

# Alain Roussel

## List of Publications by Year in descending order

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64  
papers

4,392  
citations

94433

37  
h-index

110387

64  
g-index

64  
all docs

64  
docs citations

64  
times ranked

5079  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 detection using a nanobody-functionalized voltammetric device. <i>Communications Medicine</i> , 2022, 2, .	4.2	16
2	Sensing of COVID-19 spike protein in nasopharyngeal samples using a portable surface plasmon resonance diagnostic system. <i>Sensors &amp; Diagnostics</i> , 2022, 1, 1021-1031.	3.8	8
3	Preanalytical Issues and Cycle Threshold Values in SARS-CoV-2 Real-Time RT-PCR Testing: Should Test Results Include These?. <i>ACS Omega</i> , 2021, 6, 6528-6536.	3.5	63
4	Macromolecular interactions in vitro, comparing classical and novel approaches. <i>European Biophysics Journal</i> , 2021, 50, 313-330.	2.2	5
5	Anchoring the T6SS to the cell wall: Crystal structure of the peptidoglycan binding domain of the TagL accessory protein. <i>PLoS ONE</i> , 2021, 16, e0254232.	2.5	7
6	Novel <i>ACTN1</i> variants in cases of thrombocytopenia. <i>Human Mutation</i> , 2019, 40, 2258-2269.	2.5	5
7	A simple and versatile microfluidic device for efficient biomacromolecule crystallization and structural analysis by serial crystallography. <i>IUCr</i> , 2019, 6, 454-464.	2.2	23
8	Characterization of the <i>Porphyromonas gingivalis</i> Type IX Secretion Trans-envelope PorKLMNP Core Complex. <i>Journal of Biological Chemistry</i> , 2017, 292, 3252-3261.	3.4	60
9	TssA: The cap protein of the Type VI secretion system tail. <i>BioEssays</i> , 2017, 39, 1600262.	2.5	37
10	A phospholipase A <sub>1</sub> antibacterial Type VI secretion effector interacts directly with the C-terminal domain of the VgrG spike protein for delivery. <i>Molecular Microbiology</i> , 2016, 99, 1099-1118.	2.5	179
11	Cytokine Dieldel and a viral homologue suppress the IMD pathway in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 698-703.	7.1	67
12	Tissue-Specific Regulation of <i>Drosophila</i> NF- $\kappa$ B Pathway Activation by Peptidoglycan Recognition Protein SC. <i>Journal of Innate Immunity</i> , 2016, 8, 67-80.	3.8	43
13	X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. <i>Journal of Biological Chemistry</i> , 2015, 290, 13191-13201.	3.4	33
14	Biogenesis and structure of a type VI secretion membrane core complex. <i>Nature</i> , 2015, 523, 555-560.	27.8	241
15	Inhibition of Type VI Secretion by an Anti-TssM Llama Nanobody. <i>PLoS ONE</i> , 2015, 10, e0122187.	2.5	16
16	Bile-mediated activation of the <i>acrAB</i> and <i>tolC</i> multidrug efflux genes occurs mainly through transcriptional derepression of <i>ramA</i> in <i>Salmonella enterica</i> serovar Typhimurium. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2400-2406.	3.0	39
17	A Cutinase from <i>Trichoderma reesei</i> with a Lid-Covered Active Site and Kinetic Properties of True Lipases. <i>Journal of Molecular Biology</i> , 2014, 426, 3757-3772.	4.2	47
18	Crystal Structure and Self-Interaction of the Type VI Secretion Tail-Tube Protein from Enteroaggregative <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e86918.	2.5	44

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19	Molecular Engineering of Fungal GH5 and GH26 Beta-(1,4)-Mannanases toward Improvement of Enzyme Activity. PLoS ONE, 2013, 8, e79800.	2.5	26
20	Structural and Biochemical Analyses of Glycoside Hydrolase Families 5 and 26 $\beta$ -(1,4)-Mannanases from <i>Podospira anserina</i> Reveal Differences upon Manno-oligosaccharide Catalysis. Journal of Biological Chemistry, 2013, 288, 14624-14635.	3.4	80
21	Functional Analysis of PGRP-LA in <i>Drosophila</i> Immunity. PLoS ONE, 2013, 8, e69742.	2.5	56
22	Binding of the RamR Repressor to Wild-Type and Mutated Promoters of the <i>ramA</i> Gene Involved in Efflux-Mediated Multidrug Resistance in <i>Salmonella enterica</i> Serovar Typhimurium. Antimicrobial Agents and Chemotherapy, 2012, 56, 942-948.	3.2	43
23	Tissue- and Ligand-Specific Sensing of Gram-Negative Infection in <i>Drosophila</i> by PGRP-LC Isoforms and PGRP-LE. Journal of Immunology, 2012, 189, 1886-1897.	0.8	125
24	Crystal structure of greglin, a novel nonclassical Kazal inhibitor, in complex with subtilisin. FEBS Journal, 2012, 279, 4466-4478.	4.7	13
25	Crystal Structure of Diedel, a Marker of the Immune Response of <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e33416.	2.5	17
26	The <i>Drosophila</i> peptidoglycan recognition protein LF interacts with peptidoglycan recognition protein LC to downregulate the Imd pathway. EMBO Reports, 2011, 12, 327-333.	4.5	71
27	Structure-Function Analysis of Grass Clip Serine Protease Involved in <i>Drosophila</i> Toll Pathway Activation. Journal of Biological Chemistry, 2011, 286, 12300-12307.	3.4	29
28	Monalysin, a Novel Pore-Forming Toxin from the <i>Drosophila</i> Pathogen <i>Pseudomonas entomophila</i> , Contributes to Host Intestinal Damage and Lethality. PLoS Pathogens, 2011, 7, e1002259.	4.7	101
29	The N-terminal Domain of <i>Drosophila</i> Gram-negative Binding Protein 3 (GNBP3) Defines a Novel Family of Fungal Pattern Recognition Receptors. Journal of Biological Chemistry, 2009, 284, 28687-28697.	3.4	51
30	Structure of <i>Locusta migratoria</i> protease inhibitor 3 (LMPI-3) in complex with <i>Fusarium oxysporum</i> trypsin. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1165-1171.	2.5	3
31	Crystal structure of <i>Drosophila</i> PGRP-SD suggests binding to DAP-type but not lysine-type peptidoglycan. Molecular Immunology, 2008, 45, 2521-2530.	2.2	76
32	How much can a T-cell antigen receptor adapt to structurally distinct antigenic peptides?. EMBO Journal, 2007, 26, 1972-1983.	7.8	89
33	Resolution of the structure of the allergenic and antifungal banana fruit thaumatin-like protein at 1.7-Å. Biochimie, 2006, 88, 45-52.	2.6	77
34	Crystal structure at 1.45-Å resolution of the major allergen endo- $\beta$ -1,3-glucanase of banana as a molecular basis for the latex-fruit syndrome. Proteins: Structure, Function and Bioinformatics, 2006, 63, 235-242.	2.6	40
35	Structure and Interactions at the Viral Surface of the Envelope Protein E1 of Semliki Forest Virus. Structure, 2006, 14, 75-86.	3.3	118
36	Distinct orientation of the alloreactive monoclonal CD8 T cell activation program by three different peptide/MHC complexes. European Journal of Immunology, 2006, 36, 1856-1866.	2.9	19

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37	An Archaeal Peptidase Assembles into Two Different Quaternary Structures. <i>Journal of Biological Chemistry</i> , 2006, 281, 36327-36337.	3.4	35
38	Emergence of a subfamily of xylanase inhibitors within glycoside hydrolase family 18. <i>FEBS Journal</i> , 2005, 272, 1745-1755.	4.7	74
39	Structure-Activity Relationship Within the Serine Protease Inhibitors of the Pacifastin Family. <i>Protein and Peptide Letters</i> , 2005, 12, 409-414.	0.9	20
40	The H-2KkMHC Peptide-Binding Groove Anchors the Backbone of an Octameric Antigenic Peptide in an Unprecedented Mode. <i>Journal of Immunology</i> , 2005, 175, 3819-3825.	0.8	9
41	Conformational change and protein-protein interactions of the fusion protein of Semliki Forest virus. <i>Nature</i> , 2004, 427, 320-325.	27.8	332
42	Expression, refolding, crystallization and preliminary crystallographic study of MHC H-2Kk complexed with octapeptides and nonapeptides. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1278-1280.	2.5	3
43	Functional importance of Asp37 from a family 11 xylanase in the binding to two proteinaceous xylanase inhibitors from wheat. <i>FEMS Microbiology Letters</i> , 2004, 239, 9-15.	1.8	19
44	The Dual Nature of the Wheat Xylanase Protein Inhibitor XIP-I. <i>Journal of Biological Chemistry</i> , 2004, 279, 36029-36037.	3.4	111
45	Rat kidney acylase I: further characterisation and mutation studies on the involvement of Glu 147 in the catalytic process. <i>Biochimie</i> , 2003, 85, 953-962.	2.6	14
46	Specific Characterization of Substrate and Inhibitor Binding Sites of a Glycosyl Hydrolase Family 11 Xylanase from <i>Aspergillus niger</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 44035-44043.	3.4	67
47	X-ray Structure and Ligand Binding Study of a Moth Chemosensory Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 32094-32098.	3.4	173
48	Crystal Structure of the Open Form of Dog Gastric Lipase in Complex with a Phosphonate Inhibitor. <i>Journal of Biological Chemistry</i> , 2002, 277, 2266-2274.	3.4	107
49	A Hyperthermostable D-Ribose-5-Phosphate Isomerase from <i>Pyrococcus horikoshii</i> Characterization and Three-Dimensional Structure. <i>Structure</i> , 2002, 10, 877-886.	3.3	43
50	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73
51	The Fusion Glycoprotein Shell of Semliki Forest Virus. <i>Cell</i> , 2001, 105, 137-148.	28.9	471
52	Complexation of Two Proteic Insect Inhibitors to the Active Site of Chymotrypsin Suggests Decoupled Roles for Binding and Selectivity. <i>Journal of Biological Chemistry</i> , 2001, 276, 38893-38898.	3.4	58
53	Digestive lipases: From three-dimensional structure to physiology. <i>Biochimie</i> , 2000, 82, 973-986.	2.6	104
54	Crystal Structure of Human Gastric Lipase and Model of Lysosomal Acid Lipase, Two Lipolytic Enzymes of Medical Interest. <i>Journal of Biological Chemistry</i> , 1999, 274, 16995-17002.	3.4	150

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55	The structure of an entire noncovalent immunoglobulin kappa light-chain dimer (Bence-Jones protein) reveals a weak and unusual constant domains association. <i>FEBS Journal</i> , 1999, 260, 192-199.	0.2	34
56	An inactive pancreaticâ€”related protein is activated into a triglyceride-lipase by mutagenesis based on the 3-D structure. <i>Chemistry and Physics of Lipids</i> , 1998, 93, 103-114.	3.2	12
57	Structure and Activity of Rat Pancreatic Lipase-related Protein 2. <i>Journal of Biological Chemistry</i> , 1998, 273, 32121-32128.	3.4	76
58	Crystal structure of the streptococcal superantigen SPE-C: dimerization and zinc binding suggest a novel mode of interaction with MHC class II molecules. <i>Nature Structural Biology</i> , 1997, 4, 635-643.	9.7	104
59	A hypothetical complex between crystalline flavocytochrome b2 and Cytochrome c. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 408-422.	2.6	25
60	Solution conformation of human neuropeptide Y by 1H nuclear magnetic resonance and restrained molecular dynamics. <i>FEBS Journal</i> , 1992, 209, 765-771.	0.2	79
61	Conformational flexibility of a scorpion toxin active on mammals and insects: A circular dichroism study. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 164-172.	2.6	25
62	Three-Dimensionnal structures of complexes of <i>Lathyrus ochrus</i> isolectin I with glucose and mannose: Fine specificity of the monosaccharide-binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 365-376.	2.6	121
63	CRYStallize: A crystallographic symmetry display and handling subpackage in TOM/FRODO. <i>Journal of Molecular Graphics</i> , 1990, 8, 86-88.	1.1	78
64	Rapid access to an updated biological macromolecule crystallization database through artificial intelligence. <i>Journal of Crystal Growth</i> , 1990, 106, 405-409.	1.5	8