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Solvent content of protein crystals

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2108	venom of Australian tiger snake Notechis scutatus scutatus. <b>1977</b> , 15, 435-9  The crystallization of beef heart mitochondrial adenosine triphosphatase. <b>1977</b> , 492, 237-40		30
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2108 2107 2106 2105	venom of Australian tiger snake Notechis scutatus scutatus. 1977, 15, 435-9  The crystallization of beef heart mitochondrial adenosine triphosphatase. 1977, 492, 237-40  Crystallographic evidence for the structural isomorphism of deer and beef catalase. 1977, 33, 880-1  Haemoglobin crystals in the midgut of the tick Ornithodorus moubata Murray. 1977, 266, 536-8		30 5 25
2108 2107 2106 2105	venom of Australian tiger snake Notechis scutatus scutatus. 1977, 15, 435-9  The crystallization of beef heart mitochondrial adenosine triphosphatase. 1977, 492, 237-40  Crystallographic evidence for the structural isomorphism of deer and beef catalase. 1977, 33, 880-1  Haemoglobin crystals in the midgut of the tick Ornithodorus moubata Murray. 1977, 266, 536-8  Computer simulation of the solvent structure around biological macromolecules. 1978, 272, 222-6	3.4	30 5 25 148
2108 2107 2106 2105 2104	The crystallization of beef heart mitochondrial adenosine triphosphatase. 1977, 492, 237-40  Crystallographic evidence for the structural isomorphism of deer and beef catalase. 1977, 33, 880-1  Haemoglobin crystals in the midgut of the tick Ornithodorus moubata Murray. 1977, 266, 536-8  Computer simulation of the solvent structure around biological macromolecules. 1978, 272, 222-6  The X-ray structure of yeast inorganic pyrophosphatase at 5.5 [resolution. 1978, 34, 3210-3215  A crystallographic investigation of citrate synthase from pig and chicken heart muscle. <i>Biochemical</i>	3·4 6.5	30 5 25 148 4

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1892 1891 1890	Kinetics of ribulosebisphosphate carboxylase at high protein concentration. <i>Biochemical and Biophysical Research Communications</i> , 1986, 134, 506-11  Crystallization of methionyl porcine somatotropin, a genetically engineered variant of porcine growth hormone. <i>Journal of Molecular Biology</i> , 1986, 192, 159-60  Crystallization and preliminary data of Indian buffalo erythrocyte carbonic anhydrase. <i>Journal of Molecular Biology</i> , 1986, 190, 129-31  Preliminary characterization of crystals of nitrite reductase isolated from Alcaligenes faecalis strain S-6. <i>Journal of Molecular Biology</i> , 1986, 190, 135  Crystallization of a complex of cro repressor with a 17 base-pair operator. <i>Journal of Molecular</i>	6.5 6.5 6.5	5 8 5
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1814	Electron microscopy and image analysis of the complexes I and V of the mitochondrial respiratory chain. <b>1988</b> , 1, 175-99	8	3
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1651	Crystallization and preliminary X-ray analysis of gamma-aminobutyric acid transaminase. <i>Journal of Molecular Biology</i> , <b>1990</b> , 214, 821-3	6.5	8

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1635	Crystallization and preliminary X-ray diffraction analysis of oucleoside diphosphate kinase from Myxococcus xanthus. <i>Journal of Molecular Biology</i> , <b>1991</b> , 220, 5-7	6.5	7	
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1628	Crystal structure of the catalytic subunit of cyclic adenosine monophosphate-dependent protein kinase. <b>1991</b> , 253, 407-14		1587
1627	Crystallization and preliminary X-ray studies of annexin IV (endonexin), a calcium-dependent phospholipid-binding protein. <b>1991</b> , 279, 187-9		5
1626	Preliminary X-ray crystallographic analysis of tryptophanase from Escherichia coli. <b>1991</b> , 284, 270-2		8
1625	The crystal structure of fructose-1,6-bisphosphate aldolase from Drosophila melanogaster at 2.5 A resolution. <b>1991</b> , 292, 237-42		63
1624	Crystallization and preliminary X-ray analysis of methylamine-treated alpha 2-macroglobulin and 3 alpha 2-macroglobulin-proteinase complexes. <b>1991</b> , 292, 267-70		9
1623	Crystallization and preliminary X-ray diffraction data of the Fab fragment of a monoclonal antibody against apamin, a bee venom neurotoxin. <b>1991</b> , 286, 64-6		6
1622	Overproduction, purification and crystallization of Bacillus cereus oligo-1,6-glucosidase. <b>1991</b> , 290, 221	-3	7
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1617	Preparation and X-ray characterization of four new crystal forms of jacalin, a lectin from Artocarpus integrifolia. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 773-6	6.5	17
1616	Crystal structure of uncleaved ovalbumin at 1.95 A resolution. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 941-59	6.5	373
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1594	Crystallization and crystal packing of Proteus mirabilis PR catalase. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 1075-7	6.5	19
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1565	Crystallization and preliminary X-ray investigation of factor D of human complement. <i>Journal of Molecular Biology</i> , <b>1991</b> , 219, 1-3	6.5	8
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1197	Crystallization and preliminary crystallographic analysis of a 2,3-dihydroxybiphenyl dioxygenase from Pseudomonas sp. strain KKS102 having polychlorinated biphenyl (PCB)-degrading activity. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 22, 284-6	4.2	9
1196	Crystallization and preliminary X-ray crystallographic studies of nonhistone region of macroH2A.1. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 22, 290-2	4.2	3
1195	Crystallization of Thermus thermophilus histidyl-tRNA synthetase and its complex with tRNAHis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 22, 426-8	4.2	7
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1192	Crystallization and preliminary crystallographic analysis of recombinant abrin-a A-chain with ribosome inactivating activity. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 126-7	4.2	
1191	Purification, crystallization, and preliminary X-ray analysis of PepX, an X-prolyl dipeptidyl aminopeptidase from Lactococcus lactis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 278	3-8 <sup>4.2</sup>	12
1190	Crystallization of intact monoclonal antibodies. <i>Proteins: Structure, Function and Bioinformatics</i> ,		
	<b>1995</b> , 23, 285-9	4.2	42
1189		4.2	65
1189 1188	1995, 23, 285-9  Atomic and residue hydrophilicity in the context of folded protein structures. <i>Proteins: Structure</i> ,	·	
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1188	Atomic and residue hydrophilicity in the context of folded protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 536-47  Fermenter production of an artificial fab fragment, rationally designed for the antigen cystatin, and its optimized crystallization through constant domain shuffling. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 561-5  Crystallization and preliminary X-ray crystallographic analysis of ImmE7 protein of colicin E7.	4.2	65 47
1188	Atomic and residue hydrophilicity in the context of folded protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 536-47  Fermenter production of an artificial fab fragment, rationally designed for the antigen cystatin, and its optimized crystallization through constant domain shuffling. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 561-5  Crystallization and preliminary X-ray crystallographic analysis of ImmE7 protein of colicin E7. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 588-90  Crystallization and preliminary crystallographic analysis of an amylopullulanase from the hyperthermophilic archaeon Pyrococcus woesei. <i>Proteins: Structure, Function and Bioinformatics</i> ,	4.2	65 47 2
1188 1187 1186	Atomic and residue hydrophilicity in the context of folded protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 536-47  Fermenter production of an artificial fab fragment, rationally designed for the antigen cystatin, and its optimized crystallization through constant domain shuffling. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 561-5  Crystallization and preliminary X-ray crystallographic analysis of ImmE7 protein of colicin E7. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 588-90  Crystallization and preliminary crystallographic analysis of an amylopullulanase from the hyperthermophilic archaeon Pyrococcus woesei. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 595-7  Preliminary X-ray crystallographic analysis of Tritrichomonas foetus inosine-5'-monophosphate	4.2 4.2 4.2	65 47 2 9

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733	Crystallization and X-ray analysis of monodisperse human properdin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 0	1.1	4

732	Lysine-Specific Histone Demethylase 1A Regulates Macrophage Polarization and Checkpoint Molecules in the Tumor Microenvironment of Triple-Negative Breast Cancer. <b>2019</b> , 10, 1351		29	
731	Repurposing an Ancient Protein Core Structure: Structural Studies on FmtA, a Novel Esterase of Staphylococcus aureus. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 3107-3123	6.5	32	
730	Vibrio cholerae YaeO is a Structural Homologue of RNA Chaperone Hfq that Inhibits Rho-dependent Transcription Termination by Dissociating its Hexameric State. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 4749-4766	6.5	2	
7 <b>2</b> 9	Borophosphene: A New Anisotropic Dirac Cone Monolayer with a High Fermi Velocity and a Unique Self-Doping Feature. <b>2019</b> , 10, 6656-6663		23	
728	Structural insight into the carboxylesterase BioH from Klebsiella pneumoniae. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 520, 538-543	3.4	1	
727	Crystal Structure of NADPH-Dependent Methylglyoxal Reductase Gre2 from Candida Albicans. <i>Crystals</i> , <b>2019</b> , 9, 471	2.3	0	
726	Anisotropic Distribution of Ammonium Sulfate Ions in Protein Crystallization. <b>2019</b> , 19, 6004-6010		8	
725	The C-terminal domain conformational switch revealed by the crystal structure of malyl-CoA lyase from Roseiflexus castenholzii. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 518, 72-79	3.4		
724	The crystal structures of CDD-1, the intrinsic class D flactamase from the pathogenic Gram-positive bacterium Clostridioides difficile, and its complex with cefotaxime. <b>2019</b> , 208, 107391		5	
723	When Does the Onset of Multiple Stellar Populations in Star Clusters Occur? Detection of Enriched Stellar Populations in NGC 2121. <b>2019</b> , 876, 94		11	
722	Macromolecular powder diffraction. <b>2019</b> , 718-736		3	
721	Preparation of stable recombinant Osm1 noncovalently bound with flavin adenosine dinucleotide cofactor for structural study. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 159-165	1.1		
720	Crystal structure of UDP-glucose pyrophosphorylase from Yersinia pestis, a potential therapeutic target against plague. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 608	3-615	2	
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718	Lightweight Group Secret Key Generation Leveraging Non-Reconciled Received Signal Strength in Mobile Wireless Networks. <b>2019</b> ,		5	
717	Crystal Structure of FOXC2 in Complex with DNA Target. <b>2019</b> , 4, 10906-10914		2	
716	Structural characterization of a short-chain dehydrogenase/reductase from multi-drug resistant Acinetobacter baumannii. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 518, 465-471	3.4	2	
715	Redox-induced structural changes in the di-iron and di-manganese forms of Bacillus anthracis ribonucleotide reductase subunit NrdF suggest a mechanism for gating of radical access. <b>2019</b> , 24, 849-	861	6	

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710	Elucidation of the mechanism of disulfide exchange between staphylococcal thioredoxin2 and thioredoxin reductase2: A structural insight. <b>2019</b> , 160, 1-13		1
709	Structure of the Large Extracellular Loop of FtsX and Its Interaction with the Essential Peptidoglycan Hydrolase PcsB in Streptococcus pneumoniae. <b>2019</b> , 10,		20
708	Stability of cytochromes c' from psychrophilic and piezophilic Shewanella species: implications for complex multiple adaptation to low temperature and high hydrostatic pressure. <b>2019</b> , 23, 239-248		6
707	Structure of the SLy1 SAM homodimer reveals a new interface for SAM domain self-association. <i>Scientific Reports</i> , <b>2019</b> , 9, 54	4.9	6
706	Crystal Structure of the Fab Fragment of an Anti-CTLA-4 Antibody, Ipilimumab, Used for Cancer Immunotherapy. <b>2019</b> , 40, 582-585		
705	Structural basis of inhibition of the human serine hydroxymethyltransferase SHMT2 by antifolate drugs. <b>2019</b> , 593, 1863-1873		18
704	Structure and biochemical studies of a pseudomonad maleylpyruvate isomerase from Pseudomonas aeruginosa PAO1. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 514, 991-	9 <del>3</del> 4	
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700	Crystal structure of the SPRY domain of human SPSB2 in the apo state. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 412-418	1.1	2
699	Induced Aggregation of Epoxy Polysiloxane Grafted Gelatin by Organic Solvent and Green Application. <i>Molecules</i> , <b>2019</b> , 24,	4.8	1
699 698		4.8	7

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693	Novel T9 loop conformation of filamenting temperature-sensitive mutant Z from Mycobacterium tuberculosis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 359-367	1.1	
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691	Structural, Kinetic, and Mechanistic Analysis of an Asymmetric 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , <b>2019</b> , 58, 2617-2627	3.2	1
690	Structural and pharmacological evaluation of a novel non-nucleoside reverse transcriptase inhibitor as a promising long acting nanoformulation for treating HIV. <b>2019</b> , 167, 110-116		13
689	Light-Emitting Dehalogenases: Reconstruction of Multifunctional Biocatalysts. <i>ACS Catalysis</i> , <b>2019</b> , 9, 4810-4823	13.1	14
688	Crystal structures of rhamnosyltransferase UGT89C1 from Arabidopsis thaliana reveal the molecular basis of sugar donor specificity for UDP-El-rhamnose and rhamnosylation mechanism. <b>2019</b> , 99, 257-269		19
68 <sub>7</sub>	Structural analysis of a plant fatty acid amide hydrolase provides insights into the evolutionary diversity of bioactive acylethanolamides. <b>2019</b> , 294, 7419-7432		8
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685	Preliminary X-ray crystallographic studies on the Helicobacter pylori ABC transporter glutamine-binding protein GlnH. <b>2019</b> , 13, 52-58		1
684	Principles and Practice in Macromolecular X-Ray Crystallography. <b>2019</b> , 385-419		
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677	Biochemical characterization of Mycobacterium tuberculosis LexA and structural studies of its C-terminal segment. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 41-55	5.5	O
676	Structural and functional insights into the role of a cupin superfamily isomerase in the biosynthesis of Choi moiety of aeruginosin. <b>2019</b> , 205, 44-52		4
675	Molecular features of steroid-binding antidins and their use for assaying serum progesterone. <b>2019</b> , 14, e0212339		2
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661	Overexpression, purification, biochemical and structural characterization of rhamnosyltransferase UGT89C1 from Arabidopsis thaliana. <b>2019</b> , 156, 44-49		2

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658	Analysis of a new flavodiiron core structural arrangement in Flv1-ElR protein from Synechocystis sp. PCC6803. <b>2019</b> , 205, 91-102		8
657	DeepCrystal: a deep learning framework for sequence-based protein crystallization prediction. <b>2019</b> , 35, 2216-2225		21
656	Crystal Structure and Substrate Specificity of the 8-oxo-dGTP Hydrolase NUDT1 from Arabidopsis thaliana. <i>Biochemistry</i> , <b>2019</b> , 58, 887-899	3.2	3
655	Structural studies on M. tuberculosis argininosuccinate lyase and its liganded complex: Insights into catalytic mechanism. <b>2019</b> , 71, 643-652		2
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651	Modulation of RXR-DNA complex assembly by DNA context. <b>2019</b> , 481, 44-52		5
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643	Sequence, structure and function-based classification of the broadly conserved FAH superfamily reveals two distinct fumarylpyruvate hydrolase subfamilies. <b>2020</b> , 22, 270-285		3

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641	Molecular characterization of a ghrelin-l-aptamer complex. <i>Journal of Molecular Structure</i> , <b>2020</b> , 1204, 127510	3.4	3
640	The structure of a prokaryotic feruloyl-CoA hydratase-lyase from a lignin-degrading consortium with high oligomerization stability under extreme pHs. <b>2020</b> , 1868, 140344		2
639	Structural insight into bi-functional malonyl-CoA reductase. <b>2020</b> , 22, 752-765		O
638	Characterizing pathological imperfections in macromolecular crystals: lattice disorders and modulations. <b>2020</b> , 26, 3-50		3
637	Structural and functional investigation of AerF, a NADPH-dependent alkenal double bond reductase participating in the biosynthesis of Choi moiety of aeruginosin. <b>2020</b> , 209, 107415		1
636	Fulditoxin, representing a new class of dimeric snake toxins, defines novel pharmacology at nicotinic ACh receptors. <b>2020</b> , 177, 1822-1840		8
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633	Metabolic engineering of Escherichia coli for production of non-natural acetins from glycerol. <b>2020</b> , 22, 7788-7802		2
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627	Insulin polymorphism induced by two polyphenols: new crystal forms and advances in macromolecular powder diffraction. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 1065	-1079	3
626	Conformational Stability and Dynamics in Crystals Recapitulate Protein Behavior in Solution. <b>2020</b> , 119, 978-988		1
625	Protein crystal occurrence domains in selective protein crystallisation for bio-separation. <b>2020</b> , 22, 4566	5-4572	3

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623	Crystallization and Preliminary X-Ray Diffraction Analysis of the ZAD Domain of the Serendipity-d Protein from Drosophila melanogaster. <i>Crystallography Reports</i> , <b>2020</b> , 65, 593-595	0.6	
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621	LptC from Anabaena sp. PCC 7120: Expression, purification and crystallization. <b>2020</b> , 175, 105689		
620	Post-Catalytic Complexes with Emtricitabine or Stavudine and HIV-1 Reverse Transcriptase Reveal New Mechanistic Insights for Nucleotide Incorporation and Drug Resistance. <i>Molecules</i> , <b>2020</b> , 25,	4.8	1
619	Crystal Structure of Mannose Specific IIA Subunit of Phosphotransferase System from. <i>Molecules</i> , <b>2020</b> , 25,	4.8	1
618	Structural insights into Pseudomonas aeruginosaType six secretion system exported effector 8. <b>2020</b> , 212, 107651		1
617	Structural Characterization of the Essential Cell Division Protein FtsE and Its Interaction with FtsX in Streptococcus pneumoniae. <b>2020</b> , 11,		6
616	Theoretical Study of Intermolecular Interactions between Critical Residues of Membrane Protein MraY and Promising Antibiotic Muraymycin D2. <b>2020</b> , 5, 22739-22749		2
615	Molecular Packing of a Mutant of L-Asparaginase from Wolinella succinigenes in Two Crystal Modifications. <i>Crystallography Reports</i> , <b>2020</b> , 65, 586-592	0.6	1
614	Detecting the nature and solving the crystal structure of a contaminant protein from an opportunistic pathogen. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2020</b> , 76, 392-397	1.1	1
613	Exploring the gas access routes in a [NiFeSe] hydrogenase using crystals pressurized with krypton and oxygen. <b>2020</b> , 25, 863-874		2
612	Purification and Preliminary X-Ray Crystallographic Analysis of the Peptidyl-Prolyl cis <b>t</b> rans Isomerase Alr5059 from Anabaena sp. PCC 7120. <i>Crystallography Reports</i> , <b>2020</b> , 65, 1226-1230	0.6	1
611	Molecular Packing Interaction in DNA Crystals. <i>Crystals</i> , <b>2020</b> , 10, 1093	2.3	1
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605	Crystal structure of a C-type lysozyme from Litopenaeus vanamei exhibiting a high binding constant to its chitotriose inhibitor. <b>2020</b> , 100, 246-255		2
604	Structure and function of a flavin-dependent S-monooxygenase from garlic (). <b>2020</b> , 295, 11042-11055		5
603	Pterocarpan synthase (PTS) structures suggest a common quinone methide-stabilizing function in dirigent proteins and proteins with dirigent-like domains. <b>2020</b> , 295, 11584-11601		10
602	Highly-Active Recombinant Formate Dehydrogenase from Pathogenic Bacterium Staphylococcus aureus: Preparation and Crystallization. <b>2020</b> , 85, 689-696		2
601	Regioselectivity of hyoscyamine 6Ehydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. <b>2020</b> , 49, 4454-4469		9
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599	Aminobenzosuberone derivatives as PfA-M1 inhibitors: Molecular recognition and antiplasmodial evaluation. <b>2020</b> , 98, 103750		3
598	Conformational Plasticity of HLA-B27 Molecules Correlates Inversely With Efficiency of Negative T Cell Selection. <b>2020</b> , 11, 179		4
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597 596		17.4	18
	bundling. <i>Nature Communications</i> , <b>2020</b> , 11, 2905  Crystal structure and specific location of a germin-like protein with proteolytic activity from	17.4	
596	bundling. <i>Nature Communications</i> , <b>2020</b> , 11, 2905  Crystal structure and specific location of a germin-like protein with proteolytic activity from Thevetia peruviana. <b>2020</b> , 298, 110590  Crystal structure of the catalytic subunit of bovine pyruvate dehydrogenase phosphatase. <i>Acta</i>		2
596 595	bundling. Nature Communications, 2020, 11, 2905  Crystal structure and specific location of a germin-like protein with proteolytic activity from Thevetia peruviana. 2020, 298, 110590  Crystal structure of the catalytic subunit of bovine pyruvate dehydrogenase phosphatase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 292-301  GTP Preference of d-Glycero-EdHeptose-1-Phosphate Guanylyltransferase from. International	1.1	2
596 595 594	Crystal structure and specific location of a germin-like protein with proteolytic activity from Thevetia peruviana. 2020, 298, 110590  Crystal structure of the catalytic subunit of bovine pyruvate dehydrogenase phosphatase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 292-301  GTP Preference of d-Glycero-EdHeptose-1-Phosphate Guanylyltransferase from. International Journal of Molecular Sciences, 2019, 21,  Applications of X-ray Powder Diffraction in Protein Crystallography and Drug Screening. Crystals,	1.1	2 1 4
596 595 594 593	Crystal structure and specific location of a germin-like protein with proteolytic activity from Thevetia peruviana. 2020, 298, 110590  Crystal structure of the catalytic subunit of bovine pyruvate dehydrogenase phosphatase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 292-301  GTP Preference of d-Glycero-EdHeptose-1-Phosphate Guanylyltransferase from. International Journal of Molecular Sciences, 2019, 21,  Applications of X-ray Powder Diffraction in Protein Crystallography and Drug Screening. Crystals, 2020, 10, 54	1.1	2 1 4
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