Stephane Rety

List of Publications by Year in descending order

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STEDHANE RETV

#	Article	IF	CITATIONS
1	EF-hand calcium-binding proteins. Current Opinion in Structural Biology, 2000, 10, 637-643.	5.7	458
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	S100–ANNEXIN COMPLEXES: SOME INSIGHTS FROM STRUCTURAL STUDIES. Cell Biology International, 2000, 24, 799-802.	3.0	56
11	Regulation of DEAH/RHA Helicases by G-Patch Proteins. BioMed Research International, 2015, 2015, 1-9.	1.9	56
12	Sequential domain assembly of ribosomal protein S3 drives 40S subunit maturation. Nature Communications, 2016, 7, 10336.	12.8	55
13	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
14	Chaperoning 5S RNA assembly. Genes and Development, 2015, 29, 1432-1446.	5.9	54
15	Structural and Dynamical Insights into the Opening Mechanism of P. aeruginosa OprM Channel. Structure, 2010, 18, 507-517.	3.3	53
16	The H/ACA RNP assembly factor SHQ1 functions as an RNA mimic. Genes and Development, 2011, 25, 2398-2408.	5.9	50
17	Insights into the structural and mechanistic basis of multifunctional S. cerevisiae Pif1p helicase. Nucleic Acids Research, 2018, 46, 1486-1500.	14.5	43
18	RNA Mimicry by the Fap7 Adenylate Kinase in Ribosome Biogenesis. PLoS Biology, 2014, 12, e1001860.	5.6	37

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19	Molecular Mechanistic Insights into Drosophila DHX36-Mediated G-Quadruplex Unfolding: A Structure-Based Model. Structure, 2018, 26, 403-415.e4.	3.3	35
20	The <i>Bacteroides sp. 3_1_23</i> Pif1 protein is a multifunctional helicase. Nucleic Acids Research, 2015, 43, 8942-8954.	14.5	31
21	Functional link between DEAH/RHA helicase Prp43 activation and ATP base binding. Nucleic Acids Research, 2017, 45, 1539-1552.	14.5	27
22	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
23	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
24	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
25	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
26	Functional diversification in the <i>Nudix hydrolase</i> gene family drives sesquiterpene biosynthesis in <i>Rosa</i> × <i>wichurana</i> . Plant Journal, 2020, 104, 185-199.	5.7	21
27	Crystal Structure of an EAL Domain in Complex with Reaction Product 5â€2-pGpG. PLoS ONE, 2012, 7, e52424.	2.5	19
28	Voltageâ€gating of aquaporins, a putative conserved safety mechanism during ionic stresses. FEBS Letters, 2021, 595, 41-57.	2.8	18
29	<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
30	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
31	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
32	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
33	The Crystal Structure of Annexin A8 is Similar to that of Annexin A3. Journal of Molecular Biology, 2005, 345, 1131-1139.	4.2	11
34	Endogenous Bos taurus RECQL is predominantly monomeric and more active than oligomers. Cell Reports, 2021, 36, 109688.	6.4	11
35	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
36	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

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37	Crystal structures of N-terminally truncated telomerase reverse transcriptase from fungi. Nucleic Acids Research, 2021, 49, 4768-4781.	14.5	7
38	Structural mechanism underpinning <i>Thermus oshimai</i> Pif1â€mediated Gâ€quadruplex unfolding. EMBO Reports, 2022, 23, .	4.5	6
39	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
40	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
41	Crystal structure of Escherichiaâ€,coli DEAH/RHA helicase HrpB. Biochemical and Biophysical Research Communications, 2018, 504, 334-339.	2.1	5
42	The N-terminal of NBPF15 causes multiple types of aggregates and mediates phase transition. Biochemical Journal, 2020, 477, 445-458.	3.7	5
43	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
44	Structure ofEscherichia colitryptophanase purified from an alkaline-stressed bacterial culture. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1378-1383.	0.8	2
45	Structural study of the function of Candida Albicans Pif1. Biochemical and Biophysical Research Communications, 2021, 567, 190-194.	2.1	2
46	A Perspective for Ménière's Disease: In Silico Investigations of Dexamethasone as a Direct Modulator of AQP2. Biomolecules, 2022, 12, 511.	4.0	2
47	The fluorescent protein stability assay: an efficient method for monitoring intracellular protein stability. BioTechniques, 2021, 70, 336-344.	1.8	1
48	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
49	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