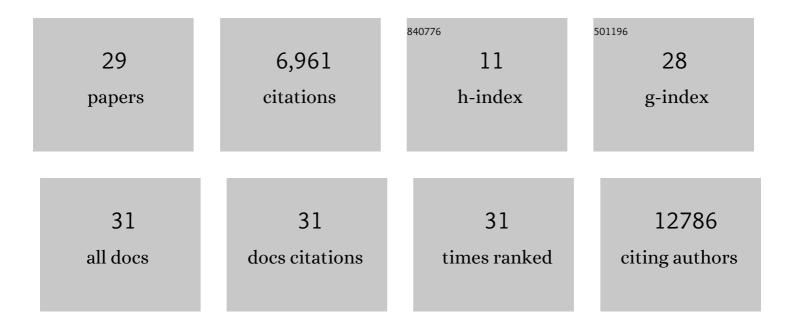
Xavier Robert

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Scaffolding Protein GspB/OutB Facilitates Assembly of the Dickeya dadantii Type 2 Secretion System by Anchoring the Outer Membrane Secretin Pore to the Inner Membrane and to the Peptidoglycan Cell Wall. MBio, 2022, 13, e0025322.	4.1	2
2	ldentification of 2-(4-N,N-Dimethylaminophenyl)-5-methyl-1-phenethyl-1H-benzimidazole targeting HIV-1 CA capsid protein and inhibiting HIV-1 replication in cellulo. BMC Pharmacology & Toxicology, 2022, 23, .	2.4	0
3	Structure–function analysis of pectate lyase Pel3 reveals essential facets of protein recognition by the bacterial type 2 secretion system. Journal of Biological Chemistry, 2021, 296, 100305.	3.4	6
4	Pyrazol(in)e derivatives of curcumin analogs as a new class of anti-Trypanosoma cruzi agents. Future Medicinal Chemistry, 2021, 13, 701-714.	2.3	5
5	Identification of a Potential Inhibitor of the FIV p24 Capsid Protein and Characterization of Its Binding Site. Biochemistry, 2021, 60, 1896-1908.	2.5	3
6	Exploring molecular determinants of <i>polysaccharide lyase family 6–1 enzyme</i> activity. Glycobiology, 2021, 31, 1557-1570.	2.5	9
7	Novel and selective inactivators of Triosephosphate isomerase with anti-trematode activity. Scientific Reports, 2020, 10, 2587.	3.3	12
8	Human H4 tail stimulates HIV-1 integration through binding to the carboxy-terminal domain of integrase. Nucleic Acids Research, 2019, 47, 3607-3618.	14.5	15
9	Looking for Novel Capsid Protein Multimerization Inhibitors of Feline Immunodeficiency Virus. Pharmaceuticals, 2018, 11, 67.	3.8	7
10	Au courant computation of the PDB to audit diffraction anisotropy of soluble and membrane proteins. Data in Brief, 2018, 19, 753-757.	1.0	3
11	Identification and visualization of protein binding regions with the ArDock server. Nucleic Acids Research, 2018, 46, W417-W422.	14.5	11
12	X-ray diffraction reveals the intrinsic difference in the physical properties of membrane and soluble proteins. Scientific Reports, 2017, 7, 17013.	3.3	13
13	Modulation of the functional association between the HIV-1 intasome and the nucleosome by histone amino-terminal tails. Retrovirology, 2017, 14, 54.	2.0	15
14	Deciphering key features in protein structures with the new ENDscript server. Nucleic Acids Research, 2014, 42, W320-W324.	14.5	5,136
15	Substrate recognition by the bacterial type <scp>II</scp> secretion system: more than a simple interaction. Molecular Microbiology, 2014, 94, 126-140.	2.5	38
16	Mutations inducing an active-site aperture inRhizobiumsp. sucrose isomerase confer hydrolytic activity. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 298-307.	2.5	11
17	PelN Is a New Pectate Lyase of Dickeya dadantii with Unusual Characteristics. Journal of Bacteriology, 2013, 195, 2197-2206.	2.2	48
18	Dynamic Interplay between the Periplasmic and Transmembrane Domains of GspL and GspM in the Type II Secretion System, PLoS ONE, 2013, 8, e79562.	2.5	34

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19	A Crystal Structure of the Catalytic Core Domain of an Avian Sarcoma and Leukemia Virus Integrase Suggests an Alternate Dimeric Assembly. PLoS ONE, 2011, 6, e23032.	2.5	11
20	The Extended Conformation of the 2.9-Ã Crystal Structure of the Three-PASTA Domain of a Ser/Thr Kinase from the Human Pathogen Staphylococcus aureus. Journal of Molecular Biology, 2010, 404, 847-858.	4.2	40
21	Structural determinants of product specificity of sucrose isomerases. FEBS Letters, 2009, 583, 1964-1968.	2.8	22
22	Crystallization and initial X-ray diffraction study of the three PASTA domains of the Ser/Thr kinase Stk1 from the human pathogenStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1187-1189.	0.7	2
23	Multiâ€site substrate binding and interplay in barley αâ€amylase 1. FEBS Letters, 2008, 582, 2567-2571.	2.8	18
24	Insights into sucrose isomerization from crystal structures of thePseudomonas mesoacidophilaMX-45 sucrose isomerase, MutB. Biocatalysis and Biotransformation, 2008, 26, 111-119.	2.0	5
25	Trehalulose Synthase Native and Carbohydrate Complexed Structures Provide Insights into Sucrose Isomerization. Journal of Biological Chemistry, 2007, 282, 28126-28136.	3.4	69
26	Oligosaccharide Binding to Barley α-Amylase 1. Journal of Biological Chemistry, 2005, 280, 32968-32978.	3.4	67
27	The Structure of Barley α-Amylase Isozyme 1 Reveals a Novel Role of Domain C in Substrate Recognition and Binding. Structure, 2003, 11, 973-984.	3.3	142
28	ESPript/ENDscript: extracting and rendering sequence and 3D information from atomic structures of proteins. Nucleic Acids Research, 2003, 31, 3320-3323.	14.5	1,207
29	Expression, purification and preliminary crystallographic studies of α-amylase isozyme 1 from barley seeds. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 683-686.	2.5	10