

# Ehmke Pohl

## List of Publications by Citations

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135  
ext. papers

4,063  
ext. citations

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avg, IF

4.83  
L-index

#	Paper	IF	Citations
125	The PILATUS 1M detector. <i>Journal of Synchrotron Radiation</i> , <b>2006</b> , 13, 120-30	2.4	390
124	Metal-adeninate vertices for the construction of an exceptionally porous metal-organic framework. <i>Nature Communications</i> , <b>2012</b> , 3, 604	17.4	312
123	Architecture of a protein central to iron homeostasis: crystal structure and spectroscopic analysis of the ferric uptake regulator. <i>Molecular Microbiology</i> , <b>2003</b> , 47, 903-15	4.1	278
122	Ab initio determination of the crystal structure of cytochrome c6 and comparison with plastocyanin. <i>Structure</i> , <b>1995</b> , 3, 1159-69	5.2	131
121	Crystal structure of a cobalt-activated diphtheria toxin repressor-DNA complex reveals a metal-binding SH3-like domain. <i>Journal of Molecular Biology</i> , <b>1999</b> , 292, 653-67	6.5	117
120	Crystal structure of the iron-dependent regulator (IdeR) from <i>Mycobacterium tuberculosis</i> shows both metal binding sites fully occupied. <i>Journal of Molecular Biology</i> , <b>1999</b> , 285, 1145-56	6.5	104
119	Crystal structure and function of the zinc uptake regulator FurB from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 9914-9922	5.4	100
118	Differential dimer activities of the transcription factor Oct-1 by DNA-induced interface swapping. <i>Molecular Cell</i> , <b>2001</b> , 8, 569-80	17.6	100
117	The structure of the chloroplast F1-ATPase at 3.2 Å resolution. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 1345-52	5.4	100
116	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , <b>2003</b> , 83, 223-49	2.6	86
115	Michael Adducts of (Alkynylcarbene)pentacarbonylchromium Complexes: Formation, Stereochemistry, and Thermal Rearrangement. <i>Chemische Berichte</i> , <b>1992</b> , 125, 2051-2065		81
114	High-resolution structure of the diphtheria toxin repressor complexed with cobalt and manganese reveals an SH3-like third domain and suggests a possible role of phosphate as co-corepressor. <i>Biochemistry</i> , <b>1996</b> , 35, 12292-302	3.2	79
113	A new, simple access to pentacarbonyl(3-aminoallenylidene)chromium complexes. <i>Organometallics</i> , <b>1993</b> , 12, 2556-2564	3.8	73
112	Modulation of global low-frequency motions underlies allosteric regulation: demonstration in CRP/FNR family transcription factors. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001651	9.7	61
111	Contribution of the intramolecular disulfide bridge to the folding stability of REIv, the variable domain of a human immunoglobulin kappa light chain. <i>Folding &amp; Design</i> , <b>1996</b> , 1, 431-40		59
110	Protein-ligand interactions investigated by thermal shift assays (TSA) and dual polarization interferometry (DPI). <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 36-44		56
109	The crystal structure of the zinc phosphodiesterase from <i>Escherichia coli</i> provides insight into function and cooperativity of tRNase Z-family proteins. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 1607-14	3.5	54

108	Mechanism of the Schiff base forming fructose-1,6-bisphosphate aldolase: structural analysis of reaction intermediates. <i>Biochemistry</i> , <b>2005</b> , 44, 4222-9	3.2	52
107	Motion of the DNA-binding domain with respect to the core of the diphtheria toxin repressor (DtxR) revealed in the crystal structures of apo- and holo-DtxR. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 22420-7	5.4	49
106	Improvements in G protein-coupled receptor purification yield light stable rhodopsin crystals. <i>Journal of Structural Biology</i> , <b>2006</b> , 156, 497-504	3.4	48
105	Structure of octreotide, a somatostatin analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1995</b> , 51, 48-59		45
104	Structural Basis of allosteric regulation and substrate specificity of the non-phosphorylating glyceraldehyde 3-Phosphate dehydrogenase from <i>Thermoproteus tenax</i> . <i>Journal of Molecular Biology</i> , <b>2004</b> , 341, 815-28	6.5	44
103	The three-dimensional structure of cystathionine beta-lyase from <i>Arabidopsis</i> and its substrate specificity. <i>Plant Physiology</i> , <b>2001</b> , 126, 631-42	6.6	43
102	Structural conservation between the actin monomer-binding sites of twinfilin and actin-depolymerizing factor (ADF)/cofilin. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 43089-95	5.4	41
101	Crystal structure of an archaeal class I aldolase and the evolution of (betaalpha) <sub>8</sub> barrel proteins. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 47253-60	5.4	39
100	Erste Kristallstruktur eines Selenans; Metall(II)-Komplexe mit dem 2,4,6-Tris(trifluormethyl)selenophenolat-Liganden. <i>Zeitschrift Fur Anorganische Und Allgemeine Chemie</i> , <b>1994</b> , 620, 41-47	1.3	36
99	Synthesis, characterization, and molecular structures of supermesitylgallium- and supermesitylindium dihalides. <i>Inorganic Chemistry</i> , <b>1993</b> , 32, 3343-3346	5.1	34
98	Comparison of high-resolution structures of the diphtheria toxin repressor in complex with cobalt and zinc at the cation-anion binding site. <i>Protein Science</i> , <b>1997</b> , 6, 1114-8	6.3	33
97	Automation of the EMBL Hamburg protein crystallography beamline BW7B. <i>Journal of Synchrotron Radiation</i> , <b>2004</b> , 11, 372-7	2.4	32
96	Structure and function of a regulated archaeal triosephosphate isomerase adapted to high temperature. <i>Journal of Molecular Biology</i> , <b>2004</b> , 342, 861-75	6.5	31
95	Coordinated 1-Aza-1,3-butadienes: Stable Intermediates in the Formation of Pyridines from [(E)Aminoethenyl]carbene]chromium Complexes. <i>Chemische Berichte</i> , <b>1993</b> , 126, 2535-2541		29
94	The crystal structure of the allosteric non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeum <i>Thermoproteus tenax</i> . <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 19938-45	5.4	28
93	A tight tunable range for Ni(II) sensing and buffering in cells. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 409-414	11.7	27
92	Structure, function and evolution of the Archaeal class I fructose-1,6-bisphosphate aldolase. <i>Biochemical Society Transactions</i> , <b>2004</b> , 32, 259-63	5.1	27
91	The Role of Protein-Ligand Contacts in Allosteric Regulation of the <i>Escherichia coli</i> Catabolite Activator Protein. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 22225-35	5.4	25

90	The crystal structure of non-modified and bipyridine-modified PNA duplexes. <i>Chemistry - A European Journal</i> , <b>2010</b> , 16, 11867-75	4.8	25
89	Ab initio structure determination of the lantibiotic mersacidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2000</b> , 56, 705-13		25
88	1.7 A structure of the stabilized REIv mutant T39K. Application of local NCS restraints. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 1158-67		25
87	The Metal-Dependent Regulators FurA and FurB from Mycobacterium Tuberculosis. <i>International Journal of Molecular Sciences</i> , <b>2008</b> , 9, 1548-60	6.3	23
86	Reduction of X-ray-induced radiation damage of macromolecular crystals by data collection at 15 K: a systematic study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 302-9		23
85	A unique dynamin-related protein is essential for mitochondrial fission in <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007512	7.6	22
84	The crystal structures of apo and cAMP-bound GlxR from <i>Corynebacterium glutamicum</i> reveal structural and dynamic changes upon cAMP binding in CRP/FNR family transcription factors. <i>PLoS ONE</i> , <b>2014</b> , 9, e113265	3.7	21
83	Synthese, Struktur und Umlagerung von Chlorbis(2,4,6-tri-tert-butylphenyl)gallan. <i>Chemische Berichte</i> , <b>1993</b> , 126, 2255-2257		21
82	A chemical potentiator of copper-accumulation used to investigate the iron-regulons of <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , <b>2014</b> , 93, 317-30	4.1	20
81	Absolute configurations of Emycin D, E and F; mimicry of centrosymmetric space groups by mixtures of chiral stereoisomers. <i>Acta Crystallographica Section B: Structural Science</i> , <b>1999</b> , 55, 607-616		20
80	Conjugate Addition of 3-Butyn-2-one to Anilines in Ethanol: Alkene Geometric Insights through In Situ FTIR Monitoring. <i>Journal of Organic Chemistry</i> , <b>2016</b> , 81, 7557-65	4.2	20
79	New active leads for tuberculosis booster drugs by structure-based drug discovery. <i>Organic and Biomolecular Chemistry</i> , <b>2017</b> , 15, 10245-10255	3.9	18
78	The Effectors and Sensory Sites of Formaldehyde-responsive Regulator FrmR and Metal-sensing Variant. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 19502-16	5.4	18
77	Preparation and properties of centrally bridgehead-substituted hexacyclo[4.4.0.0.2,1.0.3,5.0.4,8.0.7,9]decanes ("diademanes") and related (CH) <sub>10</sub> hydrocarbons. <i>Chemistry - A European Journal</i> , <b>2003</b> , 9, 5481-8	4.8	18
76	Anion-coordinating residues at binding site 1 are essential for the biological activity of the diphtheria toxin repressor. <i>Infection and Immunity</i> , <b>1999</b> , 67, 1806-11	3.7	18
75	BT: a comprehensive toolbox for the analysis of protein motion. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 183	3.6	17
74	A nucleotide phosphatase activity in the nucleotide binding domain of an orphan resistance protein from rice. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 4023-32	5.4	17
73	The molecular basis of the interactions between synthetic retinoic acid analogues and the retinoic acid receptors. <i>MedChemComm</i> , <b>2017</b> , 8, 578-592	5	16

72	Global low-frequency motions in protein allostery: CAP as a model system. <i>Biophysical Reviews</i> , <b>2015</b> , 7, 175-182	3.7	16
71	The Molecular and Crystal Structure of the Glycopeptide A-40926 Aglycone. <i>Helvetica Chimica Acta</i> , <b>1996</b> , 79, 1916-1924	2	16
70	Air/Liquid Interfacial Nanoassembly of Molecular Building Blocks into Preferentially Oriented Porous Organic Nanosheet Crystals via Hydrogen Bonding. <i>ACS Nano</i> , <b>2017</b> , 11, 10875-10882	16.7	15
69	Structure solution of DNA-binding proteins and complexes with ARCIMBOLDO libraries. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 1743-57		15
68	The calcium-dependent protein kinase 1 from <i>Toxoplasma gondii</i> as target for structure-based drug design. <i>Parasitology</i> , <b>2018</b> , 145, 210-218	2.7	15
67	Changes in the quaternary structure and function of MjHSP16.5 attributable to deletion of the IXI motif and introduction of the substitution, R107G, in the $\beta$ -crystallin domain. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20120327	5.8	14
66	Crystal structure and stereochemical studies of KD(P)G aldolase from <i>Thermoproteus tenax</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 72, 35-43	4.2	14
65	Darstellung und Struktur von Thallium(I)-2,4,6-tris(trifluormethyl)thiophenolat, einer Verbindung mit faltblattartig-polymerem Aufbau. <i>Chemische Berichte</i> , <b>1991</b> , 124, 1127-1129		14
64	Functional and phylogenetic evidence of a bacterial origin for the first enzyme in sphingolipid biosynthesis in a phylum of eukaryotic protozoan parasites. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 12208-12219	5.4	13
63	Structures of quinoxaline antibiotics. <i>Acta Crystallographica Section B: Structural Science</i> , <b>1995</b> , 51 (Pt 6), 987-99		13
62	Practical synthetic strategies towards lipophilic 6-iodotetrahydroquinolines and -dihydroquinolines. <i>Beilstein Journal of Organic Chemistry</i> , <b>2016</b> , 12, 1851-1862	2.5	13
61	A tale of tails: deciphering the contribution of terminal tails to the biochemical properties of two Dps proteins from <i>Streptomyces coelicolor</i> . <i>Cellular and Molecular Life Sciences</i> , <b>2014</b> , 71, 4911-26	10.3	12
60	Crystal structure of the caseinolytic protease gene regulator, a transcriptional activator in actinomycetes. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 5208-16	5.4	12
59	The First Structure of a Lithiated Cyanamide; Synthesis of (PhNCNLi $\square$ HMPA) <sub>n</sub> by Extrusion of N <sub>2</sub> and S from 5-Phenylamino-1,2,3,4-thiazotriazole with Li Reagents and HMPA. <i>Angewandte Chemie International Edition in English</i> , <b>1993</b> , 32, 1769-1771		12
58	Fluorescent Retinoic Acid Analogues as Probes for Biochemical and Intracellular Characterization of Retinoid Signaling Pathways. <i>ACS Chemical Biology</i> , <b>2019</b> , 14, 369-377	4.9	12
57	How to Stabilize Protein: Stability Screens for Thermal Shift Assays and Nano Differential Scanning Fluorimetry in the Virus-X Project. <i>Journal of Visualized Experiments</i> , <b>2019</b> ,	1.6	10
56	The crystal structure of ferritin from <i>Chlorobium tepidum</i> reveals a new conformation of the 4-fold channel for this protein family. <i>Biochimie</i> , <b>2014</b> , 106, 39-47	4.6	10
55	Structural evidence for a proton transfer pathway coupled with haem reduction of cytochrome c" from <i>Methylophilus methylotrophus</i> . <i>Journal of Biological Inorganic Chemistry</i> , <b>2006</b> , 11, 189-96	3.7	10

54	Structures of three diphtheria toxin repressor (DtxR) variants with decreased repressor activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 619-27		10
53	Crystallization of redox-insensitive Oct1 POU domain with different DNA-response elements. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 1634-8		10
52	Multistate binding in pyridoxine 5'-phosphate synthase: 1.96 Å crystal structure in complex with 1-deoxy-D-xylulose phosphate. <i>Biochemistry</i> , <b>2002</b> , 41, 11649-57	3.2	10
51	A rapid method for positioning small flexible molecules, nucleic acids, and large protein fragments in experimental electron density maps <b>1999</b> , 36, 512-525		10
50	A database method for automated map interpretation in protein crystallography <b>1999</b> , 36, 526-541		10
49	Crystal Structure and Packing of Isocyclosporin A. <i>Helvetica Chimica Acta</i> , <b>1996</b> , 79, 1635-1642	2	10
48	A C-terminal CXCL8 peptide based on chemokine-glycosaminoglycan interactions reduces neutrophil adhesion and migration during inflammation. <i>Immunology</i> , <b>2019</b> , 157, 173-184	7.8	9
47	Probing biological activity through structural modelling of ligand-receptor interactions of 2,4-disubstituted thiazole retinoids. <i>Bioorganic and Medicinal Chemistry</i> , <b>2018</b> , 26, 1560-1572	3.4	9
46	Porphyrin-based Coordination Polymer Composed of Layered Pillarless Two-dimensional Networks. <i>Chemistry Letters</i> , <b>2014</b> , 43, 1161-1163	1.7	9
45	Facility Update: The New Protein Crystallography Beamline X10SA at the Swiss Light Source. <i>Synchrotron Radiation News</i> , <b>2006</b> , 19, 24-26	0.6	9
44	Dilithiation of Two Diphenyl Ethers Each Containing Two NHCH <sub>2</sub> CH <sub>2</sub> Y (Y = OMe, NMe <sub>2</sub> ) Side Arms in ortho Positions: Assembly of Adamantanoid Li <sub>4</sub> O <sub>2</sub> N <sub>4</sub> Cores. <i>Angewandte Chemie International Edition in English</i> , <b>1993</b> , 32, 1182-1184		9
43	GSP4PDB: a web tool to visualize, search and explore protein-ligand structural patterns. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 85	3.6	8
42	Structural and docking studies of potent ethionamide boosters. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>2013</b> , 69, 1243-50		8
41	Zweifache Borylierung von Benzolderivaten mit (Diisoalkylamino)boradiyl-Einheiten. <i>Chemische Berichte</i> , <b>1991</b> , 124, 1907-1912		8
40	AFAL: a web service for profiling amino acids surrounding ligands in proteins. <i>Journal of Computer-Aided Molecular Design</i> , <b>2014</b> , 28, 1069-76	4.2	7
39	High-level over-expression, purification, and crystallization of a novel phospholipase C/sphingomyelinase from <i>Pseudomonas aeruginosa</i> . <i>Protein Expression and Purification</i> , <b>2013</b> , 90, 40-6	2	7
38	Crystal Structures of Two Modifications of [3,O-didehydro-mebmt1, val2]-cyclosporin and comparison of three different X-ray data sets. <i>Helvetica Chimica Acta</i> , <b>1995</b> , 78, 355-366	2	7
37	Going to extremes - a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , <b>2021</b> , 368,	2.9	7

36	Novel Fluorescence Competition Assay for Retinoic Acid Binding Proteins. <i>ACS Medicinal Chemistry Letters</i> , <b>2018</b> , 9, 1297-1300	4.3	7
35	Synthesis and molecular structure of a perfluorinated pyridyl carbanion. <i>Journal of Fluorine Chemistry</i> , <b>2012</b> , 133, 33-37	2.1	6
34	A silk purse from a sow's ear-bioinspired materials based on $\beta$ -helical coiled coils. <i>Current Opinion in Cell Biology</i> , <b>2015</b> , 32, 131-7	9	6
33	Overview of the tunable beamlines for protein crystallography at the EMBL Hamburg Outstation; an analysis of current and future usage and developments. <i>Journal of Synchrotron Radiation</i> , <b>2001</b> , 8, 1113-20	2.4	6
32	Darstellung und Kristallstruktur von $[(\text{Me}_3\text{SiCH}_2)_2\text{InP}(\text{H})\text{Ad}]_2$ . <i>Zeitschrift Fur Anorganische Und Allgemeine Chemie</i> , <b>1992</b> , 611, 92-94	1.3	6
31	Structure of bis- $\mu$ [(trimethylsilylmethanolato-O)-bis(trimethylsilylmethyl)gallium] and bis- $\mu$ [(trimethylsilylmethanolato-O)-bis(trimethylsilylmethyl)indium]. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1993</b> , 49, 1309-1311		6
30	Relative Binding Energies Predict Crystallographic Binding Modes of Ethionamide Booster Lead Compounds. <i>Journal of Physical Chemistry Letters</i> , <b>2019</b> , 10, 2244-2249	6.4	5
29	Crystal structures of the Bacillus subtilis prophage lytic cassette proteins XepA and YomS. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 1028-1039	5.5	5
28	Anion-Coordinating Residues at Binding Site 1 Are Essential for the Biological Activity of the Diphtheria Toxin Repressor. <i>Infection and Immunity</i> , <b>1999</b> , 67, 1806-1811	3.7	5
27	Obtaining Tertiary Protein Structures by the ab Initio Interpretation of Small Angle X-ray Scattering Data. <i>Journal of Chemical Theory and Computation</i> , <b>2020</b> , 16, 1985-2001	6.4	4
26	Self-assembly in the metallation of bis(aminoaryl) ethers. <i>Tetrahedron</i> , <b>1995</b> , 51, 579-590	2.4	4
25	Polycyclische Verbindungen aus 2,5-Norbornadien, Isopropylbenzol und Dehalogenierungs-Produkten von Dihalogeno(diorganylamino)boranen. Reaktion von Bis(diisopropylamino)phenylboran mit Na/K-Legierung und Difluor(diisopropylamino)boran. <i>Chemische Berichte</i> , <b>1992</b> , 125, 1559-1564		4
24	Structures of amino(triphenyl)phosphonium bromide and amino(triphenyl)phosphonium hexachloroantimonate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1993</b> , 49, 1280-1283		4
23	Crystal Structure of a Hidden Protein, YcaC, a Putative Cysteine Hydrolase from Pseudomonas aeruginosa, with and without an Acrylamide Adduct. <i>International Journal of Molecular Sciences</i> , <b>2015</b> , 16, 15971-84	6.3	3
22	Structure of cyclo-(L-threonyl-D-valyl-L-prolyl-sarcosyl-N-methyl-L-valyl-OThr) at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1994</b> , 50, 100-103		3
21	Comparison of different X-ray data-collection systems using the crystal structure of octreotide. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1995</b> , 51, 60-8		3
20	Chalcones identify cTXNPx as a potential antileishmanial drug target. <i>PLoS Neglected Tropical Diseases</i> , <b>2021</b> , 15, e0009951	4.8	3
19	Crystallization and preliminary X-ray characterization of cytochrome c" from the obligate methylotroph Methylophilus methylotrophus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 580-3		2

18	Three $\eta^5$ -Unsaturated (Carbene)pentacarbonylchromium Complexes. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1995</b> , 51, 2503-2508		2
17	Structures of endo- and exo-3-acetoxy-2,4-diethoxy-6-(2-oxo-1,3-oxazolidin-3-ylcarbonyl)-3,4-dihydro-2H-pyran. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1993</b> , 49, 1850-1852		2
16	Structure of 2,4,6-tri(tert-butyl)aniline at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1993</b> , 49, 2141-2143		2
15	Multiple Occurrences of a 168-Nucleotide Deletion in SARS-CoV-2 ORF8, Unnoticed by Standard Amplicon Sequencing and Variant Calling Pipelines. <i>Viruses</i> , <b>2021</b> , 13,	6.2	2
14	Classical pathways of gene regulation by retinoids. <i>Methods in Enzymology</i> , <b>2020</b> , 637, 151-173	1.7	1
13	Structure of 4,6-bis(trifluoromethyl)-2,2-bis[2,4,6-tris(trifluoromethyl)phenylthio]-1-thiabenzocyclobutene. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1993</b> , 49, 1026-1028		1
12	Flavonoid-based inhibitors of the Phi-class glutathione transferase from black-grass to combat multiple herbicide resistance. <i>Organic and Biomolecular Chemistry</i> , <b>2021</b> , 19, 9211-9222	3.9	1
11	Functional Analyses of a Putative, Membrane-Bound, Peroxisomal Protein Import Mechanism from the Apicomplexan Protozoan. <i>Genes</i> , <b>2018</b> , 9,	4.2	1
10	CPR-C4 is a highly conserved novel protease from the Candidate Phyla Radiation with remote structural homology to human vasohibins.. <i>Journal of Biological Chemistry</i> , <b>2022</b> , 101919	5.4	1
9	A Diaza-cyclo-tetradecadieneBis(pyrido-silafuran) Ring System. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1995</b> , 51, 2145-2147		0
8	Structure-functional relationship of cellular retinoic acid-binding proteins I and II interacting with natural and synthetic ligands. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 164-175	5.5	0
7	Multi-scale Approaches to Dynamical Transmission of Protein Allostery <b>2015</b> , 141-152		
6	Crystallization and preliminary X-ray analysis of the <i>Thermoplasma acidophilum</i> 20S proteasome in complex with protein substrates. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 899-902		
5	(2E,4'S)-2-(4'-Benzyl-2'-oxo-3'-oxazolidinylcarbonyl)-3-phenylacrylic Acid Methyl Ester. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1996</b> , 52, 246-248		
4	(2R)-3-[(4S)-4-Benzyl-2-oxo-3-oxazolidinyl]-3-oxo-2-[(1R,2S)-2-vinylcyclohexyl]propionic Acid Methyl Ester and (2R)-3-[(4S)-4-Benzyl-2-oxo-3-oxazolidinyl]-3-oxo-2-[(1R,2S)-2-vinylcyclopentyl]propionic Acid Methyl Ester. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1996</b> , 52, 2029-2032		
3	(+)-N-Trichloroacetyl-7,8-dimethoxy-1-vinyl-2,3,4,5-tetrahydro-1H-3-benzazepine at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1994</b> , 50, 1978-1980		
2	Structure of ( $\beta$ )-1[tert-butoxy-3a $\beta$ ,4 $\beta$ ,6,7,7a-hexahydro-7a $\beta$ -methyl-5-oxo-4 $\beta$ -indancarboxylic acid methyl ester at 153 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , <b>1993</b> , 49, 1654-1655		
1	Crystal structure of the GDP-bound GTPase domain of Rab5a from <i>Leishmania donovani</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2020</b> , 76, 544-556	1.1	



