

# Bostjan Kobe

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

253  
papers

14,952  
citations

60  
h-index

118  
g-index

269  
ext. papers

17,228  
ext. citations

7.6  
avg, IF

6.6  
L-index

#	Paper	IF	Citations
253	Structural basis of NLR activation and innate immune signalling in plants.. <i>Immunogenetics</i> , <b>2022</b> , 74, 5	3.2	8
252	Inhibition of the master regulator of <i>Listeria monocytogenes</i> virulence enables bacterial clearance from spacious replication vacuoles in infected macrophages.. <i>PLoS Pathogens</i> , <b>2022</b> , 18, e1010166	7.6	0
251	Crystal structure of the Toll/interleukin-1 receptor (TIR) domain of IL-1R10 provides structural insights into TIR domain signaling.. <i>FEBS Letters</i> , <b>2022</b> ,	3.8	1
250	The transmembrane adaptor SCIMP recruits tyrosine kinase Syk to phosphorylate Toll-like receptors to mediate selective inflammatory outputs.. <i>Journal of Biological Chemistry</i> , <b>2022</b> , 101857	5.4	0
249	Structural and biochemical characterization of <i>Acinetobacter baumannii</i> ZnuA.. <i>Journal of Inorganic Biochemistry</i> , <b>2022</b> , 231, 111787	4.2	0
248	Neurotoxin-mediated --potent activation of the axon degeneration regulator SARM1. <i>ELife</i> , <b>2021</b> , 10,	8.9	6
247	Structural Evolution of TIR-Domain Signalosomes. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 784484	8.4	2
246	SARM1 is a metabolic sensor activated by an increased NMN/NAD ratio to trigger axon degeneration. <i>Neuron</i> , <b>2021</b> , 109, 1118-1136.e11	13.9	54
245	MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. <i>Nature Communications</i> , <b>2021</b> , 12, 2578	17.4	11
244	DEFECTIVE EMBRYO AND MERISTEMS genes are required for cell division and gamete viability in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009561	6	0
243	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> , <b>2021</b> , 231, 2282-2296	9.8	10
242	A Novel NAD Signaling Mechanism in Axon Degeneration and its Relationship to Innate Immunity. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 703532	5.6	6
241	PR1-mediated defence via C-terminal peptide release is targeted by a fungal pathogen effector. <i>New Phytologist</i> , <b>2021</b> , 229, 3467-3480	9.8	18
240	Active site architecture reveals coordination sphere flexibility and specificity determinants in a group of closely related molybdoenzymes. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100672	5.4	1
239	A Trap-Door Mechanism for Zinc Acquisition by AdcA. <i>MBio</i> , <b>2021</b> , 12,	7.8	5
238	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. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 598778	8.4	4
237	Conformation of the Solute-Binding Protein AdcAll Influences Zinc Uptake in. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2021</b> , 11, 729981	5.9	2

236	Structural features of <i>Cryptococcus neoformans</i> bifunctional GAR/AIR synthetase may present novel antifungal drug targets. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 297, 101091	5.4	0
235	Crystal structure determination of the armadillo repeat domain of <i>Drosophila</i> SARM1 using MIRAS phasing. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2021</b> , 77, 364-373	1.1	2
234	Nicotinic acid mononucleotide is an allosteric SARM1 inhibitor promoting axonal protection. <i>Experimental Neurology</i> , <b>2021</b> , 345, 113842	5.7	6
233	Molybdenum Enzymes and How They Support Virulence in Pathogenic Bacteria. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 615860	5.7	11
232	Molecular basis of regio- and stereo-specificity in biosynthesis of bacterial heterodimeric diketopiperazines. <i>Nature Communications</i> , <b>2020</b> , 11, 6251	17.4	6
231	Evolutionary model of protein secondary structure capable of revealing new biological relationships. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2020</b> , 88, 1251-1259	4.2	
230	All major cholesterol-dependent cytolysins use glycans as cellular receptors. <i>Science Advances</i> , <b>2020</b> , 6, eaaz4926	14.3	27
229	Vaccinia Virus Immunomodulator A46: Destructive Interactions with MAL and MyD88 Shown by Negative-Stain Electron Microscopy. <i>Structure</i> , <b>2020</b> , 28, 1271-1287.e5	5.2	3
228	Targeting multiple epitopes on the spike protein: a new hope for COVID-19 antibody therapy. <i>Signal Transduction and Targeted Therapy</i> , <b>2020</b> , 5, 208	21	2
227	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1340-1348	26.6	6
226	Regulation of signaling by cooperative assembly formation in mammalian innate immunity signalosomes by molecular mimics. <i>Seminars in Cell and Developmental Biology</i> , <b>2020</b> , 99, 96-114	7.5	10
225	Structure and Metal Binding Properties of YtgA. <i>Journal of Bacteriology</i> , <b>2019</b> , 202,	3.5	3
224	NAD cleavage activity by animal and plant TIR domains in cell death pathways. <i>Science</i> , <b>2019</b> , 365, 793-799	35.3	183
223	Handling of nutrient copper in the bacterial envelope. <i>Metallomics</i> , <b>2019</b> , 11, 50-63	4.5	30
222	Animal NLRs continue to inform plant NLR structure and function. <i>Archives of Biochemistry and Biophysics</i> , <b>2019</b> , 670, 58-68	4.1	15
221	The Plant "Resistosome": Structural Insights into Immune Signaling. <i>Cell Host and Microbe</i> , <b>2019</b> , 26, 193-201	20.1	38
220	The Single Nucleotide Polymorphism Mal-D96N Mice Provide New Insights into Functionality of Mal in TLR Immune Responses. <i>Journal of Immunology</i> , <b>2019</b> , 202, 2384-2396	5.3	1
219	Death, TIR, and RHIM: Self-assembling domains involved in innate immunity and cell-death signaling. <i>Journal of Leukocyte Biology</i> , <b>2019</b> , 105, 363-375	6.5	26

218	Autoimmunity and effector recognition in <i>Arabidopsis thaliana</i> can be uncoupled by mutations in the RRS1-R immune receptor. <i>New Phytologist</i> , <b>2019</b> , 222, 954-965	9.8	4
217	Structural and functional insights into the modulation of the activity of a flax cytokinin oxidase by flax rust effector AvrL567-A. <i>Molecular Plant Pathology</i> , <b>2019</b> , 20, 211-222	5.7	7
216	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> , <b>2018</b> , 51, 97-111	3.8	41
215	Structural and Functional Characterization of a Cross-Reactive Dengue Virus Neutralizing Antibody that Recognizes a Cryptic Epitope. <i>Structure</i> , <b>2018</b> , 26, 51-59.e4	5.2	29
214	Crystal structure and insights into the oligomeric state of UDP-glucose pyrophosphorylase from sugarcane. <i>PLoS ONE</i> , <b>2018</b> , 13, e0193667	3.7	8
213	DNA mismatch repair proteins MLH1 and PMS2 can be imported to the nucleus by a classical nuclear import pathway. <i>Biochimie</i> , <b>2018</b> , 146, 87-96	4.6	9
212	Crystal structure of the <i>Melampsora lini</i> effector AvrP reveals insights into a possible nuclear function and recognition by the flax disease resistance protein P. <i>Molecular Plant Pathology</i> , <b>2018</b> , 19, 1196-1209	5.7	14
211	Pathological mutations differentially affect the self-assembly and polymerisation of the innate immune system signalling adaptor molecule MyD88. <i>BMC Biology</i> , <b>2018</b> , 16, 149	7.3	14
210	Megahertz serial crystallography. <i>Nature Communications</i> , <b>2018</b> , 9, 4025	17.4	104
209	Antifungal benzo[b]thiophene 1,1-dioxide IMPDH inhibitors exhibit pan-assay interference (PAINS) profiles. <i>Bioorganic and Medicinal Chemistry</i> , <b>2018</b> , 26, 5408-5419	3.4	6
208	Structural characterisation of the HT3 motif of the polyhistidine triad protein D from <i>Streptococcus pneumoniae</i> . <i>FEBS Letters</i> , <b>2018</b> , 592, 2341-2350	3.8	3
207	Production of small cysteine-rich effector proteins in <i>Escherichia coli</i> for structural and functional studies. <i>Molecular Plant Pathology</i> , <b>2017</b> , 18, 141-151	5.7	18
206	Multiple functional self-association interfaces in plant TIR domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E2046-E2052	11.5	72
205	GMP Synthase Is Required for Virulence Factor Production and Infection by. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 3049-3059	5.4	13
204	Towards the structure of the TIR-domain signalosome. <i>Current Opinion in Structural Biology</i> , <b>2017</b> , 43, 122-130	8.1	42
203	A non-uniform sampling approach enables studies of dilute and unstable proteins. <i>Journal of Biomolecular NMR</i> , <b>2017</b> , 68, 119-127	3	9
202	The molecular mechanisms of signaling by cooperative assembly formation in innate immunity pathways. <i>Molecular Immunology</i> , <b>2017</b> , 86, 23-37	4.3	68
201	Blood Group Antigen Recognition via the Group A Streptococcal M Protein Mediates Host Colonization. <i>MBio</i> , <b>2017</b> , 8,	7.8	18

200	ADS lyase is an enzyme essential for virulence whose crystal structure reveals features exploitable in antifungal drug design. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 11829-11839	5.4	9
199	PhosphoPICK-SNP: quantifying the effect of amino acid variants on protein phosphorylation. <i>Bioinformatics</i> , <b>2017</b> , 33, 1773-1781	7.2	7
198	Animal NLRs provide structural insights into plant NLR function. <i>Annals of Botany</i> , <b>2017</b> , 119, 827-702	4.1	48
197	Emerging Insights into the Functions of Pathogenesis-Related Protein 1. <i>Trends in Plant Science</i> , <b>2017</b> , 22, 871-879	13.1	150
196	Solution structure of the TLR adaptor MAL/TIRAP reveals an intact BB loop and supports MAL Cys91 glutathionylation for signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6480-E6489	11.5	28
195	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. <i>Nature Structural and Molecular Biology</i> , <b>2017</b> , 24, 743-751	17.6	82
194	Recombinant and epitope-based vaccines on the road to the market and implications for vaccine design and production. <i>Human Vaccines and Immunotherapeutics</i> , <b>2016</b> , 12, 763-7	4.4	57
193	Disruption of de Novo Adenosine Triphosphate (ATP) Biosynthesis Abolishes Virulence in <i>Cryptococcus neoformans</i> . <i>ACS Infectious Diseases</i> , <b>2016</b> , 2, 651-663	5.5	13
192	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> , <b>2016</b> , 113, 12856-12861	11.5	72
191	TRIF-dependent TLR signaling, its functions in host defense and inflammation, and its potential as a therapeutic target. <i>Journal of Leukocyte Biology</i> , <b>2016</b> , 100, 27-45	6.5	88
190	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. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 2120-31	6.5	13
189	Comparative Analysis of the Flax Immune Receptors L6 and L7 Suggests an Equilibrium-Based Switch Activation Model. <i>Plant Cell</i> , <b>2016</b> , 28, 146-59	11.6	69
188	Structural Biology and Regulation of Protein Import into the Nucleus. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 2060-90	6.5	140
187	Structure and Function of the TIR Domain from the Grape NLR Protein RPV1. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 1850	6.2	32
186	Multiple Domain Associations within the Arabidopsis Immune Receptor RPP1 Regulate the Activation of Programmed Cell Death. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1005769	7.6	54
185	Wheat PR-1 proteins are targeted by necrotrophic pathogen effector proteins. <i>Plant Journal</i> , <b>2016</b> , 88, 13-25	6.9	60
184	Structural basis of thiol-based regulation of formaldehyde detoxification in <i>H. influenzae</i> by a MerR regulator with no sensor region. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 6981-93	20.1	5
183	Protein crystal screening and characterization for serial femtosecond nanocrystallography. <i>Scientific Reports</i> , <b>2016</b> , 6, 25345	4.9	17

182	Prediction of kinase-specific phosphorylation sites through an integrative model of protein context and sequence. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2016</b> , 1864, 1599-608	4	9
181	Dysregulation of transition metal ion homeostasis is the molecular basis for cadmium toxicity in <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 6418	17.4	77
180	Fusion-protein-assisted protein crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 861-9	1.1	19
179	Discovery of novel pneumococcal surface antigen A (PsaA) inhibitors using a fragment-based drug design approach. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 1511-20	4.9	17
178	TRAF2 recruitment via T61 in CD30 drives NFB activation and enhances hESC survival and proliferation. <i>Molecular Biology of the Cell</i> , <b>2015</b> , 26, 993-1006	3.5	7
177	Characterizing the conformational dynamics of metal-free PsaA using molecular dynamics simulations and electron paramagnetic resonance spectroscopy. <i>Biophysical Chemistry</i> , <b>2015</b> , 207, 51-60	3.5	8
176	PhosphoPICK: modelling cellular context to map kinase-substrate phosphorylation events. <i>Bioinformatics</i> , <b>2015</b> , 31, 382-9	7.2	26
175	Recombinant production of functional full-length and truncated human TRAM/TICAM-2 adaptor protein involved in Toll-like receptor and interferon signaling. <i>Protein Expression and Purification</i> , <b>2015</b> , 106, 31-40	2	3
174	Computer-aided design of T-cell epitope-based vaccines: addressing population coverage. <i>International Journal of Immunogenetics</i> , <b>2015</b> , 42, 313-21	2.3	12
173	Stability of the octameric structure affects plasminogen-binding capacity of streptococcal enolase. <i>PLoS ONE</i> , <b>2015</b> , 10, e0121764	3.7	8
172	A linker strategy for the production and crystallization of Toll/interleukin-1 receptor/resistance protein domain complexes. <i>Protein Engineering, Design and Selection</i> , <b>2015</b> , 28, 137-45	1.9	3
171	Structure and function of Toll/interleukin-1 receptor/resistance protein (TIR) domains. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , <b>2015</b> , 20, 250-61	5.4	92
170	A bioinformatics tool for epitope-based vaccine design that accounts for human ethnic diversity: application to emerging infectious diseases. <i>Vaccine</i> , <b>2015</b> , 33, 1267-73	4.1	27
169	Heterogeneous nucleation is required for crystallization of the ZnuA domain of pneumococcal AdcA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 1459-64	1.1	4
168	Structural and Biochemical Analysis of a Single Amino-Acid Mutant of WzzBSF That Alters Lipopolysaccharide O-Antigen Chain Length in <i>Shigella flexneri</i> . <i>PLoS ONE</i> , <b>2015</b> , 10, e0138266	3.7	6
167	Structural basis for assembly and function of a heterodimeric plant immune receptor. <i>Science</i> , <b>2014</b> , 344, 299-303	33.3	228
166	Mechanism of bacterial interference with TLR4 signaling by <i>Brucella</i> Toll/interleukin-1 receptor domain-containing protein TcbB. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 654-68	5.4	47
165	Imperfect coordination chemistry facilitates metal ion release in the Psa permease. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 35-41	11.7	103



164	Structural basis of interaction of bipartite nuclear localization signal from <i>Agrobacterium</i> VirD2 with rice importin- $\alpha$ <i>Molecular Plant</i> , <b>2014</b> , 7, 1061-1064	14.4	8
163	The TLR signaling adaptor TRAM interacts with TRAF6 to mediate activation of the inflammatory response by TLR4. <i>Journal of Leukocyte Biology</i> , <b>2014</b> , 96, 427-36	6.5	25
162	Dynamics of re-constitution of the human nuclear proteome after cell division is regulated by NLS-adjacent phosphorylation. <i>Cell Cycle</i> , <b>2014</b> , 13, 3551-64	4.7	19
161	International Year of Crystallography. <i>Australian Journal of Chemistry</i> , <b>2014</b> , 67, 1718	1.2	
160	The nuclear immune receptor RPS4 is required for RRS1SLH1-dependent constitutive defense activation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004655	6	70
159	Small-Angle X-Ray Scattering for the Discerning Macromolecular Crystallographer. <i>Australian Journal of Chemistry</i> , <b>2014</b> , 67, 1786	1.2	2
158	AdcA and AdcAll employ distinct zinc acquisition mechanisms and contribute additively to zinc homeostasis in <i>Streptococcus pneumoniae</i> . <i>Molecular Microbiology</i> , <b>2014</b> , 91, 834-51	4.1	76
157	Diversity and variability of NOD-like receptors in fungi. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 3137-58	3.9	53
156	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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 2777-8		
155	PREDIVAC: CD4+ T-cell epitope prediction for vaccine design that covers 95% of HLA class II DR protein diversity. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 52	3.6	43
154	Purification, crystallization and preliminary X-ray analysis of adenylosuccinate synthetase from the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1033-6		2
153	Crystallization and X-ray diffraction analysis of the N-terminal domain of the Toll-like receptor signalling adaptor protein TRIF/TICAM-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 766-70		4
152	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> , <b>2013</b> , 69, 2495-505		26
151	The distribution of different classes of nuclear localization signals (NLSs) in diverse organisms and the utilization of the minor NLS-binding site in plant nuclear import factor importin- $\alpha$ <i>Plant Signaling and Behavior</i> , <b>2013</b> , 8,	2.5	8
150	A glutathione-dependent detoxification system is required for formaldehyde resistance and optimal survival of <i>Neisseria meningitidis</i> in biofilms. <i>Antioxidants and Redox Signaling</i> , <b>2013</b> , 18, 743-55	8.4	23
149	DLocalMotif: a discriminative approach for discovering local motifs in protein sequences. <i>Bioinformatics</i> , <b>2013</b> , 29, 39-46	7.2	10
148	Structure-informed design of an enzymatically inactive vaccine component for group A <i>Streptococcus</i> . <i>MBio</i> , <b>2013</b> , 4,	7.8	16
147	The structure of the caspase recruitment domain of BinCARD reveals that all three cysteines can be oxidized. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 774-84		9

146	The TLR signalling adaptor TRIF/TICAM-1 has an N-terminal helical domain with structural similarity to IFIT proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2420-30		11
145	Crystallization and preliminary X-ray diffraction analyses of the TIR domains of three TIR-NB-LRR proteins that are involved in disease resistance in <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1275-80		5
144	Distinctive conformation of minor site-specific nuclear localization signals bound to importin- $\beta$ . <i>Traffic</i> , <b>2013</b> , 14, 1144-54	5.7	36
143	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> , <b>2013</b> , 110, 17594-9	11.5	50
142	Structural characterisation of the nuclear import receptor importin alpha in complex with the bipartite NLS of Prp20. <i>PLoS ONE</i> , <b>2013</b> , 8, e82038	3.7	20
141	Crystallization and preliminary X-ray diffraction analysis of the flax cytokinin oxidase LuCKX1.1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1094-6		2
140	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analysis of the TIR domain from the <i>Brucella melitensis</i> TIR-domain-containing protein TcpB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1167-70		1
139	Structural basis of high-affinity nuclear localization signal interactions with importin- $\beta$ . <i>Traffic</i> , <b>2012</b> , 13, 532-48	5.7	70
138	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 637-48		20
137	Structural basis of nuclear import of flap endonuclease 1 (FEN1). <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 743-50		10
136	Crystal structure of rice importin- $\beta$ and structural basis of its interaction with plant-specific nuclear localization signals. <i>Plant Cell</i> , <b>2012</b> , 24, 5074-88	11.6	37
135	Mapping the stabilome: a novel computational method for classifying metabolic protein stability. <i>BMC Systems Biology</i> , <b>2012</b> , 6, 60	3.5	4
134	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. <i>Journal of Molecular Medicine</i> , <b>2012</b> , 90, 1197-207	5.5	40
133	De novo GTP biosynthesis is critical for virulence of the fungal pathogen <i>Cryptococcus neoformans</i> . <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002957	7.6	45
132	Intramolecular interaction influences binding of the Flax L5 and L6 resistance proteins to their AvrL567 ligands. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1003004	7.6	76
131	Adaptors in toll-like receptor signaling and their potential as therapeutic targets. <i>Current Drug Targets</i> , <b>2012</b> , 13, 1360-74	3	59
130	Wzy-dependent bacterial capsules as potential drug targets. <i>Current Drug Targets</i> , <b>2012</b> , 13, 1421-31	3	12
129	Prokaryotic substrate-binding proteins as targets for antimicrobial therapies. <i>Current Drug Targets</i> , <b>2012</b> , 13, 1400-10	3	32



128	Computational modelling of linear motif-mediated protein interactions. <i>Current Topics in Medicinal Chemistry</i> , <b>2012</b> , 12, 1553-61	3	8
127	Residues in domain III of the dengue virus envelope glycoprotein involved in cell-surface glycosaminoglycan binding. <i>Journal of General Virology</i> , <b>2012</b> , 93, 72-82	4.9	76
126	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. <i>Nature Genetics</i> , <b>2011</b> , 44, 165-9	36.3	145
125	A molecular mechanism for bacterial susceptibility to zinc. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002357	7.6	281
124	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> , <b>2011</b> , 9, 200-211	23.4	243
123	Structural basis of importin- $\beta$ -mediated nuclear transport for Ku70 and Ku80. <i>Journal of Molecular Biology</i> , <b>2011</b> , 412, 226-34	6.5	32
122	Structural mix-n-match reveals molecular secrets of platelets. <i>Blood</i> , <b>2011</b> , 118, 5065-6	2.2	1
121	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> , <b>2011</b> , 24, 897-906	3.6	116
120	Crystal structure of importin- $\beta$ bound to a peptide bearing the nuclear localisation signal from chloride intracellular channel protein 4. <i>FEBS Journal</i> , <b>2011</b> , 278, 1662-75	5.7	19
119	Molecular basis for specificity of nuclear import and prediction of nuclear localization. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2011</b> , 1813, 1562-77	4.9	284
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4	Potent activation of SARM1 by NMN analogue VMN underlies vacor neurotoxicity		8
3	Evolutionary model of protein secondary structure capable of revealing new biological relationships		1

- 2 Nicotinic acid mononucleotide is an allosteric SARM1 inhibitor promoting axonal protection 1
- 1 Crystal structure determination of the armadillo repeat domain of Drosophila SARM1 using MIRAS phasing 1