

CITATION REPORT

List of articles citing

Inference of macromolecular assemblies from crystalline state

DOI: 10.1016/j.jmb.2007.05.022

Journal of Molecular Biology, 2007, 372, 774-97.

Source: <https://exaly.com/paper-pdf/42057827/citation-report.pdf>

Version: 2024-04-27

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
2202	Crystal Structure of a Histone Deacetylase Homologue from <i>Pseudomonas aeruginosa</i> .		
2201	Structural Insights into the <i>Drosophila melanogaster</i> Retinol Dehydrogenase, a Member of the Short-Chain Dehydrogenase/Reductase Family.		
2200	Inter-Enzyme Allosteric Regulation of Chorismate Mutase in <i>Corynebacterium glutamicum</i> : Structural Basis of Feedback Activation by Trp.		
2199	Visualization of Bacterial Microcompartment Facet Assembly Using High-Speed Atomic Force Microscopy.		
2198	HheG, a Halohydrin Dehalogenase with Activity on Cyclic Epoxides.		
2197	Deactivation Pathway of Ras GTPase Underlies Conformational Substates as Targets for Drug Design.		
2196	Dynamic Structural Changes Accompany the Production of Dihydroxypropanesulfonate by Sulfolactaldehyde Reductase.		
2195	Synthetic Antibody Binding to a Preorganized RNA Domain of Hepatitis C Virus Internal Ribosome Entry Site Inhibits Translation.		
2194	Stabilization of Cyclin-Dependent Kinase 4 by Methionyl-tRNA Synthetase in p16INK4a-Negative Cancer.		
2193	Molecular Signatures of Fusion Proteins in Cancer.		
2192	Role of Coiled-Coil Registry Shifts in the Activation of Human Bicaudal D2 for Dynein Recruitment upon Cargo Binding.		
2191	Experimental and Computational Studies Delineate the Role of Asparagine 177 in Hydride Transfer for <i>E. coli</i> Thymidylate Synthase.		
2190	Structural Basis for Selectivity in Flavin-Dependent Monooxygenase-Catalyzed Oxidative Dearomatization.		
2189	Interdomain and Intermodule Organization in Epimerization Domain Containing Nonribosomal Peptide Synthetases.		
2188	Catalytic Cycle of Glycoside Hydrolase BglX from <i>Pseudomonas aeruginosa</i> and Its Implications for Biofilm Formation.		
2187	Xray Crystallographic Structure of Oligomers Formed by a Toxic Hairpin Derived from Synuclein: Trimers and Higher-Order Oligomers.		
2186	Binary Protein Crystals for the Assembly of Inorganic Nanoparticle Superlattices.		

2185	Balancing Specificity and Promiscuity in Enzyme Evolution: Multidimensional Activity Transitions in the Alkaline Phosphatase Superfamily.		
2184	Structural and Mechanistic Basis for Anaerobic Ergothioneine Biosynthesis.		
2183	An Alternative Active Site Architecture for O ₂ Activation in the Ergothioneine Biosynthetic EgtB from <i>Chloracidobacterium thermophilum</i> .		
2182	An Asymmetric Reductase That Intercepts Acyclic Imino Acids Produced in Situ by a Partner Oxidase.		
2181	Cooperative Assembly of Hsp70 Subdomain Clusters.		
2180	Predicting the Affinity of Peptides to Major Histocompatibility Complex Class II by Scoring Molecular Dynamics Simulations.		
2179	Structural Basis for DNA Gyrase Interaction with Coumermycin A1.		
2178	Protein databases on the internet. 2004 , Chapter 19, Unit 19.4		11
2177	Structure of PlcR: Insights into virulence regulation and evolution of quorum sensing in Gram-positive bacteria. 2007 , 104, 18490-5		119
2176	A structural overview of the vertebrate prion proteins. 2007 , 1, 185-97		29
2175	Structural basis for light-dependent signaling in the dimeric LOV domain of the photosensor YtvA. <i>Journal of Molecular Biology</i> , 2007 , 373, 112-26	6.5	191
2174	Crystal structures of the staphylococcal toxin SSL5 in complex with sialyl Lewis X reveal a conserved binding site that shares common features with viral and bacterial sialic acid binding proteins. <i>Journal of Molecular Biology</i> , 2007 , 374, 1298-308	6.5	57
2173	Preliminary X-ray crystallographic studies of a tetrameric phospholipase A2 formed by two isoforms of crotoxin B from <i>Crotalus durissus terrificus</i> venom. 2007 , 63, 1067-9		5
2172	Dimerization of inositol monophosphatase <i>Mycobacterium tuberculosis</i> SuhB is not constitutive, but induced by binding of the activator Mg ²⁺ . 2007 , 7, 55		13
2171	PiQSi: protein quaternary structure investigation. 2007 , 15, 1364-7		91
2170	Characterization of substrate binding and catalysis in the potential antibacterial target N-acetylglucosamine-1-phosphate uridylyltransferase (GlmU). 2007 , 16, 2657-66		33
2169	The leucine-rich repeat structure. 2008 , 65, 2307-33		325
2168	Relating Macromolecular Function and Association: The Structural Basis of Protein-DNA and RNA Recognition. 2008 , 1, 327-338		11

2167	The before and afters of molecular replacement. 2008 , 64, 17-24	10
2166	Structure of wild-type Plk-1 kinase domain in complex with a selective DARPIn. 2008 , 64, 339-53	30
2165	Structure of the C-terminal domain of the arginine repressor protein from <i>Mycobacterium tuberculosis</i> . 2008 , 64, 950-6	5
2164	Structure of HsaD, a steroid-degrading hydrolase, from <i>Mycobacterium tuberculosis</i> . 2008 , 64, 2-7	29
2163	Structures of an alanine racemase from <i>Bacillus anthracis</i> (BA0252) in the presence and absence of (R)-1-aminoethylphosphonic acid (L-Ala-P). 2008 , 64, 327-33	15
2162	Structure of <i>Staphylococcus aureus</i> 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase. 2008 , 64, 343-50	27
2161	Dimerization effect of sucrose octasulfate on rat FGF1. 2008 , 64, 448-52	4
2160	Structure of <i>Deinococcus radiodurans</i> tunicamycin-resistance protein (TmrD), a phosphotransferase. 2008 , 64, 479-86	5
2159	A covalent S-F heterodimer of leucotoxin reveals molecular plasticity of beta-barrel pore-forming toxins. 2008 , 71, 485-96	22
2158	Insights into the role of oligomeric state on the biological activities of crotoxin: crystal structure of a tetrameric phospholipase A2 formed by two isoforms of crotoxin B from <i>Crotalus durissus terrificus</i> venom. 2008 , 72, 883-91	46
2157	Crystal structure of an ADP-ribosylated protein with a cytidine deaminase-like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Å resolution. 2008 , 71, 1546-52	6
2156	Crystal structure of YagE, a putative DHDS-like protein from <i>Escherichia coli</i> K12. 2008 , 71, 2102-8	3
2155	Crystal structure of an alkaline serine protease from <i>Nesterenkonia</i> sp. defines a novel family of secreted bacterial proteases. 2008 , 73, 1072-5	3
2154	Identification of pharmacological chaperones for Gaucher disease and characterization of their effects on beta-glucocerebrosidase by hydrogen/deuterium exchange mass spectrometry. 2008 , 9, 2650-62	68
2153	Crystallographic structure and substrate-binding interactions of the molybdate-binding protein of the phytopathogen <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . 2008 , 1784, 393-9	20
2152	Crystal structure of <i>Mycobacterium tuberculosis</i> Rv0760c at 1.50 Å resolution, a structural homolog of Delta(5)-3-ketosteroid isomerase. 2008 , 1784, 1625-32	8
2151	Biochemical and structural insights of the early glycosylation steps in calicheamicin biosynthesis. 2008 , 15, 842-53	47
2150	The structure of an archaeal homodimeric ligase which has RNA circularization activity. 2008 , 17, 1336-45	24

2149	Structural evidence for substrate-induced synergism and half-sites reactivity in biotin carboxylase. 2008 , 17, 1706-18	57
2148	Crystal structure of LpxC from <i>Pseudomonas aeruginosa</i> complexed with the potent BB-78485 inhibitor. 2008 , 17, 450-7	39
2147	Crystallographic and biochemical studies revealing the structural basis for antizyme inhibitor function. 2008 , 17, 793-802	39
2146	High affinity interaction between a bivalve C-type lectin and a biantennary complex-type N-glycan revealed by crystallography and microcalorimetry. 2008 , 283, 30112-20	33
2145	Structure of Vps26B and mapping of its interaction with the retromer protein complex. 2008 , 9, 366-79	86
2144	Crystal structures of <i>Drosophila</i> mutant translin and characterization of translin variants reveal the structural plasticity of translin proteins. 2008 , 275, 4235-49	11
2143	Structural and functional studies on a mesophilic stationary phase survival protein (Sur E) from <i>Salmonella typhimurium</i> . 2008 , 275, 5855-64	10
2142	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. 2008 , 456, 107-11	138
2141	Crystal structure of the ZP-N domain of ZP3 reveals the core fold of animal egg coats. 2008 , 456, 653-7	104
2140	More complicated than it looks: assembly of Notch pathway transcription complexes. 2008 , 27, 5099-109	122
2139	Understanding the molecular machinery of genetics through 3D structures. 2008 , 9, 141-51	59
2138	Structure and functional properties of the <i>Bacillus subtilis</i> transcriptional repressor Rex. 2008 , 69, 466-78	110
2137	Comprehensive inventory of protein complexes in the Protein Data Bank from consistent classification of interfaces. 2008 , 9, 234	22
2136	Crystal structure of the ternary FimC-FimF(t)-FimD(N) complex indicates conserved pilus chaperone-subunit complex recognition by the usher FimD. 2008 , 582, 651-5	39
2135	X-ray structure of the metal-sensor CnrX in both the apo- and copper-bound forms. 2008 , 582, 3954-8	19
2134	A selective blocker of Kv1.2 and Kv1.3 potassium channels from the venom of the scorpion <i>Centruroides suffusus suffusus</i> . 2008 , 76, 1142-54	41
2133	A double mutation of MBP(83-99) peptide induces IL-4 responses and antagonizes IFN-gamma responses. 2008 , 200, 77-89	28
2132	Crystal structures of <i>Toxoplasma gondii</i> pterin-4a-carbinolamine dehydratase and comparisons with mammalian and parasite orthologues. 2008 , 158, 131-8	5

2131	Crystal packing of a bacteriophage MS2 coat protein mutant corresponds to octahedral particles. 2008 , 17, 1731-9		14
2130	Thioredoxin as a fusion tag for carrier-driven crystallization. 2008 , 17, 2070-9		29
2129	Protein-protein interaction and quaternary structure. 2008 , 41, 133-80		296
2128	The leptospiral antigen Lp49 is a two-domain protein with putative protein binding function. 2008 , 163, 53-60		8
2127	Amyloid-beta-anti-amyloid-beta complex structure reveals an extended conformation in the immunodominant B-cell epitope. <i>Journal of Molecular Biology</i> , 2008 , 377, 181-92	6.5	45
2126	Crystal structures of the clock protein EA4 from the silkworm <i>Bombyx mori</i> . <i>Journal of Molecular Biology</i> , 2008 , 377, 630-5	6.5	18
2125	Structural insights into rice BGlu1 beta-glucosidase oligosaccharide hydrolysis and transglycosylation. <i>Journal of Molecular Biology</i> , 2008 , 377, 1200-15	6.5	68
2124	The crystal structure of beta-alanine synthase from <i>Drosophila melanogaster</i> reveals a homooctameric helical turn-like assembly. <i>Journal of Molecular Biology</i> , 2008 , 377, 1544-59	6.5	31
2123	The crystal structure of DehI reveals a new alpha-haloacid dehalogenase fold and active-site mechanism. <i>Journal of Molecular Biology</i> , 2008 , 378, 284-94	6.5	46
2122	Crystal structure of the peptidoglycan recognition protein at 1.8 Å resolution reveals dual strategy to combat infection through two independent functional homodimers. <i>Journal of Molecular Biology</i> , 2008 , 378, 923-32	6.5	12
2121	Snapshots of a Y-family DNA polymerase in replication: substrate-induced conformational transitions and implications for fidelity of Dpo4. <i>Journal of Molecular Biology</i> , 2008 , 379, 317-30	6.5	77
2120	Structural analysis of the Saf pilus by electron microscopy and image processing. <i>Journal of Molecular Biology</i> , 2008 , 379, 174-87	6.5	26
2119	A putative alpha-helical porin from <i>Corynebacterium glutamicum</i> . <i>Journal of Molecular Biology</i> , 2008 , 379, 482-91	6.5	28
2118	Structure of an Fab-protease complex reveals a highly specific non-canonical mechanism of inhibition. <i>Journal of Molecular Biology</i> , 2008 , 380, 351-60	6.5	54
2117	Structure and mode of action of a mosquitocidal holotoxin. <i>Journal of Molecular Biology</i> , 2008 , 381, 150-0.5		34
2116	Statistical analysis of interface similarity in crystals of homologous proteins. <i>Journal of Molecular Biology</i> , 2008 , 381, 487-507	6.5	86
2115	Dissecting NGF interactions with TrkA and p75 receptors by structural and functional studies of an anti-NGF neutralizing antibody. <i>Journal of Molecular Biology</i> , 2008 , 381, 881-96	6.5	34
2114	The crystal structure of CHIR-AB1: a primordial avian classical Fc receptor. <i>Journal of Molecular Biology</i> , 2008 , 381, 1012-24	6.5	27

2113	Structural and kinetic properties of a beta-hydroxyacid dehydrogenase involved in nicotinate fermentation. <i>Journal of Molecular Biology</i> , 2008 , 382, 802-11	6.5	11
2112	Crystal structure of the Ig1 domain of the neural cell adhesion molecule NCAM2 displays domain swapping. <i>Journal of Molecular Biology</i> , 2008 , 382, 1113-20	6.5	7
2111	C4-dicarboxylates sensing mechanism revealed by the crystal structures of DctB sensor domain. <i>Journal of Molecular Biology</i> , 2008 , 383, 49-61	6.5	66
2110	Structure of Staphylococcus aureus EsxA suggests a contribution to virulence by action as a transport chaperone and/or adaptor protein. <i>Journal of Molecular Biology</i> , 2008 , 383, 603-14	6.5	52
2109	The crystal structure of enamidase: a bifunctional enzyme of the nicotinate catabolism. <i>Journal of Molecular Biology</i> , 2008 , 384, 837-47	6.5	7
2108	Three-dimensional structures of Pseudomonas aeruginosa PvcA and PvcB, two proteins involved in the synthesis of 2-isocyano-6,7-dihydroxycoumarin. <i>Journal of Molecular Biology</i> , 2008 , 384, 193-205	6.5	23
2107	Crystal structure of the arginine repressor protein in complex with the DNA operator from Mycobacterium tuberculosis. <i>Journal of Molecular Biology</i> , 2008 , 384, 1330-40	6.5	14
2106	Specificity and reactivity in menaquinone biosynthesis: the structure of Escherichia coli MenD (2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexadiene-1-carboxylate synthase). <i>Journal of Molecular Biology</i> , 2008 , 384, 1353-68	6.5	35
2105	A fence-like coat for the nuclear pore membrane. 2008 , 32, 815-26		104
2104	Mannosylation of mutated MBP83-99 peptides diverts immune responses from Th1 to Th2. 2008 , 45, 3661-70		28
2103	A bony fish immunological receptor of the NITR multigene family mediates allogeneic recognition. 2008 , 29, 228-37		33
2102	Implications for kinetochore-microtubule attachment from the structure of an engineered Ndc80 complex. 2008 , 133, 427-39		403
2101	Dissecting protein-RNA recognition sites. 2008 , 36, 2705-16		93
2100	Role of a conserved glutamine residue in tuning the catalytic activity of Escherichia coli cytochrome c nitrite reductase. 2008 , 47, 3789-99		32
2099	Crystallography and protein-protein interactions: biological interfaces and crystal contacts. 2008 , 36, 1438-41		53
2098	The Protein Data Bank (PDB), its related services and software tools as key components for in silico guided drug discovery. 2008 , 51, 7021-40		81
2097	Regulation of protein function: crystal packing interfaces and conformational dimerization. 2008 , 47, 6583-9		18
2096	Designed protein-protein association. 2008 , 319, 206-9		117

2095	Changes at the KinA PAS-A dimerization interface influence histidine kinase function. 2008 , 47, 4051-64	49
2094	Structural and functional characterization of the c-terminal domain of the ecdysteroid phosphate phosphatase from <i>bombyx mori</i> reveals a new enzymatic activity. 2008 , 47, 12135-45	12
2093	Changes in quaternary structure in the signaling mechanisms of PAS domains. 2008 , 47, 12078-86	43
2092	A covalent linker allows for membrane targeting of an oxylipin biosynthetic complex. 2008 , 47, 10665-76	11
2091	The structure of FSTL3.activin A complex. Differential binding of N-terminal domains influences follistatin-type antagonist specificity. 2008 , 283, 32831-8	52
2090	Crystal structure of fosfomycin resistance kinase FomA from <i>Streptomyces wedmorensis</i> . 2008 , 283, 28518-26	20
2089	PilF is an outer membrane lipoprotein required for multimerization and localization of the <i>Pseudomonas aeruginosa</i> Type IV pilus secretin. 2008 , 190, 6961-9	81
2088	Binding to DNA of the RNA-polymerase II C-terminal domain allows discrimination between Cdk7 and Cdk9 phosphorylation. 2009 , 37, 1260-8	17
2087	Crystal structure of the FeS cluster-containing nucleotide excision repair helicase XPD. 2008 , 6, e149	177
2086	Crystal structures of F420-dependent glucose-6-phosphate dehydrogenase FGD1 involved in the activation of the anti-tuberculosis drug candidate PA-824 reveal the basis of coenzyme and substrate binding. 2008 , 283, 17531-41	66
2085	A survey of available tools and web servers for analysis of protein-protein interactions and interfaces. 2009 , 10, 217-32	118
2084	Crystal structure of human liver Delta4-3-ketosteroid 5beta-reductase (AKR1D1) and implications for substrate binding and catalysis. 2008 , 283, 16830-9	60
2083	The crystal structure of the human toll-like receptor 10 cytoplasmic domain reveals a putative signaling dimer. 2008 , 283, 11861-5	148
2082	Structural basis of human triosephosphate isomerase deficiency: mutation E104D is related to alterations of a conserved water network at the dimer interface. 2008 , 283, 23254-63	56
2081	Identification of noncollagenous sites encoding specific interactions and quaternary assembly of alpha 3 alpha 4 alpha 5(IV) collagen: implications for Alport gene therapy. 2008 , 283, 35070-7	13
2080	Structure and evolution of a novel dimeric enzyme from a clinically important bacterial pathogen. 2008 , 283, 27598-27603	78
2079	Crystal structure of human plasma platelet-activating factor acetylhydrolase: structural implication to lipoprotein binding and catalysis. 2008 , 283, 31617-24	64
2078	Structure and function of sedoheptulose-7-phosphate isomerase, a critical enzyme for lipopolysaccharide biosynthesis and a target for antibiotic adjuvants. 2008 , 283, 2835-45	50

2077	Structural insight into bioremediation of triphenylmethane dyes by <i>Citrobacter</i> sp. triphenylmethane reductase. 2008 , 283, 31981-90	30
2076	Structural and functional analysis of AsbF: origin of the stealth 3,4-dihydroxybenzoic acid subunit for petrobactin biosynthesis. 2008 , 105, 17133-8	47
2075	Structural analysis of a periplasmic binding protein in the tripartite ATP-independent transporter family reveals a tetrameric assembly that may have a role in ligand transport. 2008 , 283, 32812-20	22
2074	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein-protein interactions. 2008 , 24, 652-8	72
2073	The cysteine-rich interdomain region from the highly variable plasmodium falciparum erythrocyte membrane protein-1 exhibits a conserved structure. 2008 , 4, e1000147	43
2072	Vaccinia virus proteins A52 and B14 Share a Bcl-2-like fold but have evolved to inhibit NF-kappaB rather than apoptosis. 2008 , 4, e1000128	121
2071	FutA2 is a ferric binding protein from <i>Synechocystis</i> PCC 6803. 2008 , 283, 12520-7	47
2070	Structure of the DNA repair helicase hel308 reveals DNA binding and autoinhibitory domains. 2008 , 283, 5118-26	61
2069	The C-terminal region of Ge-1 presents conserved structural features required for P-body localization. 2008 , 14, 1991-8	23
2068	Crystal structure and kinetic study of dihydrodipicolinate synthase from <i>Mycobacterium tuberculosis</i> . 2008 , 411, 351-60	69
2067	The crystal structure of the periplasmic domain of the <i>Escherichia coli</i> membrane protein insertase YidC contains a substrate binding cleft. 2008 , 283, 9350-8	49
2066	Insights into the catalytic mechanism of tyrosine phenol-lyase from X-ray structures of quinonoid intermediates. 2008 , 283, 29206-14	29
2065	Crystal structure of the avian reovirus inner capsid protein sigmaA. 2008 , 82, 11208-16	16
2064	PixE promotes dark oligomerization of the BLUF photoreceptor PixD. 2008 , 105, 11715-9	56
2063	Molecular dynamics characterization of protein crystal contacts in aqueous solutions. 2008 , 101, 248102	38
2062	Crystal structure and carbohydrate analysis of Nipah virus attachment glycoprotein: a template for antiviral and vaccine design. 2008 , 82, 11628-36	89
2061	Discrimination between biological interfaces and crystal-packing contacts. 2008 , 1, 99-113	20
2060	Computational structural analysis: multiple proteins bound to DNA. 2008 , 3, e3243	10

2059	Mycobacterium tuberculosis glucosyl-3-phosphoglycerate synthase: structure of a key enzyme in methylglucose lipopolysaccharide biosynthesis. 2008 , 3, e3748	18
2058	Intervening with urinary tract infections using anti-adhesives based on the crystal structure of the FimH-oligomannose-3 complex. 2008 , 3, e2040	176
2057	. 2009 ,	24
2056	Optimized null model for protein structure networks. 2009 , 4, e5967	26
2055	The crystal structure of the Escherichia coli autoinducer-2 processing protein LsrF. 2009 , 4, e6820	13
2054	Bioinformatics and structural characterization of a hypothetical protein from Streptococcus mutans: implication of antibiotic resistance. 2009 , 4, e7245	12
2053	Dual roles of Lys(57) at the dimer interface of human mitochondrial NAD(P) ⁺ -dependent malic enzyme. 2009 , 420, 201-9	6
2052	Structural and biochemical characterization of the wild type PCSK9-EGF(AB) complex and natural familial hypercholesterolemia mutants. 2009 , 284, 1313-23	100
2051	Chaperones of F1-ATPase. 2009 , 284, 17138-17146	23
2050	An asymmetric model for Na ⁺ -translocating glutaconyl-CoA decarboxylases. 2009 , 284, 28401-28409	10
2049	High-affinity IgE recognition of a conformational epitope of the major respiratory allergen Phl p 2 as revealed by X-ray crystallography. 2009 , 182, 2141-51	92
2048	Crystal structure and function of a DARPin neutralizing inhibitor of lactococcal phage TP901-1: comparison of DARPin and camelid VHH binding mode. 2009 , 284, 30718-26	51
2047	Identification and structural analysis of type I collagen sites in complex with fibronectin fragments. 2009 , 106, 4195-200	75
2046	Crystal structure of the catalytic domain of the tumor-associated human carbonic anhydrase IX. 2009 , 106, 16233-8	399
2045	Structure of the vesicular stomatitis virus nucleocapsid in complex with the nucleocapsid-binding domain of the small polymerase cofactor, P. 2009 , 106, 11713-8	91
2044	Complex structure of Bacillus subtilis RibG: the reduction mechanism during riboflavin biosynthesis. 2009 , 284, 1725-31	12
2043	Structural insight into the activation mechanism of human pancreatic prophospholipase A2. 2009 , 284, 16659-16666	22
2042	Crystal structure of procaspase-1 zymogen domain reveals insight into inflammatory caspase autoactivation. 2009 , 284, 6546-53	60

2041	Molecular mimicry in innate immunity: crystal structure of a bacterial TIR domain. 2009 , 284, 21386-92	64
2040	The structure of CrgA from <i>Neisseria meningitidis</i> reveals a new octameric assembly state for LysR transcriptional regulators. 2009 , 37, 4545-58	51
2039	Model for eukaryotic tail-anchored protein binding based on the structure of Get3. 2009 , 106, 14849-54	70
2038	Crystal structure of KorA bound to operator DNA: insight into repressor cooperation in RP4 gene regulation. 2009 , 37, 1915-24	14
2037	Crystal structure of a novel conformational state of the flavivirus NS3 protein: implications for polyprotein processing and viral replication. 2009 , 83, 12895-906	97
2036	Architectural nucleoporins Nup157/170 and Nup133 are structurally related and descend from a second ancestral element. 2009 , 284, 28442-28452	67
2035	Dimerization and protein binding specificity of the U2AF homology motif of the splicing factor Puf60. 2009 , 284, 630-639	49
2034	Crystal packing analysis of murine VDAC1 crystals in a lipidic environment reveals novel insights on oligomerization and orientation. 2009 , 3, 167-70	40
2033	The nature of the TRAP-Anti-TRAP complex. 2009 , 106, 2176-81	22
2032	Intrinsic disorder in protein interactions: insights from a comprehensive structural analysis. 2009 , 5, e1000316	91
2031	ATP and MO25alpha regulate the conformational state of the STRADalpha pseudokinase and activation of the LKB1 tumour suppressor. 2009 , 7, e1000126	109
2030	Dimerization of hepatitis E virus capsid protein E2s domain is essential for virus-host interaction. 2009 , 5, e1000537	107
2029	Crystal structure of native RPE65, the retinoid isomerase of the visual cycle. 2009 , 106, 17325-30	124
2028	Heme uptake across the outer membrane as revealed by crystal structures of the receptor-hemophore complex. 2009 , 106, 1045-50	130
2027	Extensive DNA mimicry by the ArdA anti-restriction protein and its role in the spread of antibiotic resistance. 2009 , 37, 4887-97	80
2026	Crystal structure of a mammalian CTP: phosphocholine cytidyltransferase catalytic domain reveals novel active site residues within a highly conserved nucleotidyltransferase fold. 2009 , 284, 33535-48	47
2025	Crystal structures of YkuI and its complex with second messenger cyclic Di-GMP suggest catalytic mechanism of phosphodiester bond cleavage by EAL domains. 2009 , 284, 13174-84	78
2024	Crystal structure and assembly of the functional <i>Nanoarchaeum equitans</i> tRNA splicing endonuclease. 2009 , 37, 5793-802	22

2023	Crystal structure of the N-terminal domain of anaphase-promoting complex subunit 7. 2009 , 284, 15137-46	19
2022	The sequence-structure relationship and protein function prediction. 2009 , 19, 357-62	65
2021	Fold space unlimited. 2009 , 19, 312-20	19
2020	Structural and biophysical studies of the human IL-7/IL-7Ralpha complex. 2009 , 17, 54-65	69
2019	Structural analysis of the GGDEF-EAL domain-containing c-di-GMP receptor FimX. 2009 , 17, 1104-16	140
2018	Structural plasticity of eph receptor A4 facilitates cross-class ephrin signaling. 2009 , 17, 1386-97	73
2017	Predicting protein-protein binding sites in membrane proteins. 2009 , 10, 312	26
2016	Crystal structure of a soluble decoy receptor IL-22BP bound to interleukin-22. 2009 , 583, 1072-7	38
2015	The crystal structure of a hyperthermoactive exopolysaccharidase from <i>Thermotoga maritima</i> reveals a unique tetramer. 2009 , 583, 3665-70	20
2014	Metal-mediated self-assembly of a beta-sandwich protein. 2009 , 15, 12672-80	7
2013	Structural modeling and biochemical studies reveal insights into the molecular basis of the recognition of beta-2-microglobulin by antibody BBM.1. 2009 , 22, 465-73	3
2012	Domain-ligand mapping for enzymes. 2010 , 23, 194-208	4
2011	Modification of protein crystal packing by systematic mutations of surface residues: implications on biotemplating and crystal porosity. 2009 , 104, 444-57	12
2010	X-ray crystal structure of GarR-tartronate semialdehyde reductase from <i>Salmonella typhimurium</i> . 2009 , 10, 249-53	12
2009	The three-dimensional structure of diaminopimelate decarboxylase from <i>Mycobacterium tuberculosis</i> reveals a tetrameric enzyme organisation. 2009 , 10, 209-17	9
2008	Data deposition and annotation at the worldwide protein data bank. 2009 , 42, 1-13	104
2007	Structural insight into function and regulation of carnitine palmitoyltransferase. 2009 , 66, 2489-501	39
2006	The ATP-binding cassette family: a structural perspective. 2009 , 66, 3111-26	83

2005	The crystal structure of the protein YhaK from Escherichia coli reveals a new subclass of redox sensitive enterobacterial bicupins. 2009 , 74, 18-31	16
2004	Crystal structure of the DUF54 family protein PH1010 from hyperthermophilic archaea Pyrococcus horikoshii OT3. 2009 , 74, 256-60	1
2003	Defining and characterizing protein surface using alpha shapes. 2009 , 76, 1-12	55
2002	An unusually small dimer interface is observed in all available crystal structures of cytosolic sulfotransferases. 2009 , 75, 289-95	14
2001	Crystal structure of a novel Sm-like protein of putative cyanophage origin at 2.60 Å resolution. 2009 , 75, 296-307	14
2000	X-ray structure of Danio rerio secretagoin: A hexa-EF-hand calcium sensor. 2009 , 76, 477-83	17
1999	Crystal structure of the Bacillus anthracis nucleoside diphosphate kinase and its characterization reveals an enzyme adapted to perform under stress conditions. 2009 , 76, 496-506	12
1998	Crystal structure of TTHA1264, a putative M16-family zinc peptidase from Thermus thermophilus HB8 that is homologous to the beta subunit of mitochondrial processing peptidase. 2009 , 75, 774-80	13
1997	Crystal structure of KaiC-like protein PH0186 from hyperthermophilic archaea Pyrococcus horikoshii OT3. 2009 , 75, 1035-9	13
1996	Combining interface core and whole interface descriptors in postscan processing of protein-protein docking models. 2009 , 77, 297-318	15
1995	X-ray crystallographic studies of RNase A variants engineered at the most destabilizing positions of the main hydrophobic core: further insight into protein stability. 2009 , 77, 658-69	7
1994	Cohesin diversity revealed by the crystal structure of the anchoring cohesin from Ruminococcus flavefaciens. 2009 , 77, 699-709	15
1993	Assessment of ligand binding residue predictions in CASP8. 2009 , 77 Suppl 9, 138-46	31
1992	The dimeric structure of Sulfolobus solfataricus thioredoxin A2 and the basis of its thermostability. 2009 , 77, 1004-8	5
1991	Mutations of key hydrophobic surface residues of 11 beta-hydroxysteroid dehydrogenase type 1 increase solubility and monodispersity in a bacterial expression system. 2009 , 18, 1552-63	8
1990	Structure and electrostatic property of cytoplasmic domain of ZntB transporter. 2009 , 18, 2043-52	12
1989	Crystal structure of a 3B3 variant—a broadly neutralizing HIV-1 scFv antibody. 2009 , 18, 2429-41	13
1988	The crystal structures of macrophage migration inhibitory factor from Plasmodium falciparum and Plasmodium berghei. 2009 , 18, 2578-91	29

1987	Structure and function of GlnU from <i>Mycobacterium tuberculosis</i> . 2009 , 65, 275-83	46
1986	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn ²⁺ -binding FCD domains. 2009 , 65, 356-65	28
1985	The F4 fimbrial chaperone FaeE is stable as a monomer that does not require self-capping of its pilin-interactive surfaces. 2009 , 65, 411-20	5
1984	Structure of SRP14 from the <i>Schizosaccharomyces pombe</i> signal recognition particle. 2009 , 65, 421-33	7
1983	Structure of the sporulation histidine kinase inhibitor Sda from <i>Bacillus subtilis</i> and insights into its solution state. 2009 , 65, 574-81	9
1982	Structure of the C-terminal domain of nsp4 from feline coronavirus. 2009 , 65, 839-46	18
1981	Structure of the Calx-beta domain of the integrin beta4 subunit: insights into function and cation-independent stability. 2009 , 65, 858-71	25
1980	Structure of the single-stranded DNA-binding protein from <i>Streptomyces coelicolor</i> . 2009 , 65, 974-9	5
1979	The effect of a proline residue on the rate of growth and the space group of alpha-spectrin SH3-domain crystals. 2009 , 65, 1247-52	7
1978	Structure of the X (ADRP) domain of nsp3 from feline coronavirus. 2009 , 65, 1292-300	15
1977	Structures of the apo and holo forms of formate dehydrogenase from the bacterium <i>Moraxella</i> sp. C-1: towards understanding the mechanism of the closure of the interdomain cleft. 2009 , 65, 1315-25	26
1976	Structures of restriction endonuclease HindIII in complex with its cognate DNA and divalent cations. 2009 , 65, 1326-33	11
1975	Structure of the twin-arginine signal-binding protein DmsD from <i>Escherichia coli</i> . 2009 , 65, 746-50	15
1974	Crystallization and preliminary X-ray diffraction analysis of crotoxin B from <i>Crotalus durissus collilineatus</i> venom. 2009 , 65, 1011-3	5
1973	The high-resolution structure of the extracellular domain of human CD69 using a novel polymer. 2009 , 65, 1258-60	13
1972	Structure of the first PDZ domain of human PSD-93. 2009 , 65, 1254-7	9
1971	Structure of hypothetical Mo-cofactor biosynthesis protein B (ST2315) from <i>Sulfolobus tokodaii</i> . 2009 , 65, 1200-3	2
1970	Structure of SurE protein from <i>Aquifex aeolicus</i> VF5 at 1.5 Å resolution. 2009 , 65, 1204-8	6

1969	The structure of an archaeal ribose-5-phosphate isomerase from <i>Methanocaldococcus jannaschii</i> (MJ1603). 2009 , 65, 1214-7	5
1968	Structural and phylogenetic analysis of a conserved actinobacteria-specific protein (ASP1; SCO1997) from <i>Streptomyces coelicolor</i> . 2009 , 9, 40	10
1967	Biochemical and structural characterization of alanine racemase from <i>Bacillus anthracis</i> (Ames). 2009 , 9, 53	30
1966	The crystal structure of <i>Haloferax volcanii</i> proliferating cell nuclear antigen reveals unique surface charge characteristics due to halophilic adaptation. 2009 , 9, 55	38
1965	Initial insight into the function of the lysosomal 66.3 kDa protein from mouse by means of X-ray crystallography. 2009 , 9, 56	13
1964	Structural insight into the essential PB1-PB2 subunit contact of the influenza virus RNA polymerase. 2009 , 28, 1803-11	145
1963	Structure and function of a complex between chorismate mutase and DAHP synthase: efficiency boost for the junior partner. 2009 , 28, 2128-42	38
1962	The structure of myostatin:follistatin 288: insights into receptor utilization and heparin binding. 2009 , 28, 2662-76	117
1961	The structure of an integrin/talin complex reveals the basis of inside-out signal transduction. 2009 , 28, 3623-32	251
1960	The structure of a cytolytic alpha-helical toxin pore reveals its assembly mechanism. 2009 , 459, 726-30	250
1959	AcsD catalyzes enantioselective citrate desymmetrization in siderophore biosynthesis. 2009 , 5, 174-82	56
1958	Protein structure homology modeling using SWISS-MODEL workspace. 2009 , 4, 1-13	908
1957	Molecular architecture of the Nup84-Nup145C-Sec13 edge element in the nuclear pore complex lattice. 2009 , 16, 1173-7	70
1956	Substitution of residues at the double dimer interface affects the stability and oligomerization of goose delta-crystallin. 2009 , 276, 5126-36	2
1955	A single intersubunit salt bridge affects oligomerization and catalytic activity in a bacterial quinone reductase. 2009 , 276, 5263-74	32
1954	Uneven twins: comparison of two enantiocomplementary hydroxynitrile lyases with alpha/beta-hydrolase fold. 2009 , 141, 166-73	49
1953	The 1.4 Å crystal structure of the large and cold-active <i>Vibrio</i> sp. alkaline phosphatase. 2009 , 1794, 297-308	42
1952	Structural organization of WrbA in apo- and holoprotein crystals. 2009 , 1794, 1288-98	11

1951	Cloning and characterisation of dihydrodipicolinate synthase from the pathogen <i>Neisseria meningitidis</i> . 2009 , 1794, 1168-74		29
1950	Crystal structure of a phospholipase A(2) homolog complexed with p-bromophenacyl bromide reveals important structural changes associated with the inhibition of myotoxic activity. 2009 , 1794, 1583-90		31
1949	Structural redesign of lipase B from <i>Candida antarctica</i> by circular permutation and incremental truncation. <i>Journal of Molecular Biology</i> , 2009 , 393, 191-201	6.5	52
1948	Structure and inhibition of human diamine oxidase. 2009 , 48, 9810-22		77
1947	Structure and function of <i>Bacillus subtilis</i> YphP, a prokaryotic disulfide isomerase with a CXC catalytic motif. 2009 , 48, 8664-71		35
1946	Dihydroorotase from the hyperthermophile <i>Aquifex aeolicus</i> is activated by stoichiometric association with aspartate transcarbamoylase and forms a one-pot reactor for pyrimidine biosynthesis. 2009 , 48, 766-78		33
1945	Macrophage scavenger receptor A mediates adhesion to apolipoproteins A-I and E. 2009 , 48, 11858-71		37
1944	The structure of the UbcH8-ubiquitin complex shows a unique ubiquitin interaction site. 2009 , 48, 12169-79		41
1943	Structural artifacts in protein-ligand X-ray structures: implications for the development of docking scoring functions. 2009 , 52, 5673-84		45
1942	Ring1B contains a ubiquitin-like docking module for interaction with Cbx proteins. 2009 , 48, 10542-8		34
1941	Impaired protofibril formation in fibrinogen gamma N308K is due to altered D:D and "A:a" interactions. 2009 , 48, 8656-63		11
1940	Control of protein oligomerization symmetry by metal coordination: C2 and C3 symmetrical assemblies through Cu(II) and Ni(II) coordination. 2009 , 48, 2726-8		60
1939	Folding and association of thermophilic dimeric and trimeric DsrEFH proteins: Tm0979 and Mth1491. 2009 , 48, 2891-906		11
1938	Crystal structure of Baeyer-Villiger monooxygenase MtmOIV, the key enzyme of the mithramycin biosynthetic pathway. 2009 , 48, 4476-87		68
1937	Identification of continuous interaction sites in PLA(2)-based protein complexes by peptide arrays. 2009 , 91, 1482-92		15
1936	Structures of asymmetric ClpX hexamers reveal nucleotide-dependent motions in a AAA+ protein-unfolding machine. 2009 , 139, 744-56		218
1935	Open-closed conformational change revealed by the crystal structures of 3-keto-L-gulonate 6-phosphate decarboxylase from <i>Streptococcus mutans</i> . 2009 , 381, 429-33		1
1934	The quaternary structure of <i>Escherichia coli</i> N-acetylneuraminase lyase is essential for functional expression. 2009 , 388, 107-11		10

1933	Structure of the Enterococcus faecalis EIIA(gnt) PTS component. 2009 , 388, 626-9		4
1932	Structure-function relationships of the outer membrane translocon Wza investigated by cryo-electron microscopy and mutagenesis. 2009 , 166, 172-82		11
1931	Comparative structural studies on Lys49-phospholipases A(2) from Bothrops genus reveal their myotoxic site. 2009 , 167, 106-16		51
1930	The dimer formed by the periplasmic domain of EpsL from the Type 2 Secretion System of Vibrio parahaemolyticus. 2009 , 168, 313-22		34
1929	Crystal structure of the resuscitation-promoting factor (DeltaDUF)RpFB from M. tuberculosis. <i>Journal of Molecular Biology</i> , 2009 , 385, 153-62	6.5	64
1928	Vancomycin forms ligand-mediated supramolecular complexes. <i>Journal of Molecular Biology</i> , 2009 , 385, 200-11	6.5	32
1927	Structure and action of the myxobacterial chondrochloren halogenase CndH: a new variant of FAD-dependent halogenases. <i>Journal of Molecular Biology</i> , 2009 , 385, 520-30	6.5	53
1926	Crystal structure of SpoVT, the final modulator of gene expression during spore development in Bacillus subtilis. <i>Journal of Molecular Biology</i> , 2009 , 386, 962-75	6.5	18
1925	Structural base for enzymatic cyclodextrin hydrolysis. <i>Journal of Molecular Biology</i> , 2009 , 385, 606-17	6.5	25
1924	The crystal structure of ATP-bound phosphofructokinase from Trypanosoma brucei reveals conformational transitions different from those of other phosphofructokinases. <i>Journal of Molecular Biology</i> , 2009 , 385, 1519-33	6.5	28
1923	Domain organization in Clostridium botulinum neurotoxin type E is unique: its implication in faster translocation. <i>Journal of Molecular Biology</i> , 2009 , 386, 233-45	6.5	137
1922	Conformations of NhaA, the Na/H exchanger from Escherichia coli, in the pH-activated and ion-translocating states. <i>Journal of Molecular Biology</i> , 2009 , 386, 351-65	6.5	33
1921	Crystal structures of mite allergens Der f 1 and Der p 1 reveal differences in surface-exposed residues that may influence antibody binding. <i>Journal of Molecular Biology</i> , 2009 , 386, 520-30	6.5	64
1920	Crystal structure of the IrrE protein, a central regulator of DNA damage repair in deinococcaceae. <i>Journal of Molecular Biology</i> , 2009 , 386, 704-16	6.5	54
1919	Solution structure of human zeta-COP: direct evidences for structural similarity between COP I and clathrin-adaptor coats. <i>Journal of Molecular Biology</i> , 2009 , 386, 903-12	6.5	20
1918	Structural and functional studies of the biotin protein ligase from Aquifex aeolicus reveal a critical role for a conserved residue in target specificity. <i>Journal of Molecular Biology</i> , 2009 , 387, 129-46	6.5	33
1917	Structural basis for catalysis of a tetrameric class IIa fructose 1,6-bisphosphate aldolase from Mycobacterium tuberculosis. <i>Journal of Molecular Biology</i> , 2009 , 386, 1038-53	6.5	33
1916	Crystal structures of Limulus SAP-like pentraxin reveal two molecular aggregations. <i>Journal of Molecular Biology</i> , 2009 , 386, 1240-54	6.5	16

1915	The oligomeric assembly of the novel haem-degrading protein HbpS is essential for interaction with its cognate two-component sensor kinase. <i>Journal of Molecular Biology</i> , 2009 , 386, 1108-22	6.5	21
1914	First inactive conformation of CK2 alpha, the catalytic subunit of protein kinase CK2. <i>Journal of Molecular Biology</i> , 2009 , 386, 1212-21	6.5	27
1913	Crystal structure of the full-length sorbitol operon regulator SorC from <i>Klebsiella pneumoniae</i> : structural evidence for a novel transcriptional regulation mechanism. <i>Journal of Molecular Biology</i> , 2009 , 387, 759-70	6.5	11
1912	Crystal structure of LipL32, the most abundant surface protein of pathogenic <i>Leptospira</i> spp. <i>Journal of Molecular Biology</i> , 2009 , 387, 1229-38	6.5	46
1911	The structure of the arginine repressor from <i>Mycobacterium tuberculosis</i> bound with its DNA operator and Co-repressor, L-arginine. <i>Journal of Molecular Biology</i> , 2009 , 388, 85-97	6.5	12
1910	Conformations of NhaA, the Na ⁺ /H ⁺ exchanger from <i>Escherichia coli</i> , in the pH-activated and ion-translocating states. <i>Journal of Molecular Biology</i> , 2009 , 388, 659-72	6.5	38
1909	Insights into positive and negative requirements for protein-protein interactions by crystallographic analysis of the beta-lactamase inhibitory proteins BLIP, BLIP-I, and BLP. <i>Journal of Molecular Biology</i> , 2009 , 389, 289-305	6.5	33
1908	Structures of glycinamide ribonucleotide transformylase (PurN) from <i>Mycobacterium tuberculosis</i> reveal a novel dimer with relevance to drug discovery. <i>Journal of Molecular Biology</i> , 2009 , 389, 722-33	6.5	10
1907	An ion-channel modulator from the saliva of the brown ear tick has a highly modified Kunitz/BPTI structure. <i>Journal of Molecular Biology</i> , 2009 , 389, 734-47	6.5	36
1906	The three-dimensional Structure of a mycobacterial DapD provides insights into DapD diversity and reveals unexpected particulars about the enzymatic mechanism. <i>Journal of Molecular Biology</i> , 2009 , 389, 863-79	6.5	18
1905	Contributions of interfacial residues of human Interleukin15 to the specificity and affinity for its private alpha-receptor. <i>Journal of Molecular Biology</i> , 2009 , 389, 880-94	6.5	13
1904	The X-ray crystal structure of the phage lambda tail terminator protein reveals the biologically relevant hexameric ring structure and demonstrates a conserved mechanism of tail termination among diverse long-tailed phages. <i>Journal of Molecular Biology</i> , 2009 , 389, 938-51	6.5	46
1903	Structure and calcium-binding activity of LipL32, the major surface antigen of pathogenic <i>Leptospira</i> sp. <i>Journal of Molecular Biology</i> , 2009 , 390, 722-36	6.5	35
1902	The crystal structures of human S100A12 in apo form and in complex with zinc: new insights into S100A12 oligomerisation. <i>Journal of Molecular Biology</i> , 2009 , 391, 536-51	6.5	82
1901	Intermodular linker flexibility revealed from crystal structures of adjacent cellulosomal cohesins of <i>Acetivibrio cellulolyticus</i> . <i>Journal of Molecular Biology</i> , 2009 , 391, 86-97	6.5	21
1900	Dimer interface migration in a viral sulfhydryl oxidase. <i>Journal of Molecular Biology</i> , 2009 , 391, 758-68	6.5	25
1899	Crystal structure of Miner1: The redox-active 2Fe-2S protein causative in Wolfram Syndrome 2. <i>Journal of Molecular Biology</i> , 2009 , 392, 143-53	6.5	91
1898	The structural basis of beta-peptide-specific cleavage by the serine protease cyanophycinase. <i>Journal of Molecular Biology</i> , 2009 , 392, 393-404	6.5	15

1897	Structure and function of the FeoB G-domain from <i>Methanococcus jannaschii</i> . <i>Journal of Molecular Biology</i> , 2009 , 392, 405-19	6.5	25
1896	Crystal structure of the frizzled-like cysteine-rich domain of the receptor tyrosine kinase MuSK. <i>Journal of Molecular Biology</i> , 2009 , 393, 1-9	6.5	57
1895	Crystal structure of the hexameric catabolic ornithine transcarbamylase from <i>Lactobacillus hilgardii</i> : Structural insights into the oligomeric assembly and metal binding. <i>Journal of Molecular Biology</i> , 2009 , 393, 425-34	6.5	13
1894	Determinants for the activation and autoinhibition of the diguanylate cyclase response regulator WspR. <i>Journal of Molecular Biology</i> , 2009 , 393, 619-33	6.5	105
1893	Structure of the mature Streptococcal cysteine protease exotoxin mSpeB in its active dimeric form. <i>Journal of Molecular Biology</i> , 2009 , 393, 693-703	6.5	14
1892	Crystal structure of the antitoxin-toxin protein complex RelB-RelE from <i>Methanococcus jannaschii</i> . <i>Journal of Molecular Biology</i> , 2009 , 393, 898-908	6.5	36
1891	Periplasmic domains of <i>Pseudomonas aeruginosa</i> PilN and PilO form a stable heterodimeric complex. <i>Journal of Molecular Biology</i> , 2009 , 394, 143-59	6.5	61
1890	Crystal Structures of the histidine acid phosphatase from <i>Francisella tularensis</i> provide insight into substrate recognition. <i>Journal of Molecular Biology</i> , 2009 , 394, 893-904	6.5	11
1889	Structure of the Yeast DEAD box protein Mss116p reveals two wedges that crimp RNA. 2009 , 35, 598-609		108
1888	Analysis of B-cell epitopes from the allergen Hev b 6.02 revealed by using blocking antibodies. 2009 , 46, 668-76		10
1887	The betagamma-crystallin superfamily contains a universal motif for binding calcium. 2009 , 48, 12180-90		56
1886	Applications of Graph Theory in Chemo- and Bioinformatics. 221-243		
1885	Genome and proteome annotation: organization, interpretation and integration. 2009 , 6, 129-47		36
1884	Structural insights into tail-anchored protein binding and membrane insertion by Get3. 2009 , 106, 21131-6		75
1883	From Protein Structure to Function with Bioinformatics. 2009 ,		19
1882	High-affinity recognition of lanthanide(III) chelate complexes by a reprogrammed human lipocalin 2. 2009 , 131, 3565-76		53
1881	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. 2009 , 5, 1456-72		8
1880	Biomedical informatics. Preface. 2009 , 569, v		

1879	The structure of CDK4/cyclin D3 has implications for models of CDK activation. 2009 , 106, 4171-6	84
1878	Structural analysis of a multifunctional, tandemly repeated inositol polyphosphatase. <i>Journal of Molecular Biology</i> , 2009 , 392, 75-86	6.5 11
1877	Structure of the Notch1-negative regulatory region: implications for normal activation and pathogenic signaling in T-ALL. 2009 , 113, 4381-90	128
1876	Crystal structure of protein Z-dependent inhibitor complex shows how protein Z functions as a cofactor in the membrane inhibition of factor X. 2009 , 114, 3662-7	37
1875	Crystal structure of bucaïn, a three-fingered toxin from the venom of the Malayan krait (<i>Bungarus candidus</i>). 2009 , 16, 1473-7	6
1874	Influence of quaternary conformation on the biological activities of the Asp49-phospholipases A2s from snake venoms. 2009 , 16, 852-9	12
1873	The intriguing phospholipases A2 homologues: relevant structural features on myotoxicity and catalytic inactivity. 2009 , 16, 887-93	22
1872	Role of a PA14 domain in determining substrate specificity of a glycoside hydrolase family 3 β -glucosidase from <i>Kluyveromyces marxianus</i> . 2010 , 431, 39-49	83
1871	Structure of an Ebf1:DNA complex reveals unusual DNA recognition and structural homology with Rel proteins. 2010 , 24, 2270-5	35
1870	Crystal structure and collagen-binding site of immune inhibitory receptor LAIR-1: unexpected implications for collagen binding by platelet receptor GPVI. 2010 , 115, 1364-73	49
1869	Crystal structure of the human transcription elongation factor DSIF hSpt4 subunit in complex with the hSpt5 dimerization interface. 2009 , 425, 373-80	23
1868	RING domain dimerization is essential for RNF4 function. 2010 , 431, 23-9	65
1867	Structure at 1.0 Å resolution of a high-potential iron-sulfur protein involved in the aerobic respiratory chain of <i>Rhodothermus marinus</i> . 2010 , 15, 303-13	17
1866	Protein subunit interfaces: A statistical analysis of hot spots in Sm proteins. 2010 , 16, 1743-51	5
1865	Cloning, overexpression, purification and preliminary characterization of human septin 8. 2010 , 29, 328-35	2
1864	Structure of <i>Trypanosoma brucei</i> glutathione synthetase: domain and loop alterations in the catalytic cycle of a highly conserved enzyme. 2010 , 170, 93-9	9
1863	Crystal structure of the APOBEC3G catalytic domain reveals potential oligomerization interfaces. 2010 , 18, 28-38	104
1862	A TNF-like trimeric lectin domain from <i>Burkholderia cenocepacia</i> with specificity for fucosylated human histo-blood group antigens. 2010 , 18, 59-72	61

1861	AlgK is a TPR-containing protein and the periplasmic component of a novel exopolysaccharide secretin. 2010 , 18, 265-73	82
1860	Structure of the GLD-1 homodimerization domain: insights into STAR protein-mediated translational regulation. 2010 , 18, 377-89	23
1859	Molecular basis for shared cytokine recognition revealed in the structure of an unusually high affinity complex between IL-13 and IL-13Ralpha2. 2010 , 18, 332-42	92
1858	A single mutation promotes amyloidogenicity through a highly promiscuous dimer interface. 2010 , 18, 563-70	35
1857	Crystal structure of an intracellular subtilisin reveals novel structural features unique to this subtilisin family. 2010 , 18, 744-55	16
1856	Molecular basis for the association of human E4B U box ubiquitin ligase with E2-conjugating enzymes UbcH5c and Ubc4. 2010 , 18, 955-65	35
1855	Crystal structures of Phd-Doc, HigA, and YeeU establish multiple evolutionary links between microbial growth-regulating toxin-antitoxin systems. 2010 , 18, 996-1010	59
1854	Structure and cellular roles of the RMI core complex from the bloom syndrome dissolvasome. 2010 , 18, 1149-58	30
1853	Folding, DNA recognition, and function of GIY-YIG endonucleases: crystal structures of R.Eco29kl. 2010 , 18, 1321-31	30
1852	Crystal structure of group II chaperonin in the open state. 2010 , 18, 1270-9	34
1851	MoDEL (Molecular Dynamics Extended Library): a database of atomistic molecular dynamics trajectories. 2010 , 18, 1399-409	100
1850	WD40 proteins propel cellular networks. 2010 , 35, 565-74	410
1849	ATP-dependent MurE ligase in Mycobacterium tuberculosis: biochemical and structural characterisation. 2010 , 90, 16-24	41
1848	Structural characterization of a family of cytochromes c(7) involved in Fe(III) respiration by Geobacter sulfurreducens. 2010 , 1797, 222-32	45
1847	Structure of the GTPase and GDI domains of FeoB, the ferrous iron transporter of Legionella pneumophila. 2010 , 584, 733-8	24
1846	Structure of translation initiation factor 1 from Mycobacterium tuberculosis and inferred binding to the 30S ribosomal subunit. 2010 , 584, 1011-5	7
1845	A disulfide driven domain swap switches off the activity of Shigella lpaH9.8 E3 ligase. 2010 , 584, 4163-8	29
1844	Crystal contacts as nature's docking solutions. 2010 , 31, 133-43	218

1843	Biocatalysis with thermostable enzymes: structure and properties of a thermophilic 'ene'-reductase related to old yellow enzyme. 2010 , 11, 197-207	94
1842	Recent developments in cyclin-dependent kinase biochemical and structural studies. 2010 , 1804, 511-9	83
1841	Structure and catalytic mechanism of the beta-carbonic anhydrases. 2010 , 1804, 362-73	121
1840	Structural characterization of acylimine-containing blue and red chromophores in mTagBFP and TagRFP fluorescent proteins. 2010 , 17, 333-41	80
1839	Structural and mechanistic studies on Ebutyrobetaine hydroxylase. 2010 , 17, 1316-24	70
1838	AMINONET ² tool to construct and visualize amino acid networks, and to calculate topological parameters. 2010 , 43, 367-369	8
1837	Structure of a family 3b' carbohydrate-binding module from the Cel9V glycoside hydrolase from <i>Clostridium thermocellum</i> : structural diversity and implications for carbohydrate binding. 2010 , 66, 33-43	16
1836	Structure of the <i>Methanothermobacter thermoautotrophicus</i> exosome RNase PH ring. 2010 , 66, 522-8	7
1835	Structure of dehaloperoxidase B at 1.58 Å resolution and structural characterization of the AB dimer from <i>Amphitrite ornata</i> . 2010 , 66, 529-38	25
1834	Structure determination of the minimal complex between Tfb5 and Tfb2, two subunits of the yeast transcription/DNA-repair factor TFIIH: a retrospective study. 2010 , 66, 745-55	3
1833	The high-resolution structure of pig heart succinyl-CoA:3-oxoacid coenzyme A transferase. 2010 , 66, 797-805	6
1832	Structure of the <i>Escherichia coli</i> RNA polymerase alpha subunit C-terminal domain. 2010 , 66, 806-12	7
1831	Structures of apo and GTP-bound molybdenum cofactor biosynthesis protein MoaC from <i>Thermus thermophilus</i> HB8. 2010 , 66, 821-33	22
1830	Structure of <i>Staphylococcus aureus</i> adenylosuccinate lyase (PurB) and assessment of its potential as a target for structure-based inhibitor discovery. 2010 , 66, 881-8	13
1829	Structural and functional analysis of Rv0554 from <i>Mycobacterium tuberculosis</i> : testing a putative role in menaquinone biosynthesis. 2010 , 66, 909-17	10
1828	Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. 2010 , 66, 979-87	10
1827	Crystallization of small proteins assisted by green fluorescent protein. 2010 , 66, 1059-66	28
1826	Structural and biochemical analyses reveal a monomeric state of the bacterial lipocalin Blc. 2010 , 66, 1308-15	13

1825	Conformational changes associated with the binding of zinc acetate at the putative active site of XcTcmJ, a cupin from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . 2010 , 66, 1347-53	4
1824	Structure of an essential bacterial protein YeaZ (TM0874) from <i>Thermotoga maritima</i> at 2.5 Å resolution. 2010 , 66, 1230-6	14
1823	The structure of the first representative of Pfam family PF06475 reveals a new fold with possible involvement in glycolipid metabolism. 2010 , 66, 1211-7	8
1822	Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. 2010 , 66, 1205-10	2
1821	The structure of Jann_2411 (DUF1470) from <i>Jannaschia</i> sp. at 1.45 Å resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. 2010 , 66, 1198-204	9
1820	Structure of the first representative of Pfam family PF09410 (DUF2006) reveals a structural signature of the calycin superfamily that suggests a role in lipid metabolism. 2010 , 66, 1153-9	15
1819	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. 2010 , 66, 1245-53	8
1818	Structures of the first representatives of Pfam family PF06938 (DUF1285) reveal a new fold with repeated structural motifs and possible involvement in signal transduction. 2010 , 66, 1218-25	7
1817	Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of the <i>Bacillus</i> chorismate mutase fold and suggest a role in amino-acid metabolism. 2010 , 66, 1182-9	2
1816	A new crystal form of human diamine oxidase. 2010 , 66, 137-42	9
1815	The structure of DinB from <i>Geobacillus stearothermophilus</i> : a representative of a unique four-helix-bundle superfamily. 2010 , 66, 219-24	10
1814	A triclinic crystal form of <i>Escherichia coli</i> 4-diphosphocytidyl-2C-methyl-D-erythritol kinase and reassessment of the quaternary structure. 2010 , 66, 237-41	9
1813	The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. 2010 , 66, 1160-6	15
1812	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. 2010 , 66, 1167-73	3
1811	Dramatic improvement of crystal quality for low-temperature-grown rabbit muscle aldolase. 2010 , 66, 595-600	1
1810	The structure of PhaZ7 at atomic (1.2 Å) resolution reveals details of the active site and suggests a substrate-binding mode. 2010 , 66, 648-54	11
1809	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved β-barrel core domain and an auxiliary C-terminal treble-clef zinc finger. 2010 , 66, 1335-46	7
1808	Structure of a putative NTP pyrophosphohydrolase: YP_001813558.1 from <i>Exiguobacterium sibiricum</i> 255-15. 2010 , 66, 1237-44	2

1807	Near-atomic resolution analysis of BipD, a component of the type III secretion system of <i>Burkholderia pseudomallei</i> . 2010 , 66, 990-3	8
1806	Structure of <i>Bacteroides thetaiotaomicron</i> BT2081 at 2.05 Å resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. 2010 , 66, 1287-96	1
1805	High-resolution structure of an alpha-spectrin SH3-domain mutant with a redesigned hydrophobic core. 2010 , 66, 1023-7	3
1804	Structural analysis of <i>Bacillus pumilus</i> phenolic acid decarboxylase, a lipocalin-fold enzyme. 2010 , 66, 1407-14	21
1803	Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. 2010 , 66, 1274-80	9
1802	The homodimeric GBS1074 from <i>Streptococcus agalactiae</i> . 2010 , 66, 1421-5	13
1801	Structure of Hsp33/YOR391Cp from the yeast <i>Saccharomyces cerevisiae</i> . 2010 , 66, 1557-61	5
1800	A biophysical elucidation for less toxicity of agglutinin than abrin-a from the seeds of <i>Abrus precatorius</i> in consequence of crystal structure. 2010 , 17, 34	19
1799	Evidence for alternative quaternary structure in a bacterial Type III secretion system chaperone. 2010 , 10, 21	16
1798	Thermodynamic and structural insights into CSL-DNA complexes. 2010 , 19, 34-46	30
1797	Structure of the catalytic domain of the human mitochondrial Lon protease: proposed relation of oligomer formation and activity. 2010 , 19, 987-99	37
1796	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. 2010 , 19, 1031-43	244
1795	The short-chain oxidoreductase Q9HYA2 from <i>Pseudomonas aeruginosa</i> PAO1 contains an atypical catalytic center. 2010 , 19, 1097-103	1
1794	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP. 2010 , 19, 1439-43	12
1793	The crystal structure of the <i>Mycobacterium tuberculosis</i> Rv3019c-Rv3020c ESX complex reveals a domain-swapped heterotetramer. 2010 , 19, 1692-703	24
1792	Crystal structure of human thioredoxin revealing an unraveled helix and exposed S-nitrosation site. 2010 , 19, 1801-6	18
1791	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp23.1, a putative chaperone. 2010 , 19, 1812-6	10
1790	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. 2010 , 19, 2131-40	12

1789	The structure and NO binding properties of the nitrophorin-like heme-binding protein from <i>Arabidopsis thaliana</i> gene locus At1g79260.1. 2010 , 78, 917-31	41
1788	Heterologous quaternary structure of CXCL12 and its relationship to the CC chemokine family. 2010 , 78, 1331-7	35
1787	Amino acid substitutions at protein-protein interfaces that modulate the oligomeric state. 2010 , 78, 1563-74	11
1786	Structure of human CLIC3 at 2 Å resolution. 2010 , 78, 1594-600	22
1785	p-Coumaric acid decarboxylase from <i>Lactobacillus plantarum</i> : structural insights into the active site and decarboxylation catalytic mechanism. 2010 , 78, 1662-76	39
1784	Structural investigation of transcriptional regulator HlyIIIR: influence of a disordered region on protein fold and dimerization. 2010 , 78, 1870-7	2
1783	Crystal structure of an eIF4G-like protein from <i>Danio rerio</i> . 2010 , 78, 1803-6	2
1782	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. 2010 , 78, 1992-8	9
1781	Crystal structures of holo and Cu-deficient Cu/Zn-SOD from the silkworm <i>Bombyx mori</i> and the implications in amyotrophic lateral sclerosis. 2010 , 78, 1999-2004	10
1780	Structure and oligomerization of the PilC type IV pilus biogenesis protein from <i>Thermus thermophilus</i> . 2010 , 78, 2049-57	41
1779	Self-association of TPR domains: Lessons learned from a designed, consensus-based TPR oligomer. 2010 , 78, 2131-43	41
1778	Structure of full-length class I chitinase from rice revealed by X-ray crystallography and small-angle X-ray scattering. 2010 , 78, 2295-305	37
1777	CRK: an evolutionary approach for distinguishing biologically relevant interfaces from crystal contacts. 2010 , 78, 2707-13	23
1776	Side-chain rotamer transitions at protein-protein interfaces. 2010 , 78, 3219-25	15
1775	Structure of FocB--a member of a family of transcription factors regulating fimbrial adhesin expression in uropathogenic <i>Escherichia coli</i> . 2010 , 277, 3368-81	7
1774	A coleopteran triosephosphate isomerase: X-ray structure and phylogenetic impact of insect sequences. 2010 , 19, 35-48	6
1773	Structural studies on the full-length LysR-type regulator TsaR from <i>Comamonas testosteroni</i> T-2 reveal a novel open conformation of the tetrameric LTTR fold. 2010 , 75, 1199-214	60
1772	Structural basis of respiratory syncytial virus neutralization by motavizumab. 2010 , 17, 248-50	121

1771	The structure of the catalytic subunit FANCL of the Fanconi anemia core complex. 2010 , 17, 294-8	61
1770	How baculovirus polyhedra fit square pegs into round holes to robustly package viruses. 2010 , 29, 505-14	82
1769	Structural basis for the function of DEAH helicases. 2010 , 11, 180-6	88
1768	Structural basis for receptor recognition of vitamin-B(12)-intrinsic factor complexes. 2010 , 464, 445-8	86
1767	Structural basis of semaphorin-plexin signalling. 2010 , 467, 1118-22	168
1766	Visualization of macromolecular structures. 2010 , 7, S42-55	107
1765	Phenotypic variability, neurological outcome and genetics background of 6-pyruvoyl-tetrahydropterin synthase deficiency. 2010 , 77, 249-57	48
1764	The minimal autoinhibited unit of the guanine nucleotide exchange factor intersectin. 2010 , 5, e11291	17
1763	Crystal structure of the RNA recognition motif of yeast translation initiation factor eIF3b reveals differences to human eIF3b. 2010 , 5, e12784	9
1762	Comparative structural analysis of human DEAD-box RNA helicases. 2010 , 5, e12791	72
1761	Structural profiling of endogenous S-nitrosocysteine residues reveals unique features that accommodate diverse mechanisms for protein S-nitrosylation. 2010 , 107, 16958-63	216
1760	Functional differences of invariant and highly conserved residues in the extracellular domain of the glycoprotein hormone receptors. 2010 , 285, 34813-27	15
1759	Structure of the FoxM1 DNA-recognition domain bound to a promoter sequence. 2010 , 38, 4527-38	78
1758	The mechanism and control of DNA transfer by the conjugative relaxase of resistance plasmid pCU1. 2010 , 38, 5929-43	21
1757	Plastid-associated porphobilinogen synthase from <i>Toxoplasma gondii</i> : kinetic and structural properties validate therapeutic potential. 2010 , 285, 22122-31	30
1756	Implications of the HIV-1 Rev dimer structure at 3.2 Å resolution for multimeric binding to the Rev response element. 2010 , 107, 5810-4	106
1755	Identification, subcellular localization, biochemical properties, and high-resolution crystal structure of <i>Trypanosoma brucei</i> UDP-glucose pyrophosphorylase. 2010 , 20, 1619-30	25
1754	Drug resistance against HCV NS3/4A inhibitors is defined by the balance of substrate recognition versus inhibitor binding. 2010 , 107, 20986-91	146

1753	Structural basis for substrate activation and regulation by cystathionine beta-synthase (CBS) domains in cystathionine {beta}-synthase. 2010 , 107, 20958-63	280
1752	High-resolution x-ray structure and functional analysis of the murine norovirus 1 capsid protein protruding domain. 2010 , 84, 5695-705	66
1751	Structural and kinetic analysis of free methionine-R-sulfoxide reductase from <i>Staphylococcus aureus</i> : conformational changes during catalysis and implications for the catalytic and inhibitory mechanisms. 2010 , 285, 25044-52	10
1750	PDBe: Protein Data Bank in Europe. 2010 , 38, D308-17	86
1749	Structural and functional characterization of the transcriptional repressor CsoR from <i>Thermus thermophilus</i> HB8. 2010 , 156, 1993-2005	45
1748	ZBP1 recognition of beta-actin zipcode induces RNA looping. 2010 , 24, 148-58	129
1747	Crystallographic structure of porcine adenovirus type 4 fiber head and galectin domains. 2010 , 84, 10558-68	18
1746	Structure of the nucleoprotein binding domain of Mokola virus phosphoprotein. 2010 , 84, 1089-96	26
1745	H-NS forms a superhelical protein scaffold for DNA condensation. 2010 , 107, 15728-32	130
1744	Structural determination of functional domains in early B-cell factor (EBF) family of transcription factors reveals similarities to Rel DNA-binding proteins and a novel dimerization motif. 2010 , 285, 25875-9	18
1743	Global conformational change associated with the two-step reaction catalyzed by <i>Escherichia coli</i> lipote-protein ligase A. 2010 , 285, 9971-9980	28
1742	Structural characterization of apical membrane antigen 1 (AMA1) from <i>Toxoplasma gondii</i> . 2010 , 285, 15644-15652	38
1741	The N domain of human angiotensin-I-converting enzyme: the role of N-glycosylation and the crystal structure in complex with an N domain-specific phosphinic inhibitor, RXP407. 2010 , 285, 35685-93	59
1740	Neuroplastin-55 binds to and signals through the fibroblast growth factor receptor. 2010 , 24, 1139-50	42
1739	Quality assessment of protein model-structures using evolutionary conservation. 2010 , 26, 1299-307	41
1738	Symmetry versus Asymmetry in the Molecules of Life: Homomeric Protein Assemblies. 2010 , 2, 884-906	16
1737	ComSin: database of protein structures in bound (complex) and unbound (single) states in relation to their intrinsic disorder. 2010 , 38, D283-7	24
1736	Crystal structure of the P2 C-repressor: a binder of non-palindromic direct DNA repeats. 2010 , 38, 7778-90	10

1735	PyETV: a PyMOL evolutionary trace viewer to analyze functional site predictions in protein complexes. 2010 , 26, 2981-2	35
1734	Shedding of large functionally active CD11/CD18 Integrin complexes from leukocyte membranes during synovial inflammation distinguishes three types of arthritis through differential epitope exposure. 2010 , 185, 4154-68	35
1733	Metal templated design of protein interfaces. 2010 , 107, 1827-32	112
1732	The coxsackievirus-adenovirus receptor reveals complex homophilic and heterophilic interactions on neural cells. 2010 , 30, 2897-910	48
1731	ANCHOR: a web server and database for analysis of protein-protein interaction binding pockets for drug discovery. 2010 , 38, W407-11	88
1730	Structural and functional characterization of an RNase HI domain from the bifunctional protein Rv2228c from <i>Mycobacterium tuberculosis</i> . 2010 , 192, 2878-86	22
1729	Structure and folding of a designed knotted protein. 2010 , 107, 20732-7	102
1728	Evolution of new enzymatic function by structural modulation of cysteine reactivity in <i>Pseudomonas fluorescens</i> isocyanide hydratase. 2010 , 285, 29651-61	27
1727	Implications for collagen binding from the crystallographic structure of fibronectin 6FnI1-2FnII7FnI. 2010 , 285, 33764-70	26
1726	Ferredoxin:NADPH oxidoreductase is recruited to thylakoids by binding to a polyproline type II helix in a pH-dependent manner. 2010 , 107, 19260-5	46
1725	Dimeric architecture of the Hendra virus attachment glycoprotein: evidence for a conserved mode of assembly. 2010 , 84, 6208-17	75
1724	Mutational analyses reveal that the staphylococcal immune evasion molecule Sbi and complement receptor 2 (CR2) share overlapping contact residues on C3d: implications for the controversy regarding the CR2/C3d cocrystal structure. 2010 , 184, 1946-55	33
1723	Structural basis for the blockage of IL-2 signaling by therapeutic antibody basiliximab. 2010 , 184, 1361-8	27
1722	Structural and kinetic analysis of <i>Schwanniomyces occidentalis</i> invertase reveals a new oligomerization pattern and the role of its supplementary domain in substrate binding. 2010 , 285, 13930-41	60
1721	Inferred Biomolecular Interaction Server--a web server to analyze and predict protein interacting partners and binding sites. 2010 , 38, D518-24	66
1720	Structure and biochemical analysis of the heparin-induced E1 dimer of the amyloid precursor protein. 2010 , 107, 5381-6	81
1719	The multifunctional protein in peroxisomal beta-oxidation: structure and substrate specificity of the <i>Arabidopsis thaliana</i> protein MFP2. 2010 , 285, 24066-77	34
1718	Crystal structure of <i>Leishmania major</i> oligopeptidase B gives insight into the enzymatic properties of a trypanosomatid virulence factor. 2010 , 285, 39249-59	45

1717	Crystal structure of CCM3, a cerebral cavernous malformation protein critical for vascular integrity. 2010 , 285, 24099-107	63
1716	Crystal structure of aminomethyltransferase in complex with dihydrolipoyl-H-protein of the glycine cleavage system: implications for recognition of lipoyl protein substrate, disease-related mutations, and reaction mechanism. 2010 , 285, 18684-92	22
1715	Structural and kinetic characterization of 4-hydroxy-4-methyl-2-oxoglutarate/4-carboxy-4-hydroxy-2-oxoadipate aldolase, a protocatechuate degradation enzyme evolutionarily convergent with the HpaI and DmpG pyruvate aldolases. 2010 , 285, 36608-15	27
1714	Structural and biochemical characterization of peroxiredoxin Qbeta from <i>Xylella fastidiosa</i> : catalytic mechanism and high reactivity. 2010 , 285, 16051-65	40
1713	An antibody as surrogate receptor reveals determinants of activity of an innate immune peptide antibiotic. 2010 , 285, 35750-8	6
1712	Structural basis for substrate selectivity in human maltase-glucoamylase and sucrase-isomaltase N-terminal domains. 2010 , 285, 17763-70	138
1711	Functional hybrid rubisco enzymes with plant small subunits and algal large subunits: engineered rbcS cDNA for expression in <i>Chlamydomonas</i> . 2010 , 285, 19833-41	105
1710	Structural basis for the interaction between the growth factor-binding protein GRB10 and the E3 ubiquitin ligase NEDD4. 2010 , 285, 42130-9	22
1709	Structural and mechanistic studies on <i>Klebsiella pneumoniae</i> 2-Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase. 2010 , 285, 35446-54	16
1708	Substrate-mediated stabilization of a tetrameric drug target reveals Achilles heel in anthrax. 2010 , 285, 5188-95	41
1707	Structural analysis of <i>Thermus thermophilus</i> HB27 mannosyl-3-phosphoglycerate synthase provides evidence for a second catalytic metal ion and new insight into the retaining mechanism of glycosyltransferases. 2010 , 285, 17857-68	11
1706	Boron toxicity tolerance in barley through reduced expression of the multifunctional aquaporin HvNIP2;1. 2010 , 153, 1706-15	135
1705	Molecular basis for association of PIPKI gamma-p90 with clathrin adaptor AP-2. 2010 , 285, 2734-49	24
1704	A conserved protein interaction interface on the type 5 G protein beta subunit controls proteolytic stability and activity of R7 family regulator of G protein signaling proteins. 2010 , 285, 41100-12	14
1703	Structural insights into the catalytic mechanism of bacterial guanosine-diphospho-D-mannose pyrophosphorylase and its regulation by divalent ions. 2010 , 285, 27468-27476	24
1702	Structure of lactococcal phage p2 baseplate and its mechanism of activation. 2010 , 107, 6852-7	124
1701	Structural insight into M-band assembly and mechanics from the titin-obscurin-like-1 complex. 2010 , 107, 2908-13	56
1700	The structural and energetic basis for high selectivity in a high-affinity protein-protein interaction. 2010 , 107, 10080-5	101

1699	tRNA(His) guanylyltransferase (THG1), a unique 3'-5' nucleotidyl transferase, shares unexpected structural homology with canonical 5'-3' DNA polymerases. 2010 , 107, 20305-10	44
1698	Interaction of decay-accelerating factor with echovirus 7. 2010 , 84, 12665-74	33
1697	Structural basis of immunosuppression by the therapeutic antibody daclizumab. 2010 , 20, 1361-71	21
1696	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. 2010 , 16, 1205-16	13
1695	Structural basis of cell wall cleavage by a staphylococcal autolysin. 2010 , 6, e1000807	62
1694	A computational analysis of the antigenic properties of haemagglutinin in influenza A H3N2. 2010 , 26, 1403-8	34
1693	Adaptive divergence of ancient gene duplicates in the avian MHC class II beta. 2010 , 27, 2360-74	57
1692	Unloading RNAs in the cytoplasm. 2010 , 1, 139-143	8
1691	Structure of a major antigenic site on the respiratory syncytial virus fusion glycoprotein in complex with neutralizing antibody 101F. 2010 , 84, 12236-44	83
1690	The structure of the poxvirus A33 protein reveals a dimer of unique C-type lectin-like domains. 2010 , 84, 2502-10	23
1689	Crystal structure and functional insights of hemopexin fold protein from grass pea. 2010 , 152, 1842-50	19
1688	Structural and functional characterization of a novel homodimeric three-finger neurotoxin from the venom of <i>Ophiophagus hannah</i> (king cobra). 2010 , 285, 8302-15	63
1687	Mechanisms of protein oligomerization, the critical role of insertions and deletions in maintaining different oligomeric states. 2010 , 107, 20352-7	115
1686	Homodimeric enzymes as drug targets. 2010 , 17, 826-46	37
1685	Visualizing the metal-binding versatility of copper trafficking sites. 2010 , 49, 7798-810	24
1684	Pressure perturbation calorimetry and the thermodynamics of noncovalent interactions in water: comparison of protein-protein, protein-ligand, and cyclodextrin-adamantane complexes. 2010 , 114, 16228-35	25
1683	The crystal structure of the human nascent polypeptide-associated complex domain reveals a nucleic acid-binding region on the NACA subunit. 2010 , 49, 2890-6	20
1682	Structural studies of BmooMPalpha-I, a non-hemorrhagic metalloproteinase from <i>Bothrops moojeni</i> venom. 2010 , 55, 361-8	35

1681	Intermolecular interactions in a 44 kDa interferon-receptor complex detected by asymmetric reverse-protonation and two-dimensional NOESY. 2010 , 49, 5117-33	19
1680	Conformational selection in the recognition of the snurportin importin beta binding domain by importin beta. 2010 , 49, 5042-7	16
1679	Domain organization in <i>Candida glabrata</i> THI6, a bifunctional enzyme required for thiamin biosynthesis in eukaryotes. 2010 , 49, 9922-34	14
1678	Identification of carbonic anhydrase I immunodominant epitopes recognized by specific autoantibodies which indicate an improved prognosis in patients with malignancy after autologous stem cell transplantation. 2010 , 9, 5171-9	9
1677	Structure of the bacteriophage T4 long tail fiber receptor-binding tip. 2010 , 107, 20287-92	130
1676	Crystal structure of arginase from <i>Plasmodium falciparum</i> and implications for L-arginine depletion in malarial infection. 2010 , 49, 5600-8	32
1675	Delta12-prostaglandin J2 as a product and ligand of human serum albumin: formation of an unusual covalent adduct at His146. 2010 , 132, 824-32	55
1674	Reversible phase transitions in self-assembled monolayers at the liquid-solid interface: temperature-controlled opening and closing of nanopores. 2010 , 132, 5084-90	204
1673	Are scoring functions in protein-protein docking ready to predict interactomes? Clues from a novel binding affinity benchmark. 2010 , 9, 2216-25	196
1672	X-ray Study of Protein-Protein Complexes and Analysis of Interfaces. 2010 , 1-24	1
1671	Crystal structure of the cofactor-independent monooxygenase SnoaB from <i>Streptomyces nogalater</i> : implications for the reaction mechanism. 2010 , 49, 934-44	33
1670	Insights into the specificity of thioredoxin reductase-thioredoxin interactions. A structural and functional investigation of the yeast thioredoxin system. 2010 , 49, 3317-26	50
1669	Mutation of archaeal isopentenyl phosphate kinase highlights mechanism and guides phosphorylation of additional isoprenoid monophosphates. 2010 , 5, 589-601	22
1668	Crystallographic and nuclear magnetic resonance evaluation of the impact of peptide binding to the second PDZ domain of protein tyrosine phosphatase 1E. 2010 , 49, 9280-91	55
1667	X-ray structures of isopentenyl phosphate kinase. 2010 , 5, 517-27	23
1666	Structural insights into substrate specificity and solvent tolerance in alcohol dehydrogenase ADH-'A' from <i>Rhodococcus ruber</i> DSM 44541. 2010 , 46, 6314-6	54
1665	Mutational analysis of VIM-2 reveals an essential determinant for metallo-beta-lactamase stability and folding. 2010 , 54, 3197-204	46
1664	The mechanism of prion inhibition by HET-S. 2010 , 38, 889-99	71

1663	Exploring peptide mimics for the production of antibodies against discontinuous protein epitopes. 2010 , 47, 1137-48		24
1662	Comparative structural studies of two natural isoforms of ammodytoxin, phospholipases A2 from <i>Vipera ammodytes ammodytes</i> which differ in neurotoxicity and anticoagulant activity. 2010 , 169, 360-9		33
1661	Structure of dihydropyrimidinase from <i>Sinorhizobium meliloti</i> CECT4114: new features in an amidohydrolase family member. 2010 , 169, 200-8		27
1660	Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from <i>Thermoplasma acidophilum</i> . 2010 , 169, 304-11		13
1659	Inhibition of Toll-like receptors TLR4 and 7 signaling pathways by SIGIRR: a computational approach. 2010 , 169, 323-30		54
1658	The crystal structure of <i>Escherichia coli</i> spermidine synthase SpeE reveals a unique substrate-binding pocket. 2010 , 169, 277-85		18
1657	<i>Bacillus licheniformis</i> Anti-TRAP can assemble into two types of dodecameric particles with the same symmetry but inverted orientation of trimers. 2010 , 170, 127-33		3
1656	Atomic structure of vimentin coil 2. 2010 , 170, 369-76		81
1655	Crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase from the hyperthermophile <i>Thermotoga maritima</i> for insights into the coordination of conformational changes and an inhibitor binding. 2010 , 170, 532-9		22
1654	Comparison between apo and complexed structures of bothropstoxin-I reveals the role of Lys122 and Ca(2+)-binding loop region for the catalytically inactive Lys49-PLA(2)s. 2010 , 171, 31-43		39
1653	The structure of tryptophanyl-tRNA synthetase from <i>Giardia lamblia</i> reveals divergence from eukaryotic homologs. 2010 , 171, 238-43		10
1652	The crystal structure of the novobiocin biosynthetic enzyme NovP: the first representative structure for the TylF O-methyltransferase superfamily. <i>Journal of Molecular Biology</i> , 2010 , 395, 390-407 ^{6.5}		26
1651	Evolution of protein binding modes in homooligomers. <i>Journal of Molecular Biology</i> , 2010 , 395, 860-70	6.5	57
1650	Crystal structure of the ATPase subunit and its substrate-dependent association with the GATase subunit: a novel regulatory mechanism for a two-subunit-type GMP synthetase from <i>Pyrococcus horikoshii</i> OT3. <i>Journal of Molecular Biology</i> , 2010 , 395, 417-29	6.5	15
1649	Ligand-mediated dimerization of the Met receptor tyrosine kinase by the bacterial invasion protein InlB. <i>Journal of Molecular Biology</i> , 2010 , 395, 522-32	6.5	39
1648	A single mutation at the sheet switch region results in conformational changes favoring lambda6 light-chain fibrillogenesis. <i>Journal of Molecular Biology</i> , 2010 , 396, 280-92	6.5	38
1647	Binding of S-methyl-5'-thioadenosine and S-adenosyl-L-methionine to protein MJ0100 triggers an open-to-closed conformational change in its CBS motif pair. <i>Journal of Molecular Biology</i> , 2010 , 396, 800-20 ^{6.5}	6.5	41
1646	The crystal structure and activity of a putative trypanosomal nucleoside phosphorylase reveal it to be a homodimeric uridine phosphorylase. <i>Journal of Molecular Biology</i> , 2010 , 396, 1244-59	6.5	14

1645	Structural basis of substrate binding in WsaF, a rhamnosyltransferase from <i>Geobacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 2010 , 397, 436-47	6.5	19
1644	Crystal structure of the first eubacterial Mre11 nuclease reveals novel features that may discriminate substrates during DNA repair. <i>Journal of Molecular Biology</i> , 2010 , 397, 647-63	6.5	37
1643	A single-domain llama antibody potently inhibits the enzymatic activity of botulinum neurotoxin by binding to the non-catalytic alpha-exosite binding region. <i>Journal of Molecular Biology</i> , 2010 , 397, 1106-18	6.5	66
1642	Structural and functional analyses of beta-glucosidase 3B from <i>Thermotoga neapolitana</i> : a thermostable three-domain representative of glycoside hydrolase 3. <i>Journal of Molecular Biology</i> , 2010 , 397, 724-39	6.5	96
1641	Structure of bacteriophage T4 endonuclease II mutant E118A, a tetrameric GIY-YIG enzyme. <i>Journal of Molecular Biology</i> , 2010 , 397, 1003-16	6.5	6
1640	The subunit interfaces of weakly associated homodimeric proteins. <i>Journal of Molecular Biology</i> , 2010 , 398, 146-60	6.5	91
1639	The x-ray crystal structure of the first RNA recognition motif and site-directed mutagenesis suggest a possible HuR redox sensing mechanism. <i>Journal of Molecular Biology</i> , 2010 , 397, 1231-44	6.5	37
1638	Nonantibiotic properties of tetracyclines: structural basis for inhibition of secretory phospholipase A2. <i>Journal of Molecular Biology</i> , 2010 , 398, 83-96	6.5	27
1637	Crystal structure of sulfide:quinone oxidoreductase from <i>Acidithiobacillus ferrooxidans</i> : insights into sulfidotrophic respiration and detoxification. <i>Journal of Molecular Biology</i> , 2010 , 398, 292-305	6.5	74
1636	Crystal structures of the CBS and DRTGG domains of the regulatory region of <i>Clostridium perfringens</i> pyrophosphatase complexed with the inhibitor, AMP, and activator, diadenosine tetraphosphate. <i>Journal of Molecular Biology</i> , 2010 , 398, 400-13	6.5	30
1635	The crystal structure of protein MJ1225 from <i>Methanocaldococcus jannaschii</i> shows strong conservation of key structural features seen in the eukaryal gamma-AMPK. <i>Journal of Molecular Biology</i> , 2010 , 399, 53-70	6.5	26
1634	Functional states of homooligomers: insights from the evolution of glycosyltransferases. <i>Journal of Molecular Biology</i> , 2010 , 399, 196-206	6.5	32
1633	Crystal structure of the intermediate complex of the arginine repressor from <i>Mycobacterium tuberculosis</i> bound with its DNA operator reveals detailed mechanism of arginine repression. <i>Journal of Molecular Biology</i> , 2010 , 399, 240-54	6.5	6
1632	Geometric similarities of protein-protein interfaces at atomic resolution are only observed within homologous families: an exhaustive structural classification study. <i>Journal of Molecular Biology</i> , 2010 , 399, 526-40	6.5	16
1631	Structural and biochemical characterization of a halophilic archaeal alkaline phosphatase. <i>Journal of Molecular Biology</i> , 2010 , 400, 52-62	6.5	20
1630	Oligomeric state in the crystal structure of modular FAD synthetase provides insights into its sequential catalysis in prokaryotes. <i>Journal of Molecular Biology</i> , 2010 , 400, 218-30	6.5	37
1629	Crystal structure of human RNA helicase A (DHX9): structural basis for unselective nucleotide base binding in a DEAD-box variant protein. <i>Journal of Molecular Biology</i> , 2010 , 400, 768-82	6.5	31
1628	Crystal Structure of the 2-Oxoglutarate- and Fe(II)-Dependent Lysyl Hydroxylase JMJD6. <i>Journal of Molecular Biology</i> , 2010 ,	6.5	74

1627	P. aeruginosa PilT structures with and without nucleotide reveal a dynamic type IV pilus retraction motor. <i>Journal of Molecular Biology</i> , 2010 , 400, 1011-21	6.5	69
1626	The structure of the FnIII Tandem A77-A78 points to a periodically conserved architecture in the myosin-binding region of titin. <i>Journal of Molecular Biology</i> , 2010 , 401, 843-53	6.5	25
1625	Structure and reactivity of Bacillus subtilis MenD catalyzing the first committed step in menaquinone biosynthesis. <i>Journal of Molecular Biology</i> , 2010 , 401, 253-64	6.5	28
1624	Structure and function of P19, a high-affinity iron transporter of the human pathogen Campylobacter jejuni. <i>Journal of Molecular Biology</i> , 2010 , 401, 590-604	6.5	28
1623	Structure-based annotation of a novel sugar isomerase from the pathogenic E. coli O157:H7. <i>Journal of Molecular Biology</i> , 2010 , 401, 866-81	6.5	25
1622	Crystal structure of glyceraldehyde-3-phosphate dehydrogenase 1 from methicillin-resistant Staphylococcus aureus MRSA252 provides novel insights into substrate binding and catalytic mechanism. <i>Journal of Molecular Biology</i> , 2010 , 401, 949-68	6.5	32
1621	Molecular basis for complement recognition and inhibition determined by crystallographic studies of the staphylococcal complement inhibitor (SCIN) bound to C3c and C3b. <i>Journal of Molecular Biology</i> , 2010 , 402, 17-29	6.5	32
1620	Structural conservation of components in the amino acid sensing branch of the TOR pathway in yeast and mammals. <i>Journal of Molecular Biology</i> , 2010 , 402, 388-98	6.5	49
1619	Computational design of a chain-specific tetracycline repressor heterodimer. <i>Journal of Molecular Biology</i> , 2010 , 403, 371-85	6.5	6
1618	Crystal structure of zebrafish hatching enzyme 1 from the zebrafish Danio rerio. <i>Journal of Molecular Biology</i> , 2010 , 402, 865-78	6.5	32
1617	Diversity of bisubstrate binding modes of adenosine analogue-oligoarginine conjugates in protein kinase a and implications for protein substrate interactions. <i>Journal of Molecular Biology</i> , 2010 , 403, 66-77	6.5	25
1616	Crystal structure of Hexachlorocyclohexane Dehydrochlorinase LinA from Sphingobium japonicum UT26. <i>Journal of Molecular Biology</i> , 2010 , 403, 260-9	6.5	33
1615	TolA modulates the oligomeric status of YbgF in the bacterial periplasm. <i>Journal of Molecular Biology</i> , 2010 , 403, 270-85	6.5	31
1614	Full-length structures of BenM and two variants reveal different oligomerization schemes for LysR-type transcriptional regulators. <i>Journal of Molecular Biology</i> , 2010 , 404, 568-86	6.5	48
1613	Gradual adaptive changes of a protein facing high salt concentrations. <i>Journal of Molecular Biology</i> , 2010 , 404, 493-505	6.5	35
1612	Crystal structure of human interferon- β in complex with its high-affinity receptor interferon- β R1. <i>Journal of Molecular Biology</i> , 2010 , 404, 650-64	6.5	59
1611	Microcin J25 triggers cytochrome c release through irreversible damage of mitochondrial proteins and lipids. 2010 , 42, 273-81		16
1610	Sorting of the Alzheimer's disease amyloid precursor protein mediated by the AP-4 complex. 2010 , 18, 425-36		190

1609	In vitro receptor binding properties of a "painless" NGF mutein, linked to hereditary sensory autonomic neuropathy type V. 2010 , 391, 824-9	38
1608	A large-scale conformational change couples membrane recruitment to cargo binding in the AP2 clathrin adaptor complex. 2010 , 141, 1220-9	252
1607	Insights into egg coat assembly and egg-sperm interaction from the X-ray structure of full-length ZP3. 2010 , 143, 404-15	112
1606	Crotoxin: novel activities for a classic beta-neurotoxin. 2010 , 55, 1045-60	86
1605	Exploring the dihydrodipicolinate synthase tetramer: how resilient is the dimer-dimer interface?. 2010 , 494, 58-63	30
1604	Disruption of quaternary structure in Escherichia coli dihydrodipicolinate synthase (DHDPS) generates a functional monomer that is no longer inhibited by lysine. 2010 , 503, 202-6	11
1603	Directed evolution of a thermostable quorum-quenching lactonase from the amidohydrolase superfamily. 2010 , 285, 40911-20	66
1602	Crystal structure of the aspartyl-tRNA synthetase from Entamoeba histolytica. 2010 , 169, 95-100	13
1601	Homomeric protein complexes: evolution and assembly. 2010 , 38, 879-82	24
1600	Catalysis and inhibition of Mycobacterium tuberculosis methionine aminopeptidase. 2010 , 53, 1329-37	29
1599	Data Mining Techniques for the Life Sciences. 2010 ,	9
1598	Biochemical characterization of the transcriptional regulator BzdR from Azoarcus sp. CIB. 2010 , 285, 35694-705	23
1597	Intrinsic disorder and protein multibinding in domain, terminal, and linker regions. 2010 , 6, 1821-8	19
1596	Position 552 in a FMRFamide-gated Na(+) channel affects the gating properties and the potency of FMRFamide. 2010 , 27, 440-8	5
1595	Structural analysis of Saccharomyces cerevisiae alpha-galactosidase and its complexes with natural substrates reveals new insights into substrate specificity of GH27 glycosidases. 2010 , 285, 28020-33	31
1594	Crystal structure of bacteriophage SPP1 distal tail protein (gp19.1): a baseplate hub paradigm in gram-positive infecting phages. 2010 , 285, 36666-73	62
1593	Structural determinants underlying photoprotection in the photoactive orange carotenoid protein of cyanobacteria. 2010 , 285, 18364-75	114
1592	An accurate classification of native and non-native protein-protein interactions using supervised and semi-supervised learning approaches. 2010 ,	

1591	Regioselective deacetylation based on teicoplanin-complexed Orf2* crystal structures. 2011 , 7, 1224-31	19
1590	EspR, a key regulator of <i>Mycobacterium tuberculosis</i> virulence, adopts a unique dimeric structure among helix-turn-helix proteins. 2011 , 108, 13450-5	28
1589	Identification of cytoplasmic and membrane-associated complexes in human embryonic stem cells using blue native PAGE. 2011 , 7, 2688-701	6
1588	Structural basis for the neutralization and genotype specificity of hepatitis E virus. 2011 , 108, 10266-71	95
1587	Heterogeneous and homogeneous crystal nucleation in colloidal hard-sphere like microgels at low metastabilities. 2011 , 7, 11267	26
1586	Evolution of a new enzyme for carbon disulphide conversion by an acidothermophilic archaeon. 2011 , 478, 412-6	78
1585	Dehaloperoxidase-hemoglobin from <i>Amphitrite ornata</i> is primarily a monomer in solution. 2011 , 115, 4266-72	10
1584	The crystal structure of <i>Escherichia coli</i> group 4 capsule protein GfcC reveals a domain organization resembling that of Wza. 2011 , 50, 5465-76	20
1583	Modular mechanism of Wnt signaling inhibition by Wnt inhibitory factor 1. 2011 , 18, 886-93	113
1582	Molecular modeling and molecular dynamics simulation studies of Delta-Notch complex. 2011 , 29, 297-310	2
1581	Broad distribution of energetically important contacts across an extended protein interface. 2011 , 133, 10038-41	32
1580	The crystal structure of necrosis- and ethylene-inducing protein 2 from the causal agent of cacao's Witches' Broom disease reveals key elements for its activity. 2011 , 50, 9901-10	21
1579	Evidence of the participation of remote residues in the catalytic activity of Co-type nitrile hydratase from <i>Pseudomonas putida</i> . 2011 , 50, 4923-35	39
1578	Three clusters of conformational states in p450cam reveal a multistep pathway for closing of the substrate access channel. 2011 , 50, 693-703	46
1577	Flavin-induced oligomerization in <i>Escherichia coli</i> adaptive response protein AidB. 2011 , 50, 10159-69	6
1576	The protein common interface database (ProtCID)--a comprehensive database of interactions of homologous proteins in multiple crystal forms. 2011 , 39, D761-70	65
1575	Structure of the USP15 N-terminal domains: a β -hairpin mediates close association between the DUSP and UBL domains. 2011 , 50, 7995-8004	22
1574	Molecular basis of the thermostability and thermophilicity of laminarinases: X-ray structure of the hyperthermostable laminarinase from <i>Rhodothermus marinus</i> and molecular dynamics simulations. 2011 , 115, 7940-9	23

1573	Stabilization of a protein nanocage through the plugging of a protein-protein interfacial water pocket. 2011 , 50, 4029-37	21
1572	The Chp1-Tas3 core is a multifunctional platform critical for gene silencing by RITS. 2011 , 18, 1351-7	31
1571	Systematic computational prediction of protein interaction networks. 2011 , 8, 035008	30
1570	Structure and activity of <i>Aspergillus nidulans</i> copper amine oxidase. 2011 , 50, 5718-30	21
1569	Automated protein structure modeling with SWISS-MODEL Workspace and the Protein Model Portal. 2012 , 857, 107-36	106
1568	Three-dimensional structure of mannosyl-3-phosphoglycerate phosphatase from <i>Thermus thermophilus</i> HB27: a new member of the haloalcanolic acid dehalogenase superfamily. 2011 , 50, 9551-67	8
1567	Crystal structures of a halophilic archaeal malate synthase from <i>Haloferax volcanii</i> and comparisons with isoforms A and G. 2011 , 11, 23	14
1566	Thermodynamic characterization of the binding interaction between the histone demethylase LSD1/KDM1 and CoREST. 2011 , 50, 546-57	17
1565	Fragment growing induces conformational changes in acetylcholine-binding protein: a structural and thermodynamic analysis. 2011 , 133, 5363-71	63
1564	Glutathione transferases of <i>Phanerochaete chrysosporium</i> : S-glutathionyl-p-hydroquinone reductase belongs to a new structural class. 2011 , 286, 9162-73	35
1563	Stability of domain structures in multi-domain proteins. 2011 , 1, 40	66
1562	Focused evolution of HIV-1 neutralizing antibodies revealed by structures and deep sequencing. 2011 , 333, 1593-602	688
1561	Host cell invasion by apicomplexan parasites: insights from the co-structure of AMA1 with a RON2 peptide. 2011 , 333, 463-7	145
1560	Observation of intermolecular interactions in large protein complexes by 2D-double difference nuclear Overhauser enhancement spectroscopy: application to the 44 kDa interferon-receptor complex. 2011 , 133, 14755-64	12
1559	Mutational and structural studies of the PixD BLUF output signal that affects light-regulated interactions with PixE. 2011 , 50, 6365-75	27
1558	Crystallographic proof for an extended hydrogen-bonding network in small prolyl isomerases. 2011 , 133, 20096-9	26
1557	Amphiphilic nanotubes in the crystal structure of a biosurfactant protein hydrophobin HFBII. 2011 , 47, 9843-5	5
1556	The crystal structure of an oxygen-tolerant hydrogenase uncovers a novel iron-sulphur centre. 2011 , 479, 249-52	295

1555	Crystal structure determination and dynamic studies of Mycobacterium tuberculosis Cytidine deaminase in complex with products. 2011 , 509, 108-15	6
1554	Crystal structure and immunogenicity of the class C acid phosphatase from Pasteurella multocida. 2011 , 509, 76-81	4
1553	The crystal structure of rice (<i>Oryza sativa</i> L.) Os4BGlu12, an oligosaccharide and tuberonic acid glucoside-hydrolyzing β -glucosidase with significant thioglucosylhydrolase activity. 2011 , 510, 62-72	25
1552	A tetrameric structure is not essential for activity in dihydrodipicolinate synthase (DHDPS) from Mycobacterium tuberculosis. 2011 , 512, 154-9	16
1551	Structure of <i>Candida albicans</i> methionine synthase determined by employing surface residue mutagenesis. 2011 , 513, 19-26	7
1550	Structural basis of the 9-fold symmetry of centrioles. 2011 , 144, 364-75	263
1549	The mechanism of linkage-specific ubiquitin chain elongation by a single-subunit E2. 2011 , 144, 769-81	217
1548	Structural linkage between ligand discrimination and receptor activation by type I interferons. 2011 , 146, 621-32	253
1547	Molecular architecture of the transport channel of the nuclear pore complex. 2011 , 147, 590-602	87
1546	The molecular basis of CRL4DDB2/CSA ubiquitin ligase architecture, targeting, and activation. 2011 , 147, 1024-39	294
1545	The molecular basis for the endocytosis of small R-SNAREs by the clathrin adaptor CALM. 2011 , 147, 1118-31	140
1544	Crystal structure of the cysteine protease inhibitor 2 from <i>Entamoeba histolytica</i> : functional convergence of a common protein fold. 2011 , 471, 45-52	14
1543	Crystal structure of Bn IV in complex with myristic acid: a Lys49 myotoxic phospholipase AII from <i>Bothrops neuwiedi</i> venom. 2011 , 93, 513-8	18
1542	Structure of <i>Leishmania major</i> methionyl-tRNA synthetase in complex with intermediate products methionyladenylate and pyrophosphate. 2011 , 93, 570-82	36
1541	Tight association of N-terminal and catalytic subunits of rabbit 12/15-lipoxygenase is important for protein stability and catalytic activity. 2011 , 1811, 1001-10	15
1540	Molecular evolution and selection pressure in alpha-class carbonic anhydrase family members. 2011 , 1814, 1854-61	5
1539	Structure of a novel class II phospholipase D: catalytic cleft is modified by a disulphide bridge. 2011 , 409, 622-7	38
1538	Inverted repeats in the promoter as an autoregulatory sequence for TcrX in Mycobacterium tuberculosis. 2011 , 415, 17-23	9

1537	Structural analyses of a purine biosynthetic enzyme from <i>Mycobacterium tuberculosis</i> reveal a novel bound nucleotide. 2011 , 286, 40706-16		7
1536	Structural and functional analysis of three β -glucosidases from bacterium <i>Clostridium cellulovorans</i> , fungus <i>Trichoderma reesei</i> and termite <i>Neotermes koshunensis</i> . 2011 , 173, 46-56		142
1535	Structures of a key interaction protein from the <i>Trypanosoma brucei</i> editosome in complex with single domain antibodies. 2011 , 174, 124-36		23
1534	Crystal structure of <i>Salmonella typhimurium</i> 2-methylcitrate synthase: Insights on domain movement and substrate specificity. 2011 , 174, 58-68		6
1533	The crystal structure of the leptospiral hypothetical protein LIC12922 reveals homology with the periplasmic chaperone SurA. 2011 , 173, 312-22		8
1532	Structural basis for pH dependent monomer-dimer transition of 3,4-dihydroxy 2-butanone-4-phosphate synthase domain from <i>Mycobacterium tuberculosis</i> . 2011 , 174, 374-84		7
1531	Designed ankyrin repeat protein binders for the crystallization of AcrB: plasticity of the dominant interface. 2011 , 174, 269-81		20
1530	A novel heterotetrameric structure of the crenarchaeal PCNA2-PCNA3 complex. 2011 , 174, 443-50		11
1529	Crystal structure of the 30 K protein from the silkworm <i>Bombyx mori</i> reveals a new member of the β -trefoil superfamily. 2011 , 175, 97-103		24
1528	Molecular architecture of mouse activating NKR-P1 receptors. 2011 , 175, 434-41		30
1527	Crystal structures of <i>Pseudomonas aeruginosa</i> guanidinobutyrase and guanidinopropionase, members of the ureohydrolase superfamily. 2011 , 175, 329-38		10
1526	The unusual extended C-terminal helix of the peroxisomal β -hydrolase Lpx1 is involved in dimer contacts but dispensable for dimerization. 2011 , 175, 362-71		17
1525	Crystal structure of the TL29 protein from <i>Arabidopsis thaliana</i> : an APX homolog without peroxidase activity. 2011 , 176, 24-31		13
1524	Binding site and interlobe interactions of the ionotropic glutamate receptor GluK3 ligand binding domain revealed by high resolution crystal structure in complex with (S)-glutamate. 2011 , 176, 307-14		20
1523	Structural characterization of HBXIP: the protein that interacts with the anti-apoptotic protein survivin and the oncogenic viral protein HBx. <i>Journal of Molecular Biology</i> , 2011 , 405, 331-40	6.5	26
1522	Specific inhibition of the aspartate aminotransferase of <i>Plasmodium falciparum</i> . <i>Journal of Molecular Biology</i> , 2011 , 405, 956-71	6.5	32
1521	The structure of the CRISPR-associated protein Csa3 provides insight into the regulation of the CRISPR/Cas system. <i>Journal of Molecular Biology</i> , 2011 , 405, 939-55	6.5	72
1520	The Structure of <i>Physarum polycephalum</i> hemagglutinin I suggests a minimal carbohydrate recognition domain of legume lectin fold. <i>Journal of Molecular Biology</i> , 2011 , 405, 560-9	6.5	4

1519	The filamentous phages fd and IF1 use different mechanisms to infect Escherichia coli. <i>Journal of Molecular Biology</i> , 2011 , 405, 989-1003	6.5	21
1518	Crystal structure of arrestin-3 reveals the basis of the difference in receptor binding between two non-visual subtypes. <i>Journal of Molecular Biology</i> , 2011 , 406, 467-78	6.5	150
1517	A product analog bound form of 3-oxoadipate-enol-lactonase (PcaD) reveals a multifunctional role for the divergent cap domain. <i>Journal of Molecular Biology</i> , 2011 , 406, 649-58	6.5	31
1516	The crystal structure of l-sorbose reductase from <i>Gluconobacter frateurii</i> complexed with NADPH and l-sorbose. <i>Journal of Molecular Biology</i> , 2011 , 407, 543-55	6.5	14
1515	Ligand bound structures of a glycosyl hydrolase family 30 glucuronoxylan xylanohydrolase. <i>Journal of Molecular Biology</i> , 2011 , 407, 92-109	6.5	62
1514	Energetics of SecA dimerization. <i>Journal of Molecular Biology</i> , 2011 , 408, 87-98	6.5	27
1513	Interaction between nucleosome assembly protein 1-like family members. <i>Journal of Molecular Biology</i> , 2011 , 407, 647-60	6.5	27
1512	Crystal structure of R120G disease mutant of human B-crystallin domain dimer shows closure of a groove. <i>Journal of Molecular Biology</i> , 2011 , 408, 118-34	6.5	95
1511	Simultaneous formation of right- and left-handed anti-parallel coiled-coil interfaces by a coil2 fragment of human lamin A. <i>Journal of Molecular Biology</i> , 2011 , 408, 135-46	6.5	25
1510	The double-length tyrosyl-tRNA synthetase from the eukaryote <i>Leishmania major</i> forms an intrinsically asymmetric pseudo-dimer. <i>Journal of Molecular Biology</i> , 2011 , 409, 159-76	6.5	30
1509	Structural analysis of a novel class of R-M controller proteins: C.Csp231I from <i>Citrobacter</i> sp. RFL231. <i>Journal of Molecular Biology</i> , 2011 , 409, 177-88	6.5	11
1508	The crystal structure of death receptor 6 (DR6): a potential receptor of the amyloid precursor protein (APP). <i>Journal of Molecular Biology</i> , 2011 , 409, 189-201	6.5	22
1507	The extra-membranous domains of the competence protein HofQ show DNA binding, flexibility and a shared fold with type I KH domains. <i>Journal of Molecular Biology</i> , 2011 , 409, 642-53	6.5	18
1506	Probing dimerization and structural flexibility of mammalian lipoxygenases by small-angle X-ray scattering. <i>Journal of Molecular Biology</i> , 2011 , 409, 654-68	6.5	30
1505	Structural analysis of a putative aminoglycoside N-acetyltransferase from <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , 2011 , 410, 411-23	6.5	14
1504	Structure and organisation of SinR, the master regulator of biofilm formation in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2011 , 411, 597-613	6.5	29
1503	The crystal structure of zebrafish S100Z: implications for calcium-promoted S100 protein oligomerisation. <i>Journal of Molecular Biology</i> , 2011 , 411, 1072-82	6.5	7
1502	The structure of BRMS1 nuclear export signal and SNX6 interacting region reveals a hexamer formed by antiparallel coiled coils. <i>Journal of Molecular Biology</i> , 2011 , 411, 1114-27	6.5	12

1501	The dimeric structure of the Cpn60.2 chaperonin of <i>Mycobacterium tuberculosis</i> at 2.8 Å reveals possible modes of function. <i>Journal of Molecular Biology</i> , 2011 , 412, 192-203	6.5	23
1500	Crystal structure of crotoxin reveals key residues involved in the stability and toxicity of this potent heterodimeric β -neurotoxin. <i>Journal of Molecular Biology</i> , 2011 , 412, 176-91	6.5	75
1499	Structure of the food-poisoning <i>Clostridium perfringens</i> enterotoxin reveals similarity to the aerolysin-like pore-forming toxins. <i>Journal of Molecular Biology</i> , 2011 , 413, 138-49	6.5	70
1498	The structures of <i>Thermoplasma volcanium</i> phosphoribosyl pyrophosphate synthetase bound to ribose-5-phosphate and ATP analogs. <i>Journal of Molecular Biology</i> , 2011 , 413, 844-56	6.5	14
1497	High-throughput genetic identification of functionally important regions of the yeast DEAD-box protein Mss116p. <i>Journal of Molecular Biology</i> , 2011 , 413, 952-72	6.5	14
1496	Crystal structure of the passenger domain of the <i>Escherichia coli</i> autotransporter EspP. <i>Journal of Molecular Biology</i> , 2011 , 413, 985-1000	6.5	33
1495	A disulfide-free single-domain V(L) intrabody with blocking activity towards huntingtin reveals a novel mode of epitope recognition. <i>Journal of Molecular Biology</i> , 2011 , 414, 337-55	6.5	31
1494	Structure of the <i>Escherichia coli</i> phosphonate binding protein PhnD and rationally optimized phosphonate biosensors. <i>Journal of Molecular Biology</i> , 2011 , 414, 356-69	6.5	46
1493	The crystal structure of odorant binding protein 7 from <i>Anopheles gambiae</i> exhibits an outstanding adaptability of its binding site. <i>Journal of Molecular Biology</i> , 2011 , 414, 401-12	6.5	66
1492	Structure and dynamics of a stabilized coiled-coil domain in the P-TEFb regulator Hexim1. <i>Journal of Molecular Biology</i> , 2011 , 414, 639-53	6.5	10
1491	Molecular mechanisms of viral and host cell substrate recognition by hepatitis C virus NS3/4A protease. 2011 , 85, 6106-16		37
1490	Accelerated Macromolecular Solution Structure Recovery. 2011 ,		
1489	Modulation of the pharmacological activities of secretory phospholipase A2 from <i>Crotalus durissus cascavella</i> induced by naringin. 2011 , 16, 738-61		2
1488	Co-crystal structures of inhibitors with MRCK β a key regulator of tumor cell invasion. 2011 , 6, e24825		29
1487	Identification of amino acids that account for long-range interactions in two triosephosphate isomerases from pathogenic trypanosomes. 2011 , 6, e18791		13
1486	Crystal structure of the heteromolecular chaperone, AscE-AscG, from the type III secretion system in <i>Aeromonas hydrophila</i> . 2011 , 6, e19208		11
1485	Critical factors governing the difference in antizyme-binding affinities between human ornithine decarboxylase and antizyme inhibitor. 2011 , 6, e19253		16
1484	Identification of the allosteric regulatory site of insulin. 2011 , 6, e20864		26

1483	Structural and sequence analysis of imelysin-like proteins implicated in bacterial iron uptake. 2011 , 6, e21875	15
1482	An inserted β subdomain shapes the catalytic pocket of <i>Lactobacillus johnsonii</i> cinnamoyl esterase. 2011 , 6, e23269	32
1481	An angiotensin I-converting enzyme mutation (Y465D) causes a dramatic increase in blood ACE via accelerated ACE shedding. 2011 , 6, e25952	31
1480	Crystal structure of thrombin in complex with S-variegain: insights of a novel mechanism of inhibition and design of tunable thrombin inhibitors. 2011 , 6, e26367	34
1479	A novel N-acetylglutamate synthase architecture revealed by the crystal structure of the bifunctional enzyme from <i>Maricaulis maris</i> . 2011 , 6, e28825	12
1478	X-ray structural studies of the entire extracellular region of the serine/threonine kinase PrkC from <i>Staphylococcus aureus</i> . 2011 , 435, 33-41	44
1477	Crystal structure of a novel type of odorant-binding protein from <i>Anopheles gambiae</i> , belonging to the C-plus class. 2011 , 437, 423-30	42
1476	Structure of the leukemia oncogene LMO2: implications for the assembly of a hematopoietic transcription factor complex. 2011 , 117, 2146-56	51
1475	The P(2)' residue is a key determinant of mesotrypsin specificity: engineering a high-affinity inhibitor with anticancer activity. 2011 , 440, 95-105	30
1474	Archaeal RNA polymerase: the influence of the protruding stalk in crystal packing and preliminary biophysical analysis of the Rpo13 subunit. 2011 , 39, 25-30	9
1473	Functional and structural characterization of a novel mannosyl-3-phosphoglycerate synthase from <i>Rubrobacter xylanophilus</i> reveals its dual substrate specificity. 2011 , 79, 76-93	17
1472	Atypical DNA recognition mechanism used by the EspR virulence regulator of <i>Mycobacterium tuberculosis</i> . 2011 , 82, 251-64	20
1471	Crystal structure of an ascomycete fungal laccase from <i>Thielavia arenaria</i> --common structural features of asco-laccases. 2011 , 278, 2283-95	61
1470	Insights into the Rrf2 repressor family--the structure of CymR, the global cysteine regulator of <i>Bacillus subtilis</i> . 2011 , 278, 2689-701	40
1469	Quaternary structure, conformational variability and global motions of phosphoglucosamine mutase. 2011 , 278, 3298-307	9
1468	Characterization of an oxidoreductase from the arylamine N-acetyltransferase operon in <i>Mycobacterium smegmatis</i> . 2011 , 278, 4824-32	2
1467	Regulation and structure of YahD, a copper-inducible β serine hydrolase of <i>Lactococcus lactis</i> IL1403. 2011 , 314, 57-66	5
1466	Structural basis for MOF and MSL3 recruitment into the dosage compensation complex by MSL1. 2011 , 18, 142-9	75

1465	Structural basis of substrate discrimination and integrin binding by autotaxin. 2011 , 18, 198-204	203
1464	Three-dimensional structure of a viral genome-delivery portal vertex. 2011 , 18, 597-603	117
1463	Conformational changes in IgE contribute to its uniquely slow dissociation rate from receptor FcεRI. 2011 , 18, 571-6	91
1462	Structure of Importin13-Ubc9 complex: nuclear import and release of a key regulator of sumoylation. 2011 , 30, 427-38	27
1461	Substrate recognition by complement convertases revealed in the C5-cobra venom factor complex. 2011 , 30, 606-16	61
1460	Structure of the HECT:ubiquitin complex and its role in ubiquitin chain elongation. 2011 , 12, 342-9	121
1459	Structural characterization of the multidomain regulatory protein Rv1364c from Mycobacterium tuberculosis. 2011 , 19, 56-69	19
1458	Realizing the allosteric potential of the tetrameric protein kinase A R1holoenzyme. 2011 , 19, 265-76	35
1457	Interferon-inducible protein 16: insight into the interaction with tumor suppressor p53. 2011 , 19, 418-29	69
1456	Combining Bayes classification and point group symmetry under Boolean framework for enhanced protein quaternary structure inference. 2011 , 19, 304-12	22
1455	Structure and activity of a novel archaeal β -CASP protein with N-terminal KH domains. 2011 , 19, 622-32	26
1454	Relative solvent accessible surface area predicts protein conformational changes upon binding. 2011 , 19, 859-67	120
1453	The crystal structure of the β neurexin-1 extracellular region reveals a hinge point for mediating synaptic adhesion and function. 2011 , 19, 767-78	56
1452	The structure of neurexin 1 β reveals features promoting a role as synaptic organizer. 2011 , 19, 779-89	55
1451	Insights into the evolution of a complex virus from the crystal structure of vaccinia virus D13. 2011 , 19, 1011-20	59
1450	Crystal structure of cGMP-dependent protein kinase reveals novel site of interchain communication. 2011 , 19, 1317-27	50
1449	Structural basis for complex formation between human IRSp53 and the translocated intimin receptor Tir of enterohemorrhagic E. coli. 2011 , 19, 1294-306	24
1448	Unusual, dual endo- and exonuclease activity in the degradosome explained by crystal structure analysis of RNase J1. 2011 , 19, 1241-51	43

1447	Phosphorylation in protein-protein binding: effect on stability and function. 2011 , 19, 1807-15	192
1446	Phosphorylation at the interface. 2011 , 19, 1726-7	4
1445	Evolving specificity from variability for protein interaction domains. 2011 , 36, 183-90	34
1444	Characterization of a new phosphatase from Plasmodium. 2011 , 179, 69-79	18
1443	A structural basis for Staphylococcal complement subversion: X-ray structure of the complement-binding domain of Staphylococcus aureus protein Sbi in complex with ligand C3d. 2011 , 48, 452-62	13
1442	CD4-binding site alterations in CCR5-using HIV-1 envelopes influencing gp120-CD4 interactions and fusogenicity. 2011 , 410, 418-28	23
1441	Exploiting the high-resolution crystal structure of Staphylococcus aureus MenH to gain insight into enzyme activity. 2011 , 11, 19	12
1440	Structural characterization of a ribose-5-phosphate isomerase B from the pathogenic fungus Coccidioides immitis. 2011 , 11, 39	6
1439	Crystal structures of LacD from Staphylococcus aureus and LacD.1 from Streptococcus pyogenes: insights into substrate specificity and virulence gene regulation. 2011 , 585, 307-12	4
1438	Structural basis for a new tetracycline resistance mechanism relying on the TetX monooxygenase. 2011 , 585, 1061-6	69
1437	MEMO associated with an ErbB2 receptor phosphopeptide reveals a new phosphotyrosine motif. 2011 , 585, 2688-92	3
1436	Structural basis of coagulation factor V recognition for cleavage by RVV-V. 2011 , 585, 3020-5	25
1435	Hell's Gate globin I: an acid and thermostable bacterial hemoglobin resembling mammalian neuroglobin. 2011 , 585, 3250-8	26
1434	Glycolipids that elicit IFN- γ -biased responses from natural killer T cells. 2011 , 18, 1620-30	33
1433	Caught in self-interaction: evolutionary and functional mechanisms of protein homooligomerization. 2011 , 8, 035007	75
1432	Prediction of protein-protein interactions: unifying evolution and structure at protein interfaces. 2011 , 8, 035006	47
1431	The nucleotide-binding domain 2 of the human transporter protein MRP6. 2011 , 43, 465-71	16
1430	Nine crystal structures determine the substrate envelope of the MDR HIV-1 protease. 2011 , 30, 173-83	23

1429	Protein structure reports in JIMD--an important enhancement of journal scope. 2011 , 34, 563-4	
1428	Crystal structure of tarocystatin-papain complex: implications for the inhibition property of group-2 phytocystatins. 2011 , 234, 243-54	30
1427	ISC-like [2Fe-2S] ferredoxin (FdxB) dimer from <i>Pseudomonas putida</i> JCM 20004: structural and electron-nuclear double resonance characterization. 2011 , 16, 923-35	11
1426	dockYard--a repository to assist modeling of protein-protein docking. 2011 , 17, 599-606	2
1425	Kinetic and structural evidence of the alkenal/one reductase specificity of human β -crystallin. 2011 , 68, 1065-77	12
1424	The crystal structure of an esterase from the hyperthermophilic microorganism <i>Pyrobaculum calidifontis</i> VA1 explains its enantioselectivity. 2011 , 91, 1061-72	50
1423	Protein structure databases. 2011 , 48, 183-98	6
1422	Crystal structures of <i>Burkholderia cenocepacia</i> dihydropteroate synthase in the apo-form and complexed with the product 7,8-dihydropteroate. 2011 , 11, 21	17
1421	Structural comparison of tRNA m(1)A58 methyltransferases revealed different molecular strategies to maintain their oligomeric architecture under extreme conditions. 2011 , 11, 48	18
1420	Large-scale experimental studies show unexpected amino acid effects on protein expression and solubility in vivo in <i>E. coli</i> . 2011 , 1, 6	21
1419	Diffusion of hydrophobin proteins in solution and interactions with a graphite surface. 2011 , 4, 9	13
1418	Novel approach to controlled protein crystallization through ligandation of yttrium cations. 2011 , 44, 755-762	53
1417	The Protein Data Bank in Europe (PDBe): bringing structure to biology. 2011 , 67, 324-30	25
1416	Overview of the CCP4 suite and current developments. 2011 , 67, 235-42	8847
1415	Structure of the effector-binding domain of the LysR-type transcription factor RovM from <i>Yersinia pseudotuberculosis</i> . 2011 , 67, 81-90	8
1414	Structural characterization of CalO1: a putative orsellinic acid methyltransferase in the calicheamicin-biosynthetic pathway. 2011 , 67, 197-203	15
1413	Structure of the sortase AcSrtC-1 from <i>Actinomyces oris</i> . 2011 , 67, 212-7	21
1412	Macromolecular complexes in crystals and solutions. 2011 , 67, 376-85	44

1411	Presenting your structures: the CCP4mg molecular-graphics software. 2011 , 67, 386-94	908
1410	Scaffoldin-borne family 3b carbohydrate-binding module from the cellulosome of <i>Bacteroides cellulosolvens</i> : structural diversity and significance of calcium for carbohydrate binding. 2011 , 67, 506-15	16
1409	Crystallographic determination of the disease-associated T1184R variant of complement regulator factor H. 2011 , 67, 593-600	7
1408	High-resolution X-ray structure of the rabbit histidine triad nucleotide-binding protein 1 (rHINT1)-adenosine complex at 1.10 Å resolution. 2011 , 67, 601-7	5
1407	Structure of 2-oxo-3-deoxygalactonate kinase from <i>Klebsiella pneumoniae</i> . 2011 , 67, 678-89	4
1406	Structural features of peroxisomal catalase from the yeast <i>Hansenula polymorpha</i> . 2011 , 67, 690-8	10
1405	High-resolution structure of a retroviral protease folded as a monomer. 2011 , 67, 907-14	15
1404	The structure of <i>Serratia marcescens</i> Lip, a membrane-bound component of the type VI secretion system. 2011 , 67, 1065-72	26
1403	Deriving the ultrastructure of crustacyanin using lower-resolution structural and biophysical methods. 2011 , 18, 79-83	9
1402	Structure of the dimeric form of CTP synthase from <i>Sulfolobus solfataricus</i> . 2011 , 67, 201-8	18
1401	Pentapeptide-repeat proteins that act as topoisomerase poison resistance factors have a common dimer interface. 2011 , 67, 296-302	24
1400	Structure of the extended-spectrum β-lactamase TEM-72 inhibited by citrate. 2011 , 67, 303-6	10
1399	Crystallization and preliminary X-ray analysis of mannosyl-3-phosphoglycerate phosphatase from <i>Thermus thermophilus</i> HB27. 2011 , 67, 390-6	1
1398	BrabA.11339.a: anomalous diffraction and ligand binding guide towards the elucidation of the function of a 'putative β-lactamase-like protein' from <i>Brucella melitensis</i> . 2011 , 67, 1106-12	4
1397	Structure of nitrilotriacetate monooxygenase component B from <i>Mycobacterium thermoresistibile</i> . 2011 , 67, 1100-5	13
1396	Structure of thymidylate kinase from <i>Ehrlichia chaffeensis</i> . 2011 , 67, 1090-4	1
1395	Structure of the <i>Drosophila melanogaster</i> Rab6 GTPase at 1.4 Å resolution. 2011 , 67, 744-8	3
1394	Crystallization and preliminary X-ray analysis of a putative sensor histidine kinase domain: the C-terminal domain of HksP4 from <i>Aquifex aeolicus</i> VF5. 2011 , 67, 803-7	0

1393	Structure of triosephosphate isomerase from <i>Cryptosporidium parvum</i> . 2011 , 67, 1095-9	1
1392	Structure of fructose bisphosphate aldolase from <i>Encephalitozoon cuniculi</i> . 2011 , 67, 1055-9	2
1391	Structure of filamin A immunoglobulin-like repeat 10 from <i>Homo sapiens</i> . 2011 , 67, 871-6	11
1390	Structure of fumarate hydratase from <i>Rickettsia prowazekii</i> , the agent of typhus and suspected relative of the mitochondria. 2011 , 67, 1123-8	3
1389	Structures of respiratory syncytial virus nucleocapsid protein from two crystal forms: details of potential packing interactions in the native helical form. 2011 , 67, 1179-83	14
1388	Structure of 3-ketoacyl-(acyl-carrier-protein) reductase from <i>Rickettsia prowazekii</i> at 2.25 Å resolution. 2011 , 67, 1118-22	9
1387	Purification, crystallization and diffraction studies of the methyltransferases BT_2972 and BVU_3255 from antibiotic-resistant pathogens of the genus <i>Bacteroides</i> from the human intestine. 2011 , 67, 1359-62	
1386	Structure of cellobiose phosphorylase from <i>Clostridium thermocellum</i> in complex with phosphate. 2011 , 67, 1345-9	20
1385	Crystallographic analysis of the C-terminal domain of the <i>Escherichia coli</i> lipoprotein BamC. 2011 , 67, 1350-8	19
1384	Structure of hyperthermophilic α-glucosidase from <i>Pyrococcus furiosus</i> . 2011 , 67, 1473-9	23
1383	Structure of the H107R variant of the extracellular domain of mouse NKR-P1A at 2.3 Å resolution. 2011 , 67, 1519-23	6
1382	Comprehensive, atomic-level characterization of structurally characterized protein-protein interactions: the PICCOLO database. 2011 , 12, 313	44
1381	The UlaG protein family defines novel structural and functional motifs grafted on an ancient RNase fold. 2011 , 11, 273	5
1380	The crystal structure of alanine racemase from <i>Streptococcus pneumoniae</i> , a target for structure-based drug design. 2011 , 11, 116	24
1379	Structural studies on the enzyme complex isopropylmalate isomerase (LeuCD) from <i>Mycobacterium tuberculosis</i> . 2011 , 79, 35-49	17
1378	Structural, functional, and bioinformatics studies reveal a new snake venom homologue phospholipase A ₂ class. 2011 , 79, 61-78	36
1377	Crystal structure of isoamyl acetate-hydrolyzing esterase from <i>Saccharomyces cerevisiae</i> reveals a novel active site architecture and the basis of substrate specificity. 2011 , 79, 662-8	13
1376	Crystal structure of curcuminoid synthase CUS from <i>Oryza sativa</i> . 2011 , 79, 669-73	6

1375	Insights into <i>Mycoplasma genitalium</i> metabolism revealed by the structure of MG289, an extracytoplasmic thiamine binding lipoprotein. 2011 , 79, 528-36	7
1374	Structures of parasitic CDPK domains point to a common mechanism of activation. 2011 , 79, 803-20	71
1373	Structure of the C-terminal heme-binding domain of THAP domain containing protein 4 from <i>Homo sapiens</i> . 2011 , 79, 1337-41	20
1372	Crystal structure of a bacterial phosphoglucomutase, an enzyme involved in the virulence of multiple human pathogens. 2011 , 79, 1215-29	23
1371	Structural basis for a ribofuranosyl binding protein: insights into the furanose specific transport. 2011 , 79, 1352-7	4
1370	Crystal structure of the GAF-B domain from human phosphodiesterase 5. 2011 , 79, 1682-7	3
1369	Structure of an archaeal-type phosphoenolpyruvate carboxylase sensitive to inhibition by aspartate. 2011 , 79, 1820-9	6
1368	The structure of a D-xylose isomerase from the B regulon of <i>Bacillus subtilis</i> . 2011 , 79, 2015-9	12
1367	Crystal structure of a metal-dependent phosphoesterase (YP_910028.1) from <i>Bifidobacterium adolescentis</i> : Computational prediction and experimental validation of phosphoesterase activity. 2011 , 79, 2146-60	11
1366	Cover and spacer insertions: small nonhydrophobic accessories that assist protein oligomerization. 2011 , 79, 2372-9	11
1365	Structure of the catalytic domain of glucuronoyl esterase Cip2 from <i>Hypocrea jecorina</i> . 2011 , 79, 2588-92	43
1364	Docking and free energy simulations to predict conformational domains involved in hCG-LH receptor interactions using recombinant antibodies. 2011 , 79, 3108-22	6
1363	Assessment of ligand-binding residue predictions in CASP9. 2011 , 79 Suppl 10, 126-36	59
1362	Assessment of template based protein structure predictions in CASP9. 2011 , 79 Suppl 10, 37-58	133
1361	The crystal structures of the <i>Salmonella</i> type III secretion system tip protein SipD in complex with deoxycholate and chenodeoxycholate. 2011 , 20, 75-86	54
1360	Crystal structure of the sensory domain of <i>Escherichia coli</i> CadC, a member of the ToxR-like protein family. 2011 , 20, 656-69	18
1359	Self-association studies of the bifunctional N-acetylglucosamine-1-phosphate uridyltransferase from <i>Escherichia coli</i> . 2011 , 20, 745-52	3
1358	Crystal structure of New Delhi metallo- β -lactamase reveals molecular basis for antibiotic resistance. 2011 , 20, 1484-91	135

1357	Crystal structure of N-domain of FKBP22 from <i>Shewanella</i> sp. SIB1: dimer dissociation by disruption of Val-Leu knot. 2011 , 20, 1755-64	10
1356	Rational disruption of the oligomerization of the mini-ferritin <i>E. coli</i> DPS through protein-protein interface mutation. 2011 , 20, 1907-17	22
1355	Feature-based classification of native and non-native protein-protein interactions: Comparing supervised and semi-supervised learning approaches. 2011 , 11, 4321-30	9
1354	Contribution of Non-Canonical Interactions to the Stability of Sm/LSm Oligomeric Assemblies. 2011 , 30, 430-42	4
1353	Using correlated parameters for improved ranking of protein-protein docking decoys. 2011 , 32, 787-96	12
1352	Crystal structure of an arthritogenic anticollagen immune complex. 2011 , 63, 3740-8	22
1351	Small angle X-ray scattering as a complementary tool for high-throughput structural studies. 2011 , 95, 517-30	58
1350	Re-structuring protein crystals porosity for biotemplating by chemical modification of lysine residues. 2011 , 108, 1-11	10
1349	Tolerance of α -diketone hydrolases as representatives of the crotonase superfamily towards organic solvents. 2011 , 108, 2815-22	6
1348	Inter-subunit interactions in erythroid and non-erythroid spectrins. 2011 , 1814, 420-7	5
1347	The lipoproteins of cyanobacterial photosystem II. 2011 , 104, 191-203	46
1346	Non-covalent interactions across subunit interfaces in Sm proteins. 2011 , 271, 18-26	4
1345	Protein modifications giving rise to homo-oligomers. 2011 , 103, 187-229	
1344	Novel pentameric structure of the diarrhea-inducing region of the rotavirus enterotoxigenic protein NSP4. 2011 , 85, 12721-32	21
1343	Crystal structure of the human astrovirus capsid spike. 2011 , 108, 12681-6	63
1342	COCOMAPS: a web application to analyze and visualize contacts at the interface of biomolecular complexes. 2011 , 27, 2915-6	159
1341	Structural and immunologic characterization of Ara h 1, a major peanut allergen. 2011 , 286, 39318-27	74
1340	Structural basis for antiviral inhibition of the main protease, 3C, from human enterovirus 93. 2011 , 85, 10764-73	16

1339	Kinked β -strands mediate high-affinity recognition of mRNA targets by the germ-cell regulator DAZL. 2011 , 108, 18266-71	46
1338	The RCSB Protein Data Bank: redesigned web site and web services. 2011 , 39, D392-401	461
1337	A structural model of the Sgt2 protein and its interactions with chaperones and the Get4/Get5 complex. 2011 , 286, 34325-34	50
1336	PCNA directs type 2 RNase H activity on DNA replication and repair substrates. 2011 , 39, 3652-66	88
1335	Structure of QnrB1, a plasmid-mediated fluoroquinolone resistance factor. 2011 , 286, 25265-73	64
1334	Structural basis for the role of the Sir3 AAA+ domain in silencing: interaction with Sir4 and unmethylated histone H3K79. 2011 , 25, 1835-46	33
1333	Structural insights into cis element recognition of non-polyadenylated RNAs by the Nab3-RRM. 2011 , 39, 337-46	23
1332	A prominent β -hairpin structure in the winged-helix domain of RECQ1 is required for DNA unwinding and oligomer formation. 2011 , 39, 1703-17	48
1331	The E3 ubiquitin ligase- and protein phosphatase 2A (PP2A)-binding domains of the Alpha4 protein are both required for Alpha4 to inhibit PP2A degradation. 2011 , 286, 17665-71	39
1330	Crystal structures of two active proliferating cell nuclear antigens (PCNAs) encoded by <i>Thermococcus kodakaraensis</i> . 2011 , 108, 2711-6	27
1329	Structural basis for complement factor I control and its disease-associated sequence polymorphisms. 2011 , 108, 12839-44	92
1328	Structural basis for two-component system inhibition and pilus sensing by the auxiliary CpxP protein. 2011 , 286, 9805-14	50
1327	Characterization of the interactions between the nucleoprotein and the phosphoprotein of Henipavirus. 2011 , 286, 13583-602	51
1326	Adaptive evolution of threonine deaminase in plant defense against insect herbivores. 2011 , 108, 5897-902	57
1325	High-resolution structural insights on the sugar-recognition and fusion tag properties of a versatile β -trefoil lectin domain from the mushroom <i>Laetiporus sulphureus</i> . 2011 , 21, 1349-61	30
1324	A dimeric Rep protein initiates replication of a linear archaeal virus genome: implications for the Rep mechanism and viral replication. 2011 , 85, 925-31	34
1323	Molecular rearrangements involved in the capsid shell maturation of bacteriophage T7. 2011 , 286, 234-42	49
1322	Structure of the PilM-PilN inner membrane type IV pilus biogenesis complex from <i>Thermus thermophilus</i> . 2011 , 286, 24434-42	61

1321	M-ORBIS: mapping of molecular binding sites and surfaces. 2011 , 39, 30-43	9
1320	Structural basis of neutralization of the major toxic component from the scorpion <i>Centruroides noxius</i> Hoffmann by a human-derived single-chain antibody fragment. 2011 , 286, 20892-900	14
1319	HIV-1 escape from the CCR5 antagonist maraviroc associated with an altered and less-efficient mechanism of gp120-CCR5 engagement that attenuates macrophage tropism. 2011 , 85, 4330-42	63
1318	Structure and binding analysis of <i>Polyporus squamosus</i> lectin in complex with the Neu5Ac{alpha}2-6Gal{beta}1-4GlcNAc human-type influenza receptor. 2011 , 21, 973-84	51
1317	BISC: binary subcomplexes in proteins database. 2011 , 39, D705-11	4
1316	PKA phosphorylation of NDE1 is DISC1/PDE4 dependent and modulates its interaction with LIS1 and NDEL1. 2011 , 31, 9043-54	62
1315	Structure of <i>Burkholderia cepacia</i> UDP-glucose dehydrogenase (UGD) BceC and role of Tyr10 in final hydrolysis of UGD thioester intermediate. 2011 , 193, 3978-87	21
1314	Structure of the periplasmic stress response protein CpxP. 2011 , 193, 2149-57	38
1313	Crystal structure of <i>Archaeoglobus fulgidus</i> CTP:inositol-1-phosphate cytidyltransferase, a key enzyme for di-myo-inositol-phosphate synthesis in (hyper)thermophiles. 2011 , 193, 2177-85	13
1312	Temperature-sensitive mutants of RNase E in <i>Salmonella enterica</i> . 2011 , 193, 6639-50	6
1311	SDM--a server for predicting effects of mutations on protein stability and malfunction. 2011 , 39, W215-22	343
1310	Structure-activity analysis of cathepsin K/chondroitin 4-sulfate interactions. 2011 , 286, 8988-98	25
1309	Defining a structural and kinetic rationale for paralogous copies of phenylacetate-CoA ligases from the cystic fibrosis pathogen <i>Burkholderia cenocepacia</i> J2315. 2011 , 286, 15577-85	25
1308	Structure of human C8 protein provides mechanistic insight into membrane pore formation by complement. 2011 , 286, 17585-92	77
1307	Characterization of a dipartite iron uptake system from uropathogenic <i>Escherichia coli</i> strain F11. 2011 , 286, 25317-30	28
1306	Mapping the I{kappa}B kinase beta (IKKbeta)-binding interface of the B14 protein, a vaccinia virus inhibitor of IKKbeta-mediated activation of nuclear factor kappaB. 2011 , 286, 20727-35	43
1305	Molecular basis for the unique role of the AAA+ chaperone ClpV in type VI protein secretion. 2011 , 286, 30010-21	79
1304	βGalactosidase/sucrose kinase (AgaSK), a novel bifunctional enzyme from the human microbiome coupling galactosidase and kinase activities. 2011 , 286, 40814-23	21

1303	Molecular recognition of leucine-aspartate repeat (LD) motifs by the focal adhesion targeting homology domain of cerebral cavernous malformation 3 (CCM3). 2011 , 286, 26138-47	31
1302	Molecular analysis of the interaction of the snake venom rhodocytin with the platelet receptor CLEC-2. 2011 , 3, 991-1003	9
1301	Compensated pathogenic deviations. 2011 , 2, 281-92	3
1300	Toward the estimation of the absolute quality of individual protein structure models. 2011 , 27, 343-50	1357
1299	Crystal structure of human natural cytotoxicity receptor NKp30 and identification of its ligand binding site. 2011 , 108, 6223-8	58
1298	Molecular recognition of chymotrypsin by the serine protease inhibitor ecotin from <i>Yersinia pestis</i> . 2011 , 286, 24015-22	12
1297	New insights into the mechanism of odorant detection by the malaria-transmitting mosquito <i>Anopheles gambiae</i> . 2011 , 286, 34175-83	24
1296	Atomic structure of bacteriophage Sf6 tail needle knob. 2011 , 286, 30867-30877	26
1295	Structures of <i>Phytophthora</i> RXLR effector proteins: a conserved but adaptable fold underpins functional diversity. 2011 , 286, 35834-35842	131
1294	The crystal structure and mechanism of an unusual oxidoreductase, GilR, involved in gilvocarcin V biosynthesis. 2011 , 286, 23533-43	18
1293	The structure of the plakin domain of plectin reveals a non-canonical SH3 domain interacting with its fourth spectrin repeat. 2011 , 286, 12429-38	37
1292	Crystal Structure of the cis-Dimer of Nectin-1: implications for the architecture of cell-cell junctions. 2011 , 286, 12659-69	41
1291	Structural and biological properties of the <i>Drosophila</i> insulin-like peptide 5 show evolutionary conservation. 2011 , 286, 661-73	43
1290	Novel folding and stability defects cause a deficiency of human glutathione transferase omega 1. 2011 , 286, 4271-9	23
1289	Insights into association of the NuRD complex with FOG-1 from the crystal structure of an RbAp48-FOG-1 complex. 2011 , 286, 1196-203	70
1288	Structural basis of tumor suppressor in lung cancer 1 (TSLC1) binding to differentially expressed in adenocarcinoma of the lung (DAL-1/4.1B). 2011 , 286, 4511-6	22
1287	TCRs used in cancer gene therapy cross-react with MART-1/Melan-A tumor antigens via distinct mechanisms. 2011 , 187, 2453-63	98
1286	Idas, a novel phylogenetically conserved geminin-related protein, binds to geminin and is required for cell cycle progression. 2011 , 286, 23234-46	38

1285	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. 2011 , 480, 336-43	682
1284	Computational design of a symmetric homodimer using β -strand assembly. 2011 , 108, 20562-7	63
1283	Crystal structure of <i>Bacillus anthracis</i> phosphoglucosamine mutase, an enzyme in the peptidoglycan biosynthetic pathway. 2011 , 193, 4081-7	22
1282	The <i>Leishmania donovani</i> UMP synthase is essential for promastigote viability and has an unusual tetrameric structure that exhibits substrate-controlled oligomerization. 2011 , 286, 20930-41	28
1281	Unexpected diversity of chlorite dismutases: a catalytically efficient dimeric enzyme from <i>Nitrobacter winogradskyi</i> . 2011 , 193, 2408-17	66
1280	The virulence factor PEB4 (Cj0596) and the periplasmic protein Cj1289 are two structurally related SurA-like chaperones in the human pathogen <i>Campylobacter jejuni</i> . 2011 , 286, 21254-65	27
1279	X-ray structure and site-directed mutagenesis analysis of the <i>Escherichia coli</i> colicin M immunity protein. 2011 , 193, 205-14	18
1278	Ligand-induced conformational changes within a hexameric Acyl-CoA thioesterase. 2011 , 286, 35643-35649	9
1277	Crystal structures of <i>Staphylococcus epidermidis</i> mevalonate diphosphate decarboxylase bound to inhibitory analogs reveal new insight into substrate binding and catalysis. 2011 , 286, 23900-10	25
1276	The structure of the kinesin-1 motor-tail complex reveals the mechanism of autoinhibition. 2011 , 333, 883-5	118
1275	Structural and functional analysis of a new subfamily of glycosyltransferases required for glycosylation of serine-rich streptococcal adhesins. 2011 , 286, 27048-57	25
1274	Remote control of regioselectivity in acyl-acyl carrier protein-desaturases. 2011 , 108, 16594-9	51
1273	Molecular basis of 1,6-anhydro bond cleavage and phosphoryl transfer by <i>Pseudomonas aeruginosa</i> 1,6-anhydro-N-acetylmuramic acid kinase. 2011 , 286, 12283-91	21
1272	Structure and mechanism of the lipooligosaccharide sialyltransferase from <i>Neisseria meningitidis</i> . 2011 , 286, 37237-48	30
1271	Crystal structure of β -barrel assembly machinery BamCD protein complex. 2011 , 286, 39116-21	60
1270	Crystal structure of uronate dehydrogenase from <i>Agrobacterium tumefaciens</i> . 2011 , 286, 27294-300	25
1269	Crystal structure of heterodimeric hexaprenyl diphosphate synthase from <i>Micrococcus luteus</i> B-P 26 reveals that the small subunit is directly involved in the product chain length regulation. 2011 , 286, 3729-40	15
1268	Crystal structure of the <i>Pseudomonas aeruginosa</i> virulence factor regulator. 2011 , 193, 4069-74	10

1267	Conformational flexibility of the ligand-binding domain dimer in kainate receptor gating and desensitization. 2011 , 31, 2916-24	20
1266	Mechanism of ubiquitylation by dimeric RING ligase RNF4. 2011 , 18, 1052-9	123
1265	Mechanism of actin filament nucleation by the bacterial effector VopL. 2011 , 18, 1068-74	49
1264	Structures of SAS-6 suggest its organization in centrioles. 2011 , 331, 1196-9	240
1263	Structural basis for the removal of ubiquitin and interferon-stimulated gene 15 by a viral ovarian tumor domain-containing protease. 2011 , 108, 2222-7	74
1262	PDBe: Protein Data Bank in Europe. 2011 , 39, D402-10	48
1261	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. 2011 , 108, 14879-84	105
1260	Protein-protein binding affinity prediction on a diverse set of structures. 2011 , 27, 3002-9	86
1259	The ancestral role of ATP hydrolysis in type II topoisomerases: prevention of DNA double-strand breaks. 2011 , 39, 6327-39	48
1258	Structure-based approach to rationally design a chimeric protein for an effective vaccine against Group B Streptococcus infections. 2011 , 108, 10278-83	107
1257	Changes in dynamics upon oligomerization regulate substrate binding and allostery in amino acid kinase family members. 2011 , 7, e1002201	40
1256	Structural and functional studies on the interaction of GspC and GspD in the type II secretion system. 2011 , 7, e1002228	74
1255	Towards a structural comprehension of bacterial type VI secretion systems: characterization of the TssJ-TssM complex of an Escherichia coli pathovar. 2011 , 7, e1002386	99
1254	Structural insights into quinolone antibiotic resistance mediated by pentapeptide repeat proteins: conserved surface loops direct the activity of a Qnr protein from a gram-negative bacterium. 2011 , 39, 3917-27	61
1253	The crystal structure of the ubiquitin-like (UBL) domain of human homologue A of Rad23 (hHR23A) protein. 2011 , 24, 131-8	3
1252	Xwalk: computing and visualizing distances in cross-linking experiments. 2011 , 27, 2163-4	104
1251	Architecture of the flagellar rotor. 2011 , 30, 2962-71	75
1250	Crystal structures of an archaeal class II DNA photolyase and its complex with UV-damaged duplex DNA. 2011 , 30, 4437-49	68

1249	The binding of triclosan to SmeT, the repressor of the multidrug efflux pump SmeDEF, induces antibiotic resistance in <i>Stenotrophomonas maltophilia</i> . 2011 , 7, e1002103	77
1248	Membrane remodeling by the double-barrel scaffolding protein of poxvirus. 2011 , 7, e1002239	33
1247	Molecular recognition of the Tes LIM2-3 domains by the actin-related protein Arp7A. 2011 , 286, 11543-54	26
1246	Structural basis for cell surface patterning through NetrinG-NGL interactions. 2011 , 30, 4479-88	41
1245	Structural basis for partial redundancy in a class of transcription factors, the LIM homeodomain proteins, in neural cell type specification. 2011 , 286, 42971-80	31
1244	Structure of a light-activated LOV protein dimer that regulates transcription. 2011 , 4, ra50	92
1243	A conserved lysine residue of plant Whirly proteins is necessary for higher order protein assembly and protection against DNA damage. 2012 , 40, 258-69	38
1242	Functional comparison of <i>Deinococcus radiodurans</i> Dps proteins suggests distinct in vivo roles. 2012 , 447, 381-91	19
1241	A flexible brace maintains the assembly of a hexameric replicative helicase during DNA unwinding. 2012 , 40, 2271-83	12
1240	Assessing the range of kinase autoinhibition mechanisms in the insulin receptor family. 2012 , 448, 213-20	65
1239	Insights into Chi recognition from the structure of an AddAB-type helicase-nuclease complex. 2012 , 31, 1568-78	49
1238	Biochemical identification and crystal structure of kynurenine formamidase from <i>Drosophila melanogaster</i> . 2012 , 446, 253-60	23
1237	Insights into ubiquitin-conjugating enzyme/ co-activator interactions from the structure of the Pex4p:Pex22p complex. 2012 , 31, 391-402	46
1236	A stomatin dimer modulates the activity of acid-sensing ion channels. 2012 , 31, 3635-46	48
1235	The substrate/product-binding modes of a novel GH120 β -xylosidase (XylC) from <i>Thermoanaerobacterium saccharolyticum</i> JW/SL-YS485. 2012 , 448, 401-7	14
1234	MpaA is a murein-tripeptide-specific zinc carboxypeptidase that functions as part of a catabolic pathway for peptidoglycan-derived peptides in ϵ proteobacteria. 2012 , 448, 329-41	8
1233	Tail-anchor targeting by a Get3 tetramer: the structure of an archaeal homologue. 2012 , 31, 707-19	30
1232	Novel <i>Clostridium thermocellum</i> type I cohesin-dockerin complexes reveal a single binding mode. 2012 , 287, 44394-405	25

1231	Structural basis for paxillin binding and focal adhesion targeting of β -parvin. 2012 , 287, 32566-77	27
1230	Mutational and structural analysis of L-N-carbamoylase reveals new insights into a peptidase M20/M25/M40 family member. 2012 , 194, 5759-68	10
1229	Substrate recognition mechanism and substrate-dependent conformational changes of an ROK family glucokinase from <i>Streptomyces griseus</i> . 2012 , 194, 607-16	20
1228	Crystal structure of the VgrG1 actin cross-linking domain of the <i>Vibrio cholerae</i> type VI secretion system. 2012 , 287, 38190-9	51
1227	Cloning, Baeyer-Villiger biooxidations, and structures of the camphor pathway 2-oxo-(B)-4,5,5-trimethylcyclopentylacetyl-coenzyme A monooxygenase of <i>Pseudomonas putida</i> ATCC 17453. 2012 , 78, 2200-12	48
1226	IBIS (Inferred Biomolecular Interaction Server) reports, predicts and integrates multiple types of conserved interactions for proteins. 2012 , 40, D834-40	75
1225	Structure and mechanism of the polynucleotide kinase component of the bacterial Pnkp-Hen1 RNA repair system. 2012 , 18, 2277-86	18
1224	Structural mechanism of ATP-induced polymerization of the partition factor ParF: implications for DNA segregation. 2012 , 287, 26146-54	22
1223	Protein databases on the Internet. 2012 , Chapter 19, Unit 19.4.	6
1222	Crystal structure of <i>Escherichia coli</i> diaminopropionate ammonia-lyase reveals mechanism of enzyme activation and catalysis. 2012 , 287, 20369-81	13
1221	Characterization of a <i>Phanerochaete chrysosporium</i> glutathione transferase reveals a novel structural and functional class with ligandin properties. 2012 , 287, 39001-11	29
1220	Dissecting the protein-RNA interface: the role of protein surface shapes and RNA secondary structures in protein-RNA recognition. 2012 , 40, 3299-306	42
1219	Structural insights into the catalytic mechanism of <i>Escherichia coli</i> selenophosphate synthetase. 2012 , 194, 499-508	16
1218	Structural and functional characterization of VanG D-Ala:D-Ser ligase associated with vancomycin resistance in <i>Enterococcus faecalis</i> . 2012 , 287, 37583-92	14
1217	Crystal structure of the DNA-bound VapBC2 antitoxin/toxin pair from <i>Rickettsia felis</i> . 2012 , 40, 3245-58	45
1216	Structure of the cytoplasmic region of PelD, a degenerate diguanylate cyclase receptor that regulates exopolysaccharide production in <i>Pseudomonas aeruginosa</i> . 2012 , 287, 23582-93	79
1215	Invariant gly residue is important for β -defensin folding, dimerization, and function: a case study of the human neutrophil β -defensin HNP1. 2012 , 287, 18900-12	23
1214	Interactions of isolated C-terminal fragments of neural Wiskott-Aldrich syndrome protein (N-WASP) with actin and Arp2/3 complex. 2012 , 287, 34646-59	31

1213	Crystal structure of the human PRMT5:MEP50 complex. 2012 , 109, 17960-5	204
1212	Design of meningococcal factor H binding protein mutant vaccines that do not bind human complement factor H. 2012 , 80, 2667-77	22
1211	Assignment of protein sequences to existing domain and family classification systems: Pfam and the PDB. 2012 , 28, 2763-72	44
1210	Wzy-dependent bacterial capsules as potential drug targets. 2012 , 13, 1421-31	12
1209	Bioinformatics of Protein-Protein Interfaces and Small Molecule Effectors. 2012 , 7, 159-172	
1208	Structural study of TTR-52 reveals the mechanism by which a bridging molecule mediates apoptotic cell engulfment. 2012 , 26, 1339-50	13
1207	Identification of key residues for the binding of glucagon to the N-terminal domain of its receptor: an alanine scan and modeling study. 2012 , 44, 804-9	6
1206	Crystal structure of ISG54 reveals a novel RNA binding structure and potential functional mechanisms. 2012 , 22, 1328-38	59
1205	Structural analysis of an eIF3 subcomplex reveals conserved interactions required for a stable and proper translation pre-initiation complex assembly. 2012 , 40, 2294-311	57
1204	Structural Databases of Biological Macromolecules. 2012 ,	2
1203	Biochemical and structural characterization of the Arabidopsis bifunctional enzyme dethiobiotin synthetase-diaminopelargonic acid aminotransferase: evidence for substrate channeling in biotin synthesis. 2012 , 24, 1608-25	20
1202	Structural insight into how <i>Pseudomonas aeruginosa</i> peptidoglycanhydrolase Tse1 and its immunity protein Tsi1 function. 2012 , 448, 201-11	19
1201	The binding of Varp to VAMP7 traps VAMP7 in a closed, fusogenically inactive conformation. 2012 , 19, 1300-9	56
1200	The first structure of polarity suppression protein, Psu from enterobacteria phage P4, reveals a novel fold and a knotted dimer. 2012 , 287, 44667-75	16
1199	Crystal structure of the N-terminal domain of the yeast general corepressor Tup1p and its functional implications. 2012 , 287, 26528-38	17
1198	Structural basis of coactivation of liver receptor homolog-1 by β -catenin. 2012 , 109, 143-8	47
1197	Structure of Salmonella effector protein SopB N-terminal domain in complex with host Rho GTPase Cdc42. 2012 , 287, 13348-55	16
1196	Structure and mechanism of human UDP-xylose synthase: evidence for a promoting role of sugar ring distortion in a three-step catalytic conversion of UDP-glucuronic acid. 2012 , 287, 31349-58	26

1195	Solution NMR structure of the Ca ²⁺ -bound N-terminal domain of CaBP7: a regulator of golgi trafficking. 2012 , 287, 38231-43	6
1194	Structural basis for small G protein effector interaction of Ras-related protein 1 (Rap1) and adaptor protein Krev interaction trapped 1 (KRIT1). 2012 , 287, 22317-27	38
1193	Nucleoporin Nup50 stabilizes closed conformation of armadillo repeat 10 in importin β . 2012 , 287, 2022-31	21
1192	Extra-domain B in oncofetal fibronectin structurally promotes fibrillar head-to-tail dimerization of extracellular matrix protein. 2012 , 287, 17578-17588	26
1191	Crystal structures and small-angle x-ray scattering analysis of UDP-galactopyranose mutase from the pathogenic fungus <i>Aspergillus fumigatus</i> . 2012 , 287, 9041-51	30
1190	Structural basis for membrane binding specificity of the Bin/Amphiphysin/Rvs (BAR) domain of Arfaptin-2 determined by Arl1 GTPase. 2012 , 287, 25478-89	27
1189	Insights into structural network responsible for oligomerization and activity of bacterial virulence regulator caseinolytic protease P (ClpP) protein. 2012 , 287, 9484-94	46
1188	Mouse Clr-g, a ligand for NK cell activation receptor NKR-P1F: crystal structure and biophysical properties. 2012 , 189, 4881-9	18
1187	Structural basis for morpheein-type allosteric regulation of <i>Escherichia coli</i> glucosamine-6-phosphate synthase: equilibrium between inactive hexamer and active dimer. 2012 , 287, 34533-46	14
1186	Mapping ultra-weak protein-protein interactions between heme transporters of <i>Staphylococcus aureus</i> . 2012 , 287, 16477-87	42
1185	Multiple binding sites on the pyrin domain of ASC protein allow self-association and interaction with NLRP3 protein. 2012 , 287, 41732-43	103
1184	The extracellular protein factor Epf from <i>Streptococcus pyogenes</i> is a cell surface adhesin that binds to cells through an N-terminal domain containing a carbohydrate-binding module. 2012 , 287, 38178-89	17
1183	Optimizing ring assembly reveals the strength of weak interactions. 2012 , 109, 2348-53	29
1182	The molecular basis of ubiquitin-like protein NEDD8 deamidation by the bacterial effector protein Cif. 2012 , 109, E1830-8	25
1181	Structure of a calcium-dependent 11R-lipoxygenase suggests a mechanism for Ca ²⁺ regulation. 2012 , 287, 22377-86	40
1180	Structure of the heterodimer of human NONO and paraspeckle protein component 1 and analysis of its role in subnuclear body formation. 2012 , 109, 4846-50	98
1179	Structure of the nuclear factor κ -B-inducing kinase (NIK) kinase domain reveals a constitutively active conformation. 2012 , 287, 27326-34	37
1178	Mitochondrial localization and structure-based phosphate activation mechanism of Glutaminase C with implications for cancer metabolism. 2012 , 109, 1092-7	174

1177	Structure of the surface layer of the methanogenic archaean <i>Methanosarcina acetivorans</i> . 2012 , 109, 11812-7	46
1176	Structural and functional analysis of phosphorylation-specific binders of the kinase ERK from designed ankyrin repeat protein libraries. 2012 , 109, E2248-57	70
1175	Biophysical and computational fragment-based approaches to targeting protein-protein interactions: applications in structure-guided drug discovery. 2012 , 45, 383-426	74
1174	Structures of the PelD cyclic diguanylate effector involved in pellicle formation in <i>Pseudomonas aeruginosa</i> PAO1. 2012 , 287, 30191-204	30
1173	Crystal structure of N-glycosylated human glypican-1 core protein: structure of two loops evolutionarily conserved in vertebrate glypican-1. 2012 , 287, 14040-51	40
1172	Diversity in the C3b [corrected] contact residues and tertiary structures of the staphylococcal complement inhibitor (SCIN) protein family. 2012 , 287, 628-640	20
1171	Crystal structures of N-acetylmannosamine kinase provide insights into enzyme activity and inhibition. 2012 , 287, 13656-65	24
1170	The crystal structure of an intermediate dimer of aspergilloglutamic peptidase that mimics the enzyme-activation product complex produced upon autoproteolysis. 2012 , 152, 45-52	4
1169	PDBe: Protein Data Bank in Europe. 2012 , 40, D445-52	75
1168	Crystal structure of the Japanese encephalitis virus envelope protein. 2012 , 86, 2337-46	146
1167	The structure of the yeast NADH dehydrogenase (Ndi1) reveals overlapping binding sites for water- and lipid-soluble substrates. 2012 , 109, 15247-52	78
1166	Structural characterization of closely related O-antigen lipopolysaccharide (LPS) chain length regulators. 2012 , 287, 15696-705	21
1165	Cdt1 and geminin in DNA replication initiation. 2012 , 62, 71-87	18
1164	Crystal structure of a heterodimer of editosome interaction proteins in complex with two copies of a cross-reacting nanobody. 2012 , 40, 1828-40	26
1163	The crystal structure of <i>Arabidopsis</i> VSP1 reveals the plant class C-like phosphatase structure of the DDDD superfamily of phosphohydrolases. 2012 , 7, e49421	6
1162	PDBTM: Protein Data Bank of transmembrane proteins after 8 years. 2013 , 41, D524-9	178
1161	OPM database and PPM web server: resources for positioning of proteins in membranes. 2012 , 40, D370-6	917
1160	X-ray crystal structure of the streptococcal specific phage lysin PlyC. 2012 , 109, 12752-7	66

1159	Structural basis for the recognition of C20:2-GalCer by the invariant natural killer T cell receptor-like antibody L363. 2012 , 287, 1269-78	21
1158	Structural characterization and oligomerization of the TssL protein, a component shared by bacterial type VI and type IVb secretion systems. 2012 , 287, 14157-68	69
1157	Inhibiting alternative pathway complement activation by targeting the factor D exosite. 2012 , 287, 12886-92	63
1156	Insights into substrate specificity and metal activation of mammalian tetrahedral aspartyl aminopeptidase. 2012 , 287, 13356-70	27
1155	Quantitative analysis of prenylated RhoA interaction with its chaperone, RhoGDI. 2012 , 287, 26549-62	31
1154	Structural insights into the regulatory mechanism of the response regulator RocR from <i>Pseudomonas aeruginosa</i> in cyclic Di-GMP signaling. 2012 , 194, 4837-46	42
1153	Structural characterization of a conserved, calcium-dependent periplasmic protease from <i>Legionella pneumophila</i> . 2012 , 194, 4415-25	36
1152	Crystal structure of the <i>Klebsiella pneumoniae</i> NFeoB/FeoC complex and roles of FeoC in regulation of Fe ²⁺ transport by the bacterial Feo system. 2012 , 194, 6518-26	27
1151	Crystal structure of an indole-3-acetic acid amido synthetase from grapevine involved in auxin homeostasis. 2012 , 24, 4525-38	57
1150	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. 2012 , 40, 4178-92	49
1149	InterEvol database: exploring the structure and evolution of protein complex interfaces. 2012 , 40, D847-56	42
1148	Structural determinants of the α -selectivity of a bacterial aminotransferase. 2012 , 287, 28495-502	29
1147	Furin-cleaved proprotein convertase subtilisin/kexin type 9 (PCSK9) is active and modulates low density lipoprotein receptor and serum cholesterol levels. 2012 , 287, 43482-91	63
1146	On the origin and evolution of thermophily: reconstruction of functional precambrian enzymes from ancestors of <i>Bacillus</i> . 2012 , 29, 825-35	65
1145	Protein-protein docking and hot-spot prediction for drug discovery. 2012 , 18, 4607-18	37
1144	A human XRCC4-XLF complex bridges DNA. 2012 , 40, 1868-78	106
1143	Crystal structure and functional characterization of a glucosamine-6-phosphate N-acetyltransferase from <i>Arabidopsis thaliana</i> . 2012 , 443, 427-37	7
1142	Mn ²⁺ -Dependent L-Ascorbate 6-Phosphate Lactonase. 2012 ,	

1141	Computational drug design targeting protein-protein interactions. 2012 , 18, 1240-54	58
1140	Computational Drug Design Targeting Protein-Protein Interactions. 2012 , 18, 1240-1254	
1139	Large-scale mapping of human protein interactome using structural complexes. 2012 , 13, 266-71	40
1138	Getting personalized cancer genome analysis into the clinic: the challenges in bioinformatics. 2012 , 4, 61	22
1137	Roles of residues in the interface of transient protein-protein complexes before complexation. 2012 , 2, 334	23
1136	Structural and biochemical characterization of a trapped coenzyme A adduct of <i>Caenorhabditis elegans</i> glucosamine-6-phosphate N-acetyltransferase 1. 2012 , 68, 1019-29	12
1135	Structural features of the single-stranded DNA-binding protein MoSub1 from <i>Magnaporthe oryzae</i> . 2012 , 68, 1071-6	8
1134	High-resolution structure of <i>Bombyx mori</i> lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. 2012 , 68, 1140-51	13
1133	The structure of augments liver regeneration crystallized in the presence of 50 mM CdCl ₂ reveals a novel Cd ₂ Cl ₄ O ₆ cluster that aids in crystal packing. 2012 , 68, 1128-33	4
1132	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogen <i>Giardia lamblia</i> . 2012 , 68, 1194-200	8
1131	Structure of the <i>Archaeoglobus fulgidus</i> orphan ORF AF1382 determined by sulfur SAD from a moderately diffracting crystal. 2012 , 68, 1242-52	5
1130	The structure of <i>Enterococcus faecalis</i> thymidylate synthase provides clues about folate bacterial metabolism. 2012 , 68, 1232-41	22
1129	Crystallization, dehydration and experimental phasing of WbdD, a bifunctional kinase and methyltransferase from <i>Escherichia coli</i> O9a. 2012 , 68, 1371-9	5
1128	Structural polymorphism of c-di-GMP bound to an EAL domain and in complex with a type II PilZ-domain protein. 2012 , 68, 1380-92	35
1127	Crystallization and preliminary X-ray diffraction analysis of three myotoxic phospholipases A ₂ from <i>Bothrops brazili</i> venom. 2012 , 68, 935-8	1
1126	A new crystal form of human histidine triad nucleotide-binding protein 1 (hHINT1) in complex with adenosine 5'-monophosphate at 1.38 Å resolution. 2012 , 68, 883-8	10
1125	Structure of a UDP-glucose dehydrogenase from the hyperthermophilic archaeon <i>Pyrobaculum islandicum</i> . 2012 , 68, 1003-7	1
1124	Structure of anabolic ornithine carbamoyltransferase from <i>Campylobacter jejuni</i> at 2.7 Å resolution. 2012 , 68, 1018-24	3

1123	High-resolution structures of <i>Thermus thermophilus</i> enoyl-acyl carrier protein reductase in the apo form, in complex with NAD ⁺ and in complex with NAD ⁺ and triclosan. 2012 , 68, 1139-48	2
1122	Crystal structure of the glycosyltransferase SnogD from the biosynthetic pathway of nogalamycin in <i>Streptomyces nogalater</i> . 2012 , 279, 3251-63	15
1121	X-ray structure of a protease-resistant mutant form of human galectin-8 with two carbohydrate recognition domains. 2012 , 279, 3937-51	29
1120	New secreted toxins and immunity proteins encoded within the Type VI secretion system gene cluster of <i>Serratia marcescens</i> . 2012 , 86, 921-36	95
1119	Structural analysis of a dengue cross-reactive antibody complexed with envelope domain III reveals the molecular basis of cross-reactivity. 2012 , 188, 4971-9	65
1118	The native GCN4 leucine-zipper domain does not uniquely specify a dimeric oligomerization state. 2012 , 51, 9581-91	31
1117	Toward a hepatitis C virus vaccine: the structural basis of hepatitis C virus neutralization by AP33, a broadly neutralizing antibody. 2012 , 86, 12923-32	72
1116	RANKL employs distinct binding modes to engage RANK and the osteoprotegerin decoy receptor. 2012 , 20, 1971-82	85
1115	Structure of a RING E3 ligase and ubiquitin-loaded E2 primed for catalysis. 2012 , 489, 115-20	339
1114	Inhibiting the protein ubiquitination cascade by ubiquitin-mimicking short peptides. 2012 , 14, 5760-3	11
1113	High affinity peptide inhibitors of the hepatitis C virus NS3-4A protease refractory to common resistant mutants. 2012 , 287, 39224-32	14
1112	Structure of NPP1, an ectonucleotide pyrophosphatase/phosphodiesterase involved in tissue calcification. 2012 , 20, 1948-59	53
1111	Crystal structure of the HLA-DM-HLA-DR1 complex defines mechanisms for rapid peptide selection. 2012 , 151, 1557-68	123
1110	Crystal structure of calmodulin binding domain of orai1 in complex with Ca ²⁺ calmodulin displays a unique binding mode. 2012 , 287, 43030-41	52
1109	Analysis of Delta-Notch interaction by molecular modeling and molecular dynamic simulation studies. 2012 , 30, 13-29	
1108	Atypical reactive center Kunitz-type inhibitor from the sea anemone <i>Heteractis crispa</i> . 2012 , 10, 1545-65	16
1107	2P2ldb: a structural database dedicated to orthosteric modulation of protein-protein interactions. 2013 , 41, D824-7	115
1106	Structural and functional characterization of NikO, an enolpyruvyl transferase essential in nikkomycin biosynthesis. 2012 , 287, 31427-36	12

1105	Architecture of the Atg17 complex as a scaffold for autophagosome biogenesis. 2012 , 151, 1501-1512	179
1104	Crystal structure of the conserved domain of the DC lysosomal associated membrane protein: implications for the lysosomal glycocalyx. 2012 , 10, 62	60
1103	LpxI structures reveal how a lipid A precursor is synthesized. 2012 , 19, 1132-8	18
1102	The last piece in the vitamin B1 biosynthesis puzzle: structural and functional insight into yeast 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate (HMP-P) synthase. 2012 , 287, 42333-43	18
1101	Structure of a novel phosphotyrosine-binding domain in Hakai that targets E-cadherin. 2012 , 31, 1308-19	50
1100	Identification and characterization of a multifunctional dye peroxidase from a lignin-reactive bacterium. 2012 , 7, 2074-81	160
1099	Mechanistic and structural insight into the functional dichotomy between IL-2 and IL-15. 2012 , 13, 1187-95	148
1098	Neuropilins lock secreted semaphorins onto plexins in a ternary signaling complex. 2012 , 19, 1293-9	123
1097	Unique motifs and hydrophobic interactions shape the binding of modified DNA ligands to protein targets. 2012 , 109, 19971-6	162
1096	The crystal structure of the Rv0301-Rv0300 VapBC-3 toxin-antitoxin complex from <i>M. tuberculosis</i> reveals a Mg ²⁺ ion in the active site and a putative RNA-binding site. 2012 , 21, 1754-67	46
1095	Crystal structure of NirD, the small subunit of the nitrite reductase NirbD from <i>Mycobacterium tuberculosis</i> at 2.0 Å resolution. 2012 , 80, 2799-803	7
1094	Structural basis for modification of flavonol and naphthol glucoconjugates by <i>Nicotiana tabacum</i> malonyltransferase (NtMaT1). 2012 , 236, 781-93	17
1093	Molecular simulation and docking studies of Gal1p and Gal3p proteins in the presence and absence of ligands ATP and galactose: implication for transcriptional activation of GAL genes. 2012 , 26, 847-64	5
1092	The crystal structures of the β subunit of the (β) ₂ (2) tetrameric Glycyl-tRNA synthetase. 2012 , 13, 233-9	7
1091	Crystal structure of mouse RhoA:GTPβ complex in a centered lattice. 2012 , 13, 241-5	4
1090	Low-resolution structure of <i>Drosophila</i> translin. 2012 , 2, 37-46	6
1089	Structural characterization of the PliG lysozyme inhibitor family. 2012 , 180, 235-42	11
1088	How many packing contacts are observed in protein crystals?. 2012 , 180, 96-100	21

1087	Explorations of linked editosome domains leading to the discovery of motifs defining conserved pockets in editosome OB-folds. 2012 , 180, 362-73	4
1086	Structural insights into serine protease inhibition by a marine invertebrate BPTI Kunitz-type inhibitor. 2012 , 180, 271-9	15
1085	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. 2012 , 434, 257-64	14
1084	Structural basis for broad detection of genogroup II noroviruses by a monoclonal antibody that binds to a site occluded in the viral particle. 2012 , 86, 3635-46	61
1083	Structures of the Sgt2/SGTA dimerization domain with the Get5/UBL4A UBL domain reveal an interaction that forms a conserved dynamic interface. 2012 , 2, 1620-32	45
1082	Mutational analysis of phenolic acid decarboxylase from <i>Bacillus subtilis</i> (BsPAD), which converts bio-derived phenolic acids to styrene derivatives. 2012 , 2, 1568	22
1081	Chemical and structural analysis of an antibody folding intermediate trapped during glycan biosynthesis. 2012 , 134, 17554-63	62
1080	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697 α -fucosidases are active on fucosylated human milk oligosaccharides. 2012 , 78, 795-803	154
1079	Crystal structures of glycoside hydrolase family 51 β -L-arabinofuranosidase from <i>Thermotoga maritima</i> . 2012 , 76, 423-8	12
1078	An ultra-specific avian antibody to phosphorylated tau protein reveals a unique mechanism for phosphoepitope recognition. 2012 , 287, 44425-34	43
1077	fSUB: normal mode analysis with flexible substructures. 2012 , 116, 8636-45	3
1076	Protein-protein interactions and substrate channeling in orthologous and chimeric aldolase-dehydrogenase complexes. 2012 , 51, 1942-52	16
1075	Competition between anion binding and dimerization modulates <i>Staphylococcus aureus</i> phosphatidylinositol-specific phospholipase C enzymatic activity. 2012 , 287, 40317-27	12
1074	The structure of the C-terminal domain of the largest editosome interaction protein and its role in promoting RNA binding by RNA-editing ligase L2. 2012 , 40, 6966-77	16
1073	Metal binding at the <i>Deinococcus radiodurans</i> Dps-1 N-terminal metal site controls dodecameric assembly and DNA binding. 2012 , 51, 6679-89	14
1072	The 2.8 Å crystal structure of the dynein motor domain. 2012 , 484, 345-50	180
1071	Structure of 2-methylisoborneol synthase from <i>Streptomyces coelicolor</i> and implications for the cyclization of a noncanonical C-methylated monoterpene substrate. 2012 , 51, 3011-20	32
1070	Impact of quaternary structure upon bacterial cytochrome c peroxidases: does homodimerization matter?. 2012 , 51, 10008-16	7

1069	Structural insights into the conformation and oligomerization of E2~ubiquitin conjugates. 2012 , 51, 4175-87	58
1068	Crystal structures of <i>Trypanosoma cruzi</i> UDP-galactopyranose mutase implicate flexibility of the histidine loop in enzyme activation. 2012 , 51, 4968-79	23
1067	Crystal structures of <i>Xanthomonas campestris</i> OleA reveal features that promote head-to-head condensation of two long-chain fatty acids. 2012 , 51, 4138-46	23
1066	Distinct regions of the <i>Pseudomonas syringae</i> coiled-coil effector AvrRps4 are required for activation of immunity. 2012 , 109, 16371-6	51
1065	Conservation of oxidative protein stabilization in an insect homologue of parkinsonism-associated protein DJ-1. 2012 , 51, 3799-807	20
1064	Structure of a specialized acyl carrier protein essential for lipid A biosynthesis with very long-chain fatty acids in open and closed conformations. 2012 , 51, 7239-49	11
1063	Structure of geranyl diphosphate C-methyltransferase from <i>Streptomyces coelicolor</i> and implications for the mechanism of isoprenoid modification. 2012 , 51, 3003-10	27
1062	Structural investigation of the thermostability and product specificity of amylosucrase from the bacterium <i>Deinococcus geothermalis</i> . 2012 , 287, 6642-54	45
1061	Structure of a bacteriophytochrome and light-stimulated protomer swapping with a gene repressor. 2012 , 20, 1436-46	76
1060	The C-terminal priming domain is strongly associated with the main body of bacteriophage ϕ RNA-dependent RNA polymerase. 2012 , 432, 184-93	8
1059	Structural elements of primary CCR5-using HIV-1 gp120 proteins influencing sensitivity and resistance to the broadly neutralizing monoclonal antibody b12. 2012 , 432, 394-404	1
1058	Structural basis for RNA-duplex recognition and unwinding by the DEAD-box helicase Mss116p. 2012 , 490, 121-5	81
1057	Computational and experimental analysis of the transmembrane domain 4/5 dimerization interface of the serotonin 5-HT(1A) receptor. 2012 , 82, 448-63	41
1056	Structure-based prediction of protein-protein interactions on a genome-wide scale. 2012 , 490, 556-60	508
1055	Molecular determinants for antibody binding on group 1 house dust mite allergens. 2012 , 287, 7388-98	61
1054	Structural characterization of binding mode of smoking cessation drugs to nicotinic acetylcholine receptors through study of ligand complexes with acetylcholine-binding protein. 2012 , 287, 23283-93	38
1053	The structural basis for the sensing and binding of cyclic di-GMP by STING. 2012 , 19, 728-30	131
1052	Dynamic dissociating homo-oligomers and the control of protein function. 2012 , 519, 131-43	76

1051	Structure of the glycosyltransferase EryCIII in complex with its activating P450 homologue EryCII. <i>Journal of Molecular Biology</i> , 2012 , 415, 92-101	6.5	24
1050	Intra-chain 3D segment swapping spawns the evolution of new multidomain protein architectures. <i>Journal of Molecular Biology</i> , 2012 , 415, 221-35	6.5	12
1049	Structure and kinetic stability of the p63 tetramerization domain. <i>Journal of Molecular Biology</i> , 2012 , 415, 503-13	6.5	22
1048	Structural analysis of Chi1 Chitinase from Yen-Tc: the multisubunit insecticidal ABC toxin complex of <i>Yersinia entomophaga</i> . <i>Journal of Molecular Biology</i> , 2012 , 415, 359-71	6.5	45
1047	A conserved Glu-Arg salt bridge connects coevolved motifs that define the eukaryotic protein kinase fold. <i>Journal of Molecular Biology</i> , 2012 , 415, 666-79	6.5	32
1046	A reverse binding motif that contributes to specific protease inhibition by antibodies. <i>Journal of Molecular Biology</i> , 2012 , 415, 699-715	6.5	39
1045	Protein kinase domain of CTR1 from <i>Arabidopsis thaliana</i> promotes ethylene receptor cross talk. <i>Journal of Molecular Biology</i> , 2012 , 415, 768-79	6.5	33
1044	Modulating protein-protein interactions with small molecules: the importance of binding hotspots. <i>Journal of Molecular Biology</i> , 2012 , 415, 443-53	6.5	49
1043	Metal binding dictates conformation and function of the amyloid precursor protein (APP) E2 domain. <i>Journal of Molecular Biology</i> , 2012 , 416, 438-52	6.5	77
1042	Structural, bioinformatic, and in vivo analyses of two <i>Treponema pallidum</i> lipoproteins reveal a unique TRAP transporter. <i>Journal of Molecular Biology</i> , 2012 , 416, 678-96	6.5	23
1041	Structure of the ultra-high-affinity colicin E2 DNase–Im2 complex. <i>Journal of Molecular Biology</i> , 2012 , 417, 79-94	6.5	45
1040	Structurally similar but functionally diverse ZU5 domains in human erythrocyte ankyrin. <i>Journal of Molecular Biology</i> , 2012 , 417, 336-50	6.5	14
1039	Structural basis for the slow dark recovery of a full-length LOV protein from <i>Pseudomonas putida</i> . <i>Journal of Molecular Biology</i> , 2012 , 417, 362-74	6.5	42
1038	Crystal structure of bifunctional aldose-2-ulose dehydratase/isomerase from <i>Phanerochaete chrysosporium</i> with the reaction intermediate ascopyrone M. <i>Journal of Molecular Biology</i> , 2012 , 417, 279-93	6.5	3
1037	Structure-based inhibition of Norovirus RNA-dependent RNA polymerases. <i>Journal of Molecular Biology</i> , 2012 , 419, 198-210	6.5	71
1036	Crystal structure of <i>Bacillus subtilis</i> signal peptide peptidase A. <i>Journal of Molecular Biology</i> , 2012 , 419, 347-58	6.5	13
1035	Evolvability of yeast protein-protein interaction interfaces. <i>Journal of Molecular Biology</i> , 2012 , 419, 387-396	6.5	4
1034	The β -scaffold of the LOV domain of the <i>Brucella</i> light-activated histidine kinase is a key element for signal transduction. <i>Journal of Molecular Biology</i> , 2012 , 420, 112-27	6.5	22

1033	Structural and functional characterization of microcin C resistance peptidase MccF from <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , 2012 , 420, 366-83	6.5	19
1032	Structure and catalytic mechanism of a cyclic dipeptide prenyltransferase with broad substrate promiscuity. <i>Journal of Molecular Biology</i> , 2012 , 422, 87-99	6.5	57
1031	X-ray crystal structure and specificity of the <i>Plasmodium falciparum</i> malaria aminopeptidase PFM18AAP. <i>Journal of Molecular Biology</i> , 2012 , 422, 495-507	6.5	27
1030	Crystal structure of <i>Apis mellifera</i> OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. 2012 , 42, 41-50		98
1029	Evaluation of three different formats of a neutralizing single chain human antibody against toxin Cn2: neutralization capacity versus thermodynamic stability. 2012 , 143, 152-60		6
1028	Crystallographic and spectroscopic characterizations of <i>Sulfolobus solfataricus</i> TrxA1 provide insights into the determinants of thioredoxin fold stability. 2012 , 177, 506-12		5
1027	The sensor region of the ubiquitous cytosolic sensor kinase, PdtaS, contains PAS and GAF domain sensing modules. 2012 , 177, 498-505		15
1026	Structural basis of specificity in tetrameric <i>Kluyveromyces lactis</i> β -galactosidase. 2012 , 177, 392-401		78
1025	Crystal structure of a mono- and diacylglycerol lipase from <i>Malassezia globosa</i> reveals a novel lid conformation and insights into the substrate specificity. 2012 , 178, 363-9		52
1024	Structural basis for catalytic activity of a silkworm Delta-class glutathione transferase. 2012 , 1820, 1469-74		16
1023	Interaction of GAPR-1 with lipid bilayers is regulated by alternative homodimerization. 2012 , 1818, 2175-83		24
1022	Crystal structure of the Rasputin NTF2-like domain from <i>Drosophila melanogaster</i> . 2012 , 420, 188-92		10
1021	Crystal structure of <i>Plasmodium falciparum</i> thioredoxin reductase, a validated drug target. 2012 , 425, 806-11		19
1020	Structural basis of the intracellular sorting of the SNARE VAMP7 by the AP3 adaptor complex. 2012 , 22, 979-88		49
1019	CENP-T-W-S-X forms a unique centromeric chromatin structure with a histone-like fold. 2012 , 148, 487-501		183
1018	A novel dimerization interface of cyclic nucleotide binding domain, which is disrupted in presence of cAMP: implications for CNG channels gating. 2012 , 18, 4053-60		1
1017	Dynamic features of homodimer interfaces calculated by normal-mode analysis. 2012 , 21, 1503-13		4
1016	Engineered variants of InlB with an additional leucine-rich repeat discriminate between physiologically relevant and packing contacts in crystal structures of the InlB:MET complex. 2012 , 21, 1528-39		6

1015	Progressive dry-core-wet-rim hydration trend in a nested-ring topology of protein binding interfaces. 2012 , 13, 51	7
1014	CONS-COCOMAPS: a novel tool to measure and visualize the conservation of inter-residue contacts in multiple docking solutions. 2012 , 13 Suppl 4, S19	22
1013	Crystal structure of the <i>Yersinia enterocolitica</i> type III secretion chaperone SycD in complex with a peptide of the minor translocator YopD. 2012 , 12, 13	19
1012	Integrative structural modeling with small angle X-ray scattering profiles. 2012 , 12, 17	80
1011	Structural and mechanistic investigations on <i>Salmonella typhimurium</i> acetate kinase (AckA): identification of a putative ligand binding pocket at the dimeric interface. 2012 , 12, 24	24
1010	Comparison of tertiary structures of proteins in protein-protein complexes with unbound forms suggests prevalence of allostery in signalling proteins. 2012 , 12, 6	16
1009	Protein databases on the internet. 2012 , Chapter 2, Unit2.6	4
1008	Structural insights into activation of antiviral NK cell responses. 2012 , 250, 239-57	24
1007	Structure of the haptoglobin-haemoglobin complex. 2012 , 489, 456-9	161
1006	Unusual carbon fixation gives rise to diverse polyketide extender units. 2011 , 8, 117-24	57
1005	Protein interface classification by evolutionary analysis. 2012 , 13, 334	98
1004	The structural biochemistry of Zucchini implicates it as a nuclease in piRNA biogenesis. 2012 , 491, 279-83	229
1003	Structure of a force-conveying cadherin bond essential for inner-ear mechanotransduction. 2012 , 492, 128-32	110
1002	Exploiting a natural conformational switch to engineer an interleukin-2 'superkine'. 2012 , 484, 529-33	320
1001	A monomeric TIM-barrel structure from <i>Pyrococcus furiosus</i> is optimized for extreme temperatures. 2012 , 68, 1479-87	2
1000	Structure analysis of geranyl pyrophosphate methyltransferase and the proposed reaction mechanism of SAM-dependent C-methylation. 2012 , 68, 1558-69	7
999	Structure of the corrinoid:coenzyme M methyltransferase MtaA from <i>Methanosarcina mazei</i> . 2012 , 68, 1549-57	4
998	Substrate channels revealed in the trimeric <i>Lactobacillus reuteri</i> bacterial microcompartment shell protein PduB. 2012 , 68, 1642-52	47

997	Dimeric structure of the N-terminal domain of PriB protein from <i>Thermoanaerobacter tengcongensis</i> solved ab initio. 2012 , 68, 1680-9		1
996	Influence of intermolecular contacts on the structure of recombinant prolidase from <i>Thermococcus sibiricus</i> . 2012 , 68, 1275-8		5
995	Structure of ribose 5-phosphate isomerase from the probiotic bacterium <i>Lactobacillus salivarius</i> UCC118. 2012 , 68, 1427-33		7
994	ATP-dependent DNA ligase from <i>Thermococcus</i> sp. 1519 displays a new arrangement of the OB-fold domain. 2012 , 68, 1440-7		14
993	On the roles of polyvalent binding in immune recognition: perspectives in the nanoscience of immunology and the immune response to nanomedicines. 2012 , 64, 1759-81		40
992	<i>Alternaria alternata</i> allergen Alt a 1: a unique β -barrel protein dimer found exclusively in fungi. 2012 , 130, 241-7.e9		71
991	Structural and biochemical studies of the open state of Lys48-linked diubiquitin. 2012 , 1823, 2046-56		34
990	Crystal structures of triosephosphate isomerase from methicillin resistant <i>Staphylococcus aureus</i> MRSA252 provide structural insights into novel modes of ligand binding and unique conformations of catalytic loop. 2012 , 94, 2532-44		6
989	Structural insight into the molecular basis of polyextremophilicity of short-chain alcohol dehydrogenase from the hyperthermophilic archaeon <i>Thermococcus sibiricus</i> . 2012 , 94, 2628-38		19
988	The crystal structure of the intact <i>E. coli</i> RelBE toxin-antitoxin complex provides the structural basis for conditional cooperativity. 2012 , 20, 1641-8		70
987	Crystal structure of the yeast vacuolar ATPase heterotrimeric EGC(head) peripheral stalk complex. 2012 , 20, 1881-92		58
986	Structure and function of β -tetrahydrocannabinolic acid (THCA) synthase, the enzyme controlling the psychoactivity of <i>Cannabis sativa</i> . <i>Journal of Molecular Biology</i> , 2012 , 423, 96-105	6.5	75
985	Assembling of AcrB trimer in cell membrane. <i>Journal of Molecular Biology</i> , 2012 , 423, 123-34	6.5	12
984	Crystal structures of penicillin-binding protein 3 (PBP3) from methicillin-resistant <i>Staphylococcus aureus</i> in the apo and cefotaxime-bound forms. <i>Journal of Molecular Biology</i> , 2012 , 423, 351-64	6.5	38
983	The structural domains of <i>Pseudomonas aeruginosa</i> phosphorylcholine phosphatase cooperate in substrate hydrolysis: 3D structure and enzymatic mechanism. <i>Journal of Molecular Biology</i> , 2012 , 423, 503-14	6.5	5
982	Structural basis for ASPP2 recognition by the tumor suppressor p73. <i>Journal of Molecular Biology</i> , 2012 , 423, 515-27	6.5	16
981	Conservation of functionally important global motions in an enzyme superfamily across varying quaternary structures. <i>Journal of Molecular Biology</i> , 2012 , 423, 831-46	6.5	12
980	Structural analysis of the quaking homodimerization interface. <i>Journal of Molecular Biology</i> , 2012 , 423, 766-81	6.5	24

979	Structure and catalytic mechanism of nicotinate (vitamin B3) degradative enzyme maleamate amidohydrolase from <i>Bordetella bronchiseptica</i> RB50. 2012 , 51, 545-54	14
978	Structures of apo and product-bound human L-asparaginase: insights into the mechanism of autoproteolysis and substrate hydrolysis. 2012 , 51, 6816-26	37
977	Structure of a novel winged-helix like domain from human NFRKB protein. 2012 , 7, e43761	4
976	Broad and potent neutralization of HIV-1 by a gp41-specific human antibody. 2012 , 491, 406-12	624
975	Functional structural motifs for protein-ligand, protein-protein, and protein-nucleic acid interactions and their connection to supersecondary structures. 2013 , 932, 295-315	
974	The crystal structures of the tryparedoxin-tryparedoxin peroxidase couple unveil the structural determinants of <i>Leishmania</i> detoxification pathway. 2012 , 6, e1781	35
973	The cloning, expression, purification, characterization and modeled structure of <i>Caulobacter crescentus</i> β -Xylosidase I. 2012 , 28, 2879-88	19
972	Detection of KCNJ11 gene mutations in a family with neonatal diabetes mellitus: implications for therapeutic management of family members with long-standing disease. 2012 , 16, 109-14	8
971	Two structures of a thiazolinyl imine reductase from <i>Yersinia enterocolitica</i> provide insight into catalysis and binding to the nonribosomal peptide synthetase module of HMWP1. 2012 , 51, 9002-13	15
970	Structural basis of evasion of cellular adaptive immunity by HIV-1 Nef. 2012 , 19, 701-6	107
969	Structure, function, and chemical synthesis of <i>Vaejovis mexicanus</i> peptide 24: a novel potent blocker of Kv1.3 potassium channels of human T lymphocytes. 2012 , 51, 4049-61	43
968	Structural characterization of a novel <i>Chlamydia pneumoniae</i> type III secretion-associated protein, Cpn0803. 2012 , 7, e30220	11
967	Structural view of a non Pfam singleton and crystal packing analysis. 2012 , 7, e31673	0
966	Structural characterisation of Tpx from <i>Yersinia pseudotuberculosis</i> reveals insights into the binding of salicylidene acylhydrazide compounds. 2012 , 7, e32217	15
965	Macro-to-micro structural proteomics: native source proteins for high-throughput crystallization. 2012 , 7, e32498	27
964	Insight on an arginine synthesis metabolon from the tetrameric structure of yeast acetylglutamate kinase. 2012 , 7, e34734	15
963	<i>M. tuberculosis</i> sliding β -clamp does not interact directly with the NAD ⁺ -dependent DNA ligase. 2012 , 7, e35702	12
962	Linking yeast Gcn5p catalytic function and gene regulation using a quantitative, graded dominant mutant approach. 2012 , 7, e36193	11

961	Structural and mutational studies on substrate specificity and catalysis of <i>Salmonella typhimurium</i> D-cysteine desulphydrase. 2012 , 7, e36267	9
960	Analysis of domain-swapped oligomers reveals local sequence preferences and structural imprints at the linker regions and swapped interfaces. 2012 , 7, e39305	17
959	The crystal structures of dystrophin and utrophin spectrin repeats: implications for domain boundaries. 2012 , 7, e40066	22
958	Characterisation of the first enzymes committed to lysine biosynthesis in <i>Arabidopsis thaliana</i> . 2012 , 7, e40318	39
957	Structural insights into the effector-immunity system Tse1/Tsi1 from <i>Pseudomonas aeruginosa</i> . 2012 , 7, e40453	38
956	Crystal structure of a monomeric thiolase-like protein type 1 (TLP1) from <i>Mycobacterium smegmatis</i> . 2012 , 7, e41894	3
955	Crystal structure of the Sema-PSI extracellular domain of human RON receptor tyrosine kinase. 2012 , 7, e41912	25
954	¹³ C NMR reveals no evidence of n-π interactions in proteins. 2012 , 7, e42075	13
953	The "CPC clip motif": a conserved structural signature for heparin-binding proteins. 2012 , 7, e42692	30
952	Structures of human DPP7 reveal the molecular basis of specific inhibition and the architectural diversity of proline-specific peptidases. 2012 , 7, e43019	19
951	Insights into phosphate cooperativity and influence of substrate modifications on binding and catalysis of hexameric purine nucleoside phosphorylases. 2012 , 7, e44282	10
950	A green fluorescent protein containing a QFG tri-peptide chromophore: optical properties and X-ray crystal structure. 2012 , 7, e47331	5
949	Structural insight into the <i>Clostridium difficile</i> ethanolamine utilisation microcompartment. 2012 , 7, e48360	42
948	Characterization of <i>Arabidopsis</i> FPS isozymes and FPS gene expression analysis provide insight into the biosynthesis of isoprenoid precursors in seeds. 2012 , 7, e49109	26
947	Structural insight into inhibitor of apoptosis proteins recognition by a potent divalent smac-mimetic. 2012 , 7, e49527	10
946	Crystal structure of the hexachlorocyclohexane dehydrochlorinase (LinA-type2): mutational analysis, thermostability and enantioselectivity. 2012 , 7, e50373	13
945	Molecular interaction analysis of cigarette smoke carcinogens NNK and NNAL with enzymes involved in DNA repair pathways: An in silico approach. 2012 , 8, 795-800	11
944	Mining genomes of marine cyanobacteria for elements of zinc homeostasis. 2012 , 3, 142	39

943	Carbonic Anhydrase and Zinc in Plant Physiology. 2012 , 72, 140-146	24
942	Structural features and kinetic characterization of alanine racemase from <i>Staphylococcus aureus</i> (Mu50). 2012 , 68, 82-92	18
941	Structure of the cytoplasmic domain of <i>Yersinia pestis</i> YscD, an essential component of the type III secretion system. 2012 , 68, 201-9	12
940	High-resolution structures of complexes of plant S-adenosyl-L-homocysteine hydrolase (<i>Lupinus luteus</i>). 2012 , 68, 218-31	15
939	Structural insights into RipC, a putative citrate lyase β subunit from a <i>Yersinia pestis</i> virulence operon. 2012 , 68, 2-7	14
938	Lysozyme contamination facilitates crystallization of a heterotrimeric cortactin-Arg-lysozyme complex. 2012 , 68, 154-8	8
937	Structure-function relationship of assimilatory nitrite reductases from the leaf and root of tobacco based on high-resolution structures. 2012 , 21, 383-95	13
936	Structural characterization of human Uch37. 2012 , 80, 649-54	32
935	Computational protein design with explicit consideration of surface hydrophobic patches. 2012 , 80, 825-38	48
934	Crystal structure of hypothetical protein TTHB210, controlled by the σ^E /anti- σ^E regulatory system in <i>Thermus thermophilus</i> HB8, reveals a novel homodecamer. 2012 , 80, 958-62	
933	Conformational dynamics of capping protein and interaction partners: simulation studies. 2012 , 80, 1066-77	10
932	Crystal structure and fluorescence studies reveal the role of helical dimeric interface of staphylococcal FabG1 in positive cooperativity for NADPH. 2012 , 80, 1250-7	22
931	A structural mechanism for dimeric to tetrameric oligomer conversion in <i>Halomonas</i> sp. nucleoside diphosphate kinase. 2012 , 21, 498-510	13
930	Functional and structural characterization of a thermostable acetyl esterase from <i>Thermotoga maritima</i> . 2012 , 80, 1545-59	36
929	Crystal structure and biochemical properties of putrescine carbamoyltransferase from <i>Enterococcus faecalis</i> : Assembly, active site, and allosteric regulation. 2012 , 80, 1436-47	3
928	Structural and biochemical characterization of native and recombinant single insulin-like growth factor-binding domain protein (SIBD-1) from the Central American hunting spider <i>Cupiennius salei</i> (Ctenidae). 2012 , 80, 2323-9	5
927	Structural insights into catalysis by β -C-S lyase from <i>Streptococcus anginosus</i> . 2012 , 80, 2447-58	11
926	Structural analysis of the STING adaptor protein reveals a hydrophobic dimer interface and mode of cyclic di-GMP binding. 2012 , 36, 1073-86	232

925	Structural and biochemical basis of Yos9 protein dimerization and possible contribution to self-association of 3-hydroxy-3-methylglutaryl-coenzyme A reductase degradation ubiquitin-ligase complex. 2012 , 287, 8633-40	9
924	Matrix metalloproteinase-10 (MMP-10) interaction with tissue inhibitors of metalloproteinases TIMP-1 and TIMP-2: binding studies and crystal structure. 2012 , 287, 15935-46	68
923	Protein camouflage in cytochrome c-calixarene complexes. 2012 , 4, 527-33	164
922	Quaternary ammonium oxidative demethylation: X-ray crystallographic, resonance Raman, and UV-visible spectroscopic analysis of a Rieske-type demethylase. 2012 , 134, 2823-34	39
921	G-protein-coupled receptor dynamics: dimerization and activation models compared with experiment. 2012 , 40, 394-9	13
920	Quality control of disulfide bond formation in pilus subunits by the chaperone FimC. 2012 , 8, 707-13	41
919	Mapping a neutralizing epitope onto the capsid of adeno-associated virus serotype 8. 2012 , 86, 7739-51	65
918	Computational study of ligand binding in lipid transfer proteins: Structures, interfaces, and free energies of protein-lipid complexes. 2012 , 33, 1831-44	16
917	Computational design of self-assembling protein nanomaterials with atomic level accuracy. 2012 , 336, 1171-4	473
916	Structure of the receptor-binding carboxy-terminal domain of bacteriophage T7 tail fibers. 2012 , 109, 9390-5	71
915	Structural basis of Wnt recognition by Frizzled. 2012 , 337, 59-64	563
914	MMDB: 3D structures and macromolecular interactions. 2012 , 40, D461-4	85
913	Monospecific inhibitors show that both mannan-binding lectin-associated serine protease-1 (MASP-1) and -2 Are essential for lectin pathway activation and reveal structural plasticity of MASP-2. 2012 , 287, 20290-300	58
912	Dimeric α -obratoxin X-ray structure: localization of intermolecular disulfides and possible mode of binding to nicotinic acetylcholine receptors. 2012 , 287, 6725-34	28
911	Thermodynamic and structural description of allosterically regulated VEGFR-2 dimerization. 2012 , 119, 1781-8	83
910	The structure of a GH10 xylanase from <i>Fusarium oxysporum</i> reveals the presence of an extended loop on top of the catalytic cleft. 2012 , 68, 735-42	12
909	Structural and Catalytic Characterization of <i>Pichia stipitis</i> OYE 2.6, a Useful Biocatalyst for Asymmetric Alkene Reductions. 2012 , 354, 1949-1960	27
908	Tailoring a stabilized variant of hydroxynitrile lyase from <i>Arabidopsis thaliana</i> . 2012 , 13, 797-802	18

907	Hydroxynitrile lyases with β -hydrolase fold: two enzymes with almost identical 3D structures but opposite enantioselectivities and different reaction mechanisms. 2012 , 13, 1932-9	21
906	Allosteric antibody inhibition of human hepsin protease. 2012 , 442, 483-94	27
905	Structural determinants of protein kinase CK2 regulation by autoinhibitory polymerization. 2012 , 7, 1158-63	47
904	Plant UVR8 photoreceptor senses UV-B by tryptophan-mediated disruption of cross-dimer salt bridges. 2012 , 335, 1492-6	337
903	Structural studies on molecular interactions between camel peptidoglycan recognition protein, CPGRP-S, and peptidoglycan moieties N-acetylglucosamine and N-acetylmuramic acid. 2012 , 287, 22153-64	7
902	Crystal structure of a putative isochorismatase hydrolase from <i>Oleispira antarctica</i> . 2012 , 13, 27-36	20
901	Crystal structures of putative phosphoglycerate kinases from <i>B. anthracis</i> and <i>C. jejuni</i> . 2012 , 13, 15-26	7
900	Conformational changes in 2-trans-enoyl-ACP (CoA) reductase (InhA) from <i>M. tuberculosis</i> induced by an inorganic complex: a molecular dynamics simulation study. 2012 , 18, 1779-90	12
899	The conjugation protein TcpC from <i>Clostridium perfringens</i> is structurally related to the type IV secretion system protein VirB8 from Gram-negative bacteria. 2012 , 83, 275-88	63
898	Inhibition mechanism of human galectin-7 by a novel galactose-benzylphosphate inhibitor. 2012 , 279, 193-202	13
897	Structure and activity of exo-1,3/1,4- β -glucanase from marine bacterium <i>Pseudoalteromonas</i> sp. BB1 showing a novel C-terminal domain. 2012 , 279, 464-78	22
896	Conservation of structure and mechanism within the transaldolase enzyme family. 2012 , 279, 766-78	12
895	Dissecting heterogeneous molecular chaperone complexes using a mass spectrum deconvolution approach. 2012 , 19, 599-607	61
894	Breaking down order to keep cells tidy. 2012 , 19, 547-8	
893	Accommodating variety in iron-responsive elements: Crystal structure of transferrin receptor 1 B IRE bound to iron regulatory protein 1. 2012 , 586, 32-5	20
892	Crystal structure of <i>cce_0566</i> from <i>Cyanothece</i> 51142, a protein associated with nitrogen fixation in the DUF269 family. 2012 , 586, 350-5	1
891	Crystal structures of the Tudor domains of human PHF20 reveal novel structural variations on the Royal Family of proteins. 2012 , 586, 859-65	20
890	The crystal structure of the MPN domain from the COP9 signalosome subunit CSN6. 2012 , 586, 1147-53	19

889	FolX from <i>Pseudomonas aeruginosa</i> is octameric in both crystal and solution. 2012 , 586, 1160-5	3
888	Hookworm SCP/TAPS protein structure--A key to understanding host-parasite interactions and developing new interventions. 2012 , 30, 652-7	28
887	Crystal structure of the native plasminogen reveals an activation-resistant compact conformation. 2012 , 10, 1385-96	52
886	Structural basis of high-affinity nuclear localization signal interactions with importin- β . 2012 , 13, 532-48	70
885	Structural analysis, enzymatic characterization, and catalytic mechanisms of β -galactosidase from <i>Bacillus circulans</i> sp. <i>alkalophilus</i> . 2012 , 279, 1788-98	47
884	Structural role of the active-site metal in the conformation of <i>Trypanosoma brucei</i> phosphoglycerate mutase. 2012 , 279, 2012-21	16
883	Structure and stability of a thermostable carboxylesterase from the thermoacidophilic archaeon <i>Sulfolobus tokodaii</i> . 2012 , 279, 3071-84	39
882	Structural analysis of trimeric phospholipase A2 neurotoxin from the Australian taipan snake venom. 2012 , 279, 3121-35	15
881	Computational analysis of RNA-protein interaction interfaces via the Voronoi diagram. 2012 , 293, 55-64	3
880	<i>Saccharomyces cerevisiae</i> MHF complex structurally resembles the histones (H3-H4) heterotetramer and functions as a heterotetramer. 2012 , 20, 364-70	19
879	Structure of the human obesity receptor leptin-binding domain reveals the mechanism of leptin antagonism by a monoclonal antibody. 2012 , 20, 487-97	53
878	The structure of human tripeptidyl peptidase II as determined by a hybrid approach. 2012 , 20, 593-603	15
877	Crystal structures of Aureochrome1 LOV suggest new design strategies for optogenetics. 2012 , 20, 698-706	56
876	Complex structures of the abscisic acid receptor PYL3/RCAR13 reveal a unique regulatory mechanism. 2012 , 20, 780-90	62
875	Crystal structures of the outer membrane domain of intimin and invasin from enterohemorrhagic <i>E. coli</i> and enteropathogenic <i>Y. pseudotuberculosis</i> . 2012 , 20, 1233-43	69
874	Chemical shift prediction for protein structure calculation and quality assessment using an optimally parameterized force field. 2012 , 60, 1-28	27
873	Relationship between the structure and the enzymatic activity of crotoxin complex and its phospholipase A2 subunit: an in silico approach. 2012 , 35, 36-42	7
872	Structure of phosphoserine aminotransferase from <i>Mycobacterium tuberculosis</i> . 2012 , 68, 553-63	10

871	Structures of ternary complexes of aspartate-semialdehyde dehydrogenase (Rv3708c) from <i>Mycobacterium tuberculosis</i> H37Rv. 2012 , 68, 671-9	14
870	Structures of <i>Staphylococcus aureus</i> peptide deformylase in complex with two classes of new inhibitors. 2012 , 68, 784-93	4
869	Structure of a post-translationally processed heterodimeric double-headed Kunitz-type serine protease inhibitor from potato. 2012 , 68, 794-9	19
868	In praise of impurity: 30S ribosomal S15 protein-assisted crystallization of turnip yellow mosaic virus proteinase. 2012 , 68, 486-90	5
867	Structure of the regulatory domain of the LysR family regulator NMB2055 (MetR-like protein) from <i>Neisseria meningitidis</i> . 2012 , 68, 730-7	1
866	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. 2012 , 68, 527-34	1
865	The structure of an orthorhombic crystal form of a 'forced reduced' thiol peroxidase reveals lattice formation aided by the presence of the affinity tag. 2012 , 68, 522-6	2
864	Structure of a short-chain dehydrogenase/reductase from <i>Bacillus anthracis</i> . 2012 , 68, 632-7	1
863	Structure of <i>Leishmania major</i> cysteine synthase. 2012 , 68, 738-43	16
862	Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). 2012 , 68, 744-50	10
861	Identification of residues involved in NS2 homodimerization and elucidation of their impact on the HCV life cycle. 2012 , 19, 189-98	7
860	Crystal structure of 6-SST/6-SFT from <i>Pachysandra terminalis</i> , a plant fructan biosynthesizing enzyme in complex with its acceptor substrate 6-kestose. 2012 , 70, 205-19	39
859	Chromatography, mass spectrometry, and molecular modeling studies on ammodyttoxins. 2012 , 402, 2737-48	4
858	Crystal structure and functional mapping of human ASMT, the last enzyme of the melatonin synthesis pathway. 2013 , 54, 46-57	40
857	INI1/hSNF5-interaction defective HIV-1 IN mutants exhibit impaired particle morphology, reverse transcription and integration in vivo. 2013 , 10, 66	11
856	Biophysical characterization and crystal structure of the Feline Immunodeficiency Virus p15 matrix protein. 2013 , 10, 64	8
855	Structure analysis of the extracellular domain reveals disulfide bond forming-protein properties of <i>Mycobacterium tuberculosis</i> Rv2969c. 2013 , 4, 628-40	9
854	Crystal structures and biochemical studies of human lysophosphatidic acid phosphatase type 6. 2013 , 4, 548-61	4

853	The nucleoprotein of severe fever with thrombocytopenia syndrome virus processes a stable hexameric ring to facilitate RNA encapsidation. 2013 , 4, 445-55	32
852	Structural basis of bacterial defense against g-type lysozyme-based innate immunity. 2013 , 70, 1113-22	25
851	New sub-family of lysozyme-like proteins shows no catalytic activity: crystallographic and biochemical study of STM3605 protein from Salmonella Typhimurium. 2013 , 14, 1-10	2
850	Structural, kinetic and computational investigation of Vitis vinifera DHDPs reveals new insight into the mechanism of lysine-mediated allosteric inhibition. 2013 , 81, 431-46	26
849	An in vivo human-plasmablast enrichment technique allows rapid identification of therapeutic influenza A antibodies. 2013 , 14, 93-103	131
848	Structural characterization of a D-isomer specific 2-hydroxyacid dehydrogenase from Lactobacillus delbrueckii ssp. bulgaricus. 2013 , 181, 179-84	13
847	Thrombin inhibition by the serpins. 2013 , 11 Suppl 1, 254-64	42
846	Full-length structure of a sensor histidine kinase pinpoints coaxial coiled coils as signal transducers and modulators. 2013 , 21, 1127-36	140
845	Structural insights into the mechanism of GTPase activation in the GIMAP family. 2013 , 21, 550-9	26
844	Medicago truncatula histidine-containing phosphotransfer protein: structural and biochemical insights into the cytokinin transduction pathway in plants. 2013 , 280, 3709-20	13
843	Structure and activity of NADPH-dependent reductase Q1EQE0 from Streptomyces kanamyceticus, which catalyses the R-selective reduction of an imine substrate. 2013 , 14, 1372-9	69
842	The structure of the D3 domain of Plasmodium falciparum myosin tail interacting protein MTIP in complex with a nanobody. 2013 , 190, 87-91	11
841	The compact conformation of the Plasmodium knowlesi myosin tail interacting protein MTIP in complex with the C-terminal helix of myosin A. 2013 , 190, 56-9	4
840	A dodecameric ring-like structure of the N0 domain of the type II secretin from enterotoxigenic Escherichia coli. 2013 , 183, 354-362	14
839	Combinatorial design of an Anticalin directed against the extra-domain b for the specific targeting of oncofetal fibronectin. <i>Journal of Molecular Biology</i> , 2013 , 425, 780-802	6.5 53
838	Structural basis of FlIG-FlIM interaction in Helicobacter pylori. 2013 , 88, 798-812	32
837	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. 2013 , 500, 350-353	324
836	Biocatalytic Asymmetric Alkene Reduction: Crystal Structure and Characterization of a Double Bond Reductase from. 2013 , 3, 370-379	49

835	The crystal structure of methenyltetrahydromethanopterin cyclohydrolase from <i>Methanobrevibacter ruminantium</i> . 2013 , 81, 2064-70	3
834	The DNA binding mechanism of a SSB protein from <i>Lactococcus lactis</i> siphophage p2. 2013 , 1834, 1070-6	6
833	Modeling Complexes of Transmembrane Proteins: Systematic Analysis of Protein-Protein Docking Tools. 2013 , 32, 717-33	24
832	Solvation models and computational prediction of orientations of peptides and proteins in membranes. 2013 , 1063, 125-42	4
831	X-Ray Crystallography of Biological Macromolecules: Fundamentals and Applications. 2013 , 1-22	0
830	ROCK: a resource for integrative breast cancer data analysis. 2013 , 139, 907-21	27
829	Structural rearrangement of ebola virus VP40 begets multiple functions in the virus life cycle. 2013 , 154, 763-74	155
828	Structure of the PilZ-FimXEAL-c-di-GMP Complex Responsible for the Regulation of Bacterial Type IV Pilus Biogenesis. <i>Journal of Molecular Biology</i> , 2013 , 425, 2174-97	6.5 37
827	Structural and functional analysis of angucycline C-6 ketoreductase LanV involved in landomycin biosynthesis. 2013 , 52, 5304-14	15
826	MgATP regulates allostery and fiber formation in IMPDHs. 2013 , 21, 975-85	48
825	Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. 2013 , 4, 1613	64
824	Structural basis for regulation of human glucokinase by glucokinase regulatory protein. 2013 , 52, 6232-9	36
823	Structural characterization of <i>Staphylococcus aureus</i> biotin protein ligase and interaction partners: an antibiotic target. 2013 , 22, 762-73	29
822	Putative conformations of the receptor-binding domain in S protein of hCoV-EMC in complex with its receptor dipeptidyl peptidase-4. 2013 , 67, 156-8	6
821	Insights into the mechanism of drug resistance: X-ray structure analysis of multi-drug resistant HIV-1 protease ritonavir complex. 2013 , 431, 232-8	3
820	Structural templates for modeling homodimers. 2013 , 22, 1655-63	15
819	A structural modeling approach for the understanding of initiation and elongation of ALS-linked superoxide dismutase fibrils. 2013 , 19, 3695-704	4
818	Computational structure analysis of biomacromolecule complexes by interface geometry. 2013 , 47, 16-23	6

817	Structural insights into the role of <i>Bacillus subtilis</i> YwfH (BacG) in tetrahydrotyrosine synthesis. 2013 , 69, 324-32	7
816	Structural basis for signaling by exclusive EDS1 heteromeric complexes with SAG101 or PAD4 in plant innate immunity. 2013 , 14, 619-30	152
815	Structural bases for a complete myotoxic mechanism: crystal structures of two non-catalytic phospholipases A2-like from <i>Bothrops brazili</i> venom. 2013 , 1834, 2772-81	27
814	The role of salt bridges, charge density, and subunit flexibility in determining disassembly routes of protein complexes. 2013 , 21, 1325-37	71
813	Identification, characterization, and crystal structure of an aldo-keto reductase (AKR2E4) from the silkworm <i>Bombyx mori</i> . 2013 , 538, 156-63	12
812	Functional site plasticity in domain superfamilies. 2013 , 1834, 874-89	24
811	Structure and dynamics of human Nedd4-1 WW3 in complex with the ENaC PY motif. 2013 , 1834, 1632-41	25
810	Structure-based engineering of streptavidin monomer with a reduced biotin dissociation rate. 2013 , 81, 1621-33	32
809	Structural basis for the enzymatic formation of the key strawberry flavor compound 4-hydroxy-2,5-dimethyl-3(2H)-furanone. 2013 , 288, 16815-16826	19
808	Structural basis for kinesin-1: cargo recognition. 2013 , 340, 356-9	58
807	Structure of a bifunctional alcohol dehydrogenase involved in bioethanol generation in <i>Geobacillus thermoglucosidasius</i> . 2013 , 69, 2104-15	24
806	The structure of the Fnl-EGF-like tandem domain of coagulation factor XII solved using SIRAS. 2013 , 69, 94-102	7
805	The diversity of microbial aldo/keto reductases from <i>Escherichia coli</i> K12. 2013 , 202, 168-77	9
804	Understanding specificity of the mycosin proteases in ESX/type VII secretion by structural and functional analysis. 2013 , 184, 115-28	33
803	Structural and biochemical characterization of Rv2140c, a phosphatidylethanolamine-binding protein from <i>Mycobacterium tuberculosis</i> . 2013 , 587, 2936-42	9
802	Structure-function analysis of <i>Arabidopsis thaliana</i> histidine kinase AHK5 bound to its cognate phosphotransfer protein AHP1. 2013 , 6, 959-70	32
801	Design of a superior cytokine antagonist for topical ophthalmic use. 2013 , 110, 3913-8	38
800	The X-ray crystal structure of PA1374 from <i>Pseudomonas aeruginosa</i> , a putative oxidative-stress sensing transcriptional regulator. 2013 , 431, 376-81	7

799	Modeling iron-catecholates binding to NGAL protein. 2013 , 45, 111-21	13
798	Atomic structure of dual-specificity phosphatase 26, a novel p53 phosphatase. 2013 , 52, 938-48	18
797	Tryptophan-accelerated electron flow across a protein-protein interface. 2013 , 135, 15515-25	38
796	A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. 2013 , 32, 2430-8	40
795	Structural study of interaction between brinzolamide and dorzolamide inhibition of human carbonic anhydrases. 2013 , 21, 7210-5	76
794	Functional classification of immune regulatory proteins. 2013 , 21, 766-76	20
793	The crystal structure reveals the molecular mechanism of bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (Rv1415) from <i>Mycobacterium tuberculosis</i> . 2013 , 69, 1633-44	8
792	RNA polymerase I structure and transcription regulation. 2013 , 502, 650-5	150
791	Knowledge-based design of a biosensor to quantify localized ERK activation in living cells. 2013 , 20, 847-56	42
790	Probing the amino acids critical for protein oligomerisation and protein-nucleotide interaction in <i>Mycobacterium tuberculosis</i> PII protein through integration of computational and experimental approaches. 2013 , 1834, 2736-49	
789	Allophycocyanin and phycocyanin crystal structures reveal facets of phycobilisome assembly. 2013 , 1827, 311-8	60
788	Functional and structural study of the dimeric inner membrane protein SbmA. 2013 , 195, 5352-61	27
787	Structural basis of preferential binding of fucose-containing saccharide by the <i>Caenorhabditis elegans</i> galectin LEC-6. 2013 , 23, 797-805	11
786	Structural and functional studies with mytoxin II from <i>Bothrops moojeni</i> reveal remarkable similarities and differences compared to other catalytically inactive phospholipases A ₂ like. 2013 , 72, 52-63	22
785	A model of the membrane-bound cytochrome b5-cytochrome P450 complex from NMR and mutagenesis data. 2013 , 288, 22080-95	93
784	Wzi is an outer membrane lectin that underpins group 1 capsule assembly in <i>Escherichia coli</i> . 2013 , 21, 844-53	47
783	The crystal structure of an extracellular catechol oxidase from the ascomycete fungus <i>Aspergillus oryzae</i> . 2013 , 18, 917-29	35
782	The molecular basis of iron-induced oligomerization of frataxin and the role of the ferroxidation reaction in oligomerization. 2013 , 288, 8156-8167	18

781	Structural basis for the recognition of tyrosine-based sorting signals by the β A subunit of the AP-3 adaptor complex. 2013 , 288, 9563-71	27
780	Crystal structure of an HSA/FcRn complex reveals recycling by competitive mimicry of HSA ligands at a pH-dependent hydrophobic interface. 2013 , 21, 1966-78	76
779	Nucleotide-induced asymmetry within ATPase activator ring drives β 4-RNAP interaction and ATP hydrolysis. 2013 , 27, 2500-11	31
778	Structural insights into functional overlapping and differentiation among myosin V motors. 2013 , 288, 34131-34145	25
777	Structural basis for highly effective HIV-1 neutralization by CD4-mimetic miniproteins revealed by 1.5 Å cryocrystal structure of gp120 and M48U1. 2013 , 21, 1018-29	27
776	The crystal structure of the cell division amidase AmiC reveals the fold of the AMIN domain, a new peptidoglycan binding domain. 2013 , 90, 267-77	41
775	Biochemical and structural characterisation of dehydroquinase synthase from the New Zealand kiwifruit <i>Actinidia chinensis</i> . 2013 , 537, 185-91	12
774	Computational large-scale mapping of protein-protein interactions using structural complexes. 2013 , 73, 3.9.1-3.9.9	2
773	Outer domain of HIV-1 gp120: antigenic optimization, structural malleability, and crystal structure with antibody VRC-PG04. 2013 , 87, 2294-306	32
772	Hemoglobin allostery: new views on old players. <i>Journal of Molecular Biology</i> , 2013 , 425, 1515-26	6.5 9
771	Structure of the Sgt2/Get5 complex provides insights into GET-mediated targeting of tail-anchored membrane proteins. 2013 , 110, 1327-32	25
770	Crystal structure of the Psb28 accessory factor of <i>Thermosynechococcus elongatus</i> photosystem II at 2.3 Å. 2013 , 117, 375-83	9
769	An analysis of oligomerization interfaces in transmembrane proteins. 2013 , 13, 21	26
768	Antibacterial mechanisms identified through structural systems pharmacology. 2013 , 7, 102	20
767	BioSuper: a web tool for the superimposition of biomolecules and assemblies with rotational symmetry. 2013 , 13, 32	5
766	The crystal structure of sterol carrier protein 2 from <i>Yarrowia lipolytica</i> and the evolutionary conservation of a large, non-specific lipid-binding cavity. 2013 , 14, 145-53	10
765	Effect of incorporating a thiophene tail in the scaffold of acetazolamide on the inhibition of human carbonic anhydrase isoforms I, II, IX and XII. 2013 , 23, 5646-9	17
764	Insights into the mechanism of pyrrole polymerization catalysed by porphobilinogen deaminase: high-resolution X-ray studies of the <i>Arabidopsis thaliana</i> enzyme. 2013 , 69, 471-85	19

763	Crystal structure of peroxisomal targeting signal-2 bound to its receptor complex Pex7p-Pex21p. 2013 , 20, 987-93		42
762	Mechanism of transient binding and release of substrate protein during the allosteric cycle of the p97 nanomachine. 2013 , 135, 14627-36		17
761	Activation mechanism of claudin-4 by ephrin type-A receptor 2: a molecular dynamics approach. 2013 , 9, 2627-34		4
760	Zinc coordination spheres in protein structures. 2013 , 52, 10983-91		144
759	Buried and accessible surface area control intrinsic protein flexibility. <i>Journal of Molecular Biology</i> , 2013 , 425, 3250-63	6.5	44
758	Crystal structures of interleukin 17A and its complex with IL-17 receptor A. 2013 , 4, 1888		75
757	A large solvent isotope effect on protein association thermodynamics. 2013 , 52, 6595-600		8
756	Structural and functional analysis of FIP2 binding to the endosome-localised Rab25 GTPase. 2013 , 1834, 2679-90		11
755	Structural biology study of human TNF receptor associated factor 4 TRAF domain. 2013 , 4, 687-94		13
754	An open conformation determined by a structural switch for 2A protease from coxsackievirus A16. 2013 , 4, 782-92		10
753	Structural analysis of the <i>Rhizoctonia solani</i> agglutinin reveals a domain-swapping dimeric assembly. 2013 , 280, 1750-63		16
752	Spot14/Mig12 heterocomplex sequesters polymerization and restrains catalytic function of human acetyl-CoA carboxylase 2. 2013 , 26, 679-88		18
751	Thermodynamic dissection of large-scale domain motions coupled with ligand binding of enzyme I. 2013 , 22, 1602-11		3
750	Biochemical analysis and structure determination of <i>Paucimonas lemoignei</i> poly(3-hydroxybutyrate) (PHB) depolymerase PhaZ7 muteins reveal the PHB binding site and details of substrate-enzyme interactions. 2013 , 90, 649-64		20
749	Organophosphorus acid anhydrolase from <i>Alteromonas macleodii</i> : structural study and functional relationship to prolidases. 2013 , 69, 346-54		15
748	Structure of signal peptide peptidase A with C-termini bound in the active sites: insights into specificity, self-processing, and regulation. 2013 , 52, 8811-22		4
747	Structure and assembly of an inner membrane platform for initiation of type IV pilus biogenesis. 2013 , 110, E4638-47		46
746	Structure and function of an insect β -carboxylesterase (β esterase7) associated with insecticide resistance. 2013 , 110, 10177-82		84

745	Crystal structure of the dimeric coiled-coil domain of the cytosolic nucleic acid sensor LRRFIP1. 2013 , 181, 82-8	12
744	The myosin chaperone UNC-45 is organized in tandem modules to support myofilament formation in <i>C. elegans</i> . 2013 , 152, 183-95	62
743	Structure of a VP1-VP3 complex suggests how birnaviruses package the VP1 polymerase. 2013 , 87, 3229-36	13
742	The structural basis of direct glucocorticoid-mediated transrepression. 2013 , 20, 53-8	130
741	Structure of a dengue virus envelope protein late-stage fusion intermediate. 2013 , 87, 2287-93	85
740	The atomic structure of the virally encoded antifungal protein, KP6. <i>Journal of Molecular Biology</i> , 2013 , 425, 609-21	6.5 8
739	Light-induced subunit dissociation by a light-oxygen-voltage domain photoreceptor from <i>Rhodobacter sphaeroides</i> . 2013 , 52, 378-91	53
738	ACA-specific RNA sequence recognition is acquired via the loop 2 region of MazF mRNA interferase. 2013 , 81, 874-83	6
737	Crystal structure of rice importin- β and structural basis of its interaction with plant-specific nuclear localization signals. 2012 , 24, 5074-88	37
736	Functional Genomics of Metalloregulators in Cyanobacteria. 2013 , 107-156	9
735	Structure of the human ATG12~ATG5 conjugate required for LC3 lipidation in autophagy. 2013 , 20, 59-66	265
734	Evolution from the prokaryotic to the higher plant chloroplast signal recognition particle: the signal recognition particle RNA is conserved in plastids of a wide range of photosynthetic organisms. 2012 , 24, 4819-36	34
733	Natively inhibited <i>Trypanosoma brucei</i> cathepsin B structure determined by using an X-ray laser. 2013 , 339, 227-230	350
732	Structure of the St. Louis encephalitis virus postfusion envelope trimer. 2013 , 87, 818-28	25
731	Abstracting knowledge from the Protein Data Bank. 2013 , 99, 183-8	6
730	A novel mechanism of ligand binding and release in the odorant binding protein 20 from the malaria mosquito <i>Anopheles gambiae</i> . 2013 , 22, 11-21	24
729	<i>Babesia divergens</i> and <i>Neospora caninum</i> apical membrane antigen 1 structures reveal selectivity and plasticity in apicomplexan parasite host cell invasion. 2013 , 22, 114-27	29
728	Crystal structure of the small GTPase Arl6/BBS3 from <i>Trypanosoma brucei</i> . 2013 , 22, 196-203	4

727	Human C3a and C3a desArg anaphylatoxins have conserved structures, in contrast to C5a and C5a desArg. 2013 , 22, 204-12		36
726	Prediction of phenotypes of missense mutations in human proteins from biological assemblies. 2013 , 81, 199-213		16
725	S-linked protein homocysteinylation: identifying targets based on structural, physicochemical and protein-protein interactions of homocysteinyllated proteins. 2013 , 44, 1307-16		6
724	High-resolution crystal structure of the eukaryotic HMP-P synthase (THIC) from <i>Arabidopsis thaliana</i> . 2013 , 184, 438-44		18
723	Structures of CD200/CD200 receptor family and implications for topology, regulation, and evolution. 2013 , 21, 820-32		41
722	Self-assembly and conformational heterogeneity of the AXH domain of ataxin-1: an unusual example of a chameleon fold. 2013 , 104, 1304-13		16
721	Substrate specificity and oligomerization of human GMP synthetase. <i>Journal of Molecular Biology</i> , 2013 , 425, 4323-33	6.5	22
720	Structure of stem cell growth factor R-spondin 1 in complex with the ectodomain of its receptor LGR5. 2013 , 3, 1885-92		60
719	The crystal structure of an activated <i>Thermotoga maritima</i> CheY with N-terminal region of FliM. 2013 , 54, 76-83		13
718	Structural peculiarities of the (MHF1-MHF2) ₄ octamer provide a long DNA binding patch to anchor the MHF-FANCM complex to chromatin: a solution SAXS study. 2013 , 587, 2912-7		3
717	Structural insights into the mechanism and inhibition of the α -hydroxydecanoyl-acyl carrier protein dehydratase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2013 , 425, 365-77	6.5	26
716	Identification of catalytically important amino acid residues for enzymatic reduction of glyoxylate in plants. 2013 , 1834, 2663-71		11
715	Rapid IgG heavy chain cleavage by the streptococcal IgG endopeptidase IdeS is mediated by IdeS monomers and is not due to enzyme dimerization. 2013 , 587, 1818-22		13
714	The crystal structure of the luminal domain of Erv41p, a protein involved in transport between the endoplasmic reticulum and Golgi apparatus. <i>Journal of Molecular Biology</i> , 2013 , 425, 2208-18	6.5	9
713	The switch helix: a putative combinatorial relay for interprotomer communication in cGMP-dependent protein kinase. 2013 , 1834, 1346-51		6
712	Calcium binding by the PKD1 domain regulates interdomain flexibility in <i>Vibrio cholerae</i> metalloprotease PrtV. 2013 , 3, 263-70		9
711	Crystal structure of the DNA cytosine deaminase APOBEC3F: the catalytically active and HIV-1 Vif-binding domain. 2013 , 21, 1042-50		77
710	X-ray crystallographic structural characteristics of <i>Arabidopsis</i> hemoglobin I and their functional implications. 2013 , 1834, 1944-56		14

709	In human pseudouridine synthase 1 (hPus1), a C-terminal helical insert blocks tRNA from binding in the same orientation as in the Pus1 bacterial homologue TruA, consistent with their different target selectivities. <i>Journal of Molecular Biology</i> , 2013 , 425, 3875-87	6.5	20
708	RG7116, a therapeutic antibody that binds the inactive HER3 receptor and is optimized for immune effector activation. 2013 , 73, 5183-94		83
707	DXP synthase-catalyzed C-N bond formation: nitroso substrate specificity studies guide selective inhibitor design. 2013 , 14, 1309-15		23
706	X-ray structure of a superinfection exclusion lipoprotein from phage TP-J34 and identification of the tape measure protein as its target. 2013 , 89, 152-65		33
705	Crystallographic study of multi-drug resistant HIV-1 protease lopinavir complex: mechanism of drug recognition and resistance. 2013 , 437, 199-204		4
704	Structural determinants of oligomerization of (1)-pyrroline-5-carboxylate dehydrogenase: identification of a hexamerization hot spot. <i>Journal of Molecular Biology</i> , 2013 , 425, 3106-20	6.5	19
703	Conformational plasticity at the IgE-binding site of the B-cell receptor CD23. 2013 , 56, 693-7		13
702	Data_Sheet_1.PDF. 2019 ,		
701	Image_1.pdf. 2019 ,		
700	Image_2.pdf. 2019 ,		
699	Image_3.pdf. 2019 ,		
698	Image_4.pdf. 2019 ,		
697	DataSheet_1.pdf. 2019 ,		
696	Image_1.pdf. 2019 ,		
695	Image_2.pdf. 2019 ,		
694	Image_3.pdf. 2019 ,		
693	Image_4.pdf. 2019 ,		
692	Image_5.pdf. 2019 ,		

691 Image_6.pdf. **2019**,

690 Table_1.pdf. **2019**,

689 DataSheet_1.pdf. **2020**,

688 Table_1.docx. **2020**,

687 Table_2.xls. **2020**,

686 Table_3.xls. **2020**,

685 DataSheet_1.pdf. **2019**,

684 Surface Ig variable domain glycosylation affects autoantigen binding and acts as threshold for human autoreactive B cell activation.. **2022**, 8, eabm1759 4

683 Structural basis for C-type inactivation in a Shaker family voltage-gated K channel.. **2022**, 8, eabm8804 2

682 An ACE2-blocking antibody confers broad neutralization and protection against Omicron and other SARS-CoV-2 variants of concern.. **2022**, eabp9312 5

681 Anti-SARS-CoV-2 potential of Cissampelos pareira L. identified by connectivity map-based analysis and in vitro studies.. **2022**, 22, 114

680 Canavanine resistance mutation in is a missense mutation in the ubiquitin ligase adaptor gene .. **2022**, 2022, 0

679 A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in Rymv Spread.

678 SARS-CoV-2 pan-variant inhibitory peptides deter S1-ACE2 interaction and neutralize delta and omicron pseudoviruses.. **2022**, 20, 2042-2056 0

677 Structural Insight into Molecular Inhibitory Mechanism of InsP on African Swine Fever Virus mRNA-Decapping Enzyme g5Rp.. **2022**, e0190521 0

676 Molecular basis of antibiotic self-resistance in a bee larvae pathogen.. **2022**, 13, 2349 0

675 A Puzzling Protein from Variovorax paradoxus Has a PLP Fold Type IV Transaminase Structure and Binds PLP without Catalytic Lysine. **2022**, 12, 619

674 L-tyrosine-bound ThiH structure reveals C-C bond break differences within radical SAM aromatic amino acid lyases.. **2022**, 13, 2284 0

- 673 An auto-inhibited state of protein kinase G and implications for selective activation.
- 672 Structure of an influenza group 2-neutralizing antibody targeting the hemagglutinin stem supersite.. **2022**, ○
- 671 Nanobodies identify an activated state of the TRIB2 pseudokinase.
- 670 Multiple-Allele MHC Class II Epitope Engineering by a Molecular Dynamics-Based Evolution Protocol.. **2022**, 13, 862851 1
- 669 Structure and role of the linker domain of the iron surface-determinant protein IsdH in heme transportation in *Staphylococcus aureus*.. **2022**, 101995
- 668 Quantum Mechanics/Molecular Mechanics Studies on the Catalytic Mechanism of a Novel Esterase (FmtA) of .. **2022**, 4
- 667 Structural and functional characterization of TrmM in m A modification of bacterial tRNA.. **2022**, 31, e4319 ○
- 666 Functional and Structural Diversity of Bacterial Contact-Dependent Growth Inhibition Effectors.. **2022**, 9, 866854 ○
- 665 Characterization and Structural Analysis of Emodin--Methyltransferase from .. **2022**, ○
- 664 The structure of *Phocaeicola vulgatus* sialic acid acetyltransferase.. **2022**, 78, 647-657 ○
- 663 USP14-regulated allostery of the human proteasome by time-resolved cryo-EM.. **2022**, 605, 567-574 1
- 662 Reverse Engineering Analysis of the High-Temperature Reversible Oligomerization and Amyloidogenicity of PSD95-PDZ3.. **2022**, 27, ○
- 661 Structural insights into choline-O-sulfatase reveal the molecular determinants for ligand binding.. **2022**, 78, 669-682
- 660 Clade-Specific Alterations within the HIV-1 Capsid Protein with Implications for Nuclear Translocation. **2022**, 12, 695 ○
- 659 Atomic model of Vesicular Stomatitis Virus and Mechanism of Assembly. ○
- 658 Optimization of IL-1RA structure to achieve a smaller protein with a higher affinity to its receptor.. **2022**, 12, 7483 ○
- 657 Novel super-neutralizing antibody UT28K is capable of protecting against infection from a wide variety of SARS-CoV-2 variants.. **2022**, 14, 2072455 ○
- 656 Designing a novel E2-IFN- β fusion protein against CSFV by immunoinformatics and structural vaccinology approaches.. **2022**, ○

655	Structural, mechanistic and physiological insights into phospholipase A-mediated membrane phospholipid degradation in .. 2022 , 11,	1
654	Glycyrrhetic acid restricts mitochondrial energy metabolism by targeting SHMT2. 2022 , 104349	0
653	New structural insights into the PI-2 pilus from <i>Streptococcus oralis</i> , an early dental plaque colonizer.. 2022 ,	0
652	The mechanism of activation of MEK1 by B-Raf and KSR1.. 2022 , 79, 281	1
651	Structural basis of human LRG1 recognition by Magacizumab, a humanized monoclonal antibody with therapeutic potential. 2022 , 78,	0
650	Biophysical Insight into the SARS-CoV2 Spike-ACE2 Interaction and Its Modulation by Hepcidin through a Multifaceted Computational Approach.	1
649	Structural insights of a highly potent pan-neutralizing SARS-CoV-2 human monoclonal antibody.. 2022 , 119, e2120976119	2
648	The ArsH Protein Product of the <i>Paracoccus denitrificans</i> ars Operon Has an Activity of Organoarsenic Reductase and Is Regulated by a Redox-Responsive Repressor. 2022 , 11, 902	1
647	Kunitz-Type Peptides from Sea Anemones Protect Neuronal Cells against Parkinson's Disease Inductors via Inhibition of ROS Production and ATP-Induced P2X7 Receptor Activation.. 2022 , 23,	1
646	Metal-Induced Fluorescence Quenching of Photoconvertible Fluorescent Protein DendFP.. 2022 , 27,	1
645	Phenol-soluble modulins PSM β and PSM ζ form nanotubes that are cross- β amyloids.. 2022 , 119, e2121586119	0
644	Crystal structure and biochemical analysis suggest that Yj0B ATPase is a substrate-specific molecular chaperone.	
643	Advanced Insights into Catalytic and Structural Features of the Zinc-Dependent Alcohol Dehydrogenase from <i>Thaueria aromatica</i> .. 2022 ,	
642	Structural basis of sodium-dependent bile salt uptake into the liver.. 2022 ,	1
641	Posttranslational modification of microtubules by the MATCAP detyrosinase.. 2022 , 376, eabn6020	5
640	The apo-form of the <i>Vibrio cholerae</i> replicative helicase DnaB is a labile and inactive planar trimer of dimers.. 2022 ,	
639	Mapping Paratopes of Nanobodies using Native Mass Spectrometry and Ultraviolet Photodissociation.	0
638	Crystal structure of the polyketide cyclase from <i>Mycobacterium tuberculosis</i> .. 2022 , 54, 474-481	

- 637 A nucleotide-sensing oligomerization mechanism that controls NrdR-dependent transcription of ribonucleotide reductases.. **2022**, 13, 2700
- 636 Mpe1 senses the binding of pre-mRNA and controls 3' end processing by CPF.. **2022**, 0
- 635 Elucidation of the Conformational Transition of Oligopeptidase B by an Integrative Approach Based on the Combination of X-ray, SAXS, and Essential Dynamics Sampling Simulation. **2022**, 12, 712 1
- 634 Structure of the IL-27 quaternary receptor signaling complex.. **2022**, 11, 2
- 633 Structural insights into highly similar spatial organization of zinc-finger associated domains with a very low sequence similarity.. **2022**, 1
- 632 Complex Mutation Pattern of Omicron BA.2: Evading Antibodies without Losing Receptor Interactions. **2022**, 23, 5534 0
- 631 Large-Size Subunit Catalases Are Chimeric Proteins: A H₂O₂ Selecting Domain with Catalase Activity Fused to a Hsp31-Derived Domain Conferring Protein Stability and Chaperone Activity. **2022**, 11, 979 2
- 630 A truncated anti-CRISPR protein prevents spacer acquisition but not interference.. **2022**, 13, 2802 0
- 629 Cryo-EM structure of acylpeptide hydrolase reveals substrate selection by multimerization and a multi-state serine-protease triad. 0
- 628 Solid-state Nanopore Analysis on Conformation Change of DNA Polymerase I induced by DNA Substrate. 0
- 627 Architecture and Assembly Mechanism of Human LACTB. 1
- 626 Structural comparisons reveal diverse binding modes between nucleosome assembly proteins and histones. **2022**, 15, 1
- 625 In silico design and analyses of a multi-epitope vaccine against Crimean-Congo hemorrhagic fever virus through reverse vaccinology and immunoinformatics approaches. **2022**, 12, 1
- 624 Ancient plant-like terpene biosynthesis in corals. **2022**, 18, 664-669 1
- 623 Linking the thermostability of FIP-nha (*Nectria haematococca*) to its structural properties. **2022**, 1
- 622 Crystal structure of thermally stable homodimeric cytochrome c_h from *Thermus thermophilus*. **2022**, 78, 1
- 621 Structure-based interface engineering methodology in designing a thermostable amylose-forming transglucosylase. **2022**, 102074 1
- 620 High-resolution structures of the SAMHD1 dGTPase homolog from *Leeuwenhoekiella blandensis* reveal a novel mechanism of allosteric activation by dATP. **2022**, 102073 1

- 619 Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. **2022**, 7
- 618 Structural insights for neutralization of BA.1 and BA.2 Omicron variants by a broadly neutralizing SARS-CoV-2 antibody. 0
- 617 In vitro Evolution of Uracil Glycosylase Towards DnaKJ and GroEL Binding Evolves Different Misfolded States. *Journal of Molecular Biology*, **2022**, 434, 167627 6.5
- 616 The structural and functional investigation of the VapBC43 complex from *Mycobacterium tuberculosis*. **2022**, 616, 19-25
- 615 Proteome-Wide and Protein-Specific Multi-Epitope Vaccine Constructs Against the Rift Valley Fever Virus Outbreak Using Integrated Omics Approaches. **2022**, 13,
- 614 Cryo-EM structures of human A2ML1 elucidate the protease-inhibitory mechanism of the A2M family. **2022**, 13, 1
- 613 Brachypodium Antifreeze Protein Gene Products Inhibit Ice Recrystallisation, Attenuate Ice Nucleation, and Reduce Immune Response. **2022**, 11, 1475
- 612 Structural dynamics underlying gating and regulation in IP3R channel. 1
- 611 The *Toxoplasma* glucan phosphatase TgLaforin utilizes a distinct functional mechanism that can be exploited by therapeutic inhibitors. **2022**, 102089 0
- 610 Pentameric assembly of the Kv2.1 tetramerization domain. **2022**, 78, 792-802
- 609 In-silico identification of Tyr232 in AMPK β as a dephosphorylation site for the protein tyrosine phosphatase PTP-PEST.
- 608 Type II BMP and Activin receptors BMPR2 and ACVR2A share a conserved mode of growth factor recognition. **2022**, 102076 1
- 607 Antigenic structure of the human coronavirus OC43 spike reveals exposed and occluded neutralizing epitopes. **2022**, 13, 0
- 606 Competition for Dominance Within Replicating Quasispecies During Prolonged SARS-CoV-2 Infection in an Immunocompromised Host. 1
- 605 Fip1 is a multivalent interaction scaffold for processing factors in human mRNA 3' end biogenesis.
- 604 The Nse5/6-like SIMC1-SLF2 Complex Localizes SMC5/6 to Viral Replication Centers. 0
- 603 Evaluation of Current Methods to Detect Cellular Leucine-Rich Repeat Kinase 2 (LRRK2) Kinase Activity. **2022**, 1-25 0
- 602 Comparative genomic and crystal structure analyses identify a collagen glucosyltransferase from *Acanthamoeba Polyphaga* Mimivirus.

601	Crystal Structure of an Intramolecular Mesoconyl-Coenzyme A Transferase From the 3-Hydroxypropionic Acid Cycle of <i>Roseiflexus castenholzii</i> . 2022 , 13,	1
600	Structural model of the human BTG2/BABPC1 complex by combining mutagenesis, NMR chemical shift perturbation data and molecular docking. <i>Journal of Molecular Biology</i> , 2022 , 167662	6.5 0
599	Structure of the glucosyltransferase domain of TcdA in complex with RhoA provides insights into substrate recognition. 2022 , 12,	0
598	SARS-CoV-2 Omicron BA.2.12.1, BA.4, and BA.5 subvariants evolved to extend antibody evasion.	3
597	Human IgE monoclonal antibody recognition of mite allergen Der p 2 defines structural basis of an epitope for IgE cross-linking and anaphylaxis in vivo.	0
596	In silico SARS-CoV-2 vaccine development for Omicron strain using reverse vaccinology.	0
595	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. 2022 , 13, 1018	1
594	Structural basis of the IL-1 receptor TIR domain-mediated IL-1 signaling. 2022 , 104508	0
593	Conformational flexibility enables catalysis of phthalate cis-4,5-dihydrodiol dehydrogenase. 2022 , 109314	0
592	Direct interaction of a chaperone-bound type III secretion substrate with the export gate. 2022 , 13,	0
591	A comprehensive structural analysis of the ATPase domain of human DNA topoisomerase II beta bound to AMPPNP, ADP, and the bisdioxopiperazine, ICRF193. 2022 ,	0
590	Structural Characterization of a Neutralizing Nanobody With Broad Activity Against SARS-CoV-2 Variants. 2022 , 13,	
589	Structural insights into the binding of nanobody Rh57 to active RhoA-GTP. 2022 , 616, 122-128	
588	In silico study on the effects of disulfide bonds in ORF8 of SARS-CoV-2.	0
587	Crystal structure of the BREX phage defence protein BrxA. 2022 , 4, 211-219	0
586	Structural-guided fragment-based drug discovery applied to antitoxin, MAB3862 opens a new possibility of exploring the Toxin and Antitoxin for antibiotics.	
585	High-affinity anti-Arc nanobodies provide tools for structural and functional studies. 2022 , 17, e0269281	0
584	An M protein coiled coil unfurls and exposes its hydrophobic core to capture LL-37. 11,	0

583	Crystal structure of mevalonate 3,5-bisphosphate decarboxylase reveals insight into the evolution of decarboxylases in the mevalonate metabolic pathways. 2022 , 102111	1
582	The first structure of human MTHFD2L and its implications for the development of isoform-selective inhibitors.	0
581	Structural insights into the lysophospholipid brain uptake mechanism and its inhibition by syncytin-2. 2022 , 29, 604-612	0
580	Crystal structures of the molecular class A β -lactamase TEM-171 and its complexes with tazobactam. 2022 , 78,	0
579	When AlphaFold2 predictions go wrong for protein-protein complexes, is there something to be learnt?. 1-8	1
578	Assessing combinatorial diversity of aureochrome bZIPs through genome-wide screening.	
577	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. 2022 , 5,	2
576	Potent human broadly SARS-CoV-2-neutralizing IgA and IgG antibodies effective against Omicron BA.1 and BA.2. 2022 , 219,	3
575	Studies on the antiviral activity of chebulinic acid against dengue and chikungunya viruses and in silico investigation of its mechanism of inhibition. 2022 , 12,	
574	Extensive substrate recognition by the streptococcal antibody-degrading enzymes IdeS and EndoS.	
573	Sequence Divergence in the Arginase Domain of Ornithine Decarboxylase/Arginase in Fusobacteriacea Leads to Loss of Function in Oral Associated Species.	
572	Identification, structure determination and analysis of Mycobacterium smegmatis acyl-carrier protein synthase (AcpS) crystallized serendipitously. 2022 , 78,	
571	Biochemical and structural insights into an unusual, alkali-metal-independent S-adenosyl-L-homocysteine hydrolase from Synechocystis sp. PCC 6803. 2022 , 78,	
570	A single sensor controls large variations in zinc quotas in a marine cyanobacterium.	1
569	Metal cofactor stabilization by a partner protein is a widespread strategy employed for amidase activation. 2022 , 119,	0
568	Structural variations between small alarmone hydrolase dimers support different modes of regulation of the stringent response. 2022 , 102142	1
567	Structure-based electron-confurcation mechanism of the Ldh-EtfAB complex. 11,	1
566	Crystal structure of BtrK, a decarboxylase involved in the (S)-4-amino-2-hydroxybutyrate (AHBA) formation during butirosin biosynthesis. 2022 , 133576	

565	Penicillin-Binding Protein 1 (PBP1) of Staphylococcus aureus Has Multiple Essential Functions in Cell Division.	3
564	Cryo-EM structure of a type IV secretion system.	1
563	Bioinformatics Approaches to Predict Mutation Effects in the Binding Site of the Proangiogenic Molecule CD93. 2,	
562	Evolution of homo-oligomerization of methionine S-adenosyltransferases is replete with structurefunction constrains. 2022 , 31,	0
561	Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3.	
560	Primary and secondary functions of HLA-E are determined by stability and conformation of the peptide-bound complexes. 2022 , 39, 110959	0
559	AI-based structure prediction empowers integrative structural analysis of human nuclear pores. 2022 , 376,	10
558	In Vitro Neutralisation of Zika Virus by an Engineered Protein Targeting the Viral Envelope Fusion Loop.	
557	Terminase Subunits from the Pseudomonas-Phage E217.	
556	Convergence of two global regulators to coordinate expression of essential virulence determinants of Mycobacterium tuberculosis.	
555	Identification of 2-(4-N,N-Dimethylaminophenyl)-5-methyl-1-phenethyl-1H-benzimidazole targeting HIV-1 CA capsid protein and inhibiting HIV-1 replication in cellulo. 2022 , 23,	
554	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. 2022 , 13,	2
553	Evolution and activation mechanism of the flavivirus class II membrane-fusion machinery. 2022 , 13,	1
552	In Silico Designed Multi-Epitope Immunogen [pme-VAC/LGCM-2022]May Induce Both Cellular and Humoral Immunity against Treponema pallidum Infection. 2022 , 10, 1019	0
551	Structure of a HIV-1 IN-Allosteric Inhibitor Complex at 2.93 ÅResolution: Routes to Inhibitor Optimization.	
550	Protein misfolding and clearance in the pathogenesis of a new infantile onset ataxia caused by mutations in PRDX3.	0
549	Structural insights into the assembly of gp130 family cytokine signaling complexes.	0
548	LAG3 ectodomain structure reveals functional LAG interfaces for ligand and antibody recognition. 2022 , 23, 1031-1041	0

547	Recognition of the TDP-43 nuclear localization signal by importin β / β . 2022 , 39, 111007		3
546	Structural basis for host recognition and superinfection exclusion by bacteriophage T5.		
545	Neutralizing monoclonal antibodies elicited by mosaic RBD nanoparticles bind conserved sarbecovirus epitopes.		0
544	A broad and potent neutralization epitope in SARS-related coronaviruses. 2022 , 119,		2
543	Structural Characterization of L-Galactose Dehydrogenase: An Essential Enzyme for Vitamin C Biosynthesis.		0
542	Biochemical and Structural Characterization of Thermostable GH159 Glycoside Hydrolases Exhibiting β -Arabinofuranosidase Activity. 9,		
541	Structure of cytoplasmic ring of nuclear pore complex by integrative cryo-EM and AlphaFold. 2022 , 376,		5
540	Structure and dynamic association of an assembly platform subcomplex of the bacterial type II secretion system.		0
539	Hinge disulfides in human IgG2 CD40 antibodies modulate receptor signaling by regulation of conformation and flexibility. 2022 , 7,		1
538	Allosteric hotspots in the main protease of SARS-CoV-2. <i>Journal of Molecular Biology</i> , 2022 , 167748	6.5	0
537	Structure of the human RAD17RFC clamp loader and 911 checkpoint clamp bound to a dsDNA/dsDNA junction.		0
536	Molecular dissection of the glutamine synthetase-GlnR nitrogen regulatory circuitry in Gram-positive bacteria. 2022 , 13,		0
535	A panel of nanobodies recognizing conserved hidden clefts of all SARS-CoV-2 spike variants including Omicron. 2022 , 5,		1
534	Structural analysis of 1-deoxy-D-xylulose 5-phosphate synthase from <i>Pseudomonas aeruginosa</i> and <i>Klebsiella pneumoniae</i> reveals conformational changes upon cofactor binding.		
533	The Hidden Intricacies of Aquaporins: Remarkable Details in a Common Structural Scaffold. 2202056		3
532	Biophysical insight into protein-protein interactions in the Interleukin-11/Interleukin-11R/glycoprotein 130 signaling complex.		
531	Vaccine-elicited murine antibody WS6 neutralizes diverse beta-coronaviruses by recognizing a helical stem supersite of vulnerability. 2022 ,		0
530	Omicron Binding Mode: Contact Analysis and Dynamics of the Omicron Receptor-Binding Domain in Complex with ACE2.		0

529	Organism-specific differences in the binding of ketoprofen to serum albumin. 2022 , 9,	0
528	Structures of VWF tubules before and after concatemerization reveal a mechanism of disulfide bond exchange.	1
527	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. 2022 , 13,	1
526	Mechanistic insights into the rational design of masked antibodies. 2022 , 14,	0
525	Exploring protein symmetry at the RCSB Protein Data Bank.	1
524	Dual targeting factors are required for LXG toxin export by the bacterial type VIIb secretion system.	0
523	A monomeric mycobacteriophage immunity repressor utilizes two domains to recognize an asymmetric DNA sequence. 2022 , 13,	
522	Necroptosis-Mediated eCIRP Release in Sepsis. Volume 15, 4047-4059	
521	Structural and functional characterization of DdrC, a novel DNA damage-induced nucleoid associated protein involved in DNA compaction.	0
520	The nuclear egress complex of Epstein-Barr virus buds membranes through an oligomerization-driven mechanism. 2022 , 18, e1010623	
519	Broadly neutralizing antibodies target the coronavirus fusion peptide.	7
518	Antibody evasion by SARS-CoV-2 Omicron subvariants BA.2.12.1, BA.4, & BA.5.	50
517	The LH-DH module of the bacterial replicative helicases is the common binding site for DciA and other helicase loaders.	0
516	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. 2022 , 119,	0
515	Fusion of two unrelated protein domains in a chimera protein and its 3D prediction. Justification of the X-ray reference structures as a prediction benchmark.	
514	The two-domain elevator-type mechanism of zinc-transporting ZIP proteins. 2022 , 8,	1
513	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in RYMV Spread. <i>Journal of Molecular Biology</i> , 2022 , 434, 167715	6.5 1
512	Structural basis of the bHLH domains of MyoD-E47 heterodimer. 2022 , 621, 88-93	0

- 511 In silico analysis of SARS-CoV-2 spike protein N501Y and N501T mutation effects on human ACE2 binding. **2022**, 116, 108260
- 510 Measles and Nipah virus assembly: Specific lipid binding drives matrix polymerization. **2022**, 8, 0
- 509 Discovery of a Transferrin Receptor 1-Binding Aptamer and Its Application in Cancer Cell Depletion for Adoptive T-Cell Therapy Manufacturing. 2
- 508 Modeling and computational characterization of a Xanthomonas sp. Hypothetical protein identifies a remote ortholog of Burkholderia lethal factor 1. 1-13
- 507 Dynamic acylome reveals metabolite driven modifications in Syntrophomonas wolfei.
- 506 Rep15 interacts with several Rab GTPases and has a distinct fold for a Rab effector. **2022**, 13, 0
- 505 The crystal structure of CbpD clarifies substrate-specificity motifs in chitin-active lytic polysaccharide monoxygenases. **2022**, 78, 0
- 504 Suppressing crucial oncogenes of leukemia initiator cells by major royal jelly protein 2 for mediating apoptosis in myeloid and lymphoid leukemia cells. 1
- 503 Structural determinants of DNA recognition by the NO sensor NsrR and related Rrf2-type [FeS]-transcription factors. **2022**, 5, 0
- 502 De novo determination of mosquitocidal Cry11Aa and Cry11Ba structures from naturally-occurring nanocrystals. **2022**, 13, 0
- 501 A direct interaction between CPF and Pol II links RNA 3'-end processing to transcription. 1
- 500 Structural assembly of the nucleic-acid-binding Thp3Usn12Bem1 complex functioning in mRNA splicing. **2022**, 50, 8882-8897 1
- 499 Crystal structure of human NADK2 reveals a dimeric organization and active site occlusion by lysine acetylation. **2022**, 0
- 498 Antibody recognition of CD4-induced open HIV-1 Env trimers. 0
- 497 Panoramic Perspective on Human Phosphosites. **2022**, 21, 1894-1915 0
- 496 Organizing structural principles of the IL-17 ligand-receptor axis. 1
- 495 DNA-binding mechanism and evolution of Replication Protein A.
- 494 An unexpected histone chaperone function for the MIER1 histone deacetylase complex.

- 493 Anti-apoptotic Bcl-2 protein in apo and holo conformation anchored to the membrane: comparative molecular dynamics simulations. 1-15
- 492 Peptide Centric V α Specific Germline Contacts Shape a Specialist T Cell Response. 13,
- 491 Structural and mechanistic insights into the cleavage of clustered O-glycan patches-containing glycoproteins by mucinases of the human gut. **2022**, 13, 3
- 490 Human antibodies to SARS-CoV-2 with a recurring YYDRxG motif retain binding and neutralization to variants of concern including Omicron. **2022**, 5, 1
- 489 Bivalent BET Bromodomain Inhibitors Confer Increased Potency and Selectivity for BRDT via Protein Conformational Plasticity. **2022**, 65, 10441-10458 0
- 488 The Haemophilus influenzae HipBA toxin-antitoxin system adopts an unusual three-component regulatory mechanism. **2022**, 9,
- 487 Dancing with the ions: symport and antiport mechanisms of human glutamate transporters.
- 486 RL-MLZerD: Multimeric protein docking using reinforcement learning. 9, 1
- 485 R-loop formation and conformational activation mechanisms of Cas9. 3
- 484 Crystal structure of ChbG from Klebsiella pneumoniae reveals the molecular basis of diacetylchitobiose deacetylation. **2022**, 5,
- 483 Structural characterisation of a MAPR -related archaeal cytochrome b 5M protein.
- 482 Insight into the structural basis of the dual inhibitory mode of Lima bean (Phaseolus lunatus) serine protease inhibitor.
- 481 The Crystal Structure of the Defense Conferring Rice Protein OsJAC1 Reveals a Carbohydrate Binding Site on the Dirigent-like Domain. **2022**, 12, 1126 1
- 480 Mammalian derived lipocalin and secretoglobin respiratory allergens strongly bind ligands with potentially immune modulating properties. 3, 1
- 479 Structures of topoisomerase V in complex with DNA reveal unusual DNA binding mode and novel relaxation mechanism. 11,
- 478 Extensive substrate recognition by the streptococcal antibody-degrading enzymes IdeS and EndoS. 0
- 477 Crystal structure of Methanococcus jannaschii dihydroorotase.
- 476 Human anti-ACE2 monoclonal antibodies as pan-sarbecovirus prophylactic agents. 1

- 475 Structural and functional characterisation of a stable, broad-specificity multimeric sialidase from the oral pathogen *Tannerella forsythia*.
- 474 Structural characterization of aspartate-semialdehyde dehydrogenase from *Pseudomonas aeruginosa* and *Neisseria gonorrhoeae*. **2022**, 12,
- 473 Architecture and self-assembly of the jumbo bacteriophage nuclear shell. **2022**, 608, 429-435 1
- 472 Structural principles of B-cell antigen receptor assembly. 0
- 471 Structure of a fully assembled tumor-specific T cell receptor ligated by pMHC. **2022**, 185, 3201-3213.e19 4
- 470 Endogenous ligand recognition and structural transition of a human PTH receptor. **2022**, 1
- 469 Augmenting apoptosis-mediated anticancer activity of lactoperoxidase and lactoferrin by nanocombination with copper and iron hybrid nanometals. **2022**, 12, 1
- 468 SH3 domain regulation of RhoGAP activity: Crosstalk between p120RasGAP and DLC1 RhoGAP. **2022**, 13, 1
- 467 Molecular Basis for Enzymatic Aziridine Formation via Sulfate Elimination. 1
- 466 Structures of L-BC virus and its open particle provide insight into Totivirus capsid assembly. **2022**, 5, 0
- 465 Analysis of critical protein-protein interactions of SARS-CoV-2 capping and proofreading molecular machineries towards designing dual target inhibitory peptides.
- 464 Development, structure, and mechanism of synthetic antibodies that target claudin and *Clostridium perfringens* enterotoxin complexes. **2022**, 102357 0
- 463 Structural basis of transcriptional regulation by a nascent RNA element, HK022 putRNA. **2022**, 13, 0
- 462 The Protein Common Assembly Database (ProtCAD) \square A comprehensive structural resource of protein complexes.
- 461 Structural analysis of Red1 as a conserved scaffold of the RNA-targeting MTREC/PAXT complex. **2022**, 13, 0
- 460 In-Silico Characterization of von Willebrand Factor Bound to FVIII. **2022**, 12, 7855
- 459 Evidence of an intracellular interaction between the *Escherichia coli* enzymes EntC and EntB and identification of a potential electrostatic channeling surface. **2022**,
- 458 Structural Comparison of hMDH2 Complexed with Natural Substrates and Cofactors: The Importance of Phosphate Binding for Active Conformation and Catalysis. **2022**, 12, 1175 0

457	CD8 coreceptor engagement of MR1 enhances antigen responsiveness by human MAIT and other MR1-reactive T cells. 2022 , 219,	0
456	Cryo-EM Structure of a Mammalian-specific Alternative Amyloid Exon.	
455	Full structure/function analysis of all the pilin subunits in a type 4 pilus: a complex of minor pilins in <i>Streptococcus sanguinis</i> mediates binding to glycans.	0
454	Terminase subunits from the <i>Pseudomonas</i> -phage E217. 2022 , 167799	0
453	Structures of BIRC6-Client Complexes Provide Mechanism of Smac-Mediated Release of Caspases.	
452	Structural insights into partner selection for MYB and bHLH transcription factor complexes.	0
451	Structures of the mannose-6-phosphate pathway enzyme, GlcNAc-1-phosphotransferase. 2022 , 119,	
450	Molecular and in vivo studies of a glutamate-class prolyl-endopeptidase for coeliac disease therapy. 2022 , 13,	2
449	A naturally arising broad and potent CD4-binding site antibody with low somatic mutation. 2022 , 8,	1
448	Visualizing molecular interactions that determine assembly of a bullet-shaped vesicular stomatitis virus particle. 2022 , 13,	1
447	Structural insights into the assembly and activation of the IL -27 signaling complex.	1
446	Identification of IOMA-class neutralizing antibodies targeting the CD4-binding site on the HIV-1 envelope glycoprotein. 2022 , 13,	1
445	Differential modulation of collybistin conformational dynamics by the closely related GTPases Cdc42 and TC10. 14,	0
444	Structural and mechanistic analysis of a tripartite ATP-independent periplasmic TRAP transporter. 2022 , 13,	0
443	Crystal structure of the <i>Escherichia coli</i> CusS kinase core. 2022 , 214, 107883	1
442	Structural and functional studies of legumain-mycocypin complexes revealed a competitive, exosite-regulated mode of interaction. 2022 , 102502	0
441	A conserved glutathione binding site in poliovirus is a target for antivirals and vaccine stabilisation.	0
440	The Antibacterial Type VII Secretion System of <i>Bacillus subtilis</i> : Structure and Interactions of the Pseudokinase YukC/EssB.	0

- 439 An ensemble of interconverting conformations of the elemental paused transcription complex creates regulatory options. 0
- 438 Molecular dynamics simulations highlight the altered binding landscape at the spike-ACE2 interface between the Delta and Omicron variants compared to the SARS-CoV-2 original strain. **2022**, 149, 106035 0
- 437 Characterisation of a Seneca Valley virus thermostable mutant. **2022**, 575, 74-82 0
- 436 Structural basis for the substrate specificity of an S-formylglutathione hydrolase derived from *Variovorax* sp. PAMC 28711. **2022**, 629, 159-164 1
- 435 Unveiling molecular details behind improved activity at neutral to alkaline pH of an engineered DyP-type peroxidase. **2022**, 20, 3899-3910 0
- 434 Protein quaternary structures in solution are a mixture of multiple forms. 1
- 433 Protein-protein interaction prediction with deep learning: A comprehensive review. **2022**, 20, 5316-5341 0
- 432 Antibody interfaces revealed through structural mining. **2022**, 20, 4952-4968 0
- 431 The Endoplasmic Reticulum Signal Peptidase Complex. **2022**, 0
- 430 ATP-Binding Cassette Transporters: Snap-on Complexes?. **2022**, 35-82 0
- 429 Structures of a phycobilisome in light-harvesting and photoprotected states. **2022**, 609, 835-845 5
- 428 The BAF A12T mutation disrupts lamin A/C interaction, impairing robust repair of nuclear envelope ruptures in Nestor-Cuillermo progeria syndrome cells. **2022**, 50, 9260-9278 1
- 427 ~~BAF~~ and Cachd1 Proteins Are Regulators of Presynaptic Functions. **2022**, 23, 9885 1
- 426 Asymmetric horseshoe-like assembly of peroxisomal Yeast Oxalyl-CoA synthetase. 0
- 425 *Staphylococcus aureus* Exfoliative Toxin E, Oligomeric State and Flip of P186: Implications for Its Action Mechanism. **2022**, 23, 9857 1
- 424 CCP4 Cloud for structure determination and project management in macromolecular crystallography. **2022**, 78, 1079-1089 1
- 423 Structure of the Repurposed Fungal Terpene Cyclase FlvF Implicated in the C-N Bond-Forming Reaction of Flavunoidine Biosynthesis. **2022**, 61, 2014-2024 0
- 422 Structure of angiogenin dimer bound to double-stranded RNA. **2022**, 78, 330-337 0

421	Dual Targeting Factors Are Required for LXG Toxin Export by the Bacterial Type VIIb Secretion System.	0
420	Design of immunogens for eliciting antibody responses that may protect against SARS-CoV-2 variants. 2022 , 18, e1010563	0
419	Structural basis of substrate recognition by human tRNA splicing endonuclease TSEN.	0
418	LSSmScarlet2 and LSSmScarlet3, Chemically Stable Genetically Encoded Red Fluorescent Proteins with a Large Stokes Shift. 2022 , 23, 11051	1
417	A dedicated C-6 α -hydroxyacyltransferase required for biosynthesis of the glycolipid anchor for Vi antigen capsule in typhoidal Salmonella.. 2022 , 102520	0
416	The staphylococcal inhibitory protein SPIN binds to human myeloperoxidase with picomolar affinity but only dampens halide oxidation. 2022 , 102514	0
415	The structure of a polyketide synthase bimodule core. 2022 , 8,	0
414	Gain of function studies on predicted host receptors for white spot virus. 2022 ,	0
413	Molecular basis for thermal stability and affinity in a VHH : contribution of the framework region and its influence in the conformation of the CDR3.	0
412	Small-Angle X-ray Scattering (SAXS) Measurements of APOBEC3G Provide Structural Basis for Binding of Single-Stranded DNA and Processivity. 2022 , 14, 1974	0
411	Affinity-matured DLL4 ligands as broad-spectrum modulators of Notch signaling.	0
410	A monoclonal antibody targeting the Nipah virus fusion glycoprotein apex imparts protection from disease.	0
409	Human immunoglobulin repertoire analysis guides design of vaccine priming immunogens targeting HIV V2-apex broadly neutralizing antibody precursors. 2022 ,	1
408	Mechanism by which T7 bacteriophage protein Gp1.2 inhibits Escherichia coli dGTPase. 2022 , 119,	0
407	High-resolution crystal structure and chemical screening reveal pantothenate kinase as a new target for antifungal development. 2022 ,	0
406	X-ray crystallographic characterization of the SARS-CoV-2 main protease polyprotein cleavage sites essential for viral processing and maturation. 2022 , 13,	4
405	Structural basis of bacteriophage T5 infection trigger and E. coli cell wall perforation.	2
404	Structural basis of Norrin recognition by Lgr4/5/6.	0

- 403 Structural and functional characterization of chloroplast ribulose-5-phosphate-3-epimerase from the model green microalga *Chlamydomonas reinhardtii*. ○
- 402 Structural features of chloroplast trigger factor determined at 2.6 Å resolution. **2022**, 78, 1259-1272 ○
- 401 Repositioning small molecule drugs as allosteric inhibitors of the BFT-3 toxin from enterotoxigenic *Bacteroides fragilis*. **2022**, 31, ○
- 400 Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3. **2022**, 13, ○
- 399 Physical Characteristics of von Willebrand Factor Binding with Platelet Glycoprotein Ib Mutants at Residue 233 Causing Various Biological Functions.. ○
- 398 Y98 Mutation Leads to the Loss of RsfS Anti-Association Activity in *Staphylococcus aureus*. **2022**, 23, 10931 ○
- 397 Modeling of the thermal properties of SARS-CoV-2 S-protein. 9, 1
- 396 Cryo-electron microscopy and image classification reveal the existence and structure of the coxsackievirus A6 virion. **2022**, 5, ○
- 395 Multiscale Modeling of Hepatitis B Virus Capsid Assembly and Its Dimorphism. **2022**, 16, 13845-13859 ○
- 394 Hotspots and Mechanisms of Action of the Thermostable Framework of a Microbial Thermolipase. 1
- 393 Computational Dissection of the Role of Trp305 in the Regulation of the Death-Associated Protein Kinase α almodulin Interaction. **2022**, 12, 1395 ○
- 392 Structural conservation of Lassa virus glycoproteins and recognition by neutralizing antibodies. ○
- 391 Bidirectional sequestration between a bacterial hibernation factor and a glutamate metabolizing protein. **2022**, 119, ○
- 390 Structural Basis of Substrate Promiscuity and Catalysis by the Reverse Prenyltransferase N-Dimethylallyl-L-tryptophan Synthase from *Fusarium fujikuroi*. **2022**, 61, 2025-2035 ○
- 389 Nanobodies identify an activated state of the TRIB2 pseudokinase. **2022**, ○
- 388 Cellular and structural characterisation of VP1 and VP2 knockout mutants of AAV3B serotype and implications for AAV manufacturing. 1
- 387 Efficacy Evaluation of SDF-1 β -Based Polypeptides in an Acute Myocardial Infarction Model Using Structure-Based Drug Design. ○
- 386 Structural analysis of human CEACAM1 oligomerization. **2022**, 5, ○

- 385 Fip1 is a multivalent interaction scaffold for processing factors in human mRNA 3' end biogenesis. 11, 0
- 384 Improved mammalian retromer cryo-EM structures reveal a new assembly interface. **2022**, 102523 1
- 383 Substrate-induced dimerization of elaiophylin glycosyltransferase reveals a novel self-activating form of glycosyltransferase for symmetric glycosylation. **2022**, 78, 1235-1248 0
- 382 *Fusarium verticillioides* NAT1 (FDB2) N-malonyltransferase is structurally, functionally and phylogenetically distinct from its N -acetyltransferase (NAT) homologues. 0
- 381 Structure determination of an unstable macromolecular complex enabled by nanobody-peptide bridging. **2022**, 31, 0
- 380 Structural insights into crista junction formation by the Mic60-Mic19 complex. **2022**, 8, 0
- 379 Cryo-EM analyses of wild-type and oncogenic KIT mutants reveal structural oncogenic plasticity and a novel Achilles heel for therapeutic intervention. 0
- 378 Structure-based design, synthesis and biological evaluation of a NAD + analogue targeting *Pseudomonas aeruginosa* NAD kinase. 0
- 377 Structural characterization of SARS-CoV-2 dimeric ORF9b reveals potential fold-switching trigger mechanism. 0
- 376 Non-canonical *Staphylococcus aureus* pathogenicity island repression. 0
- 375 High-resolution structure of a microtubule-like tube composed of FtsZ nanobody complexes. 0
- 374 DELE1 oligomerization promotes integrated stress response activation. 0
- 373 Structural model for ligand binding and channel opening of an insect gustatory receptor. **2022**, 102573 1
- 372 Metal binding and oligomerization properties of FurC (PerR) from *Anabaena* sp. PCC7120: an additional layer of regulation?. 0
- 371 The crystal structure of a simian Foamy Virus receptor binding domain provides clues about entry into host cells. 0
- 370 High-resolution structures of a siderophore-producing cyclization domain from *Yersinia pestis* offer a refined proposal of substrate binding. **2022**, 298, 102454 0
- 369 SPACA9 is a luminal protein of human ciliary singlet and doublet microtubules. **2022**, 119, 2
- 368 Cell-free protein crystallization for nanocrystal structure determination. **2022**, 12, 0

- 367 The dimeric form of bacterial l-asparaginase YpAl is fully active. 0
- 366 Neighboring mutation-mediated enhancement of dengue virus infectivity and spread. 1
- 365 Crystal structure of the Phospholipase A and acyltransferase 4 (PLAAT4) catalytic domain. **2022**, 107903 0
- 364 Structural insights for neutralization of Omicron variants BA.1, BA.2, BA.4, and BA.5 by a broadly neutralizing SARS-CoV-2 antibody. **2022**, 8, 3
- 363 Crystal structure and biochemical analysis suggest that YjoB ATPase is a putative substrate-specific molecular chaperone. **2022**, 119, 0
- 362 Combining small angle X-ray scattering (SAXS) with protein structure predictions to characterize conformations in solution. **2022**, 0
- 361 Structural and functional basis of the universal transcription factor NusG pro-pausing activity in *Mycobacterium tuberculosis*. 0
- 360 Molecular basis of dual anti-CRISPR and auto-regulatory functions of AcrIF24. 0
- 359 Three-dimensional structure of a mycobacterial oligoribonuclease reveals a unique C-terminal tail that stabilizes the homodimer. **2022**, 102595 0
- 358 Molecular insights into DNA recognition and methylation by non-canonical type I restriction-modification systems. **2022**, 13, 0
- 357 BRD9 Inhibition by Natural Polyphenols Targets DNA Damage/Repair and Apoptosis in Human Colon Cancer Cells. **2022**, 14, 4317 1
- 356 Polymerization cycle of actin homolog MreB from a Gram-positive bacterium. 0
- 355 The protein common assembly database (ProtCAD) is a comprehensive structural resource of protein complexes. 0
- 354 Broad SARS-CoV-2 Neutralization by Monoclonal and Bispecific Antibodies Derived from a Gamma-infected Individual. 0
- 353 Structural Characterization of Protective Non-Neutralizing Antibodies targeting Crimean-Congo Hemorrhagic Fever Virus. 0
- 352 The structural basis for the self-inhibition of DNA binding by apo- σ^{70} . 0
- 351 Structural insight into Tn3 family transposition mechanism. **2022**, 13, 0
- 350 Kinetic and Structural Characterization of a Flavin-Dependent Putrescine N-Hydroxylase from *Acinetobacter baumannii*. 0

349	Stochastic chain termination in bacterial pilus assembly.	0
348	HIV-1 CD4-binding site germline antibody Env structures inform vaccine design. 2022 , 13,	0
347	Allelic compatibility in plant immune receptors facilitates engineering of new effector recognition specificities.	1
346	Structural insight into the ligand binding mechanism of aryl hydrocarbon receptor. 2022 , 13,	0
345	Zymogenic latency in an ~250-million-year-old astacin metallopeptidase. 2022 , 78, 1347-1357	1
344	Molecular mechanism of Afadin substrate recruitment to the receptor phosphatase PTPRK via its pseudophosphatase domain. 11,	0
343	The Calpain-7 protease functions together with the ESCRT-III protein IST1 within the midbody to regulate the timing and completion of abscission.	0
342	Structural basis of colibactin activation by the ClbP peptidase.	0
341	Structural and functional studies of a snake venom phospholipase A2-like protein complexed to an inhibitor from <i>Tabernaemontana catharinensis</i> . 2022 ,	0
340	Distinction between small RNA-bound and free ARGONAUTE via an N-terminal protein-protein interaction site.	0
339	Molecular analysis of a public cross-neutralizing antibody response to SARS-CoV-2. 2022 , 111650	0
338	Unravelling the regulation pathway of photosynthetic AB-GAPDH. 2022 , 78, 1399-1411	0
337	A selective and orally bioavailable VHL-recruiting PROTAC achieves SMARCA2 degradation in vivo. 2022 , 13,	5
336	Structural principles of B-cell antigen receptor assembly.	1
335	Atomic model of vesicular stomatitis virus and mechanism of assembly. 2022 , 13,	1
334	The first archaeal PET-degrading enzyme belongs to the feruloyl-esterase family.	0
333	Neutralizing monoclonal antibodies elicited by mosaic RBD nanoparticles bind conserved sarbecovirus epitopes. 2022 ,	2
332	Structure and functionality of a multimeric human COQ7:COQ9 complex. 2022 ,	0

331	Molecular basis of SARS-CoV-2 Omicron variant evasion from shared neutralizing antibody response.	0
330	Dimerization of the C-type lectin-like receptor CD93 promotes its binding to Multimerin-2 in endothelial cells. 2022 ,	0
329	Structure of the photosynthetic Calvin-Benson-Bassham sedoheptulose-1,7-bisphosphatase SBPase from the model microalga <i>Chlamydomonas reinhardtii</i> .	0
328	High-Resolution Crystal Structure of Muscle Phosphoglycerate Mutase Provides Insight into Its Nuclear Import and Role. 2022 , 23, 13198	0
327	Structural basis for Cas9 off-target activity. 2022 , 185, 4067-4081.e21	1
326	Isoform-specific inhibition of FGFR signaling achieved by a de-novo-designed mini-protein. 2022 , 41, 111545	0
325	Glycoside hydrolase subfamily GH5_57 features a highly redesigned catalytic interface to process complex hetero- β -mannans. 2022 , 78, 1358-1372	0
324	Structural basis for host recognition and superinfection exclusion by bacteriophage T5. 2022 , 119,	1
323	BACTERIAL NADQ (COG4111) IS A NUDIX-LIKE, ATP-RESPONSIVE REGULATOR OF NAD BIOSYNTHESIS. 2022 , 107917	0
322	AAA+ protease-adaptor structures reveal altered conformations and ring specialization.	1
321	Enzymatic C3-Methylation of Indoles Using Methyltransferase PsmD-Crystal Structure, Catalytic Mechanism, and Preparative Applications. 14130-14139	0
320	Selection of a PD-1 blocking antibody from a novel fully human phage display library.	0
319	Characterization of the Gateway Decarboxylase for Psilocybin Biosynthesis.	0
318	Co-translational binding of importins to nascent proteins.	0
317	A comprehensive set of ER protein disulfide isomerase family members supports the biogenesis of pro-inflammatory interleukin 12 family cytokines. 2022 , 102677	0
316	Cryo-EM Structure of the Type IV Pilus Extension ATPase from Enteropathogenic <i>Escherichia coli</i> .	0
315	Endowing homodimeric carbamoyltransferase GdmN with iterative functions through structural characterization and mechanistic studies. 2022 , 13,	0
314	Nanobodies targeting LexA autocleavage disclose a novel suppression strategy of SOS-response pathway. 2022 , 30, 1479-1493.e9	0

313	Synthesis of new sulphonate derivatives containing adamantane and 4-chlorophenyl moieties as nucleotide pyrophosphatase/phosphodiesterase-1 and -3 inhibitors. 2023 , 1274, 134494	0
312	Targeting apoptosis in MCF-7 and Ehrlich ascites carcinoma cells by saponifiable fractions from green and black Vitis vinifera seed oil. 2023 , 157, 114017	0
311	Structural insights at acidic pH of Dye-decolorizing peroxidase from Bacillus subtilis.	0
310	Dynamic acylome reveals metabolite driven modifications in Syntrophomonas wolfei. 13,	0
309	Cross-linking mass spectrometry discovers, evaluates, and validates the experimental and predicted structural proteome.	0
308	Inhibiting ACK1-mediated phosphorylation of C-terminal Src kinase counteracts prostate cancer immune checkpoint blockade resistance. 2022 , 13,	1
307	Antigenic mapping reveals sites of vulnerability on HCoV spike protein. 2022 , 5,	0
306	Rare, convergent antibodies targeting the stem helix broadly neutralize diverse betacoronaviruses. 2022 ,	0
305	Do Go Chasing Waterfalls: Enoyl Reductase (FabI) in Complex with Inhibitors Stabilizes the Tetrameric Structure and Opens Water Channels.	0
304	Cryo-EM structures of prefusion SIV envelope trimer. 2022 , 29, 1080-1091	0
303	Fragment-based computational design of antibodies targeting structured epitopes. 2022 , 8,	0
302	The Nse5/6-like SIMC1-SLF2 complex localizes SMC5/6 to viral replication centers. 11,	0
301	Co-immunization with hemagglutinin stem immunogens elicits cross-group neutralizing antibodies and broad protection against influenza A viruses. 2022 ,	1
300	Structural insights into broadly neutralizing antibodies against SARS-CoV-2 elicited by hybrid immunity. 1-52	0
299	Exploring Structural Diversity among Adhesion Devices Encoded by Lactococcal P335 Phages with AlphaFold2. 2022 , 10, 2278	0
298	Neutralizing epitopes on Clostridioides difficile toxin A revealed by the structures of two camelid VHH antibodies. 13,	0
297	A terminal functionalization strategy reveals unusual binding abilities of anti-thrombin anticoagulant aptamers. 2022 ,	0
296	Stability profile of vimentin rod domain.	0

- 295 Structural and biochemical basis of interdependent FANCI-FANCD2 ubiquitination. ○
- 294 Structures of a mobile intron retroelement poised to attack its structured DNA target. **2022**, 378, 627-634 ○
- 293 Conformational motions and ligand-binding underlying gating and regulation in IP3R channel. **2022**, 13, 1
- 292 Designed Ankyrin Repeat Proteins provide insights into the structure and function of CagI and are potent inhibitors of CagA translocation by the Helicobacter pylori type IV secretion system. ○
- 291 Designing a multi-epitope vaccine against coxsackievirus B based on immunoinformatics approaches. 13, ○
- 290 Human B Cell Epitope Map of the Lyme Disease Vaccine Antigen, OspA. ○
- 289 Structural and mutational studies suggest key residues to determine whether stomatin SPFH domains form dimers or trimers. **2022**, 32, 101384 ○
- 288 Structure and function of the NS5 methyltransferase domain from Usutu virus. **2022**, 208, 105460 ○
- 287 Structural basis of the myotoxic inhibition of the Bothrops pirajai PrTX-I by the synthetic varespladib. **2022**, 1
- 286 Cryo-EM structure of ex vivo fibrils associated with extreme AA amyloidosis prevalence in a cat shelter. **2022**, 13, ○
- 285 Protein-Protein-Binding Interfaces. **2022**, 15-37 ○
- 284 Structure, Composition, and Modeling of Protein Complexes. **2022**, 101-125 ○
- 283 BtuB TonB-dependent transporters and BtuG surface lipoproteins form stable complexes for vitamin B12 uptake in gut Bacteroides. ○
- 282 Complementary antibody lineages achieve neutralization breadth in an HIV-1 infected elite neutralizer. **2022**, 18, e1010945 ○
- 281 CryoEM Reveals Oligomeric Isomers of a Multienzyme Complex and Assembly Mechanics. ○
- 280 The Ruminococcus bromii amylosome protein Sas6 binds single and double helical β -glucan structures in starch.. ○
- 279 A unique network of attack, defence and competence on the outer membrane of the periodontitis pathogen Tannerella forsythia. ○
- 278 Molecular basis for antiviral activity of two pediatric neutralizing antibodies targeting SARS-CoV-2 Spike RBD. **2023**, 26, 105783 ○

- 277 In vitro neutralisation of Zika virus by an engineered protein targeting the viral envelope fusion loop. ○
- 276 Crystal structure of prodigiosin binding protein PgbP, a GNAT family protein, in *Serratia marcescens* FS14. **2023**, 640, 73-79 ○
- 275 The structure of a tautomerase superfamily member linked to the type VI secretion system of *Acinetobacter baumannii*. **2023**, 79, 8-16 ○
- 274 The pursuit of new alternative ways to eradicate *Helicobacter pylori* continues: Detailed characterization of interactions in the adenylosuccinate synthetase active site. **2023**, 226, 37-50 ○
- 273 Paramyxoviruses from bats: changes in receptor specificity and their role in host adaptation. **2023**, 58, 101292 ○
- 272 Structural and biochemical characterization of *Leptospira interrogans* Lsa45 reveals a penicillin-binding protein with esterase activity. **2023**, 125, 141-153 ○
- 271 Structure of human placental steroid sulfatase at 2.0 angstrom resolution: Catalysis, quaternary association, and a secondary ligand site. **2023**, 227, 106228 ○
- 270 Computer- and NMR-Aided Design of Small-Molecule Inhibitors of the Hub1 Protein. **2022**, 27, 8282 ○
- 269 Cryo-EM structures of the active NLRP3 inflammasome disk. 1
- 268 Switching of Receptor Binding Poses between Closely Related Enteroviruses. **2022**, 14, 2625 ○
- 267 Structural characterization of protective non-neutralizing antibodies targeting Crimean-Congo hemorrhagic fever virus. **2022**, 13, ○
- 266 CryoEM structure and assembly mechanism of a bacterial virus genome gatekeeper. **2022**, 13, ○
- 265 Human neutralizing antibodies to cold linear epitopes and to subdomain 1 of SARS-CoV-2. ○
- 264 Structure-based engineering of minimal Proline dehydrogenase domains for inhibitor discovery. ○
- 263 Structural Studies of Bypass of Forespore Protein C from *Bacillus Subtilis* to Reveal Its Inhibitory Molecular Mechanism for SpoIVB. **2022**, 12, 1530 ○
- 262 From primordial clocks to circadian oscillators. ○
- 261 A conserved glutathione binding site in poliovirus is a target for antivirals and vaccine stabilisation. **2022**, 5, ○
- 260 Insights into the Structure of the Highly Glycosylated Ffase from *Rhodotorula dairenensis* Enhance Its Biotechnological Potential. **2022**, 23, 14981 ○

- 259 Structural basis of tankyrase activation by polymerization. **2022**, 612, 162-169 ○
- 258 Vaccination with the Omicron spike RBD boosts broadly neutralizing antibody levels and confers sustained protection even after acquiring immunity to the original antigen. 1
- 257 High-density binding to Plasmodium falciparum circumsporozoite protein repeats by inhibitory antibody elicited in mouse with human immunoglobulin repertoire. **2022**, 18, e1010999 ○
- 256 A structural model of the profilin-formin pacemaker system for actin filament elongation. **2022**, 12, 1
- 255 Mechanisms of ion selectivity and rotor coupling in the bacterial flagellar sodium-driven stator unit. ○
- 254 cNTnC and FYTnC2, Genetically Encoded Green Calcium Indicators Based on Troponin C from Fast Animals. **2022**, 23, 14614 ○
- 253 Antiviral signaling by a cyclic nucleotide activated CRISPR protease. ○
- 252 An intact S-layer is advantageous to Clostridioides difficile within the host. ○
- 251 Structural and biochemical characterizations of Thermus thermophilus HB8 transketolase producing a heptulose. **2023**, 107, 233-245 ○
- 250 Uptake mechanism of iron-phytosiderophore from the soil based on the structure of yellow stripe transporter. **2022**, 13, ○
- 249 Next-generation retinoid X receptor agonists increase ATRA signaling in organotypic epithelium cultures and have distinct effects on receptor dynamics. **2022**, 102746 ○
- 248 Explicit versus implicit consideration of binding partners in protein-protein complex to elucidate intrinsic dynamics. ○
- 247 Structural insights into mechanism and specificity of the plant protein O-fucosyltransferase SPINDLY. **2022**, 13, ○
- 246 A broad specificity β -propeller enzyme from Rhodospirillum rubrum that hydrolyzes many lactones including β -valerolactone. **2022**, 102782 ○
- 245 Illuminating the mechanism and allosteric behavior of NanoLuc luciferase. ○
- 244 Structural basis for a human broadly neutralizing influenza A hemagglutinin stem-specific antibody including H17/18 subtypes. **2022**, 13, ○
- 243 A high-quality reference genome for the fission yeast Schizosaccharomyces osmophilus. ○
- 242 Discovery of β -Glucosidase Raises the Possibility of β -Glucosides in Nature. **2022**, 7, 47411-47423 1

- 241 Molecular mechanism of antibody neutralization of coxsackievirus A16. **2022**, 13, ○
- 240 X-ray structure and mechanism of ZgHAD , a l -2-haloacid dehalogenase from the marine Flavobacterium Zobellia galactanivorans. **2023**, 32, ○
- 239 Mapping the protein binding site of the (pro)renin receptor using in silico 3D structural analysis. ○
- 238 Structures of the Inhibitory Receptor Siglec-8 in Complex with a High-Affinity Sialoside Analogue and a Therapeutic Antibody. ○
- 237 HBD-2 variants and SARS-CoV-2: New insights into inter-individual susceptibility. 13, ○
- 236 Atmospheric hydrogen oxidation extends to the domain archaea. ○
- 235 Calmodulin variant E140G associated with long QT syndrome impairs CaMKII β autophosphorylation and L-type calcium channel (Cav1.2) inactivation. **2022**, 102777 ○
- 234 Bacterial crystalline cellulose secretion via a supramolecular BcsHD scaffold. **2022**, 8, ○
- 233 Monomer and dimer structures of cytochrome b₃ ubiquinol oxidase from Escherichia coli. ○
- 232 Tandem engagement of phosphotyrosines by the dual SH2 domains of p120RasGAP. **2022**, 30, 1603-1614.e5 ○
- 231 High-resolution cryo-EM structure of the Shigella virus Sf6 genome delivery tail machine. **2022**, 8, ○
- 230 The structure of the human LACTB filament reveals the mechanisms of assembly and membrane binding. **2022**, 20, e3001899 ○
- 229 Structural basis of sequence-specific RNA recognition by the antiviral factor APOBEC3G. **2022**, 13, ○
- 228 Structure and Dynamics of the Unassembled Nucleoprotein of Rabies Virus in Complex with Its Phosphoprotein Chaperone Module. **2022**, 14, 2813 ○
- 227 Characterization of a glycoside hydrolase endolysin from Acinetobacter baumannii phage Ab TZA1 with high antibacterial potency and novel structural features. ○
- 226 Multivalency ensures persistence of a +TIP body at specialized microtubule ends. ○
- 225 DNA-TCP complex structures reveal a unique recognition mechanism for TCP transcription factor families. 1
- 224 The structure, binding and function of a Notch transcription complex involving RBPJ and the epigenetic reader protein L3MBTL3. ○

- 223 Structure of the AlgKX modification and secretion complex required for alginate production and biofilm attachment in *Pseudomonas aeruginosa*. **2022**, 13, 0
- 222 Diethylpyrocarbonate-Based Covalent Labeling Mass Spectrometry of Protein Interactions in a Membrane Complex System. 1
- 221 From passage to inhibition: Uncovering the structural and physiological inhibitory mechanisms of MCUb in mitochondrial calcium regulation. **2023**, 37, 0
- 220 Crystal Contact Engineering for Enhanced Cross-Linking Efficiency of HheG Crystals. **2022**, 12, 1553 0
- 219 The neuronal calcium sensor NCS-1 regulates the phosphorylation state and activity of the G β chaperone and GEF Ric-8A. 0
- 218 Molecular mechanism of phosphopeptide neoantigen immunogenicity. 0
- 217 Extracellular CIRP dysregulates macrophage bacterial phagocytosis in sepsis. 0
- 216 Crystal structure and solution state of the C-terminal head region of the narxovirus receptor binding protein. 0
- 215 The Crystal Structure of *Bacillus thuringiensis* Tpp80Aa1 and Its Interaction with Galactose-Containing Glycolipids. **2022**, 14, 863 0
- 214 Probing the Role of a Conserved Phenylalanine in the Active Site of Thiocyanate Dehydrogenase. **2022**, 12, 1787 0
- 213 Crystal structure of the feruloyl esterase from *Lentilactobacillus buchneri* reveals a novel homodimeric state. 13, 0
- 212 Itch receptor MRGPRX4 interacts with the receptor activity-modifying proteins (RAMPs). 0
- 211 Explicit versus implicit consideration of binding partners in protein-protein complex to elucidate intrinsic dynamics. 0
- 210 Extensive substrate recognition by the streptococcal antibody-degrading enzymes IdeS and EndoS. **2022**, 13, 0
- 209 Nodavirus RNA Replication Crown Architecture Reveals Proto-Crown Precursor and Viral Protein A Conformational Switching. 0
- 208 The crystal structure of the EspB-EspK virulence factor-chaperone complex suggests an additional type VII secretion mechanism in *M. tuberculosis*. **2022**, 102761 0
- 207 Antibody Recognition of CD4-Induced Open HIV-1 Env Trimers. **2022**, 96, 0
- 206 A DNA damage-induced phosphorylation circuit enhances Mec1ATR-Ddc2ATRIPrecruitment to Replication Protein A.. 0

- 205 Structural Insights into Pink-eyed Dilution Protein (Oca2). ○
- 204 Hsp70 and Hsp110 Chaperones Promote Early Steps of Proteasome Assembly. **2023**, 13, 11 ○
- 203 Identification, binding, and structural characterization of single domain anti-PD-L1 antibodies inhibitory of immune regulatory proteins PD-1 and CD80. **2022**, 102769 ○
- 202 Structural Insights into the Dimeric Form of Bacillus subtilis RNase Y Using NMR and AlphaFold. **2022**, 12, 1798 ○
- 201 RanBP9 controls the oligomeric state of CTLH complex assemblies. **2023**, 102869 ○
- 200 A data-driven interpretation of the stability of organic molecular crystals. ○
- 199 Conservation and divergence of the G-interfaces of Drosophila melanogaster septins. ○
- 198 Changes within the central stalk of E. coli F1Fo ATP synthase observed after addition of ATP. **2023**, 6, 1 ○
- 197 Rhanteriol, a New Rhanterium suaveolens Desf. Lignan with Pharmacological Potential as an Inhibitor of Enzymes Involved in Neurodegeneration and Type 2 Diabetes. **2023**, 12, 301 ○
- 196 Solution x-ray scattering highlights discrepancies in Plasmodium multi-aminoacyl-tRNA synthetase complexes. ○
- 195 Structural Basis of the Inhibition of L-Methionine γ -Lyase from Fusobacterium nucleatum. **2023**, 24, 1651 ○
- 194 Emergence of an Auxin Sensing Domain in Plant-Associated Bacteria. ○
- 193 In-silico identification of Tyr232 in AMPK β as a dephosphorylation site for the protein tyrosine phosphatase PTP-PEST. ○
- 192 Molecular Dynamics Simulation as a Tool to Identify Mutual Synergistic Folding Proteins. **2023**, 24, 1790 ○
- 191 The Bacteriophage Phage-Inducible Chromosomal Island Arms Race Designs an Interkingdom Inhibitor of dUTPases. ○
- 190 Protein Engineering of Enzyme Robustness Relevant to Organic and Pharmaceutical Chemistry and Applications in Biotechnology. **2023**, 233-277 ○
- 189 New Insights into the Role of the Trypanosoma cruzi Aldo-Keto Reductase TcAKR. **2023**, 12, 85 ○
- 188 Structural basis of broad-spectrum β -lactam resistance in Staphylococcus aureus. **2023**, 613, 375-382 ○

- 187 Analysis of critical protein-protein interactions of SARS-CoV-2 capping and proofreading molecular machineries towards designing dual target inhibitory peptides. **2023**, 13, 0
- 186 Structural and Functional Characterization of the Ureidoacrylate Amidohydrolase RutB from *Escherichia coli*. 0
- 185 Phosphorylation Regulation Mechanism of $\alpha 2$ Integrin for the Binding of Filamin Revealed by Markov State Model. 0
- 184 Cryo-EM structure of hnRNPD-2 fibrils, a functional amyloid associated with limb-girdle muscular dystrophy. **2023**, 14, 1
- 183 Complexed Crystal Structure of the Dihydroorotase Domain of Human CAD Protein with the Anticancer Drug 5-Fluorouracil. **2023**, 13, 149 0
- 182 Activity of Cytosolic Ascorbate Peroxidase (APX) from *Panicum virgatum* against Ascorbate and Phenylpropanoids. **2023**, 24, 1778 0
- 181 Activity and Crystal Structure of the Adherent-Invasive *Escherichia coli* Tle3/Tli3 T6SS Effector/Immunity Complex Determined Using an AlphaFold2 Predicted Model. **2023**, 24, 1740 0
- 180 Tracking the PROTAC degradation pathway in living cells highlights the importance of ternary complex measurement for PROTAC optimization. 0
- 179 Structural insights into ligand-recognition, activation, and signaling-bias at the complement C5a receptor, C5aR1. 0
- 178 Illuminating the mechanism and allosteric behavior of NanoLuc luciferase. 0
- 177 Extracellular Fe(III) reductase structure reveals a modular organization enabling S-layer insertion and electron transfer to insoluble substrates. **2023**, 0
- 176 Structure-guided mutagenesis of the capsid protein indicates that a nanovirus requires assembled viral particles for systemic infection. **2023**, 19, e1011086 0
- 175 Structures of permuted halves of a modern ribose-binding protein. **2023**, 79, 40-49 0
- 174 IraM Remodels the RssB Segmented Helical Linker to Stabilize λ against Degradation by ClpXP. 0
- 173 Major royal jelly proteins elicited suppression of SARS-CoV-2 entry and replication with halting lung injury. **2023**, 228, 715-731 0
- 172 Targeted degradation via direct 26S proteasome recruitment. **2023**, 19, 55-63 0
- 171 Crystal structure of the *Arabidopsis* SPIRAL2 C-terminal domain reveals a p80-Katanin-like domain. 0
- 170 Potent ClpP agonists with anticancer properties bind with improved structural complementarity and alter the mitochondrial N-terminome. **2022**, 1

- 169 A sorghum ascorbate peroxidase with four binding sites has activity against ascorbate and phenylpropanoids. ○
- 168 Evolution of Rev7 interactions in eukaryotic TLS DNA polymerase Pol η **2022**, 102859 ○
- 167 Structure and dynamic association of an assembly platform subcomplex of the bacterial type II secretion system. **2022**, ○
- 166 Preparation and Structural Studies of the Silkworm Carotenoid-Binding Protein Complexed with a New Pigment. **2022**, 67, 909-917 ○
- 165 Machine learning in computational modelling of membrane protein sequences and structures: From methodologies to applications. **2023**, 21, 1205-1226 ○
- 164 The allosteric effect of the upper half of SENP1 contributes to its substrate selectivity for SUMO1 over SUMO2. 1-15 ○
- 163 Asymmetric horseshoe-like assembly of peroxisomal yeast oxalyl-CoA synthetase. **2023**, ○
- 162 Cryo-EM structure of DNA polymerase η helicase domain in complex with inhibitor novobiocin. ○
- 161 Structural characterization of HIV-1 Env heterotrimers bound to one or two CD4 receptors reveals intermediate Env conformations. ○
- 160 PTCHD1 Binds Cholesterol but Not Sonic Hedgehog, Suggesting a Distinct Cellular Function. **2023**, 24, 2682 ○
- 159 Design, Production, and Characterization of Catalytically Active Inclusion Bodies. **2023**, 49-74 ○
- 158 Trimeric Architecture Ensures the Stability and Biological Activity of the Calf Purine Nucleoside Phosphorylase: In Silico and In Vitro Studies of Monomeric and Trimeric Forms of the Enzyme. **2023**, 24, 2157 ○
- 157 Human neutralizing antibodies to cold linear epitopes and subdomain 1 of the SARS-CoV-2 spike glycoprotein. 2
- 156 Mechanisms of Sugar Aminotransferase-like Enzymes to Synthesize Stereoisomers of Non-proteinogenic Amino Acids in Natural Product Biosynthesis. ○
- 155 Staphylococcal Periscope Proteins Aap, SasG and Pls project non-canonical legume-like lectin adhesin domains from the bacterial surface. **2023**, 102936 ○
- 154 Self-recycling and partially conservative replication of mycobacterial methylmannose polysaccharides. **2023**, 6, ○
- 153 Biophysical evaluation of the oligomerization and conformational properties of the N-terminal domain of TDP-43. **2023**, 109533 ○
- 152 An unusual disulfide-linked dimerization in the fluorescent protein rsCherryRev1.4. **2023**, 79, 38-44 ○

- 151 Structure of the human CLC-7/Ostm1 complex reveals a novel state. **2023**, 53, 0306 ○
- 150 Connection between MHC class II binding and aggregation propensity: The antigenic peptide 10 of *Paracoccidioides brasiliensis* as a benchmark study. **2023**, 21, 1746-1758 ○
- 149 Probing the E1 α -E2 α and E1 α -E2 α Interactions in Binary Subcomplexes of the Human 2-Oxoglutarate Dehydrogenase and 2-Oxoadipate Dehydrogenase Complexes by Chemical Cross-Linking Mass Spectrometry and Molecular Dynamics Simulation. **2023**, 24, 4555 ○
- 148 The SAH7 Homologue of the Allergen Ole e 1 Interacts with the Putative Stress Sensor SBP1 (Selenium-Binding Protein 1) in *Arabidopsis thaliana*. **2023**, 24, 3580 ○
- 147 Screening and epitope characterization of diagnostic nanobody against total and activated *Bacteroides fragilis* toxin. 14, ○
- 146 Unique alcohol dehydrogenases involved in algal sugar utilization by marine bacteria. **2023**, 107, 2363-2384 ○
- 145 Structure and regulation of the myotonic dystrophy kinase-related Cdc42-binding kinase. **2023**, 31, 435-446.e4 ○
- 144 Structural insights into the chromodomain of Oxpecker in complex with histone H3 lysine 9 trimethylation reveal a transposon silencing mechanism by heterodimerization. **2023**, 652, 95-102 ○
- 143 Molecular determinants for differential activation of the bile acid receptor from the pathogen *Vibrio parahaemolyticus*. **2023**, 299, 104591 ○
- 142 The structure of the teleost Immunoglobulin M core provides insights on polymeric antibody evolution, assembly, and function. ○
- 141 Attractant and repellent induce opposing changes in the chemoreceptor four-helix bundle ligand-binding domain. ○
- 140 Multistep Engineering of a Penicillin G Acylase for Systematic Improvement of Crystallization Efficiency. ○
- 139 CryoEM Reveals Oligomeric Isomers of a Multienzyme Complex and Assembly Mechanics. **2023**, 100088 ○
- 138 Characterization of new highly selective pyrazolo[4,3-d]pyrimidine inhibitor of CDK7. **2023**, 161, 114492 ○
- 137 The Conserved Yeast Protein Knr4 Involved in Cell Wall Integrity Is a Multi-domain Intrinsically Disordered Protein. **2023**, 435, 168048 ○
- 136 ERREDBD undergoes dimerization and conformational rearrangement upon binding to the downstream site of the DR1 element. **2023**, 656, 16-22 ○
- 135 Unveiling mutation effects on the structural dynamics of the main protease from SARS-CoV-2 with hybrid simulation methods. **2023**, 121, 108443 ○
- 134 Characterization of two distinct neutrophil serine protease binding modes within a *Staphylococcus aureus* innate immune evasion protein family. **2023**, 299, 102969 ○

- 133 Two different alanine dehydrogenases from *Geobacillus kaustophilus*: Their biochemical characteristics and differential expression in vegetative cells and spores. **2023**, 1871, 140904 ○
- 132 Structures of the sulfite detoxifying F420-dependent enzyme from Methanococcales. ○
- 131 Crystal Structure of Inhibitor-Bound Bacterial Oligopeptidase B in the Closed State: Similarity and Difference between Protozoan and Bacterial Enzymes. **2023**, 24, 2286 ○
- 130 Mechanism of regulation of the *Helicobacter pylori* Cag β ATPase by CagZ. **2023**, 14, ○
- 129 Heterogeneity in winged helix-turn-helix and substrate DNA interactions: Insights from theory and experiments. **2023**, 124, 337-358 ○
- 128 Recognition of the CCT5 di-Glu degron by CRL4 DCAF12 is dependent on TRiC assembly. **2023**, 42, ○
- 127 DNAJB8 facilitates autophagic-lysosomal degradation of viral Vif protein and restricts HIV -1 virion infectivity by rescuing APOBEC3G expression in host cells. **2023**, 37, ○
- 126 Formation and characterization of BMP2/GDF5 and BMP4/GDF5 heterodimers. **2023**, 21, ○
- 125 Reducing affinity as a strategy to boost immunomodulatory antibody agonism. **2023**, 614, 539-547 1
- 124 Structure of pyridoxal 5'-phosphate-bound D-threonine aldolase from *Chlamydomonas reinhardtii*. **2023**, 79, 31-37 ○
- 123 The uncharacterized *Pseudomonas aeruginosa* PA4189 is a novel and efficient aminoacetaldehyde dehydrogenase. **2023**, 480, 259-281 ○
- 122 Regulation of alanine racemase activity by carboxylates and the d -type substrate d -alanine. ○
- 121 *Escherichia coli* YgiC and Yjfc Possess Peptide-Spermidine Ligase Activity. **2023**, 62, 899-911 ○
- 120 The LHDH module of bacterial replicative helicases is the common binding site for DciA and other helicase loaders. **2023**, 79, 177-187 ○
- 119 Structural Insight into the Working Mechanism of the FAD Synthetase from the Human Pathogen *Streptococcus pneumoniae*: A Molecular Docking Simulation Study. **2023**, 24, 3121 ○
- 118 Quaternary glucocorticoid receptor structure highlights allosteric interdomain communication. **2023**, 30, 286-295 ○
- 117 Atomic crystal structure and sugar specificity of a β -trefoil lectin domain from the ectomycorrhizal basidiomycete *Laccaria bicolor*. **2023**, 233, 123507 ○
- 116 A high-quality reference genome for the fission yeast *Schizosaccharomyces osmophilus*. **2023**, 13, ○

- 115 Blue-to-Red TagFT, mTagFT, mTsFT, and Green-to-FarRed mNeptusFT2 Proteins, Genetically Encoded True and Tandem Fluorescent Timers. **2023**, 24, 3279 ○
- 114 Structures of MPND Reveal the Molecular Recognition of Nucleosomes. **2023**, 24, 3368 ○
- 113 The binding mode of orphan glycyl-tRNA synthetase with tRNA supports the synthetase classification and reveals large domain movements. **2023**, 9, ○
- 112 Structural and Functional Analysis of a Highly Active Designed Phosphotriesterase for the Detoxification of Organophosphate Nerve Agents Reveals an Unpredicted Conformation of the Active Site Loop. **2023**, 62, 942-955 ○
- 111 Structures of BIRC6-client complexes provide a mechanism of SMAC-mediated release of caspases. **2023**, 379, 1105-1111 1
- 110 Structure-Based Optimization of ProteaseInhibitor Interactions to Enhance Specificity of Human Stefin-A against Falcipain-2 from the Plasmodium falciparum 3D7 Strain. **2023**, 62, 1053-1069 ○
- 109 Structural insights into agonist-binding and activation of the human complement C3a receptor. ○
- 108 Structure and dynamics of the essential endogenous mycobacterial polyketide synthase Pks13. **2023**, 30, 296-308 ○
- 107 An engineered miRNA PS-OMe miR130 inhibits acute lung injury by targeting eCIRP in sepsis. **2023**, 29, ○
- 106 Cross-protective antibodies against common endemic respiratory viruses. **2023**, 14, ○
- 105 Structures of NF- κ B p52 homodimer-DNA complexes rationalize binding mechanisms and transcription activation. 12, ○
- 104 Conformational dynamics control assembly of an extremely long bacteriophage tail tube. **2023**, 299, 103021 ○
- 103 Integration of immunoinformatics and cheminformatics to design and evaluate a multipeptide vaccine against *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* coinfection. 10, ○
- 102 A Fijivirus Major Viroplasm Protein Shows RNA-Stimulated ATPase Activity by Adopting Pentameric and Hexameric Assemblies of Dimers. ○
- 101 Structural insight into guanylyl cyclase receptor hijacking of the kinaseHsp90 regulatory mechanism. ○
- 100 Integrative structural analysis of the type III secretion system needle complex from *Shigella flexneri*. **2023**, 32, ○
- 99 Structural and Biochemical Insights into Post-Translational Arginine-to-Ornithine Peptide Modifications by an Atypical Arginase. **2023**, 18, 528-536 ○
- 98 Template-assisted covalent modification of DCAF16 underlies activity of BRD4 molecular glue degraders. ○

- 97 Crystal Structure of Mesoconyl-CoA Hydratase from *Methylobacterium extorquens* CM4. **2023**, ○
- 96 N-Glycoprofiling of SLC35A2-CDG: Patient with a Novel Hemizygous Variant. **2023**, 11, 580 ○
- 95 Structure, substrate binding and activity of a unique AAA+ protein: the BrxL phage restriction factor. ○
- 94 Engineering the Thermostability of Sucrose Synthase by Reshaping the Subunit Interaction Contributes to Efficient UDP-Glucose Production. **2023**, 71, 3832-3841 ○
- 93 Monobody Inhibitor Selective to the Phosphatase Domain of SHP2 and its Use as a Probe for Quantifying SHP2 Allosteric Regulation. **2023**, 435, 168010 ○
- 92 Broadly neutralizing anti-S2 antibodies protect against all three human betacoronaviruses that cause deadly disease. **2023**, 56, 669-686.e7 ○
- 91 Structure of the planar cell polarity cadherins Fat4 and Dachsous1. **2023**, 14, 1
- 90 Structural and biochemical characterization establishes a detailed understanding of KEAP1-CUL3 complex assembly. ○
- 89 Improved Assessment of Globularity of Protein Structures and the Ellipsoid Profile of the Biological Assemblies from the PDB. **2023**, 13, 385 ○
- 88 CDK4/6 inhibitor palbociclib promotes SARS-CoV-2 cell entry by down-regulating SKP2 dependent ACE2 degradation. **2023**, 212, 105558 ○
- 87 CvkR is a MerR-type transcriptional repressor of class 2 type V-K CRISPR-associated transposase systems. **2023**, 14, ○
- 86 Structural insights into ribonucleoprotein dissociation by nucleocapsid protein interacting with non-structural protein 3 in SARS-CoV-2. **2023**, 6, ○
- 85 Structural basis for binding of Smaug to the GPCR Smoothed and to the germline inducer Oskar. ○
- 84 Avidity engineering of human heavy-chain-only antibodies mitigates neutralization resistance of SARS-CoV-2 variants. 14, ○
- 83 Development of a human antibody fragment cross-neutralizing scorpion toxins. **2023**, 155, 165-174 ○
- 82 Uncovering the Interaction Interface Between Harpin (Hpa1) and Rice Aquaporin (OsPIP1;3) Through Protein-Protein Docking: An In Silico Approach. ○
- 81 Hile represses the activity of Hild via a mechanism distinct from that of intestinal long-chain fatty acids. ○
- 80 Ion Mobility Mass Spectrometry (IM-MS) for Structural Biology: Insights Gained by Measuring Mass, Charge, and Collision Cross Section. **2023**, 123, 2902-2949 ○

- 79 To the Understanding of Catalysis by D-Amino Acid Transaminases: A Case Study of the Enzyme from *Aminobacterium colombiense*. **2023**, 28, 2109 ○
- 78 TcpA from the *Clostridium perfringens* plasmid pCW3 is more closely related to the DNA translocase FtsK than to coupling proteins. **2023**, 31, 455-463.e4 ○
- 77 Hierarchical graph learning for protein-protein interaction. **2023**, 14, ○
- 76 Ubiquitin-like conjugation by bacterial cGAS enhances anti-phage defence. **2023**, 616, 326-331 ○
- 75 Characterization of new highly selective pyrazolo[4,3-d]pyrimidine inhibitor of CDK7. ○
- 74 The NGF R100W Mutation, Associated with Hereditary Sensory Autonomic Neuropathy Type V, Specifically Affects the Binding Energetic Landscapes of NGF and of Its Precursor proNGF and p75NTR. **2023**, 12, 364 ○
- 73 PrePPI: A structure informed proteome-wide database of protein-protein interactions. ○
- 72 Heteromerization of Dopamine D2 and Oxytocin Receptor in Adult Striatal Astrocytes. **2023**, 24, 4677 ○
- 71 Preclinical safety and efficacy of a therapeutic antibody that targets SARS-CoV-2 at the sotrovimab face but is escaped by Omicron. **2023**, 26, 106323 ○
- 70 Structure of the *T. brucei* kinetoplastid RNA editing substrate-binding complex core component, RESC5. **2023**, 18, e0282155 ○
- 69 The dynamic nature of netrin-1 and the structural basis for glycosaminoglycan fragment-induced filament formation. **2023**, 14, 1
- 68 Structure of a HIV-1 IN-Allosteric inhibitor complex at 2.93 Å resolution: Routes to inhibitor optimization. **2023**, 19, e1011097 ○
- 67 First pan-specific vNAR against human TGF-β as a potential therapeutic application: in silico modeling assessment. **2023**, 13, ○
- 66 A molecular basis for tetramer destabilization and aggregation of transthyretin Ala97Ser. **2023**, 32, ○
- 65 Crystal structure and identification of amino acid residues for catalysis and binding of GH3 AnBX αxylosidase from *Aspergillus niger*. **2023**, 107, 2335-2349 ○
- 64 The crystal structure of a simian Foamy Virus receptor binding domain provides clues about entry into host cells. **2023**, 14, ○
- 63 Monomer and dimer structures of cytochrome bo₃ ubiquinol oxidase from *Escherichia coli*. **2023**, 32, ○
- 62 Designer molecules of the synaptic organizer MDGA1 reveal 3D conformational control of biological function. **2023**, 299, 104586 ○

- 61 A novel mAb broadly neutralizes SARS-CoV-2 VOCs in vitro and in vivo, including the Omicron variants. **2023**, 95, ○
- 60 Design of Synthetic Hydrogel Compositions for Noncovalent Protein Recognition. ○
- 59 Structural basis of GAIN domain autoproteolysis and cleavage-resistance in the adhesion G-protein coupled receptors. ○
- 58 Heterocomplex structure of a polyketide synthase component involved in modular backbone halogenation. **2023**, ○
- 57 A splicing variant of EDS1 from *Vitis vinifera* forms homodimers but no heterodimers with PAD4. **2023**, 32, ○
- 56 Novel exported bifunctional fusion enzymes with chorismate mutase and cyclohexadienyl dehydratase activity: shikimate pathway enzymes teamed up in no man's land. ○
- 55 The Josephin domain (JD) containing proteins are predicted to bind to the same interactors: Implications for spinocerebellar ataxia type 3 (SCA3) studies using *Drosophila melanogaster* mutants. 16, ○
- 54 Structures of trehalose-6-phosphate synthase, Tps1, from the fungal pathogen *Cryptococcus neoformans*: a target for novel antifungals. ○
- 53 Cryo-EM structures of anti-malarial antibody L9 with circumsporozoite protein reveal trimeric L9 association and complete 27-residue epitope. **2023**, 31, 480-491.e4 ○
- 52 Production of neutralizing antibody fragment variants in the cytoplasm of *E. coli* for rapid screening: SARS-CoV-2 a case study. **2023**, 13, ○
- 51 PrePPI: A Structure Informed Proteome-wide Database of Protein-Protein Interactions. **2023**, 168052 ○
- 50 Structural insights into the assembly of gp130 family cytokine signaling complexes. **2023**, 9, ○
- 49 MERS virus spike protein HTL-epitopes selection and multi-epitope vaccine design using computational biology. 1-16 ○
- 48 Structural context of homomeric interactions in the Ig domain of the MPZ (P0) myelin adhesion protein and relation to Charcot-Marie-Tooth disease phenotype variants. ○
- 47 Identification of a peptide ligand for human ALDH3A1 through peptide phage display: Prediction and characterization of protein interaction sites and inhibition of ALDH3A1 enzymatic activity. 10, ○
- 46 Structure of Dimeric Lipoprotein Lipase Reveals a Pore for Hydrolysis of Acyl Chains. ○
- 45 From primordial clocks to circadian oscillators. **2023**, 616, 183-189 ○
- 44 Modeling of Protein Complexes. **2023**, 349-371 ○

- 43 Structural insights into the regulation of peptidoglycan DL-endopeptidases by inhibitory protein IseA. **2023**, ○
- 42 Structural basis of bacteriophage T5 infection trigger and E. coli cell wall perforation. **2023**, 9, ○
- 41 ClpC2 protects mycobacteria against a natural antibiotic targeting ClpC1-dependent protein degradation. **2023**, 6, ○
- 40 Modification of DNA by a viral enzyme and charged tRNA. ○
- 39 Crystal structures of dimeric and heptameric mtHsp60 reveal the mechanism of chaperonin inactivation. **2023**, 6, e202201753 ○
- 38 Mechanism of antibody-specific deglycosylation and immune evasion by Streptococcal IgG-specific endoglycosidases. **2023**, 14, ○
- 37 Direct Blockade of the Norovirus Histo-Blood Group Antigen Binding Pocket by Nanobodies. ○
- 36 Structural Characterization of Neisseria gonorrhoeae Bacterial Peroxidase Insights into the Catalytic Cycle of Bacterial Peroxidases. **2023**, 24, 6246 ○
- 35 3,4-Dihydroxyphenylacetaldehyde synthase evolved an ordered and distinct active site to promote elastic cuticle formation and blood intake in Aedes aegypti. ○
- 34 BRCA1-BARD1 combines multiple chromatin recognition modules to bridge nascent nucleosomes. ○
- 33 Itch receptor MRGPRX4 interacts with the receptor activity-modifying proteins (RAMPs). **2023**, 104664 ○
- 32 Novel glycoside hydrolase family enzymes from Escherichia coli are associated with osmo-regulated periplasmic glucan synthesis. ○
- 31 Rational strategies for enhancing mAb binding to SARS-CoV-2 variants through CDR diversification and antibody-escape prediction. 14, ○
- 30 Structural and mechanistic insights into activation of the human RNA ligase RTCB by Arcease. ○
- 29 Protein language models can capture protein quaternary state. ○
- 28 Pseudouridine-Modifying Enzymes SapB and SapH Control Entry into the Pseudouridimycin Biosynthetic Pathway. **2023**, 18, 794-802 ○
- 27 Modular adjuvant-free pan-HLA-DR-immunotargeting subunit vaccine against SARS-CoV-2 elicits broad sarbecovirus-neutralizing antibody responses. **2023**, 42, 112391 ○
- 26 Crystal Structure and Functional Characterization of an S-Formylglutathione Hydrolase (BuSFGH) from Burkholderiaceae sp.. **2023**, 13, 621 ○

- 25 Extended DNA threading through a dual-engine motor module of the activating signal co-integrator 1 complex. **2023**, 14,
- 24 Crystal structure of a highly conserved enteroviral 5' cloverleaf RNA replication element. **2023**, 14,
- 23 Antibodies that neutralize all current SARS-CoV-2 variants of concern by conformational locking.
- 22 BopN is a Gatekeeper of the Bordetella Type III Secretion System.
- 21 Structural basis of spike RBM-specific human antibodies counteracting broad SARS-CoV-2 variants. **2023**, 6,
- 20 Structural basis of sensory receptor evolution in octopus. **2023**, 616, 373-377
- 19 Sensory specializations drive octopus and squid behaviour. **2023**, 616, 378-383
- 18 Pangenomic Study of *Fusobacterium nucleatum* Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.
- 17 Identification and characterization of endo- and exo-hydrolases cleaving the β - and β -D-arabinofuranosidic bonds of lipoarabinomannan and arabinogalactan of *Mycobacteria*.
- 16 Structure-function Analyses Reveal Key Molecular Determinants of HIV-1 CRF01_AE Resistance to the Entry Inhibitor Temsavir.
- 15 Histone divergence in *Trypanosoma brucei* results in unique alterations to nucleosome structure.
- 14 Genetic drift and genome reduction in the plant pathogen *Candidatus Liberibacter solanacearum* shapes a new enzyme in lysine biosynthesis.
- 13 CryoEM and stability analysis of virus-like particles of potyvirus and ipomovirus infecting a common host. **2023**, 6,
- 12 Soluble domains of cytochrome c-556 and Rieske iron-sulfur protein from *Chlorobaculum tepidum*: Crystal structures and interaction analysis. **2023**, 100101
- 11 Crystal structures of 17-beta-hydroxysteroid dehydrogenase 13.
- 10 The structure of a 12-segmented dsRNA reovirus: New insights into capsid stabilization and organization. **2023**, 19, e1011341
- 9 DNA-binding mechanism and evolution of replication protein A. **2023**, 14,
- 8 TRIM56 coiled-coil domain structure provides insights into its E3 ligase functions. **2023**,

- 7 A potential histone-chaperone activity for the MIER1 histone deacetylase complex. ○
- 6 Factors Affecting the Stability of the Trimer of 2'-Deoxyuridine 5'-Triphosphate Nucleotide Hydrolase from *Escherichia coli*. **2023**, 57, 312-319 ○
- 5 Combined Structural and Computational Study of the mRubyFT Fluorescent Timer Locked in Its Blue Form. **2023**, 24, 7906 ○
- 4 Structural insight into an anti-BRIL Fab as a G-protein-coupled receptor crystallization chaperone. **2023**, 79, 435-441 ○
- 3 Structural and biochemical characterization establishes a detailed understanding of KEAP1-CUL3 complex assembly. **2023**, 204, 215-225 ○
- 2 Pathogenic HER3 dimerization domain mutations create a structural bias towards un-conventional EGFR-HER3 signalling axis in breast cancer. **2023**, 242, 124765 ○
- 1 Annotating Macromolecular Complexes in the Protein Data Bank: Improving the FAIRness of Structure Data. ○