

# Daniel John Rigden

## List of Publications by Year in descending order

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218  
papers

11,459  
citations

36691

53  
h-index

46524

93  
g-index

233  
all docs

233  
docs citations

233  
times ranked

20759  
citing authors

#	ARTICLE	IF	CITATIONS
1	WHISTLE server: A high-accuracy genomic coordinate-based machine learning platform for RNA modification prediction. <i>Methods</i> , 2022, 203, 378-382.	1.9	11
2	m5C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m5C) epitranscriptome. <i>Nucleic Acids Research</i> , 2022, 50, D196-D203.	6.5	53
3	findMySequence: a neural-network-based approach for identification of unknown proteins in X-ray crystallography and cryo-EM. <i>IUCr</i> , 2022, 9, 86-97.	1.0	34
4	Carboxyl Methyltransferase Catalysed Formation of Mono- and Dimethyl Esters under Aqueous Conditions: Application in Cascade Biocatalysis. <i>Angewandte Chemie - International Edition</i> , 2022, , .	7.2	7
5	Carboxyl Methyltransferase Catalysed Formation of Mono- and Dimethyl Esters under Aqueous Conditions: Application in Cascade Biocatalysis. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	0
6	The 2022 <i>Nucleic Acids Research</i> database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2022, 50, D1-D10.	6.5	50
7	MrParse: finding homologues in the PDB and the EBI AlphaFold database for molecular replacement and more. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 553-559.	1.1	12
8	RMDisease: a database of genetic variants that affect RNA modifications, with implications for epitranscriptome pathogenesis. <i>Nucleic Acids Research</i> , 2021, 49, D1396-D1404.	6.5	65
9	m6A-Atlas: a comprehensive knowledgebase for unraveling the N <sup>6</sup> -methyladenosine (m6A) epitranscriptome. <i>Nucleic Acids Research</i> , 2021, 49, D134-D143.	6.5	185
10	<i>Bodo saltans</i> (Kinetoplastida) is dependent on a novel <i>Paracaedibacter</i> -like endosymbiont that possesses multiple putative toxin-antitoxin systems. <i>ISME Journal</i> , 2021, 15, 1680-1694.	4.4	11
11	ConPlot: web-based application for the visualization of protein contact maps integrated with other data. <i>Bioinformatics</i> , 2021, 37, 2763-2765.	1.8	7
12	Evolution, structure and emerging roles of C1ORF112 in DNA replication, DNA damage responses, and cancer. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 4365-4376.	2.4	14
13	Bisphenol A Inhibits the Transporter Function of the Blood-Brain Barrier by Directly Interacting with the ABC Transporter Breast Cancer Resistance Protein (BCRP). <i>International Journal of Molecular Sciences</i> , 2021, 22, 5534.	1.8	16
14	ConsRM: collection and large-scale prediction of the evolutionarily conserved RNA methylation sites, with implications for the functional epitranscriptome. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	34
15	Attention-based multi-label neural networks for integrated prediction and interpretation of twelve widely occurring RNA modifications. <i>Nature Communications</i> , 2021, 12, 4011.	5.8	61
16	High-accuracy protein structure prediction in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1687-1699.	1.5	220
17	Evaluation of model refinement in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1852-1869.	1.5	21
18	Assessing the utility of CASP14 models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1752-1769.	1.5	47

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19	Prophages encode phage-defense systems with cognate self-immunity. <i>Cell Host and Microbe</i> , 2021, 29, 1620-1633.e8.	5.1	50
20	The 2021 <i>Nucleic Acids Research</i> database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2021, 49, D1-D9.	6.5	100
21	Redeployment of automated <i>MrBUMP</i> search-model identification for map fitting in cryo-EM. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1378-1385.	1.1	3
22	Multitasking in the gut: the X-ray structure of the multidomain BbgIII from <i>Bifidobacterium bifidum</i> offers possible explanations for its alternative functions. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1564-1578.	1.1	0
23	The X-ray structure of juvenile hormone diol kinase from the silkworm <i>Bombyx mori</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 465-472.	0.4	0
24	The 27th annual <i>Nucleic Acids Research</i> database issue and molecular biology database collection. <i>Nucleic Acids Research</i> , 2020, 48, D1-D8.	6.5	470
25	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1587-1604.	1.9	38
26	Structural annotation of the conserved carbohydrate esterase vb_24B_21 from Shiga toxin-encoding bacteriophage $\phi$ 24B. <i>Journal of Structural Biology</i> , 2020, 212, 107596.	1.3	2
27	m7GHub: deciphering the location, regulation and pathogenesis of internal mRNA N7-methylguanosine (m7G) sites in human. <i>Bioinformatics</i> , 2020, 36, 3528-3536.	1.8	85
28	Maturation of the functional mouse CRES amyloid from globular form. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16363-16372.	3.3	7
29	Informatics investigations into anti-thyroid drug induced agranulocytosis associated with multiple HLA-B alleles. <i>PLoS ONE</i> , 2020, 15, e0220754.	1.1	3
30	In silico prediction of structure and function for a large family of transmembrane proteins that includes human Tmem41b. <i>F1000Research</i> , 2020, 9, 1395.	0.8	13
31	Protein Phosphohistidine Phosphatases of the HP Superfamily. <i>Methods in Molecular Biology</i> , 2020, 2077, 93-107.	0.4	2
32	Extending the scope of coiled-coil crystal structure solution by <i>AMPLE</i> through improved <i>ab initio</i> modelling. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 272-284.	1.1	7
33	Helical ensembles outperform ideal helices in molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 962-970.	1.1	2
34	In silico prediction of structure and function for a large family of transmembrane proteins that includes human Tmem41b. <i>F1000Research</i> , 2020, 9, 1395.	0.8	14
35	Using <i>Phaser</i> and ensembles to improve the performance of <i>SIMBAD</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1-8.	1.1	7
36	The heparin-binding proteome in normal pancreas and murine experimental acute pancreatitis. <i>PLoS ONE</i> , 2019, 14, e0217633.	1.1	27

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37	WHISTLE: a high-accuracy map of the human N6-methyladenosine (m6A) epitranscriptome predicted using a machine learning approach. <i>Nucleic Acids Research</i> , 2019, 47, e41-e41.	6.5	177
38	Molecular replacement using structure predictions from databases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 1051-1062.	1.1	15
39	Autophosphorylation Is a Mechanism of Inhibition in Twitchin Kinase. <i>Journal of Molecular Biology</i> , 2018, 430, 793-805.	2.0	3
40	Candidate-gene based GWAS identifies reproducible DNA markers for metabolic pyrethroid resistance from standing genetic variation in East African <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2018, 8, 2920.	1.6	51
41	Large scale ab initio modeling of structurally uncharacterized antimicrobial peptides reveals known and novel folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 548-565.	1.5	13
42	The 2018 <i>Nucleic Acids Research</i> database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2018, 46, D1-D7.	6.5	106
43	Structure and function of Per-ARNT-Sim domains and their possible role in the life-cycle biology of <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2018, 219, 52-66.	0.5	16
44	Genome-wide transcriptional analyses in <i>Anopheles</i> mosquitoes reveal an unexpected association between salivary gland gene expression and insecticide resistance. <i>BMC Genomics</i> , 2018, 19, 225.	1.2	27
45	Critical assessment of approaches for molecular docking to elucidate associations of HLA alleles with adverse drug reactions. <i>Molecular Immunology</i> , 2018, 101, 488-499.	1.0	14
46	Ensembles generated from crystal structures of single distant homologues solve challenging molecular-replacement cases in <i>AMPLE</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 183-193.	1.1	16
47	Recent developments in <i>MrBUMP</i> : better search-model preparation, graphical interaction with search models, and solution improvement and assessment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 167-182.	1.1	35
48	<i>SIMBAD</i> : a sequence-independent molecular-replacement pipeline. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 595-605.	1.1	25
49	The 24th annual <i>Nucleic Acids Research</i> database issue: a look back and upcoming changes. <i>Nucleic Acids Research</i> , 2017, 45, D1-D11.	6.5	144
50	Genome-wide association study of nevirapine hypersensitivity in a sub-Saharan African HIV-infected population. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, dkw545.	1.3	42
51	Prediction of Protein Function from Theoretical Models. , 2017, , 467-498.		3
52	ConKit: a python interface to contact predictions. <i>Bioinformatics</i> , 2017, 33, 2209-2211.	1.8	17
53	Clareosin: a novel sexually dimorphic urinary lipocalin in the bank vole, <i>Myodes glareolus</i> . <i>Open Biology</i> , 2017, 7, 170135.	1.5	7
54	Probing Medin Monomer Structure and its Amyloid Nucleation Using <sup>13</sup> C-Direct Detection NMR in Combination with Structural Bioinformatics. <i>Scientific Reports</i> , 2017, 7, 45224.	1.6	13

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55	<i>SIMBAD</i> : a sequence-independent molecular replacement pipeline. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1004-C1004.	0.0	1
56	Applications of contact predictions to structural biology. <i>IUCr</i> , 2017, 4, 291-300.	1.0	39
57	Novel compound heterozygous ASXL3 mutation causing Bainbridge-ropers like syndrome and primary IGF1 deficiency. <i>International Journal of Pediatric Endocrinology (Springer)</i> , 2017, 2017, 8.	1.6	9
58	Approaches to <i>ab initio</i> molecular replacement of $\alpha$ -helical transmembrane proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 985-996.	1.1	6
59	GPO.4 from bacteriophage T7: in silico characterisation of its structure and interaction with E. coli FtsZ. <i>BMC Research Notes</i> , 2016, 9, 343.	0.6	3
60	Potential DNA binding and nuclease functions of ComEC domains characterized <i>in silico</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1431-1442.	1.5	31
61	Biophysical Analysis of the N-Terminal Domain from the Human Protein Phosphatase 1 Nuclear Targeting Subunit PNUTS Suggests an Extended Transcription Factor TFIIIS-Like Fold. <i>Protein Journal</i> , 2016, 35, 340-345.	0.7	6
62	Exploration of pathomechanisms triggered by a single-nucleotide polymorphism in titin's I-band: the cardiomyopathy-linked mutation T2580I. <i>Open Biology</i> , 2016, 6, 160114.	1.5	17
63	CARP interacts with titin at a unique helical N2A sequence and at the domain Ig81 to form a structured complex. <i>FEBS Letters</i> , 2016, 590, 3098-3110.	1.3	22
64	The centrosomal Deubiquitylase USP21 regulates Gli1 transcriptional activity and stability.. <i>Journal of Cell Science</i> , 2016, 129, 4001-4013.	1.2	30
65	The industrial melanism mutation in British peppered moths is a transposable element. <i>Nature</i> , 2016, 534, 102-105.	13.7	386
66	The 2016 database issue of <i>Nucleic Acids Research</i> and an updated molecular biology database collection. <i>Nucleic Acids Research</i> , 2016, 44, D1-D6.	6.5	119
67	Residue contacts predicted by evolutionary covariance extend the application of <i>ab initio</i> molecular replacement to larger and more challenging protein folds. <i>IUCr</i> , 2016, 3, 259-270.	1.0	17
68	Contemporary evolution of resistance at the major insecticide target site gene <i>Ace1</i> by mutation and copy number variation in the malaria mosquito <i>Anopheles gambiae</i> . <i>Molecular Ecology</i> , 2015, 24, 2656-2672.	2.0	63
69	Structural advances on titin: towards an atomic understanding of multi-domain functions in myofilament mechanics and scaffolding. <i>Biochemical Society Transactions</i> , 2015, 43, 850-855.	1.6	20
70	ATG24 Represses Autophagy and Differentiation and Is Essential for Homeostasy of the Flagellar Pocket in <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2015, 10, e0130365.	1.1	14
71	The 2015 <i>Nucleic Acids Research</i> Database Issue and Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2015, 43, D1-D5.	6.5	79
72	Exploring the speed and performance of molecular replacement with <i>AMPLE</i> using <i>QUARK</i> <i>ab initio</i> protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 338-343.	2.5	25

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73	Transcriptomic Analysis of Shiga-Toxigenic Bacteriophage Carriage Reveals a Profound Regulatory Effect on Acid Resistance in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 8118-8125.	1.4	60
74	Routine phasing of coiled-coil protein crystal structures with <i>AMPLE</i> . <i>IUCr</i> , 2015, 2, 198-206.	1.0	24
75	Lpg0393 of <i>Legionella pneumophila</i> Is a Guanine-Nucleotide Exchange Factor for Rab5, Rab21 and Rab22. <i>PLoS ONE</i> , 2015, 10, e0118683.	1.1	16
76	Crystal Structure of the Nipah Virus Phosphoprotein Tetramerization Domain. <i>Journal of Virology</i> , 2014, 88, 758-762.	1.5	63
77	Extracellular calcium triggers unique transcriptional programs and modulates staurosporine-induced cell death in <i>Neurospora crassa</i> . <i>Microbial Cell</i> , 2014, 1, 289-302.	1.4	8
78	Molecular basis for the fold organization and sarcomeric targeting of the muscle atrogin MuRF1. <i>Open Biology</i> , 2014, 4, 130172.	1.5	17
79	Structural genomics analysis of uncharacterized protein families overrepresented in human gut bacteria identifies a novel glycoside hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 112.	1.2	13
80	Conversion of a Disulfide Bond into a Thioacetal Group during Echinomycin Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 824-828.	7.2	29
81	Structure- and context-based analysis of the GxGYxYP family reveals a new putative class of Glycoside Hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 196.	1.2	8
82	The 2014 <i>Nucleic Acids Research</i> Database Issue and an updated NAR online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2014, 42, D1-D6.	6.5	81
83	Titin kinase is an inactive pseudokinase scaffold that supports MuRF1 recruitment to the sarcomeric M-line. <i>Open Biology</i> , 2014, 4, 140041.	1.5	52
84	<i>AMPLE</i> : a cluster-and-truncate approach to solve the crystal structures of small proteins using rapidly computed <i>ab initio</i> models. Corrigendum. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1174-1174.	2.5	4
85	Metabolic and Target-Site Mechanisms Combine to Confer Strong DDT Resistance in <i>Anopheles gambiae</i> . <i>PLoS ONE</i> , 2014, 9, e92662.	1.1	102
86	Evidence for Loss of a Partial Flagellar Glycolytic Pathway during Trypanosomatid Evolution. <i>PLoS ONE</i> , 2014, 9, e103026.	1.1	5
87	Employing in vitro directed molecular evolution for the selection of $\beta$ -amylase variant inhibitors with activity toward cotton boll weevil enzyme. <i>Journal of Biotechnology</i> , 2013, 167, 377-385.	1.9	7
88	Ubiquitination of the glycosomal matrix protein receptor PEX5 in <i>Trypanosoma brucei</i> by PEX4 displays novel features. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 3076-3092.	1.9	32
89	Deubiquitylases From Genes to Organism. <i>Physiological Reviews</i> , 2013, 93, 1289-1315.	13.1	350
90	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296

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91	Application of the <i>AMPLE</i> cluster-and-truncate approach to NMR structures for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2194-2201.	2.5	13
92	Mechanistic and functional diversity in the mechanosensory kinases of the titin-like family. <i>Biochemical Society Transactions</i> , 2013, 41, 1066-1071.	1.6	23
93	The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013, 2, 154.	0.8	2
94	The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013, 2, 154.	0.8	3
95	Systematic survey of deubiquitinase localization identifies USP21 as a regulator of centrosome- and microtubule-associated functions. <i>Molecular Biology of the Cell</i> , 2012, 23, 1095-1103.	0.9	106
96	Genomic determinants of sporulation in <i>Bacilli</i> and <i>Clostridia</i> : towards the minimal set of sporulation-specific genes. <i>Environmental Microbiology</i> , 2012, 14, 2870-2890.	1.8	235
97	A new family of bacterial DNA repair proteins annotated by the integration of non-homology, distant homology and structural bioinformatic methods. <i>FEBS Letters</i> , 2012, 586, 3908-3913.	1.3	3
98	Rab14 and Its Exchange Factor FAM116 Link Endocytic Recycling and Adherens Junction Stability in Migrating Cells. <i>Developmental Cell</i> , 2012, 22, 952-966.	3.1	158
99	<i>AMPLE</i> : a cluster-and-truncate approach to solve the crystal structures of small proteins using rapidly computed <i>ab initio</i> models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1622-1631.	2.5	109
100	mRNA 3' Tagging Is Induced by Nonsense-Mediated Decay and Promotes Ribosome Dissociation. <i>Molecular and Cellular Biology</i> , 2012, 32, 2585-2595.	1.1	39
101	Evaluating Caveolin Interactions: Do Proteins Interact with the Caveolin Scaffolding Domain through a Widespread Aromatic Residue-Rich Motif?. <i>PLoS ONE</i> , 2012, 7, e44879.	1.1	101
102	Prediction of antimicrobial peptides based on the adaptive neuro-fuzzy inference system application. <i>Biopolymers</i> , 2012, 98, 280-287.	1.2	58
103	Trypanosomes contain two highly different isoforms of peroxin PEX13 involved in glycosome biogenesis. <i>FEBS Letters</i> , 2012, 586, 1765-1771.	1.3	25
104	<i>Ab Initio</i> Modeling Led Annotation Suggests Nucleic Acid Binding Function for Many DUFs. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 431-438.	1.0	25
105	Comparative Genomics of the Anopheline Glutathione S-Transferase Epsilon Cluster. <i>PLoS ONE</i> , 2011, 6, e29237.	1.1	19
106	Autophagy in parasitic protists: Unique features and drug targets. <i>Molecular and Biochemical Parasitology</i> , 2011, 177, 83-99.	0.5	111
107	Identification and modelling of a PPM protein phosphatase fold in the <i>Legionella pneumophila</i> deAMPylase SidD. <i>FEBS Letters</i> , 2011, 585, 2749-2754.	1.3	12
108	Structural variability of the ubiquitin specific protease DUSP-UBL double domains. <i>FEBS Letters</i> , 2011, 585, 3385-3390.	1.3	23

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109	Ferric iron uptake genes are differentially expressed in the presence of copper sulfides in <i>Acidithiobacillus ferrooxidans</i> strain LR. <i>Antonie Van Leeuwenhoek</i> , 2011, 99, 609-617.	0.7	7
110	Improving Cry8Ka toxin activity towards the cotton boll weevil ( <i>Anthonomus grandis</i> ). <i>BMC Biotechnology</i> , 2011, 11, 85.	1.7	36
111	Characterization of the relationship between integrase, excisionase and antirepressor activities associated with a superinfecting Shiga toxin encoding bacteriophage. <i>Nucleic Acids Research</i> , 2011, 39, 2116-2129.	6.5	51
112	Autophagy in protists. <i>Autophagy</i> , 2011, 7, 127-158.	4.3	148
113	Characterisation of a Desmosterol Reductase Involved in Phytosterol Dealkylation in the Silkworm, <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2011, 6, e21316.	1.1	23
114	New Structural and Functional Contexts of the Dx[DN]xDG Linear Motif: Insights into Evolution of Calcium-Binding Proteins. <i>PLoS ONE</i> , 2011, 6, e21507.	1.1	53
115	Mining metagenomic data for novel domains: BACON, a new carbohydrate-binding module. <i>FEBS Letters</i> , 2010, 584, 2421-2426.	1.3	41
116	Distinct roles for Caf1, Ccr4, Edc3 and CutA in the coordination of transcript deadenylation, decapping and P-body formation in <i>Aspergillus nidulans</i> . <i>Molecular Microbiology</i> , 2010, 76, 503-516.	1.2	26
117	Family-wide characterization of the DENN domain Rab GDP-GTP exchange factors. <i>Journal of Cell Biology</i> , 2010, 191, 367-381.	2.3	260
118	CUCU Modification of mRNA Promotes Decapping and Transcript Degradation in <i>Aspergillus nidulans</i> . <i>Molecular and Cellular Biology</i> , 2010, 30, 460-469.	1.1	48
119	Mammalian Atg18 (WIPI2) localizes to omegasome-anchored phagophores and positively regulates LC3 lipidation. <i>Autophagy</i> , 2010, 6, 506-522.	4.3	566
120	Autophagy in protists: examples of secondary loss, lineage-specific innovations, and the conundrum of remodeling a single mitochondrion. <i>Autophagy</i> , 2009, 5, 784-794.	4.3	56
121	Identification of novel aspartic proteases from <i>Strongyloides ratti</i> and characterisation of their evolutionary relationships, stage-specific expression and molecular structure. <i>BMC Genomics</i> , 2009, 10, 611.	1.2	20
122	Identification, characterization and essentiality of the unusual peroxin 13 from <i>Trypanosoma brucei</i> . <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2009, 1793, 516-527.	1.9	28
123	Ab initio protein modelling reveals novel human MIT domains. <i>FEBS Letters</i> , 2009, 583, 872-878.	1.3	17
124	Does distant homology with Evf reveal a lipid binding site in <i>Bacillus thuringiensis</i> cytolytic toxins?. <i>FEBS Letters</i> , 2009, 583, 1555-1560.	1.3	11
125	PrfA protein of <i>Bacillus</i> species: Prediction and demonstration of endonuclease activity on DNA. <i>Protein Science</i> , 2009, 11, 2370-2381.	3.1	16
126	Molecular Dynamics and Electrochemical Investigations of a pH-Responsive Peptide Monolayer. <i>Journal of Physical Chemistry C</i> , 2009, 113, 6792-6799.	1.5	13



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127	Cathepsin L Digestion of Nanobioconjugates upon Endocytosis. ACS Nano, 2009, 3, 2461-2468.	7.3	110
128	From Protein Structure to Function with Bioinformatics. , 2009, , .		29
129	Prediction of Protein Function from Theoretical Models. , 2009, , 293-317.		0
130	Molecular replacement using <i>ab initio</i> polyaniline models generated with ROSETTA. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1288-1291.	2.5	30
131	Order within a mosaic distribution of mitochondrial <i>c</i> -type cytochrome biogenesis systems?. FEBS Journal, 2008, 275, 2385-2402.	2.2	79
132	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium Anoxybacillus flavithermus WK1. Genome Biology, 2008, 9, R161.	13.9	71
133	Sequence analysis of GerM and SpoVS, uncharacterized bacterial <i>sp</i> sporulation proteins with widespread phylogenetic distribution. Bioinformatics, 2008, 24, 1793-1797.	1.8	30
134	The histidine phosphatase superfamily: structure and function. Biochemical Journal, 2008, 409, 333-348.	1.7	172
135	The protein that binds to DNA base J in trypanosomatids has features of a thymidine hydroxylase. Nucleic Acids Research, 2007, 35, 2107-2115.	6.5	84
136	Jaburetox-2Ec: An insecticidal peptide derived from an isoform of urease from the plant Canavalia ensiformis. Peptides, 2007, 28, 2042-2050.	1.2	78
137	Acyl Carrier Protein Phosphodiesterase (AcpH) of Escherichia coli is a Non-Canonical Member of the HD Phosphatase/Phosphodiesterase Family. Biochemistry, 2007, 46, 129-136.	1.2	23
138	An unsuspected ecdysteroid/steroid phosphatase activity in the key T-cell regulator, Sts-1: Surprising relationship to insect ecdysteroid phosphate phosphatase. Proteins: Structure, Function and Bioinformatics, 2007, 67, 720-731.	1.5	24
139	Structural flexibility in Trypanosoma brucei enolase revealed by X-ray crystallography and molecular dynamics. FEBS Journal, 2007, 274, 5077-5089.	2.2	41
140	Alternate Structural Conformations of Streptococcus pneumoniae Hyaluronan Lyase: Insights into Enzyme Flexibility and Underlying Molecular Mechanism of Action. Journal of Molecular Biology, 2006, 358, 1165-1178.	2.0	21
141	Molecular modeling and inhibitory activity of cowpea cystatin against bean bruchid pests. Proteins: Structure, Function and Bioinformatics, 2006, 63, 662-670.	1.5	11
142	Genome-based identification and characterization of a putative mucin-binding protein from the surface of Streptococcus pneumoniae. Proteins: Structure, Function and Bioinformatics, 2006, 66, 547-558.	1.5	21
143	Understanding the cell in terms of structure and function: insights from structural genomics. Current Opinion in Biotechnology, 2006, 17, 457-464.	3.3	19
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