</b> , 3, 39-42	64
1859	Crystal structure of the human K2P TRAAK, a lipid- and mechano-sensitive K <sup>+</sup> ion channel. <b>2012</b> , 335, 436-41	307
1858	Structural characterisation of Tpx from <i>Yersinia pseudotuberculosis</i> reveals insights into the binding of salicylidene acylhydrazide compounds. <b>2012</b> , 7, e32217	15
1857	Comparative analysis of the heptahelical transmembrane bundles of G protein-coupled receptors. <b>2012</b> , 7, e35802	4
1856	The structure of the oligomerization domain of Lsr2 from <i>Mycobacterium tuberculosis</i> reveals a mechanism for chromosome organization and protection. <b>2012</b> , 7, e38542	28
1855	Crystal structures of human pyridoxal kinase in complex with the neurotoxins, ginkgotoxin and theophylline: insights into pyridoxal kinase inhibition. <b>2012</b> , 7, e40954	22
1854	A green fluorescent protein containing a QFG tri-peptide chromophore: optical properties and X-ray crystal structure. <b>2012</b> , 7, e47331	5
1853	Structural variation and uniformity among tetraloop-receptor interactions and other loop-helix interactions in RNA crystal structures. <b>2012</b> , 7, e49225	19
1852	Structures of the human poly (ADP-ribose) glycohydrolase catalytic domain confirm catalytic mechanism and explain inhibition by ADP-HPD derivatives. <b>2012</b> , 7, e50889	38
1851	Piperidinols that show anti-tubercular activity as inhibitors of arylamine N-acetyltransferase: an essential enzyme for mycobacterial survival inside macrophages. <b>2012</b> , 7, e52790	20
1850	Crystal structure of <i>Proteus mirabilis</i> lipase, a novel lipase from the <i>Proteus</i> /psychrophilic subfamily of lipase family I.1. <b>2012</b> , 7, e52890	18
1849	Flexibility of the flap in the active site of BACE1 as revealed by crystal structures and molecular dynamics simulations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 13-25	70
1848	Rapid visualization of hydrogen positions in protein neutron crystallographic structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 35-41	24
1847	Optimal fine Blicing for single-photon-counting pixel detectors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 42-56	80

1846	Single-wavelength phasing strategy for quasi-racemic protein crystal diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 62-8	9
1845	The use of trimethylamine N-oxide as a primary precipitating agent and related methylamine osmolytes as cryoprotective agents for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 69-81	23
1844	Structural features and kinetic characterization of alanine racemase from <i>Staphylococcus aureus</i> (Mu50). <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 82-92	18
1843	Structure of a compact conformation of linear diubiquitin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 102-8	26
1842	Four complete turns of a curved 3 $\pi$ helix at atomic resolution: the crystal structure of the peptaibol trichovirin I-4A in a polar environment suggests a transition to $\pi$ helix for membrane function. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 109-16	15
1841	Structural basis of the strict phospholipid binding specificity of the pleckstrin homology domain of human eveltin-2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 117-23	10
1840	A corrected space group for <i>Sulfolobus sulfataricus</i> 5'-deoxy-5'-methylthioadenosine phosphorylase II. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 249-52	2
1839	Structural studies on <i>Mycobacterium tuberculosis</i> DXR in complex with the antibiotic FR-900098. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 134-43	15
1838	Covalent modifications of the catalytic tyrosine in octahaem cytochrome c nitrite reductase and their effect on the enzyme activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 144-53	11
1837	Structure of an RNA/DNA dodecamer corresponding to the HIV-1 polypurine tract at 1.6 $\text{\AA}$ resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 169-75	1
1836	Structure of the effector-binding domain of the arabinose repressor AraR from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 176-85	10
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1830	Structure and function of CYP108D1 from <i>Novosphingobium aromaticivorans</i> DSM12444: an aromatic hydrocarbon-binding P450 enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 277-91	20
1829	Structure and function of the <i>Clostridium thermocellum</i> cellobiohydrolase A X1-module repeat: enhancement through stabilization of the CbhA complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 292-9	13

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1827	High-pressure-induced water penetration into 3-isopropylmalate dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 300-9	33
1826	Structure of the catalytic domain of the <i>Clostridium thermocellum</i> cellulase CelT. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 310-20	12
1825	Expression, purification, crystallization and preliminary X-ray diffraction analysis of a ribokinase from the thermohalophile <i>Halothermothrix orenii</i> . <b>2012</b> , 68, 240-3	2
1824	Crystallization and preliminary X-ray diffraction analysis of orotate phosphoribosyltransferase from the human malaria parasite <i>Plasmodium falciparum</i> . <b>2012</b> , 68, 244-6	2
1823	Crystallization and preliminary X-ray crystallographic analysis of the membrane-binding haemprotein nitrophorin 7 from <i>Rhodnius prolixus</i> . <b>2012</b> , 68, 37-40	5
1822	Molecular cloning, overexpression, purification, crystallization and preliminary X-ray diffraction studies of histidinol phosphate aminotransferase (HisC2) from <i>Mycobacterium tuberculosis</i> . <b>2012</b> , 68, 32-6	5
1821	Overproduction, purification, crystallization and preliminary X-ray diffraction analysis of Cockayne syndrome protein A in complex with DNA damage-binding protein 1. <b>2012</b> , 68, 45-8	
1820	Crystallization and preliminary X-ray crystallographic studies of the outer membrane cytochrome OmcA from <i>Shewanella oneidensis</i> MR-1. <b>2012</b> , 68, 53-5	
1819	Protein expression, crystallization and preliminary X-ray crystallographic analysis of chicken interferon- $\beta$ receptor $\beta$ chain. <b>2012</b> , 68, 41-4	1
1818	Crystallization and preliminary X-ray crystallographic analysis of the $\beta$ -N-acetylglucosaminidase CbsA from <i>Thermotoga neapolitana</i> . <b>2012</b> , 68, 56-8	2
1817	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of human $\beta$ -galactosidase. <b>2012</b> , 68, 73-7	2
1816	Activation of legumain involves proteolytic and conformational events, resulting in a context- and substrate-dependent activity profile. <b>2012</b> , 68, 24-31	55
1815	Structure of CBM3b of the major cellulosomal scaffoldin subunit ScaA from <i>Acetivibrio cellulolyticus</i> . <b>2012</b> , 68, 8-13	8
1814	Crystallization and preliminary X-ray analysis of pyridoxine 4-oxidase, the first enzyme in pyridoxine degradation pathway I. <b>2012</b> , 68, 66-8	2
1813	Improving the diffraction of apoA-IV crystals through extreme dehydration. <b>2012</b> , 68, 105-10	10
1812	Purification, crystallization and preliminary X-ray diffraction analysis of the IL-20-IL-20R1-IL-20R2 complex. <b>2012</b> , 68, 89-92	
1811	Three-dimensional structure of a thermophilic family GH11 xylanase from <i>Thermobifida fusca</i> . <b>2012</b> , 68, 141-4	9

1810	Structure of the interleukin-2 tyrosine kinase Src homology 2 domain; comparison between X-ray and NMR-derived structures. <b>2012</b> , 68, 145-53	5
1809	Expression, purification and preliminary crystallographic studies of NahF, a salicylaldehyde dehydrogenase from <i>Pseudomonas putida</i> G7 involved in naphthalene degradation. <b>2012</b> , 68, 93-7	12
1808	Expression, purification, crystallization and preliminary crystallographic analysis of a thermostable DNA ligase from the archaeon <i>Thermococcus sibiricus</i> . <b>2012</b> , 68, 163-5	6
1807	Crystallization of the C-terminal domain of the bacteriophage T7 fibre protein gp17. <b>2012</b> , 68, 166-71	10
1806	Room-temperature ultrahigh-resolution time-of-flight neutron and X-ray diffraction studies of H/D-exchanged crambin. <b>2012</b> , 68, 119-23	8
1805	Purification, crystallization and preliminary X-ray crystallographic studies of the <i>Mycobacterium tuberculosis</i> DNA gyrase CTD. <b>2012</b> , 68, 178-80	5
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1803	A new crystal lattice structure of <i>Helicobacter pylori</i> neutrophil-activating protein (HP-NAP). <b>2012</b> , 68, 134-40	6
1802	Crystallization and preliminary X-ray crystallographic analysis of dioscorin from <i>Dioscorea japonica</i> . <b>2012</b> , 68, 193-5	1
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1800	Cloning, expression, crystallization and preliminary X-ray crystallographic analysis of aspartyl aminopeptidase from the <i>apeB</i> gene of <i>Pseudomonas aeruginosa</i> . <b>2012</b> , 68, 207-10	1
1799	Purification, crystallization and preliminary X-ray diffraction analysis of the Hsp40 protein CPIP1 from <i>Nicotiana tabacum</i> . <b>2012</b> , 68, 236-9	1
1798	Refolding, purification and crystallization of the FrpB outer membrane iron transporter from <i>Neisseria meningitidis</i> . <b>2012</b> , 68, 231-5	8
1797	Crystallization and preliminary X-ray analysis of the <i>Clostridium botulinum</i> type D nontoxic nonhaemagglutinin. <b>2012</b> , 68, 227-30	1
1796	Structures of dimethylsulfoniopropionate-dependent demethylase from the marine organism <i>Pelagabacter ubique</i> . <b>2012</b> , 21, 289-98	21
1795	High-resolution crystal structure of FKBP12 from <i>Aedes aegypti</i> . <b>2012</b> , 21, 1080-4	5
1794	Crystal structure of a supercharged variant of the human enteropeptidase light chain. <b>2012</b> , 80, 1907-10	10
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1792	Structural analysis of the STING adaptor protein reveals a hydrophobic dimer interface and mode of cyclic di-GMP binding. <b>2012</b> , 36, 1073-86	232
1791	Linking crystallographic model and data quality. <b>2012</b> , 336, 1030-3	1329
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1789	Structure of the catalytic core module of the Chaetomium thermophilum family GH6 cellobiohydrolase Cel6A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 875-82	17
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1785	Structural plasticity of tubulin assembly probed by vinca-domain ligands. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 927-34	59
1784	A frontier in the understanding of synaptic plasticity: solving the structure of the postsynaptic density. <b>2012</b> , 34, 599-608	17
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1782	Structural analysis of coxsackievirus A7 reveals conformational changes associated with uncoating. <b>2012</b> , 86, 7207-15	31
1781	Structural tuning of the fluorescent protein iLOV for improved photostability. <b>2012</b> , 287, 22295-304	104
1780	Metal-directed, chemically tunable assembly of one-, two- and three-dimensional crystalline protein arrays. <b>2012</b> , 4, 375-82	301
1779	Current methods in structural proteomics and its applications in biological sciences. <b>2012</b> , 2, 89-113	17
1778	Crystal structures of putative phosphoglycerate kinases from B. anthracis and C. jejuni. <b>2012</b> , 13, 15-26	7
1777	Crystal structures of the Chromobacterium violaceum transaminase reveal major structural rearrangements upon binding of coenzyme PLP. <b>2012</b> , 279, 779-92	99
1776	Structural and biochemical insight into glycogenin inactivation by the glycogenosis-causing T82M mutation. <b>2012</b> , 586, 254-7	2
1775	Crystal structures of the coil 2B fragment and the globular tail domain of human lamin B1. <b>2012</b> , 586, 314-8	28

1774	Crystal structure of cce_0566 from Cyanothece 51142, a protein associated with nitrogen fixation in the DUF269 family. <b>2012</b> , 586, 350-5	1
1773	Protein folding by 'levels of separation': a hypothesis. <b>2012</b> , 586, 962-6	5
1772	Crystal structure of periplasmic catechol-siderophore binding protein VctP from <i>Vibrio cholerae</i> at 1.7 Å resolution. <b>2012</b> , 586, 1240-4	14
1771	Conformational changes upon ligand binding in the essential class II fumarase Rv1098c from <i>Mycobacterium tuberculosis</i> . <b>2012</b> , 586, 1606-11	17
1770	Creation and biochemical analysis of a broad-specific claudin binder. <b>2012</b> , 33, 3464-74	37
1769	The structure of Ca <sup>2+</sup> -loaded S100A2 at 1.3 Å resolution. <b>2012</b> , 279, 1799-810	7
1768	Exploiting structural biology in the fight against parasitic diseases. <b>2012</b> , 28, 124-30	4
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1765	Moonlighting by different stressors: crystal structure of the chaperone species of a 2-Cys peroxiredoxin. <b>2012</b> , 20, 429-39	85
1764	Increasing sequence diversity with flexible backbone protein design: the complete redesign of a protein hydrophobic core. <b>2012</b> , 20, 1086-96	45
1763	Structural insights into Atg10-mediated formation of the autophagy-essential Atg12-Atg5 conjugate. <b>2012</b> , 20, 1244-54	52
1762	CrystFEL: a software suite for snapshot serial crystallography. <b>2012</b> , 45, 335-341	314
1761	Statistical quality indicators for electron-density maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 454-67	96
1760	Use of noncrystallographic symmetry for automated model building at medium to low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 446-53	1
1759	PDB_REDO: constructive validation, more than just looking for errors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 484-96	160
1758	Exploiting structure similarity in refinement: automated NCS and target-structure restraints in BUSTER. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 368-80	432
1757	Low-resolution refinement tools in REFMAC5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 404-17	179

1756	Handling ligands with Coot. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 425-30	94
1755	Challenges and surprises that arise with nucleic acids during model building and refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 441-5	4
1754	Towards automated crystallographic structure refinement with phenix.refine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 352-67	3236
1753	JLigand: a graphical tool for the CCP4 template-restraint library. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 431-40	293
1752	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 521-30	22
1751	Structural changes caused by radiation-induced reduction and radiolysis: the effect of X-ray absorbed dose in a fungal multicopper oxidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 564-77	42
1750	Ribosome engineering to promote new crystal forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 578-83	23
1749	Formylglycinamide ribonucleotide amidotransferase from <i>Salmonella typhimurium</i> : role of ATP complexation and the glutaminase domain in catalytic coupling. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 627-36	7
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1747	Structural and functional characterization of the C-terminal catalytic domain of SSV1 integrase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 659-70	11
1746	Structures of ternary complexes of aspartate-semialdehyde dehydrogenase (Rv3708c) from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 671-9	14
1745	Three-dimensional structure of a schistosome serpin revealing an unusual configuration of the helical subdomain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 686-94	5
1744	Structure-function studies of an unusual 3-methyladenine DNA glycosylase II (AlkA) from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 703-12	14
1743	Two high-resolution structures of potato endo-1,3- $\beta$ -glucanase reveal subdomain flexibility with implications for substrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 713-23	12
1742	Protonation-state determination in proteins using high-resolution X-ray crystallography: effects of resolution and completeness. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 800-9	36
1741	A single mutation reforms the binding activity of an adhesion-deficient family 3 carbohydrate-binding module. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 819-28	11
1740	High-resolution structures of <i>Neotermes koshunensis</i> $\beta$ -glucosidase mutants provide insights into the catalytic mechanism and the synthesis of glucoconjugates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 829-38	26
1739	The structure of a <i>Xanthomonas</i> general stress protein involved in citrus canker reveals its flavin-binding property. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 846-53	6

1738	Purification, crystallization and preliminary X-ray analysis of PPD6, a PsbP-domain protein from <i>Arabidopsis thaliana</i> . <b>2012</b> , 68, 278-80	8
1737	Expression, purification, crystallization and preliminary crystallographic analysis of PilA from the nontypeable <i>Haemophilus influenzae</i> type IV pilus. <b>2012</b> , 68, 284-7	1
1736	Crystallization and X-ray structure analysis of a thermostable penicillin G acylase from <i>Alcaligenes faecalis</i> . <b>2012</b> , 68, 273-7	7
1735	Structure of a bacterial cytoplasmic cyclophilin A in complex with a tetrapeptide. <b>2012</b> , 68, 259-64	5
1734	Crystallization and preliminary X-ray analysis of FlgA, a periplasmic protein essential for flagellar P-ring assembly. <b>2012</b> , 68, 310-3	2
1733	Structural analysis of 3-isopropylmalate dehydrogenase from the obligate piezophile <i>Shewanella benthica</i> DB21MT-2 and the nonpiezophile <i>Shewanella oneidensis</i> MR-1. <b>2012</b> , 68, 265-8	17
1732	Crystallization and preliminary X-ray analysis of alginate importer from <i>Sphingomonas</i> sp. A1. <b>2012</b> , 68, 317-20	1
1731	Structure of recombinant human carboxylesterase 1 isolated from whole cabbage looper larvae. <b>2012</b> , 68, 269-72	6
1730	Crystallization and preliminary X-ray studies of an electron-transfer complex of ferredoxin and ferredoxin-dependent glutamate synthase from the cyanobacterium <i>Leptolyngbya boryana</i> . <b>2012</b> , 68, 324-7	2
1729	Purification, crystallization and preliminary X-ray diffraction analysis of the Fyn SH2 domain and its complex with a phosphotyrosine peptide. <b>2012</b> , 68, 359-64	1
1728	Crystallization and preliminary X-ray crystallographic characterization of a cyclic nucleotide-binding homology domain from the mouse EAG potassium channel. <b>2012</b> , 68, 337-9	3
1727	Crystallization and preliminary X-ray analysis of the subclass B3 metallo- $\beta$ -lactamase SMB-1 that confers carbapenem resistance. <b>2012</b> , 68, 343-6	3
1726	Cloning, purification, crystallization and preliminary X-ray analysis of the <i>Burkholderia pseudomallei</i> L1 ribosomal protein. <b>2012</b> , 68, 347-50	
1725	Crystallization and crystallographic analysis of the ligand-binding domain of the <i>Pseudomonas putida</i> chemoreceptor McpS in complex with malate and succinate. <b>2012</b> , 68, 428-31	1
1724	Overproduction, purification and crystallization of PfTic22, a component of the import apparatus from the apicoplast of <i>Plasmodium falciparum</i> . <b>2012</b> , 68, 351-4	2
1723	Crystallization and preliminary crystallographic characterization of the N-terminal Kunitz domain of boophilin. <b>2012</b> , 68, 436-9	3
1722	Crystallization of a novel metal-containing cupin from <i>Acidobacterium</i> sp. and preliminary diffraction data analysis. <b>2012</b> , 68, 451-4	3
1721	Structure of MurA (UDP-N-acetylglucosamine enolpyruvyl transferase) from <i>Vibrio fischeri</i> in complex with substrate UDP-N-acetylglucosamine and the drug fosfomycin. <b>2012</b> , 68, 382-5	14

1720	Crystallization and preliminary X-ray diffraction analysis of human endoplasmic reticulum aminopeptidase 2. <b>2012</b> , 68, 468-71	6
1719	Purification, crystallization and preliminary X-ray analysis of the aminoglycoside-6'-acetyltransferase AAC(6')-Im. <b>2012</b> , 68, 472-5	1
1718	Crystallization and preliminary X-ray analysis of stationary phase survival protein E (SurE) from <i>Xylella fastidiosa</i> in two crystal forms. <b>2012</b> , 68, 464-7	1
1717	Structures of the pleckstrin homology domain of <i>Saccharomyces cerevisiae</i> Avo1 and its human orthologue Sin1, an essential subunit of TOR complex 2. <b>2012</b> , 68, 386-92	22
1716	Detection and analysis of unusual features in the structural model and structure-factor data of a birch pollen allergen. <b>2012</b> , 68, 366-76	15
1715	In praise of impurity: 30S ribosomal S15 protein-assisted crystallization of turnip yellow mosaic virus proteinase. <b>2012</b> , 68, 486-90	5
1714	Structural analysis of <i>Pneumocystis carinii</i> dihydrofolate reductase complexed with NADPH and 2,4-diamino-6-[2-(5-carboxypent-1-yn-1-yl)-5-methoxybenzyl]-5-methylpyrido[2,3-d]pyrimidine. <b>2012</b> , 68, 418-23	1
1713	Structure of the tetradecanucleotide d(CCCCGGTACCGGG)2 as an A-DNA duplex. <b>2012</b> , 68, 393-9	10
1712	Structure of the His269Arg mutant of the rat aldose reductase-like protein AKR1B14 complexed with NADPH. <b>2012</b> , 68, 400-3	1
1711	Initial crystallographic studies of a small heat-shock protein from <i>Xylella fastidiosa</i> . <b>2012</b> , 68, 535-9	2
1710	Purification, crystallization and preliminary X-ray analysis of OsAREB8 from rice, a member of the AREB/ABF family of bZIP transcription factors, in complex with its cognate DNA. <b>2012</b> , 68, 491-4	3
1709	Structure of <i>Escherichia coli</i> aspartate decarboxylase Asn72Ala: probing the role of Asn72 in pyruvoyl cofactor formation. <b>2012</b> , 68, 414-7	4
1708	On-column ligand exchange for structure-based drug design: a case study with human 11 $\beta$ -hydroxysteroid dehydrogenase type 1. <b>2012</b> , 68, 601-5	
1707	Purification, crystallization and preliminary X-ray crystallographic analysis of 3-ketosteroid $\Delta^1$ -dehydrogenase from <i>Rhodococcus erythropolis</i> SQ1. <b>2012</b> , 68, 551-6	12
1706	Structure of the catalytic chain of <i>Methanococcus jannaschii</i> aspartate transcarbamoylase in a hexagonal crystal form: insights into the path of carbamoyl phosphate to the active site of the enzyme. <b>2012</b> , 68, 527-34	1
1705	New crystal structure of the proteasome-dedicated chaperone Rpn14 at 1.6 Å resolution. <b>2012</b> , 68, 517-21	1
1704	The structure of an orthorhombic crystal form of a 'forced reduced' thiol peroxidase reveals lattice formation aided by the presence of the affinity tag. <b>2012</b> , 68, 522-6	2
1703	Crystallization and preliminary characterization of chloromuconolactone dehalogenase from <i>Rhodococcus opacus</i> 1CP. <b>2012</b> , 68, 591-5	2

1702	Crystallization and preliminary X-ray diffraction analysis of the SOD-TAT fusion protein. <b>2012</b> , 68, 543-6	3
1701	Crystallization and preliminary X-ray crystallographic analysis of hydroquinone dioxygenase from <i>Sphingomonas</i> sp. TTNP3. <b>2012</b> , 68, 588-90	3
1700	The precursor form of <i>Hansenula polymorpha</i> copper amine oxidase 1 in complex with CuI and Coll. <b>2012</b> , 68, 501-10	4
1699	Use of differential scanning fluorimetry to optimize the purification and crystallization of PLP-dependent enzymes. <b>2012</b> , 68, 596-600	19
1698	Crystallization and preliminary crystallographic analysis of D-aspartate oxidase from porcine kidney. <b>2012</b> , 68, 644-6	3
1697	Structure of the GDP-bound G domain of the RGK protein Rem2. <b>2012</b> , 68, 626-31	9
1696	Crystallization and preliminary X-ray analysis of the haloalkane dehalogenase DatA from <i>Agrobacterium tumefaciens</i> C58. <b>2012</b> , 68, 652-4	2
1695	Purification, crystallization and preliminary X-ray crystallographic analysis of the ATPase domain of human TAP in nucleotide-free and ADP-, vanadate- and azide-complexed forms. <b>2012</b> , 68, 655-8	
1694	Crystallization and preliminary crystallographic studies of both components of the staphylococcal LukE-LukD leukotoxin. <b>2012</b> , 68, 663-7	3
1693	The ParE2-PaaA2 toxin-antitoxin complex from <i>Escherichia coli</i> O157 forms a heterododecamer in solution and in the crystal. <b>2012</b> , 68, 724-9	6
1692	Structure of human ADAM-8 catalytic domain complexed with batimastat. <b>2012</b> , 68, 616-21	7
1691	Expression, purification, crystallization and preliminary X-ray analysis of <i>Plasmodium falciparum</i> GTP:AMP phosphotransferase. <b>2012</b> , 68, 671-4	
1690	Crystallization and preliminary X-ray crystallographic analysis of bacterial tRNA(Sec) in complex with seryl-tRNA synthetase. <b>2012</b> , 68, 678-82	2
1689	Crystallization and preliminary X-ray analysis of the C-terminal domain of CCM2, part of a novel adaptor protein involved in cerebral cavernous malformations. <b>2012</b> , 68, 683-6	3
1688	A model for 3-methyladenine recognition by 3-methyladenine DNA glycosylase I (TAG) from <i>Staphylococcus aureus</i> . <b>2012</b> , 68, 610-5	3
1687	Cloning, purification, crystallization and preliminary X-ray studies of human $\beta$ -microglobulin. <b>2012</b> , 68, 692-4	1
1686	Overexpression, purification, crystallization and preliminary X-ray analysis of putative molybdenum cofactor biosynthesis protein C (MoaC2) from <i>Mycobacterium tuberculosis</i> H37Rv. <b>2012</b> , 68, 687-91	5
1685	Crystallization and preliminary crystallographic studies of CCM3 in complex with the C-terminal domain of MST4. <b>2012</b> , 68, 760-3	4

1684	Crystallization and preliminary X-ray analysis of the reductase component of p-hydroxyphenylacetate 3-hydroxylase from <i>Acinetobacter baumannii</i> . <b>2012</b> , 68, 720-3	2
1683	Crystallization of the novel S-adenosyl-L-methionine-dependent C-methyltransferase CouO from <i>Streptomyces rishiriensis</i> and preliminary diffraction data analysis. <b>2012</b> , 68, 698-700	1
1682	Expression, purification, crystallization and preliminary X-ray diffraction analysis of the apo form of InsP5 2-K from <i>Arabidopsis thaliana</i> . <b>2012</b> , 68, 701-4	1
1681	Crystallization and preliminary X-ray analysis of a novel halotolerant feruloyl esterase identified from a soil metagenomic library. <b>2012</b> , 68, 767-70	2
1680	Structure of a short-chain dehydrogenase/reductase from <i>Bacillus anthracis</i> . <b>2012</b> , 68, 632-7	1
1679	Cloning, purification, crystallization and preliminary X-ray crystallographic analysis of a cyclophilin A-like protein from <i>Piriformospora indica</i> . <b>2012</b> , 68, 709-12	6
1678	Cloning, purification, crystallization and preliminary X-ray diffraction crystallographic study of acyl-protein thioesterase 1 from <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 68, 775-7	
1677	Crystallization and preliminary X-ray diffraction analysis of the high molecular weight ketoacyl reductase FabG4 complexed with NADH. <b>2012</b> , 68, 786-9	4
1676	Purification, crystallization and preliminary crystallographic analysis of the adhesion domain of Epf from <i>Streptococcus pyogenes</i> . <b>2012</b> , 68, 793-7	2
1675	Crystallization and preliminary X-ray crystallographic analysis of an ice-binding protein (FfIBP) from <i>Flavobacterium frigidis</i> PS1. <b>2012</b> , 68, 806-9	23
1674	Purification and crystallization of yeast Ent1 ENTH domain. <b>2012</b> , 68, 820-3	3
1673	Crystallization and preliminary X-ray analysis of the C-terminal domain of $\beta$ COP, a medium-sized subunit of the COPI complex involved in membrane trafficking. <b>2012</b> , 68, 829-31	
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1671	Two crystal forms of a helix-rich fatty acid- and retinol-binding protein, Na-FAR-1, from the parasitic nematode <i>Necator americanus</i> . <b>2012</b> , 68, 835-8	5
1670	Expression, purification, crystallization and preliminary X-ray diffraction analysis of Deg5 from <i>Arabidopsis thaliana</i> . <b>2012</b> , 68, 839-41	1
1669	Folding of an all-helical Greek-key protein monitored by quenched-flow hydrogen-deuterium exchange and NMR spectroscopy. <b>2012</b> , 41, 41-51	3
1668	Synergistic effects of mutations in cytochrome P450cam designed to mimic CYP101D1. <b>2013</b> , 52, 5396-402	16
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1660	Structural and thermodynamic insights into the recognition of native proteins by anti-peptide antibodies. <b>2013</b> , 425, 2027-2038	5
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1653	Crystal structure of shrimp arginine kinase in binary complex with arginine-a molecular view of the phosphagen precursor binding to the enzyme. <b>2013</b> , 45, 511-8	18
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1634	Structural insights into the role of Bacillus subtilis YwfH (BacG) in tetrahydrotyrosine synthesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 324-32	7
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1630	Structure of an atypical periplasmic adaptor from a multidrug efflux pump of the spirochete <i>Borrelia burgdorferi</i> . <b>2013</b> , 587, 2984-8	15
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1562	Diaryl- and triaryl-pyrrole derivatives: inhibitors of the MDM2-p53 and MDMX-p53 protein-protein interactions $\square$ Electronic supplementary information (ESI) available: Experimental details for compound synthesis, analytical data for all compounds and intermediates. Details for the biological evaluation. Further details for the modeling. Table of combustion analysis data. See DOI:	20
1561	Structural basis of intersubunit recognition in elongin BC-cullin 5-SOCS box ubiquitin-protein ligase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1587-97	26
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1516	The role of T56 in controlling the flexibility of the distal histidine in dehaloperoxidase-hemoglobin from <i>Amphitrite ornata</i> . <b>2013</b> , 1834, 2020-9	7
1515	Structure of a truncation mutant of the nuclear export factor CRM1 provides insights into the auto-inhibitory role of its C-terminal helix. <b>2013</b> , 21, 1338-49	10
1514	Structural analysis of an epsilon-class glutathione transferase from housefly, <i>Musca domestica</i> . <b>2013</b> , 430, 1206-11	9
1513	The structure of the RLIP76 RhoGAP-Ral binding domain dyad: fixed position of the domains leads to dual engagement of small G proteins at the membrane. <b>2013</b> , 21, 2131-42	9
1512	Conformational plasticity at the IgE-binding site of the B-cell receptor CD23. <b>2013</b> , 56, 693-7	13
1511	Crystal structure of Src-like adaptor protein 2 reveals close association of SH3 and SH2 domains through $\beta$ -sheet formation. <b>2013</b> , 25, 2702-8	10
1510	The crystal structure of a novel phosphopantothenate synthetase from the hyperthermophilic archaea, <i>Thermococcus onnurineus</i> NA1. <b>2013</b> , 439, 533-8	4
1509	Three sites and you are out: ternary synergistic allostery controls aromatic amino acid biosynthesis in <i>Mycobacterium tuberculosis</i> . <b>2013</b> , 425, 1582-92	30
1508	Structure of internalin InlK from the human pathogen <i>Listeria monocytogenes</i> . <b>2013</b> , 425, 4520-9	16
1507	Crystal structure of wild-type and mutant human Ap4A hydrolase. <b>2013</b> , 432, 16-21	8
1506	Structural determination of importin alpha in complex with beak and feather disease virus capsid nuclear localization signal. <b>2013</b> , 438, 680-5	9
1505	Crystallographic snapshots along the reaction pathway of nucleoside triphosphate diphosphohydrolases. <b>2013</b> , 21, 1460-75	39

1504	X-ray structure of the V301L aldol-keto reductase 1B10 complexed with NADP(+) and the potent aldose reductase inhibitor fidarestat: implications for inhibitor binding and selectivity. <b>2013</b> , 202, 178-85	11
1503	Crystal structures of the ternary complex of APH(4)-Ia/Hph with hygromycin B and an ATP analog using a thermostable mutant. <b>2013</b> , 183, 76-85	11
1502	BRMS151-98 and BRMS151-84 are crystal oligomeric coiled coils with different oligomerization states, which behave as disordered protein fragments in solution. <b>2013</b> , 425, 2147-63	5
1501	Crystal structure of phospholipase A1 from <i>Streptomyces albidoflavus</i> NA297. <b>2013</b> , 182, 192-6	23
1500	Structure and T cell inhibition properties of B7 family member, B7-H3. <b>2013</b> , 21, 707-17	67
1499	A Trp199Glu MauG variant reveals a role for Trp199 interactions with pre-methylamine dehydrogenase during tryptophan tryptophylquinone biosynthesis. <b>2013</b> , 587, 1736-41	2
1498	Redox state-dependent changes in the crystal structure of [NiFeSe] hydrogenase from <i>Desulfovibrio vulgaris</i> Hildenborough. <b>2013</b> , 38, 8664-8682	31
1497	A novel crystal form of pyrrolysyl-tRNA synthetase reveals the pre- and post-aminoacyl-tRNA synthesis conformational states of the adenylate and aminoacyl moieties and an asparagine residue in the catalytic site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 5-15	13
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1494	The structure of the deacetylase domain of <i>Escherichia coli</i> PgaB, an enzyme required for biofilm formation: a circularly permuted member of the carbohydrate esterase 4 family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 44-51	12
1493	Structures of aminophenol dioxygenase in complex with intermediate, product and inhibitor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 32-43	15
1492	The structure of a novel glucuronoyl esterase from <i>Myceliophthora thermophila</i> gives new insights into its role as a potential biocatalyst. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 63-73	29
1491	Structure and ligand-binding properties of the biogenic amine-binding protein from the saliva of a blood-feeding insect vector of <i>Trypanosoma cruzi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 105-13	15
1490	Placement of molecules in (not out of) the cell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2-4	4
1489	Adenosine kinase from <i>Schistosoma mansoni</i> : structural basis for the differential incorporation of nucleoside analogues. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 126-36	12
1488	To scavenge or not to scavenge, that is STILL the question. <b>2013</b> , 20, 23-36	31
1487	The AEROPATH project targeting <i>Pseudomonas aeruginosa</i> : crystallographic studies for assessment of potential targets in early-stage drug discovery. <b>2013</b> , 69, 25-34	28

1486	Crystallization and preliminary X-ray crystallographic analysis of UDP-glucuronic acid:flavonol-3-O-glucuronosyltransferase (VvGT5) from the grapevine <i>Vitis vinifera</i> . <b>2013</b> , 69, 65-8	2
1485	Structure of <i>Pisum sativum</i> Rubisco with bound ribulose 1,5-bisphosphate. <b>2013</b> , 69, 10-4	4
1484	Preliminary crystallographic analysis of a polyadenylate synthase from Megavirus. <b>2013</b> , 69, 53-6	1
1483	Mechanism-based covalent neuraminidase inhibitors with broad-spectrum influenza antiviral activity. <b>2013</b> , 340, 71-5	154
1482	Understanding how noncatalytic carbohydrate binding modules can display specificity for xyloglucan. <b>2013</b> , 288, 4799-809	29
1481	Structure, dynamics, evolution, and function of a major scaffold component in the nuclear pore complex. <b>2013</b> , 21, 560-71	48
1480	The architecture of EssB, an integral membrane component of the type VII secretion system. <b>2013</b> , 21, 595-603	12
1479	Genetically encoded calcium indicators for multi-color neural activity imaging and combination with optogenetics. <b>2013</b> , 6, 2	487
1478	Allosteric inhibition of hypoxia inducible factor-2 with small molecules. <b>2013</b> , 9, 271-6	196
1477	Molecular architecture and functional analysis of NetB, a pore-forming toxin from <i>Clostridium perfringens</i> . <b>2013</b> , 288, 3512-22	71
1476	Structure of LdtMt2, an L,D-transpeptidase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 432-41	26
1475	Re-engineering protein interfaces yields copper-inducible ferritin cage assembly. <b>2013</b> , 9, 169-76	139
1474	Expression, purification, crystallization and preliminary X-ray diffraction analysis of carbonyl reductase from <i>Candida parapsilosis</i> ATCC 7330. <b>2013</b> , 69, 313-5	6
1473	Structural insight into potent broad-spectrum inhibition with reversible recyclization mechanism: avibactam in complex with CTX-M-15 and <i>Pseudomonas aeruginosa</i> AmpC $\beta$ -lactamases. <b>2013</b> , 57, 2496-505	154
1472	Crystal structure of an RNA-bound 11-subunit eukaryotic exosome complex. <b>2013</b> , 495, 70-5	175
1471	Accelerated maturation of Tk-subtilisin by a Leu->Pro mutation at the C-terminus of the propeptide, which reduces the binding of the propeptide to Tk-subtilisin. <b>2013</b> , 280, 994-1006	12
1470	Studies on an (S)-2-amino-3-(3-hydroxy-5-methyl-4-isoxazolyl)propionic acid (AMPA) receptor antagonist IKM-159: asymmetric synthesis, neuroactivity, and structural characterization. <b>2013</b> , 56, 2283-93	20
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1468	Adaptation of aminoacyl-tRNA synthetase catalytic core to carrier protein aminoacylation. <b>2013</b> , 21, 614-26	9
1467	Crystallization and preliminary X-ray diffraction analysis of three recombinant mutants of Vaccinia virus uracil DNA glycosylase. <b>2013</b> , 69, 295-301	5
1466	Structure of the Trypanosoma cruzi protein tyrosine phosphatase TcPTP1, a potential therapeutic target for Chagas' disease. <b>2013</b> , 187, 1-8	7
1465	Discovery of thieno[3,2-d]pyrimidine-6-carboxamides as potent inhibitors of SIRT1, SIRT2, and SIRT3. <b>2013</b> , 56, 3666-79	153
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1463	AutoDrug: fully automated macromolecular crystallography workflows for fragment-based drug discovery. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 796-803	16
1462	Spirocyclic β-site amyloid precursor protein cleaving enzyme 1 (BACE1) inhibitors: from hit to lowering of cerebrospinal fluid (CSF) amyloid β in a higher species. <b>2013</b> , 56, 3379-403	43
1461	Structure of the cytoplasmic domain of TcpE, the inner membrane core protein required for assembly of the Vibrio cholerae toxin-coregulated pilus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 513-9	8
1460	Clostridium perfringens epsilon toxin H149A mutant as a platform for receptor binding studies. <b>2013</b> , 22, 650-9	31
1459	Structural and functional characterization of a noncanonical nucleoside triphosphate pyrophosphatase from Thermotoga maritima. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 184-93	3
1458	Structure of a complete four-domain chitinase from Moritella marina, a marine psychrophilic bacterium. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 821-9	32
1457	The role of structural bioinformatics resources in the era of integrative structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 710-21	14
1456	Crystal structure of the O <sub>2</sub> -tolerant membrane-bound hydrogenase 1 from Escherichia coli in complex with its cognate cytochrome b. <b>2013</b> , 21, 184-190	79
1455	Chemoenzymatic synthesis of new 2,4-syn-functionalized (S)-glutamate analogues and structure-activity relationship studies at ionotropic glutamate receptors and excitatory amino acid transporters. <b>2013</b> , 56, 1614-28	36
1454	Crystal structure of a eukaryotic phosphate transporter. <b>2013</b> , 496, 533-6	170
1453	Nucleotide binding and conformational switching in the hexameric ring of a AAA <sup>+</sup> machine. <b>2013</b> , 153, 628-39	91
1452	The 1.6 Å resolution structure of a FRET-optimized Cerulean fluorescent protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 767-73	6
1451	The mechanism of E. coli RNA polymerase regulation by ppGpp is suggested by the structure of their complex. <b>2013</b> , 50, 430-6	133

1450	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6?-FCR3 of the Plasmodium falciparum VAR2CSA protein. <b>2013</b> , 69, 270-4	2
1449	Design, synthesis, and molecular modeling of novel pyrido[2,3-d]pyrimidine analogues as antifolates; application of Buchwald-Hartwig aminations of heterocycles. <b>2013</b> , 56, 4422-41	33
1448	Species-specific detection of the antiviral small-molecule compound CMA by STING. <b>2013</b> , 32, 1440-50	123
1447	Rational HIV immunogen design to target specific germline B cell receptors. <b>2013</b> , 340, 711-6	519
1446	Crystallization and preliminary X-ray crystallographic analysis of the functional form of BinB binary toxin from Bacillus sphaericus. <b>2013</b> , 69, 170-3	3
1445	Targeted inhibition of mutant IDH2 in leukemia cells induces cellular differentiation. <b>2013</b> , 340, 622-6	619
1444	A bilirubin-inducible fluorescent protein from eel muscle. <b>2013</b> , 153, 1602-11	187
1443	Crystal structures of the viral protease Npro imply distinct roles for the catalytic water in catalysis. <b>2013</b> , 21, 929-38	18
1442	Crystallization and preliminary crystallographic studies of AAL-2, a novel lectin from Agrocybe aegerita that binds nonreducing terminal N-acetylglucosamine. <b>2013</b> , 69, 650-2	4
1441	Ligand promiscuity within the internal cavity of Epiphyas postvittana Takeout 1 protein. <b>2013</b> , 182, 259-63	10
1440	Dissecting the structural determinants for the difference in mechanical stability of silk and amyloid beta-sheet stacks. <b>2013</b> , 15, 8765-71	20
1439	Peptide crystal simulations reveal hidden dynamics. <b>2013</b> , 135, 7938-48	28
1438	Yellow fluorescent protein phiYFPv (Phialidium): structure and structure-based mutagenesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1005-12	15
1437	The structure of cardiac troponin C regulatory domain with bound Cd <sup>2+</sup> reveals a closed conformation and unique ion coordination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 722-34	8
1436	Scaffold-focused virtual screening: prospective application to the discovery of TTK inhibitors. <b>2013</b> , 53, 1100-12	26
1435	Discovery of (R)-2-amino-6-borono-2-(2-(piperidin-1-yl)ethyl)hexanoic acid and congeners as highly potent inhibitors of human arginases I and II for treatment of myocardial reperfusion injury. <b>2013</b> , 56, 2568-80	56
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1433	Identification of a cation transport pathway in Neisseria meningitidis PorB. <b>2013</b> , 81, 830-40	11

1432	Fragment-based ligand design of novel potent inhibitors of tankyrases. <b>2013</b> , 56, 4497-508	55
1431	The differences in binding 12-carbon aliphatic ligands by bovine $\beta$ -lactoglobulin isoform A and B studied by isothermal titration calorimetry and X-ray crystallography. <b>2013</b> , 26, 357-67	27
1430	Structure of a human IgA1 Fab fragment at 1.55 Å resolution: potential effect of the constant domains on antigen-affinity modulation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 388-97	20
1429	Structure and functional studies of the ribonuclease binase Glu43Ala/Phe81Ala mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 991-6	10
1428	Structure, recombinant expression and mutagenesis studies of the catalase with oxidase activity from <i>Scytalidium thermophilum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 398-408	7
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1426	Crystal structure, SAXS and kinetic mechanism of hyperthermophilic ADP-dependent glucokinase from <i>Thermococcus litoralis</i> reveal a conserved mechanism for catalysis. <b>2013</b> , 8, e66687	24
1425	The structure of the KtrAB potassium transporter. <b>2013</b> , 496, 323-8	81
1424	Reversal of the substrate specificity of CMP N-glycosidase to dCMP. <b>2013</b> , 52, 4037-47	13
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1422	Structural consequences of cutting a binding loop: two circularly permuted variants of streptavidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 968-77	5
1421	Simulation of modulated protein crystal structure and diffraction data in a supercell and in superspace. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1062-72	7
1420	The use of VLD (vive la difference) in the molecular-replacement approach: a pipeline. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1038-44	8
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1418	Structure of a double-stranded DNA (6-4) photoproduct in complex with the 64M-5 antibody Fab. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 504-12	8
1417	Crystallization and preliminary structural analysis of dibenzothiophene monooxygenase (DszC) from <i>Rhodococcus erythropolis</i> . <b>2013</b> , 69, 597-601	11
1416	Protein recognition by short peptide reversible inhibitors of the chromatin-modifying LSD1/CoREST lysine demethylase. <b>2013</b> , 8, 1677-82	50
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1414	Assembly of a stack of ligands in the binding site of an acetylcholine-binding protein. <b>2013</b> , 4, 1875	43
1413	Trans and cis effects of axial fluoroalkyl ligands in vitamin B12 analogues: relationship between alkyl- and fluoroalkyl-cobalamins. <b>2013</b> , 52, 13392-401	6
1412	The lid domain of the MCP hydrolase DxnB2 contributes to the reactivity toward recalcitrant PCB metabolites. <b>2013</b> , 52, 5685-5695	12
1411	Cyclin-dependent kinase inhibitor dinaciclib interacts with the acetyl-lysine recognition site of bromodomains. <b>2013</b> , 8, 2360-5	113
1410	CSAR benchmark exercise 2011-2012: evaluation of results from docking and relative ranking of blinded congeneric series. <b>2013</b> , 53, 1853-70	107
1409	Structural studies of hydroxylamine oxidoreductase reveal a unique heme cofactor and a previously unidentified interaction partner. <b>2013</b> , 52, 6211-8	48
1408	Metal binding properties of Escherichia coli YjiA, a member of the metal homeostasis-associated COG0523 family of GTPases. <b>2013</b> , 52, 1788-1801	37
1407	Expression, crystallization and preliminary X-ray analysis of rice L-galactose dehydrogenase. <b>2013</b> , 69, 809-11	2
1406	"Snapshots" of ispinesib-induced conformational changes in the mitotic kinesin Eg5. <b>2013</b> , 288, 18588-98	21
1405	A nanobody binding to non-amyloidogenic regions of the protein human lysozyme enhances partial unfolding but inhibits amyloid fibril formation. <b>2013</b> , 117, 13245-13258	33
1404	Structure and assembly of the NOT module of the human CCR4-NOT complex. <b>2013</b> , 20, 1289-97	74
1403	Structure of isochorismate synthase DhbC from Bacillus anthracis. <b>2013</b> , 69, 956-61	
1402	Structural insights into incorporation of norbornene amino acids for click modification of proteins. <b>2013</b> , 14, 2114-8	30
1401	Autoinhibition and phosphorylation-induced activation of phospholipase C- $\beta$ isozymes. <b>2013</b> , 52, 4810-9	22
1400	Heterochromatin protein Sir3 induces contacts between the amino terminus of histone H4 and nucleosomal DNA. <b>2013</b> , 110, 8495-500	46
1399	Mapping the conformational space accessible to BACE2 using surface mutants and cocrystals with Fab fragments, Fynomers and Xaperones. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1124-37	26
1398	A highly selective dual insulin receptor (IR)/insulin-like growth factor 1 receptor (IGF-1R) inhibitor derived from an extracellular signal-regulated kinase (ERK) inhibitor. <b>2013</b> , 288, 28068-77	10
1397	Subangstrom resolution X-ray structure details aquaporin-water interactions. <b>2013</b> , 340, 1346-1349	147

1396	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. <b>2013</b> , 46, 804-810	77
1395	The structure of Rv3717 reveals a novel amidase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2543-54	22
1394	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. <b>2013</b> , 56, 794-803	34
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1392	Structure of parkin reveals mechanisms for ubiquitin ligase activation. <b>2013</b> , 340, 1451-5	348
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1390	Specificity of Processing $\alpha$ -glucosidase I is guided by the substrate conformation: crystallographic and in silico studies. <b>2013</b> , 288, 13563-74	47
1389	Cloning, overexpression, purification and crystallization of the CRN12 coiled-coil domain from <i>Leishmania donovani</i> . <b>2013</b> , 69, 535-9	4
1388	Coiled-coil dimerization of the LOV2 domain of the blue-light photoreceptor phototropin 1 from <i>Arabidopsis thaliana</i> . <b>2013</b> , 69, 1316-21	29
1387	Structure and enzymatic mechanism of a moonlighting dUTPase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2298-308	20
1386	Molecular insight into substrate recognition and catalysis of Baeyer-Villiger monooxygenase MtmOIV, the key frame-modifying enzyme in the biosynthesis of anticancer agent mithramycin. <b>2013</b> , 8, 2466-77	28
1385	Secreted proteases control autolysin-mediated biofilm growth of <i>Staphylococcus aureus</i> . <b>2013</b> , 288, 29440-52	64
1384	Crystal structures and functional characterization of wild-type CYP101D1 and its active site mutants. <b>2013</b> , 52, 8898-906	16
1383	Plant multifunctional nuclease TBN1 with unexpected phospholipase activity: structural study and reaction-mechanism analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 213-26	11
1382	The copper active site of CBM33 polysaccharide oxygenases. <b>2013</b> , 135, 6069-77	143
1381	Structure of the inositol-1-phosphate cytidyltransferase from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1808-17	1
1380	P450cin active site water: implications for substrate binding and solvent accessibility. <b>2013</b> , 52, 5039-50	14
1379	Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant <i>Staphylococcus aureus</i> . <b>2013</b> , 14, 97-108	5

1378	Three-dimensional structure of the Rhodobacter sphaeroides RC-LH1-PufX complex: dimerization and quinone channels promoted by PufX. <b>2013</b> , 52, 7575-85	109
1377	Structure of a dinuclear iron cluster-containing $\alpha$ -hydroxylase active in antibiotic biosynthesis. <b>2013</b> , 52, 6662-71	32
1376	A substrate-assisted mechanism of nucleophile activation in a Ser-His-Asp containing C-C bond hydrolase. <b>2013</b> , 52, 7428-38	12
1375	Structural basis for a hand-like site in the calcium sensor CatchER with fast kinetics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2309-19	5
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1372	Principles of sustained enzymatic hydrogen oxidation in the presence of oxygen--the crucial influence of high potential Fe-S clusters in the electron relay of [NiFe]-hydrogenases. <b>2013</b> , 135, 2694-707	82
1371	Expression, crystallization and preliminary X-ray crystallographic analysis of cellobiose 2-epimerase from <i>Dictyoglomus turgidum</i> DSM 6724. <b>2013</b> , 69, 1163-6	2
1370	Structural and biochemical characterization of compounds inhibiting <i>Mycobacterium tuberculosis</i> pantothenate kinase. <b>2013</b> , 288, 18260-70	23
1369	The crystal structures of the tri-functional <i>Chloroflexus aurantiacus</i> and bi-functional <i>Rhodobacter sphaeroides</i> malyl-CoA lyases and comparison with CitE-like superfamily enzymes and malate synthases. <b>2013</b> , 13, 28	10
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1363	Structural basis of protein phosphatase 2A stable latency. <b>2013</b> , 4, 1699	44
1362	Conformational stability of fibrillar amyloid-beta oligomers via protofilament pair formation - a systematic computational study. <b>2013</b> , 8, e70521	59
1361	On the catalytic mechanism of dimeric dUTPases. <b>2013</b> , 456, 81-8	22

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1359	Crystal structure of the FAD-containing ferredoxin-NADP <sup>+</sup> reductase from the plant pathogen <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <b>2013</b> , 2013, 906572	4
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1354	Atomic resolution description of the interaction between the nucleoprotein and phosphoprotein of Hendra virus. <b>2013</b> , 9, e1003631	56
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1340	Structural basis of subtilase cytotoxin SubAB assembly. <b>2013</b> , 288, 27505-27516	15
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1331	Crystal structures of B-DNA dodecamer containing the epigenetic modifications 5-hydroxymethylcytosine or 5-methylcytosine. <b>2013</b> , 41, 9891-900	55
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1268	Visual automated macromolecular model building. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 635-41	49
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1217	Improvements in the order, isotropy and electron density of glypican-1 crystals by controlled dehydration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2524-33	10

1216	Structure of human apurinic/aprimidinic endonuclease 1 with the essential Mg <sup>2+</sup> cofactor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2555-62	31
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1213	Crystallographic structure determination of B10 mutants of <i>Vitreoscilla</i> hemoglobin: role of Tyr29 (B10) in the structure of the ligand-binding site. <b>2013</b> , 69, 215-22	4
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1144	Crystallization and preliminary X-ray crystallographic analysis of the curli transporter CsgG. <b>2013</b> , 69, 1349-53	6
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1118	Crystallization and X-ray crystallographic analysis of the cap-binding domain of influenza A virus H1N1 polymerase subunit PB2. <b>2013</b> , 69, 280-3	3
1117	Overexpression, crystallization and preliminary X-ray crystallographic analysis of hypothetical protein SAV0479 from <i>Staphylococcus aureus</i> Mu50. <b>2013</b> , 69, 405-7	
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1085	Crystal structure and enzymatic activity of an ADAMTS-13 mutant with the East Asian-specific P475S polymorphism. <b>2013</b> , 11, 1399-406	16
1084	Structure, biochemical characterization and analysis of the pleomorphism of carboxylesterase Cest-2923 from <i>Lactobacillus plantarum</i> WCFS1. <b>2013</b> , 280, 6658-71	29
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1076	Role of Ca <sup>2+</sup> in folding the tandem $\beta$ -sandwich extender domains of a bacterial ice-binding adhesin. <b>2013</b> , 280, 5919-32	17
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1061	Crystal structures of the DNA-binding domain tetramer of the p53 tumor suppressor family member p73 bound to different full-site response elements. <b>2013</b> , 288, 4744-54	14
1060	The structure of a <i>Streptomyces avermitilis</i> $\beta$ -rhamnosidase reveals a novel carbohydrate-binding module CBM67 within the six-domain arrangement. <b>2013</b> , 288, 12376-85	51
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983	Molecular recognition of the neurotransmitter acetylcholine by an acetylcholine binding protein reveals determinants of binding to nicotinic acetylcholine receptors. <b>2014</b> , 9, e91232	30

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981	Esterase LpEst1 from <i>Lactobacillus plantarum</i> : a novel and atypical member of the $\beta$ hydrolase superfamily of enzymes. <b>2014</b> , 9, e92257	17
980	Structural, kinetic and proteomic characterization of acetyl phosphate-dependent bacterial protein acetylation. <b>2014</b> , 9, e94816	178
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941	Zinc finger oxidation of Fpg/Nei DNA glycosylases by 2-thioxanthine: biochemical and X-ray structural characterization. <b>2014</b> , 42, 10748-61	7
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930	Crystal structure of the dithiol oxidase DsbA enzyme from <i>proteus mirabilis</i> bound non-covalently to an active site peptide ligand. <b>2014</b> , 289, 19810-22	15
929	A PDB-wide, evolution-based assessment of protein-protein interfaces. <b>2014</b> , 14, 22	34

928	Crystallization and preliminary X-ray crystallographic analysis of latent isoform PPO4 mushroom ( <i>Agaricus bisporus</i> ) tyrosinase. <b>2014</b> , 70, 263-6	54
927	Structural characterization of the putative ABC-type 2 transporter from <i>Thermotoga maritima</i> MSB8. <b>2014</b> , 15, 215-22	1
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925	Impact of residues remote from the catalytic centre on enzyme catalysis of copper nitrite reductase. <b>2014</b> , 5, 4395	30
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920	Control of KirBac3.1 potassium channel gating at the interface between cytoplasmic domains. <b>2014</b> , 289, 143-51	17
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918	Biochemical and structural insights into microtubule perturbation by CopN from <i>Chlamydia pneumoniae</i> . <b>2014</b> , 289, 25199-210	17
917	Structure and mechanism of cysteine peptidase gingipain K (Kgp), a major virulence factor of <i>Porphyromonas gingivalis</i> in periodontitis. <b>2014</b> , 289, 32291-32302	52
916	Altered peptide ligands revisited: vaccine design through chemically modified HLA-A2-restricted T cell epitopes. <b>2014</b> , 193, 4803-13	29
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908	ATP-induced electron transfer by redox-selective partner recognition. <b>2014</b> , 5, 4626	15
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906	Identification of the docking site between a type III secretion system ATPase and a chaperone for effector cargo. <b>2014</b> , 289, 23734-44	26
905	Structure of the epimerization domain of tyrocidine synthetase A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 1442-52	35
904	Atomic resolution crystal structure of glutaredoxin 1 from Plasmodium falciparum and comparison with other glutaredoxins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 91-100	11
903	Crystallization and preliminary X-ray study of Vibrio cholerae uridine phosphorylase in complex with 6-methyluracil. <b>2014</b> , 70, 60-3	6
902	Restricted diversity of antigen binding residues of antibodies revealed by computational alanine scanning of 227 antibody-antigen complexes. <b>2014</b> , 426, 3729-3743	46
901	The 2.2 Å resolution structure of the catalase-peroxidase KatG from Synechococcus elongatus PCC7942. <b>2014</b> , 70, 288-93	8
900	Neutron structure of the cyclic glucose-bound xylose isomerase E186Q mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 414-20	14
899	Disarming Burkholderia pseudomallei: structural and functional characterization of a disulfide oxidoreductase (DsbA) required for virulence in vivo. <b>2014</b> , 20, 606-17	43
898	RNA mimicry by the fap7 adenylate kinase in ribosome biogenesis. <b>2014</b> , 12, e1001860	33
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468	Non-canonical <i>Staphylococcus aureus</i> pathogenicity island repression.	0
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466	High-resolution structure of a microtubule-like tube composed of FtsZ $\alpha$ homobody complexes.	0
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264	Structural basis of Qng1-mediated salvage of the micronutrient queuine from queuosine-5'-monophosphate as the biological substrate.	0
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