

Christian Betzel

List of Publications by Year in descending order

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303
papers

8,467
citations

70961

41
h-index

64668

79
g-index

309
all docs

309
docs citations

309
times ranked

9375
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular structure of the acyl-enzyme intermediate in β -lactam hydrolysis at 1.7 Å... resolution. <i>Nature</i> , 1992, 359, 700-705.	13.7	614
2	Three-dimensional structure of system I of photosynthesis at 6 Å... resolution. <i>Nature</i> , 1993, 361, 326-331.	13.7	411
3	Natively Inhibited <i>Trypanosoma brucei</i> Cathepsin B Structure Determined by Using an X-ray Laser. <i>Science</i> , 2013, 339, 227-230.	6.0	393
4	Topography of cyclodextrin inclusion complexes, part 20. Circular and flip-flop hydrogen bonding in β -cyclodextrin undecahydrate: a neutron diffraction study. <i>Journal of the American Chemical Society</i> , 1984, 106, 7545-7557.	6.6	348
5	Enzymatic toxins from snake venom: structural characterization and mechanism of catalysis. <i>FEBS Journal</i> , 2011, 278, 4544-4576.	2.2	233
6	Room-temperature macromolecular serial crystallography using synchrotron radiation. <i>IUCr</i> , 2014, 1, 204-212.	1.0	221
7	Serial crystallography on <i>in vivo</i> grown microcrystals using synchrotron radiation. <i>IUCr</i> , 2014, 1, 87-94.	1.0	204
8	In vivo protein crystallization opens new routes in structural biology. <i>Nature Methods</i> , 2012, 9, 259-262.	9.0	193
9	Three-dimensional structure of proteinase K at 0.15-nm resolution. <i>FEBS Journal</i> , 1988, 178, 155-171.	0.2	171
10	Crystal structure of the alkaline proteinase Savinase [®] from <i>Bacillus lentus</i> at 1.4 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 223, 427-445.	2.0	155
11	Megahertz serial crystallography. <i>Nature Communications</i> , 2018, 9, 4025.	5.8	147
12	Structure of a Serine Protease Proteinase K from <i>Tritirachium album limber</i> at 0.98 Å... Resolution. <i>Biochemistry</i> , 2001, 40, 3080-3088.	1.2	128
13	Exosomal cellular prion protein drives fibrillization of amyloid beta and counteracts amyloid beta-mediated neurotoxicity. <i>Journal of Neurochemistry</i> , 2016, 137, 88-100.	2.1	117
14	Structure of catalase-A from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1999, 286, 135-149.	2.0	106
15	The refined crystal structure of <i>Pseudomonas putida</i> lipoamide dehydrogenase complexed with NAD ⁺ at 2.45 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 13, 336-351.	1.5	102
16	Crystal structure of catalase HPII from <i>Escherichia coli</i> . <i>Structure</i> , 1995, 3, 491-502.	1.6	99
17	Dimerization of the Major Birch Pollen Allergen Bet v 1 Is Important for its In Vivo IgE-Cross-Linking Potential in Mice. <i>Journal of Immunology</i> , 2005, 175, 6645-6650.	0.4	92
18	Snake Venom Peptides: Tools of Biodiscovery. <i>Toxins</i> , 2018, 10, 474.	1.5	83

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19	.beta.-D-Cellotetraose Hemihydrate as a Structural Model for Cellulose II. An X-ray Diffraction Study. <i>Journal of the American Chemical Society</i> , 1995, 117, 11397-11406.	6.6	80
20	Structure and function of proteins involved in milk allergies. <i>Biomedical Applications</i> , 2001, 756, 183-187.	1.7	77
21	Proteome analysis of snake venom toxins: pharmacological insights. <i>Expert Review of Proteomics</i> , 2008, 5, 787-797.	1.3	77
22	Crystal structure of a mirror-image L-RNA aptamer (Spiegelmer) in complex with the natural L-protein target CCL2. <i>Nature Communications</i> , 2015, 6, 6923.	5.8	77
23	The Structure of a Functional Unit from the Wall of a Gastropod Hemocyanin Offers a Possible Mechanism for Cooperativity. <i>Biochemistry</i> , 2003, 42, 6341-6346.	1.2	76
24	The Venomics of <i>Bothrops alternatus</i> is a Pool of Acidic Proteins with Predominant Hemorrhagic and Coagulopathic Activities. <i>Journal of Proteome Research</i> , 2010, 9, 2422-2437.	1.8	69
25	Comparative Analysis of the Venom Proteomes of <i>Vipera ammodytes ammodytes</i> and <i>Vipera ammodytes meridionalis</i> . <i>Journal of Proteome Research</i> , 2008, 7, 866-886.	1.8	66
26	Snake venomomics of the Siamese Russell's viper (<i>Daboia russelli siamensis</i>) – Relation to pharmacological activities. <i>Journal of Proteomics</i> , 2009, 72, 256-269.	1.2	66
27	Real-Time Observation of Protein Dense Liquid Cluster Evolution during Nucleation in Protein Crystallization. <i>Crystal Growth and Design</i> , 2017, 17, 954-958.	1.4	65
28	Structural insights into the catalytic mechanism of sphingomyelinases D and evolutionary relationship to glycerophosphodiester phosphodiesterases. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 323-329.	1.0	63
29	Crystal Structure of Mistletoe Lectin I from <i>Viscum album</i> . <i>Biochemical and Biophysical Research Communications</i> , 1999, 257, 418-424.	1.0	60
30	Snake Venomic of <i>Crotalus durissus terrificus</i> – Correlation with Pharmacological Activities. <i>Journal of Proteome Research</i> , 2010, 9, 2302-2316.	1.8	60
31	Three-dimensional structure of the Fab fragment of a neutralizing antibody to human rhinovirus serotype 2. <i>Protein Science</i> , 1992, 1, 1154-1161.	3.1	58
32	Active-site geometry of proteinase K. <i>FEBS Letters</i> , 1986, 197, 105-110.	1.3	55
33	Structural basis for branching enzyme activity of glycoside hydrolase family 57: Structure and stability studies of a novel branching enzyme from the hyperthermophilic archaeon <i>Thermococcus Kodakaraensis</i> KOD1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 547-557.	1.5	54
34	Modeling of Oxidized PTH (oxPTH) and Non-oxidized PTH (n-oxPTH) Receptor Binding and Relationship of Oxidized to Non-Oxidized PTH in Children with Chronic Renal Failure, Adult Patients on Hemodialysis and Kidney Transplant Recipients. <i>Kidney and Blood Pressure Research</i> , 2013, 37, 240-251.	0.9	52
35	Structural characterization of β^2 -sheeted oligomers formed on the pathway of oxidative prion protein aggregation in vitro. <i>Journal of Structural Biology</i> , 2007, 157, 308-320.	1.3	51
36	CHL1 Is a Selective Organizer of the Presynaptic Machinery Chaperoning the SNARE Complex. <i>PLoS ONE</i> , 2010, 5, e12018.	1.1	51

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37	A TIM barrel protein without enzymatic activity? Crystal-structure of narbonin at 1.8 Å... resolution. FEBS Letters, 1992, 306, 80-84.	1.3	50
38	The crystal structure of an "All Locked"™ nucleic acid duplex. Nucleic Acids Research, 2010, 38, 6729-6736.	6.5	49
39	Crystal structure of vipoxin at 2.0 Å...: an example of regulation of a toxic function generated by molecular evolution. FEBS Letters, 1997, 412, 573-577.	1.3	47
40	X-ray structural studies of the fungal laccase from <i>Cerrena maxima</i> . Journal of Biological Inorganic Chemistry, 2006, 11, 963-973.	1.1	47
41	Structure of the Lassa Virus Nucleoprotein Revealed by X-ray Crystallography, Small-angle X-ray Scattering, and Electron Microscopy. Journal of Biological Chemistry, 2011, 286, 38748-38756.	1.6	47
42	Dynamic Light Scattering (DLS). Bioanalysis, 2019, , 173-193.	0.1	43
43	Thrombin-like enzymes from snake venom: Structural characterization and mechanism of action. International Journal of Biological Macromolecules, 2018, 114, 788-811.	3.6	41
44	Structure of Free <i>Thermus flavus</i> 5 S rRNA at 1.3 nm Resolution from Synchrotron X-ray Solution Scattering. Journal of Biological Chemistry, 2000, 275, 31283-31288.	1.6	40
45	Native and Inhibited Structure of a Mu class-related Glutathione S-transferase from <i>Plasmodium falciparum</i> . Journal of Biological Chemistry, 2004, 279, 1336-1342.	1.6	40
46	Atomic structure of the <i>Serratia marcescens</i> endonuclease at 1.1 Å... resolution and the enzyme reaction mechanism. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 567-572.	2.5	39
47	Structure of the neurotoxic complex vipoxin at 1.4 Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1552-1559.	2.5	39
48	Crystal Structure of the Disintegrin Heterodimer from Saw-Scaled Viper (<i>Echis carinatus</i>) at 1.9 Å... Resolution. Biochemistry, 2005, 44, 11058-11066.	1.2	38
49	Dynamic Light Scattering in Protein Crystallization Droplets: Adaptations for Analysis and Optimization of Crystallization Processes. Crystal Growth and Design, 2008, 8, 1628-1634.	1.4	37
50	Structure of the polypeptide crotamine from the Brazilian rattlesnake <i>Crotalus durissus terrificus</i> . Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1958-1964.	2.5	37
51	Crystal structure of domain E of <i>Thermus flavus</i> 5S rRNA: a helical RNA structure including a hairpin loop. FEBS Letters, 1998, 429, 211-215.	1.3	36
52	<i>Trypanosoma brucei</i> ATG8: Structural insights into autophagic-like mechanisms in protozoa. Autophagy, 2009, 5, 1085-1091.	4.3	36
53	Proteomic analysis of the rare Uracoan rattlesnake <i>Crotalus vegrandis</i> venom: Evidence of a broad arsenal of toxins. Toxicon, 2015, 107, 234-251.	0.8	35
54	Comparative Analysis of the Human and Chicken Prion Protein Copper Binding Regions at pH 6.5. Journal of Biological Chemistry, 2005, 280, 13987-13992.	1.6	34

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55	<i>Pseudechis australis</i> Venomics: Adaptation for a Defense against Microbial Pathogens and Recruitment of Body Transferrin. <i>Journal of Proteome Research</i> , 2011, 10, 2440-2464.	1.8	34
56	Cm ³⁺ /Eu ³⁺ induced structural, mechanistic and functional implications for calmodulin. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 21213-21222.	1.3	34
57	The first crystal structure of an RNA racemate. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 659-664.	2.5	33
58	Molecular crowding and RNA synergize to promote phase separation, microtubule interaction, and seeding of Tau condensates. <i>EMBO Journal</i> , 2022, 41, e108882.	3.5	33
59	Crystallization of proteins under microgravity. <i>FEBS Letters</i> , 1989, 259, 194-198.	1.3	31
60	UV-light-induced conversion and aggregation of prion proteins. <i>Free Radical Biology and Medicine</i> , 2009, 46, 1353-1361.	1.3	31
61	Efficient UV detection of protein crystals enabled by fluorescence excitation at wavelengths longer than 300 nm. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 478-484.	0.7	31
62	Immunosuppressive Yersinia Effector YopM Binds DEAD Box Helicase DDX3 to Control Ribosomal S6 Kinase in the Nucleus of Host Cells. <i>PLoS Pathogens</i> , 2016, 12, e1005660.	2.1	31
63	Atomic Structure and Biochemical Characterization of an RNA Endonuclease in the N Terminus of Andes Virus L Protein. <i>PLoS Pathogens</i> , 2016, 12, e1005635.	2.1	31
64	Heating Affects Structure, Enterocyte Adsorption and Signalling, As Well as Immunogenicity of the Peanut Allergen Ara h 2. <i>The Open Allergy Journal</i> , 2011, 4, 24-34.	0.5	31
65	Crystal structure of a complex between thermitase from <i>Thermoactinomyces vulgaris</i> and the leech inhibitor eglin. <i>FEBS Letters</i> , 1988, 236, 171-178.	1.3	30
66	Real-time investigation of dynamic protein crystallization in living cells. <i>Structural Dynamics</i> , 2015, 2, 041712.	0.9	29
67	Crystal Structure of a Complex Formed between a Snake Venom Phospholipase A2 and a Potent Peptide Inhibitor Phe-Leu-Ser-Tyr-Lys at 1.8 Å Resolution. <i>Journal of Biological Chemistry</i> , 2002, 277, 41079-41085.	1.6	28
68	Structure of the functional domain of the major grass-pollen allergen Phlp 5b. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1175-1181.	2.5	28
69	Venom on ice: First insights into Antarctic octopus venoms. <i>Toxicon</i> , 2010, 56, 897-913.	0.8	28
70	Venomomics of the Australian eastern brown snake (<i>Pseudonaja textilis</i>): Detection of new venom proteins and splicing variants. <i>Toxicon</i> , 2015, 107, 252-265.	0.8	28
71	Systematic analysis of protein-detergent complexes applying dynamic light scattering to optimize solutions for crystallization trials. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 75-81.	0.4	28
72	Isolation and characterization of Bradykinin potentiating peptides from <i>Agkistrodon bilineatus</i> venom. <i>Proteome Science</i> , 2016, 14, 1.	0.7	28

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73	Structure of the Major Cytosolic Glutathione S-Transferase from the Parasitic Nematode <i>Onchocerca volvulus</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 12630-12636.	1.6	27
74	Purification, crystallization and preliminary X-ray study of the fungal laccase from <i>Cerrena maxima</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 954-957.	0.7	27
75	Polysaccharide binding sites in hyaluronate lyase – crystal structures of native phage-encoded hyaluronate lyase and its complexes with ascorbic acid and lactose. <i>FEBS Journal</i> , 2009, 276, 3392-3402.	2.2	27
76	The structure of a native L-amino acid oxidase, the major component of the <i>Vipera ammodytes ammodytes</i> venom, reveals dynamic active site and quaternary structure stabilization by divalent ions. <i>Molecular BioSystems</i> , 2011, 7, 379-384.	2.9	27
77	Highly affine and selective aptamers against cholera toxin as capture elements in magnetic bead-based sandwich ELISA. <i>Journal of Biotechnology</i> , 2018, 269, 35-42.	1.9	27
78	Flip-Flop Hydrogen Bonds in β -Cyclodextrin? A Generally Valid Principle in Polysaccharides?. <i>Angewandte Chemie International Edition in English</i> , 1983, 22, 883-884.	4.4	26
79	Amino Acid Sequence and Glycosylation of Functional Unit R _{H2} -e from <i>Rapana thomasiana</i> (Gastropod) Hemocyanin. <i>Archives of Biochemistry and Biophysics</i> , 2002, 399, 149-158.	1.4	26
80	Stability of subtilisins and related proteinases (subtilases). <i>International Journal of Peptide and Protein Research</i> , 1995, 45, 391-400.	0.1	26
81	Crystallization and Preliminary X-ray Analysis of a Low Density Lipoprotein from Human Plasma. <i>Journal of Biological Chemistry</i> , 1996, 271, 28731-28733.	1.6	25
82	Crystal Structure of Himalayan Mistletoe Ribosome-inactivating Protein Reveals the Presence of a Natural Inhibitor and a New Functionally Active Sugar-binding Site. <i>Journal of Biological Chemistry</i> , 2005, 280, 20712-20721.	1.6	25
83	Crystal structures of the complexes of a group IIA phospholipase A 2 with two natural anti-inflammatory agents, anisic acid, and atropine reveal a similar mode of binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 89-100.	1.5	25
84	Structural insights into selectivity and cofactor binding in snake venom L-amino acid oxidases. <i>Biochemical and Biophysical Research Communications</i> , 2012, 421, 124-128.	1.0	25
85	Crystallization and preliminary X-ray diffraction studies of an alkaline protease from <i>Bacillus lentus</i> . <i>Journal of Molecular Biology</i> , 1988, 204, 803-804.	2.0	24
86	Crystallization and preliminary diffraction studies of 5 S rRNA from the thermophilic bacterium <i>Thermus flavus</i> . <i>Journal of Molecular Biology</i> , 1991, 219, 399-402.	2.0	24
87	Strategy to design peptide inhibitors: Structure of a complex of proteinase K with a designed octapeptide inhibitor N ^α -Acetyl-Pro ^α -Ala ^α -Pro ^α -Phe ^α -DAla ^α -Ala ^α -Ala ^α -NH ₂ at 2.5 Å... resolution. <i>Protein Science</i> , 1996, 5, 2453-2458.	1.1	24
88	Crystallization and Preliminary Diffraction Data of a Major Pollen Allergen. <i>Journal of Biological Chemistry</i> , 1996, 271, 27193-27196.	1.6	24
89	Venom peptide analysis of <i>Vipera ammodytes meridionalis</i> (Viperinae) and <i>Bothrops jararacussu</i> (Crotalinae) demonstrates subfamily-specificity of the peptidome in the family Viperidae. <i>Molecular BioSystems</i> , 2011, 7, 3298.	2.9	24
90	Impact of methionine oxidation as an initial event on the pathway of human prion protein conversion. <i>Prion</i> , 2013, 7, 404-411.	0.9	24

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91	Primary Structure and Molecular Modeling of Mistletoe Lectin I from <i>Viscum album</i> . <i>Biochemical and Biophysical Research Communications</i> , 1998, 247, 367-372.	1.0	23
92	Detection of native peptides as potent inhibitors of enzymes. <i>FEBS Journal</i> , 2005, 272, 562-572.	2.2	23
93	The XBI BioLab for life science experiments at the European XFEL. <i>Journal of Applied Crystallography</i> , 2021, 54, 7-21.	1.9	23
94	Cavity Mutants of Savinase, α . <i>Journal of Molecular Biology</i> , 1994, 242, 193-202.	2.0	22
95	Crystal structure of subtilisin DY, a random mutant of subtilisin Carlsberg. <i>FEBS Journal</i> , 1998, 257, 309-318.	0.2	22
96	Mistletoe lectin I in complex with galactose and lactose reveals distinct sugar-binding properties. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 17-25.	0.7	22
97	MRSA Infections: From Classical Treatment to Suicide Drugs. <i>Current Medicinal Chemistry</i> , 2014, 21, 1809-1819.	1.2	22
98	Crystallographic Studies of Savinase, a Subtilisin-like Proteinase, at pH 10.5. <i>FEBS Journal</i> , 1994, 224, 507-518.	0.2	21
99	Asp49 phospholipase A2 ϵ elaidoylamide complex: a new mode of inhibition. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 1314-1321.	1.0	21
100	Oligomerization of the proteolytic products is an intrinsic property of prion proteins. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 1278-1286.	1.0	21
101	Structure of mistletoe lectin I from <i>Viscum album</i> in complex with the phytohormone zeatin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 1590-1595.	1.1	21
102	Protein microheterogeneity and crystal habits: The case of epidermal growth factor receptor isoforms as isolated in a multicompartement electrolyzer with isoelectric membranes. <i>Journal of Chromatography A</i> , 1994, 679, 181-189.	1.8	20
103	Lysine as a Critical Amino Acid for IgE Binding in Phl p 5b C Terminus. <i>International Archives of Allergy and Immunology</i> , 2006, 140, 285-294.	0.9	20
104	First experimental evidence for the preferential stabilization of the natural D- over the nonnatural L-configuration in nucleic acids. <i>Rna</i> , 2007, 13, 1877-1880.	1.6	20
105	Structure of the Extracellular Glutathione S-Transferase OvGST1 from the Human Pathogenic Parasite <i>Onchocerca volvulus</i> . <i>Journal of Molecular Biology</i> , 2008, 377, 501-511.	2.0	20
106	Elapid Snake Venom Analyses Show the Specificity of the Peptide Composition at the Level of Genera <i>Naja</i> and <i>Notechis</i> . <i>Toxins</i> , 2014, 6, 850-868.	1.5	20
107	<i>Pseudechis guttatus</i> venom proteome: Insights into evolution and toxin clustering. <i>Journal of Proteomics</i> , 2014, 110, 32-44.	1.2	20
108	Electronic damage in S atoms in a native protein crystal induced by an intense X-ray free-electron laser pulse. <i>Structural Dynamics</i> , 2015, 2, 041703.	0.9	20

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109	Utilisation of adsorption and desorption for simultaneously improving protein crystallisation success rate and crystal quality. <i>Scientific Reports</i> , 2014, 4, 7308.	1.6	20
110	Reliably distinguishing protein nanocrystals from amorphous precipitate by means of depolarized dynamic light scattering. <i>Journal of Applied Crystallography</i> , 2015, 48, 1476-1484.	1.9	20
111	<i>In vivo</i> protein crystallization in combination with highly brilliant radiation sources offers novel opportunities for the structural analysis of post-translationally modified eukaryotic proteins. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 929-937.	0.4	20
112	Structure of the proteinase inhibitor eglin c with hydrolysed reactive centre at 2.0 Å... resolution. <i>FEBS Letters</i> , 1993, 317, 185-188.	1.3	19
113	First look at RNA in L-configuration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1-7.	2.5	19
114	Single-drop optimization of protein crystallization. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 994-998.	0.7	19
115	A multicrystal diffraction data-collection approach for studying structural dynamics with millisecond temporal resolution. <i>IUCr</i> , 2016, 3, 393-401.	1.0	19
116	Analysis of self-assembly of S-layer protein slp-B53 from <i>Lysinibacillus sphaericus</i> . <i>European Biophysics Journal</i> , 2017, 46, 77-89.	1.2	19
117	X-Ray structure of the antibiotic bacitracin A. <i>FEBS Letters</i> , 1991, 285, 115-119.	1.3	18
118	Structure of a ternary complex of proteinase K, mercury, and a substrate analogue hexapeptide at 2.2 Å resolution. , 1996, 25, 195-201.		18
119	Structure of the heterodimeric neurotoxic complex viperotoxin F (RV-4/RV-7) from the venom of <i>Vipera russelli formosensis</i> at 1.9 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1679-1687.	2.5	18
120	Structure of a novel ribosome-inactivating protein from a hemi-parasitic plant inhabiting the northwestern Himalayas. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2295-2304.	2.5	18
121	Preliminary investigation of the three-dimensional structure of <i>Salmonella typhimurium</i> uridine phosphorylase in the crystalline state. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 337-340.	0.7	18
122	The X-ray structure of <i>Salmonella typhimurium</i> uridine nucleoside phosphorylase complexed with 2,2'-anhydrouridine, phosphate and potassium ions at 1.86 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 51-60.	2.5	18
123	Three-dimensional model of the honeybee venom allergen Api m 7: structural and functional insights. <i>Molecular BioSystems</i> , 2010, 6, 1056.	2.9	18
124	Structural insights into serine protease inhibition by a marine invertebrate BPTI Kunitz-type inhibitor. <i>Journal of Structural Biology</i> , 2012, 180, 271-279.	1.3	18
125	Protein phase separation and determinants of in cell crystallization. <i>Traffic</i> , 2020, 21, 220-230.	1.3	18
126	Interactions of the Neurotoxin Vipoxin in Solution Studied by Dynamic Light Scattering. <i>Biophysical Journal</i> , 2004, 86, 461-466.	0.2	17

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127	Crystallographic portrayal of different conformational states of a Lys49 phospholipase A2 homologue: Insights into structural determinants for myotoxicity and dimeric configuration. <i>International Journal of Biological Macromolecules</i> , 2012, 51, 209-214.	3.6	17
128	Monitoring and Scoring Counter-Diffusion Protein Crystallization Experiments in Capillaries by in situ Dynamic Light Scattering. <i>PLoS ONE</i> , 2012, 7, e33545.	1.1	17
129	Three-dimensional Structure of a Kunitz-type Inhibitor in Complex with an Elastase-like Enzyme. <i>Journal of Biological Chemistry</i> , 2015, 290, 14154-14165.	1.6	17
130	Effect of Audible Sound on Protein Crystallization. <i>Crystal Growth and Design</i> , 2016, 16, 705-713.	1.4	17
131	Crystallization and preliminary diffraction studies of the structural domain E of <i>Thermus flavus</i> 2S rRNA. <i>FEBS Letters</i> , 1995, 374, 292-294.	1.3	16
132	Crystal structure of a complex formed between proteolytically-generated lactoferrin fragment and proteinase K. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 33, 30-38.	1.5	16
133	Crystal structure of a novel myotoxic Arg49 phospholipase A2 homolog (zhaoermiatoxin) from <i>Zhaoermia mangshanensis</i> snake venom: Insights into Arg49 coordination and the role of Lys122 in the polarization of the C-terminus. <i>Toxicon</i> , 2008, 51, 723-735.	0.8	16
134	Isolation, identification and functional profile of excretory secretory peptides from <i>Onchocerca ochengi</i> . <i>Acta Tropica</i> , 2015, 142, 156-166.	0.9	16
135	Spider venoms phospholipases D: A structural review. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 1054-1065.	3.6	16
136	Microfluidic Chips for <i>In Situ</i> Crystal X-ray Diffraction and <i>In Situ</i> Dynamic Light Scattering for Serial Crystallography. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	16
137	Crystallization and preliminary X-ray diffraction studies of intact EF-Tu from <i>Thermus aquaticus</i> YT-1. <i>FEBS Letters</i> , 1988, 240, 139-142.	1.3	15
138	Autoproteolytic stability of a trypsin from the marine crab <i>Cancer pagurus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2008, 370, 566-571.	1.0	15
139	Multi-channel <i>in situ</i> dynamic light scattering instrumentation enhancing biological small-angle X-ray scattering experiments at the PETRA III beamline P12. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 361-372.	1.0	15
140	The Sequence and a Three-Dimensional Structural Analysis Reveal Substrate Specificity among Snake Venom Phosphodiesterases. <i>Toxins</i> , 2019, 11, 625.	1.5	15
141	Crystallization of the bifunctional proteinase/amylase inhibitor PKI-3 and of its complex with proteinase K. <i>FEBS Letters</i> , 1986, 197, 111-114.	1.3	14
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