

Benjamin Lang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/650178/publications.pdf>

Version: 2024-02-01

17
papers

2,926
citations

759233

12
h-index

888059

17
g-index

19
all docs

19
docs citations

19
times ranked

7286
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of long non-coding RNAs and RNA binding proteins in breast cancer subtypes. <i>Scientific Reports</i> , 2022, 12, 693.	3.3	14
2	DualSeqDB: the host-pathogen dual RNA sequencing database for infection processes. <i>Nucleic Acids Research</i> , 2021, 49, D687-D693.	14.5	11
3	A community effort to bring structure to disorder. <i>Nature Methods</i> , 2021, 18, 454-455.	19.0	19
4	Matrix-screening reveals a vast potential for direct protein-protein interactions among RNA binding proteins. <i>Nucleic Acids Research</i> , 2021, 49, 6702-6721.	14.5	10
5	Determination of primary microRNA processing in clinical samples by targeted pri-miR-sequencing. <i>Rna</i> , 2020, 26, 1726-1730.	3.5	5
6	BacFITBase: a database to assess the relevance of bacterial genes during host infection. <i>Nucleic Acids Research</i> , 2019, 48, D511-D516.	14.5	9
7	RNAct: Protein-RNA interaction predictions for model organisms with supporting experimental data. <i>Nucleic Acids Research</i> , 2019, 47, D601-D606.	14.5	80
8	The eukaryotic linear motif resource - 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.	14.5	183
9	An Integrative Study of Protein-RNA Condensates Identifies Scaffolding RNAs and Reveals Players in Fragile X-Associated Tremor/Ataxia Syndrome. <i>Cell Reports</i> , 2018, 25, 3422-3434.e7.	6.4	62
10	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline. <i>Nature Communications</i> , 2018, 9, 4004.	12.8	71
11	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.	6.4	192
12	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	47.7	1,618
13	Proteomic Analysis of Mitotic RNA Polymerase II Reveals Novel Interactors and Association With Proteins Dysfunctional in Disease. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011767.	3.8	13
14	Evolutionary selection for protein aggregation. <i>Biochemical Society Transactions</i> , 2012, 40, 1032-1037.	3.4	32
15	An Expanded Oct4 Interaction Network: Implications for Stem Cell Biology, Development, and Disease. <i>Cell Stem Cell</i> , 2010, 6, 382-395.	11.1	338
16	Methods to Reconstruct and Compare Transcriptional Regulatory Networks. <i>Methods in Molecular Biology</i> , 2009, 541, 163-180.	0.9	36
17	High-affinity DNA binding sites for H-NS provide a molecular basis for selective silencing within proteobacterial genomes. <i>Nucleic Acids Research</i> , 2007, 35, 6330-6337.	14.5	231