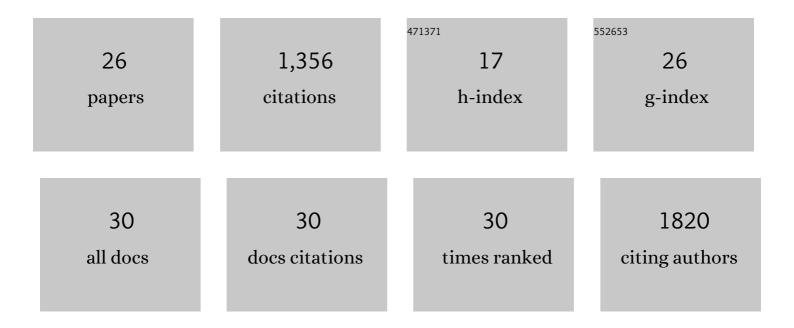
## Jerome Basquin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8210940/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Structural and Biochemical Insights to the Role of the CCR4-NOT Complex and DDX6 ATPase in MicroRNA Repression. Molecular Cell, 2014, 54, 751-765.	4.5	276
2	Structure of Full-Length SMC and Rearrangements Required for Chromosome Organization. Molecular Cell, 2017, 67, 334-347.e5.	4.5	151
3	Architecture of the Nuclease Module of the Yeast Ccr4-Not Complex: the Not1-Caf1-Ccr4 Interaction. Molecular Cell, 2012, 48, 207-218.	4.5	131
4	Self-organization of <i>parS</i> centromeres by the ParB CTP hydrolase. Science, 2019, 366, 1129-1133.	6.0	110
5	Structure of a Human 4E-T/DDX6/CNOT1 Complex Reveals the Different Interplay of DDX6-Binding Proteins with the CCR4-NOT Complex. Cell Reports, 2015, 13, 703-711.	2.9	95
6	Insights into catalysis and function of phosphoribosyl-linked serine ubiquitination. Nature, 2018, 557, 734-738.	13.7	84
7	Structural basis of outer dynein arm intraflagellar transport by the transport adaptor protein ODA16 and the intraflagellar transport protein IFT46. Journal of Biological Chemistry, 2017, 292, 7462-7473.	1.6	48
8	Distinct and evolutionary conserved structural features of the human nuclear exosome complex. ELife, 2018, 7, .	2.8	47
9	Sen1 has unique structural features grafted on the architecture of the Upf1â€like helicase family. EMBO Journal, 2017, 36, 1590-1604.	3.5	45
10	Structural insights into the interaction of the nuclear exosome helicase Mtr4 with the preribosomal protein Nop53. Rna, 2017, 23, 1780-1787.	1.6	42
11	The MTR4 helicase recruits nuclear adaptors of the human RNA exosome using distinct arch-interacting motifs. Nature Communications, 2019, 10, 3393.	5.8	41
12	Binding of IFT22 to the intraflagellar transport complex is essential for flagellum assembly. EMBO Journal, 2019, 38, .	3.5	38
13	Crystal structure of intraflagellar transport protein 80 reveals a homo-dimer required for ciliogenesis. ELife, 2018, 7, .	2.8	36
14	Architecture of the Ubiquitylation Module of the Yeast Ccr4-Not Complex. Structure, 2015, 23, 921-928.	1.6	33
15	Nse5/6 inhibits the Smc5/6 ATPase and modulates DNA substrate binding. EMBO Journal, 2021, 40, e107807.	3.5	30
16	CUL5-ARIH2 E3-E3 ubiquitin ligase structure reveals cullin-specific NEDD8 activation. Nature Chemical Biology, 2021, 17, 1075-1083.	3.9	30
17	Long-wavelength native-SAD phasing: opportunities and challenges. IUCrJ, 2019, 6, 373-386.	1.0	22
18	Structural insights into the nucleic acid remodeling mechanisms of the yeast THO-Sub2 complex. ELife, 2020.9	2.8	21

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19	To Process or to Decay: A Mechanistic View of the Nuclear RNA Exosome. Cold Spring Harbor Symposia on Quantitative Biology, 2019, 84, 155-163.	2.0	16
20	Multifaceted N-Degron Recognition and Ubiquitylation by GID/CTLH E3 Ligases. Journal of Molecular Biology, 2022, 434, 167347.	2.0	15
21	Structural basis of PETISCO complex assembly during piRNA biogenesis in <i>C. elegans</i> . Genes and Development, 2021, 35, 1304-1323.	2.7	14
22	Purification and crystal structure of human ODA16 : Implications for ciliary import of outer dynein arms by the intraflagellar transport machinery. Protein Science, 2020, 29, 1502-1510.	3.1	12
23	A rod conformation of the <i>Pyrococcus furiosus</i> Rad50 coiled coil. Proteins: Structure, Function and Bioinformatics, 2021, 89, 251-255.	1.5	8
24	Evolution of a histone variant involved in compartmental regulation of NAD metabolism. Nature Structural and Molecular Biology, 2021, 28, 1009-1019.	3.6	7
25	Complex Reconstitution from Individual Protein Modules. Advances in Experimental Medicine and Biology, 2016, 896, 305-314.	0.8	3
26	Substrate-Based Design of Cytosolic Nucleotidase IIIB Inhibitors and Structural Insights into Inhibition Mechanism. Pharmaceuticals, 2022, 15, 554.	1.7	1