

Robert B Russell

List of Publications by Year in descending order

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178
papers

27,254
citations

9756

73
h-index

6454

157
g-index

189
all docs

189
docs citations

189
times ranked

32049
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006, 440, 631-636.	13.7	2,347
2	Principles of MicroRNA Target Recognition. <i>PLoS Biology</i> , 2005, 3, e85.	2.6	2,019
3	bantam Encodes a Developmentally Regulated microRNA that Controls Cell Proliferation and Regulates the Proapoptotic Gene hid in <i>Drosophila</i> . <i>Cell</i> , 2003, 113, 25-36.	13.5	1,889
4	Protein Disorder Prediction. <i>Structure</i> , 2003, 11, 1453-1459.	1.6	1,119
5	Animal MicroRNAs Confer Robustness to Gene Expression and Have a Significant Impact on 3'UTR Evolution. <i>Cell</i> , 2005, 123, 1133-1146.	13.5	979
6	GlobPlot: exploring protein sequences for globularity and disorder. <i>Nucleic Acids Research</i> , 2003, 31, 3701-3708.	6.5	869
7	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012, 488, 100-105.	13.7	765
8	Systematic Discovery of In Vivo Phosphorylation Networks. <i>Cell</i> , 2007, 129, 1415-1426.	13.5	702
9	Identification of <i>Drosophila</i> MicroRNA Targets. <i>PLoS Biology</i> , 2003, 1, e60.	2.6	689
10	Multiple protein sequence alignment from tertiary structure comparison: Assignment of global and residue confidence levels. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 14, 309-323.	1.5	622
11	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2007, 36, D919-D922.	6.5	518
12	WD40 proteins propel cellular networks. <i>Trends in Biochemical Sciences</i> , 2010, 35, 565-574.	3.7	518
13	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	6.0	440
14	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012, 44, 1316-1320.	9.4	389
15	Illuminating G-Protein-Coupling Selectivity of GPCRs. <i>Cell</i> , 2019, 177, 1933-1947.e25.	13.5	387
16	Structure-Based Assembly of Protein Complexes in Yeast. <i>Science</i> , 2004, 303, 2026-2029.	6.0	367
17	Interrogating protein interaction networks through structural biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5896-5901.	3.3	330
18	Amino Acid Properties and Consequences of Substitutions. , 0, , 289-316.		327

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19	Systematic Discovery of New Recognition Peptides Mediating Protein Interaction Networks. <i>PLoS Biology</i> , 2005, 3, e405.	2.6	310
20	Linear motifs: Evolutionary interaction switches. <i>FEBS Letters</i> , 2005, 579, 3342-3345.	1.3	299
21	Structural systems biology: modelling protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 188-197.	16.1	298
22	The Relationship Between Sequence and Interaction Divergence in Proteins. <i>Journal of Molecular Biology</i> , 2003, 332, 989-998.	2.0	296
23	The Natural History of Protein Domains. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002, 31, 45-71.	18.3	286
24	On the Evolution of Protein Folds: Are Similar Motifs in Different Protein Folds the Result of Convergence, Insertion, or Relics of an Ancient Peptide World?. <i>Journal of Structural Biology</i> , 2001, 134, 191-203.	1.3	276
25	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	6.0	267
26	A structural perspective on protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2004, 14, 313-324.	2.6	260
27	Analysis and prediction of functional sub-types from protein sequence alignments. <i>Journal of Molecular Biology</i> , 2000, 303, 61-76.	2.0	245
28	Detection of protein three-dimensional side-chain patterns: new examples of convergent evolution. <i>Journal of Molecular Biology</i> , 1998, 279, 1211-1227.	2.0	241
29	Peptide-mediated interactions in biological systems: new discoveries and applications. <i>Current Opinion in Biotechnology</i> , 2008, 19, 344-350.	3.3	232
30	Changes in mitochondrial genetic codes as phylogenetic characters: Two examples from the flatworms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11359-11364.	3.3	223
31	Supersites within superfolds. Binding site similarity in the absence of homology 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 1998, 282, 903-918.	2.0	221
32	InterPreTS: protein Interaction Prediction through Tertiary Structure. <i>Bioinformatics</i> , 2003, 19, 161-162.	1.8	214
33	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. <i>Nature Communications</i> , 2016, 7, 11491.	5.8	207
34	Recognition of analogous and homologous protein folds: analysis of sequence and structure conservation 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1997, 269, 423-439.	2.0	204
35	GABA _{B2} Is Essential for G-Protein Coupling of the GABA _B Receptor Heterodimer. <i>Journal of Neuroscience</i> , 2001, 21, 8043-8052.	1.7	203
36	New roles for structure in biology and drug discovery. , 2000, 7, 928-930.		189

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37	Ten thousand interactions for the molecular biologist. <i>Nature Biotechnology</i> , 2004, 22, 1317-1321.	9.4	186
38	A recurrent 11q aberration pattern characterizes a subset of MYC-negative high-grade B-cell lymphomas resembling Burkitt lymphoma. <i>Blood</i> , 2014, 123, 1187-1198.	0.6	185
39	Peptides mediating interaction networks: new leads at last. <i>Current Opinion in Biotechnology</i> , 2006, 17, 465-471.	3.3	183
40	PepSite: prediction of peptide-binding sites from protein surfaces. <i>Nucleic Acids Research</i> , 2012, 40, W423-W427.	6.5	174
41	Structural Features can be Unconserved in Proteins with Similar Folds. <i>Journal of Molecular Biology</i> , 1994, 244, 332-350.	2.0	169
42	Crosstalk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	3.2	169
43	A Model for Statistical Significance of Local Similarities in Structure. <i>Journal of Molecular Biology</i> , 2003, 326, 1307-1316.	2.0	161
44	3did: interacting protein domains of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2004, 33, D413-D417.	6.5	160
45	Structural similarity between the p17 matrix protein of HIV-1 and interferon- β . <i>Nature</i> , 1994, 370, 666-668.	13.7	158
46	SMARCA4-mutated atypical teratoid/rhabdoid tumors are associated with inherited germline alterations and poor prognosis. <i>Acta Neuropathologica</i> , 2014, 128, 453-456.	3.9	155
47	The C-Terminal Domains of the GABA _B Receptor Subunits Mediate Intracellular Trafficking But Are Not Required for Receptor Signaling. <i>Journal of Neuroscience</i> , 2001, 21, 1203-1210.	1.7	153
48	Annotation in three dimensions. PINTS: Patterns in Non-homologous Tertiary Structures. <i>Nucleic Acids Research</i> , 2003, 31, 3341-3344.	6.5	151
49	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	3.2	146
50	The mutational pattern of primary lymphoma of the central nervous system determined by whole-exome sequencing. <i>Leukemia</i> , 2015, 29, 677-685.	3.3	139
51	Accurate Prediction of Peptide Binding Sites on Protein Surfaces. <i>PLoS Computational Biology</i> , 2009, 5, e1000335.	1.5	138
52	Protein Fold Recognition by Mapping Predicted Secondary Structures. <i>Journal of Molecular Biology</i> , 1996, 259, 349-365.	2.0	134
53	Illuminating the Onco-GPCRome: Novel G protein-coupled receptor-driven oncocrine networks and targets for cancer immunotherapy. <i>Journal of Biological Chemistry</i> , 2019, 294, 11062-11086.	1.6	129
54	Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. <i>Accounts of Chemical Research</i> , 2008, 41, 617-627.	7.6	123

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55	DILIMOT: discovery of linear motifs in proteins. <i>Nucleic Acids Research</i> , 2006, 34, W350-W355.	6.5	121
56	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015, 47, 1316-1325.	9.4	119
57	Swaposins: circular permutations within genes encoding saposin homologues. <i>Trends in Biochemical Sciences</i> , 1995, 20, 179-180.	3.7	116
58	A Dynamic Structural Model for Estrogen Receptor- α Activation by Ligands, Emphasizing the Role of Interactions between Distant A and E Domains. <i>Molecular Cell</i> , 2002, 10, 1019-1032.	4.5	114
59	Identification of distant homologues of fibroblast growth factors suggests a common ancestor for all β -trefoil proteins 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2000, 302, 1041-1047.	2.0	111
60	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017, 13, 936.	3.2	108
61	Geminate Structures of African Cassava Mosaic Virus. <i>Journal of Virology</i> , 2004, 78, 6758-6765.	1.5	107
62	EZH1/CXorf67 mimics K27M mutated oncohistones and functions as an intrinsic inhibitor of PRC2 function in aggressive posterior fossa ependymoma. <i>Neuro-Oncology</i> , 2019, 21, 878-889.	0.6	106
63	Systematic searches for molecular synapomorphies in model metazoan genomes give some support for Ecdysozoa after accounting for the idiosyncrasies of <i>Caenorhabditis elegans</i> . <i>Evolution & Development</i> , 2004, 6, 164-169.	1.1	104
64	CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019, 14, e0216705.	1.1	104
65	Predictions without templates: New folds, secondary structure, and contacts in CASP5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 436-456.	1.5	103
66	Illuminating drug discovery with biological pathways. <i>FEBS Letters</i> , 2005, 579, 1872-1877.	1.3	100
67	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	5.8	99
68	Conservation analysis and structure prediction of the SH2 family of phosphotyrosine binding domains. <i>FEBS Letters</i> , 1992, 304, 15-20.	1.3	96
69	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. <i>Nucleic Acids Research</i> , 2015, 43, e10-e10.	6.5	95
70	Exon structure conservation despite low sequence similarity: a relic of dramatic events in evolution?. <i>EMBO Journal</i> , 2001, 20, 5354-5360.	3.5	93
71	The third dimension for protein interactions and complexes. <i>Trends in Biochemical Sciences</i> , 2002, 27, 633-638.	3.7	91
72	Targeting and tinkering with interaction networks. <i>Nature Chemical Biology</i> , 2008, 4, 666-673.	3.9	90

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73	A complex prediction: three-dimensional model of the yeast exosome. <i>EMBO Reports</i> , 2002, 3, 628-635.	2.0	89
74	Amino-Acid Properties and Consequences of Substitutions. , 0, , 311-342.		88
75	Landscape of nuclear transport receptor cargo specificity. <i>Molecular Systems Biology</i> , 2017, 13, 962.	3.2	88
76	Protein complexes: structure prediction challenges for the 21st century. <i>Current Opinion in Structural Biology</i> , 2005, 15, 15-22.	2.6	85
77	Recurrent mutation of <i>JAK3</i> in T-cell prolymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 309-316.	1.5	79
78	The Limits of Protein Secondary Structure Prediction Accuracy from Multiple Sequence Alignment. <i>Journal of Molecular Biology</i> , 1993, 234, 951-957.	2.0	75
79	Differential localization of coatamer complex isoforms within the Golgi apparatus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4425-4430.	3.3	75
80	Molecular dissection of human Argonaute proteins by DNA shuffling. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 818-826.	3.6	74
81	A careful disorderliness in the proteome: Sites for interaction and targets for future therapies. <i>FEBS Letters</i> , 2008, 582, 1271-1275.	1.3	71
82	The three-dimensional molecular structure of the desmosomal plaque. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6480-6485.	3.3	71
83	Sialidase-like Asp-boxes: Sequence-similar structures within different protein folds. <i>Protein Science</i> , 2001, 10, 285-292.	3.1	70
84	The mutational landscape of Burkitt-like lymphoma with 11q aberration is distinct from that of Burkitt lymphoma. <i>Blood</i> , 2019, 133, 962-966.	0.6	69
85	Functional Analysis of H-Ryk, an Atypical Member of the Receptor Tyrosine Kinase Family. <i>Molecular and Cellular Biology</i> , 1999, 19, 6427-6440.	1.1	66
86	Potential artefacts in protein-interaction networks. <i>FEBS Letters</i> , 2002, 530, 253-254.	1.3	64
87	Genes encoding members of the <i>JAK-STAT</i> pathway or epigenetic regulators are recurrently mutated in T-cell prolymphocytic leukaemia. <i>British Journal of Haematology</i> , 2016, 173, 265-273.	1.2	64
88	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019, 10, 1635.	5.8	64
89	Synthesis of a new family of water-soluble tertiary phosphine ligands and of their rhodium(I) complexes; olefin hydrogenation in aqueous and biphasic media. <i>Journal of Organometallic Chemistry</i> , 1991, 419, 403-415.	0.8	63
90	Fast Fitting of Atomic Structures to Low-resolution Electron Density Maps by Surface Overlap Maximization. <i>Journal of Molecular Biology</i> , 2004, 338, 783-793.	2.0	58

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91	KIAA0556 is a novel ciliary basal body component mutated in Joubert syndrome. <i>Genome Biology</i> , 2015, 16, 293.	3.8	56
92	A more complete, complexed and structured interactome. <i>Current Opinion in Structural Biology</i> , 2007, 17, 370-377.	2.6	53
93	An automated stochastic approach to the identification of the protein specificity determinants and functional subfamilies. <i>Algorithms for Molecular Biology</i> , 2010, 5, 29.	0.3	53
94	Recurrent <i>RHOA</i> mutations in pediatric Burkitt lymphoma treated according to the NHL-BFM protocols. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 911-916.	1.5	51
95	Domain insertion. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1407-1410.	1.0	48
96	Protein fold irregularities that hinder sequence analysis. <i>Current Opinion in Structural Biology</i> , 1998, 8, 364-371.	2.6	48
97	Cryptogenic cholestasis in young and adults: ATP8B1, ABCB11, ABCB4, and TJP2 gene variants analysis by high-throughput sequencing. <i>Journal of Gastroenterology</i> , 2018, 53, 945-958.	2.3	47
98	Defining clinical subgroups and genotype-phenotype correlations in NBAS-associated disease across 110 patients. <i>Genetics in Medicine</i> , 2020, 22, 610-621.	1.1	46
99	Crystal Structure of an Archaeal Class I Aldolase and the Evolution of (12±)8 Barrel Proteins. <i>Journal of Biological Chemistry</i> , 2003, 278, 47253-47260.	1.6	45
100	Finding Functional Sites in Structural Genomics Proteins. <i>Structure</i> , 2004, 12, 1405-1412.	1.6	44
101	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017, 13, e1005462.	1.5	44
102	Fold recognition using sequence and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 141-148.	1.5	43
103	Structure of the full-length HPr kinase/phosphatase from <i>Staphylococcus xylosus</i> at 1.95 Å resolution: Mimicking the product/substrate of the phospho transfer reactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3458-3463.	3.3	43
104	Negative protein-protein interaction datasets derived from large-scale two-hybrid experiments. <i>Methods</i> , 2012, 58, 343-348.	1.9	38
105	Combining specificity determining and conserved residues improves functional site prediction. <i>BMC Bioinformatics</i> , 2009, 10, 174.	1.2	37
106	The serine protease inhibitor canonical loop conformation: examples found in extracellular hydrolases, toxins, cytokines and viral proteins 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 296, 325-334.	2.0	35
107	CASH a β -helix domain widespread among carbohydrate-binding proteins. <i>Trends in Biochemical Sciences</i> , 2002, 27, 59-62.	3.7	32
108	Taking the mystery out of biological networks. <i>EMBO Reports</i> , 2004, 5, 349-350.	2.0	31

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109	The <i>PCBP1</i> gene encoding poly(rc) binding protein i is recurrently mutated in Burkitt lymphoma. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 555-564.	1.5	29
110	Structure-based systems biology: a zoom lens for the cell. <i>FEBS Letters</i> , 2005, 579, 1854-1858.	1.3	27
111	An SH2-SH3 domain hybrid. <i>Nature</i> , 1993, 364, 765-765.	13.7	26
112	Combinations of Protein-Chemical Complex Structures Reveal New Targets for Established Drugs. <i>PLoS Computational Biology</i> , 2011, 7, e1002043.	1.5	25
113	RNAi screen identifies KIF15 as a novel regulator of integrin endocytic trafficking. <i>Journal of Cell Science</i> , 2014, 127, 2433-47.	1.2	25
114	Protein structure prediction. <i>Nature</i> , 1993, 361, 505-506.	13.7	24
115	Modular architecture of nucleotide-binding pockets. <i>Nucleic Acids Research</i> , 2010, 38, 3809-3816.	6.5	24
116	Topic Pages: PLoS Computational Biology Meets Wikipedia. <i>PLoS Computational Biology</i> , 2012, 8, e1002446.	1.5	23
117	The Interaction of Munc18-1 Helix 11 and 12 with the Central Region of the VAMP2 SNARE Motif Is Essential for SNARE Templating and Synaptic Transmission. <i>ENeuro</i> , 2020, 7, ENEURO.0278-20.2020.	0.9	23
118	Structure Prediction: How good are we?. <i>Current Biology</i> , 1995, 5, 488-490.	1.8	21
119	Interactions between the Fyn SH3 domain and adaptor protein Cbp/PAG derived ligands, effects on kinase activity and affinity. <i>FEBS Journal</i> , 2008, 275, 4863-4874.	2.2	21
120	Insights into cancer severity from biomolecular interaction mechanisms. <i>Scientific Reports</i> , 2016, 6, 34490.	1.6	21
121	Molecular switch from MYC to MYCN expression in MYC protein negative Burkitt lymphoma cases. <i>Blood Cancer Journal</i> , 2019, 9, 91.	2.8	21
122	Next Generation Protein Structure Predictions and Genetic Variant Interpretation. <i>Journal of Molecular Biology</i> , 2021, 433, 167180.	2.0	21
123	Fold recognition without folds. <i>Protein Science</i> , 2002, 11, 1575-1579.	3.1	20
124	Structural similarity to link sequence space: New potential superfamilies and implications for structural genomics. <i>Protein Science</i> , 2002, 11, 1101-1116.	3.1	20
125	Rare, functional, somatic variants in gene families linked to cancer genes: GPCR signaling as a paradigm. <i>Oncogene</i> , 2019, 38, 6491-6506.	2.6	20
126	PRECOG: PREDicting COupling probabilities of G-protein coupled receptors. <i>Nucleic Acids Research</i> , 2019, 47, W395-W401.	6.5	20

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127	Content Disputes in Wikipedia Reflect Geopolitical Instability. PLoS ONE, 2011, 6, e20902.	1.1	20
128	Fold recognition from sequence comparisons. Proteins: Structure, Function and Bioinformatics, 2001, 45, 68-75.	1.5	19
129	The hard cell: From proteomics to a whole cell model. FEBS Letters, 2007, 581, 2870-2876.	1.3	18
130	Domain Recombination: A Workhorse for Evolutionary Innovation. Science Signaling, 2010, 3, pe30.	1.6	18
131	Evolutionary relationship between the bacterial HPr kinase and the ubiquitous PEP-carboxykinase: expanding the P-loop nucleotidyl transferase superfamily. FEBS Letters, 2002, 517, 1-6.	1.3	15
132	Understanding the role of genetic variability in <i>LRRK2</i> in Indian population. Movement Disorders, 2019, 34, 496-505.	2.2	14
133	ProtChemSI: a network of protein-chemical structural interactions. Nucleic Acids Research, 2012, 40, D549-D553.	6.5	12
134	Structural similarity to bridge sequence space: Finding new families on the bridges. Protein Science, 2005, 14, 1305-1314.	3.1	11
135	Molecular Biology of Human Renin and Its Gene. , 1991, 47, 211-258.		11
136	Predicting function from structure: examples of the serine protease inhibitor canonical loop conformation found in extracellular proteins. Computers & Chemistry, 2001, 26, 31-39.	1.2	10
137	Characterizing Protein Interactions Employing a Genome-Wide siRNA Cellular Phenotyping Screen. PLoS Computational Biology, 2014, 10, e1003814.	1.5	10
138	RhoGAP19D inhibits Cdc42 laterally to control epithelial cell shape and prevent invasion. Journal of Cell Biology, 2021, 220, .	2.3	10
139	Cancer genetics meets biomolecular mechanism“bridging an age“old gulf. FEBS Letters, 2018, 592, 463-474.	1.3	9
140	A lipid-binding domain in Wnt: a case of mistaken identity?. Current Biology, 1999, 9, R717-R719.	1.8	8
141	Understanding and Predicting Protein Assemblies with 3D Structures. Comparative and Functional Genomics, 2003, 4, 410-415.	2.0	8
142	Proline-Rich Regions in Transcriptional Complexes: Heading in Many Directions. Science's STKE: Signal Transduction Knowledge Environment, 2007, 2007, pe1-pe1.	4.1	8
143	Genetic variants affecting equivalent protein family positions reflect human diversity. Scientific Reports, 2017, 7, 12771.	1.6	8
144	A novel binding site in catalase is suggested by structural similarity to the calycin superfamily. Protein Engineering, Design and Selection, 1996, 9, 107-111.	1.0	7

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145	Classification of Protein Folds. Molecular Biotechnology, 2002, 20, 017-028.	1.3	7

146	A shortcut to peptides to modulate platelets. , 2007, 3, 83-84.		7
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163	A structural perspective on protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2004, 14, 313-313.	2.6	0
164	Classification of Protein Folds. , 2005, , 903-919.		0
165	Spotlight on Rob Russell. <i>FEBS Letters</i> , 2005, 579, 4043-4043.	1.3	0
166	Predicting molecular mechanism and adverse effects of biopharmaceuticals—A novel on-line tool for toxicologists. <i>Toxicology</i> , 2007, 240, 191-192.	2.0	0
167	Structural Systems Biology: Modeling Interactions and Networks for Systems Studies. , 2014, , 9-19.		0
168	Using mode of action framework in prediction of skin toxicity. <i>Toxicology Letters</i> , 2014, 229, S163-S164.	0.4	0
169	A systems biology approach towards the prediction of ciliopathy mechanisms. <i>Cilia</i> , 2015, 4, .	1.8	0
170	From proteomic data to networks: statistics and methods reveal ciliary protein interaction landscape. <i>Cilia</i> , 2015, 4, .	1.8	0
171	Systematic exploration of the ciliary protein landscape by large-scale affinity proteomics. <i>Cilia</i> , 2015, 4, .	1.8	0
172	Data Sources for Signature Discovery in Toxicology. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 95-108.	0.1	0
173	Systems biology approach to identify mechanism of toxicity of pioglitazone. <i>Toxicology Letters</i> , 2017, 280, S283.	0.4	0
174	Studying how genetic variants affect mechanism in biological systems. <i>Essays in Biochemistry</i> , 2018, 62, 575-582.	2.1	0
175	EPEN-04. CXorf67 MIMICS ONCOGENIC HISTONE H3 K27M MUTATIONS AND FUNCTIONS AS INTRINSIC INHIBITOR OF PRC2 FUNCTION IN AGGRESSIVE POSTERIOR FOSSA EPENDYMOMA. <i>Neuro-Oncology</i> , 2019, 21, ii78-ii78.	0.6	0
176	Identifying structural details for protein-protein interactions. <i>FASEB Journal</i> , 2006, 20, A35.	0.2	0
177	Systems-wide analysis of protein complexes in <i>Saccharomyces cerevisiae</i> . <i>FASEB Journal</i> , 2007, 21, A211.	0.2	0
178	Prediction of Protein Structure from Multiple Sequence Alignment. , 1993, , 209-220.		0