Patrick Kemmeren

List of Publications by Year
in descending order

23 papers	2,394 citations	567281 15 h-index	677142 22 g-index
29 all docs	29 docs citations	29 times ranked	3848 citing authors

#	Article	IF	Citations
1	Improved Gene Fusion Detection in Childhood Cancer Diagnostics Using RNA Sequencing. JCO Precision Oncology, 2022, 6, e2000504.	3.0	9
2	Structural variant detection in cancer genomes: computational challenges and perspectives for precision oncology. Npj Precision Oncology, 2021, 5, 15.	5.4	30
3	A systematic analysis of genetic interactions and their underlying biology in childhood cancer. Communications Biology, 2021, 4, 1139.	4.4	2
4	DNA Methylation Profiling Identifies Distinct Clusters in Angiosarcomas. Clinical Cancer Research, 2020, 26, 93-100.	7.0	34
5	A framework for exhaustive modelling of genetic interaction patterns using Petri nets. Bioinformatics, 2020, 36, 2142-2149.	4.1	3
6	An Optimized Chromatin Immunoprecipitation Protocol for Quantification of Protein-DNA Interactions. STAR Protocols, 2020, 1, 100020.	1.2	15
7	An organoid biobank for childhood kidney cancers that captures disease and tissue heterogeneity. Nature Communications, 2020, 11, 1310.	12.8	183
8	Genome‐wide off‐rates reveal how DNA binding dynamics shape transcription factor function. Molecular Systems Biology, 2020, 16, e9885.	7.2	14
9	The ability of transcription factors to differentially regulate gene expression is a crucial component of the mechanism underlying inversion, a frequently observed genetic interaction pattern. PLoS Computational Biology, 2019, 15, e1007061.	3.2	4
10	Molecular mechanisms that distinguish TFIID housekeeping from regulatable SAGA promoters. EMBO Journal, 2017, 36, 274-290.	7.8	53
11	Growth condition dependency is the major cause of non-responsiveness upon genetic perturbation. PLoS ONE, 2017, 12, e0173432.	2.5	3
12	Proteome-wide Changes in Protein Turnover Rates in C.Âelegans Models of Longevity and Age-Related Disease. Cell Reports, 2016, 16, 3041-3051.	6.4	54
13	A high-resolution gene expression atlas of epistasis between gene-specific transcription factors exposes potential mechanisms for genetic interactions. BMC Biology, 2015, 13, 112.	3.8	21
14	The Genomic Landscape of Compensatory Evolution. PLoS Biology, 2014, 12, e1001935.	5.6	150
15	Cell cycle population effects in perturbation studies. Molecular Systems Biology, 2014, 10, 732.	7.2	118
16	Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors. Cell, 2014, 157, 740-752.	28.9	248
17	A Consensus of Core Protein Complex Compositions for Saccharomyces cerevisiae. Molecular Cell, 2010, 38, 916-928.	9.7	91
18	Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. Cell, 2010, 143, 991-1004.	28.9	123

#	Article	IF	Citations
19	Epistatic relationships reveal the functional organization of yeast transcription factors. Molecular Systems Biology, 2010, 6, 420.	7.2	50
20	Functional Organization of the S. cerevisiae Phosphorylation Network. Cell, 2009, 136, 952-963.	28.9	235
21	Toward a Comprehensive Atlas of the Physical Interactome of Saccharomyces cerevisiae. Molecular and Cellular Proteomics, 2007, 6, 439-450.	3.8	692
22	Predicting gene function through systematic analysis and quality assessment of high-throughput data. Bioinformatics, 2005, 21, 1644-1652.	4.1	24
23	Protein Interaction Verification and Functional Annotation by Integrated Analysis of Genome-Scale Data. Molecular Cell, 2002, 9, 1133-1143.	9.7	221