Jiri Damborsky

List of Publications by Year
in descending order

271	12,657	30070	36028
papers	citations	54 h-index	97 g-index

296	296	296	12152
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CAVER 3.0: A Tool for the Analysis of Transport Pathways in Dynamic Protein Structures. PLoS Computational Biology, 2012, 8, e1002708.	3.2	991
2	PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology, 2014, 10, e1003440.	3.2	593
3	Strategies for Stabilization of Enzymes in Organic Solvents. ACS Catalysis, 2013, 3, 2823-2836.	11.2	514
4	CAVER: a new tool to explore routes from protein clefts, pockets and cavities. BMC Bioinformatics, 2006, 7, 316.	2.6	453
5	Machine Learning in Enzyme Engineering. ACS Catalysis, 2020, 10, 1210-1223.	11.2	250
6	CAVER Analyst 2.0: analysis and visualization of channels and tunnels in protein structures and molecular dynamics trajectories. Bioinformatics, 2018, 34, 3586-3588.	4.1	244
7	Bioremediation 3.0: Engineering pollutant-removing bacteria in the times of systemic biology. Biotechnology Advances, 2017, 35, 845-866.	11.7	240
8	Redesigning dehalogenase access tunnels as a strategy for degrading an anthropogenic substrate. Nature Chemical Biology, 2009, 5, 727-733.	8.0	238
9	Gates of Enzymes. Chemical Reviews, 2013, 113, 5871-5923.	47.7	216
10	Computational tools for designing and engineering enzymes. Current Opinion in Chemical Biology, 2014, 19, 8-16.	6.1	185
11	HotSpot Wizard 3.0: web server for automated design of mutations and smart libraries based on sequence input information. Nucleic Acids Research, 2018, 46, W356-W362.	14.5	171
12	HotSpot Wizard: a web server for identification of hot spots in protein engineering. Nucleic Acids Research, 2009, 37, W376-W383.	14.5	160
13	PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLoS Computational Biology, 2016, 12, e1004962.	3.2	149
14	Exacerbation of substrate toxicity by IPTG in Escherichia coli BL21(DE3) carrying a synthetic metabolic pathway. Microbial Cell Factories, 2015, 14, 201.	4.0	145
15	FireProt: Energy- and Evolution-Based Computational Design of Thermostable Multiple-Point Mutants. PLoS Computational Biology, 2015, 11, e1004556.	3.2	144
16	Caver Web 1.0: identification of tunnels and channels in proteins and analysis of ligand transport. Nucleic Acids Research, 2019, 47, W414-W422.	14.5	138
17	CAVER Analyst 1.0: graphic tool for interactive visualization and analysis of tunnels and channels in protein structures. Bioinformatics, 2014, 30, 2684-2685.	4.1	135
18	Engineering enzyme access tunnels. Biotechnology Advances, 2019, 37, 107386.	11.7	128

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19	Haloalkane dehalogenases: Biotechnological applications. Biotechnology Journal, 2013, 8, 32-45.	3.5	126
20	Crystal Structure of the Haloalkane Dehalogenase fromSphingomonas paucimobilisUT26â€,â€¡. Biochemistry, 2000, 39, 14082-14086.	2.5	118
21	Modification of Activity and Specificity of Haloalkane Dehalogenase from Sphingomonas paucimobilis UT26 by Engineering of Its Entrance Tunnel. Journal of Biological Chemistry, 2003, 278, 52622-52628.	3.4	115
22	Engineering Enzyme Stability and Resistance to an Organic Cosolvent by Modification of Residues in the Access Tunnel. Angewandte Chemie - International Edition, 2013, 52, 1959-1963.	13.8	113
23	Biodegradation of 1,2,3-Trichloropropane through Directed Evolution and Heterologous Expression of a Haloalkane Dehalogenase Gene. Applied and Environmental Microbiology, 2002, 68, 3582-3587.	3.1	112
24	CAVER: Algorithms for Analyzing Dynamics of Tunnels in Macromolecules. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 505-517.	3.0	108
25	FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research, 2017, 45, W393-W399.	14.5	104
26	Mechanism-Based Design of Efficient PET Hydrolases. ACS Catalysis, 2022, 12, 3382-3396.	11.2	104
27	Computational tools for designing and engineering biocatalysts. Current Opinion in Chemical Biology, 2009, 13, 26-34.	6.1	99
28	Enantioselectivity of Haloalkane Dehalogenases and its Modulation by Surface Loop Engineering. Angewandte Chemie - International Edition, 2010, 49, 6111-6115.	13.8	96
29	Substrate specificity of haloalkane dehalogenases. Biochemical Journal, 2011, 435, 345-354.	3.7	92
30	Pathways and Mechanisms for Product Release in the Engineered Haloalkane Dehalogenases Explored Using Classical and Random Acceleration Molecular Dynamics Simulations. Journal of Molecular Biology, 2009, 392, 1339-1356.	4.2	89
31	Computational Design of Stable and Soluble Biocatalysts. ACS Catalysis, 2019, 9, 1033-1054.	11.2	87
32	Rad52 SUMOylation affects the efficiency of the DNA repair. Nucleic Acids Research, 2010, 38, 4708-4721.	14.5	85
33	Engineering a de Novo Transport Tunnel. ACS Catalysis, 2016, 6, 7597-7610.	11.2	84
34	Crystal Structure of Haloalkane Dehalogenase LinB from Sphingomonas paucimobilis UT26 at 0.95 Ã... Resolution:â€‰ Dynamics of Catalytic Residues,. Biochemistry, 2004, 43, 870-878.	2.5	82
35	Phylogenetic analysis of haloalkane dehalogenases. Proteins: Structure, Function and Bioinformatics, 2007, 67, 305-316.	2.6	82
36	Catalytic Mechanism of the Haloalkane Dehalogenase LinB from Sphingomonas paucimobilis UT26. Journal of Biological Chemistry, 2003, 278, 45094-45100.	3.4	80

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37	HotSpot Wizard 2.0: automated design of site-specific mutations and smart libraries in protein engineering. Nucleic Acids Research, 2016, 44, W479-W487.	14.5	76
38	Software tools for identification, visualization and analysis of protein tunnels and channels. Biotechnology Advances, 2013, 31, 38-49.	11.7	74
39	Two Rhizobial Strains, Mesorhizobium loti MAFF303099 and Bradyrhizobium japonicum USDA110, Encode Haloalkane Dehalogenases with Novel Structures and Substrate Specificities. Applied and Environmental Microbiology, 2005, 71, 4372-4379.	3.1	73
40	Degradation of Î²-Hexachlorocyclohexane by Haloalkane Dehalogenase LinB from Sphingomonas paucimobilis UT26. Applied and Environmental Microbiology, 2005, 71, 2183-2185.	3.1	72
41	Molecular Dissection of Interactions between Rad51 and Members of the Recombination-Repair Group. Molecular and Cellular Biology, 2001, 21, 966-976.	2.3	70
42	Reaction Mechanism and Stereochemistry of Î³-Hexachlorocyclohexane Dehydrochlorinase LinA. Journal of Biological Chemistry, 2001, 276, 7734-7740.	3.4	70
43	Halide-Stabilizing Residues of Haloalkane Dehalogenases Studied by Quantum Mechanic Calculations and Site-Directed Mutagenesisâ€. Biochemistry, 2002, 41, 14272-14280.	2.5	69
44	Quantitative Analysis of Substrate Specificity of Haloalkane Dehalogenase LinB fromSphingomonas paucimobilisUT26â€. Biochemistry, 2005, 44, 3390-3401.	2.5	68
45	Characterization of a Novel Thermostable Mn(II)-dependent 2,3-Dihydroxybiphenyl 1,2-Dioxygenase from a Polychlorinated Biphenyl- and Naphthalene-degrading Bacillus sp. JF8. Journal of Biological Chemistry, 2003, 278, 21483-21492.	3.4	66
46	Enzymes fight chemical weapons. Biotechnology Journal, 2006, 1, 1370-1380.	3.5	66
47	SoluProt: prediction of soluble protein expression in Escherichia coli. Bioinformatics, 2021, 37, 23-28.	4.1	66
48	Enzyme Tunnels and Gates As Relevant Targets in Drug Design. Medicinal Research Reviews, 2017, 37, 1095-1139.	10.5	65
49	FireProtDB: database of manually curated protein stability data. Nucleic Acids Research, 2021, 49, D319-D324.	14.5	63
50	Degradation of Î²-hexachlorocyclohexane by haloalkane dehalogenase LinB from Î³-hexachlorocyclohexane-utilizing bacterium Sphingobium sp. MI1205. Archives of Microbiology, 2007, 188, 313-325.	2.2	62
51	A Single Mutation in a Tunnel to the Active Site Changes the Mechanism and Kinetics of Product Release in Haloalkane Dehalogenase LinB. Journal of Biological Chemistry, 2012, 287, 29062-29074.	3.4	61
52	Repositioning the Catalytic Triad Aspartic Acid of Haloalkane Dehalogenase:â€‰ Effects on Stability, Kinetics, and Structure. Biochemistry, 1997, 36, 9571-9580.	2.5	59
53	Molecular orbital calculations to describe microbial reductive dechlorination of polychlorinated dioxins. Environmental Toxicology and Chemistry, 1998, 17, 988-997.	4.3	58
54	Fluorescence-based biosensor for monitoring of environmental pollutants: From concept to field application. Biosensors and Bioelectronics, 2016, 84, 97-105.	10.1	58

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55	Exploration of Enzyme Diversity by Integrating Bioinformatics with Expression Analysis and Biochemical Characterization. ACS Catalysis, 2018, 8, 2402-2412.	11.2	58
56	Analysis of the reaction mechanism and substrate specificity of haloalkane dehalogenases by sequential and structural comparisons. Protein Engineering, Design and Selection, 1999, 12, 989-998.	2.1	57
57	Development of an enzymatic fiber-optic biosensor for detection of halogenated hydrocarbons. Analytical and Bioanalytical Chemistry, 2010, 398, 1891-1898.	3.7	57
58	Comparison of the QSAR models for toxicity and biodegradability of anilines and phenols. Chemosphere, 1997, 34, 429-446.	8.2	54
59	Cloning, Biochemical Properties, and Distribution of Mycobacterial Haloalkane Dehalogenases. Applied and Environmental Microbiology, 2005, 71, 6736-6745.	3.1	54
60	Immobilized Synthetic Pathway for Biodegradation of Toxic Recalcitrant Pollutant 1,2,3-Trichloropropane. Environmental Science & Technology, 2014, 48, 6859-6866.	10.0	54
61	Engineering theÂprotein dynamics of anÂancestral luciferase. Nature Communications, 2021, 12, 3616.	12.8	54
62	Identification of tunnels in proteins, nucleic acids, inorganic materials and molecular ensembles. Biotechnology Journal, 2007, 2, 62-67.	3.5	53
63	New Functional Handle for Use as a Self-Reporting Contrast and Delivery Agent in Nanomedicine. Journal of the American Chemical Society, 2013, 135, 9518-9524.	13.7	52
64	Dynamics and hydration explain failed functional transformation in dehalogenase design. Nature Chemical Biology, 2014, 10, 428-430.	8.0	52
65	Dehalogenation of Haloalkanes byMycobacterium tuberculosisH37Rv and Other Mycobacteria. Applied and Environmental Microbiology, 2000, 66, 219-222.	3.1	51
66	CaverDock: a molecular docking-based tool to analyse ligand transport through protein tunnels and channels. Bioinformatics, 2019, 35, 4986-4993.	4.1	51
67	EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities. Nucleic Acids Research, 2020, 48, W104-W109.	14.5	51
68	Multi-pathogen infections and Alzheimerâ€™s disease. Microbial Cell Factories, 2021, 20, 25.	4.0	51
69	Computational design of enzymes for biotechnological applications. Biotechnology Advances, 2021, 47, 107696.	11.7	51
70	A Molecular Modeling Study of the Catalytic Mechanism of Haloalkane Dehalogenase:â€‰ 1. Quantum Chemical Study of the First Reaction Step. Journal of Chemical Information and Computer Sciences, 1997, 37, 562-568.	2.8	50
71	Cloning and Expression of the Haloalkane Dehalogenase Gene dhmA from Mycobacterium avium N85 and Preliminary Characterization of DhmA. Applied and Environmental Microbiology, 2002, 68, 3724-3730.	3.1	50
72	Impact of the access tunnel engineering on catalysis is strictly ligandâ€specific. FEBS Journal, 2018, 285, 1456-1476.	4.7	50

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73	Exploring the Structure and Activity of Haloalkane Dehalogenase from Sphingomonas paucimobilis UT26: Evidence for Product- and Water-Mediated Inhibition,. Biochemistry, 2002, 41, 4847-4855.	2.5	49
74	Computerâ€assisted engineering of hyperstable fibroblast growth factor 2. Biotechnology and Bioengineering, 2018, 115, 850-862.	3.3	49
75	Instability restricts signaling of multiple fibroblast growth factors. Cellular and Molecular Life Sciences, 2015, 72, 2445-2459.	5.4	48
76	Identification of the catalytic triad in the haloalkane dehalogenase fromSphingomonas paucimobilisUT26. FEBS Letters, 1999, 446, 177-181.	2.8	47
77	Novosphingobium barchaimii sp. nov., isolated from hexachlorocyclohexane-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 667-672.	1.7	46
78	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
79	Mechanism-guided tunnel engineering to increase the efficiency of a flavin-dependent halogenase. Nature Catalysis, 2022, 5, 534-544.	34.4	46
80	Construction and Characterization of Histidine-Tagged Haloalkane Dehalogenase (LinB) of a New Substrate Class from a Î³-Hexachlorocyclohexane-Degrading Bacterium, Sphingomonas paucimobilis UT26. Protein Expression and Purification, 1999, 17, 299-304.	1.3	45
81	High occurrence of BRCA1 intragenic rearrangements in hereditary breast and ovarian cancer syndrome in the Czech Republic. BMC Medical Genetics, 2007, 8, 32.	2.1	45
82	Ancestral Haloalkane Dehalogenases Show Robustness and Unique Substrate Specificity. ChemBioChem, 2017, 18, 1448-1456.	2.6	45
83	Structural Biology and Protein Engineering of Thrombolytics. Computational and Structural Biotechnology Journal, 2019, 17, 917-938.	4.1	45
84	Structureâ€“specificity relationships for haloalkane dehalogenases. Environmental Toxicology and Chemistry, 2001, 20, 2681-2689.	4.3	44
85	Suppression of protein inactivation during freezing by minimizing pH changes using ionic cryoprotectants. International Journal of Pharmaceutics, 2016, 509, 41-49.	5.2	44
86	Haloalkane Dehalogenase LinB fromSphingomonas paucimobilisUT26:Â X-ray Crystallographic Studies of Dehalogenation of Brominated Substratesâ€,â€¡. Biochemistry, 2003, 42, 10104-10112.	2.5	43
87	Substrate inhibition by the blockage of product release and its control by tunnel engineering. RSC Chemical Biology, 2021, 2, 645-655.	4.1	43
88	Comparative Binding Energy Analysis of the Substrate Specificity of Haloalkane Dehalogenase from Xanthobacter autotrophicus GJ10. Biochemistry, 2001, 40, 8905-8917.	2.5	42
89	Nanosecond Time-Dependent Stokes Shift at the Tunnel Mouth of Haloalkane Dehalogenases. Journal of the American Chemical Society, 2009, 131, 494-501.	13.7	42
90	A Pseudomonas putida Strain Genetically Engineered for 1,2,3-Trichloropropane Bioremediation. Applied and Environmental Microbiology, 2014, 80, 5467-5476.	3.1	42

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91	Tetrachloroethene-dehalogenating bacteria. Folia Microbiologica, 1999, 44, 247-262.	2.3	40
92	Identification of protein fold and catalytic residues of Î³-hexachlorocyclohexane dehydrochlorinase LinA. Proteins: Structure, Function and Bioinformatics, 2001, 45, 471-477.	2.6	40
93	Functionally relevant motions of haloalkane dehalogenases occur in the specificity-modulating cap domains. Protein Science, 2002, 11, 1206-1217.	7.6	40
94	Computer-Assisted Engineering of the Synthetic Pathway for Biodegradation of a Toxic Persistent Pollutant. ACS Synthetic Biology, 2014, 3, 172-181.	3.8	39
95	Balancing the Stabilityâ€“Activity Tradeâ€Off by Fineâ€Tuning Dehalogenase Access Tunnels. ChemCatChem, 2015, 7, 648-659.	3.7	39
96	Interfacing Microwells with Nanoliter Compartments: A Sampler Generating High-Resolution Concentration Gradients for Quantitative Biochemical Analyses in Droplets. Analytical Chemistry, 2015, 87, 624-632.	6.5	39
97	Exploration of Protein Unfolding by Modelling Calorimetry Data from Reheating. Scientific Reports, 2017, 7, 16321.	3.3	39
98	Web-based tools for computational enzyme design. Current Opinion in Structural Biology, 2021, 69, 19-34.	5.7	38
99	FireProtASR: A Web Server for Fully Automated Ancestral Sequence Reconstruction. Briefings in Bioinformatics, 2021, 22, .	6.5	37
100	Biochemical Characteristics of the Novel Haloalkane Dehalogenase DatA, Isolated from the Plant Pathogen Agrobacterium tumefaciens C58. Applied and Environmental Microbiology, 2011, 77, 1881-1884.	3.1	36
101	Characterization of Protein Glycosylation in Francisella tularensis subsp. holarctica. Molecular and Cellular Proteomics, 2012, 11, M111.015016-1-M111.015016-12.	3.8	36
102	Organic coâ€solvents affect activity, stability and enantioselectivity of haloalkane dehalogenases. Biotechnology Journal, 2013, 8, 719-729.	3.5	36
103	Enzyme-Based Test Strips for Visual or Photographic Detection and Quantitation of Gaseous Sulfur Mustard. Analytical Chemistry, 2016, 88, 6044-6049.	6.5	36
104	Plectin repeats and modules: strategic cysteines and their presumed impact on cytolinker functions. BioEssays, 2001, 23, 1064-1069.	2.5	35
105	Stepwise dissection and visualization of the catalytic mechanism of haloalkane dehalogenase LinB using molecular dynamics simulations and computer graphics. Journal of Molecular Graphics and Modelling, 2007, 26, 643-651.	2.4	35
106	Computational Study of Protein-Ligand Unbinding for Enzyme Engineering. Frontiers in Chemistry, 2018, 6, 650.	3.6	35
107	Biochemical Characterization of Haloalkane Dehalogenases DrbA and DmbC, Representatives of a Novel Subfamily. Applied and Environmental Microbiology, 2009, 75, 5157-5160.	3.1	34
108	Biochemical Characterization of a Novel Haloalkane Dehalogenase from a Cold-Adapted Bacterium. Applied and Environmental Microbiology, 2012, 78, 4995-4998.	3.1	33

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109	Interaction of organic solvents with protein structures at protein-solvent interface. Journal of Molecular Modeling, 2013, 19, 4701-4711.	1.8	33
110	Expansion of Access Tunnels and Activeâ€Site Cavities Influence Activity of Haloalkane Dehalogenases in Organic Cosolvents. ChemBioChem, 2013, 14, 890-897.	2.6	33
111	Light-Emitting Dehalogenases: Reconstruction of Multifunctional Biocatalysts. ACS Catalysis, 2019, 9, 4810-4823.	11.2	33
112	A Molecular Modeling Study of the Catalytic Mechanism of Haloalkane Dehalogenase. 2. Quantum Chemical Study of Complete Reaction Mechanism. Journal of Chemical Information and Computer Sciences, 1998, 38, 736-741.	2.8	32
113	Maximizing the Efficiency of Multienzyme Process by Stoichiometry Optimization. ChemBioChem, 2014, 15, 1891-1895.	2.6	31
114	CalFitter: a web server for analysis of protein thermal denaturation data. Nucleic Acids Research, 2018, 46, W344-W349.	14.5	30
115	Fibroblast Growth Factor 2 Protein Stability Provides Decreased Dependence on Heparin for Induction of FGFR Signaling and Alters ERK Signaling Dynamics. Frontiers in Cell and Developmental Biology, 2019, 7, 331.	3.7	30
116	Effects of developmental nicotine exposure in rats on decision-making in adulthood. Behavioural Pharmacology, 2012, 23, 34-42.	1.7	29
117	Sphingobium baderi sp. nov., isolated from a hexachlorocyclohexane dump site. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 673-678.	1.7	29
118	TRITON: in silico construction of protein mutants and prediction of their activities. Bioinformatics, 2000, 16, 845-846.	4.1	28
119	Comparison of catalysis by haloalkane dehalogenases in aqueous solutions of deep eutectic and organic solvents. Green Chemistry, 2014, 16, 2754-2761.	9.0	28
120	Fructose 1â€phosphate is the one and only physiological effector of the Cra (FruR) regulator of Pseudomonas putida. FEBS Open Bio, 2014, 4, 377-386.	2.3	28
121	Exploring the challenges of computational enzyme design by rebuilding the active site of a dehalogenase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 389-394.	7.1	28
122	Quantitative structure-function and structure-stability relationships of purposely modified proteins. Protein Engineering, Design and Selection, 1998, 11, 21-30.	2.1	27
123	Identification of Salmonella enterica serovar Typhimurium genes associated with growth suppression in stationary-phase nutrient broth cultures and in the chicken intestine. Archives of Microbiology, 2002, 178, 411-420.	2.2	27
124	Physiological and proteomic approaches to evaluate the role of sterol binding in elicitin-induced resistance. Journal of Experimental Botany, 2012, 63, 2203-2215.	4.8	27
125	Substrate Anchoring and Flexibility Reduction in CYP153A_{M.aq} Leads to Highly Improved Efficiency toward Octanoic Acid. ACS Catalysis, 2021, 11, 3182-3189.	11.2	27
126	Exploring mechanism of enzyme catalysis by on-chip transient kinetics coupled with global data analysis and molecular modeling. CheM, 2021, 7, 1066-1079.	11.7	27

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127	TRITON: graphic software for rational engineering of enzymes. Trends in Biochemical Sciences, 2001, 26, 71-73.	7.5	26
128	DspA from Strongylocentrotus purpuratus: The first biochemically characterized haloalkane dehalogenase of non-microbial origin. Biochimie, 2013, 95, 2091-2096.	2.6	26
129	Mechanism of enhanced conversion of 1,2,3-trichloropropane by mutant haloalkane dehalogenase revealed by molecular modeling. Journal of Computer-Aided Molecular Design, 2006, 20, 375-383.	2.9	25
130	Weak Activity of Haloalkane Dehalogenase LinB with 1,2,3-Trichloropropane Revealed by X-Ray Crystallography and Microcalorimetry. Applied and Environmental Microbiology, 2007, 73, 2005-2008.	3.1	25
131	Site-Specific Analysis of Protein Hydration Based on Unnatural Amino Acid Fluorescence. Journal of the American Chemical Society, 2015, 137, 4988-4992.	13.7	25
132	Wedelolactone Acts as Proteasome Inhibitor in Breast Cancer Cells. International Journal of Molecular Sciences, 2017, 18, 729.	4.1	25
133	Molecular Gating of an Engineered Enzyme Captured in Real Time. Journal of the American Chemical Society, 2018, 140, 17999-18008.	13.7	25
134	Second step of hydrolytic dehalogenation in haloalkane dehalogenase investigated by QM/MM methods. Proteins: Structure, Function and Bioinformatics, 2008, 70, 707-717.	2.6	24
135	CaverDock: A Novel Method for the Fast Analysis of Ligand Transport. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1625-1638.	3.0	24
136	Lincomycin Biosynthesis Involves a Tyrosine Hydroxylating Heme Protein of an Unusual Enzyme Family. PLoS ONE, 2013, 8, e79974.	2.5	24
137	Biochemical characterization of broad-specificity enzymes using multivariate experimental design and a colorimetric microplate assay: characterization of the haloalkane dehalogenase mutants. Journal of Microbiological Methods, 2001, 44, 149-157.	1.6	23
138	Role of SdiA in Salmonella enterica serovar Typhimurium physiology and virulence. Archives of Microbiology, 2002, 178, 94-101.	2.2	23
139	The new platinum-based anticancer agent LA-12 induces retinol binding protein 4 in vivo. Proteome Science, 2011, 9, 68.	1.7	23
140	Mechanism-Based Discovery of Novel Substrates of Haloalkane Dehalogenases Using in Silico Screening. Journal of Chemical Information and Modeling, 2015, 55, 54-62.	5.4	23
141	Computational Analysis of Protein Tunnels and Channels. Methods in Molecular Biology, 2018, 1685, 25-42.	0.9	23
142	Tools for computational design and high-throughput screening of therapeutic enzymes. Advanced Drug Delivery Reviews, 2022, 183, 114143.	13.7	23
143	Analysis of transactivation capability and conformation of p53 temperature-dependent mutants and their reactivation by amifostine in yeast. Oncogene, 2008, 27, 1243-1252.	5.9	22
144	Stereoselectivity and conformational stability of haloalkane dehalogenase DbjA from Bradyrhizobiumâ€ƒjaponicum USDA110: the effect of pH and temperature. FEBS Journal, 2011, 278, 2728-2738.	4.7	22

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145	Catalytic Cycle of Haloalkane Dehalogenases Toward Unnatural Substrates Explored by Computational Modeling. Journal of Chemical Information and Modeling, 2017, 57, 1970-1989.	5.4	22
146	Reconstruction of Mycobacterial Dehalogenase Rv2579 by Cumulative Mutagenesis of Haloalkane Dehalogenase LinB. Applied and Environmental Microbiology, 2003, 69, 2349-2355.	3.1	21
147	Conjugation of 5(6)-carboxyfluorescein and 5(6)-carboxynaphthofluorescein with bovine serum albumin and their immobilization for optical pH sensing. Sensors and Actuators B: Chemical, 2012, 161, 93-99.	7.8	21
148	Computational Tools for Designing Smart Libraries. Methods in Molecular Biology, 2014, 1179, 291-314.	0.9	21
149	Impact of Orthogonal Signal Correction (OSC) on the Predictive Ability of CoMFA Models for the Ciliate Toxicity of Nitrobenzenes Dedicated to Professor Werner Klein, Schmallenberg (Germany), on the oaccastion of his 65th birthday. QSAR and Combinatorial Science, 2002, 21, 3.	1.2	20
150	Exploring the Binding Sites of the Haloalkane Dehalogenase DhlA from Xanthobacter autotrophicus GJ10. Biochemistry, 2007, 46, 9239-9249.	2.5	20
151	The effect of a unique halideâ€stabilizing residue on the catalytic properties of haloalkane dehalogenase <scp>D</scp>at<scp>A</scp> from <scp>A</scp>grobacteriumÂtumefaciens<scp>C</scp>58. FEBS Journal, 2013, 280, 3149-3159.	4.7	20
152	Cation-Specific Effects on Enzymatic Catalysis Driven by Interactions at the Tunnel Mouth. Journal of Physical Chemistry B, 2013, 117, 6394-6402.	2.6	20
153	Structural and functional analysis of a novel haloalkane dehalogenase with two halide-binding sites. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1884-1897.	2.5	20
154	Evolutionary Analysis As a Powerful Complement to Energy Calculations for Protein Stabilization. ACS Catalysis, 2018, 8, 9420-9428.	11.2	20
155	Controlled Oil/Water Partitioning of Hydrophobic Substrates Extending the Bioanalytical Applications of Droplet-Based Microfluidics. Analytical Chemistry, 2019, 91, 10008-10015.	6.5	20
156	A Nonconventional Archaeal Fluorinase Identified by In Silico Mining for Enhanced Fluorine Biocatalysis. ACS Catalysis, 2022, 12, 6570-6577.	11.2	20
157	Computational site-directed mutagenesis of haloalkane dehalogenase in position 172. Protein Engineering, Design and Selection, 1998, 11, 901-907.	2.1	19
158	Comparative binding energy analysis of haloalkane dehalogenase substrates: modelling of enzyme-substrate complexes by molecular docking and quantum mechanical calculations. Journal of Computer-Aided Molecular Design, 2003, 17, 299-311.	2.9	19
159	Fast Screening of Inhibitor Binding/Unbinding Using Novel Software Tool CaverDock. Frontiers in Chemistry, 2019, 7, 709.	3.6	19
160	Quantitative Structure-Function Relationships of the Single-Point Mutants of Haloalkane Dehalogenase: A Multivariate Approach. QSAR and Combinatorial Science, 1997, 16, 126-135.	1.2	18
161	QSAR for acute toxicity of saturated and unsaturated halogenated aliphatic compounds. Chemosphere, 1998, 36, 1345-1365.	8.2	18
162	Construction of Cryptogein Mutants, a Proteinaceous Elicitor fromPhytophthora, with Altered Abilities To Induce a Defense Reaction in Tobacco Cellsâ€. Biochemistry, 2005, 44, 6565-6572.	2.5	18

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163	Sphingobium czechense sp. nov., isolated from a hexachlorocyclohexane dump site. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 723-728.	1.7	18
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