

Katja Luck

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8299782/publications.pdf>

Version: 2024-02-01

15
papers

3,132
citations

623574

14
h-index

996849

15
g-index

19
all docs

19
docs citations

19
times ranked

5591
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226. | 13.5 | 1,199 |
| 2 | A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408. | 13.7 | 724 |
| 3 | Network-based prediction of protein interactions. <i>Nature Communications</i> , 2019, 10, 1240. | 5.8 | 293 |
| 4 | ELM—the database of eukaryotic linear motifs. <i>Nucleic Acids Research</i> , 2012, 40, D242-D251. | 6.5 | 290 |
| 5 | Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017, 42, 342-354. | 3.7 | 129 |
| 6 | The emerging contribution of sequence context to the specificity of protein interactions mediated by PDZ domains. <i>FEBS Letters</i> , 2012, 586, 2648-2661. | 1.3 | 108 |
| 7 | Quantifying domain-ligand affinities and specificities by high-throughput holdup assay. <i>Nature Methods</i> , 2015, 12, 787-793. | 9.0 | 80 |
| 8 | Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019, 10, 3907. | 5.8 | 57 |
| 9 | 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, 745-763. | 2.0 | 43 |
| 10 | Phage display can select over-hydrophobic sequences that may impair prediction of natural domain-peptide interactions. <i>Bioinformatics</i> , 2011, 27, 899-902. | 1.8 | 38 |
| 11 | Putting into Practice Domain-Linear Motif Interaction Predictions for Exploration of Protein Networks. <i>PLoS ONE</i> , 2011, 6, e25376. | 1.1 | 37 |
| 12 | KEPE—a motif frequently superimposed on sumoylation sites in metazoan chromatin proteins and transcription factors. <i>Bioinformatics</i> , 2009, 25, 1-5. | 1.8 | 34 |
| 13 | Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018, 430, 1024-1050. | 2.0 | 32 |
| 14 | Precision medicine — networks to the rescue. <i>Current Opinion in Biotechnology</i> , 2020, 63, 177-189. | 3.3 | 30 |
| 15 | The Eukaryotic Linear Motif Resource (ELM): Regulatory Sites in Proteins. <i>Nature Precedings</i> , 2009, , . | 0.1 | 1 |