

# Hannes Braberg

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

6,027  
citations

516710

16  
h-index

610901

24  
g-index

28  
all docs

28  
docs citations

28  
times ranked

12753  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative structure determination of histones H3 and H4 using genetic interactions. FEBS Journal, 2023, 290, 2565-2575.	4.7	0
2	From systems to structure " using genetic data to model protein structures. Nature Reviews Genetics, 2022, 23, 342-354.	16.3	14
3	Evolution of enhanced innate immune evasion by SARS-CoV-2. Nature, 2022, 602, 487-495.	27.8	237
4	Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. Molecular Cell, 2021, 81, 2201-2215.e9.	9.7	10
5	Systems-level effects of allosteric perturbations to a model molecular switch. Nature, 2021, 599, 152-157.	27.8	13
6	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
7	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	12.6	24
8	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
9	Genetic analysis reveals functions of atypical polyubiquitin chains. ELife, 2018, 7, .	6.0	12
10	Nonsense-mediated decay regulates key components of homologous recombination. Nucleic Acids Research, 2016, 44, 5218-5230.	14.5	18
11	Genetic interaction analysis of point mutations enables interrogation of gene function at a residue-level resolution. BioEssays, 2014, 36, 706-713.	2.5	9
12	Adventures in time and space. RNA Biology, 2014, 11, 313-319.	3.1	37
13	Quantitative analysis of triple-mutant genetic interactions. Nature Protocols, 2014, 9, 1867-1881.	12.0	15
14	From Structure to Systems: High-Resolution, Quantitative Genetic Analysis of RNA Polymerase II. Cell, 2013, 154, 775-788.	28.9	132
15	A Lipid E-MAP Identifies Ubx2 as a Critical Regulator of Lipid Saturation and Lipid Bilayer Stress. Molecular Cell, 2013, 51, 519-530.	9.7	127
16	Systematic Triple-Mutant Analysis Uncovers Functional Connectivity between Pathways Involved in Chromosome Regulation. Cell Reports, 2013, 3, 2168-2178.	6.4	36
17	SALIGN: a web server for alignment of multiple protein sequences and structures. Bioinformatics, 2012, 28, 2072-2073.	4.1	72
18	RNA Polymerase II Carboxyl-terminal Domain Phosphorylation Regulates Protein Stability of the Set2 Methyltransferase and Histone H3 Di- and Trimethylation at Lysine 36. Journal of Biological Chemistry, 2012, 287, 3249-3256.	3.4	50

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Functional Organization of the <i>S. cerevisiae</i> Phosphorylation Network. <i>Cell</i> , 2009, 136, 952-963.	28.9	235
22	High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . <i>Nature Methods</i> , 2008, 5, 781-787.	19.0	214
23	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
24	Protein complex compositions predicted by structural similarity. <i>Nucleic Acids Research</i> , 2006, 34, 2943-2952.	14.5	56