Philip M Kim

List of Publications by Year
in descending order

60	4,451	186265 28	138484 58
papers	citations	h-index	g-index

63	63	63	7287
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Deep generative modeling for protein design. Current Opinion in Structural Biology, 2022, 72, 226-236.	5.7	39
2	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.	7.5	3
3	PepNN: a deep attention model for the identification of peptide binding sites. Communications Biology, 2022, 5, .	4.4	16
4	ELASPIC2 (EL2): Combining Contextualized Language Models and Graph Neural Networks to Predict Effects of Mutations. Journal of Molecular Biology, 2021, 433, 166810.	4.2	24
5	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. STAR Protocols, 2021, 2, 100505.	1.2	5
6	Rapid protein model refinement by deep learning. Nature Computational Science, 2021, 1, 456-457.	8.0	0
7	Computational Design of Potent D-Peptide Inhibitors of SARS-CoV-2. Journal of Medicinal Chemistry, 2021, 64, 14955-14967.	6.4	28
8	A Method to Calculate the Relative Binding Free Energy Differences of Î±-Helical Stapled Peptides. Journal of Organic Chemistry, 2020, 85, 1644-1651.	3.2	5
9	Fast and Flexible Protein Design Using Deep Graph Neural Networks. Cell Systems, 2020, 11, 402-411.e4.	6.2	121
10	The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. Nucleic Acids Research, 2020, 48, 6382-6402.	14.5	4
11	Largeâ€scale survey and database of high affinity ligands for peptide recognition modules. Molecular Systems Biology, 2020, 16, e9310.	7.2	22
12	Predicting changes in protein stability caused by mutation using sequenceâ€and structureâ€based methods in a CAGI5 blind challenge. Human Mutation, 2019, 40, 1414-1423.	2.5	28
13	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	2.5	16
14	A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domainâ€“Peptide Interactions. ACS Synthetic Biology, 2019, 8, 918-928.	3.8	6
15	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. Journal of Molecular Biology, 2019, 431, 336-350.	4.2	20
16	Rapid and accurate structureâ€based therapeutic peptide design using GPU accelerated thermodynamic integration. Proteins: Structure, Function and Bioinformatics, 2019, 87, 236-244.	2.6	7
17	Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. Methods in Molecular Biology, 2019, 1851, 1-17.	0.9	12
18	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.	7.1	89

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19	The Chemical Fluctuation Theorem governing gene expression. Nature Communications, 2018, 9, 297.	12.8	29
20	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. Nature Structural and Molecular Biology, 2018, 25, 1093-1102.	8.2	31
21	The present and the future of motif-mediated proteinâ€“protein interactions. Current Opinion in Structural Biology, 2018, 50, 162-170.	5.7	23
22	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. Structure, 2017, 25, 1598-1610.e3.	3.3	105
23	Large-Scale Interaction Profiling of Protein Domains Through Proteomic Peptide-Phage Display Using Custom Peptidomes. Methods in Molecular Biology, 2017, 1518, 213-226.	0.9	1
24	Strategies to Develop Inhibitors of Motif-Mediated Protein-Protein Interactions as Drug Leads. Annual Review of Pharmacology and Toxicology, 2017, 57, 39-60.	9.4	37
25	Non-base-contacting residues enable kaleidoscopic evolution of metazoan C2H2 zinc finger DNA binding. Genome Biology, 2017, 18, 167.	8.8	33
26	A computational approach for designing D-proteins with non-canonical amino acid optimised binding affinity. PLoS ONE, 2017, 12, e0187524.	2.5	8
27	Data driven flexible backbone protein design. PLoS Computational Biology, 2017, 13, e1005722.	3.2	13
28	JBASE: Joint Bayesian Analysis of Subphenotypes and Epistasis. Bioinformatics, 2016, 32, 203-210.	4.1	8
29	Protein engineering by highly parallel screening of computationally designed variants. Science Advances, 2016, 2, e1600692.	10.3	32
30	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.	2.6	0
31	Motif mediated protein-protein interactions as drug targets. Cell Communication and Signaling, 2016, 14, 8.	6.5	76
32	ELASPIC web-server: proteome-wide structure-based prediction of mutation effects on protein stability and binding affinity. Bioinformatics, 2016, 32, 1589-1591.	4.1	55
33	Proteomic peptide phage display uncovers novel interactions of the PDZ1â€2 supramodule of syntenin. FEBS Letters, 2016, 590, 3-12.	2.8	24
34	Pooled screening for antiproliferative inhibitors of protein-protein interactions. Nature Chemical Biology, 2016, 12, 275-281.	8.0	37
35	A high-throughput pipeline for the production of synthetic antibodies for analysis of ribonucleoprotein complexes. Rna, 2016, 22, 636-655.	3.5	22
36	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189.	6.4	22

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37	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. Nature Biotechnology, 2015, 33, 555-562.	17.5	271
38	A structural approach reveals how neighbouring C2H2 zinc fingers influence DNA binding specificity. Nucleic Acids Research, 2015, 43, 9147-9157.	14.5	44
39	Combining Structural Modeling with Ensemble Machine Learning to Accurately Predict Protein Fold Stability and Binding Affinity Effects upon Mutation. PLoS ONE, 2014, 9, e107353.	2.5	71
40	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, 2542-2547.	7.1	124
41	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in Escherichia coli. PLoS Genetics, 2014, 10, e1004120.	3.5	96
42	A systematic approach to identify novel cancer drug targets using machine learning, inhibitor design and high-throughput screening. Genome Medicine, 2014, 6, 57.	8.2	101
43	Interpreting protein networks with three-dimensional structures. Nature Methods, 2013, 10, 43-44.	19.0	7
44	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. PLoS Computational Biology, 2013, 9, e1003030.	3.2	62
45	Network Evolution: Rewiring and Signatures of Conservation in Signaling. PLoS Computational Biology, 2012, 8, e1002411.	3.2	30
46	Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the hostâ€“pathogen interaction space. Methods, 2012, 57, 508-518.	3.8	49
47	Elucidation of the binding preferences of peptide recognition modules: SH3 and PDZ domains. FEBS Letters, 2012, 586, 2631-2637.	2.8	43
48	An omics perspective of protein disorder. Molecular BioSystems, 2012, 8, 185-193.	2.9	12
49	Computational structural analysis of protein interactions and networks. Proteomics, 2012, 12, 1697-1705.	2.2	14
50	The multipleâ€specificity landscape of modular peptide recognition domains. Molecular Systems Biology, 2011, 7, 484.	7.2	78
51	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.	3.8	16
52	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. Science Signaling, 2010, 3, ra12.	3.6	341
53	MOTIPS: Automated Motif Analysis for Predicting Targets of Modular Protein Domains. BMC Bioinformatics, 2010, 11, 243.	2.6	28
54	Coevolution of PDZ domainâ€“ligand interactions analyzed by high-throughput phage display and deep sequencing. Molecular BioSystems, 2010, 6, 1782.	2.9	107

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55	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. PLoS Biology, 2009, 7, e1000218.	5.6	172
56	The role of disorder in interaction networks: a structural analysis. Molecular Systems Biology, 2008, 4, 179.	7.2	206
57	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, 1865-1874.	5.5	126
58	The Importance of Bottlenecks in Protein Networks: Correlation with Gene Essentiality and Expression Dynamics. PLoS Computational Biology, 2007, 3, e59.	3.2	849
59	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, 20274-20279.	7.1	132
60	Relating Three-Dimensional Structures to Protein Networks Provides Evolutionary Insights. Science, 2006, 314, 1938-1941.	12.6	447