

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
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274
all docs

274
docs citations

274
times ranked

16462
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of the surface ligand on the performance of electrochemical SARS-CoV-2 antigen biosensors. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 103-113.	1.9	17
2	Present Impact of AlphaFold2 Revolution on Structural Biology, and an Illustration With the Structure Prediction of the Bacteriophage J-1 Host Adhesion Device. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	18
3	Structure Prediction and Analysis of Hepatitis E Virus Non-Structural Proteins from the Replication and Transcription Machinery by AlphaFold2. <i>Viruses</i> , 2022, 14, 1537.	1.5	8
4	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
5	Crystal structures of two camelid nanobodies raised against GldL, a component of the type IX secretion system from <i>Flavobacterium johnsoniae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 171-176.	0.4	2
6	The Odorant-Binding Proteins of the Spider Mite <i>Tetranychus urticae</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6828.	1.8	7
7	A new non-classical fold of varroa odorant-binding proteins reveals a wide open internal cavity. <i>Scientific Reports</i> , 2021, 11, 13172.	1.6	4
8	Anchoring the T6SS to the cell wall: Crystal structure of the peptidoglycan binding domain of the TagL accessory protein. <i>PLoS ONE</i> , 2021, 16, e0254232.	1.1	7
9	Biogenesis of a Bacteriophage Long Non-Contractile Tail. <i>Journal of Molecular Biology</i> , 2021, 433, 167112.	2.0	6
10	Structure and Topology Prediction of Phage Adhesion Devices Using AlphaFold2: The Case of Two <i>Oenococcus oeni</i> Phages. <i>Microorganisms</i> , 2021, 9, 2151.	1.6	18
11	Wine Phenolic Compounds Differently Affect the Host-Killing Activity of Two Lytic Bacteriophages Infecting the Lactic Acid Bacterium <i>Oenococcus oeni</i> . <i>Viruses</i> , 2020, 12, 1316.	1.5	9
12	Structure of odorant binding proteins and chemosensory proteins determined by X-ray crystallography. <i>Methods in Enzymology</i> , 2020, 642, 151-167.	0.4	2
13	Structural Insights into Lactococcal Siphophage p2 Baseplate Activation Mechanism. <i>Viruses</i> , 2020, 12, 878.	1.5	7
14	Crystal structure of Type IX secretion system PorE C-terminal domain from <i>Porphyromonas gingivalis</i> in complex with a peptidoglycan fragment. <i>Scientific Reports</i> , 2020, 10, 7384.	1.6	12
15	Conserved and Diverse Traits of Adhesion Devices from Siphoviridae Recognizing Proteinaceous or Saccharidic Receptors. <i>Viruses</i> , 2020, 12, 512.	1.5	34
16	Revisiting the host adhesion determinants of <i>Streptococcus thermophilus</i> siphophages. <i>Microbial Biotechnology</i> , 2020, 13, 1765-1779.	2.0	20
17	The CWPS Rubik's cube: Linking diversity of cell wall polysaccharide structures with the encoded biosynthetic machinery of selected <i>Lactococcus lactis</i> strains. <i>Molecular Microbiology</i> , 2020, 114, 582-596.	1.2	19
18	Novel Genus of Phages Infecting <i>Streptococcus thermophilus</i> : Genomic and Morphological Characterization. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	22

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19	Characterization of the First Virulent Phage Infecting <i>Oenococcus oeni</i> , the Queen of the Cellars. <i>Frontiers in Microbiology</i> , 2020, 11, 596541.	1.5	12
20	Ubiquitous Carbohydrate Binding Modules Decorate 936 Lactococcal Siphophage Virions. <i>Viruses</i> , 2019, 11, 631.	1.5	19
21	High-Throughput Protein Production Combined with High- Throughput SELEX Identifies an Extensive Atlas of <i>Ciona robusta</i> Transcription Factor DNA-Binding Specificities. <i>Methods in Molecular Biology</i> , 2019, 2025, 487-517.	0.4	15
22	Cas9 Allosteric Inhibition by the Anti-CRISPR Protein AcrIIA6. <i>Molecular Cell</i> , 2019, 76, 922-937.e7.	4.5	44
23	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
24	Towards a complete structural deciphering of Type VI secretion system. <i>Current Opinion in Structural Biology</i> , 2018, 49, 77-84.	2.6	78
25	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
26	A Decade of <i>Streptococcus thermophilus</i> Phage Evolution in an Irish Dairy Plant. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	35
27	Structureâ€“Function Analysis of the C-Terminal Domain of the Type VI Secretion TssB Tail Sheath Subunit. <i>Journal of Molecular Biology</i> , 2018, 430, 297-309.	2.0	6
28	Structure of the type VI secretion system TssKâ€“TssFâ€“TssG baseplate subcomplex revealed by cryo-electron microscopy. <i>Nature Communications</i> , 2018, 9, 5385.	5.8	37
29	Identification of Dual Receptor Binding Protein Systems in Lactococcal 936 Group Phages. <i>Viruses</i> , 2018, 10, 668.	1.5	12
30	Biochemical and Structural Characterization of TesA, a Major Thioesterase Required for Outer-Envelope Lipid Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2018, 430, 5120-5136.	2.0	22
31	Functional carbohydrate binding modules identified in evolved dits from siphophages infecting various Gramâ€“positive bacteria. <i>Molecular Microbiology</i> , 2018, 110, 777-795.	1.2	32
32	Widespread anti-CRISPR proteins in virulent bacteriophages inhibit a range of Cas9 proteins. <i>Nature Communications</i> , 2018, 9, 2919.	5.8	147
33	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
34	Characterization of the <i>Porphyromonas gingivalis</i> Type IX Secretion Trans-envelope PorKLMNP Core Complex. <i>Journal of Biological Chemistry</i> , 2017, 292, 3252-3261.	1.6	60
35	Evolved distal tail carbohydrate binding modules of <i>actobacillus</i> phage <i>â€“1</i> : a novel type of antiâ€“receptor widespread among lactic acid bacteria phages. <i>Molecular Microbiology</i> , 2017, 104, 608-620.	1.2	35
36	Camelid nanobodies used as crystallization chaperones for different constructs of PorM, a component of the type IX secretion system from <i>Porphyromonas gingivalis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 286-293.	0.4	17

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37	Reverse chemical ecology: Olfactory proteins from the giant panda and their interactions with putative pheromones and bamboo volatiles. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9802-E9810.	3.3	86
38	TssA: The cap protein of the Type VI secretion system tail. BioEssays, 2017, 39, 1600262.	1.2	37
39	Type VI secretion TssK baseplate protein exhibits structural similarity with phage receptor-binding proteins and evolved to bind the membrane complex. Nature Microbiology, 2017, 2, 17103.	5.9	48
40	Genetic and functional characterisation of the lactococcal P335 phage-host interactions. BMC Genomics, 2017, 18, 146.	1.2	29
41	Host recognition by lactic acid bacterial phages. FEMS Microbiology Reviews, 2017, 41, S16-S26.	3.9	35
42	Bivalent Llama Single-Domain Antibody Fragments against Tumor Necrosis Factor Have Picomolar Potencies due to Intramolecular Interactions. Frontiers in Immunology, 2017, 8, 867.	2.2	57
43	Neutralization of Human Interleukin 23 by Multivalent Nanobodies Explained by the Structure of Cytokineâ€“Nanobody Complex. Frontiers in Immunology, 2017, 8, 884.	2.2	35
44	Structure of the host-recognition device of Staphylococcus aureus phage Î•11. Scientific Reports, 2016, 6, 27581.	1.6	42
45	An essential role for the baseplate protein Gp45 in phage adsorption to Staphylococcus aureus. Scientific Reports, 2016, 6, 26455.	1.6	61
46	Structural Mimicry of Receptor Interaction by Antagonistic Interleukin-6 (IL-6) Antibodies. Journal of Biological Chemistry, 2016, 291, 13846-13854.	1.6	24
47	Structureâ€“Function Analysis of the TssL Cytoplasmic Domain Reveals a New Interaction between the Type VI Secretion Baseplate and Membrane Complexes. Journal of Molecular Biology, 2016, 428, 4413-4423.	2.0	33
48	Characterization of prophages containing â€œevolvedâ€•Dit/Tal modules in the genome of Lactobacillus casei BL23. Applied Microbiology and Biotechnology, 2016, 100, 9201-9215.	1.7	22
49	Structure and specificity of the Type VI secretion system ClpV-TssC interaction in enteroaggregative Escherichia coli. Scientific Reports, 2016, 6, 34405.	1.6	31
50	Functional and structural dissection of the tape measure protein of lactococcal phage TP901-1. Scientific Reports, 2016, 6, 36667.	1.6	75
51	A phospholipase A₁ antibacterial Type VI secretion effector interacts directly with the Câ€“terminal domain of the VgrG spike protein for delivery. Molecular Microbiology, 2016, 99, 1099-1118.	1.2	179
52	The Baseplate of Lactobacillus delbrueckii Bacteriophage Ld17 Harbors a Glycerophosphodiesterase. Journal of Biological Chemistry, 2016, 291, 16816-16827.	1.6	11
53	Combining somatic mutations present in different <i>in vivo</i> affinity-matured antibodies isolated from immunized <i>Lama glama</i> yields ultra-potent antibody therapeutics. Protein Engineering, Design and Selection, 2016, 29, 123-133.	1.0	10
54	<i>Lactococcus lactis</i> phage TP901â€“1 as a model for <i>Siphoviridae</i> virion assembly. Bacteriophage, 2016, 6, e1123795.	1.9	15

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55	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
56	Priming and polymerization of a bacterial contractile tail structure. <i>Nature</i> , 2016, 531, 59-63.	13.7	127
57	X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. <i>Journal of Biological Chemistry</i> , 2015, 290, 13191-13201.	1.6	33
58	Crystallization and preliminary X-ray analysis of the C-terminal fragment of PorM, a subunit of the <i>Porphyromonas gingivalis</i> type IX secretion system. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 71-74.	0.4	6
59	Camelid nanobodies: killing two birds with one stone. <i>Current Opinion in Structural Biology</i> , 2015, 32, 1-8.	2.6	101
60	The targeted recognition of <i>Lactococcus lactis</i> phages to their polysaccharide receptors. <i>Molecular Microbiology</i> , 2015, 96, 875-886.	1.2	39
61	Bacteriophage module reshuffling results in adaptive host range as exemplified by the baseplate model of listerial phage A118. <i>Virology</i> , 2015, 484, 86-92.	1.1	11
62	Biogenesis and structure of a type VI secretion membrane core complex. <i>Nature</i> , 2015, 523, 555-560.	13.7	241
63	Production, crystallization and X-ray diffraction analysis of a complex between a fragment of the TssM T6SS protein and a camelid nanobody. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 266-271.	0.4	6
64	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
65	Inhibition of Type VI Secretion by an Anti-TssM Llama Nanobody. <i>PLoS ONE</i> , 2015, 10, e0122187.	1.1	16
66	Structure and Assembly of TP901-1 Virion Unveiled by Mutagenesis. <i>PLoS ONE</i> , 2015, 10, e0131676.	1.1	19
67	Structures and host-adhesion mechanisms of lactococcal siphophages. <i>Frontiers in Microbiology</i> , 2014, 5, 3.	1.5	63
68	Differences in Lactococcal Cell Wall Polysaccharide Structure Are Major Determining Factors in Bacteriophage Sensitivity. <i>MBio</i> , 2014, 5, e00880-14.	1.8	98
69	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
70	Cryo-Electron Microscopy Structure of Lactococcal Siphophage 1358 Virion. <i>Journal of Virology</i> , 2014, 88, 8900-8910.	1.5	30
71	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
72	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

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73	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
74	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
75	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
76	Biochemical and structural characterization of non-glycosylated <i>Yarrowia lipolytica</i> LIP2 lipase. <i>European Journal of Lipid Science and Technology</i> , 2013, 115, 429-441.	1.0	12
77	X-ray structure of a superinfection exclusion lipoprotein from phage TP34 and identification of the tape measure protein as its target. <i>Molecular Microbiology</i> , 2013, 89, 152-165.	1.2	43
78	Ligands for Pheromone-Sensing Neurons Are Not Conformationally Activated Odorant Binding Proteins. <i>PLoS Biology</i> , 2013, 11, e1001546.	2.6	151
79	A Toxin-Antitoxin Module of <i>Salmonella</i> Promotes Virulence in Mice. <i>PLoS Pathogens</i> , 2013, 9, e1003827.	2.1	111
80	The First Structure of a Mycobacteriophage, the <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> Phage Araucaria. <i>Journal of Virology</i> , 2013, 87, 8099-8109.	1.5	35
81	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
82	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
83	Structure, Adsorption to Host, and Infection Mechanism of Virulent Lactococcal Phage p2. <i>Journal of Virology</i> , 2013, 87, 12302-12312.	1.5	85
84	Structure and activity of <i>AbiQ</i> , a lactococcal endoribonuclease belonging to the type III toxin-antitoxin system. <i>Molecular Microbiology</i> , 2013, 87, 756-768.	1.2	57
85	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
86	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
87	Dissection of the TssB-TssC Interface during Type VI Secretion Sheath Complex Formation. <i>PLoS ONE</i> , 2013, 8, e81074.	1.1	19
88	Crystal Structure of the VgrG1 Actin Cross-linking Domain of the <i>Vibrio cholerae</i> Type VI Secretion System. <i>Journal of Biological Chemistry</i> , 2012, 287, 38190-38199.	1.6	60
89	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
90	Involvement of the Major Capsid Protein and Two Early-Expressed Phage Genes in the Activity of the Lactococcal Abortive Infection Mechanism <i>AbiT</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 6890-6899.	1.4	28

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91	Structure of the phage TP901-1 1.8ÅMDa baseplate suggests an alternative host adhesion mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8954-8958.	3.3	121
92	Structural Characterization and Oligomerization of the TssL Protein, a Component Shared by Bacterial Type VI and Type IVb Secretion Systems. Journal of Biological Chemistry, 2012, 287, 14157-14168.	1.6	91
93	Crystal structure of Apis mellifera OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. Insect Biochemistry and Molecular Biology, 2012, 42, 41-50.	1.2	135
94	Structural biology of type VI secretion systems. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 1102-1111.	1.8	191
95	Crystal Structure of ATVORF273, a New Fold for a Thermo- and Acido-Stable Protein from the Acidianus Two-Tailed Virus. PLoS ONE, 2012, 7, e45847.	1.1	7
96	A Common Evolutionary Origin for Tailed-Bacteriophage Functional Modules and Bacterial Machineries. Microbiology and Molecular Biology Reviews, 2011, 75, 423-433.	2.9	234
97	The Crystal Structure of Odorant Binding Protein 7 from Anopheles gambiae Exhibits an Outstanding Adaptability of Its Binding Site. Journal of Molecular Biology, 2011, 414, 401-412.	2.0	76
98	High-throughput protein expression screening and purification in Escherichia coli. Methods, 2011, 55, 65-72.	1.9	80
99	Crystal structure of a novel type of odorant-binding protein from <i>Anopheles gambiae</i> , belonging to the C-plus class. Biochemical Journal, 2011, 437, 423-430.	1.7	52
100	Lactococcal phage p2 ORF35â€šak3 is an ATPase involved in DNA recombination and AbiK mechanism. Molecular Microbiology, 2011, 80, 102-116.	1.2	23
101	Construction of two Lactococcus lactis expression vectors combining the Gateway and the Nlsin Controlled Expression systems. Plasmid, 2011, 66, 129-135.	0.4	17
102	Expanding the molecular toolbox for Lactococcus lactis: construction of an inducible thioredoxin gene fusion expression system. Microbial Cell Factories, 2011, 10, 66.	1.9	28
103	Unraveling Lactococcal Phage Baseplate Assembly by Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.009787.	2.5	24
104	Deciphering the Xcp Pseudomonas aeruginosa Type II Secretion Machinery through Multiple Interactions with Substrates. Journal of Biological Chemistry, 2011, 286, 40792-40801.	1.6	91
105	The Opening of the SPP1 Bacteriophage Tail, a Prevalent Mechanism in Gram-positive-infecting Siphophages. Journal of Biological Chemistry, 2011, 286, 25397-25405.	1.6	40
106	Towards a Structural Comprehension of Bacterial Type VI Secretion Systems: Characterization of the TssJ-TssM Complex of an Escherichia coli Pathovar. PLoS Pathogens, 2011, 7, e1002386.	2.1	132
107	Effect of Rickettsial Toxin VapC on Its Eukaryotic Host. PLoS ONE, 2011, 6, e26528.	1.1	51
108	Mammalian G protein-coupled receptor expression in Escherichia coli: II. Refolding and biophysical characterization of mouse cannabinoid receptor 1 and human parathyroid hormone receptor 1. Analytical Biochemistry, 2010, 401, 74-80.	1.1	45

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109	Getting the best out of long-wavelength X-rays: <i>de novo</i> chlorine/sulfur SAD phasing of a structural protein from ATV. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 304-308.	2.5	37
110	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP. <i>Protein Science</i> , 2010, 19, 1439-1443.	3.1	12
111	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp23.1, a putative chaperone. <i>Protein Science</i> , 2010, 19, 1812-1816.	3.1	11
112	ORF157 from the Archaeal Virus <i>Acidianus</i> Filamentous Virus 1 Defines a New Class of Nuclease. <i>Journal of Virology</i> , 2010, 84, 5025-5031.	1.5	14
113	Lactococcal Abortive Infection Protein AbiV Interacts Directly with the Phage Protein SaV and Prevents Translation of Phage Proteins. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7085-7092.	1.4	23
114	Structure and Molecular Assignment of Lactococcal Phage TP901-1 Baseplate. <i>Journal of Biological Chemistry</i> , 2010, 285, 39079-39086.	1.6	55
115	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
116	Deciphering the function of lactococcal phage ul36 Sak domains. <i>Journal of Structural Biology</i> , 2010, 170, 462-469.	1.3	20
117	Solution and electron microscopy characterization of lactococcal phage baseplates expressed in <i>Escherichia coli</i> . <i>Journal of Structural Biology</i> , 2010, 172, 75-84.	1.3	35
118	Crystal Structure of Bacteriophage SPP1 Distal Tail Protein (gp19.1). <i>Journal of Biological Chemistry</i> , 2010, 285, 36666-36673.	1.6	70
119	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
120	Crystal Structure of ORF12 from <i>Lactococcus lactis</i> Phage p2 Identifies a Tape Measure Protein Chaperone. <i>Journal of Bacteriology</i> , 2009, 191, 728-734.	1.0	26
121	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
122	Crystal Structure of a Chimeric Receptor Binding Protein Constructed from Two Lactococcal Phages. <i>Journal of Bacteriology</i> , 2009, 191, 3220-3225.	1.0	22
123	<i>Acidianus</i> filamentous virus 1 coat proteins display a helical fold spanning the filamentous archaeal viruses lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21155-21160.	3.3	41
124	The crystal structure of ORF14 from <i>Sulfolobus islandicus</i> filamentous virus. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 1020-1022.	1.5	7
125	The thermo- and acid-stable ORF99 from the archaeal virus AFV1. <i>Protein Science</i> , 2009, 18, 1316-1320.	3.1	13
126	Camelid nanobodies raised against an integral membrane enzyme, nitric oxide reductase. <i>Protein Science</i> , 2009, 18, 619-628.	3.1	28

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127	Crystal structure of AFV1â€02, a protein from the acidianus filamentous virus 1. <i>Protein Science</i> , 2009, 18, 845-849.	3.1	7
128	Structure and function of phage p2 ORF34_{p2}, a new type of singleâ€stranded DNA binding protein. <i>Molecular Microbiology</i> , 2009, 73, 1156-1170.	1.2	15
129	Mammalian G-protein-coupled receptor expression in <i>Escherichia coli</i> : I. High-throughput large-scale production as inclusion bodies. <i>Analytical Biochemistry</i> , 2009, 386, 147-155.	1.1	34
130	Production and biophysical characterization of the CorA transporter from <i>Methanosarcina mazei</i> . <i>Analytical Biochemistry</i> , 2009, 388, 115-121.	1.1	18
131	Surfactant Poloxamer 188 as a New Crystallizing Agent for Urate Oxidase. <i>Crystal Growth and Design</i> , 2009, 9, 4199-4206.	1.4	9
132	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
133	High-throughput automated refolding screening of inclusion bodies. <i>Protein Science</i> , 2009, 13, 2782-2792.	3.1	134
134	There is a baby in the bath water: AcrB contamination is a major problem in membrane-protein crystallization. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 880-885.	0.7	40
135	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	9.0	763
136	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
137	A Topological Model of the Baseplate of Lactococcal Phage Tuc2009. <i>Journal of Biological Chemistry</i> , 2008, 283, 2716-2723.	1.6	51
138	Differential Substrate Specificity and Kinetic Behavior of <i>Escherichia coli</i> YfdW and <i>Oxalobacter formigenes</i> Formyl Coenzyme A Transferase. <i>Journal of Bacteriology</i> , 2008, 190, 2556-2564.	1.0	22
139	Crystal structure of AFV3-109, a highly conserved protein from crenarchaeal viruses. <i>Virology Journal</i> , 2007, 4, 12.	1.4	31
140	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
141	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
142	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
143	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
144	Crystallization and preliminary X-ray diffraction analysis of protein 14 from <i>Sulfolobus islandicus</i> filamentous virus (SIFV). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 884-886.	0.7	4

#	ARTICLE	IF	CITATIONS
145	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
146	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
147	Crystal Structure of the Receptor-Binding Protein Head Domain from <i>Lactococcus lactis</i> Phage bIL170. <i>Journal of Virology</i> , 2006, 80, 9331-9335.	1.5	62
148	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
149	Modular Structure of the Receptor Binding Proteins of <i>Lactococcus lactis</i> Phages. <i>Journal of Biological Chemistry</i> , 2006, 281, 14256-14262.	1.6	102
150	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
151	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
152	Automated expression and solubility screening of His-tagged proteins in 96-well format. <i>Analytical Biochemistry</i> , 2005, 346, 77-84.	1.1	65
153	A mutation designed to alter crystal packing permits structural analysis of a tight-binding fluorescein-scFv complex. <i>Protein Science</i> , 2005, 14, 2537-2549.	3.1	27
154	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
155	VaZyMoLO: a tool to define and classify modularity in viral proteins. <i>Journal of General Virology</i> , 2005, 86, 743-749.	1.3	45
156	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
157	Glu-Q-tRNA ^{Asp} synthetase coded by the <i>yadB</i> gene, a new paralog of aminoacyl-tRNA synthetase that glutamylates tRNA ^{Asp} anticodon. <i>Biochimie</i> , 2005, 87, 847-861.	1.3	31
158	Crystal structure of the conserved hypothetical protein Rv1155 from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2005, 579, 215-221.	1.3	25
159	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
160	A minimalist glutamyl-tRNA synthetase dedicated to aminoacylation of the tRNA ^{Asp} QUC anticodon. <i>Nucleic Acids Research</i> , 2004, 32, 2768-2775.	6.5	43
161	From The Cover: An aminoacyl-tRNA synthetase-like protein encoded by the <i>Escherichia coli yadB</i> 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
162	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

#	ARTICLE	IF	CITATIONS
163	Crystal structures of bovine odorant-binding protein in complex with odorant molecules. FEBS Journal, 2004, 271, 3832-3842.	0.2	51
164	Expression and characterization of the protein Rv1399c from Mycobacterium tuberculosis. FEBS Journal, 2004, 271, 3953-3961.	0.2	61
165	Structural aspects of sexual attraction and chemical communication in insects. Trends in Biochemical Sciences, 2004, 29, 257-264.	3.7	269
166	Crystal structure of E. coli yddE protein reveals a striking homology with diaminopimelate epimerase. Proteins: Structure, Function and Bioinformatics, 2004, 55, 764-767.	1.5	7
167	Structure of Escherichia coli YhdH, a putative quinone oxidoreductase. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1855-1862.	2.5	15
168	Directed in Vitro Evolution and Crystallographic Analysis of a Peptide-binding Single Chain Antibody Fragment (scFv) with Low Picomolar Affinity. Journal of Biological Chemistry, 2004, 279, 18870-18877.	1.6	160
169	Crystal structure and reactivity of YbdL from Escherichia coli identify a methionine aminotransferase function. FEBS Letters, 2004, 571, 141-146.	1.3	18
170	Plant stress proteins of the thaumatin-like family discovered in animals. FEBS Letters, 2004, 572, 3-7.	1.3	49
171	The Escherichia coli YadB Gene Product Reveals a Novel Aminoacyl-tRNA Synthetase Like Activity. Journal of Molecular Biology, 2004, 337, 273-283.	2.0	45
172	Crystal Structure of E. coli Alcohol Dehydrogenase YqhD: Evidence of a Covalently Modified NADP Coenzyme. Journal of Molecular Biology, 2004, 342, 489-502.	2.0	92
173	Crystal Structure and Kinetics Identify Escherichia coli YdcW Gene Product as a Medium-chain Aldehyde Dehydrogenase. Journal of Molecular Biology, 2004, 343, 29-41.	2.0	66
174	The crystal structure of the Escherichia coli lipocalin Blc suggests a possible role in phospholipid binding. FEBS Letters, 2004, 562, 183-188.	1.3	45
175	Domain swapping of a llama VHH domain builds a crystal-wide β^2 -sheet structure. FEBS Letters, 2004, 564, 35-40.	1.3	32
176	Crystallization and preliminary crystallographic study of a pheromone-binding protein from the cockroach Leucophaea maderae. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 916-918.	2.5	4
177	Optimization of crystals from nanodrops: crystallization and preliminary crystallographic study of a pheromone-binding protein from the honeybee Apis mellifera L. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 919-921.	2.5	19
178	Structural genomics of the SARS coronavirus: cloning, expression, crystallization and preliminary crystallographic study of the Nsp9 protein. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1628-1631.	2.5	34
179	Medium-Scale Structural Genomics: Strategies for Protein Expression and Crystallization. Accounts of Chemical Research, 2003, 36, 165-172.	7.6	116
180	Quaternary structure of alpha-crustacyanin from lobster as seen by small-angle X-ray scattering. FEBS Letters, 2003, 544, 189-193.	1.3	19

#	ARTICLE	IF	CITATIONS
181	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
182	The Crystal Structure of the Escherichia coli YfdW Gene Product Reveals a New Fold of Two Interlaced Rings Identifying a Wide Family of CoA Transferases. <i>Journal of Biological Chemistry</i> , 2003, 278, 34582-34586.	1.6	34
183	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
184	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
185	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
186	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
187	Three Camelid VHH Domains in Complex with Porcine Pancreatic $\hat{I}\pm$ -Amylase. <i>Journal of Biological Chemistry</i> , 2002, 277, 23645-23650.	1.6	145
188	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
189	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
190	Control of domain swapping in bovine odorant-binding protein. <i>Biochemical Journal</i> , 2002, 365, 739-748.	1.7	50
191	Cyanide Binding to cd1 Nitrite Reductase from <i>Pseudomonas aeruginosa</i> : Role of the Active-Site His369 in Ligand Stabilization. <i>Biochemical and Biophysical Research Communications</i> , 2002, 291, 1-7.	1.0	19
192	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
193	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73
194	Boar salivary lipocalin. <i>FEBS Journal</i> , 2002, 269, 2449-2456.	0.2	52
195	Solution structure and backbone dynamics of an antigen-free heavy chain variable domain (VHH) from Llama. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 546-555.	1.5	33
196	Crystal structure of aphrodisin, a sex pheromone from female hamster11 Edited by R Huber. <i>Journal of Molecular Biology</i> , 2001, 305, 459-469.	2.0	46
197	Selection, Characterization and X-ray Structure of Anti-ampicillin Single-chain Fv Fragments from Phage-displayed Murine Antibody Libraries. <i>Journal of Molecular Biology</i> , 2001, 309, 671-685.	2.0	36
198	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

#	ARTICLE	IF	CITATIONS
199	Lateral recognition of a dye hapten by a llama VHH domain. <i>Journal of Molecular Biology</i> , 2001, 311, 123-129.	2.0	85
200	Domain Swing Upon His to Ala Mutation in Nitrite Reductase of <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2001, 312, 541-554.	2.0	22
201	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
202	Chemosensory protein from the moth <i>Mamestra brassicae</i> . <i>FEBS Journal</i> , 2001, 268, 4731-4739.	0.2	29
203	Recombinant chemosensory protein (CSP2) from the moth <i>Mamestra brassicae</i> : crystallization and preliminary crystallographic study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 137-139.	2.5	11
204	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
205	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
206	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
207	A novel type of catalytic copper cluster in nitrous oxide reductase. <i>Nature Structural Biology</i> , 2000, 7, 191-195.	9.7	280
208	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
209	Structural and Genomic Correlates of Hyperthermostability. <i>Journal of Biological Chemistry</i> , 2000, 275, 32383-32386.	1.6	246
210	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
211	Crystal structure of a cohesin module from <i>Clostridium cellulolyticum</i> : implications for dockerin recognition. <i>Journal of Molecular Biology</i> , 2000, 304, 189-200.	2.0	59
212	Digestive lipases: From three-dimensional structure to physiology. <i>Biochimie</i> , 2000, 82, 973-986.	1.3	104
213	Camelid Heavy-Chain Variable Domains Provide Efficient Combining Sites to Haptens. <i>Biochemistry</i> , 2000, 39, 1217-1222.	1.2	144
214	Does the Reduction of c Heme Trigger the Conformational Change of Crystalline Nitrite Reductase?. <i>Journal of Biological Chemistry</i> , 1999, 274, 14997-15004.	1.6	31
215	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
216	Recombinant pheromone binding protein 1 from <i>Mamestra brassicae</i> (MbraPBP1) . Functional and structural characterization. <i>FEBS Journal</i> , 1999, 264, 707-716.	0.2	41

#	ARTICLE	IF	CITATIONS
217	The structure of an entire noncovalent immunoglobulin kappa light-chain dimer (Bence-Jones protein) reveals a weak and unusual constant domains association. <i>FEBS Journal</i> , 1999, 260, 192-199.	0.2	34
218	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
219	MAD Structure of Pseudomonas nautica Dimeric Cytochrome c552 Mimics the 4-Dihemic Cytochrome Domain Association. <i>Journal of Molecular Biology</i> , 1999, 289, 1017-1028.	2.0	30
220	Crystal structure of a ternary complex between human chorionic gonadotropin (hCG) and two Fv fragments specific for the α 1 and α 2-subunits. Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 289, 1375-1385.	2.0	62
221	Insight into odorant perception: the crystal structure and binding characteristics of antibody fragments directed against the musk odorant traseolide. <i>Journal of Molecular Biology</i> , 1999, 292, 855-869.	2.0	7
222	An inactive pancreatic-related protein is activated into a triglyceride-lipase by mutagenesis based on the 3-D structure. <i>Chemistry and Physics of Lipids</i> , 1998, 93, 103-114.	1.5	12
223	Molecular cloning and bacterial expression of a general odorant-binding protein from the cabbage armyworm <i>Mamestra brassicae</i> . <i>FEBS Journal</i> , 1998, 258, 768-774.	0.2	34
224	Structure-function relationships of pancreatic lipases. <i>Lipid - Fett</i> , 1998, 100, 96-102.	0.6	7
225	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
226	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
227	Structure and Activity of Rat Pancreatic Lipase-related Protein 2. <i>Journal of Biological Chemistry</i> , 1998, 273, 32121-32128.	1.6	76
228	[5] Pancreatic lipases and their complexes with colipases and inhibitors: Crystallization and crystal packing. <i>Methods in Enzymology</i> , 1997, 284, 107-119.	0.4	14
229	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
230	Pancreatic Lipase Structure-Function Relationships by Domain Exchange. <i>Biochemistry</i> , 1997, 36, 239-248.	1.2	89
231	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
232	Crystal structure of cutinase covalently inhibited by a triglyceride analogue. <i>Protein Science</i> , 1997, 6, 275-286.	3.1	77
233	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
234	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

#	ARTICLE	IF	CITATIONS
235	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
236	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
237	The crystal structure of a llama heavy chain variable domain. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 752-757.	3.6	131
238	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
239	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
240	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
241	The 2.6 Å refined structure of the <i>Escherichia coli</i> recombinant <i>Saccharomyces cerevisiae</i> flavocytochrome <i>b₂</i> sulfite complex. <i>Protein Science</i> , 1994, 3, 303-313.	3.1	33
242	Interactions of plant lectins with the components of the bacterial cell wall peptidoglycan. <i>Biochemical Systematics and Ecology</i> , 1994, 22, 153-159.	0.6	30
243	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
244	Cutinase, a lipolytic enzyme with a preformed oxyanion hole. <i>Biochemistry</i> , 1994, 33, 83-89.	1.2	176
245	Crystallization and Preliminary X-ray Diffraction Studies of the Soluble 14 kDa β -Galactoside-binding Lectin from Bovine Heart. <i>Journal of Molecular Biology</i> , 1994, 235, 787-789.	2.0	19
246	Horse Pancreatic Lipase. <i>Journal of Molecular Biology</i> , 1994, 238, 709-732.	2.0	106
247	Crystallization and Preliminary X-ray Analysis of a New Crystal form of Nitrite Reductase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 1994, 243, 347-350.	2.0	8
248	A hypothetical complex between crystalline flavocytochrome <i>b₂</i> and Cytochrome <i>c</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 408-422.	1.5	25
249	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
250	Crystallization of Pancreatic Procolipase and of its Complex with Pancreatic Lipase. <i>Journal of Molecular Biology</i> , 1993, 229, 552-554.	2.0	37
251	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
252	Engineering cysteine mutants to obtain crystallographic phases with a cutinase from <i>Fusarium solani</i> pisi. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 157-165.	1.0	26

#	ARTICLE	IF	CITATIONS
253	Crystallization and preliminary X-ray diffraction study of Lathyrus ochrus isolectin II complexed to the human lactotransferrin N2 fragment. <i>Journal of Molecular Biology</i> , 1992, 227, 938-941.	2.0	13
254	Isoform purification of gastric lipases. <i>Journal of Molecular Biology</i> , 1992, 225, 147-153.	2.0	39
255	Fusarium solani cutinase is a lipolytic enzyme with a catalytic serine accessible to solvent. <i>Nature</i> , 1992, 356, 615-618.	13.7	414
256	Structure of the pancreatic lipase-procolipase complex. <i>Nature</i> , 1992, 359, 159-162.	13.7	374
257	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
258	Monoclonal antibody 117,C-11 recognizes three exposed regions on the surface of the Lathyrus ochrus isolectin I. <i>Immunology Letters</i> , 1991, 30, 47-51.	1.1	2
259	Three-Dimensionnal structures of complexes of Lathyrus ochrus 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
260	CRYStallize: A crystallographic symmetry display and handling subpackage in TOM/FRODO. <i>Journal of Molecular Graphics</i> , 1990, 8, 86-88.	1.7	78
261	Co-crystallization and preliminary X-ray diffraction studies of Lathyrus ochrus isolectin I with Di- and trisaccharides, and a biantennary octosaccharide. <i>Journal of Molecular Biology</i> , 1990, 213, 211-213.	2.0	10
262	Crystallization and preliminary X-ray study of a recombinant cutinase from Fusarium solani pisi. <i>Journal of Molecular Biology</i> , 1990, 215, 215-216.	2.0	19
263	X-ray crystal structure determination and refinement at 1.9 Å... resolution of isolectin I from the seeds of Lathyrus ochrus. <i>Journal of Molecular Biology</i> , 1990, 214, 571-584.	2.0	92
264	Crystallization and preliminary X-ray study of horse pancreatic lipase. <i>Journal of Molecular Biology</i> , 1989, 205, 259-261.	2.0	27
265	Amino acid sequence determination and three-dimensional modelling of thioredoxin from the photosynthetic bacterium Rhodobacter sphaeroides Y. <i>FEBS Journal</i> , 1988, 172, 413-419.	0.2	24
266	Subunit III of ruminant procarboxypeptidase A-S6 complexes and pancreatic proteases E a new family of pancreatic serine endopeptidases?. <i>FEBS Letters</i> , 1988, 232, 91-95.	1.3	15
267	Crystallization and preliminary X-ray studies of two isolectins from the seeds of Lathyrus ochrus. <i>Journal of Molecular Biology</i> , 1988, 202, 685-687.	2.0	8
268	Crystallization, preliminary X-ray study and crystal activity of the hydrogenase from Desulfovibrio gigas. <i>Journal of Molecular Biology</i> , 1987, 195, 969-971.	2.0	26
269	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
270	Crystallization and preliminary X-ray study of subunit III of the bovine pancreatic procarboxypeptidase A-S6 ternary complex. <i>Journal of Molecular Biology</i> , 1986, 189, 709-710.	2.0	5

#	ARTICLE	IF	CITATIONS
271	The inactive subunit of ruminant procarboxypeptidase A-S6 complexes. Structural basis of inactivity and physiological role. FEBS Journal, 1986, 157, 531-538.	0.2	23