Stephane Rety

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Perspective for Ménière's Disease: In Silico Investigations of Dexamethasone as a Direct Modulator of AQP2. Biomolecules, 2022, 12, 511.	4.0	2
2	Structural mechanism underpinning <i>Thermus oshimai</i> Pif1â€mediated Gâ€quadruplex unfolding. EMBO Reports, 2022, 23, .	4.5	6
3	Voltageâ€gating of aquaporins, a putative conserved safety mechanism during ionic stresses. FEBS Letters, 2021, 595, 41-57.	2.8	18
4	Structural and functional studies of SF1B Pif1 from <i>Thermus oshimai</i> reveal dimerization-induced helicase inhibition. Nucleic Acids Research, 2021, 49, 4129-4143.	14.5	15
5	Crystal structures of N-terminally truncated telomerase reverse transcriptase from fungi. Nucleic Acids Research, 2021, 49, 4768-4781.	14.5	7
6	The fluorescent protein stability assay: an efficient method for monitoring intracellular protein stability. BioTechniques, 2021, 70, 336-344.	1.8	1
7	Structural study of the function of Candida Albicans Pif1. Biochemical and Biophysical Research Communications, 2021, 567, 190-194.	2.1	2
8	Endogenous Bos taurus RECQL is predominantly monomeric and more active than oligomers. Cell Reports, 2021, 36, 109688.	6.4	11
9	Functional diversification in the <i>Nudix hydrolase</i> gene family drives sesquiterpene biosynthesis in <i>Rosa</i> Å— <i>wichurana</i> . Plant Journal, 2020, 104, 185-199.	5.7	21
10	The N-terminal of NBPF15 causes multiple types of aggregates and mediates phase transition. Biochemical Journal, 2020, 477, 445-458.	3.7	5
11	Structural analysis reveals a "molecular calipers―mechanism for a LATERAL ORGAN BOUNDARIES DOMAIN transcription factor protein from wheat. Journal of Biological Chemistry, 2019, 294, 142-156.	3.4	21
12	Molecular Mechanistic Insights into Drosophila DHX36-Mediated G-Quadruplex Unfolding: A Structure-Based Model. Structure, 2018, 26, 403-415.e4.	3.3	35
13	Insights into the structural and mechanistic basis of multifunctional S. cerevisiae Pif1p helicase. Nucleic Acids Research, 2018, 46, 1486-1500.	14.5	43
14	Structural model of the full-length Ser/Thr protein kinase StkP from S. pneumoniae and its recognition of peptidoglycan fragments. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3666-3679.	3.5	9
15	Crystal structure of Escherichiaâ€,coli DEAH/RHA helicase HrpB. Biochemical and Biophysical Research Communications, 2018, 504, 334-339.	2.1	5
16	A helical bundle in the N-terminal domain of the BLM helicase mediates dimer and potentially hexamer formation. Journal of Biological Chemistry, 2017, 292, 5909-5920.	3.4	14
17	<i>Escherichia coli </i> <scp>DNA</scp> polymerase I can disrupt Gâ€quadruplex structures during <scp>DNA</scp> replication. FEBS Journal, 2017, 284, 4051-4065.	4.7	17
18	Crystal structure of the active form of native human thymidylate synthase in the absence of bound substrates. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 336-341.	0.8	5

STEPHANE RETY

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19	Functional link between DEAH/RHA helicase Prp43 activation and ATP base binding. Nucleic Acids Research, 2017, 45, 1539-1552.	14.5	27
20	Sequential domain assembly of ribosomal protein S3 drives 40S subunit maturation. Nature Communications, 2016, 7, 10336.	12.8	55
21	Crystal structures of the BsPif1 helicase reveal that a major movement of the 2B SH3 domain is required for DNA unwinding. Nucleic Acids Research, 2016, 44, 2949-2961.	14.5	25
22	Structure ofEscherichia colitryptophanase purified from an alkaline-stressed bacterial culture. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1378-1383.	0.8	2
23	The <i>Bacteroides sp. 3_1_23</i> Pif1 protein is a multifunctional helicase. Nucleic Acids Research, 2015, 43, 8942-8954.	14.5	31
24	Regulation of DEAH/RHA Helicases by G-Patch Proteins. BioMed Research International, 2015, 2015, 1-9.	1.9	56
25	Chaperoning 5S RNA assembly. Genes and Development, 2015, 29, 1432-1446.	5.9	54
26	RNA Mimicry by the Fap7 Adenylate Kinase in Ribosome Biogenesis. PLoS Biology, 2014, 12, e1001860.	5.6	37
27	Genetic Analysis of the Biosynthesis of 2-Methoxy-3-Isobutylpyrazine, a Major Grape-Derived Aroma Compound Impacting Wine Quality Â. Plant Physiology, 2013, 162, 604-615.	4.8	89
28	Structural, Functional, and Evolutionary Analysis of the Unusually Large Stilbene Synthase Gene Family in Grapevine Â. Plant Physiology, 2012, 160, 1407-1419.	4.8	138
29	Functional and Structural Insights of a Staphylococcus aureus Apoptotic-like Membrane Peptide from a Toxin-Antitoxin Module. Journal of Biological Chemistry, 2012, 287, 43454-43463.	3.4	60
30	Crystal Structure of an EAL Domain in Complex with Reaction Product 5′-pGpG. PLoS ONE, 2012, 7, e52424.	2.5	19
31	The H/ACA RNP assembly factor SHQ1 functions as an RNA mimic. Genes and Development, 2011, 25, 2398-2408.	5.9	50
32	Structural and Dynamical Insights into the Opening Mechanism of P. aeruginosa OprM Channel. Structure, 2010, 18, 507-517.	3.3	53
33	Structural studies of the catalytic core of the primate foamy virus (PFV-1) integrase. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 881-886.	0.7	3
34	Scent evolution in Chinese roses. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5927-5932.	7.1	86
35	The structural comparison of the bacterial PepX and human DPP-IV reveals sites for the design of inhibitors of PepX activity. FEBS Journal, 2005, 272, 2050-2059.	4.7	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 ofBacillus anthracisspores. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 344-349.	2.5	5

STEPHANE RETY

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37	The Crystal Structure of the Bacillus anthracis Spore Surface Protein BclA Shows Remarkable Similarity to Mammalian Proteins. Journal of Biological Chemistry, 2005, 280, 43073-43078.	3.4	54
38	The Crystal Structure of Annexin A8 is Similar to that of Annexin A3. Journal of Molecular Biology, 2005, 345, 1131-1139.	4.2	11
39	Crystal structure of BclA, a protein of the exosporium of the spore ofBacillus anthracis. Acta Crystallographica Section A: Foundations and Advances, 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. FEBS Letters, 2002, 527, 15-21.	2.8	65
41	The Human Protein HSPC021 Interacts with Int-6 and Is Associated with Eukaryotic Translation Initiation Factor 3. Journal of Biological Chemistry, 2001, 276, 45988-45995.	3.4	26
42	S100–ANNEXIN COMPLEXES: SOME INSIGHTS FROM STRUCTURAL STUDIES. Cell Biology International, 2000, 24, 799-802.	3.0	56
43	EF-hand calcium-binding proteins. Current Opinion in Structural Biology, 2000, 10, 637-643.	5.7	458
44	Structural basis of the Ca2+-dependent association between S100C (S100A11) and its target, the N-terminal part of annexin I. Structure, 2000, 8, 175-184.	3.3	176
45	S100 protein–annexin interactions: a model of the (Anx2-p11)2 heterotetramer complex. Biochimica Et Biophysica Acta - Molecular Cell Research, 2000, 1498, 181-191.	4.1	25
46	The crystal structure of a complex of p11 with the annexin II N-terminal peptide. Nature Structural Biology, 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. Protein Science, 1996, 5, 405-413.	7.6	10
48	Crystal structure of the SH2 domain of the protein SHC: pH-dependent self-association. Acta Crystallographica Section A: Foundations and Advances, 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. Protein Engineering, Design and Selection, 1994, 7, 543-550.	2.1	79