Wladek Minor

List of Publications by Year in Descending Order

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217 papers	34,659 citations	49 h-index	186 g-index
283 ext. papers	36,550 ext. citations	5.2 avg, IF	7.45 L-index

#	Paper	IF	Citations
217	Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol.. *Protein Science*, **2022**,	6.3	3
216	New ligand-binding sites identified in the crystal structures of lactoglobulin complexes with desipramine.. *IUCrJ*, **2022**, 9, 386-398	4.7	0
215	Optimal structure determination from sub-optimal diffraction data. *Protein Science*, **2021**,	6.3	5
214	Gcn5-Related Acetyltransferases (GNATs) With a Catalytic Serine Residue Can Play Ping-Pong Too. *Frontiers in Molecular Biosciences*, **2021**, 8, 646046	5.6	4
213	Recognizing and validating ligands with CheckMyBlob. *Nucleic Acids Research*, **2021**, 49, W86-W92	20.1	1
212	Detecting anomalies in X-ray diffraction images using convolutional neural networks. *Expert Systems With Applications*, **2021**, 174, 114740-114740	7.8	2
211	A study on the structure, mechanism, and biochemistry of kanamycin B dioxygenase (KanJ)-an enzyme with a broad range of substrates. *FEBS Journal*, **2021**, 288, 1366-1386	5.7	1
210	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. *Protein Science*, **2021**, 30, 115-124	6.3	11
209	Synchrotron Radiation as a Tool for Macromolecular X-Ray Crystallography: a XXI Century Perspective. *Nuclear Instruments & Methods in Physics Research B*, **2021**, 489, 30-40	1.2	1
208	Rapid response to emerging biomedical challenges and threats. *IUCrJ*, **2021**, 8, 395-407	4.7	1
207	virusMED: an atlas of hotspots of viral proteins. *IUCrJ*, **2021**, 8,	4.7	2
206	State-of-the-Art Data Management: Improving the Reproducibility, Consistency, and Traceability of Structural Biology and in Vitro Biochemical Experiments. *Methods in Molecular Biology*, **2021**, 2199, 209-236	1.4	3
205	Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. *FEBS Journal*, **2020**, 287, 3703-3718	5.7	25
204	Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. *Journal of Medicinal Chemistry*, **2020**, 63, 6847-6862	8.3	15
203	Regioselectivity of hyoscyamine 6hydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. *Dalton Transactions*, **2020**, 49, 4454-4469	4.3	9
202	Assessment of Crystallographic Structure Quality and Proteinligand Complex Structure Validation **2020**, 253-275		2
201	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. *IUCrJ*, **2020**, 7,	4.7	7

200	Molstack: A platform for interactive presentations of electron density and cryo-EM maps and their interpretations. *Protein Science*, **2020**, 29, 120-127	6.3	6
199	Structural and biochemical analysis of Bacillus anthracis prephenate dehydrogenase reveals an unusual mode of inhibition by tyrosine via the ACT domain. *FEBS Journal*, **2020**, 287, 2235-2255	5.7	1
198	Structure of the Complex of an Iminopyridinedione Protein Tyrosine Phosphatase 4A3 Phosphatase Inhibitor with Human Serum Albumin. *Molecular Pharmacology*, **2020**, 98, 648-657	4.3	3
197	Comparison of metal-bound and unbound structures of aminopeptidase B proteins from Escherichia coli and Yersinia pestis. *Protein Science*, **2020**, 29, 1618-1628	6.3	1
196	On the evolution of the quality of macromolecular models in the PDB. *FEBS Journal*, **2020**, 287, 2685-2698	5.7	7
195	Testosterone meets albumin - the molecular mechanism of sex hormone transport by serum albumins. *Chemical Science*, **2019**, 10, 1607-1618	9.4	24
194	Pyrimidine biosynthesis in pathogens - Structures and analysis of dihydroorotases from Yersinia pestis and Vibrio cholerae. *International Journal of Biological Macromolecules*, **2019**, 136, 1176-1187	7.9	7
193	Automatic recognition of ligands in electron density by machine learning. *Bioinformatics*, **2019**, 35, 452-461	7.2	17
192	Energetics of interactions in the solid state of 2-hydroxy-8--quinoline derivatives (= Cl, Br, I, S-Ph): comparison of Hirshfeld atom, X-ray wavefunction and multipole refinements. *IUCrJ*, **2019**, 6, 868-883	4.7	5
191	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 455-457	5.5	7
190	The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. *Structural Dynamics*, **2019**, 6, 064301	3.2	12
189	Characterizing metal-binding sites in proteins with X-ray crystallography. *Nature Protocols*, **2018**, 13, 1062-1090	18.8	47
188	Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. *Biochemistry*, **2018**, 57, 963-977	3.2	11
187	Detect, correct, retract: How to manage incorrect structural models. *FEBS Journal*, **2018**, 285, 444-466	5.7	31
186	Molstack-Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. *Protein Science*, **2018**, 27, 86-94	6.3	25
185	Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. *BMC Evolutionary Biology*, **2018**, 18, 199	3	8
184	A Gcn5-Related N-Acetyltransferase (GNAT) Capable of Acetylating Polymyxin B and Colistin Antibiotics in Vitro. *Biochemistry*, **2018**, 57, 7011-7020	3.2	9
183	Refining the macromolecular model - achieving the best agreement with the data from X-ray diffraction experiment. *Crystallography Reviews*, **2018**, 24, 236-262	1.3	24

182	A transient post-translational modification of active site cysteine alters binding properties of the parkinsonism protein DJ-1. *Biochemical and Biophysical Research Communications*, **2018**, 504, 328-333	3.4	9
181	A close look onto structural models and primary ligands of metallo-β-lactamases. *Drug Resistance Updates*, **2018**, 40, 1-12	23.2	36
180	Differences in substrate specificity of V. cholerae FabH enzymes suggest new approaches for the development of novel antibiotics and biofuels. *FEBS Journal*, **2018**, 285, 2900-2921	5.7	1
179	Antigenic Determinants of Der p 1: Specificity and Cross-Reactivity Associated with IgE Antibody Recognition. *Journal of Immunology*, **2017**, 198, 1334-1344	5.3	10
178	Optimization of overexpression of a chaperone protein of steroid C25 dehydrogenase for biochemical and biophysical characterization. *Protein Expression and Purification*, **2017**, 134, 47-62	2	4
177	Data mining of iron(II) and iron(III) bond-valence parameters, and their relevance for macromolecular crystallography. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 316-325	5.5	23
176	Generating enzyme and radical-mediated bisubstrates as tools for investigating Gcn5-related N-acetyltransferases. *FEBS Letters*, **2017**, 591, 2348-2361	3.8	5
175	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2017**, 1865, 55-64	4	8
174	Sharing Big Data. *IUCrJ*, **2017**, 4, 3-4	4.7	2
173	CheckMyMetal: a macromolecular metal-binding validation tool. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 223-233	5.5	172
172	Databases, Repositories, and Other Data Resources in Structural Biology. *Methods in Molecular Biology*, **2017**, 1607, 643-665	1.4	4
171	A public database of macromolecular diffraction experiments. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 1181-1193	5.5	75
170	Dissecting the Structural Elements for the Activation of β-Ketoacyl-(Acyl Carrier Protein) Reductase from Vibrio cholerae. *Journal of Bacteriology*, **2016**, 198, 463-76	3.5	11
169	Fitmunk: improving protein structures by accurate, automatic modeling of side-chain conformations. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 266-80	5.5	25
168	Crystal structure of equine serum albumin in complex with cetirizine reveals a novel drug binding site. *Molecular Immunology*, **2016**, 71, 143-151	4.3	15
167	Safeguarding Structural Data Repositories against Bad Apples. *Structure*, **2016**, 24, 216-20	5.2	29
166	The young person's guide to the PDB. *Postepy Biochemii*, **2016**, 62, 242-249	0	1
165	Correcting the record of structural publications requires joint effort of the community and journal editors. *FEBS Journal*, **2016**, 283, 4452-4457	5.7	24

164	Protein purification and crystallization artifacts: The tale usually not told. *Protein Science*, **2016**, 25, 720-33	6.3	31
163	Recombinant production of enzymatically active male contraceptive drug target hTSSK2 - Localization of the TSKS domain phosphorylated by TSSK2. *Protein Expression and Purification*, **2016** , 121, 88-96	2	8
162	The impact of structural genomics: the first quindecennial. *Journal of Structural and Functional Genomics*, **2016**, 17, 1-16		52
161	Circulatory zinc transport is controlled by distinct interdomain sites on mammalian albumins. *Chemical Science*, **2016**, 7, 6635-6648	9.4	41
160	Data to knowledge: how to get meaning from your result. *IUCrJ*, **2015**, 2, 45-58	4.7	10
159	X-ray crystallography over the past decade for novel drug discovery - where are we heading next?. *Expert Opinion on Drug Discovery*, **2015**, 10, 975-89	6.2	38
158	Structural Analysis of Der p 1-Antibody Complexes and Comparison with Complexes of Proteins or Peptides with Monoclonal Antibodies. *Journal of Immunology*, **2015**, 195, 307-16	5.3	16
157	100 Years later: Celebrating the contributions of x-ray crystallography to allergy and clinical immunology. *Journal of Allergy and Clinical Immunology*, **2015**, 136, 29-37.e10	11.5	22
156	Sperm Lysozyme-Like Protein 1 (SLLP1), an intra-acrosomal oolemmal-binding sperm protein, reveals filamentous organization in protein crystal form. *Andrology*, **2015**, 3, 756-71	4.2	6
155	Crystallography and chemistry should always go together: a cautionary tale of protein complexes with cisplatin and carboplatin. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 1965-79		41
154	Magnesium-binding architectures in RNA crystal structures: validation, binding preferences, classification and motif detection. *Nucleic Acids Research*, **2015**, 43, 3789-801	20.1	63
153	The major cockroach allergen Bla g 4 binds tyramine and octopamine. *Molecular Immunology*, **2014**, 60, 86-94	4.3	12
152	Double trouble-Buffer selection and His-tag presence may be responsible for nonreproducibility of biomedical experiments. *Protein Science*, **2014**, 23, 1359-68	6.3	55
151	The crystal structure of pyrimidine/thiamin biosynthesis precursor-like domain-containing protein CAE31940 from proteobacterium Bordetella bronchiseptica RB50, and evolutionary insight into the NMT1/THI5 family. *Journal of Structural and Functional Genomics*, **2014**, 15, 73-81		
150	Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. *Nature Protocols*, **2014**, 9, 156-70	18.8	200
149	Factors correlating with significant differences between X-ray structures of myoglobin. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 481-91		9
148	Structural characterization of the putative ABC-type 2 transporter from Thermotoga maritima MSB8. *Journal of Structural and Functional Genomics*, **2014**, 15, 215-22		1
147	The future of crystallography in drug discovery. *Expert Opinion on Drug Discovery*, **2014**, 9, 125-37	6.2	51

146	Edc3 function in yeast and mammals is modulated by interaction with NAD-related compounds. *G3: Genes, Genomes, Genetics*, **2014**, 4, 613-22	3.2	9
145	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. *IUCrJ*, **2014**, 1, 179-93	4.7	51
144	Data management in the modern structural biology and biomedical research environment. *Methods in Molecular Biology*, **2014**, 1140, 1-25	1.4	25
143	The quality and validation of structures from structural genomics. *Methods in Molecular Biology*, **2014**, 1091, 297-314	1.4	18
142	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. *FEBS Journal*, **2013**, 280, 5705-36	5.7	73
141	Broad-substrate screen as a tool to identify substrates for bacterial Gcn5-related N-acetyltransferases with unknown substrate specificity. *Protein Science*, **2013**, 22, 222-30	6.3	37
140	Structural, functional, and inhibition studies of a Gcn5-related N-acetyltransferase (GNAT) superfamily protein PA4794: a new C-terminal lysine protein acetyltransferase from pseudomonas aeruginosa. *Journal of Biological Chemistry*, **2013**, 288, 30223-30235	5.4	30
139	Structure of isochorismate synthase DhbC from Bacillus anthracis. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 956-61		
138	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. *Molecular Immunology*, **2013**, 56, 794-803	4.3	34
137	Serum albumins-unusual allergens. *Biochimica Et Biophysica Acta - General Subjects*, **2013**, 1830, 5375-81	4	72
136	Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant Staphylococcus aureus. *Journal of Structural and Functional Genomics*, **2013**, 14, 97-108		5
135	Ultratight crystal packing of a 10 kDa protein. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 464-70		9
134	Structural and functional insight into the universal stress protein family. *Evolutionary Applications*, **2013**, 6, 434-49	4.8	60
133	Asymmetric synthesis and evaluation of a hydroxyphenylamide voltage-gated sodium channel blocker in human prostate cancer xenografts. *Bioorganic and Medicinal Chemistry*, **2012**, 20, 2180-8	3.4	17
132	Structural characterization of Helicobacter pylori dethiobiotin synthetase reveals differences between family members. *FEBS Journal*, **2012**, 279, 1093-105	5.7	11
131	Structural and immunologic characterization of bovine, horse, and rabbit serum albumins. *Molecular Immunology*, **2012**, 52, 174-82	4.3	600
130	Structure of a short-chain dehydrogenase/reductase from Bacillus anthracis. *Acta Crystallographica Section F: Structural Biology Communications*, **2012**, 68, 632-7		1
129	Identification of unknown protein function using metabolite cocktail screening. *Structure*, **2012**, 20, 1715-25	5.2	37

128	Structure of anabolic ornithine carbamoyltransferase from Campylobacter jejuni at 2.7 □ resolution. *Acta Crystallographica Section F: Structural Biology Communications*, **2012**, 68, 1018-24		3
127	Assessing the accuracy of template-based structure prediction metaservers by comparison with structural genomics structures. *Journal of Structural and Functional Genomics*, **2012**, 13, 213-25		10
126	Substrate specificity of mammalian N-terminal □-amino methyltransferase NRMT. *Biochemistry*, **2012**, 51, 5942-50	3.2	40
125	Molecular determinants for antibody binding on group 1 house dust mite allergens. *Journal of Biological Chemistry*, **2012**, 287, 7388-98	5.4	61
124	Structure of Escherichia coli RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the rut operon. *Acta Crystallographica Section F: Structural Biology Communications*, **2012**, 68, 1294-9		12
123	Alternaria alternata allergen Alt a 1: a unique □-barrel protein dimer found exclusively in fungi. *Journal of Allergy and Clinical Immunology*, **2012**, 130, 241-7.e9	11.5	71
122	Mechanism of N10-formyltetrahydrofolate synthetase derived from complexes with intermediates and inhibitors. *Protein Science*, **2012**, 21, 219-28	6.3	17
121	A multi-faceted analysis of RutD reveals a novel family of □/□-hydrolases. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 2359-68	4.2	5
120	Crystal structure of a putative isochorismatase hydrolase from Oleispira antarctica. *Journal of Structural and Functional Genomics*, **2012**, 13, 27-36		20
119	Crystal structures of putative phosphoglycerate kinases from B. anthracis and C. jejuni. *Journal of Structural and Functional Genomics*, **2012**, 13, 15-26		7
118	Molecular basis for phosphospecific recognition of histone H3 tails by Survivin paralogues at inner centromeres. *Molecular Biology of the Cell*, **2012**, 23, 1457-66	3.5	43
117	Single enantiomer of YK-4-279 demonstrates specificity in targeting the oncogene EWS-FLI1. *Oncotarget*, **2012**, 3, 172-82	3.3	67
116	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. *FASEB Journal*, **2012**, 26, lb194	0.9	
115	X-ray crystallography: Assessment and validation of protein-small molecule complexes for drug discovery. *Expert Opinion on Drug Discovery*, **2011**, 6, 771-782	6.2	46
114	Structural analysis of a putative aminoglycoside N-acetyltransferase from Bacillus anthracis. *Journal of Molecular Biology*, **2011**, 410, 411-23	6.5	14
113	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. *Journal of Structural and Functional Genomics*, **2011**, 12, 45-54		60
112	Crystal structure of a putative transcriptional regulator SCO0520 from Streptomyces coelicolor A3(2) reveals an unusual dimer among TetR family proteins. *Journal of Structural and Functional Genomics*, **2011**, 12, 149-57		4
111	The HP1a disordered C terminus and chromo shadow domain cooperate to select target peptide partners. *ChemBioChem*, **2011**, 12, 1084-96	3.8	41

110	The Enzyme Function Initiative. *Biochemistry*, **2011**, 50, 9950-62	3.2	140
109	Structural and immunologic characterization of Ara h 1, a major peanut allergen. *Journal of Biological Chemistry*, **2011**, 286, 39318-27	5.4	74
108	NRMT is an alpha-N-methyltransferase that methylates RCC1 and retinoblastoma protein. *Nature*, **2010**, 466, 1125-8	50.4	82
107	Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from Thermoplasma acidophilum. *Journal of Structural Biology*, **2010**, 169, 304-11	3.4	13
106	To automate or not to automate: this is the question. *Journal of Structural and Functional Genomics*, **2010**, 11, 211-21		23
105	Unmet challenges of structural genomics. *Current Opinion in Structural Biology*, **2010**, 20, 587-97	8.1	40
104	An experimental charge density of HEPES. *Acta Crystallographica Section B: Structural Science*, **2010**, 66, 482-92		14
103	Diffraction data analysis in the presence of radiation damage. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 426-36		49
102	Is too PcreativePlanguage acceptable in crystallography?. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 1041-2		2
101	New surface contacts formed upon reductive lysine methylation: improving the probability of protein crystallization. *Protein Science*, **2010**, 19, 1395-404	6.3	24
100	HOW TO USE THE PSI STRUCTURAL GENOMICS KNOWLEDGEBASE TO ENABLE RESEARCH. *FASEB Journal*, **2010**, 24, 902.2	0.9	
99	PHotPmacromolecular crystals. *Crystal Growth and Design*, **2009**, 10, 580	3.5	6
98	X-ray diffraction experiment--the last experiment in the structure elucidation process. *Advances in Protein Chemistry and Structural Biology*, **2009**, 77, 23-40	5.3	8
97	Structural and functional characterizations of SsgB, a conserved activator of developmental cell division in morphologically complex actinomycetes. *Journal of Biological Chemistry*, **2009**, 284, 25268-79	5.4	17
96	Benefits of structural genomics for drug discovery research. *Infectious Disorders - Drug Targets*, **2009**, 9, 459-74	1.1	23
95	The protein structure initiative structural genomics knowledgebase. *Nucleic Acids Research*, **2009**, 37, D365-8	20.1	80
94	The crystal structure of the AF2331 protein from Archaeoglobus fulgidus DSM 4304 forms an unusual interdigitated dimer with a new type of alpha + beta fold. *Protein Science*, **2009**, 18, 2410-9	6.3	7
93	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from Streptococcus pyogenes. *BMC Structural Biology*, **2009**, 9, 75	2.7	6

92	Crystal structures of mite allergens Der f 1 and Der p 1 reveal differences in surface-exposed residues that may influence antibody binding. *Journal of Molecular Biology*, **2009**, 386, 520-30	6.5	64
91	2,4-Dichloro-benzaldehyde. *Acta Crystallographica Section E: Structure Reports Online*, **2009**, 66, o243		1
90	The Protein Structure Initiative Structural Genomics Knowledgebase. *FASEB Journal*, **2009**, 23, 858.10	0.9	
89	Determination of protein structures--a series of fortunate events. *Biophysical Journal*, **2008**, 95, 1-9	2.9	110
88	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. *Journal of Organic Chemistry*, **2008**, 73, 4388-97	4.2	11
87	Structural insight into the mechanism of substrate specificity and catalytic activity of an HD-domain phosphohydrolase: the 5Pdeoxyribonucleotidase YfbR from Escherichia coli. *Journal of Molecular Biology*, **2008**, 378, 215-26	6.5	57
86	Crystal structure of the MACPF domain of human complement protein C8 alpha in complex with the C8 gamma subunit. *Journal of Molecular Biology*, **2008**, 379, 331-42	6.5	69
85	Asymmetric synthesis of 2,3-dihydro-2-arylquinazolin-4-ones: methodology and application to a potent fluorescent tubulin inhibitor with anticancer activity. *Journal of Medicinal Chemistry*, **2008**, 51, 4620-31	8.3	150
84	Function-biased choice of additives for optimization of protein crystallization - the case of the putative thioesterase PA5185 from Pseudomonas aeruginosa PAO1. *Crystal Growth and Design*, **2008**, 8, 4054-4061	3.5	2
83	A novel family of sequence-specific endoribonucleases associated with the clustered regularly interspaced short palindromic repeats. *Journal of Biological Chemistry*, **2008**, 283, 20361-71	5.4	156
82	Biochemical and structural characterization of apolipoprotein A-I binding protein, a novel phosphoprotein with a potential role in sperm capacitation. *Endocrinology*, **2008**, 149, 2108-20	4.8	37
81	Data mining of metal ion environments present in protein structures. *Journal of Inorganic Biochemistry*, **2008**, 102, 1765-76	4.2	240
80	Targeting a uniquely nonspecific prenyl synthase with bisphosphonates to combat cryptosporidiosis. *Chemistry and Biology*, **2008**, 15, 1296-306		35
79	Analysis of solvent content and oligomeric states in protein crystals--does symmetry matter?. *Protein Science*, **2008**, 17, 623-32	6.3	44
78	Protein crystallography for non-crystallographers, or how to get the best (but not more) from published macromolecular structures. *FEBS Journal*, **2008**, 275, 1-21	5.7	187
77	2,3-Difluoro-benzoic acid. *Acta Crystallographica Section E: Structure Reports Online*, **2008**, 64, o466		3
76	Phosphorylation regulates SIRT1 function. *PLoS ONE*, **2008**, 3, e4020	3.7	216
75	Stacks of DMANH+ scaffolding for ribbon shaped Cl bridged oxonium ions. *CrystEngComm*, **2007**, 9, 152-157	3.3	6

74	3-(1-Pyridinio)propanesulfonate and 3-(benzyldimethylammonio)propanesulfonate monohydrate. *Acta Crystallographica Section C: Crystal Structure Communications*, **2007**, 63, o114-6		3
73	An extremely SAD case: structure of a putative redox-enzyme maturation protein from Archaeoglobus fulgidus at 3.4 A resolution. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 348-54		22
72	The many faces of radiation-induced changes. *Journal of Synchrotron Radiation*, **2007**, 14, 24-33	2.4	41
71	3-(1-Methylpiperidinio)-1-propanesulfonate. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o282-o283		1
70	N,N,N?,N?-Tetrakis(carboxymethyl)-2,2?-(ethylenedioxy)dianilinium dichloride dihydrate. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o754-o756		1
69	2-(Biphenyl-4-yl)-2,3-dihydroquinazolin-4(1H)-one. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o891-o893		
68	3-Iodo-L-tyrosine hemihydrate. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o1557-o1559		
67	2-Amino-4-(4-chloro-3-methylphenyl)-5-propyl-1,3-thiazolium iodide. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o1598-o1600		
66	trans-1-Hydroxycyclopentan-2-aminium chloride. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o2697-o2698		
65	Dexamethasone at 119 K. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o2791-o2793		9
64	Absolute configuration from a redetermination of (+)-5-bromo-1-[(2R,4S,5R)-4-hydroxy-5-(hydroxymethyl)oxolan-2-yl]pyrimidine-2,4-dione at 118 (2) K. *Acta Crystallographica Section E: Structure Reports Online*, **2007**, 63, o4159-o4160		
63	In situ proteolysis for protein crystallization and structure determination. *Nature Methods*, **2007**, 4, 1019-21	21.6	181
62	Structural genomics: keeping up with expanding knowledge of the protein universe. *Current Opinion in Structural Biology*, **2007**, 17, 347-53	8.1	40
61	Crystal structure of RNase T, an exoribonuclease involved in tRNA maturation and end turnover. *Structure*, **2007**, 15, 417-28	5.2	32
60	Crystal structures of TM0549 and NE1324--two orthologs of E. coli AHAS isozyme III small regulatory subunit. *Protein Science*, **2007**, 16, 1360-7	6.3	17
59	Crystal structure of a transcriptional regulator TM1030 from Thermotoga maritima solved by an unusual MAD experiment. *Journal of Structural Biology*, **2007**, 159, 424-32	3.4	8
58	The tetramer structure of the Nervy homology two domain, NHR2, is critical for AML1/ETO's activity. *Cancer Cell*, **2006**, 9, 249-60	24.3	104
57	Continua of interactions between pairs of atoms in molecular crystals. *Chemistry - A European Journal*, **2006**, 12, 1941-9	4.8	69

56	Map2mod--a server for evaluation of crystallographic models and their agreement with electron density maps. *Bioinformatics*, **2006**, 22, 1660-1	7.2	4
55	DENZO and SCALEPACK **2006**, 226-235		27
54	Kinetic, spectroscopic, and structural investigations of the soybean lipoxygenase-1 first-coordination sphere mutant, Asn694Gly. *Biochemistry*, **2006**, 45, 10233-42	3.2	15
53	Crystal structure of Pseudomonas aeruginosa SPM-1 provides insights into variable zinc affinity of metallo-beta-lactamases. *Journal of Molecular Biology*, **2006**, 357, 890-903	6.5	79
52	Crystal structure of 6-(4-difluoromethoxy-3-methoxyphenyl)-3(2H)- pyridazinone, C12H10F2N2O3. *Zeitschrift Fur Kristallographie - New Crystal Structures*, **2006**, 221, 359-360	0.2	
51	Crystal structure of 2,6-dichlorobenzaldehyde, C7H4Cl2O. *Zeitschrift Fur Kristallographie - New Crystal Structures*, **2006**, 221, 545-546	0.2	
50	HKL-3000: the integration of data reduction and structure solution--from diffraction images to an initial model in minutes. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 859-66		1457
49	3-(Ethyldimethylammonio)propanesulfonate. *Acta Crystallographica Section E: Structure Reports Online*, **2006**, 62, o5757-o5759		2
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