Philip M Kim

List of Publications by Citations

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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.

59 papers	3,261 citations	26 h-index	57 g-index
63 ext. papers	3,996 ext. citations	9.3 avg, IF	5.11 L-index

#	Paper	IF	Citations
59	The importance of bottlenecks in protein networks: correlation with gene essentiality and expression dynamics. *PLoS Computational Biology*, **2007**, 3, e59	5	657
58	Relating three-dimensional structures to protein networks provides evolutionary insights. *Science*, **2006**, 314, 1938-41	33.3	388
57	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. *Science Signaling*, **2010**, 3, ra12	8.8	262
56	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. *Nature Biotechnology*, **2015**, 33, 555-62	44.5	194
55	The role of disorder in interaction networks: a structural analysis. *Molecular Systems Biology*, **2008**, 4, 179	12.2	167
54	Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins. *PLoS Biology*, **2009**, 7, e1000218	9.7	151
53	Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. *Genome Research*, **2008**, 18, 1865-74	9.7	114
52	Positive selection at the protein network periphery: evaluation in terms of structural constraints and cellular context. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 20274-9	11.5	111
51	Coevolution of PDZ domain-ligand interactions analyzed by high-throughput phage display and deep sequencing. *Molecular BioSystems*, **2010**, 6, 1782-90		85
50	Large-scale interaction profiling of PDZ domains through proteomic peptide-phage display using human and viral phage peptidomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 2542-7	11.5	82
49	Quantitative genome-wide genetic interaction screens reveal global epistatic relationships of protein complexes in Escherichia coli. *PLoS Genetics*, **2014**, 10, e1004120	6	71
48	A systematic approach to identify novel cancer drug targets using machine learning, inhibitor design and high-throughput screening. *Genome Medicine*, **2014**, 6, 57	14.4	67
47	The multiple-specificity landscape of modular peptide recognition domains. *Molecular Systems Biology*, **2011**, 7, 484	12.2	67
46	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. *Structure*, **2017**, 25, 1598-1610.e3	5.2	56
45	Method to generate highly stable D-amino acid analogs of bioactive helical peptides using a mirror image of the entire PDB. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 1505-1510	11.5	54
44	Combining structural modeling with ensemble machine learning to accurately predict protein fold stability and binding affinity effects upon mutation. *PLoS ONE*, **2014**, 9, e107353	3.7	53
43	Motif mediated protein-protein interactions as drug targets. *Cell Communication and Signaling*, **2016**, 14, 8	7.5	52

42	Distinct types of disorder in the human proteome: functional implications for alternative splicing. *PLoS Computational Biology*, **2013**, 9, e1003030	5	48
41	Elucidation of the binding preferences of peptide recognition modules: SH3 and PDZ domains. *FEBS Letters*, **2012**, 586, 2631-7	3.8	39
40	ELASPIC web-server: proteome-wide structure-based prediction of mutation effects on protein stability and binding affinity. *Bioinformatics*, **2016**, 32, 1589-91	7.2	37
39	Fast and Flexible Protein Design Using Deep Graph Neural Networks. *Cell Systems*, **2020**, 11, 402-411.e4	10.6	37
38	Computational analysis of interactomes: current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. *Methods*, **2012**, 57, 508-18	4.6	35
37	A structural approach reveals how neighbouring C2H2 zinc fingers influence DNA binding specificity. *Nucleic Acids Research*, **2015**, 43, 9147-57	20.1	30
36	Strategies to Develop Inhibitors of Motif-Mediated Protein-Protein Interactions as Drug Leads. *Annual Review of Pharmacology and Toxicology*, **2017**, 57, 39-60	17.9	27
35	Network evolution: rewiring and signatures of conservation in signaling. *PLoS Computational Biology*, **2012**, 8, e1002411	5	27
34	Pooled screening for antiproliferative inhibitors of protein-protein interactions. *Nature Chemical Biology*, **2016**, 12, 275-81	11.7	26
33	MOTIPS: automated motif analysis for predicting targets of modular protein domains. *BMC Bioinformatics*, **2010**, 11, 243	3.6	25
32	Protein engineering by highly parallel screening of computationally designed variants. *Science Advances*, **2016**, 2, e1600692	14.3	21
31	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. *Nature Structural and Molecular Biology*, **2018**, 25, 1093-1102	17.6	21
30	Non-base-contacting residues enable kaleidoscopic evolution of metazoan C2H2 zinc finger DNA binding. *Genome Biology*, **2017**, 18, 167	18.3	20
29	The Chemical Fluctuation Theorem governing gene expression. *Nature Communications*, **2018**, 9, 297	17.4	18
28	Proteomic peptide phage display uncovers novel interactions of the PDZ1-2 supramodule of syntenin. *FEBS Letters*, **2016**, 590, 3-12	3.8	18
27	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. *Cell Reports*, **2015**, 12, 183-9	10.6	17
26	A high-throughput pipeline for the production of synthetic antibodies for analysis of ribonucleoprotein complexes. *Rna*, **2016**, 22, 636-55	5.8	16
25	The present and the future of motif-mediated protein-protein interactions. *Current Opinion in Structural Biology*, **2018**, 50, 162-170	8.1	15

24	Predicting changes in protein stability caused by mutation using sequence-and structure-based methods in a CAGI5 blind challenge. *Human Mutation*, **2019**, 40, 1414-1423	4.7	14
23	Identification of specificity determining residues in peptide recognition domains using an information theoretic approach applied to large-scale binding maps. *BMC Biology*, **2011**, 9, 53	7.3	14
22	Computational structural analysis of protein interactions and networks. *Proteomics*, **2012**, 12, 1697-705	4.8	13
21	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. *Human Mutation*, **2019**, 40, 1392-1399	4.7	11
20	Large-scale survey and database of high affinity ligands for peptide recognition modules. *Molecular Systems Biology*, **2020**, 16, e9310	12.2	11
19	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. *Journal of Molecular Biology*, **2019**, 431, 336-350	6.5	11
18	An omics perspective of protein disorder. *Molecular BioSystems*, **2012**, 8, 185-93		10
17	Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. *Methods in Molecular Biology*, **2019**, 1851, 1-17	1.4	9
16	Data driven flexible backbone protein design. *PLoS Computational Biology*, **2017**, 13, e1005722	5	8
15	Fast and flexible design of novel proteins using graph neural networks		6
14	A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domain-Peptide Interactions. *ACS Synthetic Biology*, **2019**, 8, 918-928	5.7	5
13	A computational approach for designing D-proteins with non-canonical amino acid optimised binding affinity. *PLoS ONE*, **2017**, 12, e0187524	3.7	5
12	Computational Design of Potent D-Peptide Inhibitors of SARS-CoV-2. *Journal of Medicinal Chemistry* , **2021**, 64, 14955-14967	8.3	5
11	ELASPIC2 (EL2): Combining Contextualized Language Models and Graph Neural Networks to Predict Effects of Mutations. *Journal of Molecular Biology*, **2021**, 433, 166810	6.5	5
10	Rapid and accurate structure-based therapeutic peptide design using GPU accelerated thermodynamic integration. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 236-244	4.2	5
9	JBASE: Joint Bayesian Analysis of Subphenotypes and Epistasis. *Bioinformatics*, **2016**, 32, 203-10	7.2	4
8	A Method to Calculate the Relative Binding Free Energy Differences of □Helical Stapled Peptides. *Journal of Organic Chemistry*, **2020**, 85, 1644-1651	4.2	3
7	PepNN: a deep attention model for the identification of peptide binding sites		3

6	Deep generative modeling for protein design.. *Current Opinion in Structural Biology*, **2021**, 72, 226-236	8.1	2
5	Large-Scale Interaction Profiling of Protein Domains Through Proteomic Peptide-Phage Display Using Custom Peptidomes. *Methods in Molecular Biology*, **2017**, 1518, 213-226	1.4	1
4	The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. *Nucleic Acids Research*, **2020**, 48, 6382-6402	20.1	1
3	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. *STAR Protocols*, **2021**, 2, 100505	1.4	1
2	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. *BMC Bioinformatics*, **2016**, 17, 150	3.6	
1	Phage display identification of nanomolar ligands for human NEDD4-WW3: Energetic and dynamic implications for the development of broad-spectrum antivirals.. *International Journal of Biological Macromolecules*, **2022**, 207, 308-323	7.9	