Bostjan Kobe

List of Publications by Citations

Source: https://exaly.com/author-pdf/2114184/bostjan-kobe-publications-by-citations.pdf
Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

253	14,952	60	118
papers	citations	h-index	g-index
269	17,228	7.6	6.6
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
253	The leucine-rich repeat as a protein recognition motif. *Current Opinion in Structural Biology*, **2001**, 11, 725-32	8.1	1218
252	The leucine-rich repeat: a versatile binding motif. *Trends in Biochemical Sciences*, **1994**, 19, 415-21	10.3	1028
251	A structural basis of the interactions between leucine-rich repeats and protein ligands. *Nature*, **1995**, 374, 183-6	50.4	599
250	Direct protein interaction underlies gene-for-gene specificity and coevolution of the flax resistance genes and flax rust avirulence genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 8888-93	11.5	592
249	Crystal structure of porcine ribonuclease inhibitor, a protein with leucine-rich repeats. *Nature*, **1993**, 366, 751-6	50.4	572
248	Uses for JNK: the many and varied substrates of the c-Jun N-terminal kinases. *Microbiology and Molecular Biology Reviews*, **2006**, 70, 1061-95	13.2	417
247	Proteins with leucine-rich repeats. *Current Opinion in Structural Biology*, **1995**, 5, 409-16	8.1	334
246	Structural basis of recognition of monopartite and bipartite nuclear localization sequences by mammalian importin-alpha. *Journal of Molecular Biology*, **2000**, 297, 1183-94	6.5	316
245	Autoinhibition by an internal nuclear localization signal revealed by the crystal structure of mammalian importin alpha. *Nature Structural Biology*, **1999**, 6, 388-97		303
244	Molecular basis for specificity of nuclear import and prediction of nuclear localization. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2011**, 1813, 1562-77	4.9	284
243	A molecular mechanism for bacterial susceptibility to zinc. *PLoS Pathogens*, **2011**, 7, e1002357	7.6	281
242	Structural and functional analysis of a plant resistance protein TIR domain reveals interfaces for self-association, signaling, and autoregulation. *Cell Host and Microbe*, **2011**, 9, 200-211	23.4	243
241	Structural basis for assembly and function of a heterodimeric plant immune receptor. *Science*, **2014**, 344, 299-303	33.3	228
240	When protein folding is simplified to protein coiling: the continuum of solenoid protein structures. *Trends in Biochemical Sciences*, **2000**, 25, 509-15	10.3	228
239	Discovering sequence motifs with arbitrary insertions and deletions. *PLoS Computational Biology*, **2008**, 4, e1000071	5	224
238	Crystal structures of fusion proteins with large-affinity tags. *Protein Science*, **2003**, 12, 1313-22	6.3	217
237	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. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 4319-24	11.5	192

236	Conformational behavior of Escherichia coli OmpA signal peptides in membrane mimetic environments. *Biochemistry*, **1993**, 32, 4881-94	3.2	192
235	Structural basis of autoregulation of phenylalanine hydroxylase. *Nature Structural Biology*, **1999**, 6, 442-8		188
234	NAD cleavage activity by animal and plant TIR domains in cell death pathways. *Science*, **2019**, 365, 793-799	33.3	183
233	Active site-directed protein regulation. *Nature*, **1999**, 402, 373-6	50.4	181
232	Mechanism of ribonuclease inhibition by ribonuclease inhibitor protein based on the crystal structure of its complex with ribonuclease A. *Journal of Molecular Biology*, **1996**, 264, 1028-43	6.5	177
231	Structural basis and prediction of substrate specificity in protein serine/threonine kinases. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 74-9	11.5	171
230	Emerging Insights into the Functions of Pathogenesis-Related Protein 1. *Trends in Plant Science*, **2017**, 22, 871-879	13.1	150
229	Structural basis for the specificity of bipartite nuclear localization sequence binding by importin-alpha. *Journal of Biological Chemistry*, **2003**, 278, 27981-7	5.4	150
228	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. *Nature Genetics*, **2011**, 44, 165-9	36.3	145
227	Structural Biology and Regulation of Protein Import into the Nucleus. *Journal of Molecular Biology*, **2016**, 428, 2060-90	6.5	140
226	Biophysical characterization of interactions involving importin-alpha during nuclear import. *Journal of Biological Chemistry*, **2001**, 276, 34189-98	5.4	129
225	Ca2+/S100 regulation of giant protein kinases. *Nature*, **1996**, 380, 636-9	50.4	127
224	The Role of histidine residues in low-pH-mediated viral membrane fusion. *Structure*, **2006**, 14, 1481-7	5.2	120
223	An autoactive mutant of the M flax rust resistance protein has a preference for binding ATP, whereas wild-type M protein binds ADP. *Molecular Plant-Microbe Interactions*, **2011**, 24, 897-906	3.6	116
222	Crystal structures of flax rust avirulence proteins AvrL567-A and -D reveal details of the structural basis for flax disease resistance specificity. *Plant Cell*, **2007**, 19, 2898-912	11.6	112
221	Functional and structural properties of mammalian acyl-coenzyme A thioesterases. *Progress in Lipid Research*, **2010**, 49, 366-77	14.3	106
220	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 14879-84	11.5	105
219	Megahertz serial crystallography. *Nature Communications*, **2018**, 9, 4025	17.4	104

218	Imperfect coordination chemistry facilitates metal ion release in the Psa permease. *Nature Chemical Biology*, **2014**, 10, 35-41	11.7	103
217	Assessment of the ability to model proteins with leucine-rich repeats in light of the latest structural information. *Protein Science*, **2002**, 11, 1082-90	6.3	99
216	The AvrM effector from flax rust has a structured C-terminal domain and interacts directly with the M resistance protein. *Molecular Plant-Microbe Interactions*, **2010**, 23, 49-57	3.6	97
215	Role of flanking sequences and phosphorylation in the recognition of the simian-virus-40 large T-antigen nuclear localization sequences by importin-alpha. *Biochemical Journal*, **2003**, 375, 339-49	3.8	94
214	Structure and function of Toll/interleukin-1 receptor/resistance protein (TIR) domains. *Apoptosis: an International Journal on Programmed Cell Death*, **2015**, 20, 250-61	5.4	92
213	TRIF-dependent TLR signaling, its functions in host defense and inflammation, and its potential as a therapeutic target. *Journal of Leukocyte Biology*, **2016**, 100, 27-45	6.5	88
212	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. *Nature Structural and Molecular Biology*, **2017**, 24, 743-751	17.6	82
211	Substrate specificity of protein kinases and computational prediction of substrates. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2005**, 1754, 200-9	4	80
210	In silico screening of small molecule libraries using the dengue virus envelope E protein has identified compounds with antiviral activity against multiple flaviviruses. *Antiviral Research*, **2009**, 84, 234-41	10.8	78
209	Dysregulation of transition metal ion homeostasis is the molecular basis for cadmium toxicity in Streptococcus pneumoniae. *Nature Communications*, **2015**, 6, 6418	17.4	77
208	AdcA and AdcAII employ distinct zinc acquisition mechanisms and contribute additively to zinc homeostasis in Streptococcus pneumoniae. *Molecular Microbiology*, **2014**, 91, 834-51	4.1	76
207	Intramolecular interaction influences binding of the Flax L5 and L6 resistance proteins to their AvrL567 ligands. *PLoS Pathogens*, **2012**, 8, e1003004	7.6	76
206	Residues in domain III of the dengue virus envelope glycoprotein involved in cell-surface glycosaminoglycan binding. *Journal of General Virology*, **2012**, 93, 72-82	4.9	76
205	Multiple functional self-association interfaces in plant TIR domains. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E2046-E2052	11.5	72
204	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 12856-12861	11.5	72
203	Quantitative structural analysis of importin-□flexibility: paradigm for solenoid protein structures. *Structure*, **2010**, 18, 1171-83	5.2	72
202	Structural basis of high-affinity nuclear localization signal interactions with importin-□*Traffic*, **2012** , 13, 532-48	5.7	70
201	The nuclear immune receptor RPS4 is required for RRS1SLH1-dependent constitutive defense activation in Arabidopsis thaliana. *PLoS Genetics*, **2014**, 10, e1004655	6	70

200	UpaH is a newly identified autotransporter protein that contributes to biofilm formation and bladder colonization by uropathogenic Escherichia coli CFT073. *Infection and Immunity*, **2010**, 78, 1659-69	3.7	70
199	Comparative Analysis of the Flax Immune Receptors L6 and L7 Suggests an Equilibrium-Based Switch Activation Model. *Plant Cell*, **2016**, 28, 146-59	11.6	69
198	The molecular mechanisms of signaling by cooperative assembly formation in innate immunity pathways. *Molecular Immunology*, **2017**, 86, 23-37	4.3	68
197	Crystallization of a trimeric human T cell leukemia virus type 1 gp21 ectodomain fragment as a chimera with maltose-binding protein. *Protein Science*, **1998**, 7, 1612-9	6.3	65
196	An inflammatory role for the mammalian carboxypeptidase inhibitor latexin: relationship to cystatins and the tumor suppressor TIG1. *Structure*, **2005**, 13, 309-17	5.2	64
195	Structural basis for recruitment of tandem hotdog domains in acyl-CoA thioesterase 7 and its role in inflammation. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 10382-7	11.5	61
194	Identification of novel target sites and an inhibitor of the dengue virus E protein. *Journal of Computer-Aided Molecular Design*, **2009**, 23, 333-41	4.2	60
193	Wheat PR-1 proteins are targeted by necrotrophic pathogen effector proteins. *Plant Journal*, **2016**, 88, 13-25	6.9	60
192	Adaptors in toll-like receptor signaling and their potential as therapeutic targets. *Current Drug Targets*, **2012**, 13, 1360-74	3	59
191	Recombinant and epitope-based vaccines on the road to the market and implications for vaccine design and production. *Human Vaccines and Immunotherapeutics*, **2016**, 12, 763-7	4.4	57
190	Predikin and PredikinDB: a computational framework for the prediction of protein kinase peptide specificity and an associated database of phosphorylation sites. *BMC Bioinformatics*, **2008**, 9, 245	3.6	54
189	Turn up the HEAT. *Structure*, **1999**, 7, R91-7	5.2	54
188	SARM1 is a metabolic sensor activated by an increased NMN/NAD ratio to trigger axon degeneration. *Neuron*, **2021**, 109, 1118-1136.e11	13.9	54
187	Multiple Domain Associations within the Arabidopsis Immune Receptor RPP1 Regulate the Activation of Programmed Cell Death. *PLoS Pathogens*, **2016**, 12, e1005769	7.6	54
186	Diversity and variability of NOD-like receptors in fungi. *Genome Biology and Evolution*, **2014**, 6, 3137-58	3.9	53
185	Crystallography and protein-protein interactions: biological interfaces and crystal contacts. *Biochemical Society Transactions*, **2008**, 36, 1438-41	5.1	53
184	Defining the structural basis of human plasminogen binding by streptococcal surface enolase. *Journal of Biological Chemistry*, **2009**, 284, 17129-17137	5.4	52
183	The myosin-I-binding protein Acan125 binds the SH3 domain and belongs to the superfamily of leucine-rich repeat proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **1997**, 94, 3685-90	11.5	51

182	Histidine protonation and the activation of viral fusion proteins. *Biochemical Society Transactions*, **2008**, 36, 43-5	5.1	51
181	Structures of the flax-rust effector AvrM reveal insights into the molecular basis of plant-cell entry and effector-triggered immunity. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 17594-9	11.5	50
180	Probing the specificity of binding to the major nuclear localization sequence-binding site of importin-alpha using oriented peptide library screening. *Journal of Biological Chemistry*, **2010**, 285, 19935-46	5.4	49
179	Animal NLRs provide structural insights into plant NLR function. *Annals of Botany*, **2017**, 119, 827-702	4.1	48
178	Mechanism of bacterial interference with TLR4 signaling by Brucella Toll/interleukin-1 receptor domain-containing protein TcpB. *Journal of Biological Chemistry*, **2014**, 289, 654-68	5.4	47
177	Soybean nodule autoregulation receptor kinase phosphorylates two kinase-associated protein phosphatases in vitro. *Journal of Biological Chemistry*, **2008**, 283, 25381-25391	5.4	47
176	De novo GTP biosynthesis is critical for virulence of the fungal pathogen Cryptococcus neoformans. *PLoS Pathogens*, **2012**, 8, e1002957	7.6	45
175	PREDIVAC: CD4+ T-cell epitope prediction for vaccine design that covers 95% of HLA class II DR protein diversity. *BMC Bioinformatics*, **2013**, 14, 52	3.6	43
174	Towards the structure of the TIR-domain signalosome. *Current Opinion in Structural Biology*, **2017**, 43, 122-130	8.1	42
173	Improved success of sparse matrix protein crystallization screening with heterogeneous nucleating agents. *PLoS ONE*, **2007**, 2, e1091	3.7	42
172	An optimized SEC-SAXS system enabling high X-ray dose for rapid SAXS assessment with correlated UV measurements for biomolecular structure analysis. *Journal of Applied Crystallography*, **2018**, 51, 97-111	3.8	41
171	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. *Journal of Molecular Medicine*, **2012**, 90, 1197-207	5.5	40
170	The Plant "Resistosome": Structural Insights into Immune Signaling. *Cell Host and Microbe*, **2019**, 26, 193-201	23.4	38
169	Crystal structure of rice importin-□and structural basis of its interaction with plant-specific nuclear localization signals. *Plant Cell*, **2012**, 24, 5074-88	11.6	37
168	United we stand: combining structural methods. *Current Opinion in Structural Biology*, **2008**, 18, 617-22	8.1	37
167	Predicting protein kinase specificity: Predikin update and performance in the DREAM4 challenge. *PLoS ONE*, **2011**, 6, e21169	3.7	37
166	Distinctive conformation of minor site-specific nuclear localization signals bound to importin-□ *Traffic*, **2013**, 14, 1144-54	5.7	36
165	Functional implications of the human T-lymphotropic virus type 1 transmembrane glycoprotein helical hairpin structure. *Journal of Virology*, **2000**, 74, 6614-21	6.6	36

164	Federated repositories of X-ray diffraction images. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, D64, 810-4		35
163	Structural interpretation of mutations in phenylalanine hydroxylase protein aids in identifying genotype-phenotype correlations in phenylketonuria. *European Journal of Human Genetics*, **2000**, 8, 683-96	5.3	35
162	Structural basis of importin-□mediated nuclear transport for Ku70 and Ku80. *Journal of Molecular Biology*, **2011**, 412, 226-34	6.5	32
161	Prokaryotic substrate-binding proteins as targets for antimicrobial therapies. *Current Drug Targets*, **2012**, 13, 1400-10	3	32
160	Structure and Function of the TIR Domain from the Grape NLR Protein RPV1. *Frontiers in Plant Science*, **2016**, 7, 1850	6.2	32
159	Handling of nutrient copper in the bacterial envelope. *Metallomics*, **2019**, 11, 50-63	4.5	30
158	Structural and Functional Characterization of a Cross-Reactive Dengue Virus Neutralizing Antibody that Recognizes a Cryptic Epitope. *Structure*, **2018**, 26, 51-59.e4	5.2	29
157	Cortactin adopts a globular conformation and bundles actin into sheets. *Journal of Biological Chemistry*, **2008**, 283, 16187-93	5.4	29
156	FHA domain boundaries of the dun1p and rad53p cell cycle checkpoint kinases. *FEBS Letters*, **2000**, 471, 141-6	3.8	29
155	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	11.5	28
154	Essential role of the N-terminal autoregulatory sequence in the regulation of phenylalanine hydroxylase. *FEBS Letters*, **2001**, 488, 196-200	3.8	28
153	All major cholesterol-dependent cytolysins use glycans as cellular receptors. *Science Advances*, **2020**, 6, eaaz4926	14.3	27
152	A bioinformatics tool for epitope-based vaccine design that accounts for human ethnic diversity: application to emerging infectious diseases. *Vaccine*, **2015**, 33, 1267-73	4.1	27
151	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, 772-82	6.5	27
150	PhosphoPICK: modelling cellular context to map kinase-substrate phosphorylation events. *Bioinformatics*, **2015**, 31, 382-9	7.2	26
149	Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2495-505		26
148	Protein kinases associated with the yeast phosphoproteome. *BMC Bioinformatics*, **2006**, 7, 47	3.6	26
147	Death, TIR, and RHIM: Self-assembling domains involved in innate immunity and cell-death signaling. *Journal of Leukocyte Biology*, **2019**, 105, 363-375	6.5	26

146	The TLR signaling adaptor TRAM interacts with TRAF6 to mediate activation of the inflammatory response by TLR4. *Journal of Leukocyte Biology*, **2014**, 96, 427-36	6.5	25
145	Importin-beta is a GDP-to-GTP exchange factor of Ran: implications for the mechanism of nuclear import. *Journal of Biological Chemistry*, **2009**, 284, 22549-58	5.4	25
144	The Predikin webserver: improved prediction of protein kinase peptide specificity using structural information. *Nucleic Acids Research*, **2008**, 36, W286-90	20.1	25
143	A glutathione-dependent detoxification system is required for formaldehyde resistance and optimal survival of Neisseria meningitidis in biofilms. *Antioxidants and Redox Signaling*, **2013**, 18, 743-55	8.4	23
142	Crystallization of importin alpha, the nuclear-import receptor. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 561-3		23
141	Identification of disulfide-containing chemical cross-links in proteins using MALDI-TOF/TOF-mass spectrometry. *Analytical Chemistry*, **2008**, 80, 5036-43	7.8	21
140	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 637-48		20
139	Structural characterisation of the nuclear import receptor importin alpha in complex with the bipartite NLS of Prp20. *PLoS ONE*, **2013**, 8, e82038	3.7	20
138	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. *Proteins: Structure, Function and Bioinformatics*, **2008**, 70, 1142-6	4.2	20
137	An automatable screen for the rapid identification of proteins amenable to refolding. *Proteomics*, **2006**, 6, 1750-7	4.8	20
136	Comparison of three commercial sparse-matrix crystallization screens. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 769-72		20
135	Fusion-protein-assisted protein crystallization. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 861-9	1.1	19
134	Dynamics of re-constitution of the human nuclear proteome after cell division is regulated by NLS-adjacent phosphorylation. *Cell Cycle*, **2014**, 13, 3551-64	4.7	19
133	Crystal structure of importin-□bound to a peptide bearing the nuclear localisation signal from chloride intracellular channel protein 4. *FEBS Journal*, **2011**, 278, 1662-75	5.7	19
132	Verprolin cytokinesis function mediated by the Hof one trap domain. *Traffic*, **2005**, 6, 575-93	5.7	19
131	Production of small cysteine-rich effector proteins in Escherichia coli for structural and functional studies. *Molecular Plant Pathology*, **2017**, 18, 141-151	5.7	18
130	Blood Group Antigen Recognition via the Group A Streptococcal M Protein Mediates Host Colonization. *MBio*, **2017**, 8,	7.8	18
129	Modelling the structure of latexin-carboxypeptidase A complex based on chemical cross-linking and molecular docking. *Protein Engineering, Design and Selection*, **2006**, 19, 9-16	1.9	18

128	Identification and predicted structure of a leucine-rich repeat motif shared by Leishmania major proteophosphoglycan and Parasite Surface Antigen 2. *Molecular and Biochemical Parasitology*, **2000** , 107, 289-95	1.9	18
127	PR1-mediated defence via C-terminal peptide release is targeted by a fungal pathogen effector. *New Phytologist*, **2021**, 229, 3467-3480	9.8	18
126	Discovery of novel pneumococcal surface antigen A (PsaA) inhibitors using a fragment-based drug design approach. *ACS Chemical Biology*, **2015**, 10, 1511-20	4.9	17
125	Regulation and crystallization of phosphorylated and dephosphorylated forms of truncated dimeric phenylalanine hydroxylase. *Protein Science*, **1997**, 6, 1352-7	6.3	17
124	Structural proteomics: high-throughput methods. Preface. *Methods in Molecular Biology*, **2008**, 426, v-vi	1.4	17
123	Protein crystal screening and characterization for serial femtosecond nanocrystallography. *Scientific Reports*, **2016**, 6, 25345	4.9	17
122	Structure-informed design of an enzymatically inactive vaccine component for group A Streptococcus. *MBio*, **2013**, 4,	7.8	16
121	A probabilistic model of nuclear import of proteins. *Bioinformatics*, **2011**, 27, 1239-46	7.2	16
120	Protein structure determination using a combination of cross-linking, mass spectrometry, and molecular modeling. *Methods in Molecular Biology*, **2008**, 426, 459-74	1.4	16
119	Intrasteric regulation of protein kinases. *Advances in Second Messenger and Phosphoprotein Research*, **1997**, 31, 29-40		16
118	Animal NLRs continue to inform plant NLR structure and function. *Archives of Biochemistry and Biophysics*, **2019**, 670, 58-68	4.1	15
117	Principles of Kinase Regulation **2010**, 559-563		14
116	Fibroblast growth factor receptor 2 phosphorylation on serine 779 couples to 14-3-3 and regulates cell survival and proliferation. *Molecular and Cellular Biology*, **2008**, 28, 3372-85	4.8	14
115	Crystallization and preliminary X-ray analysis of porcine ribonuclease inhibitor, a protein with leucine-rich repeats. *Journal of Molecular Biology*, **1993**, 231, 137-40	6.5	14
114	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	5.7	14
113	Pathological mutations differentially affect the self-assembly and polymerisation of the innate immune system signalling adaptor molecule MyD88. *BMC Biology*, **2018**, 16, 149	7.3	14
112	GMP Synthase Is Required for Virulence Factor Production and Infection by. *Journal of Biological Chemistry*, **2017**, 292, 3049-3059	5.4	13
111	Disruption of de Novo Adenosine Triphosphate (ATP) Biosynthesis Abolishes Virulence in Cryptococcus neoformans. *ACS Infectious Diseases*, **2016**, 2, 651-663	5.5	13

110	Structural and Calorimetric Studies Demonstrate that Xeroderma Pigmentosum Type G (XPG) Can Be Imported to the Nucleus by a Classical Nuclear Import Pathway via a Monopartite NLS Sequence. *Journal of Molecular Biology*, **2016**, 428, 2120-31	6.5	13
109	Biochemical characterization of Arabidopsis developmentally regulated G-proteins (DRGs). *Protein Expression and Purification*, **2009**, 67, 88-95	2	13
108	Incorporating a TEV cleavage site reduces the solubility of nine recombinant mouse proteins. *Protein Expression and Purification*, **2006**, 50, 68-73	2	13
107	Computer-aided design of T-cell epitope-based vaccines: addressing population coverage. *International Journal of Immunogenetics*, **2015**, 42, 313-21	2.3	12
106	Wzy-dependent bacterial capsules as potential drug targets. *Current Drug Targets*, **2012**, 13, 1421-31	3	12
105	The use of Co2+ for crystallization and structure determination, using a conventional monochromatic X-ray source, of flax rust avirulence protein. *Acta Crystallographica Section F: Structural Biology Communications*, **2007**, 63, 209-13		12
104	Structural characterization of the N-terminal autoregulatory sequence of phenylalanine hydroxylase. *Protein Science*, **2002**, 11, 2041-7	6.3	12
103	Expression and biochemical analysis of the entire HIV-2 gp41 ectodomain: determinants of stability map to N- and C-terminal sequences outside the 6-helix bundle core. *FEBS Letters*, **2004**, 567, 183-8	3.8	12
102	Molybdenum Enzymes and How They Support Virulence in Pathogenic Bacteria. *Frontiers in Microbiology*, **2020**, 11, 615860	5.7	11
101	The TLR signalling adaptor TRIF/TICAM-1 has an N-terminal helical domain with structural similarity to IFIT proteins. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2420-30		11
100	Focusing in on structural genomics: the University of Queensland structural biology pipeline. *New Biotechnology*, **2006**, 23, 281-9		11
99	MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. *Nature Communications*, **2021**, 12, 2578	17.4	11
98	Structural basis of nuclear import of flap endonuclease 1 (FEN1). *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 743-50		10
97	DLocalMotif: a discriminative approach for discovering local motifs in protein sequences. *Bioinformatics*, **2013**, 29, 39-46	7.2	10
96	The crystal structure of SnTox3 from the necrotrophic fungus Parastagonospora nodorum reveals a unique effector fold and provides insight into Snn3 recognition and pro-domain protease processing of fungal effectors. *New Phytologist*, **2021**, 231, 2282-2296	9.8	10
95	Regulation of signaling by cooperative assembly formation in mammalian innate immunity signalosomes by molecular mimics. *Seminars in Cell and Developmental Biology*, **2020**, 99, 96-114	7.5	10
94	A non-uniform sampling approach enables studies of dilute and unstable proteins. *Journal of Biomolecular NMR*, **2017**, 68, 119-127	3	9
93	ADS lyase is an enzyme essential for virulence whose crystal structure reveals features exploitable in antifungal drug design. *Journal of Biological Chemistry*, **2017**, 292, 11829-11839	5.4	9

92	The structure of the caspase recruitment domain of BinCARD reveals that all three cysteines can be oxidized. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 774-84		9
91	Ligand-induced conformational changes within a hexameric Acyl-CoA thioesterase. *Journal of Biological Chemistry*, **2011**, 286, 35643-35649	5.4	9
90	Crystallization and preliminary X-ray analysis of ferric enterobactin receptor FepA, an integral membrane protein from Escherichia coli. *Acta Crystallographica Section D: Biological Crystallography* , **1998**, 54, 697-9		9
89	Functional analysis, using in vitro mutagenesis, of amino acids located in the phenylalanine hydroxylase active site. *Archives of Biochemistry and Biophysics*, **2000**, 384, 238-44	4.1	9
88	Prediction of kinase-specific phosphorylation sites through an integrative model of protein context and sequence. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2016**, 1864, 1599-608	4	9
87	DNA mismatch repair proteins MLH1 and PMS2 can be imported to the nucleus by a classical nuclear import pathway. *Biochimie*, **2018**, 146, 87-96	4.6	9
86	Characterizing the conformational dynamics of metal-free PsaA using molecular dynamics simulations and electron paramagnetic resonance spectroscopy. *Biophysical Chemistry*, **2015**, 207, 51-60	3.5	8
85	Crystal structure and insights into the oligomeric state of UDP-glucose pyrophosphorylase from sugarcane. *PLoS ONE*, **2018**, 13, e0193667	3.7	8
84	Structural basis of interaction of bipartite nuclear localization signal from Agrobacterium VirD2 with rice importin-□*Molecular Plant*, **2014**, 7, 1061-1064	14.4	8
83	Stability of the octameric structure affects plasminogen-binding capacity of streptococcal enolase. *PLoS ONE*, **2015**, 10, e0121764	3.7	8
82	The distribution of different classes of nuclear localization signals (NLSs) in diverse organisms and the utilization of the minor NLS-binding site inplantnuclear import factor importin-□*Plant Signaling and Behavior*, **2013**, 8,	2.5	8
81	Computational modelling of linear motif-mediated protein interactions. *Current Topics in Medicinal Chemistry*, **2012**, 12, 1553-61	3	8
80	Purification of the M flax-rust resistance protein expressed in Pichia pastoris. *Plant Journal*, **2007**, 50, 1107-17	6.9	8
79	A computational analysis of substrate binding strength by phosphorylase kinase and protein kinase A. *Journal of Molecular Recognition*, **2002**, 15, 104-11	2.6	8
78	Modification of recombinatorial cloning for small affinity tag fusion protein construct generation. *Analytical Biochemistry*, **2005**, 346, 327-9	3.1	8
77	Structural basis of NLR activation and innate immune signalling in plants.. *Immunogenetics*, **2022**, 74, 5	3.2	8
76	Potent activation of SARM1 by NMN analogue VMN underlies vacor neurotoxicity		8
75	PhosphoPICK-SNP: quantifying the effect of amino acid variants on protein phosphorylation. *Bioinformatics*, **2017**, 33, 1773-1781	7.2	7

74	TRAF2 recruitment via T61 in CD30 drives NFB activation and enhances hESC survival and proliferation. *Molecular Biology of the Cell*, **2015**, 26, 993-1006	3.5	7
73	Pilot studies on the parallel production of soluble mouse proteins in a bacterial expression system. *Journal of Structural and Functional Genomics*, **2005**, 6, 13-20		7
72	Complex between bovine ribonuclease A and porcine ribonuclease inhibitor crystallizes in a similar unit cell as free ribonuclease inhibitor. *Journal of Molecular Biology*, **1994**, 241, 288-91	6.5	7
71	Structural and functional insights into the modulation of the activity of a flax cytokinin oxidase by flax rust effector AvrL567-A. *Molecular Plant Pathology*, **2019**, 20, 211-222	5.7	7
70	Molecular basis of regio- and stereo-specificity in biosynthesis of bacterial heterodimeric diketopiperazines. *Nature Communications*, **2020**, 11, 6251	17.4	6
69	Crystallization and preliminary X-ray analysis of mycophenolic acid-resistant and mycophenolic acid-sensitive forms of IMP dehydrogenase from the human fungal pathogen Cryptococcus. *Acta Crystallographica Section F: Structural Biology Communications*, **2010**, 66, 1104-7		6
68	Evolutionary Conservation of the Membrane Fusion Machine. *IUBMB Life*, **1999**, 48, 151-156	4.7	6
67	Evolutionary conservation of the membrane fusion machine. *IUBMB Life*, **1999**, 48, 151-6	4.7	6
66	Neurotoxin-mediated --potent activation of the axon degeneration regulator SARM1. *ELife*, **2021**, 10,	8.9	6
65	Structural and Biochemical Analysis of a Single Amino-Acid Mutant of WzzBSF That Alters Lipopolysaccharide O-Antigen Chain Length in Shigella flexneri. *PLoS ONE*, **2015**, 10, e0138266	3.7	6
64	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. *Nature Microbiology*, **2020**, 5, 1340-1348	26.6	6
63	A Novel NAD Signaling Mechanism in Axon Degeneration and its Relationship to Innate Immunity. *Frontiers in Molecular Biosciences*, **2021**, 8, 703532	5.6	6
62	Antifungal benzo[b]thiophene 1,1-dioxide IMPDH inhibitors exhibit pan-assay interference (PAINS) profiles. *Bioorganic and Medicinal Chemistry*, **2018**, 26, 5408-5419	3.4	6
61	Nicotinic acid mononucleotide is an allosteric SARM1 inhibitor promoting axonal protection. *Experimental Neurology*, **2021**, 345, 113842	5.7	6
60	Crystallization and preliminary X-ray diffraction analyses of the TIR domains of three TIR-NB-LRR proteins that are involved in disease resistance in Arabidopsis thaliana. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 1275-80		5
59	A medium or high throughput protein refolding assay. *Methods in Molecular Biology*, **2008**, 426, 269-75	1.4	5
58	Crystallization of the C-terminal domain of the mouse brain cytosolic long-chain acyl-CoA thioesterase. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 133-5		5
57	Structural basis of thiol-based regulation of formaldehyde detoxification in H. influenzae by a MerR regulator with no sensor region. *Nucleic Acids Research*, **2016**, 44, 6981-93	20.1	5

56	A Trap-Door Mechanism for Zinc Acquisition by AdcA. *MBio*, **2021**, 12,	7.8	5
55	Mapping the stabilome: a novel computational method for classifying metabolic protein stability. *BMC Systems Biology*, **2012**, 6, 60	3.5	4
54	Crystallization and X-ray diffraction analysis of the N-terminal domain of the Toll-like receptor signalling adaptor protein TRIF/TICAM-1. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 766-70		4
53	Crystallization and X-ray diffraction analysis of the C-terminal domain of the flax rust effector protein AvrM. *Acta Crystallographica Section F: Structural Biology Communications*, **2011**, 67, 1603-7		4
52	Proteomic and electron microscopy survey of large assemblies in macrophage cytoplasm. *Molecular and Cellular Proteomics*, **2011**, 10, M111.008763	7.6	4
51	Heterogeneous nucleation is required for crystallization of the ZnuA domain of pneumococcal AdcA. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 1459-64	1.1	4
50	Autoimmunity and effector recognition in Arabidopsis thaliana can be uncoupled by mutations in the RRS1-R immune receptor. *New Phytologist*, **2019**, 222, 954-965	9.8	4
49	A Proteome-Wide Immunoinformatics Tool to Accelerate T-Cell Epitope Discovery and Vaccine Design in the Context of Emerging Infectious Diseases: An Ethnicity-Oriented Approach. *Frontiers in Immunology*, **2021**, 12, 598778	8.4	4
48	Structure and Metal Binding Properties of YtgA. *Journal of Bacteriology*, **2019**, 202,	3.5	3
47	Recombinant production of functional full-length and truncated human TRAM/TICAM-2 adaptor protein involved in Toll-like receptor and interferon signaling. *Protein Expression and Purification*, **2015**, 106, 31-40	2	3
46	A linker strategy for the production and crystallization of Toll/interleukin-1 receptor/resistance protein domain complexes. *Protein Engineering, Design and Selection*, **2015**, 28, 137-45	1.9	3
45	Crystallization, X-ray diffraction analysis and preliminary structure determination of the TIR domain from the flax resistance protein L6. *Acta Crystallographica Section F: Structural Biology Communications*, **2011**, 67, 237-40		3
44	Crystallization of the flexible nuclear import receptor importin-beta in the unliganded state. *Acta Crystallographica Section F: Structural Biology Communications*, **2009**, 65, 625-8		3
43	The many faces of platelet glycoprotein Ibalpha--thrombin interaction. *Current Protein and Peptide Science*, **2009**, 10, 551-8	2.8	3
42	Comment on Nprotein isoelectric point as a predictor for increased crystallization screening efficiencyN. *Bioinformatics*, **2004**, 20, 2169-70; author reply 2171-4	7.2	3
41	Crystallization and crystal structure determination of ribonuclease A-ribonuclease inhibitor protein complex. *Methods in Molecular Biology*, **2001**, 160, 201-11	1.4	3
40	The crystal structure of SnTox3 from the necrotrophic fungusParastagonospora nodorumreveals a unique effector fold and insights into Kex2 protease processing of fungal effectors		3
39	Vaccinia Virus Immunomodulator A46: Destructive Interactions with MAL and MyD88 Shown by Negative-Stain Electron Microscopy. *Structure*, **2020**, 28, 1271-1287.e5	5.2	3

38	Structural characterisation of the HT3 motif of the polyhistidine triad protein D from Streptococcus pneumoniae. *FEBS Letters*, **2018**, 592, 2341-2350	3.8	3
37	Purification, crystallization and preliminary X-ray analysis of adenylosuccinate synthetase from the fungal pathogen Cryptococcus neoformans. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 1033-6		2
36	Small-Angle X-Ray Scattering for the Discerning Macromolecular Crystallographer. *Australian Journal of Chemistry*, **2014**, 67, 1786	1.2	2
35	Hybrid Methods for Protein Structure Prediction **2010**, 265-277		2
34	Crystallization and preliminary X-ray diffraction analysis of importin-alpha complexed with NLS peptidomimetics. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2005**, 1750, 9-13	4	2
33	Crystallization and preliminary X-ray diffraction analysis of the flax cytokinin oxidase LuCKX1.1. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 1094-6		2
32	Interaction between plate make and protein in protein crystallisation screening. *PLoS ONE*, **2009**, 4, e7851	3.7	2
31	Structural Evolution of TIR-Domain Signalosomes. *Frontiers in Immunology*, **2021**, 12, 784484	8.4	2
30	Increasing protein crystallization screening success with heterogeneous nucleating agents. *Methods in Molecular Biology*, **2008**, 426, 403-9	1.4	2
29	Targeting multiple epitopes on the spike protein: a new hope for COVID-19 antibody therapy. *Signal Transduction and Targeted Therapy*, **2020**, 5, 208	21	2
28	Conformation of the Solute-Binding Protein AdcAII Influences Zinc Uptake in. *Frontiers in Cellular and Infection Microbiology*, **2021**, 11, 729981	5.9	2
27	Crystal structure determination of the armadillo repeat domain of Drosophila SARM1 using MIRAS phasing. *Acta Crystallographica Section F, Structural Biology Communications*, **2021**, 77, 364-373	1.1	2
26	Structural mix-n-match reveals molecular secrets of platelets. *Blood*, **2011**, 118, 5065-6	2.2	1
25	A general target selection method for crystallographic proteomics. *Methods in Molecular Biology*, **2008**, 426, 27-35	1.4	1
24	Crystal structure of the Toll/interleukin-1 receptor (TIR) domain of IL-1R10 provides structural insights into TIR domain signaling.. *FEBS Letters*, **2022**,	3.8	1
23	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analysis of the TIR domain from the Brucella melitensis TIR-domain-containing protein TcpB. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 1167-70		1
22	Evolutionary model of protein secondary structure capable of revealing new biological relationships		1
21	Nicotinic acid mononucleotide is an allosteric SARM1 inhibitor promoting axonal protection		1

20	The Single Nucleotide Polymorphism Mal-D96N Mice Provide New Insights into Functionality of Mal in TLR Immune Responses. *Journal of Immunology*, **2019**, 202, 2384-2396	5.3	1
19	Active site architecture reveals coordination sphere flexibility and specificity determinants in a group of closely related molybdoenzymes. *Journal of Biological Chemistry*, **2021**, 296, 100672	5.4	1
18	Crystal structure determination of the armadillo repeat domain of Drosophila SARM1 using MIRAS phasing		1
17	Inhibition of the master regulator of Listeria monocytogenes virulence enables bacterial clearance from spacious replication vacuoles in infected macrophages.. *PLoS Pathogens*, **2022**, 18, e1010166	7.6	0
16	Overview of the pipeline for structural and functional characterization of macrophage proteins at the university of queensland. *Methods in Molecular Biology*, **2008**, 426, 577-87	1.4	0
15	DEFECTIVE EMBRYO AND MERISTEMS genes are required for cell division and gamete viability in Arabidopsis. *PLoS Genetics*, **2021**, 17, e1009561	6	0
14	Structural features of Cryptococcus neoformans bifunctional GAR/AIR synthetase may present novel antifungal drug targets. *Journal of Biological Chemistry*, **2021**, 297, 101091	5.4	0
13	The transmembrane adaptor SCIMP recruits tyrosine kinase Syk to phosphorylate Toll-like receptors to mediate selective inflammatory outputs.. *Journal of Biological Chemistry*, **2022**, 101857	5.4	0
12	Structural and biochemical characterization of Acinetobacter baumannii ZnuA.. *Journal of Inorganic Biochemistry*, **2022**, 231, 111787	4.2	0
11	Evolutionary model of protein secondary structure capable of revealing new biological relationships. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 1251-1259	4.2	
10	International Year of Crystallography. *Australian Journal of Chemistry*, **2014**, 67, 1718	1.2	
9	Factors influencing nucleo-cytoplasmic trafficking: which matter? Response to Alvisi & JansN comment on Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 2777-8		
8	Open up review system. *Nature*, **1998**, 396, 509	50.4	
7	Principles of Kinase Regulation **2003**, 539-542		
6	Crystallization and preliminary X-ray diffraction studies of FHA domains of Dun1 and Rad53 protein kinases. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 459-61		
5	Protein Serine/Threonine Kinases **2000**, 297-310		
4	Structure and Regulation of Phenylalanine Hydroxylase, and Implications for Related Enzymes **2002** , 79-84		
3	Peptide Substrates of Cyclic Nucleotide-Dependent Protein Kinases **2003**, 495-499		

2 Conformations of wild-type and mutant OmpA signal sequences in membrane mimetic environments **1992**, 265-267

1 Substrates of Cyclic Nucleotide-Dependent Protein Kinases **2010**, 1489-1495