Gwenal Rabut

List of Publications by Year in Descending Order

23 papers	2,778 citations	20 h-index	26 g-index
26 ext. papers	3,055 ext. citations	9.3 avg, IF	4.61 L-index

#	Paper	IF	Citations
23	Protein-fragment complementation assays for large-scale analysis of protein-protein interactions. *Biochemical Society Transactions*, **2021**, 49, 1337-1348	5.1	2
22	Sensitive detection of protein ubiquitylation using a protein fragment complementation assay. *Journal of Cell Science*, **2020**, 133,	5.3	4
21	Bimolecular Fluorescence Complementation to Assay the Interactions of Ubiquitylation Enzymes in Living Yeast Cells. *Methods in Molecular Biology*, **2016**, 1449, 223-41	1.4	3
20	Protein quality control at the inner nuclear membrane. *Nature*, **2014**, 516, 410-3	50.4	134
19	CSN- and CAND1-dependent remodelling of the budding yeast SCF complex. *Nature Communications*, **2013**, 4, 1641	17.4	76
18	The TFIIH subunit Tfb3 regulates cullin neddylation. *Molecular Cell*, **2011**, 43, 488-95	17.6	35
17	Structural analysis of the conserved ubiquitin-binding motifs (UBMs) of the translesion polymerase iota in complex with ubiquitin. *Journal of Biological Chemistry*, **2011**, 286, 1364-73	5.4	34
16	Fluorescence perturbation techniques to study mobility and molecular dynamics of proteins in live cells: FRAP, photoactivation, photoconversion, and FLIP. *Cold Spring Harbor Protocols*, **2010**, 2010, pdb.top90	1.2	70
15	Rtt101 and Mms1 in budding yeast form a CUL4(DDB1)-like ubiquitin ligase that promotes replication through damaged DNA. *EMBO Reports*, **2008**, 9, 1034-40	6.5	76
14	Function and regulation of protein neddylation. ‘Protein modifications: beyond the usual suspects’ review series. *EMBO Reports*, **2008**, 9, 969-76	6.5	242
13	Systematic kinetic analysis of mitotic dis- and reassembly of the nuclear pore in living cells. *Journal of Cell Biology*, **2008**, 180, 857-65	7.3	197
12	RanBP2/Nup358 provides a major binding site for NXF1-p15 dimers at the nuclear pore complex and functions in nuclear mRNA export. *Molecular and Cellular Biology*, **2004**, 24, 1155-67	4.8	79
11	The entire Nup107-160 complex, including three new members, is targeted as one entity to kinetochores in mitosis. *Molecular Biology of the Cell*, **2004**, 15, 3333-44	3.5	218
10	Automatic real-time three-dimensional cell tracking by fluorescence microscopy. *Journal of Microscopy*, **2004**, 216, 131-7	1.9	123
9	Mapping the dynamic organization of the nuclear pore complex inside single living cells. *Nature Cell Biology*, **2004**, 6, 1114-21	23.4	364
8	Dynamics of nuclear pore complex organization through the cell cycle. *Current Opinion in Cell Biology*, **2004**, 16, 314-21	9	81
7	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. *Protein Expression and Purification*, **2003**, 31, 123-32	2	40

6	Nuclear envelope breakdown in starfish oocytes proceeds by partial NPC disassembly followed by a rapidly spreading fenestration of nuclear membranes. *Journal of Cell Biology*, **2003**, 160, 1055-68	7.3	126
5	Nucleocytoplasmic transport: diffusion channel or phase transition?. *Current Biology*, **2001**, 11, R551-4	6.3	21
4	An evolutionarily conserved NPC subcomplex, which redistributes in part to kinetochores in mammalian cells. *Journal of Cell Biology*, **2001**, 154, 1147-60	7.3	276
3	A complex of N-WASP and WIP integrates signalling cascades that lead to actin polymerization. *Nature Cell Biology*, **2000**, 2, 441-8	23.4	284
2	Differential inhibition of human immunodeficiency virus type 1 fusion, gp120 binding, and CC-chemokine activity by monoclonal antibodies to CCR5. *Journal of Virology*, **1999**, 73, 4145-55	6.6	182
1	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. *Journal of Virology*, **1998**, 72, 3464-8	6.6	109