

Wladek Minor

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217
papers

34,659
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49
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186
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283
ext. papers

36,550
ext. citations

5.2
avg, IF

7.45
L-index

#	Paper	IF	Citations
217	[20] Processing of X-ray diffraction data collected in oscillation mode. <i>Methods in Enzymology</i> , 1997 , 276, 307-326	1.7	24505
216	HKL-3000: the integration of data reduction and structure solution--from diffraction images to an initial model in minutes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 859-66		1457
215	Structural and immunologic characterization of bovine, horse, and rabbit serum albumins. <i>Molecular Immunology</i> , 2012 , 52, 174-82	4.3	600
214	Multiparametric scaling of diffraction intensities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003 , 59, 228-34		529
213	Double chromodomains cooperate to recognize the methylated histone H3 tail. <i>Nature</i> , 2005 , 438, 1181-5	50.4	416
212	Crystal structure of soybean lipoxygenase L-1 at 1.4 A resolution. <i>Biochemistry</i> , 1996 , 35, 10687-701	3.2	390
211	Structure of Sindbis virus core protein reveals a chymotrypsin-like serine proteinase and the organization of the virion. <i>Nature</i> , 1991 , 354, 37-43	50.4	261
210	Data mining of metal ion environments present in protein structures. <i>Journal of Inorganic Biochemistry</i> , 2008 , 102, 1765-76	4.2	240
209	Phosphorylation regulates SIRT1 function. <i>PLoS ONE</i> , 2008 , 3, e4020	3.7	216
208	Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. <i>Nature Protocols</i> , 2014 , 9, 156-70	18.8	200
207	Protein crystallography for non-crystallographers, or how to get the best (but not more) from published macromolecular structures. <i>FEBS Journal</i> , 2008 , 275, 1-21	5.7	187
206	In situ proteolysis for protein crystallization and structure determination. <i>Nature Methods</i> , 2007 , 4, 1019-21	21.6	181
205	CheckMyMetal: a macromolecular metal-binding validation tool. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 223-233	5.5	172
204	A novel family of sequence-specific endoribonucleases associated with the clustered regularly interspaced short palindromic repeats. <i>Journal of Biological Chemistry</i> , 2008 , 283, 20361-71	5.4	156
203	Asymmetric synthesis of 2,3-dihydro-2-arylquinazolin-4-ones: methodology and application to a potent fluorescent tubulin inhibitor with anticancer activity. <i>Journal of Medicinal Chemistry</i> , 2008 , 51, 4620-31	8.3	150
202	Crystallographic determination of the active site iron and its ligands in soybean lipoxygenase L-1. <i>Biochemistry</i> , 1993 , 32, 6320-3	3.2	147
201	The Enzyme Function Initiative. <i>Biochemistry</i> , 2011 , 50, 9950-62	3.2	140

200	Crystal structure of RhoA-GDP and its functional implications. <i>Nature Structural Biology</i> , 1997 , 4, 699-703		138
199	Determination of protein structures--a series of fortunate events. <i>Biophysical Journal</i> , 2008 , 95, 1-9	2.9	110
198	Structural and functional characterization of second-coordination sphere mutants of soybean lipoxygenase-1. <i>Biochemistry</i> , 2001 , 40, 7509-17	3.2	110
197	The tetramer structure of the Neryv homology two domain, NHR2, is critical for AML1/ETO β activity. <i>Cancer Cell</i> , 2006 , 9, 249-60	24.3	104
196	Mechanism of enolase: the crystal structure of asymmetric dimer enolase-2-phospho-D-glycerate/enolase-phosphoenolpyruvate at 2.0 Å resolution. <i>Biochemistry</i> , 1997 , 36, 12526-34	3.2	101
195	Structure of a microbial homologue of mammalian platelet-activating factor acetylhydrolases: <i>Streptomyces exfoliatus</i> lipase at 1.9 Å resolution. <i>Structure</i> , 1998 , 6, 511-9	5.2	89
194	Human thymidylate synthase is in the closed conformation when complexed with dUMP and raltitrexed, an antifolate drug. <i>Biochemistry</i> , 2001 , 40, 1897-902	3.2	88
193	NRMT is an alpha-N-methyltransferase that methylates RCC1 and retinoblastoma protein. <i>Nature</i> , 2010 , 466, 1125-8	50.4	82
192	The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , 2009 , 37, D365-8	20.1	80
191	Crystal structure of <i>Pseudomonas aeruginosa</i> SPM-1 provides insights into variable zinc affinity of metallo-beta-lactamases. <i>Journal of Molecular Biology</i> , 2006 , 357, 890-903	6.5	79
190	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 1181-1193	5.5	75
189	Structural and immunologic characterization of Ara h 1, a major peanut allergen. <i>Journal of Biological Chemistry</i> , 2011 , 286, 39318-27	5.4	74
188	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. <i>FEBS Journal</i> , 2013 , 280, 5705-36	5.7	73
187	Serum albumins-unusual allergens. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013 , 1830, 5375-81	4	72
186	<i>Alternaria alternata</i> allergen Alt a 1: a unique β barrel protein dimer found exclusively in fungi. <i>Journal of Allergy and Clinical Immunology</i> , 2012 , 130, 241-7.e9	11.5	71
185	Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , 2000 , 8, R105-10	5.2	70
184	Crystal structure of the MACPF domain of human complement protein C8 alpha in complex with the C8 gamma subunit. <i>Journal of Molecular Biology</i> , 2008 , 379, 331-42	6.5	69
183	Continua of interactions between pairs of atoms in molecular crystals. <i>Chemistry - A European Journal</i> , 2006 , 12, 1941-9	4.8	69

182	Single enantiomer of YK-4-279 demonstrates specificity in targeting the oncogene EWS-FLI1. <i>Oncotarget</i> , 2012 , 3, 172-82	3.3	67
181	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
180	Magnesium-binding architectures in RNA crystal structures: validation, binding preferences, classification and motif detection. <i>Nucleic Acids Research</i> , 2015 , 43, 3789-801	20.1	63
179	Structure of human thymidylate synthase suggests advantages of chemotherapy with noncompetitive inhibitors. <i>Journal of Biological Chemistry</i> , 2001 , 276, 14170-7	5.4	62
178	Molecular determinants for antibody binding on group 1 house dust mite allergens. <i>Journal of Biological Chemistry</i> , 2012 , 287, 7388-98	5.4	61
177	Structural and functional insight into the universal stress protein family. <i>Evolutionary Applications</i> , 2013 , 6, 434-49	4.8	60
176	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011 , 12, 45-54		60
175	Structural insight into the mechanism of substrate specificity and catalytic activity of an HD-domain phosphohydrolase: the 5Pdeoxyribonucleotidase YfbR from Escherichia coli. <i>Journal of Molecular Biology</i> , 2008 , 378, 215-26	6.5	57
174	Double trouble-Buffer selection and His-tag presence may be responsible for nonreproducibility of biomedical experiments. <i>Protein Science</i> , 2014 , 23, 1359-68	6.3	55
173	Measurement errors and their consequences in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 2031-8		55
172	The impact of structural genomics: the first quinquennial. <i>Journal of Structural and Functional Genomics</i> , 2016 , 17, 1-16		52
171	The future of crystallography in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2014 , 9, 125-37	6.2	51
170	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCrJ</i> , 2014 , 1, 179-93	4.7	51
169	Diffraction data analysis in the presence of radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 426-36		49
168	Expression, purification and the 1.8 angstroms resolution crystal structure of human neuron specific enolase. <i>Journal of Molecular Biology</i> , 2004 , 341, 1015-21	6.5	48
167	Characterizing metal-binding sites in proteins with X-ray crystallography. <i>Nature Protocols</i> , 2018 , 13, 1062-1090	18.8	47
166	Uncovering a calcium-regulated membrane-binding mechanism for soybean lipoxygenase-1. <i>Biochemistry</i> , 1998 , 37, 15481-90	3.2	47
165	X-ray crystallography: Assessment and validation of protein-small molecule complexes for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2011 , 6, 771-782	6.2	46

164	Analysis of solvent content and oligomeric states in protein crystals--does symmetry matter?. <i>Protein Science</i> , 2008 , 17, 623-32	6.3	44
163	Molecular basis for phosphospecific recognition of histone H3 tails by Survivin paralogues at inner centromeres. <i>Molecular Biology of the Cell</i> , 2012 , 23, 1457-66	3.5	43
162	Crystallography and chemistry should always go together: a cautionary tale of protein complexes with cisplatin and carboplatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1965-79		41
161	The HP1a disordered C terminus and chromo shadow domain cooperate to select target peptide partners. <i>ChemBioChem</i> , 2011 , 12, 1084-96	3.8	41
160	The many faces of radiation-induced changes. <i>Journal of Synchrotron Radiation</i> , 2007 , 14, 24-33	2.4	41
159	Circulatory zinc transport is controlled by distinct interdomain sites on mammalian albumins. <i>Chemical Science</i> , 2016 , 7, 6635-6648	9.4	41
158	Substrate specificity of mammalian N-terminal amino methyltransferase NRMT. <i>Biochemistry</i> , 2012 , 51, 5942-50	3.2	40
157	Unmet challenges of structural genomics. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 587-97	8.1	40
156	Structural genomics: keeping up with expanding knowledge of the protein universe. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 347-53	8.1	40
155	Crystal structure of human complement protein C8gamma at 1.2 Å resolution reveals a lipocalin fold and a distinct ligand binding site. <i>Biochemistry</i> , 2002 , 41, 7030-7	3.2	40
154	X-ray crystallography over the past decade for novel drug discovery - where are we heading next?. <i>Expert Opinion on Drug Discovery</i> , 2015 , 10, 975-89	6.2	38
153	Neutron scattering studies of Cd _{1-x} MnxTe (invited). <i>Journal of Applied Physics</i> , 1984 , 55, 2305-2309	2.5	38
152	Broad-substrate screen as a tool to identify substrates for bacterial Gcn5-related N-acetyltransferases with unknown substrate specificity. <i>Protein Science</i> , 2013 , 22, 222-30	6.3	37
151	Identification of unknown protein function using metabolite cocktail screening. <i>Structure</i> , 2012 , 20, 1715-25		37
150	Biochemical and structural characterization of apolipoprotein A-I binding protein, a novel phosphoprotein with a potential role in sperm capacitation. <i>Endocrinology</i> , 2008 , 149, 2108-20	4.8	37
149	A close look onto structural models and primary ligands of metallo-lactamases. <i>Drug Resistance Updates</i> , 2018 , 40, 1-12	23.2	36
148	Targeting a uniquely nonspecific prenyl synthase with bisphosphonates to combat cryptosporidiosis. <i>Chemistry and Biology</i> , 2008 , 15, 1296-306		35
147	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. <i>Molecular Immunology</i> , 2013 , 56, 794-803	4.3	34

146	Crystal structure of RNase T, an exoribonuclease involved in tRNA maturation and end turnover. <i>Structure</i> , 2007 , 15, 417-28	5.2	32
145	Protein purification and crystallization artifacts: The tale usually not told. <i>Protein Science</i> , 2016 , 25, 720-33	6.3	31
144	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018 , 285, 444-466	5.7	31
143	Structural, functional, and inhibition studies of a Gcn5-related N-acetyltransferase (GNAT) superfamily protein PA4794: a new C-terminal lysine protein acetyltransferase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2013 , 288, 30223-30235	5.4	30
142	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016 , 24, 216-20	5.2	29
141	DENZO and SCALEPACK 2006 , 226-235		27
140	The structural genomics experimental pipeline: insights from global target lists. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 201-10	4.2	27
139	The crystal structure of N(10)-formyltetrahydrofolate synthetase from <i>Moorella thermoacetica</i> . <i>Biochemistry</i> , 2000 , 39, 3920-6	3.2	26
138	Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. <i>FEBS Journal</i> , 2020 , 287, 3703-3718	5.7	25
137	Fitmunk: improving protein structures by accurate, automatic modeling of side-chain conformations. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 266-80	5.5	25
136	Data management in the modern structural biology and biomedical research environment. <i>Methods in Molecular Biology</i> , 2014 , 1140, 1-25	1.4	25
135	Molstack-Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. <i>Protein Science</i> , 2018 , 27, 86-94	6.3	25
134	Testosterone meets albumin - the molecular mechanism of sex hormone transport by serum albumins. <i>Chemical Science</i> , 2019 , 10, 1607-1618	9.4	24
133	New surface contacts formed upon reductive lysine methylation: improving the probability of protein crystallization. <i>Protein Science</i> , 2010 , 19, 1395-404	6.3	24
132	Correcting the record of structural publications requires joint effort of the community and journal editors. <i>FEBS Journal</i> , 2016 , 283, 4452-4457	5.7	24
131	Refining the macromolecular model - achieving the best agreement with the data from X-ray diffraction experiment. <i>Crystallography Reviews</i> , 2018 , 24, 236-262	1.3	24
130	Data mining of iron(II) and iron(III) bond-valence parameters, and their relevance for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 316-325	5.5	23
129	Benefits of structural genomics for drug discovery research. <i>Infectious Disorders - Drug Targets</i> , 2009 , 9, 459-74	1.1	23

128	To automate or not to automate: this is the question. <i>Journal of Structural and Functional Genomics</i> , 2010 , 11, 211-21		23
127	100 Years later: Celebrating the contributions of x-ray crystallography to allergy and clinical immunology. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 136, 29-37.e10	11.5	22
126	An extremely SAD case: structure of a putative redox-enzyme maturation protein from <i>Archaeoglobus fulgidus</i> at 3.4 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007 , 63, 348-54		22
125	Structure of human thymidylate synthase under low-salt conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 622-7		22
124	Crystal structure of a putative isochorismatase hydrolase from <i>Oleispira antarctica</i> . <i>Journal of Structural and Functional Genomics</i> , 2012 , 13, 27-36		20
123	Crystallization and preliminary structure analysis of an insect virus with T=4 quasi-symmetry: <i>Nudaurelia capensis</i> virus. <i>Acta Crystallographica Section B: Structural Science</i> , 1991 , 47, 23-29		20
122	Structure of <i>Bacillus subtilis</i> YXKO--a member of the UPF0031 family and a putative kinase. <i>Journal of Structural Biology</i> , 2002 , 139, 161-70	3.4	19
121	The quality and validation of structures from structural genomics. <i>Methods in Molecular Biology</i> , 2014 , 1091, 297-314	1.4	18
120	Automatic recognition of ligands in electron density by machine learning. <i>Bioinformatics</i> , 2019 , 35, 452-461	4.1	17
119	Asymmetric synthesis and evaluation of a hydroxyphenylamide voltage-gated sodium channel blocker in human prostate cancer xenografts. <i>Bioorganic and Medicinal Chemistry</i> , 2012 , 20, 2180-8	3.4	17
118	Mechanism of N10-formyltetrahydrofolate synthetase derived from complexes with intermediates and inhibitors. <i>Protein Science</i> , 2012 , 21, 219-28	6.3	17
117	Structural and functional characterizations of SsgB, a conserved activator of developmental cell division in morphologically complex actinomycetes. <i>Journal of Biological Chemistry</i> , 2009 , 284, 25268-79	5.4	17
116	Crystal structures of TM0549 and NE1324--two orthologs of <i>E. coli</i> AHAS isozyme III small regulatory subunit. <i>Protein Science</i> , 2007 , 16, 1360-7	6.3	17
115	Catalytic cysteine of thymidylate synthase is activated upon substrate binding. <i>Biochemistry</i> , 2000 , 39, 6969-78	3.2	17
114	Removal of salt from a salt-induced protein crystal without cross-linking. Preliminary examination of "desalted" crystals of phosphoglucomutase by X-ray crystallography at low temperature. <i>Biochemistry</i> , 1991 , 30, 6866-75	3.2	17
113	Structural Analysis of Der p 1-Antibody Complexes and Comparison with Complexes of Proteins or Peptides with Monoclonal Antibodies. <i>Journal of Immunology</i> , 2015 , 195, 307-16	5.3	16
112	Harvesting the high-hanging fruit: the structure of the YdeN gene product from <i>Bacillus subtilis</i> at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1101-7		16
111	Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 6847-6862	8.3	15

110	Crystal structure of equine serum albumin in complex with cetirizine reveals a novel drug binding site. <i>Molecular Immunology</i> , 2016 , 71, 143-151	4.3	15
109	Kinetic, spectroscopic, and structural investigations of the soybean lipoxygenase-1 first-coordination sphere mutant, Asn694Gly. <i>Biochemistry</i> , 2006 , 45, 10233-42	3.2	15
108	The structure determination of Sindbis virus core protein using isomorphous replacement and molecular replacement averaging between two crystal forms. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1992 , 48 (Pt 4), 430-42		15
107	Structural analysis of a putative aminoglycoside N-acetyltransferase from Bacillus anthracis. <i>Journal of Molecular Biology</i> , 2011 , 410, 411-23	6.5	14
106	An experimental charge density of HEPES. <i>Acta Crystallographica Section B: Structural Science</i> , 2010 , 66, 482-92		14
105	Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from Thermoplasma acidophilum. <i>Journal of Structural Biology</i> , 2010 , 169, 304-11	3.4	13
104	Cation binding and thermostability of FTHFS monovalent cation binding sites and thermostability of N10-formyltetrahydrofolate synthetase from Moorella thermoacetica. <i>Biochemistry</i> , 2000 , 39, 14481-6	3.2	13
103	The major cockroach allergen Bla g 4 binds tyramine and octopamine. <i>Molecular Immunology</i> , 2014 , 60, 86-94	4.3	12
102	Structure of Escherichia coli RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the rut operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 1294-9		12
101	Crystallization of Fe-Si-B metallic glasses studied by X-ray synchrotron radiation. <i>Journal of Materials Science</i> , 1987 , 22, 4144-4152	4.3	12
100	STUDIES OF FCC HEISENBERG ANTIFERROMAGNETS BY MONTE CARLO SIMULATION ON LARGE SPIN ARRAYS. <i>Journal De Physique Colloque</i> , 1988 , 49, C8-1551-C8-1552		12
99	Explanation of neutron diffraction phenomena observed in vibrating piezoelectric crystals. <i>Physica Status Solidi A</i> , 1972 , 9, 423-433		12
98	The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. <i>Structural Dynamics</i> , 2019 , 6, 064301	3.2	12
97	Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. <i>Biochemistry</i> , 2018 , 57, 963-977	3.2	11
96	Dissecting the Structural Elements for the Activation of β Ketoacyl-(Acyl Carrier Protein) Reductase from Vibrio cholerae. <i>Journal of Bacteriology</i> , 2016 , 198, 463-76	3.5	11
95	Structural characterization of Helicobacter pylori dethiobiotin synthetase reveals differences between family members. <i>FEBS Journal</i> , 2012 , 279, 1093-105	5.7	11
94	Synthesis and solid-state study of supramolecular host-guest assemblies: Bis[6-O,6-OP(1,2:3,4-diisopropylidene-alpha-D-galactopyranosyl)thiophosphoryl] dichalcogenides. <i>Journal of Organic Chemistry</i> , 2008 , 73, 4388-97	4.2	11
93	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021 , 30, 115-124	6.3	11

92	Antigenic Determinants of Der p 1: Specificity and Cross-Reactivity Associated with IgE Antibody Recognition. <i>Journal of Immunology</i> , 2017 , 198, 1334-1344	5.3	10
91	Data to knowledge: how to get meaning from your result. <i>IUCrJ</i> , 2015 , 2, 45-58	4.7	10
90	Assessing the accuracy of template-based structure prediction metaservers by comparison with structural genomics structures. <i>Journal of Structural and Functional Genomics</i> , 2012 , 13, 213-25		10
89	Spin waves in Fe ₂ Al ₂ Si system. <i>Solid State Communications</i> , 1983 , 46, 217-219	1.6	10
88	A phenomenological description of the paramagnet-antiferromagnet transition in Cd ₁ -Mn Te. <i>Journal of Magnetism and Magnetic Materials</i> , 1982 , 30, 215-222	2.8	10
87	Regioselectivity of hyoscyamine 6 β -hydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. <i>Dalton Transactions</i> , 2020 , 49, 4454-4463	4.3	9
86	Factors correlating with significant differences between X-ray structures of myoglobin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 481-91		9
85	Edc3 function in yeast and mammals is modulated by interaction with NAD-related compounds. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 613-22	3.2	9
84	Ultratight crystal packing of a 10 kDa protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 464-70		9
83	Dexamethasone at 119 K. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007 , 63, o2791-o2793		9
82	Crystallization and preliminary X-ray analysis of the cytoplasmic domain of human erythrocyte band 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 22, 293-7	4.2	9
81	A Gcn5-Related N-Acetyltransferase (GNAT) Capable of Acetylating Polymyxin B and Colistin Antibiotics in Vitro. <i>Biochemistry</i> , 2018 , 57, 7011-7020	3.2	9
80	A transient post-translational modification of active site cysteine alters binding properties of the parkinsonism protein DJ-1. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 504, 328-333	3.4	9
79	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017 , 1865, 55-64	4	8
78	X-ray diffraction experiment--the last experiment in the structure elucidation process. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009 , 77, 23-40	5.3	8
77	Crystal structure of a transcriptional regulator TM1030 from <i>Thermotoga maritima</i> solved by an unusual MAD experiment. <i>Journal of Structural Biology</i> , 2007 , 159, 424-32	3.4	8
76	Recombinant production of enzymatically active male contraceptive drug target hTSSK2 - Localization of the TSKS domain phosphorylated by TSSK2. <i>Protein Expression and Purification</i> , 2016 , 121, 88-96	2	8
75	Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. <i>BMC Evolutionary Biology</i> , 2018 , 18, 199	3	8

74	Pyrimidine biosynthesis in pathogens - Structures and analysis of dihydroorotases from <i>Yersinia pestis</i> and <i>Vibrio cholerae</i> . <i>International Journal of Biological Macromolecules</i> , 2019 , 136, 1176-1187	7.9	7
73	Crystal structures of putative phosphoglycerate kinases from <i>B. anthracis</i> and <i>C. jejuni</i> . <i>Journal of Structural and Functional Genomics</i> , 2012 , 13, 15-26		7
72	The crystal structure of the AF2331 protein from <i>Archaeoglobus fulgidus</i> DSM 4304 forms an unusual interdigitated dimer with a new type of alpha + beta fold. <i>Protein Science</i> , 2009 , 18, 2410-9	6.3	7
71	Using surface-bound rubidium ions for protein phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 1008-12		7
70	Phason velocities in TaS ₂ by x-ray diffuse scattering. <i>Physical Review B</i> , 1989 , 39, 1360-1362	3.3	7
69	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. <i>IUCrJ</i> , 2020 , 7,	4.7	7
68	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 455-457	5.5	7
67	On the evolution of the quality of macromolecular models in the PDB. <i>FEBS Journal</i> , 2020 , 287, 2685-2698	5.7	7
66	Sperm Lysozyme-Like Protein 1 (SLLP1), an intra-acrosomal oolemmal-binding sperm protein, reveals filamentous organization in protein crystal form. <i>Andrology</i> , 2015 , 3, 756-71	4.2	6
65	Hot macromolecular crystals. <i>Crystal Growth and Design</i> , 2009 , 10, 580	3.5	6
64	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from <i>Streptococcus pyogenes</i> . <i>BMC Structural Biology</i> , 2009 , 9, 75	2.7	6
63	Stacks of DMANH ⁺ scaffolding for ribbon shaped Cl ⁻ bridged oxonium ions. <i>CrystEngComm</i> , 2007 , 9, 152-157	3.3	6
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