

# James C Whisstock

## List of Publications by Year in descending order

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252  
papers

17,327  
citations

13865

67  
h-index

17592

121  
g-index

264  
all docs

264  
docs citations

264  
times ranked

20585  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein engineering of a stable and potent anti-inflammatory IL-37-Fc fusion with enhanced therapeutic potential. <i>Cell Chemical Biology</i> , 2022, 29, 586-596.e4.	5.2	7
2	A mechanism for hereditary angioedema caused by a lysine 311 to glutamic acid substitution in plasminogen. <i>Blood</i> , 2022, 139, 2816-2829.	1.4	17
3	Macrophage self-renewal is regulated by transient expression of PDGF and VEGF-related factor 2. <i>FEBS Journal</i> , 2022, 289, 3735-3751.	4.7	2
4	Mining folded proteomes in the era of accurate structure prediction. <i>PLoS Computational Biology</i> , 2022, 18, e1009930.	3.2	9
5	Mpeg1 is not essential for antibacterial or antiviral immunity, but is implicated in antigen presentation. <i>Immunology and Cell Biology</i> , 2022, 100, 529-546.	2.3	4
6	Structural analysis of the PTEN:P-Rex2 signaling complex reveals how cancer-associated mutations coordinate to hyperactivate Rac1. <i>Science Signaling</i> , 2021, 14, .	3.6	6
7	Characterization of the pathoimmunology of necrotizing enterocolitis reveals novel therapeutic opportunities. <i>Nature Communications</i> , 2020, 11, 5794.	12.8	53
8	Ancient but Not Forgotten: New Insights Into MPEG1, a Macrophage Perforin-Like Immune Effector. <i>Frontiers in Immunology</i> , 2020, 11, 581906.	4.8	17
9	Mapping the binding site of C1-inhibitor for polyanion cofactors. <i>Molecular Immunology</i> , 2020, 126, 8-13.	2.2	3
10	Human Plasminogen Exacerbates <i>Clostridioides difficile</i> Enteric Disease and Alters the Spore Surface. <i>Gastroenterology</i> , 2020, 159, 1431-1443.e6.	1.3	7
11	Anti-CDCP1 immuno-conjugates for detection and inhibition of ovarian cancer. <i>Theranostics</i> , 2020, 10, 2095-2114.	10.0	15
12	Automated cryo-lamella preparation for high-throughput in-situ structural biology. <i>Journal of Structural Biology</i> , 2020, 210, 107488.	2.8	70
13	Parsing the IL-37-Mediated Suppression of Inflammasome Function. <i>Cells</i> , 2020, 9, 178.	4.1	21
14	Effective targeting of intact and proteolysed CDCP1 for imaging and treatment of pancreatic ductal adenocarcinoma. <i>Theranostics</i> , 2020, 10, 4116-4133.	10.0	23
15	Solution structural model of the complex of the binding regions of human plasminogen with its M-protein receptor from <i>Streptococcus pyogenes</i> . <i>Journal of Structural Biology</i> , 2019, 208, 18-29.	2.8	8
16	Structure and Function Characterization of the a1a2 Motifs of <i>Streptococcus pyogenes</i> M Protein in Human Plasminogen Binding. <i>Journal of Molecular Biology</i> , 2019, 431, 3804-3813.	4.2	9
17	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. <i>Nature Communications</i> , 2019, 10, 4288.	12.8	65
18	Control of growth factor signalling by MACPF proteins. <i>Biochemical Society Transactions</i> , 2019, 47, 801-810.	3.4	2

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19	Structural studies of plasmin inhibition. <i>Biochemical Society Transactions</i> , 2019, 47, 541-557.	3.4	24
20	Tranexamic acid is an active site inhibitor of urokinase plasminogen activator. <i>Blood Advances</i> , 2019, 3, 729-733.	5.2	22
21	Characterising the Subsite Specificity of Urokinase-Type Plasminogen Activator and Tissue-Type Plasminogen Activator using a Sequence-Defined Peptide Aldehyde Library. <i>ChemBioChem</i> , 2019, 20, 46-50.	2.6	5
22	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. <i>Briefings in Bioinformatics</i> , 2019, 20, 2150-2166.	6.5	70
23	Brentuximab vedotin in T-cell lymphoma. <i>Expert Review of Hematology</i> , 2019, 12, 5-19.	2.2	18
24	Highly Potent and Selective Plasmin Inhibitors Based on the Sunflower Trypsin Inhibitor-1 Scaffold Attenuate Fibrinolysis in Plasma. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 552-560.	6.4	27
25	Torso-Like Is a Component of the Hemolymph and Regulates the Insulin Signaling Pathway in <i>Drosophila</i> . <i>Genetics</i> , 2018, 208, 1523-1533.	2.9	8
26	Genome-Wide Screen for New Components of the <i>Drosophila melanogaster</i> Torso Receptor Tyrosine Kinase Pathway. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 761-769.	1.8	1
27	Perforin proteostasis is regulated through its C2 domain: supra-physiological cell death mediated by T431D-perforin. <i>Cell Death and Differentiation</i> , 2018, 25, 1517-1529.	11.2	4
28	Crystal structure of TcpK in complex with oriT DNA of the antibiotic resistance plasmid pCW3. <i>Nature Communications</i> , 2018, 9, 3732.	12.8	18
29	PhosContext2vec: a distributed representation of residue-level sequence contexts and its application to general and kinase-specific phosphorylation site prediction. <i>Scientific Reports</i> , 2018, 8, 8240.	3.3	25
30	The first transmembrane region of complement component-9 acts as a brake on its self-assembly. <i>Nature Communications</i> , 2018, 9, 3266.	12.8	56
31	Antibodies: From novel repertoires to defining and refining the structure of biologically important targets. <i>Methods</i> , 2017, 116, 12-22.	3.8	6
32	Real-time visualization of perforin nanopore assembly. <i>Nature Nanotechnology</i> , 2017, 12, 467-473.	31.5	88
33	Homodimerization attenuates the anti-inflammatory activity of interleukin-37. <i>Science Immunology</i> , 2017, 2, .	11.9	51
34	Maternal Torso-Like Coordinates Tissue Folding During <i>Drosophila</i> Gastrulation. <i>Genetics</i> , 2017, 206, 1459-1468.	2.9	11
35	Cell Traversal Activity Is Important for <i>Plasmodium falciparum</i> Liver Infection in Humanized Mice. <i>Cell Reports</i> , 2017, 18, 3105-3116.	6.4	91
36	The Structural Basis for Complement Inhibition by Gigastasin, a Protease Inhibitor from the Giant Amazon Leech. <i>Journal of Immunology</i> , 2017, 199, 3883-3891.	0.8	14

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37	An Essential Role of Maspin in Embryogenesis and Tumor Suppression Letter. <i>Cancer Research</i> , 2017, 77, 5207-5207.	0.9	1
38	Perforin A key (shaped) weapon in the immunological arsenal. <i>Seminars in Cell and Developmental Biology</i> , 2017, 72, 117-123.	5.0	24
39	Regulation of perforin activation and pre-synaptic toxicity through C-terminal glycosylation. <i>EMBO Reports</i> , 2017, 18, 1775-1785.	4.5	27
40	X-ray crystal structure of plasmin with tranexamic acid-derived active site inhibitors. <i>Blood Advances</i> , 2017, 1, 766-771.	5.2	25
41	Mice Lacking Brinp2 or Brinp3, or Both, Exhibit Behaviors Consistent with Neurodevelopmental Disorders. <i>Frontiers in Behavioral Neuroscience</i> , 2016, 10, 196.	2.0	12
42	TcpM: a novel relaxase that mediates transfer of large conjugative plasmids from <i>Clostridium perfringens</i> . <i>Molecular Microbiology</i> , 2016, 99, 884-896.	2.5	36
43	N-terminal domain of <i>Bothrops asper</i> Myotoxin II Enhances the Activity of Endothelin Converting Enzyme-1 and Neprilysin. <i>Scientific Reports</i> , 2016, 6, 22413.	3.3	8
44	Development of the Cellular Immune System of <i>Drosophila</i> Requires the Membrane Attack Complex/Perforin-Like Protein Torso-Like. <i>Genetics</i> , 2016, 204, 675-681.	2.9	11
45	Structure of the poly-C9 component of the complement membrane attack complex. <i>Nature Communications</i> , 2016, 7, 10588.	12.8	112
46	Smoothing a rugged protein folding landscape by sequence-based redesign. <i>Scientific Reports</i> , 2016, 6, 33958.	3.3	22
47	Brinp1 <sup>-/-</sup> mice exhibit autism-like behaviour, altered memory, hyperactivity and increased parvalbumin-positive cortical interneuron density. <i>Molecular Autism</i> , 2016, 7, 22.	4.9	31
48	Giant MACPF/CDC pore forming toxins: A class of their own. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 475-486.	2.6	61
49	Torso-like mediates extracellular accumulation of Furin-cleaved Trunk to pattern the <i>Drosophila</i> embryo termini. <i>Nature Communications</i> , 2015, 6, 8759.	12.8	31
50	Stability of the Octameric Structure Affects Plasminogen-Binding Capacity of Streptococcal Enolase. <i>PLoS ONE</i> , 2015, 10, e0121764.	2.5	14
51	Perforin and granzymes: function, dysfunction and human pathology. <i>Nature Reviews Immunology</i> , 2015, 15, 388-400.	22.7	858
52	Stonefish toxin defines an ancient branch of the perforin-like superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15360-15365.	7.1	69
53	Analysis of Perforin Assembly by Quartz Crystal Microbalance Reveals a Role for Cholesterol and Calcium-independent Membrane Binding. <i>Journal of Biological Chemistry</i> , 2015, 290, 31101-31112.	3.4	4
54	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. <i>Bioinformatics</i> , 2015, 31, 1411-1419.	4.1	167

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55	IL-37 requires the receptors IL-18R $\alpha$ and IL-1R8 (SIGIRR) to carry out its multifaceted anti-inflammatory program upon innate signal transduction. <i>Nature Immunology</i> , 2015, 16, 354-365.	14.5	352
56	Preferential Acquisition and Activation of Plasminogen Glycoform II by PAM Positive Group A Streptococcal Isolates. <i>Biochemistry</i> , 2015, 54, 3960-3968.	2.5	4
57	Bone morphogenetic protein/retinoic acid inducible neural-specific protein (brinp) expression during <i>Danio rerio</i> development. <i>Gene Expression Patterns</i> , 2015, 18, 37-43.	0.8	9
58	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	5.6	114
59	Structural Basis for Ca <sup>2+</sup> -mediated Interaction of the Perforin C2 Domain with Lipid Membranes. <i>Journal of Biological Chemistry</i> , 2015, 290, 25213-25226.	3.4	25
60	The Phosphatidylinositol (3,4,5)-Trisphosphate-dependent Rac Exchanger 1-Ras-related C3 Botulinum Toxin Substrate 1 (P-Rex1-Rac1) Complex Reveals the Basis of Rac1 Activation in Breast Cancer Cells. <i>Journal of Biological Chemistry</i> , 2015, 290, 20827-20840.	3.4	46
61	A New Model for Pore Formation by Cholesterol-Dependent Cytolysins. <i>PLoS Computational Biology</i> , 2014, 10, e1003791.	3.2	33
62	Trunk cleavage is essential for <i>Drosophila</i> terminal patterning and can occur independently of Torso-like. <i>Nature Communications</i> , 2014, 5, 3419.	12.8	26
63	Maspin is not required for embryonic development or tumour suppression. <i>Nature Communications</i> , 2014, 5, 3164.	12.8	30
64	Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. <i>Bioinformatics</i> , 2014, 30, 71-80.	4.1	63
65	The Perforin Pore Facilitates the Delivery of Cationic Cargos. <i>Journal of Biological Chemistry</i> , 2014, 289, 9172-9181.	3.4	30
66	The Three-dimensional Structure of the Extracellular Adhesion Domain of the Sialic Acid-binding Adhesin SabA from <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6332-6340.	3.4	54
67	High resolution structure of cleaved Serpin 42A from <i>Drosophila melanogaster</i> . <i>BMC Structural Biology</i> , 2014, 14, 14.	2.3	15
68	Reconciling the Structural Attributes of Avian Antibodies. <i>Journal of Biological Chemistry</i> , 2014, 289, 15384-15392.	3.4	28
69	Capturing embryonic development from metamorphosis: how did the terminal patterning signalling pathway of <i>Drosophila</i> evolve?. <i>Current Opinion in Insect Science</i> , 2014, 1, 45-51.	4.4	9
70	A tale of two specificities: bispecific antibodies for therapeutic and diagnostic applications. <i>Trends in Biotechnology</i> , 2013, 31, 621-632.	9.3	148
71	Torso-like functions independently of Torso to regulate <i>Drosophila</i> growth and developmental timing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14688-14692.	7.1	48
72	Structural and Functional Analysis of the Pore-Forming Toxin NetB from <i>Clostridium perfringens</i> . <i>MBio</i> , 2013, 4, e00019-13.	4.1	64

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73	Torqueing about pores. <i>Nature Chemical Biology</i> , 2013, 9, 605-606.	8.0	1
74	Perforin forms transient pores on the target cell plasma membrane to facilitate rapid access of granzymes during killer cell attack. <i>Blood</i> , 2013, 121, 2659-2668.	1.4	208
75	New insights into the structure and function of the plasminogen/plasmin system. <i>Current Opinion in Structural Biology</i> , 2013, 23, 836-841.	5.7	112
76	Defining the interaction of perforin with calcium and the phospholipid membrane. <i>Biochemical Journal</i> , 2013, 456, 323-335.	3.7	16
77	The x-ray crystal structure of mannose-binding lectin-associated serine proteinase-3 reveals the structural basis for enzyme inactivity associated with the Carnevale, Mingarelli, Malpuech, and Michels (3MC) syndrome.. <i>Journal of Biological Chemistry</i> , 2013, 288, 28307.	3.4	0
78	A Molecular Switch Governs the Interaction between the Human Complement Protease C1s and Its Substrate, Complement C4. <i>Journal of Biological Chemistry</i> , 2013, 288, 15821-15829.	3.4	29
79	Structural characterization of the mechanism through which human glutamic acid decarboxylase auto-activates. <i>Bioscience Reports</i> , 2013, 33, 137-44.	2.4	16
80	Mechanistic characterization and crystal structure of a small molecule inactivator bound to plasminogen activator inhibitor-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4941-9.	7.1	27
81	The X-ray Crystal Structure of Mannose-binding Lectin-associated Serine Proteinase-3 Reveals the Structural Basis for Enzyme Inactivity Associated with the Carnevale, Mingarelli, Malpuech, and Michels (3MC) Syndrome. <i>Journal of Biological Chemistry</i> , 2013, 288, 22399-22407.	3.4	23
82	Assembling the machinery of coagulation. <i>Blood</i> , 2013, 122, 2773-2774.	1.4	2
83	RAB-Like 2 Has an Essential Role in Male Fertility, Sperm Intra-Flagellar Transport, and Tail Assembly. <i>PLoS Genetics</i> , 2012, 8, e1002969.	3.5	72
84	Efficient large-scale protein sequence comparison and gene matching to identify orthologs and co-orthologs. <i>Nucleic Acids Research</i> , 2012, 40, e44-e44.	14.5	17
85	Predicting giant transmembrane $\beta^2$ -barrel architecture. <i>Bioinformatics</i> , 2012, 28, 1299-1302.	4.1	25
86	A Versatile Monoclonal Antibody Specific to Human SERPINB5. <i>Hybridoma</i> , 2012, 31, 333-339.	0.4	3
87	The Extracellular Protein Factor Epf from <i>Streptococcus pyogenes</i> Is a Cell Surface Adhesin That Binds to Cells through an N-terminal Domain Containing a Carbohydrate-binding Module. <i>Journal of Biological Chemistry</i> , 2012, 287, 38178-38189.	3.4	18
88	X-ray crystal structure of the streptococcal specific phage lysin PlyC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12752-12757.	7.1	80
89	The AprV5 Subtilase Is Required for the Optimal Processing of All Three Extracellular Serine Proteases from <i>Dichelobacter nodosus</i> . <i>PLoS ONE</i> , 2012, 7, e47932.	2.5	12
90	X-ray Crystal Structure and Specificity of the <i>Plasmodium falciparum</i> Malaria Aminopeptidase PfM18AAP. <i>Journal of Molecular Biology</i> , 2012, 422, 495-507.	4.2	33

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91	Protecting a serial killer: pathways for perforin trafficking and self-defence ensure sequential target cell death. <i>Trends in Immunology</i> , 2012, 33, 406-412.	6.8	71
92	The X-ray Crystal Structure of Full-Length Human Plasminogen. <i>Cell Reports</i> , 2012, 1, 185-190.	6.4	189
93	Perforin evolved from a gene duplication of MPEP1, followed by a complex pattern of gene gain and loss within Euteleostomi. <i>BMC Evolutionary Biology</i> , 2012, 12, 59.	3.2	43
94	The conjugation protein TcpC from <i>Clostridium perfringens</i> is structurally related to the type IV secretion system protein VirB8 from Gram-negative bacteria. <i>Molecular Microbiology</i> , 2012, 83, 275-288.	2.5	68
95	Structural insights into multi-protein communication systems. <i>Current Opinion in Structural Biology</i> , 2012, 22, 313-315.	5.7	0
96	A Novel DNM2 Mutation Displaying Embryonic Lethality and Impaired Transferrin Uptake Identified in a Mouse ENU Mutagenesis Screen for Genes Perturbing Erythropoiesis. <i>Blood</i> , 2012, 120, 608-608.	1.4	1
97	Fingerprinting the Substrate Specificity of M1 and M17 Aminopeptidases of Human Malaria, <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2012, 7, e31938.	2.5	64
98	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. <i>PLoS ONE</i> , 2012, 7, e50300.	2.5	265
99	Synthesis of New $\alpha^1$ -Bestatin-Based Inhibitor Libraries Reveals a Novel Binding Mode in the S1 Pocket of the Essential Malaria M1 Metalloaminopeptidase. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 1655-1666.	6.4	54
100	Molecular basis of $\alpha_1$ -antitrypsin deficiency revealed by the structure of a domain-swapped trimer. <i>EMBO Reports</i> , 2011, 12, 1011-1017.	4.5	142
101	Functional analysis of the <i>Listeria monocytogenes</i> secretion chaperone PrsA2 and its multiple contributions to bacterial virulence. <i>Molecular Microbiology</i> , 2011, 80, 1530-1548.	2.5	43
102	Protection from Endogenous Perforin: Glycans and the C Terminus Regulate Exocytic Trafficking in Cytotoxic Lymphocytes. <i>Immunity</i> , 2011, 34, 879-892.	14.3	63
103	Automatic generation of protein structure cartoons with Pro-origami. <i>Bioinformatics</i> , 2011, 27, 3315-3316.	4.1	173
104	Crystallography of Serpins and Serpin Complexes. <i>Methods in Enzymology</i> , 2011, 501, 63-87.	1.0	17
105	Preface. <i>Methods in Enzymology</i> , 2011, 501, xvii-xviii.	1.0	0
106	Preface. <i>Methods in Enzymology</i> , 2011, 499, xix-xx.	1.0	0
107	Predicting Serpin/Protease Interactions. <i>Methods in Enzymology</i> , 2011, 501, 237-273.	1.0	7
108	S1 Pocket of a Bacterially Derived Subtilisin-like Protease Underpins Effective Tissue Destruction. <i>Journal of Biological Chemistry</i> , 2011, 286, 42180-42187.	3.4	17

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109	BIOINFORMATIC APPROACHES FOR PREDICTING SUBSTRATES OF PROTEASES. Journal of Bioinformatics and Computational Biology, 2011, 09, 149-178.	0.8	31
110	Bestatin-based chemical biology strategy reveals distinct roles for malaria M1- and M17-family aminopeptidases. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E526-34.	7.1	116
111	Structure/function analysis of lymphocyte perforin: role as an extrinsic tumour suppressor. Pathology, 2010, 42, S45-S46.	0.6	0
112	Plasmodium falciparum neutral aminopeptidases: new targets for anti-malarials. Trends in Biochemical Sciences, 2010, 35, 53-61.	7.5	108
113	Crystallization of the virulent and benign subtilisin-like proteases from the ovine footrot pathogen Dichelobacter nodosus. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 289-293.	0.7	3
114	The structural basis for membrane binding and pore formation by lymphocyte perforin. Nature, 2010, 468, 447-451.	27.8	364
115	Perforin: structure, function, and role in human immunopathology. Immunological Reviews, 2010, 235, 35-54.	6.0	171
116	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	2.5	47
117	MrGrid: A Portable Grid Based Molecular Replacement Pipeline. PLoS ONE, 2010, 5, e10049.	2.5	2
118	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. Bioinformatics, 2010, 26, 2076-2084.	4.1	7
119	CasCleave: towards more accurate prediction of caspase substrate cleavage sites. Bioinformatics, 2010, 26, 752-760.	4.1	148
120	Serpins Flex Their Muscle. Journal of Biological Chemistry, 2010, 285, 24307-24312.	3.4	97
121	Structure of the <i>Plasmodium falciparum</i> M17 aminopeptidase and significance for the design of drugs targeting the neutral exopeptidases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2449-2454.	7.1	80
122	Maspin (SERPINB5) Is an Obligate Intracellular Serpin. Journal of Biological Chemistry, 2010, 285, 10862-10869.	3.4	38
123	Serpins flex their muscle. I. PUTTING THE CLAMPS ON PROTEOLYSIS IN DIVERSE BIOLOGICAL SYSTEMS.. Journal of Biological Chemistry, 2010, 285, 38740.	3.4	0
124	The Subtilisin-Like Protease AprV2 Is Required for Virulence and Uses a Novel Disulphide-Tethered Exosite to Bind Substrates. PLoS Pathogens, 2010, 6, e1001210.	4.7	81
125	The Type III Effectors NleE and NleB from Enteropathogenic E. coli and OspZ from Shigella Block Nuclear Translocation of NF- $\kappa$ B p65. PLoS Pathogens, 2010, 6, e1000898.	4.7	201
126	Serpins Flex Their Muscle. Journal of Biological Chemistry, 2010, 285, 24299-24305.	3.4	128



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127	Molecular contortionism “ on the physical limits of serpin “loop-sheet” polymers. <i>Biological Chemistry</i> , 2010, 391, 973-82.	2.5	14
128	Highlight: The Biology of Proteolytic Systems. <i>Biological Chemistry</i> , 2010, 391, 837.	2.5	0
129	The X-Ray Crystal Structure of <i>Escherichia coli</i> Succinic Semialdehyde Dehydrogenase; Structural Insights into NADP+/Enzyme Interactions. <i>PLoS ONE</i> , 2010, 5, e9280.	2.5	31
130	High-throughput protein structure determination using grid computing. , 2009, , .		1
131	Structural basis for the inhibition of the essential <i>Plasmodium falciparum</i> M1 neutral aminopeptidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2537-2542.	7.1	133
132	Structure of granzyme C reveals an unusual mechanism of protease autoinhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5587-5592.	7.1	25
133	The Molecular Basis for Perforin Oligomerization and Transmembrane Pore Assembly. <i>Immunity</i> , 2009, 30, 684-695.	14.3	123
134	The role of strand 1 of the C <sup>1</sup> -sheet in the structure and function of $\alpha$ 1-antitrypsin. <i>Protein Science</i> , 2009, 10, 2518-2524.	7.6	8
135	Temperature sensitivity of human perforin mutants unmasks subtotal loss of cytotoxicity, delayed FHL, and a predisposition to cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9809-9814.	7.1	114
136	Structural Mechanisms of Inactivation in Scabies Mite Serine Protease Paralogues. <i>Journal of Molecular Biology</i> , 2009, 390, 635-645.	4.2	33
137	Structural determinants of GAD antigenicity. <i>Molecular Immunology</i> , 2009, 47, 493-505.	2.2	16
138	Modulation of the proteolytic activity of the complement protease C1s by polyanions: implications for polyanion-mediated acceleration of interaction between C1s and SERPING1. <i>Biochemical Journal</i> , 2009, 422, 295-303.	3.7	16
139	Conformational Change in the Chromatin Remodelling Protein MENT. <i>PLoS ONE</i> , 2009, 4, e4727.	2.5	3
140	Prodepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. <i>PLoS ONE</i> , 2009, 4, e7072.	2.5	40
141	Federated repositories of X-ray diffraction images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 810-814.	2.5	42
142	Serpins' mystery solved. <i>Nature</i> , 2008, 455, 1189-1190.	27.8	18
143	The MACPF/CDC family of pore-forming toxins. <i>Cellular Microbiology</i> , 2008, 10, 1765-1774.	2.1	250
144	A serpin in the cellulosome of the anaerobic fungus <i>Piromyces</i> sp. strain E2. <i>Mycological Research</i> , 2008, 112, 999-1006.	2.5	34

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145	A Structural Basis for Loop C-Sheet Polymerization in Serpins. <i>Journal of Molecular Biology</i> , 2008, 376, 1348-1359.	4.2	20
146	The Crystal Structure of DehI Reveals a New $\hat{\pm}$ -Haloacid Dehalogenase Fold and Active-Site Mechanism. <i>Journal of Molecular Biology</i> , 2008, 378, 284-294.	4.2	48
147	Elucidation of the substrate specificity of the MASP-2 protease of the lectin complement pathway and identification of the enzyme as a major physiological target of the serpin, C1-inhibitor. <i>Molecular Immunology</i> , 2008, 45, 670-677.	2.2	64
148	COOH-Terminal Clustering of Autoantibody and T-Cell Determinants on the Structure of GAD65 Provide Insights Into the Molecular Basis of Autoreactivity. <i>Diabetes</i> , 2008, 57, 1293-1301.	0.6	43
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