Yves-henri Sanejouand

List of Publications by Year
in descending order

23	1,944	687363 13	677142 22
papers	citations	h-index	g-index

25	25	25	2269
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	At least three xenon binding sites in the glycine binding domain of the N-methyl D-aspartate receptor. Archives of Biochemistry and Biophysics, 2022, 724, 109265.	3.0	0
2	A framework for the next generation of stationary cosmological models. International Journal of Modern Physics D, 2022, 31, .	2.1	8
3	On the vibrational free energy of hydrated proteins. Physical Biology, 2021, 18, 036003.	1.8	0
4	Rational Enzyme Design without Structural Knowledge: A Sequenceâ€Based Approach for Efficient Generation of Transglycosylases. Chemistry - A European Journal, 2021, 27, 10323-10334.	3.3	29
5	Normalâ€mode driven exploration of protein domain motions. Journal of Computational Chemistry, 2021, 42, 2250-2257.	3.3	3
6	Numerous severely twisted Nâ€acetylglucosamine conformations found in the protein databank. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1376-1383.	2.6	3
7	Toward the design of efficient transglycosidases: the case of the GH1 of Thermus thermophilus. Protein Engineering, Design and Selection, 2019, 32, 309-316.	2.1	5
8	Jumping between protein conformers using normal modes. Journal of Computational Chemistry, 2017, 38, 1622-1630.	3.3	13
9	Internal Water Dynamics Control the Transglycosylation/Hydrolysis Balance in the Agarase (AgaD) of Zobellia galactanivorans. ACS Catalysis, 2017, 7, 3357-3367.	11.2	23
10	A singular mutation in the hemagglutinin of the 1918 pandemic virus. Archives of Biochemistry and Biophysics, 2017, 625-626, 13-16.	3.0	1
11	Semi-rational approach for converting a GH36 Î±-glycosidase into an Î±-transglycosidase. Glycobiology, 2015, 25, 420-427.	2.5	27
12	On the relationship between low-frequency normal modes and the large-scale conformational changes of proteins. Archives of Biochemistry and Biophysics, 2015, 567, 59-65.	3.0	75
13	Use of a structural alphabet to find compatible folds for amino acid sequences. Protein Science, 2015, 24, 145-153.	7.6	9
14	Semi-rational approach for converting a GH1 Â-glycosidase into a Â-transglycosidase. Protein Engineering, Design and Selection, 2014, 27, 13-19.	2.1	65
15	Elastic Network Models: Theoretical and Empirical Foundations. Methods in Molecular Biology, 2013, 924, 601-616.	0.9	38
16	Conserved Water Molecules in Family 1 Glycosidases: A DXMS and Molecular Dynamics Study. Biochemistry, 2013, 52, 5900-5910.	2.5	34
17	NORMA: a tool for flexible fitting of high-resolution protein structures into low-resolution electron-microscopy-derived density maps. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1098-1100.	2.5	107
18	ElNemo: a normal mode web server for protein movement analysis and the generation of templates for molecular replacement. Nucleic Acids Research, 2004, 32, W610-W614.	14.5	620

#	Article	IF	Citations
19	On the potential of normal-mode analysis for solving difficult molecular-replacement problems. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 796-799.	2.5	99
20	Building-block approach for determining low-frequency normal modes of macromolecules. Proteins: Structure, Function and Bioinformatics, 2000, 41, 1-7.	2.6	421
21	New proteinlike properties of cubic lattice models. Physical Review E, 1999, 59, 942-946.	2.1	11
22	Hinge-bending motion in citrate synthase arising from normal mode calculations. Proteins: Structure, Function and Bioinformatics, 1995, 23, 557-560.	2.6	189
23	A new approach for determining low-frequency normal modes in macromolecules. Biopolymers, 1994, 34, 759-771.	2.4	160