

Katja Luck

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.

17
papers

2,020
citations

14
h-index

19
g-index

19
ext. papers

2,698
ext. citations

16.5
avg, IF

4.05
L-index

#	Paper	IF	Citations
17	A proteome-scale map of the human interactome network. <i>Cell</i> , 2014 , 159, 1212-1226	56.2	898
16	A reference map of the human binary protein interactome. <i>Nature</i> , 2020 , 580, 402-408	50.4	269
15	ELM--the database of eukaryotic linear motifs. <i>Nucleic Acids Research</i> , 2012 , 40, D242-51	20.1	251
14	Network-based prediction of protein interactions. <i>Nature Communications</i> , 2019 , 10, 1240	17.4	156
13	Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017 , 42, 342-354	10.3	95
12	The emerging contribution of sequence context to the specificity of protein interactions mediated by PDZ domains. <i>FEBS Letters</i> , 2012 , 586, 2648-61	3.8	82
11	Quantifying domain-ligand affinities and specificities by high-throughput holdup assay. <i>Nature Methods</i> , 2015 , 12, 787-93	21.6	49
10	The structural and dynamic response of MAGI-1 PDZ1 with noncanonical domain boundaries to the binding of human papillomavirus E6. <i>Journal of Molecular Biology</i> , 2011 , 406, 745-63	6.5	39
9	Putting into practice domain-linear motif interaction predictions for exploration of protein networks. <i>PLoS ONE</i> , 2011 , 6, e25376	3.7	36
8	Phage display can select over-hydrophobic sequences that may impair prediction of natural domain-peptide interactions. <i>Bioinformatics</i> , 2011 , 27, 899-902	7.2	33
7	KEPE--a motif frequently superimposed on sumoylation sites in metazoan chromatin proteins and transcription factors. <i>Bioinformatics</i> , 2009 , 25, 1-5	7.2	28
6	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018 , 430, 1024-1050	6.5	24
5	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019 , 10, 3907	17.4	21
4	Precision medicine - networks to the rescue. <i>Current Opinion in Biotechnology</i> , 2020 , 63, 177-189	11.4	17
3	A reference map of the human protein interactome		13
2	Network-based prediction of protein interactions		7
1	Towards an Essayome for binary interactome mapping		2

