

Stephane Rety

List of Publications by Year in descending order

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49
papers

2,266
citations

279487

23
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214527

47
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51
all docs

51
docs citations

51
times ranked

3190
citing authors

#	ARTICLE	IF	CITATIONS
1	A Perspective for MÃ©niÃ©reÃ©™s Disease: In Silico Investigations of Dexamethasone as a Direct Modulator of AQP2. <i>Biomolecules</i> , 2022, 12, 511.	1.8	2
2	Structural mechanism underpinning <i>Thermus oshimai</i> Pif1-mediated G-quadruplex unfolding. <i>EMBO Reports</i> , 2022, 23, .	2.0	6
3	Voltage-gating of aquaporins, a putative conserved safety mechanism during ionic stresses. <i>FEBS Letters</i> , 2021, 595, 41-57.	1.3	18
4	Structural and functional studies of SF1B Pif1 from <i>Thermus oshimai</i> reveal dimerization-induced helicase inhibition. <i>Nucleic Acids Research</i> , 2021, 49, 4129-4143.	6.5	15
5	Crystal structures of N-terminally truncated telomerase reverse transcriptase from fungi. <i>Nucleic Acids Research</i> , 2021, 49, 4768-4781.	6.5	7
6	The fluorescent protein stability assay: an efficient method for monitoring intracellular protein stability. <i>BioTechniques</i> , 2021, 70, 336-344.	0.8	1
7	Structural study of the function of <i>Candida Albicans</i> Pif1. <i>Biochemical and Biophysical Research Communications</i> , 2021, 567, 190-194.	1.0	2
8	Endogenous <i>Bos taurus</i> RECQL is predominantly monomeric and more active than oligomers. <i>Cell Reports</i> , 2021, 36, 109688.	2.9	11
9	Functional diversification in the <i>Nudix hydrolase</i> gene family drives sesquiterpene biosynthesis in <i>Rosa</i> – <i>wichurana</i> . <i>Plant Journal</i> , 2020, 104, 185-199.	2.8	21
10	The N-terminal of NBPF15 causes multiple types of aggregates and mediates phase transition. <i>Biochemical Journal</i> , 2020, 477, 445-458.	1.7	5
11	Structural analysis reveals a â€œmolecular calipersâ€ mechanism for a LATERAL ORGAN BOUNDARIES DOMAIN transcription factor protein from wheat. <i>Journal of Biological Chemistry</i> , 2019, 294, 142-156.	1.6	21
12	Molecular Mechanistic Insights into <i>Drosophila</i> DHX36-Mediated G-Quadruplex Unfolding: A Structure-Based Model. <i>Structure</i> , 2018, 26, 403-415.e4.	1.6	35
13	Insights into the structural and mechanistic basis of multifunctional <i>S. cerevisiae</i> Pif1p helicase. <i>Nucleic Acids Research</i> , 2018, 46, 1486-1500.	6.5	43
14	Structural model of the full-length Ser/Thr protein kinase StkP from <i>S. pneumoniae</i> and its recognition of peptidoglycan fragments. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 3666-3679.	2.0	9
15	Crystal structure of <i>Escherichia coli</i> DEAH/RHA helicase HrpB. <i>Biochemical and Biophysical Research Communications</i> , 2018, 504, 334-339.	1.0	5
16	A helical bundle in the N-terminal domain of the BLM helicase mediates dimer and potentially hexamer formation. <i>Journal of Biological Chemistry</i> , 2017, 292, 5909-5920.	1.6	14
17	<i>Escherichia coli</i> <i>scp</i> DNA polymerase I can disrupt G-quadruplex structures during <i>scp</i> DNA replication. <i>FEBS Journal</i> , 2017, 284, 4051-4065.	2.2	17
18	Crystal structure of the active form of native human thymidylate synthase in the absence of bound substrates. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 336-341.	0.4	5

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19	Functional link between DEAH/RHA helicase Prp43 activation and ATP base binding. <i>Nucleic Acids Research</i> , 2017, 45, 1539-1552.	6.5	27
20	Sequential domain assembly of ribosomal protein S3 drives 40S subunit maturation. <i>Nature Communications</i> , 2016, 7, 10336.	5.8	55
21	Crystal structures of the BsPif1 helicase reveal that a major movement of the 2B SH3 domain is required for DNA unwinding. <i>Nucleic Acids Research</i> , 2016, 44, 2949-2961.	6.5	25
22	Structure of <i>Escherichia coli</i> tryptophanase purified from an alkaline-stressed bacterial culture. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1378-1383.	0.4	2
23	The <i>Bacteroides sp. 3_1_23</i> Pif1 protein is a multifunctional helicase. <i>Nucleic Acids Research</i> , 2015, 43, 8942-8954.	6.5	31
24	Regulation of DEAH/RHA Helicases by G-Patch Proteins. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	56
25	Chaperoning 5S RNA assembly. <i>Genes and Development</i> , 2015, 29, 1432-1446.	2.7	54
26	RNA Mimicry by the Fap7 Adenylate Kinase in Ribosome Biogenesis. <i>PLoS Biology</i> , 2014, 12, e1001860.	2.6	37
27	Genetic Analysis of the Biosynthesis of 2-Methoxy-3-Isobutylpyrazine, a Major Grape-Derived Aroma Compound Impacting Wine Quality. <i>Plant Physiology</i> , 2013, 162, 604-615.	2.3	89
28	Structural, Functional, and Evolutionary Analysis of the Unusually Large Stilbene Synthase Gene Family in Grapevine. <i>Plant Physiology</i> , 2012, 160, 1407-1419.	2.3	138
29	Functional and Structural Insights of a <i>Staphylococcus aureus</i> Apoptotic-like Membrane Peptide from a Toxin-Antitoxin Module. <i>Journal of Biological Chemistry</i> , 2012, 287, 43454-43463.	1.6	60
30	Crystal Structure of an EAL Domain in Complex with Reaction Product 5'-pGpG. <i>PLoS ONE</i> , 2012, 7, e52424.	1.1	19
31	The H/ACA RNP assembly factor SHQ1 functions as an RNA mimic. <i>Genes and Development</i> , 2011, 25, 2398-2408.	2.7	50
32	Structural and Dynamical Insights into the Opening Mechanism of <i>P. aeruginosa</i> OprM Channel. <i>Structure</i> , 2010, 18, 507-517.	1.6	53
33	Structural studies of the catalytic core of the primate foamy virus (PFV-1) integrase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 881-886.	0.7	3
34	Scent evolution in Chinese roses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5927-5932.	3.3	86
35	The structural comparison of the bacterial PepX and human DPP-IV reveals sites for the design of inhibitors of PepX activity. <i>FEBS Journal</i> , 2005, 272, 2050-2059.	2.2	15
36	The use of high halide-ion concentrations and automated phasing procedures for the structural analysis of BclA, the major component of the exosporium of <i>Bacillus anthracis</i> spores. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 344-349.	2.5	5

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37	The Crystal Structure of the Bacillus anthracis Spore Surface Protein BclA Shows Remarkable Similarity to Mammalian Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 43073-43078.	1.6	54
38	The Crystal Structure of Annexin A8 is Similar to that of Annexin A3. <i>Journal of Molecular Biology</i> , 2005, 345, 1131-1139.	2.0	11
39	Crystal structure of BclA, a protein of the exosporium of the spore of Bacillus anthracis. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, s155-s155.	0.3	0
40	Association of the mammalian proto-oncoprotein Int-6 with the three protein complexes eIF3, COP9 signalosome and 26S proteasome. <i>FEBS Letters</i> , 2002, 527, 15-21.	1.3	65
41	The Human Protein HSPC021 Interacts with Int-6 and Is Associated with Eukaryotic Translation Initiation Factor 3. <i>Journal of Biological Chemistry</i> , 2001, 276, 45988-45995.	1.6	26
42	S100â€™ANNEXIN COMPLEXES: SOME INSIGHTS FROM STRUCTURAL STUDIES. <i>Cell Biology International</i> , 2000, 24, 799-802.	1.4	56
43	EF-hand calcium-binding proteins. <i>Current Opinion in Structural Biology</i> , 2000, 10, 637-643.	2.6	458
44	Structural basis of the Ca ²⁺ -dependent association between S100C (S100A11) and its target, the N-terminal part of annexin I. <i>Structure</i> , 2000, 8, 175-184.	1.6	176
45	S100 proteinâ€™annexin interactions: a model of the (Anx2-p11) ₂ heterotetramer complex. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2000, 1498, 181-191.	1.9	25
46	The crystal structure of a complex of p11 with the annexin II N-terminal peptide. <i>Nature Structural Biology</i> , 1999, 6, 89-95.	9.7	262
47	pHâ€™Dependent selfâ€™association of the Src homology 2 (SH2) domain of the Src homologous and collagenâ€™like (SHC) protein. <i>Protein Science</i> , 1996, 5, 405-413.	3.1	10
48	Crystal structure of the SH2 domain of the protein SHC: pH-dependent self-association. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1996, 52, C187-C187.	0.3	0
49	Probing the nature of substrate binding in Humicola lanuginosa lipase through X-ray crystallography and intuitive modelling. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 543-550.	1.0	79