Lukasz Salwinski

List of Publications by Year
in descending order

23 papers	6,221 citations	411340 20 h-index	685536 24 g-index
25 all docs	25 docs citations	25 times ranked	8094 citing authors

#	Article	IF	Citations
1	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	6.5	89
2	Bioinformatic identification of previously unrecognized amyloidogenic proteins. Journal of Biological Chemistry, 2022, 298, 101920.	1.6	4
3	Identifying amyloid-related diseases by mapping mutations in low-complexity protein domains to pathologies. Nature Structural and Molecular Biology, 2022, 29, 529-536.	3.6	11
4	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	5.8	49
5	The histone H3-H4 tetramer is a copper reductase enzyme. Science, 2020, 369, 59-64.	6.0	60
6	Bighead is a Wnt antagonist secreted by the *Xenopus* Spemann organizer that promotes Lrp6 endocytosis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9135-E9144.	3.3	38
7	Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. ELife, 2015, 4, e10935.	2.8	48
8	A new reference implementation of the PSICQUIC web service. Nucleic Acids Research, 2013, 41, W601-W606.	6.5	91
9	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	9.0	500
10	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	9.0	274
11	An Integrated Approach to Elucidate the Intra-Viral and Viral-Cellular Protein Interaction Networks of a Gamma-Herpesvirus. PLoS Pathogens, 2011, 7, e1002297.	2.1	37
12	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	0.9	31
13	Robust discrimination between self and non-self neurites requires thousands of Dscam1 isoforms. Nature, 2009, 461, 644-648.	13.7	147
14	Recurated protein interaction datasets. Nature Methods, 2009, 6, 860-861.	9.0	58
15	The MiSink Plugin: Cytoscape as a graphical interface to the Database of Interacting Proteins. Bioinformatics, 2007, 23, 2193-2195.	1.8	19
16	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. BMC Biology, 2007, 5, 44.	1.7	237
17	Submit Your Interaction Data the IMEx Way. Proteomics, 2007, 7, 28-34.	1.3	65
18	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	9.4	274

#	Article	IF	Citations
19	The Database of Interacting Proteins: 2004 update. Nucleic Acids Research, 2004, 32, 449D-451.	6.5	1,918
20	The HUPO PSI's Molecular Interaction format—a community standard for the representation of protein interaction data. Nature Biotechnology, 2004, 22, 177-183.	9.4	581
21	In silico simulation of biological network dynamics. Nature Biotechnology, 2004, 22, 1017-1019.	9.4	59
22	Computational methods of analysis of protein—protein interactions. Current Opinion in Structural Biology, 2003, 13, 377-382.	2.6	136
23	DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. Nucleic Acids Research, 2002, 30, 303-305.	6.5	1,487