

Hannes Braberg

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

6,027
citations

516710

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610901

24
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28
docs citations

28
times ranked

12753
citing authors

#	ARTICLE	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	27.8	3,542
2	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	12.6	508
3	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	27.8	237
4	Functional Organization of the <i>S. cerevisiae</i> Phosphorylation Network. <i>Cell</i> , 2009, 136, 952-963.	28.9	235
5	A Genetic Interaction Map of RNA-Processing Factors Reveals Links between Sem1/Dss1-Containing Complexes and mRNA Export and Splicing. <i>Molecular Cell</i> , 2008, 32, 735-746.	9.7	221
6	High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . <i>Nature Methods</i> , 2008, 5, 781-787.	19.0	214
7	From Structure to Systems: High-Resolution, Quantitative Genetic Analysis of RNA Polymerase II. <i>Cell</i> , 2013, 154, 775-788.	28.9	132
8	A Lipid E-MAP Identifies Ubx2 as a Critical Regulator of Lipid Saturation and Lipid Bilayer Stress. <i>Molecular Cell</i> , 2013, 51, 519-530.	9.7	127
9	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 901-908.	8.2	93
10	SALIGN: a web server for alignment of multiple protein sequences and structures. <i>Bioinformatics</i> , 2012, 28, 2072-2073.	4.1	72
11	Protein complex compositions predicted by structural similarity. <i>Nucleic Acids Research</i> , 2006, 34, 2943-2952.	14.5	56
12	RNA Polymerase II Carboxyl-terminal Domain Phosphorylation Regulates Protein Stability of the Set2 Methyltransferase and Histone H3 Di- and Trimethylation at Lysine 36. <i>Journal of Biological Chemistry</i> , 2012, 287, 3249-3256.	3.4	50
13	Adventures in time and space. <i>RNA Biology</i> , 2014, 11, 313-319.	3.1	37
14	Systematic Triple-Mutant Analysis Uncovers Functional Connectivity between Pathways Involved in Chromosome Regulation. <i>Cell Reports</i> , 2013, 3, 2168-2178.	6.4	36
15	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	12.6	24
16	Individual Lysine Acetylations on the N Terminus of <i>Saccharomyces cerevisiae</i> H2A.Z Are Highly but Not Differentially Regulated. <i>Journal of Biological Chemistry</i> , 2010, 285, 39855-39865.	3.4	22
17	Nonsense-mediated decay regulates key components of homologous recombination. <i>Nucleic Acids Research</i> , 2016, 44, 5218-5230.	14.5	18
18	Quantitative analysis of triple-mutant genetic interactions. <i>Nature Protocols</i> , 2014, 9, 1867-1881.	12.0	15

#	ARTICLE	IF	CITATIONS
19	From systems to structure “ using genetic data to model protein structures. Nature Reviews Genetics, 2022, 23, 342-354.	16.8	14
20	Systems-level effects of allosteric perturbations to a model molecular switch. Nature, 2021, 599, 152-157.	27.8	13
21	Genetic analysis reveals functions of atypical polyubiquitin chains. ELife, 2018, 7, .	6.0	12
22	Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. Molecular Cell, 2021, 81, 2201-2215.e9.	9.7	10
23	Genetic interaction analysis of point mutations enables interrogation of gene function at a residue-level resolution. BioEssays, 2014, 36, 706-713.	2.5	9
24	Integrative structure determination of histones H3 and H4 using genetic interactions. FEBS Journal, 2023, 290, 2565-2575.	4.7	0