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## Refinement of macromolecular structures by the maximum-likelihood method

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2043	Three-dimensional structure of the enzyme dimanganese catalase from <i>Thermus Thermophilus</i> at 1 Å resolution. <b>2000</b> , 45, 105-116	128
2042	Latrunculin alters the actin-monomer subunit interface to prevent polymerization. <b>2000</b> , 2, 376-8	387
2041	The crystal structure of DNA mismatch repair protein MutS binding to a G x T mismatch. <b>2000</b> , 407, 711-7	540
2040	Recent developments in software for the automation of crystallographic macromolecular structure determination. <b>2000</b> , 10, 564-8	15
2039	Crystal structure of RNA 3'-terminal phosphate cyclase, a ubiquitous enzyme with unusual topology. <b>2000</b> , 8, 13-23	26
2038	The structure of TolB, an essential component of the tol-dependent translocation system, and its protein-protein interaction with the translocation domain of colicin E9. <b>2000</b> , 8, 57-66	75
2037	The atomic-resolution structure of a novel bacterial esterase. <b>2000</b> , 8, 143-51	69
2036	A new variant of the Ntn hydrolase fold revealed by the crystal structure of L-aminopeptidase D-ala-esterase/amidase from <i>Ochrobactrum anthropi</i> . <b>2000</b> , 8, 153-62	38

2035	The structure of adenylosuccinate lyase, an enzyme with dual activity in the de novo purine biosynthetic pathway. <b>2000</b> , 8, 163-74	65
2034	The 1.8 Å crystal structure and active-site architecture of beta-ketoacyl-acyl carrier protein synthase III (FabH) from <i>Escherichia coli</i> . <b>2000</b> , 8, 185-95	188
2033	Crystal structure of Rab geranylgeranyltransferase at 2.0 Å resolution. <b>2000</b> , 8, 241-51	98
2032	The structure of the N-terminal actin-binding domain of human dystrophin and how mutations in this domain may cause Duchenne or Becker muscular dystrophy. <b>2000</b> , 8, 481-91	132
2031	Structure of cyanase reveals that a novel dimeric and decameric arrangement of subunits is required for formation of the enzyme active site. <b>2000</b> , 8, 505-14	50
2030	Crystal structure of decameric 2-Cys peroxiredoxin from human erythrocytes at 1.7 Å resolution. <b>2000</b> , 8, 605-15	275
2029	X-ray structure of <i>Escherichia coli</i> pyridoxine 5'-phosphate oxidase complexed with FMN at 1.8 Å resolution. <b>2000</b> , 8, 751-62	26
2028	The X-ray structure of the FMN-binding protein AtHal3 provides the structural basis for the activity of a regulatory subunit involved in signal transduction. <b>2000</b> , 8, 961-9	40
2027	Crystal structure of a D-aminopeptidase from <i>Ochrobactrum anthropi</i> , a new member of the 'penicillin-recognizing enzyme' family. <b>2000</b> , 8, 971-80	38
2026	Structure of nicotinamide mononucleotide adenylyltransferase: a key enzyme in NAD(+) biosynthesis. <b>2000</b> , 8, 993-1004	59
2025	Crystal structure of the molybdenum cofactor biosynthesis protein MobA from <i>Escherichia coli</i> at near-atomic resolution. <b>2000</b> , 8, 1115-25	38
2024	Effector sites in the three-dimensional structure of mammalian sperm beta-acrosin. <b>2000</b> , 8, 1179-88	39
2023	Does NMR mean "not for molecular replacement"? Using NMR-based search models to solve protein crystal structures. <b>2000</b> , 8, R213-20	29
2022	Structure and mechanism of homoserine kinase: prototype for the GHMP kinase superfamily. <b>2000</b> , 8, 1247-57	100
2021	Insights into class D beta-lactamases are revealed by the crystal structure of the OXA10 enzyme from <i>Pseudomonas aeruginosa</i> . <b>2000</b> , 8, 1289-98	120
2020	Cross-talk and ammonia channeling between active centers in the unexpected domain arrangement of glutamate synthase. <b>2000</b> , 8, 1299-308	79
2019	Substrate deformation in a hypoxanthine-guanine phosphoribosyltransferase ternary complex: the structural basis for catalysis. <b>2000</b> , 8, 1309-18	62
2018	Divalent metal cofactor binding in the kinetic folding trajectory of <i>Escherichia coli</i> ribonuclease HI. <b>2000</b> , 9, 1914-21	42

2017	Conformational flexibility in the apolipoprotein E amino-terminal domain structure determined from three new crystal forms: implications for lipid binding. <b>2000</b> , 9, 886-97	43
2016	Topography of a 2.0 Å structure of alpha1-antitrypsin reveals targets for rational drug design to prevent conformational disease. <b>2000</b> , 9, 1274-81	162
2015	A novel two-over-two alpha-helical sandwich fold is characteristic of the truncated hemoglobin family. <b>2000</b> , 19, 2424-34	199
2014	The structure and function of the beta 2-adaptin appendage domain. <b>2000</b> , 19, 4216-27	188
2013	Evolutionary transition pathways for changing peptide ligand specificity and structure. <b>2000</b> , 19, 4866-74	24
2012	The structural basis for the recognition of acetylated histone H4 by the bromodomain of histone acetyltransferase gcn5p. <b>2000</b> , 19, 6141-9	387
2011	The structural basis of the catalytic mechanism and regulation of glucose-1-phosphate thymidyltransferase (RmlA). <b>2000</b> , 19, 6652-63	158
2010	Crystal structure of the catalytic domain of human complement c1s: a serine protease with a handle. <b>2000</b> , 19, 1755-65	93
2009	The molecular basis of vancomycin resistance in clinically relevant Enterococci: crystal structure of D-alanyl-D-lactate ligase (VanA). <b>2000</b> , 97, 8921-5	53
2008	The role of cavities in protein dynamics: crystal structure of a photolytic intermediate of a mutant myoglobin. <b>2000</b> , 97, 2058-63	137
2007	Three-dimensional structure of the Fab from a human IgM cold agglutinin. <b>2000</b> , 165, 6422-8	26
2006	The conformational activation of antithrombin. A 2.85-Å structure of a fluorescein derivative reveals an electrostatic link between the hinge and heparin binding regions. <b>2000</b> , 275, 15377-83	56
2005	Binding of bisubstrate analog promotes large structural changes in the unregulated catalytic trimer of aspartate transcarbamoylase: implications for allosteric regulation. <b>2000</b> , 97, 5077-82	33
2004	Inversion of stereospecificity of vanillyl-alcohol oxidase. <b>2000</b> , 97, 9455-60	68
2003	Structural analysis of flavinylation in vanillyl-alcohol oxidase. <b>2000</b> , 275, 38654-8	55
2002	Substrate specificity in glycoside hydrolase family 10. Structural and kinetic analysis of the <i>Streptomyces lividans</i> xylanase 10A. <b>2000</b> , 275, 23020-6	58
2001	The structures of the H(C) fragment of tetanus toxin with carbohydrate subunit complexes provide insight into ganglioside binding. <b>2000</b> , 275, 8889-94	112
2000	The crystal structure of the <i>Escherichia coli</i> MobA protein provides insight into molybdopterin guanine dinucleotide biosynthesis. <b>2000</b> , 275, 40211-7	59

1999	Retrostructural analysis of metalloproteins: application to the design of a minimal model for diiron proteins. <b>2000</b> , 97, 6298-305	197
1998	Structural evidence for ligand specificity in the binding domain of the human androgen receptor. Implications for pathogenic gene mutations. <b>2000</b> , 275, 26164-71	438
1997	Inhibition of the hepatitis C virus NS3/4A protease. The crystal structures of two protease-inhibitor complexes. <b>2000</b> , 275, 7152-7	107
1996	The crystal structure of NusB from <i>Mycobacterium tuberculosis</i> . <b>2000</b> , 7, 475-8	23
1995	Minor structural consequences of alternative CUG codon usage (Ser for Leu) in <i>Candida albicans</i> exoglucanase. <b>2000</b> , 13, 735-8	15
1994	Expression, characterization and structure determination of an active site mutant (Glu202-Gln) of mini-stromelysin-1. <b>2000</b> , 13, 397-405	19
1993	Substrate specificity in glycoside hydrolase family 10. Structural and kinetic analysis of the <i>Streptomyces lividans</i> Xylanase 10A. <b>2000</b> ,	4
1992	The allosteric regulation of pyruvate kinase. <b>2000</b> , 275, 18145-52	131
1991	Correlated switch binding and signaling in bacterial chemotaxis. <b>2000</b> , 275, 19752-8	25
1990	Asp-170 is crucial for the redox properties of vanillyl-alcohol oxidase. <b>2000</b> , 275, 14799-808	36
1989	Structural characterization of protein-denaturant interactions: crystal structures of hen egg-white lysozyme in complex with DMSO and guanidinium chloride. <b>2000</b> , 13, 133-41	38
1988	Crystal structures of an oxygen-binding cytochrome c from <i>Rhodobacter sphaeroides</i> . <b>2000</b> , 275, 16050-6	29
1987	Crystal structure of the allergen Equ c 1. A dimeric lipocalin with restricted IgE-reactive epitopes. <b>2000</b> , 275, 21572-7	66
1986	The high resolution crystal structure of yeast hexokinase PII with the correct primary sequence provides new insights into its mechanism of action. <b>2000</b> , 275, 20814-21	95
1985	Crystal structure of human ornithine decarboxylase at 2.1 Å resolution: structural insights to antizyme binding. <b>2000</b> , 295, 7-16	121
1984	The tertiary structure at 1.59 Å resolution and the proposed amino acid sequence of a family-11 xylanase from the thermophilic fungus <i>Paecilomyces varioti bainier</i> . <b>2000</b> , 295, 581-93	60
1983	X-ray structure of yeast Hal2p, a major target of lithium and sodium toxicity, and identification of framework interactions determining cation sensitivity. <b>2000</b> , 295, 927-38	62
1982	Substrate binding site of naphthalene 1,2-dioxygenase: functional implications of indole binding. <b>2000</b> , 296, 701-12	135

1981	Crystal structures of an N-terminal fragment from Moloney murine leukemia virus reverse transcriptase complexed with nucleic acid: functional implications for template-primer binding to the fingers domain. <b>2000</b> , 296, 613-32	45
1980	Crystal structures of mutant monomeric hexokinase I reveal multiple ADP binding sites and conformational changes relevant to allosteric regulation. <b>2000</b> , 296, 1001-15	83
1979	High resolution crystal structure of bovine mitochondrial EF-Tu in complex with GDP. <b>2000</b> , 297, 421-36	63
1978	The crystal structure of d-glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeon <i>Methanothermus fervidus</i> in the presence of NADP(+) at 2.1 Å resolution. <b>2000</b> , 297, 481-500	31
1977	Insights into ligand-induced conformational change in Cel5A from <i>Bacillus agaradhaerens</i> revealed by a catalytically active crystal form. <b>2000</b> , 297, 819-28	46
1976	Domain swapping in the sporulation response regulator Spo0A. <b>2000</b> , 297, 757-70	61
1975	The three-dimensional structure of a <i>Plasmodium falciparum</i> cyclophilin in complex with the potent anti-malarial cyclosporin A. <b>2000</b> , 298, 123-33	34
1974	Crystallographic analysis of the reaction pathway of <i>Zoogloea ramigera</i> biosynthetic thiolase. <b>2000</b> , 297, 1171-82	92
1973	The crystal structure of a sulfurtransferase from <i>Azotobacter vinelandii</i> highlights the evolutionary relationship between the rhodanese and phosphatase enzyme families. <b>2000</b> , 298, 691-704	82
1972	High-resolution structure of the OmpA membrane domain. <b>2000</b> , 298, 273-82	264
1971	Dimethylsulfoxide reductase: an enzyme capable of catalysis with either molybdenum or tungsten at the active site. <b>2000</b> , 299, 593-600	79
1970	Crystal structure of a plant ribonuclease, RNase LE. <b>2000</b> , 298, 859-73	46
1969	Stabilization of GroEL minichaperones by core and surface mutations. <b>2000</b> , 298, 917-26	36
1968	The 1.5 Å resolution crystal structure of the carbamate kinase-like carbamoyl phosphate synthetase from the hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> , bound to ADP, confirms that this thermostable enzyme is a carbamate kinase, and provides insight into substrate binding and stability in carbamate kinases. <b>2000</b> , 299, 463-76	46
1967	Crystal structure of <i>Pseudomonas aeruginosa</i> PAK pilin suggests a main-chain-dominated mode of receptor binding. <b>2000</b> , 299, 1005-17	120
1966	Crystal structure of dodecameric vanadium-dependent bromoperoxidase from the red algae <i>Corallina officinalis</i> . <b>2000</b> , 299, 1035-49	160
1965	The structure of reduced trypanothione peroxidase reveals a decamer and insight into reactivity of 2Cys-peroxiredoxins. <b>2000</b> , 300, 903-16	143
1964	The structure of rhamnose isomerase from <i>Escherichia coli</i> and its relation with xylose isomerase illustrates a change between inter and intra-subunit complementation during evolution. <b>2000</b> , 300, 917-33	57



1963	Structures of chitobiase mutants complexed with the substrate Di-N-acetyl-d-glucosamine: the catalytic role of the conserved acidic pair, aspartate 539 and glutamate 540. <b>2000</b> , 300, 611-7	71
1962	The crystal structure of adenylosuccinate lyase from <i>Pyrobaculum aerophilum</i> reveals an intracellular protein with three disulfide bonds. <b>2000</b> , 301, 433-50	69
1961	Crystal structure of a phage library-derived single-chain Fv fragment complexed with turkey egg-white lysozyme at 2.0 Å resolution. <b>2000</b> , 301, 239-46	29
1960	Crystal structure of glycosyltrehalose trehalohydrolase from the hyperthermophilic archaeum <i>Sulfolobus solfataricus</i> . <b>2000</b> , 301, 451-64	36
1959	A comparative analysis of 23 structures of the amyloidogenic protein transthyretin. <b>2000</b> , 302, 649-69	179
1958	The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TcR molecules. <b>2000</b> , 302, 527-37	47
1957	Crystal structures of recombinant histones HMfA and HMfB from the hyperthermophilic archaeon <i>Methanothermus fervidus</i> . <b>2000</b> , 303, 35-47	88
1956	Structure of a slow processing precursor penicillin acylase from <i>Escherichia coli</i> reveals the linker peptide blocking the active-site cleft. <b>2000</b> , 302, 887-98	99
1955	Probing the catalytic mechanism of GDP-4-keto-6-deoxy-d-mannose Epimerase/Reductase by kinetic and crystallographic characterization of site-specific mutants. <b>2000</b> , 303, 77-91	43
1954	Active site modulation in the N-acetylneuraminase lyase sub-family as revealed by the structure of the inhibitor-complexed <i>Haemophilus influenzae</i> enzyme. <b>2000</b> , 303, 405-21	73
1953	Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding alcohol dehydrogenase (ABAD). <b>2000</b> , 303, 311-27	74
1952	Structures of l-fucose-1-phosphate aldolase mutants outlining motions during catalysis. <b>2000</b> , 303, 531-43	22
1951	Conformational variability of the Cu site in one subunit of bovine CuZn superoxide dismutase: the importance of mobility in the Glu119-Leu142 loop region for catalytic function. <b>2000</b> , 304, 231-41	45
1950	From minichaperone to GroEL 1: information on GroEL-polypeptide interactions from crystal packing of minichaperones. <b>2000</b> , 304, 873-81	19
1949	Structural origins of the interfacial activation in <i>Thermomyces (Humicola) lanuginosa</i> lipase. <b>2000</b> , 39, 15071-82	192
1948	Structure and function of Cdc6/Cdc18: implications for origin recognition and checkpoint control. <b>2000</b> , 6, 637-48	193
1947	Ulp1-SUMO crystal structure and genetic analysis reveal conserved interactions and a regulatory element essential for cell growth in yeast. <b>2000</b> , 5, 865-76	567
1946	The polar T1 interface is linked to conformational changes that open the voltage-gated potassium channel. <b>2000</b> , 102, 657-70	159



1945	E. coli hemolysin E (HlyE, ClyA, SheA): X-ray crystal structure of the toxin and observation of membrane pores by electron microscopy. <b>2000</b> , 100, 265-76	173
1944	The three-dimensional structure of human transaldolase. <b>2000</b> , 475, 205-8	33
1943	Insights into molybdenum cofactor deficiency provided by the crystal structure of the molybdenum cofactor biosynthesis protein MoaC. <b>2000</b> , 8, 709-18	59
1942	Structure of the RNA polymerase domain of E. coli primase. <b>2000</b> , 287, 2482-6	144
1941	Highly Efficient Synthesis of (1 → 4)-Oligo- and -Polysaccharides Using a Mutant Cellulase. <b>2000</b> , 122, 5429-5437	140
1940	Structural basis of the drastically increased initial electron transfer rate in the reaction center from a Rhodospseudomonas viridis mutant described at 2.00-Å resolution. <b>2000</b> , 275, 39364-8	49
1939	Catalytic action of fuculose 1-phosphate aldolase (class II) as derived from structure-directed mutagenesis. <b>2000</b> , 39, 6033-41	62
1938	Crystal structure of the haloalkane dehalogenase from Sphingomonas paucimobilis UT26. <b>2000</b> , 39, 14082-6	106
1937	Hybrid-cluster protein (HCP) from Desulfovibrio vulgaris (Hildenborough) at 1.6 Å resolution. <b>2000</b> , 39, 15044-54	40
1936	Dissection of malonyl-coenzyme A decarboxylation from polyketide formation in the reaction mechanism of a plant polyketide synthase. <b>2000</b> , 39, 890-902	277
1935	Mechanism of the phenylpyruvate tautomerase activity of macrophage migration inhibitory factor: properties of the P1G, P1A, Y95F, and N97A mutants. <b>2000</b> , 39, 9671-8	23
1934	Crystal structure of an enzyme-substrate complex provides insight into the interaction between human arylsulfatase A and its substrates during catalysis. <b>2001</b> , 305, 269-77	86
1933	Crystal structure and site-directed mutagenesis studies of N-carbamoyl-D-amino-acid amidohydrolase from Agrobacterium radiobacter reveals a homotetramer and insight into a catalytic cleft. <b>2001</b> , 306, 251-61	70
1932	Crystal structure of the NADP(H)-dependent ketose reductase from Bemisia argentifolii at 2.3 Å resolution. <b>2001</b> , 306, 239-50	65
1931	A thermophilic mini-chaperonin contains a conserved polypeptide-binding surface: combined crystallographic and NMR studies of the GroEL apical domain with implications for substrate interactions. <b>2001</b> , 306, 513-25	15
1930	pH-induced structural changes regulate histidine decarboxylase activity in Lactobacillus 30a. <b>2001</b> , 306, 727-32	35
1929	Family 7 cellobiohydrolases from Phanerochaete chrysosporium: crystal structure of the catalytic module of Cel7D (CBH58) at 1.32 Å resolution and homology models of the isozymes. <b>2001</b> , 314, 1097-111	91
1928	How methionyl-tRNA synthetase creates its amino acid recognition pocket upon L-methionine binding. <b>2001</b> , 306, 863-76	73

1927	Crystal structure of GerE, the ultimate transcriptional regulator of spore formation in <i>Bacillus subtilis</i> . <b>2001</b> , 306, 759-71	86
1926	An interfacial mechanism and a class of inhibitors inferred from two crystal structures of the <i>Mycobacterium tuberculosis</i> 30 kDa major secretory protein (Antigen 85B), a mycolyl transferase. <b>2001</b> , 307, 671-81	109
1925	Two divalent metal ions in the active site of a new crystal form of human apurinic/aprimidinic endonuclease, Ape1: implications for the catalytic mechanism. <b>2001</b> , 307, 1023-34	156
1924	Single mutations at the subunit interface modulate copper reactivity in <i>Photobacterium leiognathi</i> Cu,Zn superoxide dismutase. <b>2001</b> , 308, 555-63	19
1923	Two crystal structures of the cytoplasmic molybdate-binding protein ModG suggest a novel cooperative binding mechanism and provide insights into ligand-binding specificity. <b>2001</b> , 308, 1063-79	36
1922	The N-terminal domain of Homer/Vesl is a new class II EVH1 domain. <b>2001</b> , 309, 155-69	46
1921	On the mechanism of biological methane formation: structural evidence for conformational changes in methyl-coenzyme M reductase upon substrate binding. <b>2001</b> , 309, 315-30	158
1920	The crystal structure of human phosphoglucose isomerase at 1.6 Å resolution: implications for catalytic mechanism, cytokine activity and haemolytic anaemia. <b>2001</b> , 309, 447-63	84
1919	Crystal structures of YBHB and YBCL from <i>Escherichia coli</i> , two bacterial homologues to a Raf kinase inhibitor protein. <b>2001</b> , 310, 617-34	67
1918	Crystal structures of the class D beta-lactamase OXA-13 in the native form and in complex with meropenem. <b>2001</b> , 310, 859-74	60
1917	X-ray structure of TMP kinase from <i>Mycobacterium tuberculosis</i> complexed with TMP at 1.95 Å resolution. <b>2001</b> , 311, 87-100	90
1916	Structure of the soluble domain of a membrane-anchored thioredoxin-like protein from <i>Bradyrhizobium japonicum</i> reveals unusual properties. <b>2001</b> , 311, 1037-48	36
1915	Crystal structures of human gephyrin and plant Cnx1 G domains: comparative analysis and functional implications. <b>2001</b> , 312, 405-18	84
1914	Internalins from the human pathogen <i>Listeria monocytogenes</i> combine three distinct folds into a contiguous internalin domain. <b>2001</b> , 312, 783-94	100
1913	The 1.2 Å structure of a novel quorum-sensing protein, <i>Bacillus subtilis</i> LuxS. <b>2001</b> , 313, 111-22	67
1912	Crystal structures of penicillin acylase enzyme-substrate complexes: structural insights into the catalytic mechanism. <b>2001</b> , 313, 139-50	141
1911	Crystal structures of mutant forms of the <i>Bacillus caldolyticus</i> cold shock protein differing in thermal stability. <b>2001</b> , 313, 359-69	36
1910	Kinetic and crystallographic analyses support a sequential-ordered bi bi catalytic mechanism for <i>Escherichia coli</i> glucose-1-phosphate thymidyltransferase. <b>2001</b> , 313, 831-43	89

1909	Crystal structure of the dimeric phosphoenolpyruvate carboxykinase (PEPCK) from <i>Trypanosoma cruzi</i> at 2 Å resolution. <b>2001</b> , 313, 1059-72	55
1908	Channeling of ammonia in glucosamine-6-phosphate synthase. <b>2001</b> , 313, 1093-102	101
1907	The conserved methionine residue of the metzincins: a site-directed mutagenesis study. <b>2001</b> , 314, 181-6	26
1906	Cross-reactive binding of cyclic peptides to an anti-TGF $\alpha$ antibody Fab fragment: an X-ray structural and thermodynamic analysis. <b>2001</b> , 314, 293-309	42
1905	The structures of <i>Escherichia coli</i> inorganic pyrophosphatase complexed with Ca(2+) or CaPP(i) at atomic resolution and their mechanistic implications. <b>2001</b> , 314, 633-45	35
1904	Three-dimensional structures of the Mn and Mg dTDP complexes of the family GT-2 glycosyltransferase SpsA: a comparison with related NDP-sugar glycosyltransferases. <b>2001</b> , 314, 655-61	106
1903	Crystal structure of dephospho-coenzyme A kinase from <i>Haemophilus influenzae</i> . <b>2001</b> , 136, 119-25	31
1902	Crystal structure and deletion analysis show that the accessory subunit of mammalian DNA polymerase gamma, Pol gamma B, functions as a homodimer. <b>2001</b> , 7, 43-54	126
1901	Annexin A5 D226K structure and dynamics: identification of a molecular switch for the large-scale conformational change of domain III. <b>2001</b> , 493, 122-8	12
1900	Structure of bovine mitochondrial F(1)-ATPase with nucleotide bound to all three catalytic sites: implications for the mechanism of rotary catalysis. <b>2001</b> , 106, 331-41	406
1899	Co-crystal of <i>Escherichia coli</i> RNase HI with Mn <sup>2+</sup> ions reveals two divalent metals bound in the active site. <b>2001</b> , 276, 7266-71	78
1898	Structural requirements of endopolygalacturonase for the interaction with PGIP (polygalacturonase-inhibiting protein). <b>2001</b> , 98, 13425-30	113
1897	Antigen specificity and high affinity binding provided by one single loop of a camel single-domain antibody. <b>2001</b> , 276, 26285-90	119
1896	High resolution structural analyses of mutant chitinase A complexes with substrates provide new insight into the mechanism of catalysis. <b>2001</b> , 40, 11338-43	137
1895	Crystal structure of maleylacetoacetate isomerase/glutathione transferase zeta reveals the molecular basis for its remarkable catalytic promiscuity. <b>2001</b> , 40, 1567-76	108
1894	Crystal structure of heme oxygenase from the gram-negative pathogen <i>Neisseria meningitidis</i> and a comparison with mammalian heme oxygenase-1. <b>2001</b> , 40, 11552-8	127
1893	First crystal structure of Rubisco from a green alga, <i>Chlamydomonas reinhardtii</i> . <b>2001</b> , 276, 48159-64	73
1892	2.8-Å crystal structure of a nontoxic type-II ribosome-inactivating protein, ebulin I. <b>2001</b> , 43, 319-26	71

1891	Substrate flow in catalases deduced from the crystal structures of active site variants of HP11 from <i>Escherichia coli</i> . <b>2001</b> , 44, 270-81	44
1890	Space-time tradeoffs for parallel 3D reconstruction algorithms for virus-structure determination. <b>2001</b> , 13, 1083-1106	12
1889	Mixed-linkage cellooligosaccharides: a new class of glycoside hydrolase inhibitors. <b>2001</b> , 2, 319-25	20
1888	Structure of a family 15 carbohydrate-binding module in complex with xylopentaose. Evidence that xylan binds in an approximate 3-fold helical conformation. <b>2001</b> , 276, 49061-5	84
1887	Oligomerization and ligand binding in a homotetrameric hemoglobin: two high-resolution crystal structures of hemoglobin Bart's ( $\gamma(4)$ ), a marker for alpha-thalassemia. <b>2001</b> , 10, 1739-49	21
1886	An extended hydrophobic core induces EF-hand swapping. <b>2001</b> , 10, 927-33	35
1885	X-ray structure of a novel matrix metalloproteinase inhibitor complexed to stromelysin. <b>2001</b> , 10, 923-6	56
1884	CD81 extracellular domain 3D structure: insight into the tetraspanin superfamily structural motifs. <b>2001</b> , 20, 12-8	214
1883	The B-box dominates SAP-1-SRF interactions in the structure of the ternary complex. <b>2001</b> , 20, 3018-28	82
1882	X-ray structure of junctional adhesion molecule: structural basis for homophilic adhesion via a novel dimerization motif. <b>2001</b> , 20, 4391-8	167
1881	Crystal structure of the ankyrin repeat domain of Bcl-3: a unique member of the I $\kappa$ B protein family. <b>2001</b> , 20, 6180-90	60
1880	V-shaped structure of glutamyl-tRNA reductase, the first enzyme of tRNA-dependent tetrapyrrole biosynthesis. <b>2001</b> , 20, 6583-90	101
1879	Crystal structure of the Lrp-like transcriptional regulator from the archaeon <i>Pyrococcus furiosus</i> . <b>2001</b> , 20, 990-7	125
1878	Crystal structures of substrate free and complex forms of reactivated BphC, an extradiol type ring-cleavage dioxygenase. <b>2001</b> , 83, 269-79	56
1877	Crystal structure of molybdopterin synthase and its evolutionary relationship to ubiquitin activation. <b>2001</b> , 8, 42-6	115
1876	Pteridine reductase mechanism correlates pterin metabolism with drug resistance in trypanosomatid parasites. <b>2001</b> , 8, 521-5	99
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- 184 Crystal Structures of Free and Ligand-Bound Forms of the TetR / AcrR-Like Regulator SCO3201 from *Streptomyces coelicolor* Suggest a Novel Allosteric Mechanism.
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- 182 Biochemical and Structural Study of RuvC and YqgF from *Deinococcus radiodurans*.

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180	Core fucose-specific <i>Pholiota squarrosa</i> lectin ( PhoSL ) as a potent broad-spectrum inhibitor of SARS-CoV -2 infection.	
179	Dipeptidyl peptidase 9 triggers BRCA2 degradation and promotes DNA damage repair.	3
178	The exceptionally efficient quorum quenching enzyme LrSL suppresses <i>Pseudomonas aeruginosa</i> biofilm production. 13,	
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176	Structural determination of an antibody that specifically recognizes polyethylene glycol with a terminal methoxy group. <b>2022</b> , 5,	1
175	Inhibition of urease by hydroquinones: a structural and kinetic study.	
174	Visualizing Alternative Isoinformational Engineered DNA in A- and B-Forms at High Resolution.	1
173	Structural and functional studies of legumain-mycocypin complexes revealed a competitive, exosite-regulated mode of interaction. <b>2022</b> , 102502	0
172	Bacterial divisome protein FtsA forms curved antiparallel double filaments when binding to FtsN.	0
171	Hallucinating symmetric protein assemblies.	4
170	Novel tricyclic small molecule inhibitors of Nicotinamide N-methyltransferase for the treatment of metabolic disorders. <b>2022</b> , 12,	1
169	Regioselectivity in inhibition of peptide deformylase from <i>Haemophilus influenzae</i> by 4- vs 5-azaindole hydroxamic acid derivatives: Biochemical, structural and antimicrobial studies. <b>2022</b> , 128, 106095	0
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167	Structure-based rational design of a short-chain dehydrogenase/reductase for improving activity toward mycotoxin patulin. <b>2022</b> , 222, 421-428	0
166	PAC-FragmentDEL [photoactivated covalent capture of DNA-encoded fragments for hit discovery.	1
165	Antibody interfaces revealed through structural mining. <b>2022</b> , 20, 4952-4968	0
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159	Structural insights into the substrate specificity of IMP-6 and IMP-1 metallo-β-lactamases.	0
158	Hybrid in vitro/in silico analysis of low-affinity protein-protein interactions that regulate signal transduction by Sema6D.	1
157	Optimization of N-PiperidinyI-Benzimidazolone Derivatives as Potent and Selective Inhibitors of 8-Oxo Guanine DNA Glycosylase 1.	0
156	Structure-Based Study to Overcome Cross-Reactivity of Novel Androgen Receptor Inhibitors. <b>2022</b> , 11, 2785	0
155	Development and Characterization of Type I, Type II, and Type III LIM-Kinase Chemical Probes.	1
154	Plant-specific HDT family histone deacetylases are nucleoplasmins.	0
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152	Structural and functional characterization of NEMO cleavage by SARS-CoV-2 3CLpro. <b>2022</b> , 13,	3
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150	Fluorescent Proteins: Crystallization, Structural Determination, and Nonnatural Amino Acid Incorporation. <b>2023</b> , 99-119	0
149	Structure-Function analysis of <i>Lactiplantibacillus plantarum</i> DltE reveals D-alanylated lipoteichoic acids as direct symbiotic cues supporting <i>Drosophila</i> juvenile growth.	0
148	C3- and C3/C5-Epimerases Required for the Biosynthesis of the Capsular Polysaccharides from <i>Campylobacter jejuni</i> . <b>2022</b> , 61, 2036-2048	2
147	Discovery of Highly Potent and Selective Matrix Metalloproteinase-7 Inhibitors by Hybridizing the S1? Subsite Binder with Short Peptides.	0
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72	Structural and Functional Characterization of the Ureidoacrylate Amidohydrolase RutB from <i>Escherichia coli</i> .	o
71	Structural Analyses of a Dominant <i>Cryptosporidium parvum</i> Epitope Presented by H-2K b Offer New Options To Combat Cryptosporidiosis.	o
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