Tom Blundell

List of Publications by Year
in descending order

315 papers	44,143 citations	4345 89 h-index	2512 202 g-index
334 all docs	334 docs citations	334 times ranked	47900 citing authors

#	Article	IF	Citations
1	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46
2	In memoriam of Narayanaswamy Srinivasan (1962â€“2021). Proteins: Structure, Function and Bioinformatics, 2022, 90, 909-911.	1.5	3
3	Searching for New Z-DNA/Z-RNA Binding Proteins Based on Structural Similarity to Experimentally Validated ZÎ± Domain. International Journal of Molecular Sciences, 2022, 23, 768.	1.8	11
4	Structural insights into inhibitor regulation of the DNA repair protein DNA-PKcs. Nature, 2022, 601, 643-648.	13.7	36
5	Development of Inhibitors of SAICAR Synthetase (PurC) from <i>Mycobacterium abscessus</i> Using a Fragment-Based Approach. ACS Infectious Diseases, 2022, 8, 296-309.	1.8	10
6	Discovery of Novel Inhibitors of Uridine Diphosphate-<i>N</i>-Acetylenolpyruvylglucosamine Reductase (MurB) from <i>Pseudomonas aeruginosa</i>, an Opportunistic Infectious Agent Causing Death in Cystic Fibrosis Patients. Journal of Medicinal Chemistry, 2022, 65, 2149-2173.	2.9	5
7	Slipknot or Crystallographic Error: A Computational Analysis of the Plasmodium falciparum DHFR Structural Folds. International Journal of Molecular Sciences, 2022, 23, 1514.	1.8	3
8	Are There Hidden Genes in DNA/RNA Vaccines?. Frontiers in Immunology, 2022, 13, 801915.	2.2	9
9	Using Structure-guided Fragment-Based Drug Discovery to Target Pseudomonas aeruginosa Infections in Cystic Fibrosis. Frontiers in Molecular Biosciences, 2022, 9, 857000.	1.6	1
10	Unheeded SARS-CoV-2 proteins? A deep look into negative-sense RNA. Briefings in Bioinformatics, 2022, 23, .	3.2	15
11	Structural Biology â€“ Painting the Mechanistic Landscape of Biomolecules. Journal of Molecular Biology, 2022, 434, 167566.	2.0	1
12	Structural landscapes of PPI interfaces. Briefings in Bioinformatics, 2022, 23, .	3.2	13
13	In silico analysis of mutations near S1/S2 cleavage site in SARSâ€CoVâ€2 spike protein reveals increased propensity of glycosylation in Omicron strain. Journal of Medical Virology, 2022, 94, 4181-4192.	2.5	10
14	Structural Characterization of Mycobacterium abscessus Phosphopantetheine Adenylyl Transferase Ligand Interactions: Implications for Fragment-Based Drug Design. Frontiers in Molecular Biosciences, 2022, 9, .	1.6	5
15	Whole Exome Sequencing reveals NOTCH1 mutations in anaplastic large cell lymphoma and points to Notch both as a key pathway and a potential therapeutic target. Haematologica, 2021, 106, 1693-1704.	1.7	40
16	Dimers of DNA-PK create a stage for DNA double-strand break repair. Nature Structural and Molecular Biology, 2021, 28, 13-19.	3.6	67
17	SARS-CoV-2 3D database: understanding the coronavirus proteome and evaluating possible drug targets. Briefings in Bioinformatics, 2021, 22, 769-780.	3.2	31
18	Deep Learning for Proteinâ€“Protein Interaction Site Prediction. Methods in Molecular Biology, 2021, 2361, 263-288.	0.4	10

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19	A base measure of precision for protein stability predictors: structural sensitivity. BMC Bioinformatics, 2021, 22, 88.	1.2	28
20	SAP domain forms a flexible part of DNA aperture in Ku70/80. FEBS Journal, 2021, 288, 4382-4393.	2.2	13
21	The resolution revolution in X-ray diffraction, Cryo-EM and other Technologies. Progress in Biophysics and Molecular Biology, 2021, 160, 2-4.	1.4	18
22	Three Simple Properties Explain Protein Stability Change upon Mutation. Journal of Chemical Information and Modeling, 2021, 61, 1981-1988.	2.5	21
23	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i>. Science, 2021, 372, .	6.0	91
24	Editorial: Seventieth birthday Celebrations. Progress in Biophysics and Molecular Biology, 2021, 161, 1-2.	1.4	0
25	Targeting <i>Mycobacterium tuberculosis</i> CoaBC through Chemical Inhibition of 4â€²-Phosphopantothenoyl-<scp>l</scp>-cysteine Synthetase (CoaB) Activity. ACS Infectious Diseases, 2021, 7, 1666-1679.	1.8	3
26	ProtCHOIR: a tool for proteome-scale generation of homo-oligomers. Briefings in Bioinformatics, 2021, 22, .	3.2	3
27	Utilizing graph machine learning within drug discovery and development. Briefings in Bioinformatics, 2021, 22, .	3.2	90
28	Structure-Guided Computational Approaches to Unravel Druggable Proteomic Landscape of Mycobacterium leprae. Frontiers in Molecular Biosciences, 2021, 8, 663301.	1.6	2
29	COSMIC Cancer Gene Census 3D database: understanding the impacts of mutations on cancer targets. Briefings in Bioinformatics, 2021, 22, .	3.2	8
30	A small-molecule inhibitor of the BRCA2-RAD51 interaction modulates RAD51 assembly and potentiates DNA damage-induced cell death. Cell Chemical Biology, 2021, 28, 835-847.e5.	2.5	27
31	Strategies for drug target identification in Mycobacterium leprae. Drug Discovery Today, 2021, 26, 1569-1573.	3.2	11
32	Integrated human/SARS-CoV-2 metabolic models present novel treatment strategies against COVID-19. Life Science Alliance, 2021, 4, e202000954.	1.3	13
33	Stages, scaffolds and strings in the spatial organisation of non-homologous end joining: Insights from X-ray diffraction and Cryo-EM. Progress in Biophysics and Molecular Biology, 2021, 163, 60-73.	1.4	7
34	The renaissance in biophysics and molecular biology enabled by the interface of DNA repair and replication with cancer. Progress in Biophysics and Molecular Biology, 2021, 163, 1-4.	1.4	0
35	Cryo-EM of NHEJ supercomplexes provides insights into DNA repair. Molecular Cell, 2021, 81, 3400-3409.e3.	4.5	62
36	Using a synthetic switch to regulate insulin receptor activation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2111313118.	3.3	1

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37	Using cryo-EM to understand antimycobacterial resistance in the catalase-peroxidase (KatG) from Mycobacterium tuberculosis. Structure, 2021, 29, 899-912.e4.	1.6	13
38	The first resolution revolution in protein structure analysis: X-ray diffraction of polypeptide conformations and globular protein folds in 1950s and 1960s. Progress in Biophysics and Molecular Biology, 2021, 167, 32-32.	1.4	1
39	From revolutionary technologies for understanding genes and proteins to a focus on new therapeutics. Progress in Biophysics and Molecular Biology, 2021, 164, 1-2.	1.4	0
40	Predicted structural mimicry of spike receptor-binding motifs from highly pathogenic human coronaviruses. Computational and Structural Biotechnology Journal, 2021, 19, 3938-3953.	1.9	25
41	A fragment-based approach to assess the ligandability of ArgB, ArgC, ArgD and ArgF in the L-arginine biosynthetic pathway of Mycobacterium tuberculosis. Computational and Structural Biotechnology Journal, 2021, 19, 3491-3506.	1.9	16
42	Inhibiting Mycobacterium tuberculosis CoaBC by targeting an allosteric site. Nature Communications, 2021, 12, 143.	5.8	8
43	Can the SARS-CoV-2 Spike Protein Bind Integrins Independent of the RGD Sequence?. Frontiers in Cellular and Infection Microbiology, 2021, 11, 765300.	1.8	12
44	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	6.5	87
45	ProCarbDB: a database of carbohydrate-binding proteins. Nucleic Acids Research, 2020, 48, D368-D375.	6.5	17
46	A platform for target prediction of phenotypic screening hit molecules. Journal of Molecular Graphics and Modelling, 2020, 95, 107485.	1.3	1
47	Covalent inactivation of Mycobacterium thermoresistibile inosine-5â€²-monophosphate dehydrogenase (IMPDH). Bioorganic and Medicinal Chemistry Letters, 2020, 30, 126792.	1.0	2
48	Prediction of impacts of mutations on protein structure and interactions: SDM, a statistical approach, and mCSM, using machine learning. Protein Science, 2020, 29, 247-257.	3.1	58
49	Structural biology of multicomponent assemblies in DNA double-strand-break repair through non-homologous end joining. Current Opinion in Structural Biology, 2020, 61, 9-16.	2.6	21
50	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	6.5	13
51	Genomics, Computational Biology and Drug Discovery for Mycobacterial Infections: Fighting the Emergence of Resistance. Frontiers in Genetics, 2020, 11, 965.	1.1	7
52	Mechanism of efficient double-strand break repair by a long non-coding RNA. Nucleic Acids Research, 2020, 48, 10953-10972.	6.5	43
53	Systematic Investigation of the Data Set Dependency of Protein Stability Predictors. Journal of Chemical Information and Modeling, 2020, 60, 4772-4784.	2.5	37
54	Exploring the structural basis of conformational heterogeneity and autoinhibition of human cGMP-specific protein kinase IÎ± through computational modelling and molecular dynamics simulations. Computational and Structural Biotechnology Journal, 2020, 18, 1625-1638.	1.9	10

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55	Interdisciplinary research in physics, chemistry and biology is central to understanding biological processes. Progress in Biophysics and Molecular Biology, 2020, 156, 1-2.	1.4	1
56	A Personal History of Using Crystals and Crystallography to Understand Biology and Advanced Drug Discovery. Crystals, 2020, 10, 676.	1.0	1
57	HARP: a database of structural impacts of systematic missense mutations in drug targets of Mycobacterium leprae. Computational and Structural Biotechnology Journal, 2020, 18, 3692-3704.	1.9	16
58	Common mechanism of thermostability in small Î±â€•and Î²â€proteins studied by molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1233-1250.	1.5	4
59	Editorial overview: Macromolecular assemblies. Current Opinion in Structural Biology, 2020, 61, vi-viii.	2.6	0
60	Hotspots API: A Python Package for the Detection of Small Molecule Binding Hotspots and Application to Structure-Based Drug Design. Journal of Chemical Information and Modeling, 2020, 60, 1911-1916.	2.5	15
61	Fragment-Based Design of <i>Mycobacterium tuberculosis</i> InhA Inhibitors. Journal of Medicinal Chemistry, 2020, 63, 4749-4761.	2.9	27
62	Using a Fragment-Based Approach to Identify Alternative Chemical Scaffolds Targeting Dihydrofolate Reductase from <i>Mycobacterium tuberculosis</i>. ACS Infectious Diseases, 2020, 6, 2192-2201.	1.8	13
63	Fragment-based discovery of a new class of inhibitors targeting mycobacterial tRNA modification. Nucleic Acids Research, 2020, 48, 8099-8112.	6.5	20
64	Intrinsic disorder in proteins: Relevance to protein assemblies, drug design and host-pathogen interactions. Progress in Biophysics and Molecular Biology, 2020, 156, 34-42.	1.4	28
65	CCDC61/VFL3 Is a Paralog of SAS6 and Promotes Ciliary Functions. Structure, 2020, 28, 674-689.e11.	1.6	16
66	Deciphering the enzymatic target of a new family of antischistosomal agents bearing a quinazoline scaffold using complementary computational tools. Journal of Enzyme Inhibition and Medicinal Chemistry, 2020, 35, 511-523.	2.5	2
67	Computational saturation mutagenesis to predict structural consequences of systematic mutations in the beta subunit of RNA polymerase in Mycobacterium leprae. Computational and Structural Biotechnology Journal, 2020, 18, 271-286.	1.9	27
68	Druggable binding sites in the multicomponent assemblies that characterise DNA double-strand-break repair through non-homologous end joining. Essays in Biochemistry, 2020, 64, 791-806.	2.1	6
69	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.4	3
70	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in Mycobacterium tuberculosis in Southern India. Scientific Reports, 2019, 9, 10283.	1.6	32
71	Structure and dynamics of Î³-secretase with presenilin 2 compared to presenilin 1. RSC Advances, 2019, 9, 20901-20916.	1.7	24
72	Development of Inhibitors against <i>Mycobacterium abscessus</i> tRNA (m¹G37) Methyltransferase (TrmD) Using Fragment-Based Approaches. Journal of Medicinal Chemistry, 2019, 62, 7210-7232.	2.9	32

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73	Editorial. Progress in Biophysics and Molecular Biology, 2019, 141, 1-2.	1.4	0
74	Understanding the impacts of missense mutations on structures and functions of human cancer-related genes: A preliminary computational analysis of the COSMIC Cancer Gene Census. PLoS ONE, 2019, 14, e0219935.	1.1	10
75	SSEThread: Integrative threading of the DNA-PKcs sequence based on data from chemical cross-linking and hydrogen deuterium exchange. Progress in Biophysics and Molecular Biology, 2019, 147, 92-102.	1.4	8
76	Mabellini: a genome-wide database for understanding the structural proteome and evaluating prospective antimicrobial targets of the emerging pathogen Mycobacterium abscessus. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	12
77	Editorial overview: Theory and simulation: demystifying GPCRs â€“ structure, function and drug design. Current Opinion in Structural Biology, 2019, 55, vi-viii.	2.6	0
78	Multicomponent assemblies in DNA-double-strand break repair by NHEJ. Current Opinion in Structural Biology, 2019, 55, 154-160.	2.6	18
79	Understanding the structure and role of DNA-PK in NHEJ: How X-ray diffraction and cryo-EM contribute in complementary ways. Progress in Biophysics and Molecular Biology, 2019, 147, 26-32.	1.4	15
80	Structure-guided fragment-based drug discovery at the synchrotron: screening binding sites and correlations with hotspot mapping. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2019, 377, 20180422.	1.6	30
81	Synthesis and Structureâ€“Activity relationship of 1-(5-isoquinolinesulfonyl)piperazine analogues as inhibitorsÂofÂMycobacterium tuberculosis IMPDH. European Journal of Medicinal Chemistry, 2019, 174, 309-329.	2.6	25
82	The Molecular Organization of Human cGMP Specific Phosphodiesterase 6 (PDE6): Structural Implications of Somatic Mutations in Cancer and Retinitis Pigmentosa. Computational and Structural Biotechnology Journal, 2019, 17, 378-389.	1.9	20
83	Mycobacterial OtsA Structures Unveil Substrate Preference Mechanism and Allosteric Regulation by 2-Oxoglutarate and 2-Phosphoglycerate. MBio, 2019, 10, .	1.8	7
84	Mycobacterial genomics and structural bioinformatics: opportunities and challenges in drug discovery. Emerging Microbes and Infections, 2019, 8, 109-118.	3.0	26
85	Structural insights into <i>Escherichia coli</i> phosphopantothenoylcysteine synthetase by native ion mobilityâ€“mass spectrometry. Biochemical Journal, 2019, 476, 3125-3139.	1.7	4
86	Editorial. Progress in Biophysics and Molecular Biology, 2018, 132, 1-2.	1.4	1
87	Structural Implications of Mutations Conferring Rifampin Resistance in Mycobacterium leprae. Scientific Reports, 2018, 8, 5016.	1.6	41
88	Fragment-Based Approach to Targeting Inosine-5â€²-monophosphate Dehydrogenase (IMPDH) from <i>Mycobacterium tuberculosis</i>. Journal of Medicinal Chemistry, 2018, 61, 2806-2822.	2.9	51
89	The deubiquitylating enzyme UCHL3 regulates Ku80 retention at sites of DNA damage. Scientific Reports, 2018, 8, 17891.	1.6	29
90	Progress in biophysics and molecular biology: A brief history of the journal. Progress in Biophysics and Molecular Biology, 2018, 140, 1-4.	1.4	3

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91	Dissection of DNA double-strand-break repair using novel single-molecule forceps. Nature Structural and Molecular Biology, 2018, 25, 482-487.	3.6	79
92	Arginine-deprivationâ€“induced oxidative damage sterilizes <i>Mycobacterium tuberculosis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9779-9784.	3.3	97
93	Identification of new allosteric sites and modulators of AChE through computational and experimental tools. Journal of Enzyme Inhibition and Medicinal Chemistry, 2018, 33, 1034-1047.	2.5	33
94	Mutations at protein-protein interfaces: Small changes over big surfaces have large impacts on human health. Progress in Biophysics and Molecular Biology, 2017, 128, 3-13.	1.4	129
95	DNA-PKcs structure suggests an allosteric mechanism modulating DNA double-strand break repair. Science, 2017, 355, 520-524.	6.0	155
96	Structural insights into the EthRâ€“DNA interaction using native mass spectrometry. Chemical Communications, 2017, 53, 3527-3530.	2.2	17
97	Genomes, structural biology and drug discovery: combating the impacts of mutations in genetic disease and antibiotic resistance. Biochemical Society Transactions, 2017, 45, 303-311.	1.6	35
98	Fragment Screening against the EthRâ€“DNA Interaction by Native Mass Spectrometry. Angewandte Chemie - International Edition, 2017, 56, 7488-7491.	7.2	12
99	XSuLT: a web server for structural annotation and representation of sequence-structure alignments. Nucleic Acids Research, 2017, 45, W381-W387.	6.5	2
100	SDM: a server for predicting effects of mutations on protein stability. Nucleic Acids Research, 2017, 45, W229-W235.	6.5	407
101	Fragment Screening against the EthRâ€“DNA Interaction by Native Mass Spectrometry. Angewandte Chemie, 2017, 129, 7596-7599.	1.6	2
102	Fragment-Sized EthR Inhibitors Exhibit Exceptionally Strong Ethionamide Boosting Effect in Whole-Cell <i>Mycobacterium tuberculosis</i> Assays. ACS Chemical Biology, 2017, 12, 1390-1396.	1.6	24
103	Arpeggio: A Web Server for Calculating and Visualising Interatomic Interactions in Protein Structures. Journal of Molecular Biology, 2017, 429, 365-371.	2.0	340
104	TIBLE: a web-based, freely accessible resource for small-molecule binding data for mycobacterial species. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	5
105	Book Review on â€œMolecular Biology of Assemblies and Machinesâ€•by Alasdair Steven, Wolfgang Baumeister, Louise Johnson and Richard Perham. Published by Garland Science, Taylor and Francis Group. FEBS Letters, 2017, 591, 3707-3708.	1.3	0
106	Structural Biology and the Design of New Therapeutics: From HIV and Cancer to Mycobacterial Infections. Journal of Molecular Biology, 2017, 429, 2677-2693.	2.0	39
107	Achieving selectivity in space and time with DNA double-strand-break response and repair: molecular stages and scaffolds come with strings attached. Structural Chemistry, 2017, 28, 161-171.	1.0	9
108	The Inosine Monophosphate Dehydrogenase, GuaB2, Is a Vulnerable New Bactericidal Drug Target for Tuberculosis. ACS Infectious Diseases, 2017, 3, 5-17.	1.8	83

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109	Targeting tuberculosis using structure-guided fragment-based drug design. Drug Discovery Today, 2017, 22, 546-554.	3.2	36
110	Essential but Not Vulnerable: Indazole Sulfonamides Targeting Inosine Monophosphate Dehydrogenase as Potential Leads against <i>Mycobacterium tuberculosis</i>. ACS Infectious Diseases, 2017, 3, 18-33.	1.8	77
111	Target Identification of Mycobacterium tuberculosis Phenotypic Hits Using a Concerted Chemogenomic, Biophysical, and Structural Approach. Frontiers in Pharmacology, 2017, 8, 681.	1.6	22
112	DNA-PKcs, Allostery, and DNA Double-Strand Break Repair. Methods in Enzymology, 2017, 592, 145-157.	0.4	5
113	Decoding the similarities and differences among mycobacterial species. PLoS Neglected Tropical Diseases, 2017, 11, e0005883.	1.3	37
114	Protein crystallography and drug discovery: recollections of knowledge exchange between academia and industry. IUCrJ, 2017, 4, 308-321.	1.0	65
115	In silico functional dissection of saturation mutagenesis: Interpreting the relationship between phenotypes and changes in protein stability, interactions and activity. Scientific Reports, 2016, 6, 19848.	1.6	87
116	mCSM-lig: quantifying the effects of mutations on protein-small molecule affinity in genetic disease and emergence of drug resistance. Scientific Reports, 2016, 6, 29575.	1.6	120
117	Identifying Interactions that Determine Fragment Binding at Protein Hotspots. Journal of Medicinal Chemistry, 2016, 59, 4314-4325.	2.9	86
118	Virtual Screening and X-ray Crystallography Identify Non-Substrate Analog Inhibitors of Flavin-Dependent Thymidylate Synthase. Journal of Medicinal Chemistry, 2016, 59, 9269-9275.	2.9	19
119	Different DNA End Configurations Dictate Which NHEJ Components Are Most Important for Joining Efficiency. Journal of Biological Chemistry, 2016, 291, 24377-24389.	1.6	83
120	Engineering Archeal Surrogate Systems for the Development of Proteinâ€“Protein Interaction Inhibitors against Human RAD51. Journal of Molecular Biology, 2016, 428, 4589-4607.	2.0	13
121	Structureâ€activity relationship of the peptide bindingâ€motif mediating the BRCA2:RAD51 proteinâ€“protein interaction. FEBS Letters, 2016, 590, 1094-1102.	1.3	20
122	Optimization of Inhibitors of <i>Mycobacterium tuberculosis</i> Pantothenate Synthetase Based on Group Efficiency Analysis. ChemMedChem, 2016, 11, 38-42.	1.6	27
123	Structure of BRCA1-BRCT/Abraxas Complex Reveals Phosphorylation-Dependent BRCT Dimerization at DNA Damage Sites. Molecular Cell, 2016, 61, 434-448.	4.5	61
124	A fragment merging approach towards the development of small molecule inhibitors of Mycobacterium tuberculosis EthR for use as ethionamide boosters. Organic and Biomolecular Chemistry, 2016, 14, 2318-2326.	1.5	41
125	Developing Antagonists for the Met-HGF/SF Proteinâ€“Protein Interaction Using a Fragment-Based Approach. Molecular Cancer Therapeutics, 2016, 15, 3-14.	1.9	7
126	Twelve novel HGD gene variants identified in 99 alkaptonuria patients: focus on â€˜black bone diseaseâ€™ in Italy. European Journal of Human Genetics, 2016, 24, 66-72.	1.4	87

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127	Structure-guided, target-based drug discovery - exploiting genome information from HIV to mycobacterial infections. Postepy Biochemii, 2016, 62, 262-272.	0.5	2
128	Structure of Mycobacterium thermoresistibile GlgE defines novel conformational states that contribute to the catalytic mechanism. Scientific Reports, 2015, 5, 17144.	1.6	3
129	SInCReâ€"structural interactome computational resource for<i>Mycobacterium tuberculosis</i>. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	1.4	10
130	CHOPIN: a web resource for the structural and functional proteome of Mycobacterium tuberculosis. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	21
131	Protein-Protein Interactions: Structures and Druggability. NATO Science for Peace and Security Series A: Chemistry and Biology, 2015, , 141-163.	0.5	10
132	Flexibility and small pockets at proteinâ€"protein interfaces: New insights into druggability. Progress in Biophysics and Molecular Biology, 2015, 119, 2-9.	1.4	118
133	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	6.5	42
134	Germline Mutations in the <i>CDKN2B</i> Tumor Suppressor Gene Predispose to Renal Cell Carcinoma. Cancer Discovery, 2015, 5, 723-729.	7.7	88
135	Lst4, the yeast Fnip1/2 orthologue, is a DENN-family protein. Open Biology, 2015, 5, 150174.	1.5	27
136	Enriching the annotation of Mycobacterium tuberculosis H37Rv proteome using remote homology detection approaches: Insights into structure and function. Tuberculosis, 2015, 95, 14-25.	0.8	9
137	PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. Science, 2015, 347, 185-188.	6.0	252
138	Mutations in the NHEJ Component XRCC4 Cause Primordial Dwarfism. American Journal of Human Genetics, 2015, 96, 412-424.	2.6	71
139	Phosphopeptide interactions with BRCA1 BRCT domains: More than just a motif. Progress in Biophysics and Molecular Biology, 2015, 117, 143-148.	1.4	33
140	pkCSM: Predicting Small-Molecule Pharmacokinetic and Toxicity Properties Using Graph-Based Signatures. Journal of Medicinal Chemistry, 2015, 58, 4066-4072.	2.9	2,335
141	Achieving high signal-to-noise in cell regulatory systems: Spatial organization of multiprotein transmembrane assemblies of FGFR and MET receptors. Progress in Biophysics and Molecular Biology, 2015, 118, 103-111.	1.4	21
142	Platinum: a database of experimentally measured effects of mutations on structurally defined proteinâ€"ligand complexes. Nucleic Acids Research, 2015, 43, D387-D391.	6.5	81
143	Exploring the chemical space of the lysine-binding pocket of the first kringle domain of hepatocyte growth factor/scatter factor (HGF/SF) yields a new class of inhibitors of HGF/SF-MET binding. Chemical Science, 2015, 6, 6147-6157.	3.7	26
144	Smallâ€Molecule Inhibitors That Target Proteinâ€"Protein Interactions in the RAD51 Family of Recombinases. ChemMedChem, 2015, 10, 296-303.	1.6	36

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145	Analysis of HGD Gene Mutations in Patients with Alkaptonuria from the United Kingdom: Identification of Novel Mutations. JIMD Reports, 2014, 24, 3-11.	0.7	42
146	mCSM: predicting the effects of mutations in proteins using graph-based signatures. Bioinformatics, 2014, 30, 335-342.	1.8	779
147	An integrated computational approach can classify VHL missense mutations according to risk of clear cell renal carcinoma. Human Molecular Genetics, 2014, 23, 5976-5988.	1.4	21
148	DUET: a server for predicting effects of mutations on protein stability using an integrated computational approach. Nucleic Acids Research, 2014, 42, W314-W319.	6.5	664
149	Threonine 57 is required for the post-translational activation of<i>Escherichia coli</i>aspartate Î±-decarboxylase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1166-1172.	2.5	5
150	The spatial organization of non-homologous end joining: From bridging to end joining. DNA Repair, 2014, 17, 98-109.	1.3	60
151	Mycobacterium tuberculosis Dihydrofolate Reductase Reveals Two Conformational States and a Possible Low Affinity Mechanism to Antifolate Drugs. Structure, 2014, 22, 94-103.	1.6	30
152	A Spaetzle-like role for nerve growth factor Î² in vertebrate immunity to <i>Staphylococcus aureus</i>. Science, 2014, 346, 641-646.	6.0	68
153	Respiratory Flexibility in Response to Inhibition of Cytochrome <i>c</i> Oxidase in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 6962-6965.	1.4	116
154	Pantothenic Acid Biosynthesis in the Parasite Toxoplasma gondii: a Target for Chemotherapy. Antimicrobial Agents and Chemotherapy, 2014, 58, 6345-6353.	1.4	13
155	A structure-guided fragment-based approach for the discovery of allosteric inhibitors targeting the lipophilic binding site of transcription factor EthR. Biochemical Journal, 2014, 458, 387-394.	1.7	32
156	Structure of the Catalytic Region of DNA Ligase IV in Complex with an Artemis Fragment Sheds Light on Double-Strand Break Repair. Structure, 2013, 21, 672-679.	1.6	55
157	Using a Fragmentâ€Based Approach To Target Proteinâ€“Protein Interactions. ChemBioChem, 2013, 14, 332-342.	1.3	115
158	Cooperative Heparin-Mediated Oligomerization of Fibroblast Growth Factor-1 (FGF1) Precedes Recruitment of FGFR2 to Ternary Complexes. Biophysical Journal, 2013, 104, 1720-1730.	0.2	42
159	Molecular Mechanism of SSR128129E, an Extracellularly Acting, Small-Molecule, Allosteric Inhibitor of FGF Receptor Signaling. Cancer Cell, 2013, 23, 489-501.	7.7	125
160	CREDO: a structural interactomics database for drug discovery. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat049.	1.4	35
161	Integrated biophysical approach to fragment screening and validation for fragment-based lead discovery. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12984-12989.	3.3	97
162	Biophysical and computational fragment-based approaches to targeting proteinâ€“protein interactions: applications in structure-guided drug discovery. Quarterly Reviews of Biophysics, 2012, 45, 383-426.	2.4	90

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163	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. Nucleic Acids Research, 2012, 41, D499-D507.	6.5	53
164	Crystal structure of folliculin reveals a hidDENN function in genetically inherited renal cancer. Open Biology, 2012, 2, 120071.	1.5	97
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