

# Katja Luck

## List of Publications by Year in Descending Order

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

