A deliberate approach to screening for initial crystalliza macromolecules

Journal of Structural Biology 142, 170-179

DOI: 10.1016/s1047-8477(03)00048-0

Citation Report

#	Article	IF	CITATIONS
2	When less is more: a more efficient vapour-diffusion protocol. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1797-1800.	2.5	4
3	Automating the dispensing of viscous biomaterials. , 0, , .		7
4	Turning protein crystallisation from an art into a science. Current Opinion in Structural Biology, 2004, 14, 577-583.	5.7	173
5	Laboratory scale structural genomics. Journal of Structural and Functional Genomics, 2004, 5, 147-157.	1.2	17
6	Protein crystallization in the structural genomics era. Journal of Structural and Functional Genomics, 2004, 5, 3-12.	1.2	32
7	Which strategy for a protein crystallization project?. Cellular and Molecular Life Sciences, 2004, 61, 525-536.	5.4	21
8	Crystallization and X-ray diffraction analysis of ornithine cyclodeaminase fromPseudomonas putida. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 941-944.	2.5	6
9	High-throughput protein crystallography and drug discovery. Chemical Society Reviews, 2004, 33, 558.	38.1	66
10	High-throughput X-ray crystallography for drug discovery. Current Opinion in Pharmacology, 2004, 4, 490-496.	3.5	106
11	Introduction to protein crystallization. Methods, 2004, 34, 254-265.	3.8	214
12	Automated systems for protein crystallization. Methods, 2004, 34, 329-347.	3.8	29
13	Predictive models for protein crystallization. Methods, 2004, 34, 390-407.	3.8	63
15	Protein Crystallization. , 2005, , 29-48.		0
16	High Throughput Protein Crystallography. , 2005, , 61-104.		1
17	Crystal structures and proposed structural/functional classification of three protozoan proteins from the isochorismatase superfamily. Protein Science, 2005, 14, 2887-2894.	7.6	21
18	Automated high-throughput nanoliter-scale protein crystallization screening. Analytical and Bioanalytical Chemistry, 2005, 383, 1034-1041.	3.7	13
19	Automatic Classification and Pattern Discovery in High-throughput Protein Crystallization Trials. Journal of Structural and Functional Genomics, 2005, 6, 195-202.	1.2	32
20	Development of a fully automated macromolecular crystallization/observation robotic system, HTS-80. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 658-663.	2.5	10

#	Article	IF	Citations
21	Structure of human semicarbazide-sensitive amine oxidase/vascular adhesion protein-1. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1550-1562.	2.5	65
22	Crystallization of the SH2-binding site of p130Cas in complex with Lck, a Src-family kinase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 174-177.	0.7	4
23	Crystallization of a truncated soluble human semicarbazide-sensitive amine oxidase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 274-278.	0.7	14
24	Production, crystallization and X-ray characterization of chemically glycosylated hen egg-white lysozyme. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 435-438.	0.7	13
25	Practical implementations for improving the throughput in a manual crystallization setup. Journal of Applied Crystallography, 2005, 38, 568-570.	4.5	9
26	Structure of a ribulose 5-phosphate 3-epimerase from Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2005, 62, 338-342.	2.6	20
27	Crystal structure of glyceraldehyde-3-phosphate dehydrogenase from Plasmodium falciparum at 2.25 \tilde{A} resolution reveals intriguing extra electron density in the active site. Proteins: Structure, Function and Bioinformatics, 2005, 62, 570-577.	2.6	34
28	Coupling of MBP fusion protein cleavage with sparse matrix crystallization screens to overcome problematic protein solubility. BioTechniques, 2005, 39, 476-480.	1.8	4
29	Macromolecular crystallization with microfluidic free-interface diffusion. Expert Review of Proteomics, 2005, 2, 165-172.	3.0	22
30	The Proteomics Protocols Handbook. , 2005, , .		468
31	Efficient and effective path for automated dispensing of bio-precipitant solutions. , 0, , .		6
32	Comparisons of NMR Spectral Quality and Success in Crystallization Demonstrate that NMR and X-ray Crystallography Are Complementary Methods for Small Protein Structure Determination. Journal of the American Chemical Society, 2005, 127, 16505-16511.	13.7	72
33	Structural Genomics., 0,, 273-295.		0
34	Using Fragment Cocktail Crystallography To Assist Inhibitor Design ofTrypanosoma bruceiNucleoside 2-Deoxyribosyltransferaseâ€. Journal of Medicinal Chemistry, 2006, 49, 5939-5946.	6.4	66
35	Ligand-Induced Asymmetry in Histidine Sensor Kinase Complex Regulates Quorum Sensing. Cell, 2006, 126, 1095-1108.	28.9	258
36	Structural Basis of the Suppressed Catalytic Activity of Wild-type Human Glutathione Transferase T1-1 Compared to its W234R Mutant. Journal of Molecular Biology, 2006, 355, 96-105.	4.2	36
37	The open-access high-throughput crystallization facility at EMBL Hamburg. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1446-1452.	2.5	58
38	Structure of the conserved hypothetical protein MAL13P1.257 fromPlasmodium falciparum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 180-185.	0.7	9

#	ARTICLE	IF	Citations
39	Structure of Lmaj006129AAA, a hypothetical protein from Leishmania major. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 175-179.	0.7	18
40	Purification, crystallization and preliminary X-ray diffraction analysis of pathogen-inducible oxygenase (PIOX) fromOryza sativa. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 365-367.	0.7	4
41	Structure of ribose 5-phosphate isomerase from Plasmodium falciparum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 427-431.	0.7	13
42	Thermofluor-based high-throughput stability optimization of proteins for structural studies. Analytical Biochemistry, 2006, 357, 289-298.	2.4	733
43	Atomic-resolution crystal structure of Borrelia burgdorferiouter surface protein A via surface engineering. Protein Science, 2006, 15, 1907-1914.	7.6	38
44	Blocking S-adenosylmethionine synthesis in yeast allows selenomethionine incorporation and multiwavelength anomalous dispersion phasing. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6678-6683.	7.1	45
45	The Regulation of Histidine Sensor Kinase Complexes by Quorum Sensing Signal Molecules. Methods in Enzymology, 2007, 423, 250-263.	1.0	4
46	Development of a Protease Production Platform for Structure-Based Drug Design. Current Protein and Peptide Science, 2007, 8, 439-445.	1.4	3
47	Protein crystallization in drug design: towards a rational approach. Expert Opinion on Drug Discovery, 2007, 2, 1329-1340.	5.0	3
48	A Novel Nanoliter Liquid Dispensing Technology for Protein Crystallization. , 2007, , .		O
49	Structures of Rat Cytosolic PEPCK:  Insight into the Mechanism of Phosphorylation and Decarboxylation of Oxaloacetic Acid,. Biochemistry, 2007, 46, 10078-10088.	2.5	48
50	High resolution crystal structures of the p120 RasGAP SH3 domain. Biochemical and Biophysical Research Communications, 2007, 353, 463-468.	2.1	13
51	Crystal Structure ofHomo sapiensKynureninaseâ€,‡. Biochemistry, 2007, 46, 2735-2744.	2.5	41
52	Structure and Function of the Escherichia coli Protein YmgB: A Protein Critical for Biofilm Formation and Acid-resistance. Journal of Molecular Biology, 2007, 373, 11-26.	4.2	89
53	Dynamic Screening Experiments to Maximize Hits for Crystallization. Crystal Growth and Design, 2007, 7, 2171-2175.	3.0	14
54	High-Throughput Automated System for Crystallizing Membrane Proteins in Lipidic Mesophases. IEEE Transactions on Automation Science and Engineering, 2007, 4, 129-140.	5.2	24
55	Automated Precise Liquid Dispensing System for Protein Crystallization., 2007,,.		7
56	PEG-Induced Morphologically Unstable Growth of Tetragonal Hen Egg-White Lysozyme Crystals. Crystal Growth and Design, 2007, 7, 1999-2008.	3.0	4

#	Article	IF	CITATIONS
57	Biochemical and Structural Characterization of Pseudomonas aeruginosa Bfd and FPR:  Ferredoxin NADP+ Reductase and Not Ferredoxin Is the Redox Partner of Heme Oxygenase under Iron-Starvation Conditions,. Biochemistry, 2007, 46, 12198-12211.	2.5	38
58	The structure ofPlasmodium vivaxphosphatidylethanolamine-binding protein suggests a functional motif containing a left-handed helix. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 178-182.	0.7	5
59	Oligomerization of BenM, a LysR-type transcriptional regulator: structural basis for the aggregation of proteins in this family. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 361-368.	0.7	34
60	Efficient optimization of crystallization conditions by manipulation of drop volume ratio and temperature. Protein Science, 2007, 16, 715-722.	7.6	36
61	Polymerâ€driven crystallization. Protein Science, 2007, 16, 2542-2551.	7.6	34
62	Functional insights from structural genomics. Journal of Structural and Functional Genomics, 2007, 8, 37-44.	1.2	34
63	Glycerol concentrations required for the successful vitrification of cocktail conditions in a high-throughput crystallization screen. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 287-301.	2.5	8
64	Establishing a training set through the visual analysis of crystallization trials. Part I: â ¹ /₄150â€000 images. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1123-1130.	2.5	25
65	Establishing a training set through the visual analysis of crystallization trials. Part II: crystal examples. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1131-1137.	2.5	18
66	The application and use of chemical space mapping to interpret crystallization screening results. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1240-1249.	2.5	26
67	Structure of a <i>Trypanosoma brucei</i> i > \hat{l} ± \hat{l} 2-hydrolase fold protein with unknown function. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 474-478.	0.7	5
68	Crystallization and preliminary X-ray analysis of the inducible lysine decarboxylase fromEscherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 700-706.	0.7	8
69	Purification, crystallization and preliminary X-ray diffraction analysis of the Whirly domain of StWhy2 in complex with single-stranded DNA. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1056-1059.	0.7	4
70	<i>AutoSherlock</i> : a program for effective crystallization data analysis. Journal of Applied Crystallography, 2008, 41, 1173-1176.	4.5	14
71	Hexameric ring structure of the Nâ€terminal domain of <i>Mycobacteriumâ€ftuberculosis</i> DnaB helicase. FEBS Journal, 2008, 275, 3064-3071.	4.7	46
72	Structure of the GspK–GspI–GspJ complex from the enterotoxigenic Escherichia coli type 2 secretion system. Nature Structural and Molecular Biology, 2008, 15, 462-468.	8.2	131
73	Protein crystallization: from purified protein to diffraction-quality crystal. Nature Methods, 2008, 5, 147-153.	19.0	314
74	Characterization of <i>Trypanosoma brucei</i> dihydroorotate dehydrogenase as a possible drug target; structural, kinetic and RNAi studies. Molecular Microbiology, 2008, 68, 37-50.	2.5	73

#	Article	IF	CITATIONS
75	An Extensive Study of Protein Phase Diagram Modification: Increasing Macromolecular Crystallizability by Temperature Screening. Crystal Growth and Design, 2008, 8, 4277-4283.	3.0	18
76	Structural Proteomics. Methods in Molecular Biology, 2008, 426, v-vi.	0.9	21
77	Crystal Structure of the Pyocyanin Biosynthetic Protein PhzS. Biochemistry, 2008, 47, 5281-5289.	2.5	80
78	Crystal Structure of the MACPF Domain of Human Complement Protein C8α in Complex with the C8γ Subunit. Journal of Molecular Biology, 2008, 379, 331-342.	4.2	70
79	Structures of Substrate- and Inhibitor-Bound Adenosine Deaminase from a Human Malaria Parasite Show a Dramatic Conformational Change and Shed Light on Drug Selectivity. Journal of Molecular Biology, 2008, 381, 975-988.	4.2	33
80	The Capsid of the Small RNA Phage PRR1 Is Stabilized by Metal Ions. Journal of Molecular Biology, 2008, 383, 914-922.	4.2	20
81	Three-dimensional Structures of Pseudomonas aeruginosa PvcA and PvcB, Two Proteins Involved in the Synthesis of 2-Isocyano-6,7-dihydroxycoumarin. Journal of Molecular Biology, 2008, 384, 193-205.	4.2	34
82	Recombinant bovine dihydrofolate reductase produced by mutagenesis and nested PCR of murine dihydrofolate reductase cDNA. Protein Expression and Purification, 2008, 62, 104-110.	1.3	3
83	Structural Characterization of a 140° Domain Movement in the Two-Step Reaction Catalyzed by 4-Chlorobenzoate:CoA Ligase. Biochemistry, 2008, 47, 8016-8025.	2.5	121
84	Cycling Temperature Strategy: A Method to Improve the Efficiency of Crystallization Condition Screening of Proteins. Crystal Growth and Design, 2008, 8, 4227-4232.	3.0	35
85	Designed TPR Modules as Novel Anticancer Agents. ACS Chemical Biology, 2008, 3, 161-166.	3.4	99
86	Structural and Functional Relationships in the Virulence-associated Cathepsin L Proteases of the Parasitic Liver Fluke, Fasciola hepatica. Journal of Biological Chemistry, 2008, 283, 9896-9908.	3.4	90
87	Leveraging genetic algorithm and neural network in automated protein crystal recognition., 2008, 2008, 1926-9.		10
88	Dimeric Quaternary Structure of the Prototypical Dual Specificity Phosphatase VH1. Journal of Biological Chemistry, 2009, 284, 10129-10137.	3.4	38
89	Crystal structure of dimeric cardiac L-type calcium channel regulatory domains bridged by Ca ²⁺ Â-calmodulins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5135-5140.	7.1	104
90	A MEMS Flow Sensor and Its Application in Adaptive Liquid Dispensing. , 2009, , .		1
91	Fragment-Based Cocktail Crystallography by the Medical Structural Genomics of Pathogenic Protozoa Consortium. Current Topics in Medicinal Chemistry, 2009, 9, 1678-1687.	2.1	36
92	The Role of Medical Structural Genomics in Discovering New Drugs for Infectious Diseases. PLoS Computational Biology, 2009, 5, e1000530.	3.2	34

#	Article	IF	CITATIONS
93	Toxoplasma gondii Cathepsin L Is the Primary Target of the Invasion-inhibitory Compound Morpholinurea-leucyl-homophenyl-vinyl Sulfone Phenyl. Journal of Biological Chemistry, 2009, 284, 26839-26850.	3.4	60
95	The 2.1 à crystal structure of an acylâ€CoA synthetase from <i>Methanosarcina acetivorans</i> an alternate acylâ€binding pocket for small branched acyl substrates. Proteins: Structure, Function and Bioinformatics, 2009, 77, 685-698.	2.6	18
96	Determination and application of empirically derived detergent phase boundaries to effectively crystallize membrane proteins. Protein Science, 2009, 18, 1828-1839.	7.6	31
97	Structure of NS1A effector domain from the influenza A/Udorn/72 virus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 11-17.	2.5	39
98	Crystallization and preliminary X-ray studies of the N-domain of the Wilson disease associated protein. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 621-624.	0.7	3
99	Molecular mimicry of SUMO promotes DNA repair. Nature Structural and Molecular Biology, 2009, 16, 509-516.	8.2	51
100	Interactive Crystallomic., 2009, , 225-235.		0
101	Structural Characterization of the Hemophore HasAp from <i>Pseudomonas aeruginosa</i> : NMR Spectroscopy Reveals Proteinâ^'Protein Interactions between Holo-HasAp and Hemoglobin [,] . Biochemistry, 2009, 48, 96-109.	2.5	80
102	The Crystal Structure of the Pseudomonas dacunhae Aspartate-β-Decarboxylase Dodecamer Reveals an Unknown Oligomeric Assembly for a Pyridoxal-5′-Phosphate-Dependent Enzyme. Journal of Molecular Biology, 2009, 388, 98-108.	4.2	19
103	Active-Site Gating Regulates Substrate Selectivity in a Chymotrypsin-Like Serine Protease. Journal of Molecular Biology, 2009, 389, 559-574.	4.2	62
104	A self-adjusted precise liquid handling system. , 2009, , .		2
105	High-Throughput Protein Crystallization. Advances in Protein Chemistry and Structural Biology, 2009, 77, 1-22.	2.3	20
106	Cupredoxin-like domains in haemocyanins. Biochemical Journal, 2010, 426, 373-378.	3.7	27
107	Protein crystallization analysis on the World Community Grid. Journal of Structural and Functional Genomics, 2010, 11, 61-69.	1.2	40
108	Crystal cookery $\hat{a}\in$ using high-throughput technologies and the grocery store as a teaching tool. Journal of Applied Crystallography, 2010, 43, 1189-1207.	4.5	7
109	Structure of the <i>Escherichia coli </i> RNA polymerase α subunit C-terminal domain. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 806-812.	2,5	10
110	Purification, crystallization and preliminary X-ray diffraction analysis of Cif, a virulence factor secreted byPseudomonas aeruginosa. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 26-28.	0.7	17
111	Improving the diffraction of full-length human selenomethionyl metavinculin crystals by streak-seeding. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1617-1620.	0.7	3

#	Article	IF	CITATIONS
112	The shortâ€chain oxidoreductase Q9HYA2 from <i>Pseudomonas aeruginosa</i> PAO1 contains an atypical catalytic center. Protein Science, 2010, 19, 1097-1103.	7.6	1
113	Sequence fingerprint and structural analysis of the SCOR enzyme A3DFK9 from <i>Clostridium thermocellum</i> . Proteins: Structure, Function and Bioinformatics, 2010, 78, 603-613.	2.6	1
114	Crystal structure of a designed tetratricopeptide repeat module in complex with its peptide ligand. FEBS Journal, 2010, 277, 1058-1066.	4.7	44
115	Structural Basis of Fatty Acid Substrate Binding to Cyclooxygenase-2. Journal of Biological Chemistry, 2010, 285, 22152-22163.	3.4	132
116	Present and future of membrane protein structure determination by electron crystallography. Advances in Protein Chemistry and Structural Biology, 2010, 81, 33-60.	2.3	24
117	Protein Crystallization Using Microfluidic Technologies Based on Valves, Droplets, and SlipChip. Annual Review of Biophysics, 2010, 39, 139-158.	10.0	166
118	A Cooperative <i>Escherichia coli</i> Aspartate Transcarbamoylase without Regulatory Subunits,. Biochemistry, 2010, 49, 7694-7703.	2.5	6
119	A Conserved Mode of Protein Recognition and Binding in a ParDâ^'ParE Toxinâ^'Antitoxin Complex. Biochemistry, 2010, 49, 2205-2215.	2.5	76
120	Prediction of protein crystallization outcome using a hybrid method. Journal of Structural Biology, 2010, 171, 64-73.	2.8	17
121	The structure of tryptophanyl-tRNA synthetase from Giardia lamblia reveals divergence from eukaryotic homologs. Journal of Structural Biology, 2010, 171, 238-243.	2.8	12
122	The high-throughput protein sample production platform of the Northeast Structural Genomics Consortium. Journal of Structural Biology, 2010, 172, 21-33.	2.8	125
123	The Crystal Structure and Activity of a Putative Trypanosomal Nucleoside Phosphorylase Reveal It to be a Homodimeric Uridine Phosphorylase. Journal of Molecular Biology, 2010, 396, 1244-1259.	4.2	16
124	X-ray crystallography of chemical compounds. Life Sciences, 2010, 86, 585-589.	4.3	29
125	Structural Basis for Mechanical Force Regulation of the Adhesin FimH via Finger Trap-like \hat{I}^2 Sheet Twisting. Cell, 2010, 141, 645-655.	28.9	239
126	Crystal structure of the aspartyl-tRNA synthetase from Entamoeba histolytica. Molecular and Biochemical Parasitology, 2010, 169, 95-100.	1.1	14
127	Robotic Liquid Handling System for Microdispensing of Highly Viscous Reagent. , 2011, , .		1
128	Optimization of Protein Crystallization: The OptiCryst Project. Crystal Growth and Design, 2011, 11, 2112-2121.	3.0	13
129	Structural Characterization and High-Throughput Screening of Inhibitors of PvdQ, an NTN Hydrolase Involved in Pyoverdine Synthesis. ACS Chemical Biology, 2011, 6, 1277-1286.	3.4	83

#	ARTICLE	IF	CITATIONS
130	SLS Crystallization Platform at Beamline X06DAâ€"A Fully Automated Pipeline Enabling ⟨i⟩in Situ⟨ i⟩ X-ray Diffraction Screening. Crystal Growth and Design, 2011, 11, 916-923.	3.0	88
131	What's in a Drop? Correlating Observations and Outcomes to Guide Macromolecular Crystallization Experiments. Crystal Growth and Design, 2011, 11, 651-663.	3.0	52
132	The Crystal Structures of Eukaryotic Phosphofructokinases from Baker's Yeast and Rabbit Skeletal Muscle. Journal of Molecular Biology, 2011, 407, 284-297.	4.2	45
133	One plate, two plates, a thousand plates. How crystallisation changes with large numbers of samples. Methods, 2011, 55, 73-80.	3.8	26
134	Structure determination of glycogen synthase kinase-3 from Leishmania major and comparative inhibitor structure–activity relationships with Trypanosoma brucei GSK-3. Molecular and Biochemical Parasitology, 2011, 176, 98-108.	1.1	35
135	Large-scale experimental studies show unexpected amino acid effects on protein expression and solubility in vivo in E. coli. Microbial Informatics and Experimentation, 2011, 1, 6.	7.6	30
136	CrysPage: a program for displaying images of crystallization trials, rapid comparisons and analysis. Journal of Applied Crystallography, 2011, 44, 1130-1131.	4.5	1
137	Purification, crystallization and preliminary X-ray diffraction of the G3BP1 NTF2-like domain. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 48-50.	0.7	6
138	Crystallization and preliminary diffraction analysis of the CAL PDZ domain in complex with a selective peptide inhibitor. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 600-603.	0.7	10
139	Purification and crystallization of Bacillus subtilis NrnA, a novel enzyme involved in nanoRNA degradation. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1235-1238.	0.7	4
140	Crystallization and preliminary X-ray diffraction analysis of Sfh3, a member of the Sec14 protein superfamily. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1239-1243.	0.7	12
141	Small angle Xâ€ray scattering as a complementary tool for highâ€throughput structural studies. Biopolymers, 2011, 95, 517-530.	2.4	69
142	Combining in-situ proteolysis and microseed matrix screening to promote crystallization of PrPc-nanobody complexes. Protein Engineering, Design and Selection, 2011, 24, 737-741.	2.1	17
143	Structure of Human C8 Protein Provides Mechanistic Insight into Membrane Pore Formation by Complement. Journal of Biological Chemistry, 2011, 286, 17585-17592.	3.4	94
144	The Transition from Closed to Open Conformation of Treponema pallidum Outer Membrane-associated Lipoprotein TP0453 Involves Membrane Sensing and Integration by Two Amphipathic Helices. Journal of Biological Chemistry, 2011, 286, 41656-41668.	3.4	24
145	DNA Repair and Global Sumoylation Are Regulated by Distinct Ubc9 Noncovalent Complexes. Molecular and Cellular Biology, 2011, 31, 2299-2310.	2.3	51
146	Structural conservation of an ancient tRNA sensor in eukaryotic glutaminyl-tRNA synthetase. Nucleic Acids Research, 2012, 40, 3723-3731.	14.5	14
147	Trapping and structure determination of an intermediate in the allosteric transition of aspartate transcarbamoylase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7741-7746.	7.1	7

#	Article	IF	CITATIONS
148	The Structure of Vimentin Linker 1 and Rod 1B Domains Characterized by Site-directed Spin-labeling Electron Paramagnetic Resonance (SDSL-EPR) and X-ray Crystallography. Journal of Biological Chemistry, 2012, 287, 28349-28361.	3.4	55
149	Perspectives on High-Throughput Technologies Applied to Protein Crystallization. Protein and Peptide Letters, 2012, 19, 778-783.	0.9	3
150	Crystal Structures of <i>Xanthomonas campestris</i> OleA Reveal Features That Promote Head-to-Head Condensation of Two Long-Chain Fatty Acids. Biochemistry, 2012, 51, 4138-4146.	2.5	26
151	Crystal structure of GAP50, the anchor of the invasion machinery in the inner membrane complex of Plasmodium falciparum. Journal of Structural Biology, 2012, 178, 61-73.	2.8	28
152	Structure–activity correlations of variant forms of the B pentamer of <i>Escherichia coli</i> type II heat-labile enterotoxin LT-IIb with Toll-like receptor 2 binding. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1604-1612.	2.5	9
153	1.4 X-Ray Crystallography: Crystallization. , 2012, , 34-63.		O
154	Crystallization and preliminary X-ray crystallographic studies of the outer membrane cytochrome OmcA fromShewanella oneidensisMR-1. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 53-55.	0.7	0
155	Crystal structure of the extracellular domain of human myelin protein zero. Proteins: Structure, Function and Bioinformatics, 2012, 80, 307-313.	2.6	23
156	A universal indicator dye pH assay for crystallization solutions and other high-throughput applications. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1003-1009.	2.5	13
157	Protein Modeling. , 2012, , 1095-1125.		0
158	Structural and Functional Investigation of the Intermolecular Interaction between NRPS Adenylation and Carrier Protein Domains. Chemistry and Biology, 2012, 19, 188-198.	6.0	130
159	<i>PROSPERO (i): online prediction of crystallographic success from experimental results and sequence. Journal of Applied Crystallography, 2012, 45, 598-602.</i>	4.5	0
160	On the need for an international effort to capture, share and use crystallization screening data. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 253-258.	0.7	38
161	Electron Crystallography of Soluble and Membrane Proteins. Methods in Molecular Biology, 2013, , .	0.9	8
162	Structureâ€based engineering of streptavidin monomer with a reduced biotin dissociation rate. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1621-1633.	2.6	44
163	The Structure of Yeast Glutaminyl-tRNA Synthetase and Modeling of Its Interaction with tRNA. Journal of Molecular Biology, 2013, 425, 2480-2493.	4.2	13
164	Energetic Coupling between an Oxidizable Cysteine and the Phosphorylatable N-Terminus of Human Liver Pyruvate Kinase. Biophysical Journal, 2013, 104, 380a.	0.5	13
165	Structural and Functional Analysis of the Human Nuclear Xenobiotic Receptor PXR in Complex with RXRα. Journal of Molecular Biology, 2013, 425, 2561-2577.	4.2	49

#	Article	IF	CITATIONS
166	Energetic Coupling between an Oxidizable Cysteine and the Phosphorylatable N-Terminus of Human Liver Pyruvate Kinase. Biochemistry, 2013, 52, 466-476.	2.5	37
167	Structure determination of the functional domain interaction of a chimeric nonribosomal peptide synthetase from a challenging crystal with noncrystallographic translational symmetry. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1482-1492.	2.5	23
168	Computational Screening of the Human TF-Glycome Provides a Structural Definition for the Specificity of Anti-Tumor Antibody JAA-F11. PLoS ONE, 2013, 8, e54874.	2.5	29
169	A MEMS Flow Sensor for Self-adjusted Precise Non-Contact Liquid Dispensing. Research Journal of Applied Sciences, Engineering and Technology, 2013, 5, 962-969.	0.1	0
171	Greenâ€lighting green fluorescent protein: Faster and more efficient folding by eliminating a <i>cis–trans</i> peptide isomerization event. Protein Science, 2014, 23, 400-410.	7.6	8
172	Automation in biological crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 686-696.	0.8	29
174	A high-throughput colourimetric method for the determination of pH in crystallization screens. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2367-2375.	2.5	4
175	Introduction to protein crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 2-20.	0.8	291
176	Identifying, studying and making good use of macromolecular crystals. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 993-1008.	0.8	23
177	Signature Motifs Identify an Acinetobacter Cif Virulence Factor with Epoxide Hydrolase Activity. Journal of Biological Chemistry, 2014, 289, 7460-7469.	3.4	19
178	Design of activated serine–containing catalytic triads with atomic-level accuracy. Nature Chemical Biology, 2014, 10, 386-391.	8.0	68
179	Using Time Courses To Enrich the Information Obtained from Images of Crystallization Trials. Crystal Growth and Design, 2014, 14, 261-269.	3.0	15
180	A new view on crystal harvesting. Journal of Applied Crystallography, 2014, 47, 1158-1161.	4.5	2
181	The detection and subsequent volume optimization of biological nanocrystals. Structural Dynamics, 2015, 2, 041710.	2.3	5
182	Trimeric Structure of (+)-Pinoresinol-forming Dirigent Protein at 1.95 \tilde{A} Resolution with Three Isolated Active Sites. Journal of Biological Chemistry, 2015, 290, 1308-1318.	3.4	56
183	Structural Basis for Dimerization and DNA Binding of Transcription Factor FLI1. Biochemistry, 2015, 54, 7365-7374.	2.5	17
184	Crystal Structure of the Minor Pilin CofB, the Initiator of CFA/III Pilus Assembly in Enterotoxigenic Escherichia coli. Journal of Biological Chemistry, 2015, 290, 25805-25818.	3.4	20
185	Structure of inorganic pyrophosphatase from Staphylococcus aureus reveals conformational flexibility of the active site. Journal of Structural Biology, 2015, 189, 81-86.	2.8	16

#	Article	IF	CITATIONS
186	The accurate assessment of small-angle X-ray scattering data. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 45-56.	2.5	34
187	Using isoelectric point to determine the pH for initial protein crystallization trials. Bioinformatics, 2015, 31, 1444-1451.	4.1	51
188	Analysis and Control of Protein Crystallization Using Short Peptide Tags That Change Solubility without Affecting Structure, Thermal Stability, and Function. Crystal Growth and Design, 2015, 15, 2703-2711.	3.0	22
189	Structures of lactate dehydrogenase A (LDHA) in apo, ternary and inhibitor-bound forms. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 185-195.	2.5	49
190	Crystal structure of halogenase PltA from the pyoluteorin biosynthetic pathway. Journal of Structural Biology, 2015, 192, 349-357.	2.8	28
191	Transcriptional Regulation, Metal Binding Properties and Structure of Pden1597, an Unusual Zinc Transport Protein from Paracoccus denitrificans. Journal of Biological Chemistry, 2015, 290, 11878-11889.	3.4	21
192	Structure of shikimate kinase, an <i>in vivo</i> essential metabolic enzyme in the nosocomial pathogen <i>Acinetobacter baumannii</i> , in complex with shikimate. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1736-1744.	2.5	7
193	A community resource of experimental data for <scp>NMR</scp> / <scp>X</scp> â€ray crystal structure pairs. Protein Science, 2016, 25, 30-45.	7.6	24
194	Structures of a Nonribosomal Peptide Synthetase Module Bound to MbtH-like Proteins Support a Highly Dynamic Domain Architecture. Journal of Biological Chemistry, 2016, 291, 22559-22571.	3.4	97
195	Screening of Cryoprotectants and the Multistep Soaking Method. Springer Protocols, 2016, , 139-151.	0.3	2
196	A Second RNA-Binding Site in the NS1 Protein of Influenza B Virus. Structure, 2016, 24, 1562-1572.	3.3	12
197	Structural basis for PECAM-1 homophilic binding. Blood, 2016, 127, 1052-1061.	1.4	49
198	Structure of the Neisseria meningitidis Type IV pilus. Nature Communications, 2016, 7, 13015.	12.8	124
199	N,N,O and N,O,N Meridional cis Coordination of Two Guanines to Copper(II) by d(CGCGCG) ₂ . Inorganic Chemistry, 2016, 55, 6130-6140.	4.0	10
200	Structural and Functional Characterization of Aerobactin Synthetase lucA from a Hypervirulent Pathotype of <i>Klebsiella pneumoniae</i>). Biochemistry, 2016, 55, 3559-3570.	2.5	21
201	The Response Regulator BfmR Is a Potential Drug Target for Acinetobacter baumannii. MSphere, 2016, 1, \cdot	2.9	91
202	Structures of two distinct conformations of holo-non-ribosomal peptide synthetases. Nature, 2016, 529, 235-238.	27.8	210
203	Use of Multiple Cryoprotectants to Improve Diffraction Quality from Protein Crystals. Crystal Growth and Design, 2016, 16, 1565-1571.	3.0	10

#	Article	IF	CITATIONS
204	Crystal structure of 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase from the ESKAPE pathogen <i>Acinetobacter baumannii</i> . Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 179-187.	0.8	11
205	Xâ€ray crystal structure of the Nâ€terminal region of <scp>M</scp> oloney murine leukemia virus integrase and its implications for viral DNA recognition. Proteins: Structure, Function and Bioinformatics, 2017, 85, 647-656.	2.6	9
206	Protein Modeling. , 2017, , 1589-1626.		1
207	Principles for designing proteins with cavities formed by curved \hat{l}^2 sheets. Science, 2017, 355, 201-206.	12.6	117
208	Crystallographic structure of recombinant Lactococcus lactis prolidase to support proposed structure-function relationships. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 473-480.	2.3	8
209	Protein Crystallization. Methods in Molecular Biology, 2017, 1607, 17-50.	0.9	37
210	Efficient Screening Methodology for Protein Crystallization Based on the Counter-Diffusion Technique. Crystal Growth and Design, 2017, 17, 6780-6786.	3.0	14
211	Data Analytics for Protein Crystallization. Computational Biology, 2017, , .	0.2	10
212	Introduction to Protein Crystallization. Computational Biology, 2017, , 1-20.	0.2	0
213	X-Ray Diffraction in Biology: How Can We See DNA and Proteins in Three Dimensions?., 0, , .		4
214	Automated Protocols for Macromolecular Crystallization at the MRC Laboratory of Molecular Biology. Journal of Visualized Experiments, 2018, , .	0.3	11
215	Structural and functional delineation of aerobactin biosynthesis in hypervirulent Klebsiella pneumoniae. Journal of Biological Chemistry, 2018, 293, 7841-7852.	3.4	33
216	Structure and Enzymatic Properties of an Unusual Cysteine Tryptophylquinone-Dependent Glycine Oxidase from <i>Pseudoalteromonas luteoviolacea</i>). Biochemistry, 2018, 57, 1155-1165.	2.5	18
217	Harnessing insulin- and leptin-induced oxidation of PTP1B for therapeutic development. Nature Communications, 2018, 9, 283.	12.8	39
218	Expression system for structural and functional studies of human glycosylation enzymes. Nature Chemical Biology, 2018, 14, 156-162.	8.0	182
219	In Silico Screen and Structural Analysis Identifies Bacterial Kinase Inhibitors which Act with \hat{l}^2 -Lactams To Inhibit Mycobacterial Growth. Molecular Pharmaceutics, 2018, 15, 5410-5426.	4.6	22
220	Structural analysis reveals pathomechanisms associated with pseudoxanthoma elasticum–causing mutations in the ABCC6 transporter. Journal of Biological Chemistry, 2018, 293, 15855-15866.	3.4	8
221	Crystal structures of AztD provide mechanistic insights into direct zinc transfer between proteins. Communications Biology, 2019, 2, 308.	4.4	7

#	Article	IF	CITATIONS
222	Gravity on Crystallization of Lysozyme: Slower or Faster?. Crystal Growth and Design, 2019, 19, 7402-7410.	3.0	6
223	Catalytic mechanism for the conversion of salicylate into catechol by the flavin-dependent monooxygenase salicylate hydroxylase. International Journal of Biological Macromolecules, 2019, 129, 588-600.	7.5	26
224	A systematic comparison of sitting and hanging-drop crystallization using traditional and cross-diffusion microbatch crystallization plates. Journal of Crystal Growth, 2019, 521, 1-8.	1.5	7
225	<i>BLAST</i> ing away preconceptions in crystallization trials. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 184-192.	0.8	12
226	Human Glycerol 3-Phosphate Dehydrogenase: X-ray Crystal Structures That Guide the Interpretation of Mutagenesis Studies. Biochemistry, 2019, 58, 1061-1073.	2.5	15
227	Unusual zwitterionic catalytic site of SARS–CoV-2 main protease revealed by neutron crystallography. Journal of Biological Chemistry, 2020, 295, 17365-17373.	3.4	97
228	Structural Characterization of Sphingomonas sp. KT-1 PahZ1-Catalyzed Biodegradation of Thermally Synthesized Poly(aspartic acid). ACS Sustainable Chemistry and Engineering, 2020, , .	6.7	1
229	Crystallization of ApoA1 and ApoE4 Nanolipoprotein Particles and Initial XFEL-Based Structural Studies. Crystals, 2020, 10, 886.	2.2	6
230	Pterocarpan synthase (PTS) structures suggest a common quinone methide–stabilizing function in dirigent proteins and proteins with dirigent-like domains. Journal of Biological Chemistry, 2020, 295, 11584-11601.	3.4	16
231	A Searchable Database of Crystallization Cocktails in the PDB: Analyzing the Chemical Condition Space. Patterns, 2020, 1, 100024.	5.9	8
232	Visual-X2: interactive visualization and analysis tool for protein crystallization. Network Modeling Analysis in Health Informatics and Bioinformatics, 2020, 9, 1.	2.1	4
233	Structural plasticity of SARS-CoV-2 3CL Mpro active site cavity revealed by room temperature X-ray crystallography. Nature Communications, 2020, 11, 3202.	12.8	334
234	<i>Polo</i> : an open-source graphical user interface for crystallization screening. Journal of Applied Crystallography, 2021, 54, 673-679.	4.5	3
235	Direct Observation of Protonation State Modulation in SARS-CoV-2 Main Protease upon Inhibitor Binding with Neutron Crystallography. Journal of Medicinal Chemistry, 2021, 64, 4991-5000.	6.4	36
237	Lead compounds for the development of SARS-CoV-2 3CL protease inhibitors. Nature Communications, 2021, 12, 2016.	12.8	65
238	Structure of Blood Coagulation Factor VIII in Complex With an Anti-C2 Domain Non-Classical, Pathogenic Antibody Inhibitor. Frontiers in Immunology, 2021, 12, 697602.	4.8	3
239	Sphingomonas sp. KT-1 PahZ2 Structure Reveals a Role for Conformational Dynamics in Peptide Bond Hydrolysis. Journal of Physical Chemistry B, 2021, 125, 5722-5739.	2.6	1
240	The development of Nanosota-1 as anti-SARS-CoV-2 nanobody drug candidates. ELife, 2021, 10, .	6.0	42

#	ARTICLE	IF	CITATIONS
241	Conformational flexibility determines the Nf2/merlin tumor suppressor functions. Matrix Biology Plus, 2021, 12, 100074.	3.5	10
243	X-ray and Neutron Diffraction Approaches to the Structural Analysis of Protein-Lipid Interactions. , 2006, , 63-110.		1
244	Protein Nanocrystallization. , 2006, , 1-25.		2
245	Structural Genomics of Pathogenic Protozoa: an Overview. Methods in Molecular Biology, 2008, 426, 497-513.	0.9	38
246	High-Throughput Methods for Electron Crystallography. Methods in Molecular Biology, 2013, 955, 273-296.	0.9	4
250	Structural insights into conformational switching in latency-associated peptide between transforming growth factor β-1 bound and unbound states. IUCrJ, 2020, 7, 238-252.	2.2	5
251	Room-temperature neutron and X-ray data collection of 3CL M ^{pro} from SARS-CoV-2. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 483-487.	0.8	21
252	A Novel Dimeric Inhibitor Targeting Beta2GPI in Beta2GPI/Antibody Complexes Implicated in Antiphospholipid Syndrome. PLoS ONE, 2010, 5, e15345.	2.5	27
253	Comparing Chemistry to Outcome: The Development of a Chemical Distance Metric, Coupled with Clustering and Hierarchal Visualization Applied to Macromolecular Crystallography. PLoS ONE, 2014, 9, e100782.	2.5	14
254	SAXS studies of X-ray induced disulfide bond damage: Engineering high-resolution insight from a low-resolution technique. PLoS ONE, 2020, 15, e0239702.	2.5	9
255	Michaelis-like complex of SARS-CoV-2 main protease visualized by room-temperature X-ray crystallography. IUCrJ, 2021, 8, 973-979.	2.2	25
256	Efficient Macromolecular Crystallization Using Microfluidics and Randomized Design of Screening Reagents. Methods in Molecular Biology, 2008, 426, 387-402.	0.9	1
258	Protein Modeling., 2015,, 1-37.		0
260	The use of haptic interfaces and web services in crystallography: an application for a `screen to beam' interface. Journal of Applied Crystallography, 2016, 49, 2082-2090.	4.5	1
262	Structural, Electronic, and Electrostatic Determinants for Inhibitor Binding to Subsites S1 and S2 in SARS-CoV-2 Main Protease. Journal of Medicinal Chemistry, 2021, 64, 17366-17383.	6.4	32
263	The minor pilin PilV provides a conserved adhesion site throughout the antigenically variable meningococcal type IV pilus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118 , .	7.1	10
266	High-Throughput Virtual Screening and Validation of a SARS-CoV-2 Main Protease Noncovalent Inhibitor. Journal of Chemical Information and Modeling, 2022, 62, 116-128.	5.4	54
268	Conformational flexibility in the zinc solute-binding protein ZnuA. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 128-134.	0.8	0

#	ARTICLE	IF	CITATIONS
269	Development of optimized drug-like small molecule inhibitors of the SARS-CoV-2 3CL protease for treatment of COVID-19. Nature Communications, 2022, 13, 1891.	12.8	45
270	Hit Expansion of a Noncovalent SARS-CoV-2 Main Protease Inhibitor. ACS Pharmacology and Translational Science, 2022, 5, 255-265.	4.9	17
271	Characterization of a patient-derived variant of GPX4 for precision therapy. Nature Chemical Biology, 2022, 18, 91-100.	8.0	41
272	Covalent narlaprevir- and boceprevir-derived hybrid inhibitors of SARS-CoV-2 main protease. Nature Communications, 2022, 13, 2268.	12.8	69
273	The enzyme pseudooxynicotine amine oxidase from Pseudomonas putida S16 is not an oxidase, but a dehydrogenase. Journal of Biological Chemistry, 2022, 298, 102251.	3.4	2
274	Pharmacologic Inhibition of NT5C2 Reverses Genetic and Nongenetic Drivers of 6-MP Resistance in Acute Lymphoblastic Leukemia. Cancer Discovery, 2022, 12, 2646-2665.	9.4	5
275	Computational identification of a systemic antibiotic for Gram-negative bacteria. Nature Microbiology, 2022, 7, 1661-1672.	13.3	42
276	Small-molecule allosteric inhibitors of GPX4. Cell Chemical Biology, 2022, 29, 1680-1693.e9.	5.2	21
277	Structure and Function of the Zinc Binding Protein ZrgA from Vibrio cholerae. International Journal of Molecular Sciences, 2023, 24, 548.	4.1	2
278	Al-Accelerated Design of Targeted Covalent Inhibitors for SARS-CoV-2. Journal of Chemical Information and Modeling, 2023, 63, 1438-1453.	5.4	4
279	20 years of crystal hits: progress and promise in ultrahigh-throughput crystallization screening. Acta Crystallographica Section D: Structural Biology, 2023, 79, 198-205.	2.3	3
280	The TINCR ubiquitin-like microprotein is a tumor suppressor in squamous cell carcinoma. Nature Communications, 2023, 14 , .	12.8	8
281	The Chemokine, CCL20, and Its Receptor, CCR6, in the Pathogenesis and Treatment of Psoriasis and Psoriatic Arthritis. Journal of Psoriasis and Psoriatic Arthritis, 0, , 247553032311591.	0.7	0
282	Polymer-based microfluidic device for on-chip counter-diffusive crystallization and <i>in situ</i> X-ray crystallography at room temperature. Lab on A Chip, 2023, 23, 2075-2090.	6.0	6
284	PYK-SubstitutionOME: an integrated database containing allosteric coupling, ligand affinity and mutational, structural, pathological, bioinformatic and computational information about pyruvate kinase isozymes. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	2
285	Directed evolution unlocks oxygen reactivity for a nicotine-degrading flavoenzyme. Nature Chemical Biology, $0, , .$	8.0	2
287	Dirigent isoflavene-forming PsPTS2: 3D structure, stereochemical, and kinetic characterization comparison with pterocarpan-forming PsPTS1 homolog in pea. Journal of Biological Chemistry, 2024, 300, 105647.	3.4	0
288	Structural basis for the allosteric behaviour and substrate specificity of Lactococcus lactis Prolidase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2024, 1872, 141000.	2.3	О

ARTICLE IF CITATIONS

289 Systematic enhancement of protein crystallization efficiency by bulk lysineâ€toâ€arginine (<scp>KR</scp>) 7.6 0

7.6 0