

# Sean R Collins

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

12,388  
citations

186265

28  
h-index

434195

31  
g-index

34  
all docs

34  
docs citations

34  
times ranked

13547  
citing authors

#	ARTICLE	IF	CITATIONS
1	Waves of actin and microtubule polymerization drive microtubule-based transport and neurite growth before single axon formation. <i>ELife</i> , 2016, 5, e12387.	6.0	70
2	Systematic Discovery of Human Gene Function and Principles of Modular Organization through Phylogenetic Profiling. <i>Cell Reports</i> , 2015, 10, 993-1006.	6.4	75
3	Set5 and Set1 cooperate to repress gene expression at telomeres and retrotransposons. <i>Epigenetics</i> , 2014, 9, 513-522.	2.7	28
4	Dynamic recruitment of the curvature-sensitive protein ArhGAP44 to nanoscale membrane deformations limits exploratory filopodia initiation in neurons. <i>ELife</i> , 2014, 3, e03116.	6.0	50
5	Hierarchical Modularity and the Evolution of Genetic Interactomes across Species. <i>Molecular Cell</i> , 2012, 46, 691-704.	9.7	185
6	Functional Repurposing Revealed by Comparing <i>S. pombe</i> and <i>S. cerevisiae</i> Genetic Interactions. <i>Cell</i> , 2012, 149, 1339-1352.	28.9	154
7	Evolutionary origins of STIM1 and STIM2 within ancient Ca <sup>2+</sup> signaling systems. <i>Trends in Cell Biology</i> , 2011, 21, 202-211.	7.9	89
8	A mitochondrial-focused genetic interaction map reveals a scaffold-like complex required for inner membrane organization in mitochondria. <i>Journal of Cell Biology</i> , 2011, 195, 323-340.	5.2	402
9	Site-specific acetylation mark on an essential chromatin-remodeling complex promotes resistance to replication stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10620-10625.	7.1	20
10	Orm family proteins mediate sphingolipid homeostasis. <i>FASEB Journal</i> , 2011, 25, 197.2.	0.5	0
11	Orm family proteins mediate sphingolipid homeostasis. <i>Nature</i> , 2010, 463, 1048-1053.	27.8	544
12	Quantitative Genetic Interaction Mapping Using the E-MAP Approach. <i>Methods in Enzymology</i> , 2010, 470, 205-231.	1.0	80
13	A Complex-based Reconstruction of the <i>Saccharomyces cerevisiae</i> Interactome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1361-1381.	3.8	96
14	From information to knowledge: new technologies for defining gene function. <i>Nature Methods</i> , 2009, 6, 721-723.	19.0	15
15	Functional Organization of the <i>S. cerevisiae</i> Phosphorylation Network. <i>Cell</i> , 2009, 136, 952-963.	28.9	235
16	Comprehensive Characterization of Genes Required for Protein Folding in the Endoplasmic Reticulum. <i>Science</i> , 2009, 323, 1693-1697.	12.6	646
17	An ER-Mitochondria Tethering Complex Revealed by a Synthetic Biology Screen. <i>Science</i> , 2009, 325, 477-481.	12.6	1,129
18	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008, 5, 711-718.	19.0	473

#	ARTICLE	IF	CITATIONS
19	High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . <i>Nature Methods</i> , 2008, 5, 781-787.	19.0	214
20	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
21	Conservation and Rewiring of Functional Modules Revealed by an Epistasis Map in Fission Yeast. <i>Science</i> , 2008, 322, 405-410.	12.6	328
22	CCR4/NOT complex associates with the proteasome and regulates histone methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5836-5841.	7.1	75
23	Toward a Comprehensive Atlas of the Physical Interactome of <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 439-450.	3.8	692
24	Backup without redundancy: genetic interactions reveal the cost of duplicate gene loss. <i>Molecular Systems Biology</i> , 2007, 3, 86.	7.2	143
25	Mec1/Tel1 Phosphorylation of the INO80 Chromatin Remodeling Complex Influences DNA Damage Checkpoint Responses. <i>Cell</i> , 2007, 130, 499-511.	28.9	116
26	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	27.8	806
27	A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. <i>Genome Biology</i> , 2006, 7, R63.	9.6	287
28	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	27.8	2,681
29	The physical basis of how prion conformations determine strain phenotypes. <i>Nature</i> , 2006, 442, 585-589.	27.8	552
30	Exploration of the Function and Organization of the Yeast Early Secretory Pathway through an Epistatic Miniarray Profile. <i>Cell</i> , 2005, 123, 507-519.	28.9	804
31	Cotranscriptional Set2 Methylation of Histone H3 Lysine 36 Recruits a Repressive Rpd3 Complex. <i>Cell</i> , 2005, 123, 593-605.	28.9	712
32	Mechanism of Prion Propagation: Amyloid Growth Occurs by Monomer Addition. <i>PLoS Biology</i> , 2004, 2, e321.	5.6	466