

Martin H Schaefer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1198728/publications.pdf>

Version: 2024-02-01

23
papers

1,603
citations

567247

15
h-index

610883

24
g-index

30
all docs

30
docs citations

30
times ranked

2818
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of protein complex partners as a compensatory mechanism in aneuploid tumors. <i>ELife</i> , 2022, 11, .	6.0	7
2	Silencing of SRRM4 suppresses microexon inclusion and promotes tumor growth across cancers. <i>PLoS Biology</i> , 2021, 19, e3001138.	5.6	15
3	Translational adaptation of human viruses to the tissues they infect. <i>Cell Reports</i> , 2021, 34, 108872.	6.4	15
4	DNA methylation variation along the cancer epigenome and the identification of novel epigenetic driver events. <i>Nucleic Acids Research</i> , 2021, 49, 12692-12705.	14.5	10
5	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020, 32, 108050.	6.4	64
6	Mutation bias within oncogene families is related to proliferation-specific codon usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30848-30856.	7.1	20
7	MIPPIE: the mouse integrated protein-protein interaction reference. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	14
8	Generation and Interpretation of Context-Specific Human Protein-Protein Interaction Networks with HIPPIE. <i>Methods in Molecular Biology</i> , 2020, 2074, 135-144.	0.9	4
9	Translational efficiency across healthy and tumor tissues is proliferation-related. <i>Molecular Systems Biology</i> , 2020, 16, e9275.	7.2	42
10	Negative selection in tumor genome evolution acts on essential cellular functions and the immunopeptidome. <i>Genome Biology</i> , 2018, 19, 67.	8.8	81
11	Tissue-specific DNA methylation loss during ageing and carcinogenesis is linked to chromosome structure, replication timing and cell division rates. <i>Nucleic Acids Research</i> , 2018, 46, 7022-7039.	14.5	33
12	HIPPIE v2.0: enhancing meaningfulness and reliability of protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2017, 45, D408-D414.	14.5	401
13	Spatiotemporal Proteomic Profiling of Huntington's Disease Inclusions Reveals Widespread Loss of Protein Function. <i>Cell Reports</i> , 2017, 21, 2291-2303.	6.4	107
14	A Comprehensive View of the β -Arrestinome. <i>Frontiers in Endocrinology</i> , 2017, 8, 32.	3.5	29
15	Cell type-specific properties and environment shape tissue specificity of cancer genes. <i>Scientific Reports</i> , 2016, 6, 20707.	3.3	64
16	A network of epigenetic modifiers and DNA repair genes controls tissue-specific copy number alteration preference. <i>ELife</i> , 2016, 5, .	6.0	8
17	Correcting for the study bias associated with protein-protein interaction measurements reveals differences between protein degree distributions from different cancer types. <i>Frontiers in Genetics</i> , 2015, 6, 260.	2.3	63
18	Characterizing Protein Interactions Employing a Genome-Wide siRNA Cellular Phenotyping Screen. <i>PLoS Computational Biology</i> , 2014, 10, e1003814.	3.2	10

#	ARTICLE	IF	CITATIONS
19	Protein Conservation and Variation Suggest Mechanisms of Cell Type-Specific Modulation of Signaling Pathways. PLoS Computational Biology, 2014, 10, e1003659.	3.2	28
20	Adding Protein Context to the Human Protein-Protein Interaction Network to Reveal Meaningful Interactions. PLoS Computational Biology, 2013, 9, e1002860.	3.2	70
21	Evolution and function of CAG/polyglutamine repeats in protein-protein interaction networks. Nucleic Acids Research, 2012, 40, 4273-4287.	14.5	166
22	HIPPIE: Integrating Protein Interaction Networks with Experiment Based Quality Scores. PLoS ONE, 2012, 7, e31826.	2.5	297
23	Tissue-specific subnetworks and characteristics of publicly available human protein interaction databases. Bioinformatics, 2011, 27, 2414-2421.	4.1	46