

GwenaÃ«l Rabut

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

3,251
citations

361296

20
h-index

580701

25
g-index

26
all docs

26
docs citations

26
times ranked

3704
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping the dynamic organization of the nuclear pore complex inside single living cells. <i>Nature Cell Biology</i> , 2004, 6, 1114-1121.	4.6	431
2	A complex of N-WASP and WIP integrates signalling cascades that lead to actin polymerization. <i>Nature Cell Biology</i> , 2000, 2, 441-448.	4.6	321
3	An evolutionarily conserved NPC subcomplex, which redistributes in part to kinetochores in mammalian cells. <i>Journal of Cell Biology</i> , 2001, 154, 1147-1160.	2.3	300
4	Function and regulation of protein neddylation. <i>EMBO Reports</i> , 2008, 9, 969-976.	2.0	290
5	The Entire Nup107-160 Complex, Including Three New Members, Is Targeted as One Entity to Kinetochores in Mitosis. <i>Molecular Biology of the Cell</i> , 2004, 15, 3333-3344.	0.9	250
6	Systematic kinetic analysis of mitotic dis- and reassembly of the nuclear pore in living cells. <i>Journal of Cell Biology</i> , 2008, 180, 857-865.	2.3	231
7	Differential Inhibition of Human Immunodeficiency Virus Type 1 Fusion, gp120 Binding, and CC-Chemokine Activity by Monoclonal Antibodies to CCR5. <i>Journal of Virology</i> , 1999, 73, 4145-4155.	1.5	205
8	Protein quality control at the inner nuclear membrane. <i>Nature</i> , 2014, 516, 410-413.	13.7	188
9	Nuclear envelope breakdown in starfish oocytes proceeds by partial NPC disassembly followed by a rapidly spreading fenestration of nuclear membranes. <i>Journal of Cell Biology</i> , 2003, 160, 1055-1068.	2.3	141
10	Automatic real-time three-dimensional cell tracking by fluorescence microscopy. <i>Journal of Microscopy</i> , 2004, 216, 131-137.	0.8	137
11	Alanine Substitutions of Polar and Nonpolar Residues in the Amino-Terminal Domain of CCR5 Differently Impair Entry of Macrophage- and Dualtropic Isolates of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 1998, 72, 3464-3468.	1.5	120
12	RanBP2/Nup358 Provides a Major Binding Site for NXF1-p15 Dimers at the Nuclear Pore Complex and Functions in Nuclear mRNA Export. <i>Molecular and Cellular Biology</i> , 2004, 24, 1155-1167.	1.1	98
13	Fluorescence Perturbation Techniques to Study Mobility and Molecular Dynamics of Proteins in Live Cells: FRAP, Photoactivation, Photoconversion, and FLIP. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.top90.	0.2	94
14	CSN- and CAND1-dependent remodelling of the budding yeast SCF complex. <i>Nature Communications</i> , 2013, 4, 1641.	5.8	92
15	Rtt101 and Mms1 in budding yeast form a CUL4 ^{DDB1} -like ubiquitin ligase that promotes replication through damaged DNA. <i>EMBO Reports</i> , 2008, 9, 1034-1040.	2.0	91
16	Dynamics of nuclear pore complex organization through the cell cycle. <i>Current Opinion in Cell Biology</i> , 2004, 16, 314-321.	2.6	86
17	Expression of EGFP-amino-tagged human mu opioid receptor in Drosophila Schneider 2 cells: a potential expression system for large-scale production of G-protein coupled receptors. <i>Protein Expression and Purification</i> , 2003, 31, 123-132.	0.6	43
18	The TFIIH Subunit Tfb3 Regulates Cullin Neddylation. <i>Molecular Cell</i> , 2011, 43, 488-495.	4.5	39

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19	Structural Analysis of the Conserved Ubiquitin-binding Motifs (UBMs) of the Translesion Polymerase Iota in Complex with Ubiquitin. <i>Journal of Biological Chemistry</i> , 2011, 286, 1364-1373.	1.6	36
20	Nucleocytoplasmic transport: Diffusion channel or phase transition?. <i>Current Biology</i> , 2001, 11, R551-R554.	1.8	23
21	Protein-fragment complementation assays for large-scale analysis of protein-protein interactions. <i>Biochemical Society Transactions</i> , 2021, 49, 1337-1348.	1.6	16
22	Sensitive detection of protein ubiquitylation using a protein fragment complementation assay. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	10
23	Bimolecular Fluorescence Complementation to Assay the Interactions of Ubiquitylation Enzymes in Living Yeast Cells. <i>Methods in Molecular Biology</i> , 2016, 1449, 223-241.	0.4	4
24	Towards a reproducible interactome: semantic-based detection of redundancies to unify protein-protein interaction databases. <i>Bioinformatics</i> , 2022, 38, 1685-1691.	1.8	3
25	Introduction to the pervasive role of ubiquitin-dependent protein degradation in cell regulation. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 481.	2.3	2