

Robert B Russell

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172 papers	23,116 citations	73 h-index	151 g-index
189 ext. papers	25,783 ext. citations	11.1 avg, IF	6.68 L-index

#	Paper	IF	Citations
172	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006 , 440, 631-6	50.4	2096
171	Principles of microRNA-target recognition. <i>PLoS Biology</i> , 2005 , 3, e85	9.7	1746
170	bantam encodes a developmentally regulated microRNA that controls cell proliferation and regulates the proapoptotic gene hid in Drosophila. <i>Cell</i> , 2003 , 113, 25-36	56.2	1696
169	Protein disorder prediction: implications for structural proteomics. <i>Structure</i> , 2003 , 11, 1453-9	5.2	964
168	Animal MicroRNAs confer robustness to gene expression and have a significant impact on 3'UTR evolution. <i>Cell</i> , 2005 , 123, 1133-46	56.2	890
167	GlobPlot: Exploring protein sequences for globularity and disorder. <i>Nucleic Acids Research</i> , 2003 , 31, 3701-8	20.1	752
166	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
165	Systematic discovery of in vivo phosphorylation networks. <i>Cell</i> , 2007 , 129, 1415-26	56.2	611
164	Identification of Drosophila MicroRNA targets. <i>PLoS Biology</i> , 2003 , 1, E60	9.7	591
163	Multiple protein sequence alignment from tertiary structure comparison: assignment of global and residue confidence levels. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 14, 309-23	4.2	542
162	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2008 , 36, D919-22	20.1	416
161	WD40 proteins propel cellular networks. <i>Trends in Biochemical Sciences</i> , 2010 , 35, 565-74	10.3	410
160	Proteome organization in a genome-reduced bacterium. <i>Science</i> , 2009 , 326, 1235-40	33.3	383
159	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012 , 44, 1316-20	36.3	317
158	Structure-based assembly of protein complexes in yeast. <i>Science</i> , 2004 , 303, 2026-9	33.3	308
157	Interrogating protein interaction networks through structural biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5896-901	11.5	275
156	Structural systems biology: modelling protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 188-97	48.7	264

155	The relationship between sequence and interaction divergence in proteins. <i>Journal of Molecular Biology</i> , 2003 , 332, 989-98	6.5	264
154	Systematic discovery of new recognition peptides mediating protein interaction networks. <i>PLoS Biology</i> , 2005 , 3, e405	9.7	257
153	Linear motifs: evolutionary interaction switches. <i>FEBS Letters</i> , 2005 , 579, 3342-5	3.8	246
152	Amino Acid Properties and Consequences of Substitutions289-316		246
151	Impact of genome reduction on bacterial metabolism and its regulation. <i>Science</i> , 2009 , 326, 1263-8	33.3	229
150	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	3.4	225
149	Analysis and prediction of functional sub-types from protein sequence alignments. <i>Journal of Molecular Biology</i> , 2000 , 303, 61-76	6.5	222
148	A structural perspective on protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 313-24	8.1	221
147	The natural history of protein domains. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002 , 31, 45-71		221
146	Detection of protein three-dimensional side-chain patterns: new examples of convergent evolution. <i>Journal of Molecular Biology</i> , 1998 , 279, 1211-27	6.5	217
145	Supersites within superfolds. Binding site similarity in the absence of homology. <i>Journal of Molecular Biology</i> , 1998 , 282, 903-18	6.5	199
144	InterPreTS: protein interaction prediction through tertiary structure. <i>Bioinformatics</i> , 2003 , 19, 161-2	7.2	192
143	GABA(B2) is essential for g-protein coupling of the GABA(B) receptor heterodimer. <i>Journal of Neuroscience</i> , 2001 , 21, 8043-52	6.6	189
142	Recognition of analogous and homologous protein folds: analysis of sequence and structure conservation. <i>Journal of Molecular Biology</i> , 1997 , 269, 423-39	6.5	188
141	Peptide-mediated interactions in biological systems: new discoveries and applications. <i>Current Opinion in Biotechnology</i> , 2008 , 19, 344-50	11.4	185
140	Illuminating G-Protein-Coupling Selectivity of GPCRs. <i>Cell</i> , 2019 , 177, 1933-1947.e25	56.2	181
139	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, 11359-64	11.5	175
138	Ten thousand interactions for the molecular biologist. <i>Nature Biotechnology</i> , 2004 , 22, 1317-21	44.5	169

137	New roles for structure in biology and drug discovery. <i>Nature Structural Biology</i> , 2000 , 7 Suppl, 928-30		169
136	Structural features can be unconserved in proteins with similar folds. An analysis of side-chain to side-chain contacts secondary structure and accessibility. <i>Journal of Molecular Biology</i> , 1994 , 244, 332-50	6.5	154
135	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, 1203-10	6.6	147
134	Peptides mediating interaction networks: new leads at last. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 465-71	11.4	145
133	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012 , 8, 571	12.2	144
132	A model for statistical significance of local similarities in structure. <i>Journal of Molecular Biology</i> , 2003 , 326, 1307-16	6.5	139
131	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. <i>Nature Communications</i> , 2016 , 7, 11491	17.4	134
130	PepSite: prediction of peptide-binding sites from protein surfaces. <i>Nucleic Acids Research</i> , 2012 , 40, W423-7	6.1	133
129	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010 , 6, 430	12.2	132
128	A recurrent 11q aberration pattern characterizes a subset of MYC-negative high-grade B-cell lymphomas resembling Burkitt lymphoma. <i>Blood</i> , 2014 , 123, 1187-98	2.2	131
127	Annotation in three dimensions. PINTS: Patterns in Non-homologous Tertiary Structures. <i>Nucleic Acids Research</i> , 2003 , 31, 3341-4	20.1	130
126	3did: interacting protein domains of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2005 , 33, D413-7	20.1	127
125	Structural similarity between the p17 matrix protein of HIV-1 and interferon-gamma. <i>Nature</i> , 1994 , 370, 666-8	50.4	127
124	Protein fold recognition by mapping predicted secondary structures. <i>Journal of Molecular Biology</i> , 1996 , 259, 349-65	6.5	119
123	Subunit architecture of intact protein complexes from mass spectrometry and homology modeling. <i>Accounts of Chemical Research</i> , 2008 , 41, 617-27	24.3	117
122	SMARCA4-mutated atypical teratoid/rhabdoid tumors are associated with inherited germline alterations and poor prognosis. <i>Acta Neuropathologica</i> , 2014 , 128, 453-6	14.3	116
121	Accurate prediction of peptide binding sites on protein surfaces. <i>PLoS Computational Biology</i> , 2009 , 5, e1000335	5	116
120	A dynamic structural model for estrogen receptor-alpha activation by ligands, emphasizing the role of interactions between distant A and E domains. <i>Molecular Cell</i> , 2002 , 10, 1019-32	17.6	105

119	The mutational pattern of primary lymphoma of the central nervous system determined by whole-exome sequencing. <i>Leukemia</i> , 2015 , 29, 677-85	10.7	104
118	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	36.3	101
117	Swaposins: circular permutations within genes encoding saposin homologues. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 179-80	10.3	100
116	DILIMOT: discovery of linear motifs in proteins. <i>Nucleic Acids Research</i> , 2006 , 34, W350-5	20.1	98
115	Identification of distant homologues of fibroblast growth factors suggests a common ancestor for all beta-trefoil proteins. <i>Journal of Molecular Biology</i> , 2000 , 302, 1041-7	6.5	97
114	Predictions without templates: new folds, secondary structure, and contacts in CASP5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 436-56	4.2	94
113	Geminate structures of African cassava mosaic virus. <i>Journal of Virology</i> , 2004 , 78, 6758-65	6.6	88
112	A complex prediction: three-dimensional model of the yeast exosome. <i>EMBO Reports</i> , 2002 , 3, 628-35	6.5	84
111	The third dimension for protein interactions and complexes. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 633-8	10.3	82
110	Illuminating drug discovery with biological pathways. <i>FEBS Letters</i> , 2005 , 579, 1872-7	3.8	81
109	Targeting and tinkering with interaction networks. <i>Nature Chemical Biology</i> , 2008 , 4, 666-73	11.7	80
108	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017 , 13, 936	12.2	79
107	Conservation analysis and structure prediction of the SH2 family of phosphotyrosine binding domains. <i>FEBS Letters</i> , 1992 , 304, 15-20	3.8	79
106	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	1	78
105	A systems biology approach towards the prediction of ciliopathy mechanisms. <i>Cilia</i> , 2015 , 4,	5.5	78
104	From proteomic data to networks: statistics and methods reveal ciliary protein interaction landscape. <i>Cilia</i> , 2015 , 4,	5.5	78
103	Systematic exploration of the ciliary protein landscape by large-scale affinity proteomics. <i>Cilia</i> , 2015 , 4, P89	5.5	78
102	Exon structure conservation despite low sequence similarity: a relic of dramatic events in evolution?. <i>EMBO Journal</i> , 2001 , 20, 5354-60	13	74

101	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	5.4	73
100	Protein complexes: structure prediction challenges for the 21st century. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 15-22	8.1	73
99	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, 164-9	2.6	71
98	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, 4425-30	11.5	67
97	The limits of protein secondary structure prediction accuracy from multiple sequence alignment. <i>Journal of Molecular Biology</i> , 1993 , 234, 951-7	6.5	67
96	Sialidase-like Asp-boxes: sequence-similar structures within different protein folds. <i>Protein Science</i> , 2001 , 10, 285-92	6.3	66
95	EZH1P/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	1	65
94	A careful disorderliness in the proteome: sites for interaction and targets for future therapies. <i>FEBS Letters</i> , 2008 , 582, 1271-5	3.8	63
93	Functional analysis of H-Ryk, an atypical member of the receptor tyrosine kinase family. <i>Molecular and Cellular Biology</i> , 1999 , 19, 6427-40	4.8	63
92	Recurrent mutation of JAK3 in T-cell prolymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 309-16	5	60
91	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, 6480-5	11.5	60
90	Potential artefacts in protein-interaction networks. <i>FEBS Letters</i> , 2002 , 530, 253-4	3.8	59
89	Molecular dissection of human Argonaute proteins by DNA shuffling. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 818-26	17.6	58
88	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. <i>Nucleic Acids Research</i> , 2015 , 43, e10	20.1	57
87	Fast fitting of atomic structures to low-resolution electron density maps by surface overlap maximization. <i>Journal of Molecular Biology</i> , 2004 , 338, 783-93	6.5	53
86	A more complete, complexed and structured interactome. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 370-7	8.1	52
85	Landscape of nuclear transport receptor cargo specificity. <i>Molecular Systems Biology</i> , 2017 , 13, 962	12.2	51
84	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019 , 10, 1459	17.4	49

83	CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019 , 14, e0216705	3.7	47
82	An automated stochastic approach to the identification of the protein specificity determinants and functional subfamilies. <i>Algorithms for Molecular Biology</i> , 2010 , 5, 29	1.8	47
81	Genes encoding members of the JAK-STAT pathway or epigenetic regulators are recurrently mutated in T-cell prolymphocytic leukaemia. <i>British Journal of Haematology</i> , 2016 , 173, 265-73	4.5	47
80	Protein fold irregularities that hinder sequence analysis. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 364-71	8.1	46
79	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	2.3	45
78	Recurrent RHOA mutations in pediatric Burkitt lymphoma treated according to the NHL-BFM protocols. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 911-6	5	44
77	Domain insertion. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 1407-10	1.9	43
76	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, 3458-63	11.5	41
75	Finding functional sites in structural genomics proteins. <i>Structure</i> , 2004 , 12, 1405-12	5.2	39
74	Crystal structure of an archaeal class I aldolase and the evolution of (betaalpha) ₈ barrel proteins. <i>Journal of Biological Chemistry</i> , 2003 , 278, 47253-60	5.4	39
73	Fold recognition using sequence and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 141-148	4.2	38
72	Amino-Acid Properties and Consequences of Substitutions311-342		36
71	The serine protease inhibitor canonical loop conformation: examples found in extracellular hydrolases, toxins, cytokines and viral proteins. <i>Journal of Molecular Biology</i> , 2000 , 296, 325-34	6.5	35
70	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019 , 10, 1635	17.4	33
69	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	6.9	33
68	KIAA0556 is a novel ciliary basal body component mutated in Joubert syndrome. <i>Genome Biology</i> , 2015 , 16, 293	18.3	32
67	Combining specificity determining and conserved residues improves functional site prediction. <i>BMC Bioinformatics</i> , 2009 , 10, 174	3.6	32
66	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017 , 13, e1005462	5	31

65	The mutational landscape of Burkitt-like lymphoma with 11q aberration is distinct from that of Burkitt lymphoma. <i>Blood</i> , 2019 , 133, 962-966	2.2	29
64	Taking the mystery out of biological networks. <i>EMBO Reports</i> , 2004 , 5, 349-50	6.5	26
63	Negative protein-protein interaction datasets derived from large-scale two-hybrid experiments. <i>Methods</i> , 2012 , 58, 343-8	4.6	25
62	Modular architecture of nucleotide-binding pockets. <i>Nucleic Acids Research</i> , 2010 , 38, 3809-16	20.1	24
61	Combinations of protein-chemical complex structures reveal new targets for established drugs. <i>PLoS Computational Biology</i> , 2011 , 7, e1002043	5	24
60	CASH--a beta-helix domain widespread among carbohydrate-binding proteins. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 59-62	10.3	24
59	An SH2-SH3 domain hybrid. <i>Nature</i> , 1993 , 364, 765	50.4	24
58	Structure-based systems biology: a zoom lens for the cell. <i>FEBS Letters</i> , 2005 , 579, 1854-8	3.8	23
57	Protein structure prediction. <i>Nature</i> , 1993 , 361, 505-6	50.4	23
56	An RNAi screen identifies KIF15 as a novel regulator of the endocytic trafficking of integrin. <i>Journal of Cell Science</i> , 2014 , 127, 2433-47	5.3	22
55	Defining clinical subgroups and genotype-phenotype correlations in NBAS-associated disease across 110 patients. <i>Genetics in Medicine</i> , 2020 , 22, 610-621	8.1	22
54	The PCBP1 gene encoding poly(rC) binding protein I is recurrently mutated in Burkitt lymphoma. <i>Genes Chromosomes and Cancer</i> , 2015 , 54, 555-64	5	21
53	Structure prediction. How good are we?. <i>Current Biology</i> , 1995 , 5, 488-90	6.3	21
52	Fold recognition without folds. <i>Protein Science</i> , 2002 , 11, 1575-9	6.3	19
51	Structural similarity to link sequence space: new potential superfamilies and implications for structural genomics. <i>Protein Science</i> , 2002 , 11, 1101-16	6.3	19
50	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, 4863-74	5.7	18
49	Fold recognition from sequence comparisons. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 68-75	4.2	18
48	Insights into cancer severity from biomolecular interaction mechanisms. <i>Scientific Reports</i> , 2016 , 6, 34490	4.9	16

47	Evolutionary relationship between the bacterial HPr kinase and the ubiquitous PEP-carboxykinase: expanding the P-loop nucleotidyl transferase superfamily. <i>FEBS Letters</i> , 2002 , 517, 1-6	3.8	15
46	The hard cell: from proteomics to a whole cell model. <i>FEBS Letters</i> , 2007 , 581, 2870-6	3.8	14
45	Domain recombination: a workhorse for evolutionary innovation. <i>Science Signaling</i> , 2010 , 3, pe30	8.8	13
44	Content disputes in Wikipedia reflect geopolitical instability. <i>PLoS ONE</i> , 2011 , 6, e20902	3.7	13
43	ProtChemSI: a network of protein-chemical structural interactions. <i>Nucleic Acids Research</i> , 2012 , 40, D542-53	4.5	11
42	Structural similarity to bridge sequence space: finding new families on the bridges. <i>Protein Science</i> , 2005 , 14, 1305-14	6.3	11
41	Molecular switch from MYC to MYCN expression in MYC protein negative Burkitt lymphoma cases. <i>Blood Cancer Journal</i> , 2019 , 9, 91	7	10
40	Predicting function from structure: examples of the serine protease inhibitor canonical loop conformation found in extracellular proteins. <i>Computers & Chemistry</i> , 2001 , 26, 31-9		9
39	Rare, functional, somatic variants in gene families linked to cancer genes: GPCR signaling as a paradigm. <i>Oncogene</i> , 2019 , 38, 6491-6506	9.2	8
38	Molecular biology of human renin and its gene. <i>Endocrine Reviews</i> , 1991 , 47, 211-57; discussion 257-8		8
37	Genetic variants affecting equivalent protein family positions reflect human diversity. <i>Scientific Reports</i> , 2017 , 7, 12771	4.9	7
36	Characterizing protein interactions employing a genome-wide siRNA cellular phenotyping screen. <i>PLoS Computational Biology</i> , 2014 , 10, e1003814	5	7
35	Computational identification of novel amino-acid interactions in HIV Gag via correlated evolution. <i>PLoS ONE</i> , 2012 , 7, e42468	3.7	7
34	Proline-rich regions in transcriptional complexes: heading in many directions. <i>Sciencels STKE: Signal Transduction Knowledge Environment</i> , 2007 , 2007, pe1		7
33	A novel binding site in catalase is suggested by structural similarity to the calycin superfamily. <i>Protein Engineering, Design and Selection</i> , 1996 , 9, 107-11	1.9	7
32	Cancer genetics meets biomolecular mechanism-bridging an age-old gulf. <i>FEBS Letters</i> , 2018 , 592, 463-474	3.8	6
31	Understanding and predicting protein assemblies with 3D structures. <i>Comparative and Functional Genomics</i> , 2003 , 4, 410-5		6
30	Understanding the role of genetic variability in LRRK2 in Indian population. <i>Movement Disorders</i> , 2019 , 34, 496-505	7	6

29	Next Generation Protein Structure Predictions and Genetic Variant Interpretation. <i>Journal of Molecular Biology</i> , 2021 , 433, 167180	6.5	6
28	Classification of protein folds. <i>Molecular Biotechnology</i> , 2002 , 20, 17-28	3	5
27	PRECOG: PREdicting COupling probabilities of G-protein coupled receptors. <i>Nucleic Acids Research</i> , 2019 , 47, W395-W401	20.1	4
26	Mutagenesis of N-terminal residues of feline foamy virus Gag reveals entirely distinct functions during capsid formation, particle assembly, Gag processing and budding. <i>Retrovirology</i> , 2016 , 13, 57	3.6	4
25	Hb M Dothan [beta 25/26 (B7/B8)/(GGT/GAG-->GAG//Gly/Glu-->Glu)]; a new mechanism of unstable methemoglobin variant and molecular characteristics. <i>Blood Cells, Molecules, and Diseases</i> , 2009 , 43, 235-8	2.1	4
24	Genes from liver tissue affected in phthalate treated rats, coupled with structural analysis of phthalates jointly predict testicular toxicity and elucidates possible mechanisms. <i>Toxicology</i> , 2010 , 278, 341-342	4.4	4
23	A lipid-binding domain in Wnt: a case of mistaken identity?. <i>Current Biology</i> , 1999 , 9, R717-9	6.3	4
22	Targeting and tinkering with interaction networks. <i>FEBS Letters</i> , 2008 , 582, 1219	3.8	3
21	Classification of protein folds. <i>Molecular Biotechnology</i> , 2007 , 36, 238-47	3	3
20	Systems Biology: Understanding the Biological Mosaic. <i>FEBS Letters</i> , 2005 , 579, 1771-1771	3.8	3
19	The Interaction of Munc18-1 Helix 11 and 12 with the Central Region of the VAMP2 SNARE Motif Is Essential for SNARE Templatng and Synaptic Transmission. <i>ENeuro</i> , 2020 , 7,	3.9	3
18	CiliaCarta: an integrated and validated compendium of ciliary genes		3
17	RhoGAP19D inhibits Cdc42 laterally to control epithelial cell shape and prevent invasion. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	3
16	Getting the most from your protein sequence. <i>Methods in Molecular Biology</i> , 2003 , 211, 411-30	1.4	2
15	Generation and interpretation of protein sequence and structural multiple alignments. <i>The Protein Journal</i> , 1992 , 11, 389-389		1
14	Consequences of intramolecular ionic interactions for the activation rate of human pepsinogens A and C as revealed by molecular modelling. <i>Advances in Experimental Medicine and Biology</i> , 1991 , 306, 101-5	3.6	1
13	Mechnetor: a web server for exploring protein mechanism and the functional context of genetic variants. <i>Nucleic Acids Research</i> , 2021 , 49, W366-W374	20.1	1
12	Data Sources for Signature Discovery in Toxicology. <i>Methods in Pharmacology and Toxicology</i> , 2015 , 95-108		

- 11 Structural Systems Biology: Modeling Interactions and Networks for Systems Studies **2014**, 9-19
- 10 Unraveling Mechanisms of Toxicity with the Power of Pathways: ToxWiz Tool as an Illustrative Example **2008**, 195-217
- 9 A structural perspective on protein-protein interactions. *Current Opinion in Structural Biology*, **2004**, 14, 313-313 8.1
- 8 Classification of Protein Folds **2005**, 903-919
- 7 Classification of protein folds. *Methods in Molecular Biology*, **2000**, 143, 305-24 1.4
- 6 Leveraging biochemical reactions to unravel functional impacts of cancer somatic variants affecting protein interaction interfaces. *F1000Research*, 10, 1111 3.6
- 5 A world-wide web server of protein domain assignment **2002**, 235-236
- 4 Identifying structural details for protein-protein interactions. *FASEB Journal*, **2006**, 20, A35 0.9
- 3 Systems-wide analysis of protein complexes in *Saccharomyces cerevisiae*. *FASEB Journal*, **2007**, 21, A211 0.9
- 2 Prediction of Protein Structure from Multiple Sequence Alignment **1993**, 209-220
- 1 Studying how genetic variants affect mechanism in biological systems. *Essays in Biochemistry*, **2018**, 62, 575-582 7.6