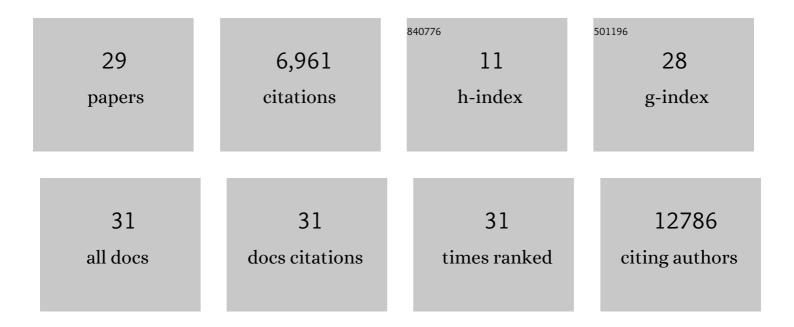
## Xavier Robert

List of Publications by Year in descending order

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XAVIED POREDT

| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Deciphering key features in protein structures with the new ENDscript server. Nucleic Acids Research, 2014, 42, W320-W324.  | 14.5 | 5,136     |
| 2  | 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     |
| 3  | 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       |
| 4  | Trehalulose Synthase Native and Carbohydrate Complexed Structures Provide Insights into Sucrose<br>Isomerization. Journal of Biological Chemistry, 2007, 282, 28126-28136.                                    | 3.4  | 69        |
| 5  | Oligosaccharide Binding to Barley α-Amylase 1. Journal of Biological Chemistry, 2005, 280, 32968-32978.   | 3.4  | 67        |
| 6  | PelN Is a New Pectate Lyase of Dickeya dadantii with Unusual Characteristics. Journal of Bacteriology,<br>2013, 195, 2197-2206.   | 2.2  | 48        |
| 7  | The Extended Conformation of the 2.9-Ã Crystal Structure of the Three-PASTA Domain of a Ser/Thr<br>Kinase from the Human Pathogen Staphylococcus aureus. Journal of Molecular Biology, 2010, 404,<br>847-858. | 4.2  | 40        |
| 8  | 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        |
| 9  | Dynamic Interplay between the Periplasmic and Transmembrane Domains of GspL and GspM in the Type II<br>Secretion System. PLoS ONE, 2013, 8, e79562.   | 2.5  | 34        |
| 10 | Structural determinants of product specificity of sucrose isomerases. FEBS Letters, 2009, 583, 1964-1968.   | 2.8  | 22        |
| 11 | Multiâ€site substrate binding and interplay in barley αâ€amylase 1. FEBS Letters, 2008, 582, 2567-2571.   | 2.8  | 18        |
| 12 | 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        |
| 13 | 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        |
| 14 | X-ray diffraction reveals the intrinsic difference in the physical properties of membrane and soluble proteins. Scientific Reports, 2017, 7, 17013.   | 3.3  | 13        |
| 15 | Novel and selective inactivators of Triosephosphate isomerase with anti-trematode activity. Scientific<br>Reports, 2020, 10, 2587.  | 3.3  | 12        |
| 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 | Identification and visualization of protein binding regions with the ArDock server. Nucleic Acids<br>Research, 2018, 46, W417-W422.   | 14.5 | 11        |
| 18 | A Crystal Structure of the Catalytic Core Domain of an Avian Sarcoma and Leukemia Virus Integrase<br>Suggests an Alternate Dimeric Assembly. PLoS ONE, 2011, 6, e23032.                                       | 2.5  | 11        |

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| #  | Article   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | 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        |
| 20 | Exploring molecular determinants of <i>polysaccharide lyase family 6–1 enzyme</i> activity.<br>Glycobiology, 2021, 31, 1557-1570.   | 2.5 | 9         |
| 21 | Looking for Novel Capsid Protein Multimerization Inhibitors of Feline Immunodeficiency Virus.<br>Pharmaceuticals, 2018, 11, 67.   | 3.8 | 7         |
| 22 | 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         |
| 23 | Insights into sucrose isomerization from crystal structures of thePseudomonas<br>mesoacidophilaMX-45 sucrose isomerase, MutB. Biocatalysis and Biotransformation, 2008, 26, 111-119.  | 2.0 | 5         |
| 24 | Pyrazol(in)e derivatives of curcumin analogs as a new class of anti-Trypanosoma cruzi agents. Future<br>Medicinal Chemistry, 2021, 13, 701-714.   | 2.3 | 5         |
| 25 | 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         |
| 26 | 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         |
| 27 | Crystallization and initial X-ray diffraction study of the three PASTA domains of the Ser/Thr kinase<br>Stk1 from the human pathogenStaphylococcus aureus. Acta Crystallographica Section F: Structural<br>Biology Communications, 2009, 65, 1187-1189. | 0.7 | 2         |
| 28 | Scaffolding Protein GspB/OutB Facilitates Assembly of the Dickeya dadantii Type 2 Secretion System by<br>Anchoring the Outer Membrane Secretin Pore to the Inner Membrane and to the Peptidoglycan Cell<br>Wall. MBio, 2022, 13, e0025322.              | 4.1 | 2         |
| 29 | Identification of 2-(4-N,N-Dimethylaminophenyl)-5-methyl-1-phenethyl-1H-benzimidazole targeting HIV-1<br>CA capsid protein and inhibiting HIV-1 replication in cellulo. BMC Pharmacology & Toxicology,<br>2022, 23, .                                   | 2.4 | 0         |