

Enrico Stura

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140
papers

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98
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140
ext. papers

10,477
ext. citations

7.9
avg, IF

5.33
L-index

#	Paper	IF	Citations
140	Crystal structures of two viral peptides in complex with murine MHC class I H-2Kb. <i>Science</i> , 1992 , 257, 919-27	33.3	808
139	Functional mimicry of a protein hormone by a peptide agonist: the EPO receptor complex at 2.8 Å. <i>Science</i> , 1996 , 273, 464-71	33.3	567
138	Crystal structure of mouse CD1: An MHC-like fold with a large hydrophobic binding groove. <i>Science</i> , 1997 , 277, 339-45	33.3	559
137	Crystallographic evidence for preformed dimers of erythropoietin receptor before ligand activation. <i>Science</i> , 1999 , 283, 987-90	33.3	545
136	Structure of a flavivirus envelope glycoprotein in its low-pH-induced membrane fusion conformation. <i>EMBO Journal</i> , 2004 , 23, 728-38	13	467
135	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 5399-404	11.5	390
134	Immune versus natural selection: antibody aldolases with enzymic rates but broader scope. <i>Science</i> , 1997 , 278, 2085-92	33.3	357
133	Crystal structure of the principal neutralization site of HIV-1. <i>Science</i> , 1994 , 264, 82-5	33.3	242
132	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 2479-83	11.5	217
131	Crystal structure of alkaline phosphatase from human placenta at 1.8 Å resolution. Implication for a substrate specificity. <i>Journal of Biological Chemistry</i> , 2001 , 276, 9158-65	5.4	208
130	Crystal structure of a human immunodeficiency virus type 1 neutralizing antibody, 50.1, in complex with its V3 loop peptide antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993 , 90, 6325-9	11.5	189
129	Crystal structure of the human urokinase plasminogen activator receptor bound to an antagonist peptide. <i>EMBO Journal</i> , 2005 , 24, 1655-63	13	181
128	An antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation. <i>Nature Structural Biology</i> , 1998 , 5, 993-1004		177
127	Routes to catalysis: structure of a catalytic antibody and comparison with its natural counterpart. <i>Science</i> , 1994 , 263, 646-52	33.3	160
126	Denmotoxin, a three-finger toxin from the colubrid snake <i>Boiga dendrophila</i> (Mangrove Catsnake) with bird-specific activity. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29030-41	5.4	157
125	Structure and mutational analysis of Rab GDP-dissociation inhibitor. <i>Nature</i> , 1996 , 381, 42-8	50.4	153
124	Irditoxin, a novel covalently linked heterodimeric three-finger toxin with high taxon-specific neurotoxicity. <i>FASEB Journal</i> , 2009 , 23, 534-45	0.9	146

123	Three-dimensional structure of an anti-steroid FabTand progesterone-FabTcomplex. <i>Journal of Molecular Biology</i> , 1993 , 231, 103-18	6.5	143
122	Structural evidence for a functional role of human tissue nonspecific alkaline phosphatase in bone mineralization. <i>Journal of Biological Chemistry</i> , 2001 , 276, 31171-8	5.4	139
121	Applications of the streak seeding technique in protein crystallization. <i>Journal of Crystal Growth</i> , 1991 , 110, 270-282	1.6	135
120	Dual conformations for the HIV-1 gp120 V3 loop in complexes with different neutralizing fabs. <i>Structure</i> , 1999 , 7, 131-42	5.2	134
119	Alphabeta T cell receptor interactions with syngeneic and allogeneic ligands: affinity measurements and crystallization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 13838-43	11.5	132
118	An antibody exo Diels-Alderase inhibitor complex at 1.95 angstrom resolution. <i>Science</i> , 1998 , 279, 1934-40	9.3	127
117	Crystal structure of Aplysia ADP ribosyl cyclase, a homologue of the bifunctional ectozyme CD38. <i>Nature Structural Biology</i> , 1996 , 3, 957-64		127
116	Strategies in the crystallization of glycoproteins and protein complexes. <i>Journal of Crystal Growth</i> , 1992 , 122, 273-285	1.6	112
115	The CuA domain of Thermus thermophilus ba3-type cytochrome c oxidase at 1.6 A resolution. <i>Nature Structural Biology</i> , 1999 , 6, 509-16		110
114	The mechanism of an inhibitory antibody on TF-initiated blood coagulation revealed by the crystal structures of human tissue factor, Fab 5G9 and TF.G9 complex. <i>Journal of Molecular Biology</i> , 1998 , 275, 873-94	6.5	105
113	Complex between Peptostreptococcus magnus protein L and a human antibody reveals structural convergence in the interaction modes of Fab binding proteins. <i>Structure</i> , 2001 , 9, 679-87	5.2	104
112	Structural analysis of antibody specificity. Detailed comparison of five FabTsteroid complexes. <i>Journal of Molecular Biology</i> , 1994 , 241, 663-90	6.5	103
111	Analytical and production seeding techniques. <i>Methods</i> , 1990 , 1, 38-49	4.6	92
110	Identification of a 13 amino acid peptide mimetic of erythropoietin and description of amino acids critical for the mimetic activity of EMP1. <i>Biochemistry</i> , 1998 , 37, 3699-710	3.2	89
109	X-ray structure of the arenavirus glycoprotein GP2 in its postfusion hairpin conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 19967-72	11.5	85
108	Third generation of matrix metalloprotease inhibitors: Gain in selectivity by targeting the depth of the S1Tcavity. <i>Biochimie</i> , 2010 , 92, 1501-8	4.6	78
107	Towards structure-based drug design: crystal structure of a multisubstrate adduct complex of glycinamide ribonucleotide transformylase at 1.96 A resolution. <i>Journal of Molecular Biology</i> , 1995 , 249, 153-75	6.5	75
106	Structural insights into the neutralization mechanism of a higher primate antibody against dengue virus. <i>EMBO Journal</i> , 2012 , 31, 767-79	13	73

105	Structure of the complex between the Fab fragment of a neutralizing antibody for type 1 poliovirus and its viral epitope. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 232-43	17.6	72
104	Crystal structure of dUTP pyrophosphatase from feline immunodeficiency virus. <i>Protein Science</i> , 1996 , 5, 2429-37	6.3	72
103	Structural studies of human placental alkaline phosphatase in complex with functional ligands. <i>Journal of Molecular Biology</i> , 2005 , 350, 441-51	6.5	70
102	Crystal structure of a ternary complex between human prostate-specific antigen, its substrate acyl intermediate and an activating antibody. <i>Journal of Molecular Biology</i> , 2008 , 376, 1021-33	6.5	69
101	Crystal structures of mite allergens Der f 1 and Der p 1 reveal differences in surface-exposed residues that may influence antibody binding. <i>Journal of Molecular Biology</i> , 2009 , 386, 520-30	6.5	64
100	Three-dimensional structure and IgE-binding properties of mature fully active Der p 1, a clinically relevant major allergen. <i>Journal of Allergy and Clinical Immunology</i> , 2006 , 117, 571-6	11.5	64
99	Crystal structure of glycinamide ribonucleotide transformylase from <i>Escherichia coli</i> at 3.0 Å resolution. A target enzyme for chemotherapy. <i>Journal of Molecular Biology</i> , 1992 , 227, 283-92	6.5	61
98	NAD binding induces conformational changes in Rho ADP-ribosylating <i>Clostridium botulinum</i> C3 exoenzyme. <i>Journal of Biological Chemistry</i> , 2002 , 277, 30950-7	5.4	57
97	On the role of the cis-proline residue in the active site of DsbA. <i>Protein Science</i> , 1999 , 8, 96-105	6.3	56
96	Crystal structure of a peptide complex of anti-influenza peptide antibody Fab 26/9. Comparison of two different antibodies bound to the same peptide antigen. <i>Journal of Molecular Biology</i> , 1994 , 241, 534-56	6.5	53
95	Nucleotide binding to glycogen phosphorylase b in the crystal. <i>Journal of Molecular Biology</i> , 1979 , 134, 639-53	6.5	52
94	Crystal structure of a human autoimmune complex between IgM rheumatoid factor RF61 and IgG1 Fc reveals a novel epitope and evidence for affinity maturation. <i>Journal of Molecular Biology</i> , 2007 , 368, 1321-31	6.5	49
93	Comparison of AMP and NADH binding to glycogen phosphorylase b. <i>Journal of Molecular Biology</i> , 1983 , 170, 529-65	6.5	48
92	Proposals for the catalytic mechanism of glycogen phosphorylase beta prompted by crystallographic studies on glucose 1-phosphate binding. <i>Journal of Molecular Biology</i> , 1980 , 140, 565-80	6.5	46
91	Crystal structure of human prostate-specific antigen in a sandwich antibody complex. <i>Journal of Molecular Biology</i> , 2011 , 414, 530-44	6.5	45
90	Crystal structure of the complex between the monomeric form of <i>Toxoplasma gondii</i> surface antigen 1 (SAG1) and a monoclonal antibody that mimics the human immune response. <i>Journal of Molecular Biology</i> , 2005 , 354, 447-58	6.5	43
89	Insights from selective non-phosphinic inhibitors of MMP-12 tailored to fit with an S1Tloop canonical conformation. <i>Journal of Biological Chemistry</i> , 2010 , 285, 35900-9	5.4	42
88	N-O-Isopropyl Sulfonamido-Based Hydroxamates as Matrix Metalloproteinase Inhibitors: Hit Selection and in Vivo Antiangiogenic Activity. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 7224-40	8.3	41

87	Molecular aspects of human FcγR interactions with IgG: functional and therapeutic consequences. <i>Immunology Letters</i> , 2006 , 106, 111-8	4.1	38
86	Crystallization of bi-functional ligand protein complexes. <i>Journal of Structural Biology</i> , 2013 , 182, 246-54	3.4	37
85	Structure of <i>Azotobacter vinelandii</i> 7Fe ferredoxin at 1.35 Å resolution and determination of the [Fe-S] bonds with 0.01 Å accuracy. <i>Journal of Molecular Biology</i> , 1998 , 278, 629-39	6.5	37
84	Reverse screening. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994 , 50, 448-55		37
83	X-ray crystallographic analysis of free and antigen-complexed Fab fragments to investigate structural basis of immune recognition. <i>Methods in Enzymology</i> , 1991 , 203, 153-76	1.7	37
82	Immunoglobulin-binding domains: Protein L from <i>Peptostreptococcus magnus</i> . <i>Biochemical Society Transactions</i> , 2003 , 31, 716-8	5.1	34
81	Mambalgin-1 Pain-relieving Peptide, Stepwise Solid-phase Synthesis, Crystal Structure, and Functional Domain for Acid-sensing Ion Channel 1a Inhibition. <i>Journal of Biological Chemistry</i> , 2016 , 291, 2616-29	5.4	33
80	Evidence for plasticity and structural mimicry at the immunoglobulin light chain-protein L interface. <i>Journal of Biological Chemistry</i> , 2002 , 277, 47500-6	5.4	33
79	Crystallization of murine major histocompatibility complex class I H-2Kb with single peptides. <i>Journal of Molecular Biology</i> , 1992 , 228, 975-82	6.5	33
78	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. <i>European Journal of Medicinal Chemistry</i> , 2016 , 111, 193-201	6.8	32
77	Fine tuning of the specificity of an anti-progesterone antibody by first and second sphere residue engineering. <i>Journal of Biological Chemistry</i> , 2005 , 280, 24880-7	5.4	32
76	Structure of the 16S rRNA pseudouridine synthase RsuA bound to uracil and UMP. <i>Nature Structural Biology</i> , 2002 , 9, 353-8		31
75	Structures of feline immunodeficiency virus dUTP pyrophosphatase and its nucleotide complexes in three crystal forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1100-9		30
74	Molecular determinants of a selective matrix metalloprotease-12 inhibitor: insights from crystallography and thermodynamic studies. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 1149-59	8.3	29
73	Simple pseudo-dipeptides with a P2Tglutamate: a novel inhibitor family of matrix metalloproteases and other metzincins. <i>Journal of Biological Chemistry</i> , 2012 , 287, 26647-56	5.4	29
72	Macromolecular crystallography with synchrotron radiation. II. Results. <i>Journal of Applied Crystallography</i> , 1983 , 16, 28-41	3.8	29
71	Transthyretin complexes with curcumin and bromo-estradiol: evaluation of solubilizing multicomponent mixtures. <i>New Biotechnology</i> , 2015 , 32, 54-64	6.4	27
70	Crystal structure of full-length human collagenase 3 (MMP-13) with peptides in the active site defines exosites in the catalytic domain. <i>FASEB Journal</i> , 2013 , 27, 4395-405	0.9	27

69	Different interactions between MT7 toxin and the human muscarinic M1 receptor in its free and N-methylscopolamine-occupied states. <i>Molecular Pharmacology</i> , 2008 , 74, 1554-63	4.3	27
68	Strategies for Protein Cryocrystallography. <i>Crystal Growth and Design</i> , 2014 , 14, 427-435	3.5	26
67	Crystal structure of a hydrophobic immunodominant antigenic site on hepatitis C virus core protein complexed to monoclonal antibody 19D9D6. <i>Journal of Immunology</i> , 2003 , 170, 1917-24	5.3	26
66	Sugar-Based Arylsulfonamide Carboxylates as Selective and Water-Soluble Matrix Metalloproteinase-12 Inhibitors. <i>ChemMedChem</i> , 2016 , 11, 1626-37	3.7	25
65	Highly specific anti-estradiol antibodies: structural characterisation and binding diversity. <i>Journal of Molecular Biology</i> , 2002 , 315, 699-712	6.5	25
64	Green mamba peptide targets type-2 vasopressin receptor against polycystic kidney disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 7154-7159	11.5	24
63	Engineering of three-finger fold toxins creates ligands with original pharmacological profiles for muscarinic and adrenergic receptors. <i>PLoS ONE</i> , 2012 , 7, e39166	3.7	24
62	Synthesis and in Vitro and in Vivo Evaluation of MMP-12 Selective Optical Probes. <i>Bioconjugate Chemistry</i> , 2016 , 27, 2407-2417	6.3	23
61	Structural basis for the NAD-hydrolysis mechanism and the ARTT-loop plasticity of C3 exoenzymes. <i>Protein Science</i> , 2008 , 17, 878-86	6.3	23
60	Structural studies of human alkaline phosphatase in complex with strontium: implication for its secondary effect in bones. <i>Protein Science</i> , 2006 , 15, 1691-700	6.3	22
59	Highly selective inhibition of myosin motors provides the basis of potential therapeutic application. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7448-E7455	11.5	21
58	Zinc-Metalloproteinase Inhibitors: Evaluation of the Complex Role Played by the Zinc-Binding Group on Potency and Selectivity. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 403-414	8.3	20
57	Crystallization of Antibodies and Antibody-Antigen Complexes. <i>ImmunoMethods</i> , 1993 , 3, 164-179		20
56	Practical Use of Glycerol in Protein Crystallization. <i>Crystal Growth and Design</i> , 2011 , 11, 2755-2762	3.5	19
55	Development of Thioaryl-Based Matrix Metalloproteinase-12 Inhibitors with Alternative Zinc-Binding Groups: Synthesis, Potentiometric, NMR, and Crystallographic Studies. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 4421-4435	8.3	18
54	A tandem of SH3-like domains participates in RNA binding in KIN17, a human protein activated in response to genotoxics. <i>Journal of Molecular Biology</i> , 2006 , 364, 764-76	6.5	18
53	Engineering protein for X-ray crystallography: the murine Major Histocompatibility Complex class II molecule I-Ad. <i>Protein Science</i> , 1998 , 7, 413-8	6.3	17
52	Crystallization of an intact monoclonal antibody (4B7) against Plasmodium falciparum malaria with peptides from the Pf25 protein antigen. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994 , 50, 556-62		17

51	Purification, sequence and crystallization of an anti-tissue factor Fab and its use for the crystallization of tissue factor. <i>Journal of Crystal Growth</i> , 1992 , 122, 253-264	1.6	17
50	Comparison of helical scan and standard rotation methods in single-crystal X-ray data collection strategies. <i>Journal of Synchrotron Radiation</i> , 2017 , 24, 42-52	2.4	16
49	A new crystal form of human transthyretin obtained with a curcumin derived ligand. <i>Journal of Structural Biology</i> , 2016 , 194, 8-17	3.4	16
48	Multicomponent mixtures for cryoprotection and ligand solubilization. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2015 , 7, 120-127	5.3	16
47	Halogen bonding controls selectivity of FRET substrate probes for MMP-9. <i>Chemistry and Biology</i> , 2014 , 21, 408-13		16
46	Structural framework for covalent inhibition of Clostridium botulinum neurotoxin A by targeting Cys165. <i>Journal of Biological Chemistry</i> , 2012 , 287, 33607-14	5.4	16
45	Structure-based secondary structure-independent approach to design protein ligands: Application to the design of Kv1.2 potassium channel blockers. <i>Journal of the American Chemical Society</i> , 2006 , 128, 16190-205	16.4	16
44	Protein L mutants for the crystallization of antibody fragments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1744-8		16
43	Structural aspects of antibodies and antibody-antigen complexes. <i>Novartis Foundation Symposium</i> , 1991 , 159, 13-28; discussion 28-39		16
42	Human TTR conformation altered by rhenium tris-carbonyl derivatives. <i>Journal of Structural Biology</i> , 2016 , 195, 353-364	3.4	15
41	Observation and characterization of the interaction between a single immunoglobulin binding domain of protein L and two equivalents of human kappa light chains. <i>Journal of Biological Chemistry</i> , 2004 , 279, 9370-8	5.4	15
40	Epitaxial jumps. <i>Journal of Crystal Growth</i> , 1999 , 196, 250-260	1.6	15
39	Crystallization and preliminary crystallographic data for an antiprogestosterone monoclonal antibody FabTand steroid-FabTcomplexes. <i>Journal of Molecular Biology</i> , 1987 , 193, 229-31	6.5	15
38	Copper mediated amyloid- β binding to Transthyretin. <i>Scientific Reports</i> , 2018 , 8, 13744	4.9	15
37	Ancestral protein resurrection and engineering opportunities of the mamba aminergic toxins. <i>Scientific Reports</i> , 2017 , 7, 2701	4.9	14
36	Screening Using Polymorphs for the Crystallization of ProteinLigand Complexes. <i>Crystal Growth and Design</i> , 2013 , 13, 1878-1888	3.5	12
35	Crystallization of macromolecular complexes: combinatorial complex crystallization. <i>Journal of Crystal Growth</i> , 2001 , 232, 573-579	1.6	12
34	In vitro affinity maturation of an anti-PSA antibody for prostate cancer diagnostic assay. <i>Journal of Molecular Biology</i> , 2011 , 414, 545-62	6.5	11

33	Bifunctional Inhibitors as a New Tool To Reduce Cancer Cell Invasion by Impairing MMP-9 Homodimerization. <i>ACS Medicinal Chemistry Letters</i> , 2017 , 8, 293-298	4.3	10
32	Diversified targets of FKBP25 and its complex with rapamycin. <i>International Journal of Biological Macromolecules</i> , 2014 , 69, 344-52	7.9	10
31	Scaffolds for protein crystallisation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1715-21		10
30	A B-cell superantigen that targets B-1 lymphocytes. <i>Current Topics in Microbiology and Immunology</i> , 2000 , 252, 251-63	3.3	10
29	Synthesis and structural analysis of halogen substituted fibril formation inhibitors of Human Transthyretin (TTR). <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2016 , 31, 40-51	5.6	10
28	Grafting of functional motifs onto protein scaffolds identified by PDB screening--an efficient route to design optimizable protein binders. <i>FEBS Journal</i> , 2013 , 280, 139-59	5.7	9
27	Effect of zinc on human IgG1 and its FcR interactions. <i>Immunology Letters</i> , 2012 , 143, 60-9	4.1	9
26	Crystallization, sequence and preliminary crystallographic data for transmission-blocking anti-malaria Fab 4B7 with cyclic peptides from the Pfs25 protein of P. falciparum. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994 , 50, 535-42		9
25	Crystallization studies of glycosylated and unglycosylated human recombinant interleukin-2. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 12, 24-30	4.2	9
24	Crystallization of macromolecular complexes:: stoichiometric variation screening. <i>Journal of Crystal Growth</i> , 2001 , 232, 580-590	1.6	8
23	A simple modification of the Q-plate for parallel screening and combinatorial crystallization. <i>Journal of Crystal Growth</i> , 2001 , 232, 545-552	1.6	8
22	X-ray crystal structure and activity of fluorenyl-based compounds as transthyretin fibrillogenesis inhibitors. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2016 , 31, 824-33	5.6	7
21	Crystallization and halide phasing of the C-terminal domain of human KIN17. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 245-8		6
20	Heparin-aggregated RANTES can be crystallised. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1670-3		6
19	Conformational exchange is critical for the productivity of an oxidative folding intermediate with buried free cysteines. <i>Journal of Molecular Biology</i> , 2010 , 403, 299-312	6.5	5
18	Improving Diffraction from 3 to 2 Å for a Complex between a Small GTPase and Its Effector by Analysis of Crystal Contacts and Use of Reverse Screening. <i>Crystal Growth and Design</i> , 2007 , 7, 2140-2146	3.5	5
17	Crystallization and preliminary X-ray diffraction data of the complex between human centrin 2 and a peptide from the protein XPC. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 649-51		5
16	Crystallization and preliminary crystallographic data for class I deoxyribose-5-phosphate aldolase from Escherichia coli: an application of reverse screening. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 22, 67-72	4.2	5

15	Crystallization and preliminary structural studies of a chorismate mutase catalytic antibody complexed with a transition state analog. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 18, 198-200	4.2	5
14	Crystallization and preliminary crystallographic data for Rab guanine nucleotide dissociation inhibitor (RabGDI) from bovine brain. <i>Journal of Molecular Biology</i> , 1994 , 244, 469-73	6.5	5
13	Crystallization of recombinant green mamba E _D a1a toxin during a lyophilization procedure and its structure determination. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 704-9		4
12	Sequence, specificity and crystallization of an oestrone-3-glucuronide antibody (3910). <i>Immunology</i> , 1997 , 90, 632-9	7.8	4
11	Crystallization of human complement component C5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 643-6		4
10	Comparison of the crystallization and crystal packing of two Fab single-site mutant protein L complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 750-4		4
9	Crystallization and preliminary crystallographic data for a ternary complex between tissue factor, factor VIIa and a BPTI-derived inhibitor. <i>Journal of Crystal Growth</i> , 1996 , 168, 260-269	1.6	4
8	Acid pH crystallization of the basic protein lysin from the spermatozoa of red abalone (<i>Haliotis rufescens</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994 , 50, 620-6		4
7	Different crystal packing in Fab-protein L semi-disordered peptide complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 744-9		3
6	Crystallization and preliminary crystallographic investigations of avian 5-aminoimidazole-4-carboxamide ribonucleotide transformylase-inosine monophosphate cyclohydrolase expressed in <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1051-4		2
5	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. <i>Biomedicine and Pharmacotherapy</i> , 2022 , 150, 113094	7.5	2
4	Protein crystallization for drug design in the last 50 years. <i>Arbor</i> , 2015 , 191, a222	0.2	1
3	Disulphide dimerised peptide creates a crystal contact in an anti-peptide antibody. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1740-3		1
2	Peptide mimetics of erythropoietin are powerful probes of receptor activation mechanisms 2002 , 536-538		
1	A peptide mimetic of erythropoietin: Critical residues and description of a minimal functional epitope 2002 , 501-503		