

Christian Cambillau

List of Publications by Year in descending order

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271
papers

20,057
citations

7069

78
h-index

15683

125
g-index

274
all docs

274
docs citations

274
times ranked

16462
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	9.0	763
2	Interfacial activation of the lipase-procolipase complex by mixed micelles revealed by X-ray crystallography. <i>Nature</i> , 1993, 362, 814-820.	13.7	712
3	Discovery of an RNA virus 3'->5' exoribonuclease that is critically involved in coronavirus RNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5108-5113.	3.3	524
4	<i>Fusarium solani</i> cutinase is a lipolytic enzyme with a catalytic serine accessible to solvent. <i>Nature</i> , 1992, 356, 615-618.	13.7	414
5	Structure of the pancreatic lipase-procolipase complex. <i>Nature</i> , 1992, 359, 159-162.	13.7	374
6	The 2.46 Å Resolution Structure of the Pancreatic Lipase-Colipase Complex Inhibited by a C11 Alkyl Phosphonate. <i>Biochemistry</i> , 1995, 34, 2751-2762.	1.2	286
7	Recognition of antigens by single-domain antibody fragments: the superfluous luxury of paired domains. <i>Trends in Biochemical Sciences</i> , 2001, 26, 230-235.	3.7	283
8	A novel type of catalytic copper cluster in nitrous oxide reductase. <i>Nature Structural Biology</i> , 2000, 7, 191-195.	9.7	280
9	Structural aspects of sexual attraction and chemical communication in insects. <i>Trends in Biochemical Sciences</i> , 2004, 29, 257-264.	3.7	269
10	The severe acute respiratory syndrome-coronavirus replicative protein nsp9 is a single-stranded RNA-binding subunit unique in the RNA virus world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3792-3796.	3.3	254
11	Structural and Genomic Correlates of Hyperthermostability. <i>Journal of Biological Chemistry</i> , 2000, 275, 32383-32386.	1.6	246
12	Architecture and assembly of the Type VI secretion system. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1664-1673.	1.9	246
13	Biogenesis and structure of a type VI secretion membrane core complex. <i>Nature</i> , 2015, 523, 555-560.	13.7	241
14	VgrG, Tae, Tle, and beyond: the versatile arsenal of Type VI secretion effectors. <i>Trends in Microbiology</i> , 2014, 22, 498-507.	3.5	240
15	A Common Evolutionary Origin for Tailed-Bacteriophage Functional Modules and Bacterial Machineries. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 423-433.	2.9	234
16	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. <i>Nature Methods</i> , 2007, 4, 13-17.	9.0	231
17	Revisiting the Specificity of <i>Mamestra brassicae</i> and <i>Antheraea polyphemus</i> Pheromone-binding Proteins with a Fluorescence Binding Assay. <i>Journal of Biological Chemistry</i> , 2001, 276, 20078-20084.	1.6	217
18	Atomic resolution (1.0 Å) crystal structure of <i>Fusarium solani</i> cutinase: stereochemical analysis. <i>Journal of Molecular Biology</i> , 1997, 268, 779-799.	2.0	211

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19	Structural and Functional Basis for ADP-Ribose and Poly(ADP-Ribose) Binding by Viral Macro Domains. <i>Journal of Virology</i> , 2006, 80, 8493-8502.	1.5	206
20	Domain swapping creates a third putative combining site in bovine odorant binding protein dimer. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 863-867.	3.6	194
21	Structural biology of type VI secretion systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1102-1111.	1.8	191
22	A phospholipase A ₂ antibacterial Type VI secretion effector interacts directly with the C-terminal domain of the VgrG spike protein for delivery. <i>Molecular Microbiology</i> , 2016, 99, 1099-1118.	1.2	179
23	Cutinase, a lipolytic enzyme with a preformed oxyanion hole. <i>Biochemistry</i> , 1994, 33, 83-89.	1.2	176
24	X-ray Structure and Ligand Binding Study of a Moth Chemosensory Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 32094-32098.	1.6	173
25	Revisiting the Catalytic CuZ Cluster of Nitrous Oxide (N ₂ O) Reductase. <i>Journal of Biological Chemistry</i> , 2000, 275, 41133-41136.	1.6	166
26	Crystal structure and mechanistic determinants of SARS coronavirus nonstructural protein 15 define an endoribonuclease family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11892-11897.	3.3	161
27	Directed in Vitro Evolution and Crystallographic Analysis of a Peptide-binding Single Chain Antibody Fragment (scFv) with Low Picomolar Affinity. <i>Journal of Biological Chemistry</i> , 2004, 279, 18870-18877.	1.6	160
28	Moth chemosensory protein exhibits drastic conformational changes and cooperativity on ligand binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5069-5074.	3.3	157
29	Ligands for Pheromone-Sensing Neurons Are Not Conformationally Activated Odorant Binding Proteins. <i>PLoS Biology</i> , 2013, 11, e1001546.	2.6	151
30	Crystal Structure of Human Gastric Lipase and Model of Lysosomal Acid Lipase, Two Lipolytic Enzymes of Medical Interest. <i>Journal of Biological Chemistry</i> , 1999, 274, 16995-17002.	1.6	150
31	Widespread anti-CRISPR proteins in virulent bacteriophages inhibit a range of Cas9 proteins. <i>Nature Communications</i> , 2018, 9, 2919.	5.8	147
32	Three Camelid VHH Domains in Complex with Porcine Pancreatic α -Amylase. <i>Journal of Biological Chemistry</i> , 2002, 277, 23645-23650.	1.6	145
33	Camelid Heavy-Chain Variable Domains Provide Efficient Combining Sites to Haptens. <i>Biochemistry</i> , 2000, 39, 1217-1222.	1.2	144
34	Crystal Structure of the Measles Virus Phosphoprotein Domain Responsible for the Induced Folding of the C-terminal Domain of the Nucleoprotein. <i>Journal of Biological Chemistry</i> , 2003, 278, 44567-44573.	1.6	143
35	Structure of lactococcal phage p2 baseplate and its mechanism of activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6852-6857.	3.3	143
36	N-terminal arm exchange is observed in the 2.15 Å... crystal structure of oxidized nitrite reductase from <i>Pseudomonas aeruginosa</i> . <i>Structure</i> , 1997, 5, 1157-1171.	1.6	142

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37	Complexes of porcine odorant binding protein with odorant molecules belonging to different chemical classes. <i>Journal of Molecular Biology</i> , 2000, 300, 127-139.	2.0	139
38	Crystal structure of <i>Apis mellifera</i> OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 41-50.	1.2	135
39	High-throughput automated refolding screening of inclusion bodies. <i>Protein Science</i> , 2009, 13, 2782-2792.	3.1	134
40	TOM: a FRODO subpackage for protein-ligand fitting with interactive energy minimization. <i>Journal of Molecular Graphics</i> , 1987, 5, 174-177.	1.7	133
41	Towards a Structural Comprehension of Bacterial Type VI Secretion Systems: Characterization of the TssJ-TssM Complex of an <i>Escherichia coli</i> Pathovar. <i>PLoS Pathogens</i> , 2011, 7, e1002386.	2.1	132
42	The crystal structure of a llama heavy chain variable domain. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 752-757.	3.6	131
43	Priming and polymerization of a bacterial contractile tail structure. <i>Nature</i> , 2016, 531, 59-63.	13.7	127
44	The Structure of the Monomeric Porcine Odorant Binding Protein Sheds Light on the Domain Swapping Mechanism. <i>Biochemistry</i> , 1998, 37, 7913-7918.	1.2	126
45	LppX is a lipoprotein required for the translocation of phthiocerol dimycocerosates to the surface of <i>Mycobacterium tuberculosis</i> . <i>EMBO Journal</i> , 2006, 25, 1436-1444.	3.5	126
46	Crystal Structure of Pig Pancreatic alpha-amylase Isoenzyme II, in Complex with the Carbohydrate Inhibitor Acarbose. <i>FEBS Journal</i> , 1996, 238, 561-569.	0.2	125
47	Three-Dimensionnal structures of complexes of <i>Lathyrus ochrus</i> isolectin I with glucose and mannose: Fine specificity of the monosaccharide-binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 365-376.	1.5	121
48	Structure of the phage TP901-1 1.8ÅMDa baseplate suggests an alternative host adhesion mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8954-8958.	3.3	121
49	Lactococcal bacteriophage p2 receptor-binding protein structure suggests a common ancestor gene with bacterial and mammalian viruses. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 85-89.	3.6	117
50	Medium-Scale Structural Genomics: Strategies for Protein Expression and Crystallization. <i>Accounts of Chemical Research</i> , 2003, 36, 165-172.	7.6	116
51	Receptor-Binding Protein of <i>Lactococcus lactis</i> Phages: Identification and Characterization of the Saccharide Receptor-Binding Site. <i>Journal of Bacteriology</i> , 2006, 188, 2400-2410.	1.0	116
52	The Crystal Structure of a Cockroach Pheromone-binding Protein Suggests a New Ligand Binding and Release Mechanism. <i>Journal of Biological Chemistry</i> , 2003, 278, 30213-30218.	1.6	115
53	Isolation of Llama Antibody Fragments for Prevention of Dandruff by Phage Display in Shampoo. <i>Applied and Environmental Microbiology</i> , 2005, 71, 442-450.	1.4	113
54	Structural genomics on membrane proteins: comparison of more than 100 GPCRs in 3 expression systems. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 77-91.	1.2	111

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55	A Toxin-Antitoxin Module of Salmonella Promotes Virulence in Mice. <i>PLoS Pathogens</i> , 2013, 9, e1003827.	2.1	111
56	Crystal Structure of the Open Form of Dog Gastric Lipase in Complex with a Phosphonate Inhibitor. <i>Journal of Biological Chemistry</i> , 2002, 277, 2266-2274.	1.6	107
57	Horse Pancreatic Lipase. <i>Journal of Molecular Biology</i> , 1994, 238, 709-732.	2.0	106
58	Structures of a legume lectin complexed with the human lactotransferrin N2 fragment, and with an isolated biantennary glycopeptide: role of the fucose moiety. <i>Structure</i> , 1994, 2, 209-219.	1.6	105
59	A pancreatic lipase with a phospholipase A1 activity: crystal structure of a chimeric pancreatic lipase-related protein 2 from guinea pig. <i>Structure</i> , 1996, 4, 1363-1374.	1.6	105
60	Structure-activity of cutinase, a small lipolytic enzyme. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1441, 185-196.	1.2	104
61	Digestive lipases: From three-dimensional structure to physiology. <i>Biochimie</i> , 2000, 82, 973-986.	1.3	104
62	Modular Structure of the Receptor Binding Proteins of Lactococcus lactis Phages. <i>Journal of Biological Chemistry</i> , 2006, 281, 14256-14262.	1.6	102
63	Camelid nanobodies: killing two birds with one stone. <i>Current Opinion in Structural Biology</i> , 2015, 32, 1-8.	2.6	101
64	TssK Is a Trimeric Cytoplasmic Protein Interacting with Components of Both Phage-like and Membrane Anchoring Complexes of the Type VI Secretion System. <i>Journal of Biological Chemistry</i> , 2013, 288, 27031-27041.	1.6	100
65	Investigation of the Relationship between Lactococcal Host Cell Wall Polysaccharide Genotype and 936 Phage Receptor Binding Protein Phylogeny. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4385-4392.	1.4	99
66	Sulfur Single-wavelength Anomalous Diffraction Crystal Structure of a Pheromone-Binding Protein from the Honeybee <i>Apis mellifera</i> L. <i>Journal of Biological Chemistry</i> , 2004, 279, 4459-4464.	1.6	98
67	Differences in Lactococcal Cell Wall Polysaccharide Structure Are Major Determining Factors in Bacteriophage Sensitivity. <i>MBio</i> , 2014, 5, e00880-14.	1.8	98
68	Contribution of Cutinase Serine 42 Side Chain to the Stabilization of the Oxyanion Transition State. <i>Biochemistry</i> , 1996, 35, 398-410.	1.2	94
69	X-ray crystal structure determination and refinement at 1.9 Å... resolution of isolectin I from the seeds of <i>Lathyrus ochrus</i> . <i>Journal of Molecular Biology</i> , 1990, 214, 571-584.	2.0	92
70	Crystal Structure of E.coli Alcohol Dehydrogenase YqhD: Evidence of a Covalently Modified NADP Coenzyme. <i>Journal of Molecular Biology</i> , 2004, 342, 489-502.	2.0	92
71	Deciphering the Xcp Pseudomonas aeruginosa Type II Secretion Machinery through Multiple Interactions with Substrates. <i>Journal of Biological Chemistry</i> , 2011, 286, 40792-40801.	1.6	91
72	Structural Characterization and Oligomerization of the TssL Protein, a Component Shared by Bacterial Type VI and Type IVb Secretion Systems. <i>Journal of Biological Chemistry</i> , 2012, 287, 14157-14168.	1.6	91

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73	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	6.5	90
74	Pancreatic Lipase Structure-Function Relationships by Domain Exchange. <i>Biochemistry</i> , 1997, 36, 239-248.	1.2	89
75	Conformational Changes Occurring upon Reduction and NO Binding in Nitrite Reductase from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 1998, 37, 13987-13996.	1.2	88
76	Structural Basis of the Honey Bee PBP Pheromone and pH-induced Conformational Change. <i>Journal of Molecular Biology</i> , 2008, 380, 158-169.	2.0	87
77	Reverse chemical ecology: Olfactory proteins from the giant panda and their interactions with putative pheromones and bamboo volatiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9802-E9810.	3.3	86
78	Lateral recognition of a dye hapten by a llama VHH domain. <i>Journal of Molecular Biology</i> , 2001, 311, 123-129.	2.0	85
79	Structure, Adsorption to Host, and Infection Mechanism of Virulent Lactococcal Phage p2. <i>Journal of Virology</i> , 2013, 87, 12302-12312.	1.5	85
80	The Insect Attractant 1-Octen-3-ol Is the Natural Ligand of Bovine Odorant-binding Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 7150-7155.	1.6	80
81	Direct in Vivo Screening of Intrabody Libraries Constructed on a Highly Stable Single-chain Framework. <i>Journal of Biological Chemistry</i> , 2002, 277, 45075-45085.	1.6	80
82	High-throughput protein expression screening and purification in <i>Escherichia coli</i> . <i>Methods</i> , 2011, 55, 65-72.	1.9	80
83	Solution conformation of human neuropeptide Y by 1H nuclear magnetic resonance and restrained molecular dynamics. <i>FEBS Journal</i> , 1992, 209, 765-771.	0.2	79
84	CRYStallize: A crystallographic symmetry display and handling subpackage in TOM/FRODO. <i>Journal of Molecular Graphics</i> , 1990, 8, 86-88.	1.7	78
85	Towards a complete structural deciphering of Type VI secretion system. <i>Current Opinion in Structural Biology</i> , 2018, 49, 77-84.	2.6	78
86	Crystal structure of cutinase covalently inhibited by a triglyceride analogue. <i>Protein Science</i> , 1997, 6, 275-286.	3.1	77
87	Structure and Activity of Rat Pancreatic Lipase-related Protein 2. <i>Journal of Biological Chemistry</i> , 1998, 273, 32121-32128.	1.6	76
88	The Crystal Structure of Odorant Binding Protein 7 from <i>Anopheles gambiae</i> Exhibits an Outstanding Adaptability of Its Binding Site. <i>Journal of Molecular Biology</i> , 2011, 414, 401-412.	2.0	76
89	Functional and structural dissection of the tape measure protein of lactococcal phage TP901-1. <i>Scientific Reports</i> , 2016, 6, 36667.	1.6	75
90	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73

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91	Crystal Structure of Bacteriophage SPP1 Distal Tail Protein (gp19.1). <i>Journal of Biological Chemistry</i> , 2010, 285, 36666-36673.	1.6	70
92	Induced refolding of a temperature denatured llama heavy-chain antibody fragment by its antigen. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 555-564.	1.5	67
93	Crystal Structure and Kinetics Identify Escherichia coli YdcW Gene Product as a Medium-chain Aldehyde Dehydrogenase. <i>Journal of Molecular Biology</i> , 2004, 343, 29-41.	2.0	66
94	Automated expression and solubility screening of His-tagged proteins in 96-well format. <i>Analytical Biochemistry</i> , 2005, 346, 77-84.	1.1	65
95	Camelid Ig V genes reveal significant human homology not seen in therapeutic target genes, providing for a powerful therapeutic antibody platform. <i>MAbs</i> , 2015, 7, 693-706.	2.6	65
96	Structures and host-adhesion mechanisms of lactococcal siphophages. <i>Frontiers in Microbiology</i> , 2014, 5, 3.	1.5	63
97	Preanalytical Issues and Cycle Threshold Values in SARS-CoV-2 Real-Time RT-PCR Testing: Should Test Results Include These?. <i>ACS Omega</i> , 2021, 6, 6528-6536.	1.6	63
98	Crystal structure of a ternary complex between human chorionic gonadotropin (hCG) and two Fv fragments specific for the $\text{I}\alpha$ and $\text{I}\beta$ -subunits 1. Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 289, 1375-1385.	2.0	62
99	Crystal Structure of the Receptor-Binding Protein Head Domain from Lactococcus lactis Phage bIL170. <i>Journal of Virology</i> , 2006, 80, 9331-9335.	1.5	62
100	Queen Bee Pheromone Binding Protein pH-Induced Domain Swapping Favors Pheromone Release. <i>Journal of Molecular Biology</i> , 2009, 390, 981-990.	2.0	62
101	Expression and characterization of the protein Rv1399c from Mycobacterium tuberculosis. <i>FEBS Journal</i> , 2004, 271, 3953-3961.	0.2	61
102	An essential role for the baseplate protein Gp45 in phage adsorption to Staphylococcus aureus. <i>Scientific Reports</i> , 2016, 6, 26455.	1.6	61
103	Crystal Structure of the VgrG1 Actin Cross-linking Domain of the Vibrio cholerae Type VI Secretion System. <i>Journal of Biological Chemistry</i> , 2012, 287, 38190-38199.	1.6	60
104	Characterization of the Porphyromonas gingivalis Type IX Secretion Trans-envelope PorKLMNP Core Complex. <i>Journal of Biological Chemistry</i> , 2017, 292, 3252-3261.	1.6	60
105	Crystal structure of a cohesin module from Clostridium cellulolyticum: implications for dockerin recognition. <i>Journal of Molecular Biology</i> , 2000, 304, 189-200.	2.0	59
106	Crystallographic study of the structure of colipase and of the interaction with pancreatic lipase. <i>Protein Science</i> , 1995, 4, 44-57.	3.1	58
107	Complexation of Two Proteic Insect Inhibitors to the Active Site of Chymotrypsin Suggests Decoupled Roles for Binding and Selectivity. <i>Journal of Biological Chemistry</i> , 2001, 276, 38893-38898.	1.6	58
108	The XcpV/GspI Pseudopilin Has a Central Role in the Assembly of a Quaternary Complex within the T2SS Pseudopilus. <i>Journal of Biological Chemistry</i> , 2009, 284, 34580-34589.	1.6	58

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109	The Atomic Structure of the Phage Tuc2009 Baseplate Tripod Suggests that Host Recognition Involves Two Different Carbohydrate Binding Modules. <i>MBio</i> , 2016, 7, e01781-15.	1.8	58
110	Dynamics of <i>Fusarium solani</i> cutinase investigated through structural comparison among different crystal forms of its variants. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 26, 442-458.	1.5	57
111	Structure and activity of <sc>AbiQ</sc>, a lactococcal endoribonuclease belonging to the type <sc>III</sc> toxin-antitoxin system. <i>Molecular Microbiology</i> , 2013, 87, 756-768.	1.2	57
112	Bivalent Llama Single-Domain Antibody Fragments against Tumor Necrosis Factor Have Picomolar Potencies due to Intramolecular Interactions. <i>Frontiers in Immunology</i> , 2017, 8, 867.	2.2	57
113	The Importance of Framework Residues H6, H7 and H10 in Antibody Heavy Chains: Experimental Evidence for a New Structural Subclassification of Antibody VH Domains. <i>Journal of Molecular Biology</i> , 2001, 309, 701-716.	2.0	55
114	Crystal Structure and Function of a DARPIn Neutralizing Inhibitor of Lactococcal Phage TP901-1. <i>Journal of Biological Chemistry</i> , 2009, 284, 30718-30726.	1.6	55
115	Structure and Molecular Assignment of Lactococcal Phage TP901-1 Baseplate. <i>Journal of Biological Chemistry</i> , 2010, 285, 39079-39086.	1.6	55
116	Visualizing a Complete Siphoviridae Member by Single-Particle Electron Microscopy: the Structure of Lactococcal Phage TP901-1. <i>Journal of Virology</i> , 2013, 87, 1061-1068.	1.5	55
117	Type IX secretion system PorM and gliding machinery GldM form arches spanning the periplasmic space. <i>Nature Communications</i> , 2018, 9, 429.	5.8	54
118	Molecular Insights on the Recognition of a <i>Lactococcus lactis</i> Cell Wall Pellicle by the Phage 1358 Receptor Binding Protein. <i>Journal of Virology</i> , 2014, 88, 7005-7015.	1.5	53
119	Boar salivary lipocalin. <i>FEBS Journal</i> , 2002, 269, 2449-2456.	0.2	52
120	Crystal structure of a novel type of odorant-binding protein from <i>Anopheles gambiae</i> , belonging to the C-plus class. <i>Biochemical Journal</i> , 2011, 437, 423-430.	1.7	52
121	Crystal structures of bovine odorant-binding protein in complex with odorant molecules. <i>FEBS Journal</i> , 2004, 271, 3832-3842.	0.2	51
122	A Topological Model of the Baseplate of Lactococcal Phage Tuc2009. <i>Journal of Biological Chemistry</i> , 2008, 283, 2716-2723.	1.6	51
123	Crystal structure of the DNA-bound VapBC2 antitoxin/toxin pair from <i>Rickettsia felis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 3245-3258.	6.5	51
124	Effect of Rickettsial Toxin VapC on Its Eukaryotic Host. <i>PLoS ONE</i> , 2011, 6, e26528.	1.1	51
125	Control of domain swapping in bovine odorant-binding protein. <i>Biochemical Journal</i> , 2002, 365, 739-748.	1.7	50
126	From The Cover: An aminoacyl-tRNA synthetase-like protein encoded by the <i>Escherichia coli</i> yadB gene glutamylates specifically tRNA ^{Asp} . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7530-7535.	3.3	50

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127	Plant stress proteins of the thaumatin-like family discovered in animals. <i>FEBS Letters</i> , 2004, 572, 3-7.	1.3	49
128	The membrane bound bacterial lipocalin Blc is a functional dimer with binding preference for lysophospholipids. <i>FEBS Letters</i> , 2006, 580, 4877-4883.	1.3	48
129	Type VI secretion TssK baseplate protein exhibits structural similarity with phage receptor-binding proteins and evolved to bind the membrane complex. <i>Nature Microbiology</i> , 2017, 2, 17103.	5.9	48
130	A Cutinase from <i>Trichoderma reesei</i> with a Lid-Covered Active Site and Kinetic Properties of True Lipases. <i>Journal of Molecular Biology</i> , 2014, 426, 3757-3772.	2.0	47
131	The gp27-like Hub of VgrG Serves as Adaptor to Promote Hcp Tube Assembly. <i>Journal of Molecular Biology</i> , 2018, 430, 3143-3156.	2.0	47
132	Crystal structure of aphrodisin, a sex pheromone from female hamster ¹ Edited by R Huber. <i>Journal of Molecular Biology</i> , 2001, 305, 459-469.	2.0	46
133	Structure and Functional Analysis of the Host Recognition Device of Lactococcal Phage Tuc2009. <i>Journal of Virology</i> , 2013, 87, 8429-8440.	1.5	46
134	A pheromone-binding protein from the cockroach <i>Leucophaea maderae</i> : cloning, expression and pheromone binding. <i>Biochemical Journal</i> , 2003, 371, 573-579.	1.7	45
135	The <i>Escherichia coli</i> YadB Gene Product Reveals a Novel Aminoacyl-tRNA Synthetase Like Activity. <i>Journal of Molecular Biology</i> , 2004, 337, 273-283.	2.0	45
136	The crystal structure of the <i>Escherichia coli</i> lipocalin Blc suggests a possible role in phospholipid binding. <i>FEBS Letters</i> , 2004, 562, 183-188.	1.3	45
137	VaZyMolO: a tool to define and classify modularity in viral proteins. <i>Journal of General Virology</i> , 2005, 86, 743-749.	1.3	45
138	Mammalian G protein-coupled receptor expression in <i>Escherichia coli</i> : II. Refolding and biophysical characterization of mouse cannabinoid receptor 1 and human parathyroid hormone receptor 1. <i>Analytical Biochemistry</i> , 2010, 401, 74-80.	1.1	45
139	Viral infection modulation and neutralization by camelid nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1371-9.	3.3	45
140	Cas9 Allosteric Inhibition by the Anti-CRISPR Protein AcrIIA6. <i>Molecular Cell</i> , 2019, 76, 922-937.e7.	4.5	44
141	Crystal Structure and Self-Interaction of the Type VI Secretion Tail-Tube Protein from Enterococcal <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e86918.	1.1	44
142	Solution structure of human corticotropin releasing factor by 1H NMR and distance geometry with restrained molecular dynamics. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 149-156.	1.0	43
143	A Hyperthermostable D-Ribose-5-Phosphate Isomerase from <i>Pyrococcus horikoshii</i> Characterization and Three-Dimensional Structure. <i>Structure</i> , 2002, 10, 877-886.	1.6	43
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