## **Christina Kiel**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Network pharmacology: curing causal mechanisms instead of treating symptoms. Trends in Pharmacological Sciences, 2022, 43, 136-150.	4.0	294
2	Recognizing and Defining True Ras Binding Domains I: Biochemical Analysis. Journal of Molecular Biology, 2005, 348, 741-758.	2.0	154
3	Engineering Signal Transduction Pathways. Cell, 2010, 140, 33-47.	13.5	112
4	Recognizing and Defining True Ras Binding Domains II: In Silico Prediction Based on Homology Modelling and Energy Calculations. Journal of Molecular Biology, 2005, 348, 759-775.	2.0	101
5	Analysis of Disease-Linked Rhodopsin Mutations Based on Structure, Function, and Protein Stability Calculations. Journal of Molecular Biology, 2011, 405, 584-606.	2.0	86
6	Analyzing Protein Interaction Networks Using Structural Information. Annual Review of Biochemistry, 2008, 77, 415-441.	5.0	85
7	A Detailed Thermodynamic Analysis of Ras/Effector Complex Interfaces. Journal of Molecular Biology, 2004, 340, 1039-1058.	2.0	81
8	The Ubiquitin Domain Superfold: Structure-based Sequence Alignments and Characterization of Binding Epitopes. Journal of Molecular Biology, 2006, 355, 821-844.	2.0	72
9	Structures in systems biology. Current Opinion in Structural Biology, 2007, 17, 378-384.	2.6	67
10	Cell Type–Specific Importance of Ras–c-Raf Complex Association Rate Constants for MAPK Signaling. Science Signaling, 2009, 2, ra38.	1.6	63
11	Integration of Protein Abundance and Structure Data Reveals Competition in the ErbB Signaling Network. Science Signaling, 2013, 6, ra109.	1.6	48
12	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. Nature Communications, 2020, 11, 499.	5.8	42
13	Challenges ahead in signal transduction: MAPK as an example. Current Opinion in Biotechnology, 2012, 23, 305-314.	3.3	39
14	A Genome-wide Ras-Effector Interaction Network. Journal of Molecular Biology, 2007, 370, 1020-1032.	2.0	34
15	The yin–yang of kinase activation and unfolding explains the peculiarity of Val600 in the activation segment of BRAF. ELife, 2016, 5, e12814.	2.8	34
16	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. Molecular Systems Biology, 2011, 7, 551.	3.2	33
17	A Comprehensive View of the β-Arrestinome. Frontiers in Endocrinology, 2017, 8, 32.	1.5	29
18	Protein Conservation and Variation Suggest Mechanisms of Cell Type-Specific Modulation of Signaling Pathways. PLoS Computational Biology, 2014, 10, e1003659.	1.5	28

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19	The Ins and Outs of RAS Effector Complexes. Biomolecules, 2021, 11, 236.	1.8	27
20	Repository of proposed pathways and protein–protein interaction networks in age-related macular degeneration. Npj Aging and Mechanisms of Disease, 2020, 6, 2.	4.5	24
21	Cell Adhesion Molecules in Normal Skin and Melanoma. Biomolecules, 2021, 11, 1213.	1.8	21
22	Dissecting the Calcium-Induced Differentiation of Human Primary Keratinocytes Stem Cells by Integrative and Structural Network Analyses. PLoS Computational Biology, 2015, 11, e1004256.	1.5	20
23	Signaling pathways in intestinal homeostasis and colorectal cancer: KRAS at centre stage. Cell Communication and Signaling, 2021, 19, 31.	2.7	19
24	Predicted â€~wiring landscape' of Ras-effector interactions in 29 human tissues. Npj Systems Biology and Applications, 2021, 7, 10.	1.4	18
25	Interaction Dynamics Determine Signaling and Output Pathway Responses. Cell Reports, 2017, 19, 136-149.	2.9	15
26	Association Rate Constants of Ras-Effector Interactions Are Evolutionarily Conserved. PLoS Computational Biology, 2008, 4, e1000245.	1.5	14
27	Structural Data in Synthetic Biology Approaches for Studying General Design Principles of Cellular Signaling Networks. Structure, 2012, 20, 1806-1813.	1.6	14
28	Simple and complex retinal dystrophies are associated with profoundly different disease networks. Scientific Reports, 2017, 7, 41835.	1.6	14
29	Analysis of Ras-effector interaction competition in large intestine and colorectal cancer context. Small GTPases, 2021, 12, 209-225.	0.7	14
30	Combining Gene–Disease Associations with Single-Cell Gene Expression Data Provides Anatomy-Specific Subnetworks in Age-Related Macular Degeneration. Network and Systems Medicine, 2020, 3, 105-121.	2.7	13
31	Reconstruction and analysis of a large-scale binary Ras-effector signaling network. Cell Communication and Signaling, 2022, 20, 24.	2.7	12
32	SAPIN: A framework for the structural analysis of protein interaction networks. Bioinformatics, 2012, 28, 2998-2999.	1.8	10
33	Assessing the correlation between mutant rhodopsin stability and the severity of retinitis pigmentosa. Molecular Vision, 2014, 20, 183-99.	1.1	10
34	SnapShot: APC/T Cell Immune Checkpoints. Cell, 2020, 183, 1142-1142.e1.	13.5	9
35	From oncogenic mutation to dynamic code. Science, 2018, 361, 844-845.	6.0	6
36	Tuneable endogenous mammalian target complementation via multiplexed plasmid-based recombineering. Scientific Reports, 2015, 5, 17432.	1.6	4

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37	Opportunities and Challenges of Whole-Cell and -Tissue Simulations of the Outer Retina in Health and Disease. Annual Review of Biomedical Data Science, 2018, 1, 131-152.	2.8	4
38	Systems level expression correlation of Ras GTPase regulators. Cell Communication and Signaling, 2018, 16, 46.	2.7	4
39	HOMELETTE: a unified interface to homology modelling software. Bioinformatics, 2022, 38, 1749-1751.	1.8	4
40	Affinity Can have Many Faces: Thermodynamic and Kinetic Properties of Ras-Effector Complex Formation. Current Chemical Biology, 2007, 1, 215-225.	0.2	2
41	TAPAS: tools to assist the targeted protein quantification of human alternative splice variants. Bioinformatics, 2014, 30, 2989-2990.	1.8	2
42	Complexities in Quantitative Systems Analysis of Signaling Networks. , 2014, , 65-88.		2
43	Engineering of Biological Pathways: Complex Formation and Signal Transduction. Methods in Molecular Biology, 2021, 2315, 59-70.	0.4	2