

Probing the transition state in enzyme catalysis by high

Nature Catalysis

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Enzyme catalysis under pressure. <i>Nature Catalysis</i> , 2019, 2, 646-647.	34.4	1
2	The Catalytic Mechanics of Dynamic Surfaces: Stimulating Methods for Promoting Catalytic Resonance. <i>ACS Catalysis</i> , 2020, 10, 12666-12695.	11.2	54
3	Proteins-Based Nanocatalysts for Energy Conversion Reactions. <i>Topics in Current Chemistry</i> , 2020, 378, 43.	5.8	3
4	Benign-by-design nature-inspired bionanoconjugates for energy conversion and storage applications. <i>Current Opinion in Green and Sustainable Chemistry</i> , 2020, 26, 100373.	5.9	5
5	Lifestyle of bacteria in deep sea. <i>Environmental Microbiology Reports</i> , 2021, 13, 15-17.	2.4	2
6	Distinct conformational dynamics and allosteric networks in alpha tryptophan synthase during active catalysis. <i>Protein Science</i> , 2021, 30, 543-557.	7.6	7
7	On Catalytic Kinetics of Enzymes. <i>Processes</i> , 2021, 9, 271.	2.8	4
9	Challenges for machine learning force fields in reproducing potential energy surfaces of flexible molecules. <i>Journal of Chemical Physics</i> , 2021, 154, 094119.	3.0	24
10	From structure to mechanism: skiing the energy landscape. <i>Nature Methods</i> , 2021, 18, 435-436.	19.0	11
11	Validating the CHARMM36m protein force field with LJ-PME reveals altered hydrogen bonding dynamics under elevated pressures. <i>Communications Chemistry</i> , 2021, 4, .	4.5	5
12	Adaptations for Pressure and Temperature in Dihydrofolate Reductases. <i>Microorganisms</i> , 2021, 9, 1706.	3.6	3
13	Making the invisible visible: Toward structural characterization of allosteric states, interaction networks, and allosteric regulatory mechanisms in protein kinases. <i>Current Opinion in Structural Biology</i> , 2021, 71, 71-78.	5.7	13
14	Local frustration determines loop opening during the catalytic cycle of an oxidoreductase. <i>ELife</i> , 2020, 9, .	6.0	13
17	Nuclear spin relaxation. <i>Nuclear Magnetic Resonance</i> , 2020, , 76-138.	0.2	0
18	Structure determination of high-energy states in a dynamic protein ensemble. <i>Nature</i> , 2022, 603, 528-535.	27.8	51
19	NMR spectroscopy, excited states and relevance to problems in cell biology – transient pre-nucleation tetramerization of huntingtin and insights into Huntington's disease. <i>Journal of Cell Science</i> , 2022, 135, .	2.0	5
20	Predicting DNA-binding protein and coronavirus protein flexibility using protein dihedral angle and sequence feature. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 497-507.	2.6	2
21	High Pressure CPMG and CEST Reveal That Cavity Position Dictates Distinct Dynamic Disorder in the PP32 Repeat Protein. <i>Journal of Physical Chemistry B</i> , 2022, 126, 10597-10607.	2.6	1

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22	Effects of high pressure on protein stability, structure, and function—Theory and applications. , 2023, , 19-48.		0
23	Insights into the Structure of Invisible Conformations of Large Methyl Group Labeled Molecular Machines from High Pressure NMR. Journal of Molecular Biology, 2023, 435, 167922.	4.2	1
24	New Insights into the Cooperativity and Dynamics of Dimeric Enzymes. Chemical Reviews, 2023, 123, 9940-9981.	47.7	2
28	Harnessing generative AI to decode enzyme catalysis and evolution for enhanced engineering. National Science Review, 0, , .	9.5	1
29	Perspectives on Computational Enzyme Modeling: From Mechanisms to Design and Drug Development. ACS Omega, 0, , .	3.5	0
30	Switching Go...-Martini for Investigating Protein Conformational Transitions and Associated Protein-Lipid Interactions. Journal of Chemical Theory and Computation, 2024, 20, 2618-2629.	5.3	0