

# Bostjan Kobe

## List of Publications by Year in descending order

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257  
papers

18,804  
citations

16411

64  
h-index

15218

126  
g-index

269  
all docs

269  
docs citations

269  
times ranked

19980  
citing authors

#	ARTICLE	IF	CITATIONS
1	The leucine-rich repeat as a protein recognition motif. <i>Current Opinion in Structural Biology</i> , 2001, 11, 725-732.	2.6	1,454
2	The leucine-rich repeat: a versatile binding motif. <i>Trends in Biochemical Sciences</i> , 1994, 19, 415-421.	3.7	1,172
3	Direct protein interaction underlies gene-for-gene specificity and coevolution of the flax resistance genes and flax rust avirulence genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8888-8893.	3.3	695
4	A structural basis of the interactions between leucine-rich repeats and protein ligands. <i>Nature</i> , 1995, 374, 183-186.	13.7	670
5	Crystal structure of porcine ribonuclease inhibitor, a protein with leucine-rich repeats. <i>Nature</i> , 1993, 366, 751-756.	13.7	612
6	Uses for JNK: the Many and Varied Substrates of the c-Jun N-Terminal Kinases. <i>Microbiology and Molecular Biology Reviews</i> , 2006, 70, 1061-1095.	2.9	488
7	A Molecular Mechanism for Bacterial Susceptibility to Zinc. <i>PLoS Pathogens</i> , 2011, 7, e1002357.	2.1	387
8	Proteins with leucine-rich repeats. <i>Current Opinion in Structural Biology</i> , 1995, 5, 409-416.	2.6	367
9	NAD <sup>+</sup> cleavage activity by animal and plant TIR domains in cell death pathways. <i>Science</i> , 2019, 365, 793-799.	6.0	357
10	Structural basis of recognition of monopartite and bipartite nuclear localization sequences by mammalian importin- $\beta$ . Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 2000, 297, 1183-1194.	2.0	356
11	Autoinhibition by an internal nuclear localization signal revealed by the crystal structure of mammalian importin alpha. , 1999, 6, 388-397.		345
12	Molecular basis for specificity of nuclear import and prediction of nuclear localization. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 1562-1577.	1.9	336
13	Structural and Functional Analysis of a Plant Resistance Protein TIR Domain Reveals Interfaces for Self-Association, Signaling, and Autoregulation. <i>Cell Host and Microbe</i> , 2011, 9, 200-211.	5.1	301
14	Structural Basis for Assembly and Function of a Heterodimeric Plant Immune Receptor. <i>Science</i> , 2014, 344, 299-303.	6.0	300
15	Discovering Sequence Motifs with Arbitrary Insertions and Deletions. <i>PLoS Computational Biology</i> , 2008, 4, e1000071.	1.5	292
16	Emerging Insights into the Functions of Pathogenesis-Related Protein 1. <i>Trends in Plant Science</i> , 2017, 22, 871-879.	4.3	271
17	When protein folding is simplified to protein coiling: the continuum of solenoid protein structures. <i>Trends in Biochemical Sciences</i> , 2000, 25, 509-515.	3.7	254
18	Crystal structures of fusion proteins with large-affinity tags. <i>Protein Science</i> , 2003, 12, 1313-1322.	3.1	229

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19	Crystal structure of human T cell leukemia virus type 1 gp21 ectodomain crystallized as a maltose-binding protein chimera reveals structural evolution of retroviral transmembrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 4319-4324.	3.3	207
20	Structural Biology and Regulation of Protein Import into the Nucleus. <i>Journal of Molecular Biology</i> , 2016, 428, 2060-2090.	2.0	204
21	Conformational behavior of Escherichia coli OmpA signal peptides in membrane mimetic environments. <i>Biochemistry</i> , 1993, 32, 4881-4894.	1.2	200
22	Structural basis of autoregulation of phenylalanine hydroxylase. <i>Nature Structural Biology</i> , 1999, 6, 442-448.	9.7	199
23	Active site-directed protein regulation. <i>Nature</i> , 1999, 402, 373-376.	13.7	196
24	Mechanism of Ribonuclease Inhibition by Ribonuclease Inhibitor Protein Based on the Crystal Structure of its Complex with Ribonuclease A. <i>Journal of Molecular Biology</i> , 1996, 264, 1028-1043.	2.0	195
25	Structural basis and prediction of substrate specificity in protein serine/threonine kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 74-79.	3.3	188
26	Structural Basis for the Specificity of Bipartite Nuclear Localization Sequence Binding by Importin- $\beta$ . <i>Journal of Biological Chemistry</i> , 2003, 278, 27981-27987.	1.6	175
27	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. <i>Nature Genetics</i> , 2012, 44, 165-169.	9.4	170
28	SARM1 is a metabolic sensor activated by an increased NMN/NAD <sup>+</sup> ratio to trigger axon degeneration. <i>Neuron</i> , 2021, 109, 1118-1136.e11.	3.8	168
29	Megahertz serial crystallography. <i>Nature Communications</i> , 2018, 9, 4025.	5.8	147
30	Biophysical Characterization of Interactions Involving Importin- $\beta$ during Nuclear Import. <i>Journal of Biological Chemistry</i> , 2001, 276, 34189-34198.	1.6	145
31	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. <i>Plant Cell</i> , 2007, 19, 2898-2912.	3.1	143
32	An Autoactive Mutant of the M Flax Rust Resistance Protein Has a Preference for Binding ATP, Whereas Wild-Type M Protein Binds ADP. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 897-906.	1.4	141
33	The Role of Histidine Residues in Low-pH-Mediated Viral Membrane Fusion. <i>Structure</i> , 2006, 14, 1481-1487.	1.6	140
34	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 743-751.	3.6	140
35	Ca <sup>2+</sup> /S100 regulation of giant protein kinases. <i>Nature</i> , 1996, 380, 636-639.	13.7	138
36	TRIF-dependent TLR signaling, its functions in host defense and inflammation, and its potential as a therapeutic target. <i>Journal of Leukocyte Biology</i> , 2016, 100, 27-45.	1.5	138

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37	Imperfect coordination chemistry facilitates metal ion release in the Psa permease. <i>Nature Chemical Biology</i> , 2014, 10, 35-41.	3.9	137
38	Functional and structural properties of mammalian acyl-coenzyme A thioesterases. <i>Progress in Lipid Research</i> , 2010, 49, 366-377.	5.3	128
39	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14879-14884.	3.3	123
40	Structure and function of Toll/interleukin-1 receptor/resistance protein (TIR) domains. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2015, 20, 250-261.	2.2	123
41	The Nuclear Immune Receptor RPS4 Is Required for RRS1SLH1-Dependent Constitutive Defense Activation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2014, 10, e1004655.	1.5	121
42	Dysregulation of transition metal ion homeostasis is the molecular basis for cadmium toxicity in <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2015, 6, 6418.	5.8	117
43	The AvrM Effector from Flax Rust Has a Structured C-Terminal Domain and Interacts Directly with the M Resistance Protein. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 49-57.	1.4	113
44	Assessment of the ability to model proteins with leucine-rich repeats in light of the latest structural information. <i>Protein Science</i> , 2002, 11, 1082-1090.	3.1	110
45	Comparative Analysis of the Flax Immune Receptors L6 and L7 Suggests an Equilibrium-Based Switch Activation Model. <i>Plant Cell</i> , 2016, 28, 146-159.	3.1	110
46	<sc>AdcA</sc> and <sc>AdcAll</sc> employ distinct zinc acquisition mechanisms and contribute additively to zinc homeostasis in <sc>S</sc> <sc>treptococcus pneumoniae</sc>. <i>Molecular Microbiology</i> , 2014, 91, 834-851.	1.2	108
47	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12856-12861.	3.3	105
48	Multiple functional self-association interfaces in plant TIR domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2046-E2052.	3.3	103
49	Role of flanking sequences and phosphorylation in the recognition of the simian-virus-40 large T-antigen nuclear localization sequences by importin- $\alpha$ . <i>Biochemical Journal</i> , 2003, 375, 339-349.	1.7	102
50	Wheat <sc>PR</sc>- $\epsilon$ 1 proteins are targeted by necrotrophic pathogen effector proteins. <i>Plant Journal</i> , 2016, 88, 13-25.	2.8	96
51	In silico screening of small molecule libraries using the dengue virus envelope E protein has identified compounds with antiviral activity against multiple flaviviruses. <i>Antiviral Research</i> , 2009, 84, 234-241.	1.9	95
52	The molecular mechanisms of signaling by cooperative assembly formation in innate immunity pathways. <i>Molecular Immunology</i> , 2017, 86, 23-37.	1.0	95
53	Intramolecular Interaction Influences Binding of the Flax L5 and L6 Resistance Proteins to their AvrL567 Ligands. <i>PLoS Pathogens</i> , 2012, 8, e1003004.	2.1	93
54	Structural Basis of High-Affinity Nuclear Localization Signal Interactions with Importin- $\alpha$ . <i>Traffic</i> , 2012, 13, 532-548.	1.3	91

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55	Quantitative Structural Analysis of Importin- $\beta$ Flexibility: Paradigm for Solenoid Protein Structures. <i>Structure</i> , 2010, 18, 1171-1183.	1.6	89
56	Substrate specificity of protein kinases and computational prediction of substrates. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1754, 200-209.	1.1	88
57	Residues in domain III of the dengue virus envelope glycoprotein involved in cell-surface glycosaminoglycan binding. <i>Journal of General Virology</i> , 2012, 93, 72-82.	1.3	88
58	Diversity and Variability of NOD-Like Receptors in Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 3137-3158.	1.1	83
59	Identification of novel target sites and an inhibitor of the dengue virus E protein. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 333-341.	1.3	77
60	UpaH Is a Newly Identified Autotransporter Protein That Contributes to Biofilm Formation and Bladder Colonization by Uropathogenic <i>Escherichia coli</i> CFT073. <i>Infection and Immunity</i> , 2010, 78, 1659-1669.	1.0	77
61	The Plant $\epsilon$ -Resistosome: Structural Insights into Immune Signaling. <i>Cell Host and Microbe</i> , 2019, 26, 193-201.	5.1	76
62	Structures of the flax-rust effector AvrM reveal insights into the molecular basis of plant-cell entry and effector-triggered immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17594-17599.	3.3	75
63	Mechanism of Bacterial Interference with TLR4 Signaling by <i>Brucella</i> Toll/Interleukin-1 Receptor Domain-containing Protein TcpB. <i>Journal of Biological Chemistry</i> , 2014, 289, 654-668.	1.6	73
64	An Inflammatory Role for the Mammalian Carboxypeptidase Inhibitor Latexin: Relationship to Cystatins and the Tumor Suppressor TIG1. <i>Structure</i> , 2005, 13, 309-317.	1.6	71
65	Structural basis for recruitment of tandem hotdog domains in acyl-CoA thioesterase 7 and its role in inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10382-10387.	3.3	71
66	Recombinant and epitope-based vaccines on the road to the market and implications for vaccine design and production. <i>Human Vaccines and Immunotherapeutics</i> , 2016, 12, 763-767.	1.4	71
67	Multiple Domain Associations within the Arabidopsis Immune Receptor RPP1 Regulate the Activation of Programmed Cell Death. <i>PLoS Pathogens</i> , 2016, 12, e1005769.	2.1	69
68	Adaptors in Toll-Like Receptor Signaling and their Potential as Therapeutic Targets. <i>Current Drug Targets</i> , 2012, 13, 1360-1374.	1.0	68
69	Crystallization of a trimeric human T cell leukemia virus type 1 gp21 ectodomain fragment as a chimera with maltose-binding protein. <i>Protein Science</i> , 1998, 7, 1612-1619.	3.1	67
70	Structural basis of SARM1 activation, substrate recognition, and inhibition by small molecules. <i>Molecular Cell</i> , 2022, 82, 1643-1659.e10.	4.5	66
71	Towards the structure of the TIR-domain signalosome. <i>Current Opinion in Structural Biology</i> , 2017, 43, 122-130.	2.6	64
72	Turn up the HEAT. <i>Structure</i> , 1999, 7, R91-R97.	1.6	62

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73	Predikin and PredikinDB: a computational framework for the prediction of protein kinase peptide specificity and an associated database of phosphorylation sites. <i>BMC Bioinformatics</i> , 2008, 9, 245.	1.2	62
74	Animal NLRs provide structural insights into plant NLR function. <i>Annals of Botany</i> , 2017, 119, mcw171.	1.4	62
75	Crystallography and protein-protein interactions: biological interfaces and crystal contacts. <i>Biochemical Society Transactions</i> , 2008, 36, 1438-1441.	1.6	61
76	Defining the Structural Basis of Human Plasminogen Binding by Streptococcal Surface Enolase. <i>Journal of Biological Chemistry</i> , 2009, 284, 17129-17137.	1.6	61
77	An optimized SEC-SAXS system enabling high X-ray dose for rapid SAXS assessment with correlated UV measurements for biomolecular structure analysis. <i>Journal of Applied Crystallography</i> , 2018, 51, 97-111.	1.9	61
78	Crystal Structure of Rice Importin- $\beta$ and Structural Basis of Its Interaction with Plant-Specific Nuclear Localization Signals. <i>Plant Cell</i> , 2013, 24, 5074-5088.	3.1	60
79	Probing the Specificity of Binding to the Major Nuclear Localization Sequence-binding Site of Importin- $\beta$ Using Oriented Peptide Library Screening. <i>Journal of Biological Chemistry</i> , 2010, 285, 19935-19946.	1.6	56
80	De novo GTP Biosynthesis Is Critical for Virulence of the Fungal Pathogen <i>Cryptococcus neoformans</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002957.	2.1	56
81	MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. <i>Nature Communications</i> , 2021, 12, 2578.	5.8	55
82	Soybean Nodule Autoregulation Receptor Kinase Phosphorylates Two Kinase-associated Protein Phosphatases in Vitro. <i>Journal of Biological Chemistry</i> , 2008, 283, 25381-25391.	1.6	54
83	Histidine protonation and the activation of viral fusion proteins. <i>Biochemical Society Transactions</i> , 2008, 36, 43-45.	1.6	54
84	PREDIVAC: CD4+ T-cell epitope prediction for vaccine design that covers 95% of HLA class II DR protein diversity. <i>BMC Bioinformatics</i> , 2013, 14, 52.	1.2	54
85	The myosin-I-binding protein Acan125 binds the SH3 domain and belongs to the superfamily of leucine-rich repeat proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 3685-3690.	3.3	52
86	Handling of nutrient copper in the bacterial envelope. <i>Metallomics</i> , 2019, 11, 50-63.	1.0	51
87	Structural basis of NLR activation and innate immune signalling in plants. <i>Immunogenetics</i> , 2022, 74, 5-26.	1.2	51
88	Improved Success of Sparse Matrix Protein Crystallization Screening with Heterogeneous Nucleating Agents. <i>PLoS ONE</i> , 2007, 2, e1091.	1.1	49
89	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. <i>Journal of Molecular Medicine</i> , 2012, 90, 1197-1207.	1.7	49
90	PR1-mediated defence via C-terminal peptide release is targeted by a fungal pathogen effector. <i>New Phytologist</i> , 2021, 229, 3467-3480.	3.5	48

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91	All major cholesterol-dependent cytolysins use glycans as cellular receptors. <i>Science Advances</i> , 2020, 6, eaaz4926.	4.7	46
92	Distinctive Conformation of Minor Siteâ€Specific Nuclear Localization Signals Bound to Importinâ€Î±. <i>Traffic</i> , 2013, 14, 1144-1154.	1.3	45
93	Death, TIR, and RHIM: Self-assembling domains involved in innate immunity and cell-death signaling. <i>Journal of Leukocyte Biology</i> , 2019, 105, 363-375.	1.5	43
94	Federated repositories of X-ray diffraction images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 810-814.	2.5	42
95	Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2495-2505.	2.5	42
96	Structure and Function of the TIR Domain from the Grape NLR Protein RPV1. <i>Frontiers in Plant Science</i> , 2016, 7, 1850.	1.7	41
97	Structural and Functional Characterization of a Cross-Reactive Dengue Virus Neutralizing Antibody that Recognizes a Cryptic Epitope. <i>Structure</i> , 2018, 26, 51-59.e4.	1.6	41
98	Predicting Protein Kinase Specificity: Predikin Update and Performance in the DREAM4 Challenge. <i>PLoS ONE</i> , 2011, 6, e21169.	1.1	41
99	Structural interpretation of mutations in phenylalanine hydroxylase protein aids in identifying genotypeâ€phenotype correlations in phenylketonuria. <i>European Journal of Human Genetics</i> , 2000, 8, 683-696.	1.4	40
100	A bioinformatics tool for epitope-based vaccine design that accounts for human ethnic diversity: Application to emerging infectious diseases. <i>Vaccine</i> , 2015, 33, 1267-1273.	1.7	40
101	United we stand: combining structural methods. <i>Current Opinion in Structural Biology</i> , 2008, 18, 617-622.	2.6	39
102	PhosphoPICK: modelling cellular context to map kinase-substrate phosphorylation events. <i>Bioinformatics</i> , 2015, 31, 382-389.	1.8	39
103	Functional Implications of the Human T-Lymphotropic Virus Type 1 Transmembrane Glycoprotein Helical Hairpin Structure. <i>Journal of Virology</i> , 2000, 74, 6614-6621.	1.5	38
104	The TLR signaling adaptor TRAM interacts with TRAF6 to mediate activation of the inflammatory response by TLR4. <i>Journal of Leukocyte Biology</i> , 2014, 96, 427-436.	1.5	38
105	Structural Basis of Importin-Î±-Mediated Nuclear Transport for Ku70 and Ku80. <i>Journal of Molecular Biology</i> , 2011, 412, 226-234.	2.0	37
106	Prokaryotic Substrate-Binding Proteins as Targets for Antimicrobial Therapies. <i>Current Drug Targets</i> , 2012, 13, 1400-1410.	1.0	35
107	Molybdenum Enzymes and How They Support Virulence in Pathogenic Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 615860.	1.5	35
108	Protein kinases associated with the yeast phosphoproteome. <i>BMC Bioinformatics</i> , 2006, 7, 47.	1.2	33



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109	Crystal structure of Mycobacterium tuberculosis ketolâ€acid reductoisomerase at 1.0 Å... resolution â€“ a potential target for antiâ€tuberculosis drug discovery. FEBS Journal, 2016, 283, 1184-1196.	2.2	33
110	Solution structure of the TLR adaptor MAL/TIRAP reveals an intact BB loop and supports MAL Cys91 glutathionylation for signaling. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6480-E6489.	3.3	33
111	Essential role of the N-terminal autoregulatory sequence in the regulation of phenylalanine hydroxylase. FEBS Letters, 2001, 488, 196-200.	1.3	32
112	Kap95p Binding Induces the Switch Loops of RanGDP to Adopt the GTP-Bound Conformation: Implications for Nuclear Import Complex Assembly Dynamics. Journal of Molecular Biology, 2008, 383, 772-782.	2.0	32
113	A Glutathione-Dependent Detoxification System Is Required for Formaldehyde Resistance and Optimal Survival of <i>Neisseria meningitidis</i> in Biofilms. Antioxidants and Redox Signaling, 2013, 18, 743-755.	2.5	32
114	Production of small cysteineâ€rich effector proteins in <i>Escherichia coli</i> for structural and functional studies. Molecular Plant Pathology, 2017, 18, 141-151.	2.0	32
115	FHA domain boundaries of the Dun1p and Rad53p cell cycle checkpoint kinases. FEBS Letters, 2000, 471, 141-146.	1.3	31
116	The Predikin webserver: improved prediction of protein kinase peptide specificity using structural information. Nucleic Acids Research, 2008, 36, W286-W290.	6.5	31
117	Cortactin Adopts a Globular Conformation and Bundles Actin into Sheets. Journal of Biological Chemistry, 2008, 283, 16187-16193.	1.6	29
118	Crystallization of importin Î±, the nuclear-import receptor. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 561-563.	2.5	28
119	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1142-1146.	1.5	28
120	A Novel NAD Signaling Mechanism in Axon Degeneration and its Relationship to Innate Immunity. Frontiers in Molecular Biosciences, 2021, 8, 703532.	1.6	28
121	Importin-Î² Is a GDP-to-GTP Exchange Factor of Ran. Journal of Biological Chemistry, 2009, 284, 22549-22558.	1.6	27
122	Computerâ€aided design of Tâ€cell epitopeâ€based vaccines: addressing population coverage. International Journal of Immunogenetics, 2015, 42, 313-321.	0.8	27
123	Structural Evolution of TIR-Domain Signalosomes. Frontiers in Immunology, 2021, 12, 784484.	2.2	27
124	Blood Group Antigen Recognition via the Group A Streptococcal M Protein Mediates Host Colonization. MBio, 2017, 8, .	1.8	25
125	Identification of Disulfide-Containing Chemical Cross-Links in Proteins Using MALDI-TOF/TOF-Mass Spectrometry. Analytical Chemistry, 2008, 80, 5036-5043.	3.2	24
126	Crystal structure of the Melampsora lini effector AvrP reveals insights into a possible nuclear function and recognition by the flax disease resistance protein P. Molecular Plant Pathology, 2018, 19, 1196-1209.	2.0	24



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127	The crystal structure of SnTox3 from the necrotrophic fungus <i>Parastagonospora nodorum</i> reveals a unique effector fold and provides insight into Snn3 recognition and pro-domain protease processing of fungal effectors. <i>New Phytologist</i> , 2021, 231, 2282-2296.	3.5	24
128	Nicotinic acid mononucleotide is an allosteric SARM1 inhibitor promoting axonal protection. <i>Experimental Neurology</i> , 2021, 345, 113842.	2.0	24
129	Leucines on a roll. <i>Nature Structural Biology</i> , 1996, 3, 977-980.	9.7	23
130	Comparison of three commercial sparse-matrix crystallization screens. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 769-772.	2.5	23
131	Crystal structure of importin $\beta$ bound to a peptide bearing the nuclear localisation signal from chloride intracellular channel protein 4. <i>FEBS Journal</i> , 2011, 278, 1662-1675.	2.2	23
132	Dynamics of re-constitution of the human nuclear proteome after cell division is regulated by NLS-adjacent phosphorylation. <i>Cell Cycle</i> , 2014, 13, 3551-3564.	1.3	23
133	Fusion-protein-assisted protein crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 861-869.	0.4	23
134	Animal NLRs continue to inform plant NLR structure and function. <i>Archives of Biochemistry and Biophysics</i> , 2019, 670, 58-68.	1.4	23
135	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. <i>Nature Microbiology</i> , 2020, 5, 1340-1348.	5.9	23
136	Molecular basis of regio- and stereo-specificity in biosynthesis of bacterial heterodimeric diketopiperazines. <i>Nature Communications</i> , 2020, 11, 6251.	5.8	23
137	An automatable screen for the rapid identification of proteins amenable to refolding. <i>Proteomics</i> , 2006, 6, 1750-1757.	1.3	22
138	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 637-648.	2.5	22
139	Structural Characterisation of the Nuclear Import Receptor Importin Alpha in Complex with the Bipartite NLS of Prp20. <i>PLoS ONE</i> , 2013, 8, e82038.	1.1	22
140	Structural Basis of Interaction of Bipartite Nuclear Localization Signal from <i>Agrobacterium</i> VirD2 with Rice Importin $\beta$ . <i>Molecular Plant</i> , 2014, 7, 1061-1064.	3.9	22
141	Protein crystal screening and characterization for serial femtosecond nanocrystallography. <i>Scientific Reports</i> , 2016, 6, 25345.	1.6	22
142	Pathological mutations differentially affect the self-assembly and polymerisation of the innate immune system signalling adaptor molecule MyD88. <i>BMC Biology</i> , 2018, 16, 149.	1.7	22
143	Neurotoxin-mediated potent activation of the axon degeneration regulator SARM1. <i>ELife</i> , 2021, 10, .	2.8	22
144	Structural Proteomics. <i>Methods in Molecular Biology</i> , 2008, 426, v-vi.	0.4	21

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145	A probabilistic model of nuclear import of proteins. <i>Bioinformatics</i> , 2011, 27, 1239-1246.	1.8	21
146	Regulation and crystallization of phosphorylated and dephosphorylated forms of truncated dimeric phenylalanine hydroxylase. <i>Protein Science</i> , 1997, 6, 1352-1357.	3.1	20
147	Verprolin Cytokinesis Function Mediated by the Hof One Trap Domain. <i>Traffic</i> , 2005, 6, 575-593.	1.3	19
148	Modelling the structure of latexin-carboxypeptidase A complex based on chemical cross-linking and molecular docking. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 9-16.	1.0	19
149	Principles of Kinase Regulation. , 2010, , 559-563.		19
150	Discovery of Novel Pneumococcal Surface Antigen A (PsaA) Inhibitors Using a Fragment-based Drug Design Approach. <i>ACS Chemical Biology</i> , 2015, 10, 1511-1520.	1.6	19
151	GMP Synthase Is Required for Virulence Factor Production and Infection by <i>Cryptococcus neoformans</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 3049-3059.	1.6	19
152	Identification and predicted structure of a leucine-rich repeat motif shared by <i>Leishmania major</i> proteophosphoglycan and Parasite Surface Antigen 2. <i>Molecular and Biochemical Parasitology</i> , 2000, 107, 289-295.	0.5	18
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