Nathalie Colloc'h

List of Publications by Year in descending order

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394421 477307 1,163 29 19 29 citations g-index h-index papers 30 30 30 1106 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Equilibria between conformational states of the Ras oncogene protein revealed by high pressure crystallography. Chemical Science, 2022, 13, 2001-2010.	7.4	17
2	Comparative study of the effects of high hydrostatic pressure <i>per se</i> and high argon pressure on urate oxidase ligand stabilization. Acta Crystallographica Section D: Structural Biology, 2022, 78, 162-173.	2.3	6
3	Method for the Identification of Potentially Bioactive Argon Binding Sites in Protein Families. Journal of Chemical Information and Modeling, 2022, 62, 1318-1327.	5.4	0
4	Behavior of B- and Z-DNA Crystals under High Hydrostatic Pressure. Crystals, 2022, 12, 871.	2.2	2
5	Ligand pathways in neuroglobin revealed by low-temperature photodissociation and docking experiments. IUCrJ, 2019, 6, 832-842.	2.2	8
6	Determinants of neuroglobin plasticity highlighted by joint coarse-grained simulations and high pressure crystallography. Scientific Reports, 2017, 7, 1858.	3.3	7
7	Mapping Hydrophobic Tunnels and Cavities in Neuroglobin with Noble Gas under Pressure. Biophysical Journal, 2017, 113, 2199-2206.	0.5	14
8	Gas-sensitive biological crystals processed in pressurized oxygen and krypton atmospheres: deciphering gas channels in proteins using a novel`soak-and-freeze' methodology. Journal of Applied Crystallography, 2016, 49, 1478-1487.	4.5	25
9	Structural Basis for Xenon Inhibition in a Cationic Pentameric Ligand-Gated Ion Channel. PLoS ONE, 2016, 11, e0149795.	2.5	31
10	Direct Evidence for a Peroxide Intermediate and a Reactive Enzyme–Substrate–Dioxygen Configuration in a Cofactorâ€free Oxidase. Angewandte Chemie - International Edition, 2014, 53, 13710-13714.	13.8	43
11	Azide inhibition of urate oxidase. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 896-902.	0.8	4
12	Functional relevance of the internal hydrophobic cavity of urate oxidase. FEBS Letters, 2014, 588, 1715-1719.	2.8	26
13	Crystallographic Studies with Xenon and Nitrous Oxide Provide Evidence for Protein-dependent Processes in the Mechanisms of General Anesthesia. Anesthesiology, 2014, 121, 1018-1027.	2.5	25
14	Xâ€ray, ESR, and quantum mechanics studies unravel a spin well in the cofactorâ€less urate oxidase. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1964-1976.	2.6	16
15	Pressureâ€response analysis of anesthetic gases xenon and nitrous oxide on urate oxidase: a crystallographic study. FASEB Journal, 2011, 25, 2266-2275.	0.5	31
16	Near-atomic resolution structures of urate oxidase complexed with its substrate and analogues: the protonation state of the ligand. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 714-724.	2.5	29
17	Xenon is an Inhibitor of Tissue-Plasminogen Activator: Adverse and Beneficial Effects in a Rat Model of Thromboembolic Stroke. Journal of Cerebral Blood Flow and Metabolism, 2010, 30, 718-728.	4.3	47
18	Structure-Function Perturbation and Dissociation of Tetrameric Urate Oxidase by High Hydrostatic Pressure. Biophysical Journal, 2010, 98, 2365-2373.	0.5	53

#	ARTICLE	IF	CITATION
19	Structural analysis of urate oxidase in complex with its natural substrate inhibited by cyanide: Mechanistic implications. BMC Structural Biology, 2008, 8, 32.	2.3	44
20	Oxygen Pressurized X-Ray Crystallography: Probing the Dioxygen Binding Site in Cofactorless Urate Oxidase and Implications for Its Catalytic Mechanism. Biophysical Journal, 2008, 95, 2415-2422.	0.5	65
21	Protein Crystallography under Xenon and Nitrous Oxide Pressure: Comparison with In Vivo Pharmacology Studies and Implications for the Mechanism of Inhaled Anesthetic Action. Biophysical Journal, 2007, 92, 217-224.	0.5	80
22	Recapture of [S]-allantoin, the product of the two-step degradation of uric acid, by urate oxidase. FEBS Letters, 2006, 580, 2087-2091.	2.8	29
23	High-Pressure Macromolecular Crystallography (HPMX): Status and prospects. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 384-390.	2.3	19
24	Urate oxidase from Aspergillus flavus: new crystal-packing contacts in relation to the content of the active site. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 218-229.	2.5	34
25	Complexed and ligand-free high-resolution structures of urate oxidase (Uox) fromAspergillus flavus: a reassignment of the active-site binding mode. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 453-462.	2.5	82
26	Modification of a reactive cysteine explains differences between rasburicase and Uricozyme, a natural Aspergillus flavus uricase. Biotechnology and Applied Biochemistry, 2002, 36, 21.	3.1	48
27	Sequence and structural features of the T-fold, an original tunnelling building unit. Proteins: Structure, Function and Bioinformatics, 2000, 39, 142-154.	2.6	55
28	Exploring hydrophobic sites in proteins with xenon or krypton. Proteins: Structure, Function and Bioinformatics, 1998, 30, 61-73.	2.6	168
29	Crystal Structure of the protein drug urate oxidase-inhibitor complex at 2.05 Ã resolution. Nature Structural and Molecular Biology, 1997, 4, 947-952.	8.2	150