Enrico Stura

List of Publications by Year
in descending order

140 papers	11,166 citations	36203 51 h-index	30010 103 g-index
140 all docs	140 docs citations	140 times ranked	10183 citing authors

#	Article	IF	Citations
1	Crystal structures of two viral peptides in complex with murine MHC class I H-2Kb. Science, 1992, 257, 919-927.	6.0	877
2	Functional Mimicry of a Protein Hormone by a Peptide Agonist: The EPO Receptor Complex at 2.8 A. Science, 1996, 273, 464-471.	6.0	621
3	Crystal Structure of Mouse CD1: An MHC-Like Fold with a Large Hydrophobic Binding Groove. Science, 1997, 277, 339-345.	6.0	596
4	Crystallographic Evidence for Preformed Dimers of Erythropoietin Receptor Before Ligand Activation. Science, 1999, 283, 987-990.	6.0	579
5	Structure of a flavivirus envelope glycoprotein in its low-pH-induced membrane fusion conformation. EMBO Journal, 2004, 23, 728-738.	3.5	526
6	Crystal structure of a Staphylococcus aureus protein A domain complexed with the Fab fragment of a human IgM antibody: Structural basis for recognition of B-cell receptors and superantigen activity. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 5399-5404.	3.3	443
7	Immune Versus Natural Selection: Antibody Aldolases with Enzymic Rates But Broader Scope. Science, 1997, 278, 2085-2092.	6.0	402
8	Crystal structure of the principal neutralization site of HIV-1. Science, 1994, 264, 82-85.	6.0	265
9	Crystal structure of an H-2Kb-ovalbumin peptide complex reveals the interplay of primary and secondary anchor positions in the major histocompatibility complex binding groove.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 2479-2483.	3.3	240
10	Crystal Structure of Alkaline Phosphatase from Human Placenta at 1.8 Ã... Resolution. Journal of Biological Chemistry, 2001, 276, 9158-9165.	1.6	234
11	Crystal structure of the human urokinase plasminogen activator receptor bound to an antagonist peptide. EMBO Journal, 2005, 24, 1655-1663.	3.5	213
12	Crystal structure of a human immunodeficiency virus type 1 neutralizing antibody, 50.1, in complex with its V3 loop peptide antigen.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 6325-6329.	3.3	211
13	An antagonist peptideâ€“EPO receptor complex suggests that receptor dimerization is not sufficient for activation. Nature Structural Biology, 1998, 5, 993-1004.	9.7	204
14	Denmotoxin, a Three-finger Toxin from the Colubrid Snake Boiga dendrophila (Mangrove Catsnake) with Bird-specific Activity. Journal of Biological Chemistry, 2006, 281, 29030-29041.	1.6	183
15	Routes to catalysis: structure of a catalytic antibody and comparison with its natural counterpart. Science, 1994, 263, 646-652.	6.0	182
16	Structural Evidence for a Functional Role of Human Tissue Nonspecific Alkaline Phosphatase in Bone Mineralization. Journal of Biological Chemistry, 2001, 276, 31171-31178.	1.6	182
17	Structure and mutational analysis of Rab GDP-dissociation inhibitor. Nature, 1996, 381, 42-48.	13.7	169
18	Irditoxin, a novel covalently linked heterodimeric threeâ€finger toxin with high taxonâ€specific neurotoxicity. FASEB Journal, 2009, 23, 534-545.	0.2	165

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19	Three-dimensional Structure of an Anti-steroid Fabâ€² and Progesterone-Fabâ€² Complex. Journal of Molecular Biology, 1993, 231, 103-118.	2.0	154
20	Applications of the streak seeding technique in protein crystallization. Journal of Crystal Growth, 1991, 110, 270-282.	0.7	147
21	Dual conformations for the HIV-1 gp120 V3 loop in complexes with different neutralizing Fabs. Structure, 1999, 7, 131-142.	1.6	145
22	Crystal structure of Aplysia ADP ribosyl cyclase, a homologue of the bifunctional ectozyme CD38. Nature Structural Biology, 1996, 3, 957-964.	9.7	142
23	An Antibody exo Diels-Alderase Inhibitor Complex at 1.95 Angstrom Resolution. Science, 1998, 279, 1934-1940.	6.0	141
24	ÂÂ T cell receptor interactions with syngeneic and allogeneic ligands: Affinity measurements and crystallization. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 13838-13843.	3.3	135
25	The CuA domain of Thermus thermophilus ba3-type cytochrome c oxidase at 1.6 A resolution. Nature Structural Biology, 1999, 6, 509-516.	9.7	131
26	Complex between Peptostreptococcus magnus Protein L and a Human Antibody Reveals Structural Convergence in the Interaction Modes of Fab Binding Proteins. Structure, 2001, 9, 679-687.	1.6	121
27	Strategies in the crystallization of glycoproteins and protein complexes. Journal of Crystal Growth, 1992, 122, 273-285.	0.7	117
28	Structural Analysis of Antibody Specificity. Journal of Molecular Biology, 1994, 241, 663-690.	2.0	113
29	The mechanism of an inhibitory antibody on TF-initiated blood coagulation revealed by the crystal structures of human tissue factor, Fab 5G9 and TFÂ·5G9 complex 1 1Edited by D. C. Rees. Journal of Molecular Biology, 1998, 275, 873-894.	2.0	113
30	X-ray structure of the arenavirus glycoprotein GP2 in its postfusion hairpin conformation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19967-19972.	3.3	101
31	Identification of a 13 Amino Acid Peptide Mimetic of Erythropoietin and Description of Amino Acids Critical for the Mimetic Activity of EMP1. Biochemistry, 1998, 37, 3699-3710.	1.2	99
32	Analytical and production seeding techniques. Methods, 1990, 1, 38-49.	1.9	98
33	Third generation of matrix metalloprotease inhibitors: Gain in selectivity by targeting the depth of the S1â€² cavity. Biochimie, 2010, 92, 1501-1508.	1.3	88
34	Structural Studies of Human Placental Alkaline Phosphatase in Complex with Functional Ligands. Journal of Molecular Biology, 2005, 350, 441-451.	2.0	85
35	Structure of the complex between the Fab fragment of a neutralizing antibody for type 1 poliovirus and its viral epitope. Nature Structural and Molecular Biology, 1995, 2, 232-243.	3.6	83
36	Structural insights into the neutralization mechanism of a higher primate antibody against dengue virus. EMBO Journal, 2012, 31, 767-779.	3.5	81

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37	Crystal Structures of Mite Allergens Der f 1 and Der p 1 Reveal Differences in Surface-Exposed Residues that May Influence Antibody Binding. Journal of Molecular Biology, 2009, 386, 520-530.	2.0	79
38	Crystal structure of dUTP pyrophosphatase from feline immunodeficiency virus. Protein Science, 1996, 5, 2429-2437.	3.1	78
39	Crystal Structure of a Ternary Complex between Human Prostate-specific Antigen, Its Substrate Acyl Intermediate and an Activating Antibody. Journal of Molecular Biology, 2008, 376, 1021-1033.	2.0	78
40	Towards Structure-based Drug Design: Crystal Structure of a Multisubstrate Adduct Complex of Glycinamide Ribonucleotide Transformylase at 1.96 Ã... Resolution. Journal of Molecular Biology, 1995, 249, 153-175.	2.0	77
41	Three-dimensional structure and IgE-binding properties of mature fully active Der p 1, a clinically relevant major allergen. Journal of Allergy and Clinical Immunology, 2006, 117, 571-576.	1.5	76
42	Crystal structure of glycinamide ribonucleotide transformylase from Escherichia coli at 3Â·0 Ã... resolution. Journal of Molecular Biology, 1992, 227, 283-292.	2.0	65
43	Crystal Structure of a Peptide Complex of Anti-influenza Peptide Antibody Fab 26/9. Journal of Molecular Biology, 1994, 241, 534-556.	2.0	65
44	Crystal Structure of a Human Autoimmune Complex between IgM Rheumatoid Factor RF61 and IgG1 Fc Reveals a Novel Epitope and Evidence for Affinity Maturation. Journal of Molecular Biology, 2007, 368, 1321-1331.	2.0	61
45	NAD Binding Induces Conformational Changes in Rho ADP-ribosylating Clostridium botulinum C3 Exoenzyme. Journal of Biological Chemistry, 2002, 277, 30950-30957.	1.6	60
46	Proposals for the catalytic mechanism of glycogen phosphorylase b prompted by crystallographic studies on glucose 1-phosphate binding. Journal of Molecular Biology, 1980, 140, 565-580.	2.0	59
47	On the role of the cisâ€proline residue in the active site of DsbA. Protein Science, 1999, 8, 96-105.	3.1	58
48	Nucleotide binding to glycogen phosphorylase b in the crystal. Journal of Molecular Biology, 1979, 134, 639-653.	2.0	57
49	Crystal Structure of Human Prostate-Specific Antigen in a Sandwich Antibody Complex. Journal of Molecular Biology, 2011, 414, 530-544.	2.0	54
50	N-O-Isopropyl Sulfonamido-Based Hydroxamates as Matrix Metalloproteinase Inhibitors: Hit Selection and in Vivo Antiangiogenic Activity. Journal of Medicinal Chemistry, 2015, 58, 7224-7240.	2.9	54
51	Comparison of AMP and NADH binding to glycogen phosphorylase b. Journal of Molecular Biology, 1983, 170, 529-565.	2.0	53
52	Crystal Structure of the Complex between the Monomeric Form of Toxoplasma gondii Surface Antigen 1 (SAG1) and a Monoclonal Antibody that Mimics the Human Immune Response. Journal of Molecular Biology, 2005, 354, 447-458.	2.0	50
53	Structure of Azotobacter vinelandii 7Fe ferredoxin at 1.35 Ã... resolution and determination of the [Fe-S] bonds with 0.01 Ã... accuracy. Journal of Molecular Biology, 1998, 278, 629-639.	2.0	48
54	Insights from Selective Non-phosphinic Inhibitors of MMP-12 Tailored to Fit with an S1â€² Loop Canonical Conformation. Journal of Biological Chemistry, 2010, 285, 35900-35909.	1.6	48

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55	Molecular aspects of human FcÎ³R interactions with IgG: Functional and therapeutic consequences. Immunology Letters, 2006, 106, 111-118.	1.1	47
56	Crystallization of bi-functional ligand protein complexes. Journal of Structural Biology, 2013, 182, 246-254.	1.3	45
57	[7] X-ray crystallographic analysis of free and antigen-complexed Fab fragments to investigate structural basis of immune recognition. Methods in Enzymology, 1991, 203, 153-176.	0.4	41
58	Reverse screening. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 448-455.	2.5	41
59	Mambalgin-1 Pain-relieving Peptide, Stepwise Solid-phase Synthesis, Crystal Structure, and Functional Domain for Acid-sensing Ion Channel 1a Inhibition. Journal of Biological Chemistry, 2016, 291, 2616-2629.	1.6	41
60	Discovery of a new selective inhibitor of A Disintegrin And Metalloprotease 10 (ADAM-10) able to reduce the shedding of NKG2D ligands in Hodgkin's lymphoma cell models. European Journal of Medicinal Chemistry, 2016, 111, 193-201.	2.6	40
61	Evidence for Plasticity and Structural Mimicry at the Immunoglobulin Light Chain-Protein L Interface. Journal of Biological Chemistry, 2002, 277, 47500-47506.	1.6	39
62	Fine Tuning of the Specificity of an Anti-progesterone Antibody by First and Second Sphere Residue Engineering. Journal of Biological Chemistry, 2005, 280, 24880-24887.	1.6	37
63	Molecular Determinants of a Selective Matrix Metalloprotease-12 Inhibitor: Insights from Crystallography and Thermodynamic Studies. Journal of Medicinal Chemistry, 2013, 56, 1149-1159.	2.9	37
64	Immunoglobulin-binding domains: Protein L from Peptostreptococcus magnus. Biochemical Society Transactions, 2003, 31, 716-718.	1.6	36
65	Sugarâ€Based Arylsulfonamide Carboxylates as Selective and Waterâ€Soluble Matrix Metalloproteinaseâ€12 Inhibitors. ChemMedChem, 2016, 11, 1626-1637.	1.6	36
66	Simple Pseudo-dipeptides with a P2â€² Glutamate. Journal of Biological Chemistry, 2012, 287, 26647-26656.	1.6	35
67	Highly selective inhibition of myosin motors provides the basis of potential therapeutic application. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7448-E7455.	3.3	34
68	Development of Thioaryl-Based Matrix Metalloproteinase-12 Inhibitors with Alternative Zinc-Binding Groups: Synthesis, Potentiometric, NMR, and Crystallographic Studies. Journal of Medicinal Chemistry, 2018, 61, 4421-4435.	2.9	34
69	Crystallization of murine major histocompatibility complex class I H-2Kb with single peptides. Journal of Molecular Biology, 1992, 228, 975-982.	2.0	33
70	Transthyretin complexes with curcumin and bromo-estradiol: evaluation of solubilizing multicomponent mixtures. New Biotechnology, 2015, 32, 54-64.	2.4	33
71	Green mamba peptide targets type-2 vasopressin receptor against polycystic kidney disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7154-7159.	3.3	33
72	Structure of the 16S rRNA pseudouridine synthase RsuA bound to uracil and UMP. Nature Structural Biology, 2002, 9, 353-8.	9.7	32

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73	Structures of feline immunodeficiency virus dUTP pyrophosphatase and its nucleotide complexes in three crystal forms. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1100-1109.	2.5	31
74	Crystal structure of fullâ€length human collagenase 3 (MMPâ€13) with peptides in the active site defines exosites in the catalytic domain. FASEB Journal, 2013, 27, 4395-4405.	0.2	31
75	Macromolecular crystallography with synchrotron radiation. II. Results. Journal of Applied Crystallography, 1983, 16, 28-41.	1.9	30
76	Highly specific anti-estradiol antibodies: structural characterisation and binding diversity 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 2002, 315, 699-712.	2.0	30
77	Strategies for Protein Cryocrystallography. Crystal Growth and Design, 2014, 14, 427-435.	1.4	29
78	Structural studies of human alkaline phosphatase in complex with strontium: Implication for its secondary effect in bones. Protein Science, 2006, 15, 1691-1700.	3.1	28
79	Different Interactions between MT7 Toxin and the Human Muscarinic M₁ Receptor in Its Free and N-Methylscopolamine-Occupied States. Molecular Pharmacology, 2008, 74, 1554-1563.	1.0	28
80	Crystal Structure of a Hydrophobic Immunodominant Antigenic Site on Hepatitis C Virus Core Protein Complexed to Monoclonal Antibody 19D9D6. Journal of Immunology, 2003, 170, 1917-1924.	0.4	27
81	Engineering of Three-Finger Fold Toxins Creates Ligands with Original Pharmacological Profiles for Muscarinic and Adrenergic Receptors. PLoS ONE, 2012, 7, e39166.	1.1	27
82	Comparison of helical scan and standard rotation methods in single-crystal X-ray data collection strategies. Journal of Synchrotron Radiation, 2017, 24, 42-52.	1.0	27
83	Zincâ€“Metalloproteinase Inhibitors: Evaluation of the Complex Role Played by the Zinc-Binding Group on Potency and Selectivity. Journal of Medicinal Chemistry, 2017, 60, 403-414.	2.9	27
84	Synthesis and in Vitro and in Vivo Evaluation of MMP-12 Selective Optical Probes. Bioconjugate Chemistry, 2016, 27, 2407-2417.	1.8	26
85	Copper mediated amyloid-Î² binding to Transthyretin. Scientific Reports, 2018, 8, 13744.	1.6	26
86	Practical Use of Glycerol in Protein Crystallization. Crystal Growth and Design, 2011, 11, 2755-2762.	1.4	25
87	Structural basis for the NADâ€hydrolysis mechanism and the ARTTâ€loop plasticity of C3 exoenzymes. Protein Science, 2008, 17, 878-886.	3.1	24
88	Halogen Bonding Controls Selectivity of FRET Substrate Probes for MMP-9. Chemistry and Biology, 2014, 21, 408-413.	6.2	24
89	Crystallization of Antibodies and Antibody-Antigen Complexes. ImmunoMethods, 1993, 3, 164-179.	0.8	22
90	Multicomponent mixtures for cryoprotection and ligand solubilization. Biotechnology Reports (Amsterdam, Netherlands), 2015, 7, 120-127.	2.1	22

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91	Structural Aspects of Antibodies and Antibodyâ€Antigen Complexes. Novartis Foundation Symposium, 1991, 159, 13-39.	1.2	21
92	Observation and Characterization of the Interaction between a Single Immunoglobulin Binding Domain of Protein L and Two Equivalents of Human Îº Light Chains. Journal of Biological Chemistry, 2004, 279, 9370-9378.	1.6	20
93	A Tandem of SH3-like Domains Participates in RNA Binding in KIN17, a Human Protein Activated in Response to Genotoxics. Journal of Molecular Biology, 2006, 364, 764-776.	2.0	20
94	Purification, sequence and crystallization of an anti-tissue factor Fab and its use for the crystallization of tissue factor. Journal of Crystal Growth, 1992, 122, 253-264.	0.7	19
95	Crystallization of an intact monoclonal antibody (4B7) against Plasmodium falciparum malaria with peptides from the Pfs25 protein antigen. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 556-562.	2.5	19
96	Engineering protein for Xâ€ray crystallography: The murine major histocompatibility complex class II molecule Iâ€A^d. Protein Science, 1998, 7, 413-418.	3.1	18
97	A new crystal form of human transthyretin obtained with a curcumin derived ligand. Journal of Structural Biology, 2016, 194, 8-17.	1.3	18
98	Crystallization and preliminary crystallographic data for an antiprogesterone monoclonal antibody Fabâ€² and steroid-Fabâ€² complexes. Journal of Molecular Biology, 1987, 193, 229-231.	2.0	17
99	Protein L mutants for the crystallization of antibody fragments. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1744-1748.	2.5	17
100	Structure-Based Secondary Structure-Independent Approach To Design Protein Ligands:Â Application to the Design of Kv1.2 Potassium Channel Blockers. Journal of the American Chemical Society, 2006, 128, 16190-16205.	6.6	17
101	Human TTR conformation altered by rhenium tris-carbonyl derivatives. Journal of Structural Biology, 2016, 195, 353-364.	1.3	17
102	Structural Framework for Covalent Inhibition of Clostridium botulinum Neurotoxin A by Targeting Cys165. Journal of Biological Chemistry, 2012, 287, 33607-33614.	1.6	16
103	Epitaxial jumps. Journal of Crystal Growth, 1999, 196, 250-260.	0.7	15
104	Synthesis and structural analysis of halogen substituted fibril formation inhibitors of Human Transthyretin (TTR). Journal of Enzyme Inhibition and Medicinal Chemistry, 2016, 31, 40-51.	2.5	15
105	Ancestral protein resurrection and engineering opportunities of the mamba aminergic toxins. Scientific Reports, 2017, 7, 2701.	1.6	15
106	Screening Using Polymorphs for the Crystallization of Proteinâ€“Ligand Complexes. Crystal Growth and Design, 2013, 13, 1878-1888.	1.4	14
107	Bifunctional Inhibitors as a New Tool To Reduce Cancer Cell Invasion by Impairing MMP-9 Homodimerization. ACS Medicinal Chemistry Letters, 2017, 8, 293-298.	1.3	13
108	Crystallization of macromolecular complexes: combinatorial complex crystallization. Journal of Crystal Growth, 2001, 232, 573-579.	0.7	12

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109	In Vitro Affinity Maturation of an Anti-PSA Antibody for Prostate Cancer Diagnostic Assay. Journal of Molecular Biology, 2011, 414, 545-562.	2.0	12
110	Scaffolds for protein crystallisation. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1715-1721.	2.5	11
111	Grafting of functional motifs onto protein scaffolds identified by <scp>PDB</scp> screening â€“ an efficient route to design optimizable protein binders. FEBS Journal, 2013, 280, 139-159.	2.2	11
112	Diversified targets of FKBP25 and its complex with rapamycin. International Journal of Biological Macromolecules, 2014, 69, 344-352.	3.6	11
113	A B-Cell Superantigen that Targets B-1 Lymphocytes. Current Topics in Microbiology and Immunology, 2000, 252, 251-263.	0.7	11
114	Crystallization, sequence and preliminary crystallographic data for transmission-blocking anti-malaria Fab 4B7 with cyclic peptides from the Pfs25 protein of P. falciparum. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 535-542.	2.5	10
115	Effect of zinc on human IgG1 and its FcÎ³R interactions. Immunology Letters, 2012, 143, 60-69.	1.1	10
116	X-ray crystal structure and activity of fluorenyl-based compounds as transthyretin fibrillogenesis inhibitors. Journal of Enzyme Inhibition and Medicinal Chemistry, 2016, 31, 824-833.	2.5	10
117	Crystallization studies of glycosylated and unglycosylated human recombinant interleukin-2. Proteins: Structure, Function and Bioinformatics, 1992, 12, 24-30.	1.5	9
118	Crystallization and preliminary crystallographic data for class I deoxyribose-5-phosphate aldolase fromEscherichia coli: An Application of Reverse Screening. Proteins: Structure, Function and Bioinformatics, 1995, 22, 67-72.	1.5	8
119	Crystallization of macromolecular complexes:. Journal of Crystal Growth, 2001, 232, 580-590.	0.7	8
120	A simple modification of the Q-plate for parallel screening and combinatorial crystallization. Journal of Crystal Growth, 2001, 232, 545-552.	0.7	8
121	Crystallization and preliminary structural studies of a chorismate mutase catalytic antibody complexed with a transition state analog. Proteins: Structure, Function and Bioinformatics, 1994, 18, 198-200.	1.5	7
122	Crystallization and halide phasing of the C-terminal domain of human KIN17. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 245-248.	0.7	7
123	Acid pH crystallization of the basic protein lysin from the spermatozoa of red abalone (Haliotis) Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	6
124	Heparin-aggregated RANTES can be crystallised. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1670-1673.	2.5	6
125	Crystallization and Preliminary Crystallographic Data for Rab Guanine Nucleotide Dissociation Inhibitor (RabGDI) from Bovine Brain. Journal of Molecular Biology, 1994, 244, 469-473.	2.0	5
126	Comparison of the crystallization and crystal packing of two Fab single-site mutant protein L complexes. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 750-754.	2.5	5

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127	Crystallization and preliminary X-ray diffraction data of the complex between human centrin 2 and a peptide from the protein XPC. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 649-651.	0.7	5
128	Improving Diffraction from 3 to 2 Ã... for a Complex between a Small GTPase and Its Effector by Analysis of Crystal Contacts and Use of Reverse Screening. Crystal Growth and Design, 2007, 7, 2140-2146.	1.4	5
129	Conformational Exchange Is Critical for the Productivity of an Oxidative Folding Intermediate with Buried Free Cysteines. Journal of Molecular Biology, 2010, 403, 299-312.	2.0	5
130	Crystallization of recombinant green mamba Ï•Da1a toxin during a lyophilization procedure and its structure determination. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 704-709.	0.7	5
131	Crystallization and preliminary crystallographic data for a ternary complex between tissue factor, factor VIIa and a BPTI-derived inhibitor. Journal of Crystal Growth, 1996, 168, 260-269.	0.7	4
132	Sequence, specificity and crystallization of an oestroneâ€3â€glucuronide antibody (3910). Immunology, 1997, 90, 632-639.	2.0	4
133	Crystallization of human complement component C5. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 643-646.	2.5	4
134	Crystallization and preliminary crystallographic investigations of avian 5-aminoimidazole-4-carboxamide ribonucleotide transformylaseâ€“inosine monophosphate cyclohydrolase expressed inEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1051-1054.	2.5	4
135	Different crystal packing in Fabâ€“protein L semi-disordered peptide complex. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 744-749.	2.5	3
136	MT9, a natural peptide from black mamba venom antagonizes the muscarinic type 2 receptor and reverses the M2R-agonist-induced relaxation in rat and human arteries. Biomedicine and Pharmacotherapy, 2022, 150, 113094.	2.5	3
137	Disulphide dimerised peptide creates a crystal contact in an anti-peptide antibody. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1740-1743.	2.5	1
138	Protein crystallization for drug design in the last 50 years. Arbor, 2015, 191, a222.	0.1	1
139	A peptide mimetic of erythropoietin: Critical residues and description of a minimal functional epitope. , 2002, , 501-503.		0
140	Peptide mimetics of erythropoietin are powerful probes of receptor activation mechanisms. , 2002, , 536-538.		0