

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	The Serpins Are an Expanding Superfamily of Structurally Similar but Functionally Diverse Proteins. <i>Journal of Biological Chemistry</i> , 2001, 276, 33293-33296.	3.4	1,069
2	Perforin and granzymes: function, dysfunction and human pathology. <i>Nature Reviews Immunology</i> , 2015, 15, 388-400.	22.7	858
3	MUSTANG: A multiple structural alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 559-574.	2.6	615
4	An overview of the serpin superfamily. <i>Genome Biology</i> , 2006, 7, 216.	9.6	550
5	Prediction of protein function from protein sequence and structure. <i>Quarterly Reviews of Biophysics</i> , 2003, 36, 307-340.	5.7	376
6	The structural basis for membrane binding and pore formation by lymphocyte perforin. <i>Nature</i> , 2010, 468, 447-451.	27.8	364
7	IL-37 requires the receptors IL-18R α 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
8	AB5 subtilase cytotoxin inactivates the endoplasmic reticulum chaperone BiP. <i>Nature</i> , 2006, 443, 548-552.	27.8	351
9	A Structural Basis for the Selection of Dominant α CD28 T Cell Receptors in Antiviral Immunity. <i>Immunity</i> , 2003, 18, 53-64.	14.3	321
10	T cell receptor recognition of a 'super-bulged' major histocompatibility complex class II bound peptide. <i>Nature Immunology</i> , 2005, 6, 1114-1122.	14.5	280
11	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. <i>PLoS ONE</i> , 2012, 7, e50300.	2.5	265
12	A Common Fold Mediates Vertebrate Defense and Bacterial Attack. <i>Science</i> , 2007, 317, 1548-1551.	12.6	261
13	The MACPF/CDC family of pore-forming toxins. <i>Cellular Microbiology</i> , 2008, 10, 1765-1774.	2.1	250
14	Conservation within the myosin motor domain: implications for structure and function. <i>Structure</i> , 1996, 4, 969-987.	3.3	224
15	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
16	The Type III Effectors NleE and NleB from Enteropathogenic <i>E. coli</i> and OspZ from <i>Shigella</i> Block Nuclear Translocation of NF- κ B p65. <i>PLoS Pathogens</i> , 2010, 6, e1000898.	4.7	201
17	Functional insights from the distribution and role of homopeptide repeat-containing proteins. <i>Genome Research</i> , 2005, 15, 537-551.	5.5	189
18	GABA production by glutamic acid decarboxylase is regulated by a dynamic catalytic loop. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 280-286.	8.2	189

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19	The X-ray Crystal Structure of Full-Length Human Plasminogen. <i>Cell Reports</i> , 2012, 1, 185-190.	6.4	189
20	The 2.6 Å... structure of antithrombin indicates a conformational change at the heparin binding site 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1997, 266, 601-609.	4.2	188
21	The major human and mouse granzymes are structurally and functionally divergent. <i>Journal of Cell Biology</i> , 2006, 175, 619-630.	5.2	187
22	An atlas of serpin conformations. <i>Trends in Biochemical Sciences</i> , 1998, 23, 63-67.	7.5	173
23	Automatic generation of protein structure cartoons with Pro-origami. <i>Bioinformatics</i> , 2011, 27, 3315-3316.	4.1	173
24	Perforin: structure, function, and role in human immunopathology. <i>Immunological Reviews</i> , 2010, 235, 35-54.	6.0	171
25	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
26	Cascleave: towards more accurate prediction of caspase substrate cleavage sites. <i>Bioinformatics</i> , 2010, 26, 752-760.	4.1	148
27	A tale of two specificities: bispecific antibodies for therapeutic and diagnostic applications. <i>Trends in Biotechnology</i> , 2013, 31, 621-632.	9.3	148
28	Phylogeny of the Serpin Superfamily: Implications of Patterns of Amino Acid Conservation for Structure and Function. <i>Genome Research</i> , 2000, 10, 1845-1864.	5.5	145
29	Molecular basis of α_1 -antitrypsin deficiency revealed by the structure of a domain-swapped trimer. <i>EMBO Reports</i> , 2011, 12, 1011-1017.	4.5	142
30	Molecular gymnastics: serpin structure, folding and misfolding. <i>Current Opinion in Structural Biology</i> , 2006, 16, 761-768.	5.7	139
31	α_1 -Antitrypsin Mmalton (Phe52-deleted) Forms Loop-Sheet Polymers in Vivo.. <i>Journal of Biological Chemistry</i> , 1995, 270, 16864-16870.	3.4	133
32	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
33	Requirement of leucine-rich repeats of glycoprotein (GP) Ib α for shear-dependent and static binding of von Willebrand factor to the platelet membrane GP Ib α -IX-V complex. <i>Blood</i> , 2000, 95, 903-910.	1.4	131
34	Antithrombin: in control of coagulation. <i>International Journal of Biochemistry and Cell Biology</i> , 2004, 36, 386-389.	2.8	128
35	Serpins Flex Their Muscle. <i>Journal of Biological Chemistry</i> , 2010, 285, 24299-24305.	3.4	128
36	The Molecular Basis for Perforin Oligomerization and Transmembrane Pore Assembly. <i>Immunity</i> , 2009, 30, 684-695.	14.3	123

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37	Bestatin-based chemical biology strategy reveals distinct roles for malaria M1- and M17-family aminopeptidases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E526-34.	7.1	116
38	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
39	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	5.6	114
40	Serpins in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2002, 19, 1881-1890.	8.9	112
41	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
42	Structure of the poly-C9 component of the complement membrane attack complex. <i>Nature Communications</i> , 2016, 7, 10588.	12.8	112
43	SH3 domains in prokaryotes. <i>Trends in Biochemical Sciences</i> , 1999, 24, 132-133.	7.5	110
44	The Type I \pm Inositol Polyphosphate 4-Phosphatase Generates and Terminates Phosphoinositide 3-Kinase Signals on Endosomes and the Plasma Membrane. <i>Molecular Biology of the Cell</i> , 2005, 16, 2218-2233.	2.1	110
45	<i>Plasmodium falciparum</i> neutral aminopeptidases: new targets for anti-malarials. <i>Trends in Biochemical Sciences</i> , 2010, 35, 53-61.	7.5	108
46	The Evolution of Enzyme Specificity in <i>Fasciola</i> spp.. <i>Journal of Molecular Evolution</i> , 2003, 57, 1-15.	1.8	106
47	Identification of a Novel Domain in Two Mammalian Inositol-polyphosphate 5-Phosphatases That Mediates Membrane Ruffle Localization. <i>Journal of Biological Chemistry</i> , 2003, 278, 11376-11385.	3.4	97
48	The Murine Orthologue of Human Antichymotrypsin. <i>Journal of Biological Chemistry</i> , 2005, 280, 43168-43178.	3.4	97
49	Serpins Flex Their Muscle. <i>Journal of Biological Chemistry</i> , 2010, 285, 24307-24312.	3.4	97
50	Conformational changes in serpins: II. the mechanism of activation of antithrombin by heparin. <i>Journal of Molecular Biology</i> , 2000, 301, 1287-1305.	4.2	93
51	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
52	POPS: A COMPUTATIONAL TOOL FOR MODELING AND PREDICTING PROTEASE SPECIFICITY. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 551-585.	0.8	89
53	Cloning and Expression of the Major Secreted Cathepsin B-Like Protein from Juvenile <i>Fasciola hepatica</i> and Analysis of Immunogenicity following Liver Fluke Infection. <i>Infection and Immunity</i> , 2003, 71, 6921-6932.	2.2	88
54	Real-time visualization of perforin nanopore assembly. <i>Nature Nanotechnology</i> , 2017, 12, 467-473.	31.5	88

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55	The Inositol Polyphosphate 5-Phosphatases and the Apurinic/Apyrimidinic Base Excision Repair Endonucleases Share a Common Mechanism for Catalysis. <i>Journal of Biological Chemistry</i> , 2000, 275, 37055-37061.	3.4	81
56	The 1.6Å... Crystal Structure of the Catalytic Domain of PlyB, a Bacteriophage Lysin Active Against <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , 2007, 366, 540-550.	4.2	81
57	The Subtilisin-Like Protease AprV2 Is Required for Virulence and Uses a Novel Disulphide-Tethered Exosite to Bind Substrates. <i>PLoS Pathogens</i> , 2010, 6, e1001210.	4.7	81
58	Structure of the <i>Plasmodium falciparum</i> M17 aminopeptidase and significance for the design of drugs targeting the neutral exopeptidases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2449-2454.	7.1	80
59	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
60	Inhibitory Activity of a Heterochromatin-associated Serpin (MENT) against Papain-like Cysteine Proteinases Affects Chromatin Structure and Blocks Cell Proliferation. <i>Journal of Biological Chemistry</i> , 2002, 277, 13192-13201.	3.4	77
61	Protein structural alignments and functional genomics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 378-382.	2.6	76
62	Cationic Sites on Granzyme B Contribute to Cytotoxicity by Promoting Its Uptake into Target Cells. <i>Molecular and Cellular Biology</i> , 2005, 25, 7854-7867.	2.3	75
63	The Structure of Chagasin in Complex with a Cysteine Protease Clarifies the Binding Mode and Evolution of an Inhibitor Family. <i>Structure</i> , 2007, 15, 535-543.	3.3	74
64	Cleaved antitrypsin polymers at atomic resolution. <i>Protein Science</i> , 2000, 9, 417-420.	7.6	73
65	Probing the Unfolding Pathway of α_1 -Antitrypsin. <i>Journal of Biological Chemistry</i> , 1999, 274, 9482-9488.	3.4	72
66	Hurpin Is a Selective Inhibitor of Lysosomal Cathepsin L and Protects Keratinocytes from Ultraviolet-Induced Apoptosis. <i>Biochemistry</i> , 2003, 42, 7381-7389.	2.5	72
67	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
68	Evidence That Serpin Architecture Intrinsically Supports Papain-like Cysteine Protease Inhibition: Engineering α_1 -Antitrypsin To Inhibit Cathepsin Proteases. <i>Biochemistry</i> , 2002, 41, 4998-5004.	2.5	71
69	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
70	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
71	Automated cryo-lamella preparation for high-throughput in-situ structural biology. <i>Journal of Structural Biology</i> , 2020, 210, 107488.	2.8	70
72	The High Resolution Crystal Structure of the Human Tumor Suppressor Maspin Reveals a Novel Conformational Switch in the G-helix. <i>Journal of Biological Chemistry</i> , 2005, 280, 22356-22364.	3.4	69

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73	Stonefish toxin defines an ancient branch of the perforin-like superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15360-15365.	7.1	69
74	Importance of the P4â€² Residue in Human Granzyme B Inhibitors and Substrates Revealed by Scanning Mutagenesis of the Proteinase Inhibitor 9 Reactive Center Loop. Journal of Biological Chemistry, 2001, 276, 15177-15184.	3.4	68
75	The conjugation protein TcpC from <i>Clostridium perfringens</i> is structurally related to the type IV secretion system protein VirB8 from Gram-negative bacteria. Molecular Microbiology, 2012, 83, 275-288.	2.5	68
76	Conformational changes in serpins: I. the native and cleaved conformations of Î± 1 -antitrypsin 1 Edited by J. M. Thornton. Journal of Molecular Biology, 2000, 296, 685-699.	4.2	67
77	Structure and function of the von Willebrand factor A1 domain: analysis with monoclonal antibodies reveals distinct binding sites involved in recognition of the platelet membrane glycoprotein Ib-IX-V complex and ristocetin-dependent activation. Blood, 2000, 95, 164-172.	1.4	65
78	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. Nature Communications, 2019, 10, 4288.	12.8	65
79	Importance of the release of strand 1C to the polymerization mechanism of inhibitory serpins. Protein Science, 1997, 6, 89-98.	7.6	64
80	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. Molecular Immunology, 2008, 45, 670-677.	2.2	64
81	Structural and Functional Analysis of the Pore-Forming Toxin NetB from <i>Clostridium perfringens</i> . MBio, 2013, 4, e00019-13.	4.1	64
82	Fingerprinting the Substrate Specificity of M1 and M17 Aminopeptidases of Human Malaria, <i>Plasmodium falciparum</i> . PLoS ONE, 2012, 7, e31938.	2.5	64
83	Protection from Endogenous Perforin: Glycans and the C Terminus Regulate Exocytic Trafficking in Cytotoxic Lymphocytes. Immunity, 2011, 34, 879-892.	14.3	63
84	CasCleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. Bioinformatics, 2014, 30, 71-80.	4.1	63
85	Conformational changes in serpins: I. the native and cleaved conformations of Î± 1 -antitrypsin 1 Edited by J. M. Thornton. Journal of Molecular Biology, 2000, 295, 651-665.	4.2	62
86	The Serpin SQN-5 Is a Dual Mechanistic-Class Inhibitor of Serine and Cysteine Proteinases. Biochemistry, 2002, 41, 3189-3199.	2.5	61
87	Giant MACPF/CDC pore forming toxins: A class of their own. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 475-486.	2.6	61
88	Expression and Purification of Recombinant Human Granzyme B from <i>Pichia pastoris</i> . Biochemical and Biophysical Research Communications, 1999, 261, 251-255.	2.1	60
89	For the record: A single amino acid substitution affects substrate specificity in cysteine proteinases from <i>Fasciola hepatica</i> . Protein Science, 2000, 9, 2567-2572.	7.6	59
90	Structural and functional analysis of the Josephin domain of the polyglutamine protein ataxin-3. Biochemical and Biophysical Research Communications, 2004, 322, 387-394.	2.1	58

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91	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
92	Synthesis of New ($\hat{\alpha}$)-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
93	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
94	Characterization of the pathoimmunology of necrotizing enterocolitis reveals novel therapeutic opportunities. <i>Nature Communications</i> , 2020, 11, 5794.	12.8	53
95	Homodimerization attenuates the anti-inflammatory activity of interleukin-37. <i>Science Immunology</i> , 2017, 2, .	11.9	51
96	The N terminus of the serpin, tengpin, functions to trap the metastable native state. <i>EMBO Reports</i> , 2007, 8, 658-663.	4.5	48
97	The Crystal Structure of DehI Reveals a New \hat{I} -Haloacid Dehalogenase Fold and Active-Site Mechanism. <i>Journal of Molecular Biology</i> , 2008, 378, 284-294.	4.2	48
98	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
99	Simple Modifications of the Serpin Reactive Site Loop Convert SCCA2 into a Cysteine Proteinase Inhibitor: A Critical Role for the P3 $\hat{\epsilon}$ Proline in Facilitating RSL Cleavage. <i>Biochemistry</i> , 2000, 39, 7081-7091.	2.5	47
100	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. <i>PLoS ONE</i> , 2010, 5, e10048.	2.5	47
101	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
102	Role of the M-loop and Reactive Center Loop Domains in the Folding and Bridging of Nucleosome Arrays by MENT. <i>Journal of Biological Chemistry</i> , 2003, 278, 43384-43393.	3.4	45
103	The 1.5 Å... Crystal Structure of a Prokaryote Serpin. <i>Structure</i> , 2003, 11, 387-397.	3.3	44
104	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
105	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
106	Perforin evolved from a gene duplication of MPEG1, followed by a complex pattern of gene gain and loss within Euteleostomi. <i>BMC Evolutionary Biology</i> , 2012, 12, 59.	3.2	43
107	Probing the Role of the F-Helix in Serpin Stability through a Single Tryptophan Substitution. <i>Biochemistry</i> , 2002, 41, 4575-4581.	2.5	42
108	The REFOLD database: a tool for the optimization of protein expression and refolding. <i>Nucleic Acids Research</i> , 2006, 34, D207-D212.	14.5	42

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109	The Crystal Structure of the Transthyretin-like Protein from <i>Salmonella dublin</i> , a Prokaryote 5-Hydroxyisourate Hydrolase. <i>Journal of Molecular Biology</i> , 2006, 359, 1389-1399.	4.2	42
110	Federated repositories of X-ray diffraction images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 810-814.	2.5	42
111	X-ray crystal structure of MENT: evidence for functional loop-sheet polymers in chromatin condensation. <i>EMBO Journal</i> , 2006, 25, 3144-3155.	7.8	41
112	Prediction of the Immunodominant Epitope of the Pyruvate Dehydrogenase Complex E2 in Primary Biliary Cirrhosis Using Phage Display. <i>Journal of Immunology</i> , 2000, 164, 3413-3419.	0.8	40
113	DNA Accelerates the Inhibition of Human Cathepsin V by Serpins. <i>Journal of Biological Chemistry</i> , 2007, 282, 36980-36986.	3.4	40
114	ProDepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. <i>PLoS ONE</i> , 2009, 4, e7072.	2.5	40
115	Conformational Epitopes on the Diabetes Autoantigen GAD65 Identified by Peptide Phage Display and Molecular Modeling. <i>Journal of Immunology</i> , 2000, 165, 3830-3838.	0.8	38
116	Serpins: Finely Balanced Conformational Traps. <i>IUBMB Life</i> , 2002, 54, 1-7.	3.4	38
117	Maspin (SERPINB5) Is an Obligate Intracellular Serpin. <i>Journal of Biological Chemistry</i> , 2010, 285, 10862-10869.	3.4	38
118	Elucidation of the Substrate Specificity of the C1s Protease of the Classical Complement Pathway. <i>Journal of Biological Chemistry</i> , 2005, 280, 39510-39514.	3.4	36
119	RCPdb: An evolutionary classification and codon usage database for repeat-containing proteins. <i>Genome Research</i> , 2007, 17, 1118-1127.	5.5	36
120	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
121	X-ray crystal structure of the fibrinolysis inhibitor Î±2-antiplasmin. <i>Blood</i> , 2008, 111, 2049-2052.	1.4	35
122	Characterization and functional analysis of Serp3: a novel myxoma virus-encoded serpin involved in virulence. <i>Journal of General Virology</i> , 2001, 82, 1407-1417.	2.9	35
123	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
124	Structural Mechanisms of Inactivation in Scabies Mite Serine Protease Paralogues. <i>Journal of Molecular Biology</i> , 2009, 390, 635-645.	4.2	33
125	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
126	A New Model for Pore Formation by Cholesterol-Dependent Cytolysins. <i>PLoS Computational Biology</i> , 2014, 10, e1003791.	3.2	33

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127	Mechanisms of serpin dysfunction in disease. <i>Expert Reviews in Molecular Medicine</i> , 2006, 8, 1-19.	3.9	32
128	REFOLD: An analytical database of protein refolding methods. <i>Protein Expression and Purification</i> , 2006, 46, 166-171.	1.3	31
129	BIOINFORMATIC APPROACHES FOR PREDICTING SUBSTRATES OF PROTEASES. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 149-178.	0.8	31
130	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
131	Brinp1 $\hat{\sim}$ / $\hat{\sim}$ 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
132	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
133	Maspin is not required for embryonic development or tumour suppression. <i>Nature Communications</i> , 2014, 5, 3164.	12.8	30
134	The Perforin Pore Facilitates the Delivery of Cationic Cargos. <i>Journal of Biological Chemistry</i> , 2014, 289, 9172-9181.	3.4	30
135	Characterization of the Specificity of Arginine-Specific Gingipains from <i>Porphyromonas gingivalis</i> Reveals Active Site Differences between Different Forms of the Enzymes. <i>Biochemistry</i> , 2003, 42, 11693-11700.	2.5	29
136	The matrix refolded. <i>Nature Methods</i> , 2005, 2, 3-3.	19.0	29
137	The High Resolution Crystal Structure of a Native Thermostable Serpin Reveals the Complex Mechanism Underpinning the Stressed to Relaxed Transition. <i>Journal of Biological Chemistry</i> , 2005, 280, 8435-8442.	3.4	29
138	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
139	Reconciling the Structural Attributes of Avian Antibodies. <i>Journal of Biological Chemistry</i> , 2014, 289, 15384-15392.	3.4	28
140	Mutagenesis of the dengue virus type 2 NS3 proteinase and the production of growth-restricted virus. <i>Journal of General Virology</i> , 2001, 82, 1647-1656.	2.9	27
141	Leucine-rich Repeats 2-4 (Leu60-Glu128) of Platelet Glycoprotein Ib \pm Regulate Shear-dependent Cell Adhesion to von Willebrand Factor. <i>Journal of Biological Chemistry</i> , 2006, 281, 26419-26423.	3.4	27
142	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
143	Regulation of perforin activation and pre $\hat{\epsilon}$ synaptic toxicity through C $\hat{\epsilon}$ terminal glycosylation. <i>EMBO Reports</i> , 2017, 18, 1775-1785.	4.5	27
144	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

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