

ProThermDB: thermodynamic database for proteins and

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Citation Report

#	ARTICLE	IF	CITATIONS
1	ProNAB: database for binding affinities of protein–nucleic acid complexes and their mutants. <i>Nucleic Acids Research</i> , 2022, 50, D1528-D1534.	6.5	20
2	Revolutionizing enzyme engineering through artificial intelligence and machine learning. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 113-125.	1.1	21
3	Assessing the performance of computational predictors for estimating protein stability changes upon missense mutations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	30
5	Reviewing Challenges of Predicting Protein Melting Temperature Change Upon Mutation Through the Full Analysis of a Highly Detailed Dataset with High-Resolution Structures. <i>Molecular Biotechnology</i> , 2021, 63, 863-884.	1.3	13
6	Evolution-aided engineering of plant specialized metabolism. <i>ABIOTECH</i> , 2021, 2, 240-263.	1.8	11
8	The Stability Landscape of de novo TIM Barrels Explored by a Modular Design Approach. <i>Journal of Molecular Biology</i> , 2021, 433, 167153.	2.0	15
10	The 2021 <i>Nucleic Acids Research</i> database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2021, 49, D1-D9.	6.5	100
11	Illustrative Tutorials for ProThermDB: Thermodynamic Database for Proteins and Mutants. <i>Current Protocols</i> , 2021, 1, e306.	1.3	0
12	Predicting protein stability changes upon single-point mutation: a thorough comparison of the available tools on a new dataset. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	57
13	Thermometer: a webserver to predict protein thermal stability. <i>Bioinformatics</i> , 2022, 38, 2060-2061.	1.8	9
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15	Artificial intelligence challenges for predicting the impact of mutations on protein stability. <i>Current Opinion in Structural Biology</i> , 2022, 72, 161-168.	2.6	45
16	Artificial intelligence based methods for hot spot prediction. <i>Current Opinion in Structural Biology</i> , 2022, 72, 209-218.	2.6	16
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18	Computational design of a cutinase for plastic biodegradation by mining molecular dynamics simulations trajectories. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 459-470.	1.9	27
20	Systematic evaluation of computational tools to predict the effects of mutations on protein stability in the absence of experimental structures. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	18
21	Systematic investigation of the link between enzyme catalysis and cold adaptation. <i>ELife</i> , 2022, 11, .	2.8	9
22	Structure–conditioned amino–acid couplings: How contact geometry affects pairwise sequence preferences. <i>Protein Science</i> , 2022, 31, 900-917.	3.1	3

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24	Large-scale design and refinement of stable proteins using sequence-only models. <i>PLoS ONE</i> , 2022, 17, e0265020.	1.1	17
25	Validating Small Molecule Chemical Probes for Biological Discovery. <i>Annual Review of Biochemistry</i> , 2022, 91, 61-87.	5.0	13
26	Turning Failures into Applications: The Problem of Protein $\Delta\Delta G$ Prediction. <i>Methods in Molecular Biology</i> , 2022, 2449, 169-185.	0.4	5
27	DDGun: an untrained predictor of protein stability changes upon amino acid variants. <i>Nucleic Acids Research</i> , 2022, 50, W222-W227.	6.5	28
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37	PROST: AlphaFold2-aware Sequence-Based Predictor to Estimate Protein Stability Changes upon Missense Mutations. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 4270-4282.	2.5	25
38	Computational approaches for predicting variant impact: An overview from resources, principles to applications. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	11
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41	Molecular Information Theory Meets Protein Folding. <i>Journal of Physical Chemistry B</i> , 2022, 126, 8655-8668.	1.2	5
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46	Accurate protein stability predictions from homology models. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 66-73.	1.9	12
47	Prediction of polyreactive and nonspecific single-chain fragment variables through structural biochemical features and protein language-based descriptors. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
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52	Beyond sequence: Structure-based machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 630-643.	1.9	3
53	Predicting protein stability changes upon mutation using a simple orientational potential. <i>Bioinformatics</i> , 2023, 39, .	1.8	6
55	How a single mutation alters the protein structure: a simulation investigation on protein tyrosine phosphatase SHP2. <i>RSC Advances</i> , 2023, 13, 4263-4274.	1.7	2
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