

Felix Frolow

List of Publications by Year in descending order

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76
papers

4,012
citations

201674

27
h-index

118850

62
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83
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docs citations

83
times ranked

4536
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel clostridial cell-surface hemicellulose-binding CBM3 proteins. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 95-104.	0.8	1
2	Directed Evolution of <i>Clostridium thermocellum</i> Î ² -Glucosidase A Towards Enhanced Thermostability. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4701.	4.1	26
3	Distinctive ligand-binding specificities of tandem PA14 biomass-sensory elements from <i>Clostridium thermocellum</i> and <i>Clostridium clariflavum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 917-930.	2.6	8
4	Light-emitting self-assembled peptide nucleic acids exhibit both stacking interactions and Watson-Crick base pairing. <i>Nature Nanotechnology</i> , 2015, 10, 353-360.	31.5	136
5	Standalone cohesin as a molecular shuttle in cellulosome assembly. <i>FEBS Letters</i> , 2015, 589, 1569-1576.	2.8	14
6	Crystal structure of the human mitochondrial chaperonin symmetrical football complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6044-6049.	7.1	92
7	Reassembly and co-crystallization of a family 9 processive endoglucanase from its component parts: structural and functional significance of the intermodular linker. <i>PeerJ</i> , 2015, 3, e1126.	2.0	29
8	Protein products obtained by site-preferred partial crosslinking in protein crystals and liberated by redissolution. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1296-1303.	3.3	7
9	Crystallization and structure determination of a symmetrical 'football' complex of the mammalian mitochondrial Hsp60-Hsp10 chaperonins. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 116-119.	0.8	26
10	Structural characterization of a novel autonomous cohesin from <i>Ruminococcus flavefaciens</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 450-456.	0.8	3
11	Fine-structural variance of family 3 carbohydrate-binding modules as extracellular biomass-sensing components of <i>Clostridium thermocellum</i> anti-Îf factors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 522-534.	2.5	26
12	Atypical Cohesin-Dockerin Complex Responsible for Cell Surface Attachment of Cellulosomal Components. <i>Journal of Biological Chemistry</i> , 2013, 288, 16827-16838.	3.4	38
13	Structure of a family 3a carbohydrate-binding module from the cellulosomal scaffoldin CipA of <i>Clostridium thermocellum</i> with flanking linkers: implications for cellulosome structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 733-737.	0.7	23
14	Crystal Structure of an Uncommon Cellulosome-Related Protein Module from <i>Ruminococcus flavefaciens</i> That Resembles Papain-Like Cysteine Peptidases. <i>PLoS ONE</i> , 2013, 8, e56138.	2.5	19
15	Crystallization and preliminary X-ray characterization of a type III cohesin-dockerin complex from the cellulosome system of <i>Ruminococcus flavefaciens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1116-1119.	0.7	4
16	Interactions Between Family 3 Carbohydrate Binding Modules (CBMs) and Cellulosomal Linker Peptides. <i>Methods in Enzymology</i> , 2012, 510, 247-259.	1.0	9
17	Structure of CBM3b of the major cellulosomal scaffoldin subunit ScaA from <i>Acetivibrio cellulolyticus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 8-13.	0.7	11
18	A single mutation reforms the binding activity of an adhesion-deficient family 3 carbohydrate-binding module. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 819-828.	2.5	16

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19	Scaffoldin-borne family 3b carbohydrate-binding module from the cellulosome of <i>Bacteroides cellulosolvens</i> : structural diversity and significance of calcium for carbohydrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 506-515.	2.5	18
20	Noncellulosomal cohesin from the hyperthermophilic archaeon <i>Archaeoglobus fulgidus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 50-60.	2.6	6
21	Restructuring protein crystals porosity for biotemplating by chemical modification of lysine residues. <i>Biotechnology and Bioengineering</i> , 2011, 108, 1-11.	3.3	10
22	Adjustment of Protein Crystal Porosity for Biotemplating: Chemical and Protein Engineering Tools. <i>AIP Conference Proceedings</i> , 2010, , .	0.4	1
23	Structure of a family 3b ² carbohydrate-binding module from the Cel9V glycoside hydrolase from <i>Clostridium thermocellum</i> : structural diversity and implications for carbohydrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 33-43.	2.5	18
24	Homology swapping of intrinsic secondary structural elements between cellulosomal types I and II cohesins and their effect on dockerin binding. <i>Pure and Applied Chemistry</i> , 2010, 82, 193-204.	1.9	1
25	Biochemical and Structural Properties of Chimeras Constructed by Exchange of Cofactor-Binding Domains in Alcohol Dehydrogenases from Thermophilic and Mesophilic Microorganisms. <i>Biochemistry</i> , 2010, 49, 1943-1953.	2.5	9
26	Modular Arrangement of a Cellulosomal Scaffoldin Subunit Revealed from the Crystal Structure of a Cohesin Dyad. <i>Journal of Molecular Biology</i> , 2010, 399, 294-305.	4.2	24
27	Thiol-disulfide organization in alliin lyase (alliinase) from garlic (<i>Allium sativum</i>). <i>Protein Science</i> , 2009, 18, 196-205.	7.6	26
28	Physical association of the catalytic and helper modules of a family 9 glycoside hydrolase is essential for activity. <i>FEBS Letters</i> , 2009, 583, 879-884.	2.8	42
29	Modification of protein crystal packing by systematic mutations of surface residues: Implications on biotemplating and crystal porosity. <i>Biotechnology and Bioengineering</i> , 2009, 104, 444-457.	3.3	13
30	Cohesin diversity revealed by the crystal structure of the anchoring cohesin from <i>Ruminococcus flavefaciens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 699-709.	2.6	16
31	Crystallization and preliminary X-ray analysis of a cohesin-like module from AF2375 of the archaeon <i>Archaeoglobus fulgidus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 275-278.	0.7	1
32	Intermodular Linker Flexibility Revealed from Crystal Structures of Adjacent Cellulosomal Cohesins of <i>Acetivibrio cellulolyticus</i> . <i>Journal of Molecular Biology</i> , 2009, 391, 86-97.	4.2	23
33	Structural basis for the enhanced thermal stability of alcohol dehydrogenase mutants from the mesophilic bacterium <i>Clostridium beijerinckii</i> : contribution of salt bridging. <i>Protein Science</i> , 2009, 11, 2561-2574.	7.6	48
34	Crystallization and preliminary X-ray analysis of <i>Acetivibrio cellulolyticus</i> cellulosomal type II cohesin module: two versions having different linker lengths. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 58-61.	0.7	4
35	Preliminary X-ray characterization of a novel type of anchoring cohesin from the cellulosome of <i>Ruminococcus flavefaciens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 77-80.	0.7	5
36	Thermal stabilization of the protozoan <i>Entamoeba histolytica</i> alcohol dehydrogenase by a single proline substitution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 711-719.	2.6	17

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37	Two Structures of Alliinase from <i>Allium sativum</i> L.: Apo Form and Ternary Complex with Aminoacrylate Reaction Intermediate Covalently Bound to the PLP Cofactor. <i>Journal of Molecular Biology</i> , 2007, 366, 611-625.	4.2	55
38	Elucidation of the mechanism and end products of glutaraldehyde crosslinking reaction by X-ray structure analysis. <i>Biotechnology and Bioengineering</i> , 2007, 98, 711-718.	3.3	169
39	Crystallization and preliminary diffraction studies of CBM3b of cellobiohydrolase 9A from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1044-1047.	0.7	7
40	Structure of alcohol dehydrogenase from <i>Entamoeba histolytica</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 541-547.	2.5	6
41	Monitoring the stability of crosslinked protein crystals biotemplates: A feasibility study. <i>Biotechnology and Bioengineering</i> , 2006, 94, 1005-1011.	3.3	23
42	Crystal Structure of a Type-II Cohesin Module from the <i>Bacteroides cellulosolvens</i> Cellulosome Reveals Novel and Distinctive Secondary Structural Elements. <i>Journal of Molecular Biology</i> , 2005, 348, 1-12.	4.2	31
43	Crystal structure of yeast V _o -ATPase subunit C reveals its stator function. <i>EMBO Reports</i> , 2004, 5, 1148-1152.	4.5	131
44	The ternary complex of <i>Pseudomonas aeruginosa</i> alcohol dehydrogenase with NADH and ethylene glycol. <i>Protein Science</i> , 2004, 13, 1547-1556.	7.6	44
45	Light-Harvesting Features Revealed by the Structure of Plant Photosystem I. <i>Photosynthesis Research</i> , 2004, 81, 239-250.	2.9	49
46	Expression, crystallization and phasing of vacuolar H ⁺ -ATPase subunit C (Vma5p) of <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1906-1909.	2.5	6
47	Evolution of photosystem I - from symmetry through pseudosymmetry to asymmetry. <i>FEBS Letters</i> , 2004, 564, 274-280.	2.8	154
48	Evolution of Organized Lariat Ether Alcohol and Diol Hydrate Macrostructures in the Solid State. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2003, 45, 251-255.	1.6	0
49	Preliminary X-ray characterization and phasing of a type II cohesin domain from the cellulosome of <i>Acetivibrio cellulolyticus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1670-1673.	2.5	22
50	Crystallization and initial X-ray diffraction studies of higher plant photosystem I. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1824-1827.	2.5	23
51	Crystal structure of plant photosystem I. <i>Nature</i> , 2003, 426, 630-635.	27.8	785
52	Thermophilic alcohol dehydrogenase from the mesophile <i>Entamoeba histolytica</i> : crystallization and preliminary X-ray characterization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 546-548.	2.5	2
53	Alliin lyase (alliinase) from garlic (<i>Allium sativum</i>): crystallization and preliminary X-ray characterization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1335-1337.	2.5	6
54	Structure of a family IIIa scaffoldin CBD from the cellulosome of <i>Clostridium cellulolyticum</i> at 2.2 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1560-1568.	2.5	48

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55	Halophilic enzymes: proteins with a grain of salt. <i>Biophysical Chemistry</i> , 2000, 86, 155-164.	2.8	360
56	Oligomeric integrity—the structural key to thermal stability in bacterial alcohol dehydrogenases. <i>Protein Science</i> , 1999, 8, 1241-1249.	7.6	39
57	Self-Assembly of a Tetrahedral Lectin into Predesigned Diamondlike Protein Crystals. <i>Angewandte Chemie - International Edition</i> , 1999, 38, 2363-2366.	13.8	74
58	Self-Assembly of a Tetrahedral Lectin into Predesigned Diamondlike Protein Crystals. <i>Angewandte Chemie - International Edition</i> , 1999, 38, 2363-2366.	13.8	3
59	Enhanced thermal stability of <i>Clostridium beijerinckii</i> alcohol dehydrogenase after strategic substitution of amino acid residues with prolines from the homologous thermophilic <i>Thermoanaerobacter brockii</i> alcohol dehydrogenase. <i>Protein Science</i> , 1998, 7, 1156-1163.	7.6	100
60	NADP-dependent bacterial alcohol dehydrogenases: crystal structure, cofactor-binding and cofactor specificity of the ADHs of <i>Clostridium beijerinckii</i> and <i>Thermoanaerobacter brockii</i> 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1998, 278, 967-981.	4.2	179
61	A cohesin domain from <i>Clostridium thermocellum</i> : the crystal structure provides new insights into cellulosome assembly. <i>Structure</i> , 1997, 5, 381-390.	3.3	119
62	Crystallization and preliminary X-ray analysis of a cohesin domain of the cellulosome from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 114-115.	2.5	6
63	Expression, purification and crystallization of a cohesin domain from the cellulosome of <i>Clostridium thermocellum</i> . <i>Journal of Biotechnology</i> , 1996, 51, 243-249.	3.8	12
64	Insights into protein adaptation to a saturated salt environment from the crystal structure of a halophilic 2Fe-2S ferredoxin. <i>Nature Structural Biology</i> , 1996, 3, 452-458.	9.7	207
65	Crystal structures of dibenzo-14-crown-4 alcohol and diol monohydrates. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 1995, 23, 85-98.	1.6	0
66	Comparison of the crystal structures of genetically engineered human manganese superoxide dismutase and manganese superoxide dismutase from <i>Thermus thermophilus</i> : Differences in dimer-dimer interaction. <i>Protein Science</i> , 1993, 2, 814-825.	7.6	57
67	Crystal Parameters of an Alcohol Dehydrogenase from the Extreme Thermophile <i>Thermoanaerobium brockii</i> . <i>Journal of Molecular Biology</i> , 1993, 230, 353-355.	4.2	9
68	Three-dimensional structures of bulge-containing DNA fragments. <i>Journal of Molecular Biology</i> , 1992, 225, 397-431.	4.2	94
69	Crown ether alcohols as bifunctional ligands for simultaneous cation complexation and anion solvation. <i>Journal of the American Chemical Society</i> , 1991, 113, 6570-6574.	13.7	26
70	The conformation of the DNA double helix in the crystal is dependent on its environment. <i>Nature</i> , 1989, 342, 456-460.	27.8	123
71	Characterization of crystals of genetically engineered human manganese superoxide dismutase. <i>Journal of Molecular Biology</i> , 1989, 206, 787-788.	4.2	24
72	The three-dimensional structure of a DNA duplex containing looped-out bases. <i>Nature</i> , 1988, 334, 82-84.	27.8	103

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73	Withanolide Y, a withanolide from a hybrid of <i>Withania somnifera</i> . <i>Phytochemistry</i> , 1987, 26, 1797-1800.	2.9	23
74	Chlorinated withanolides from <i>Withania somnifera</i> and <i>Acnistus breviflorus</i> . <i>Phytochemistry</i> , 1981, 20, 2547-2552.	2.9	54
75	Withaperuvin and 4-deoxyphysalolactone, two new ergostane-type steroids from <i>Physalis peruviana</i> (Solanaceae). <i>Journal of the Chemical Society Perkin Transactions 1</i> , 1981, , 1029.	0.9	27
76	Template Polymerization of Rhodium(I) with Rigid Bent Diisocyanide Ligands. <i>Angewandte Chemie International Edition in English</i> , 1980, 19, 633-634.	4.4	23