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	Virtual screening of potential anticancer drugs based on microbial products. Seminars in Cancer Biology, 2022, 86, 1207-1217.	9.6	6
2	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
3	Tools for computational design and high-throughput screening of therapeutic enzymes. Advanced Drug Delivery Reviews, 2022, 183, 114143.	13.7	23
4	Computer-aided engineering of staphylokinase toward enhanced affinity and selectivity for plasmin. Computational and Structural Biotechnology Journal, 2022, 20, 1366-1377.	4.1	4
5	Mechanism-Based Design of Efficient PET Hydrolases. ACS Catalysis, 2022, 12, 3382-3396.	11.2	104
6	Extended Mechanism of the Plasminogen Activator Staphylokinase Revealed by Global Kinetic Analysis: 1000-fold Higher Catalytic Activity than That of Clinically Used Alteplase. ACS Catalysis, 2022, 12, 3807-3814.	11.2	7
7	LoopGrafter: a web tool for transplanting dynamical loops for protein engineering. Nucleic Acids Research, 2022, 50, W465-W473.	14.5	11
8	CalFitter 2.0: Leveraging the power of singular value decomposition to analyse protein thermostability. Nucleic Acids Research, 2022, , .	14.5	2
9	Mechanism-Based Strategy for Optimizing HaloTag Protein Labeling. Jacs Au, 2022, 2, 1324-1337.	7.9	7
10	A Nonconventional Archaeal Fluorinase Identified by In Silico Mining for Enhanced Fluorine Biocatalysis. ACS Catalysis, 2022, 12, 6570-6577.	11.2	20
11	Mechanism-guided tunnel engineering to increase the efficiency of a flavin-dependent halogenase. Nature Catalysis, 2022, 5, 534-544.	34.4	46
12	Fast approximative methods for study of ligand transport and rational design of improved enzymes for biotechnologies. Biotechnology Advances, 2022, 60, 108009.	11.7	12
13	Increased occurrence of Treponema spp. and double-species infections in patients with Alzheimer's disease. Science of the Total Environment, 2022, 844, 157114.	8.0	7
14	FireProtASR: A Web Server for Fully Automated Ancestral Sequence Reconstruction. Briefings in Bioinformatics, 2021, 22, .	6.5	37
15	FireProtDB: database of manually curated protein stability data. Nucleic Acids Research, 2021, 49, D319-D324.	14.5	63
16	Development and Testing of Thrombolytics in Stroke. Journal of Stroke, 2021, 23, 12-36.	3.2	14
17	Substrate inhibition by the blockage of product release and its control by tunnel engineering. RSC Chemical Biology, 2021, 2, 645-655.	4.1	43
18	Multi-pathogen infections and Alzheimerâ€™s disease. Microbial Cell Factories, 2021, 20, 25.	4.0	51

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19	Fully Automated Ancestral Sequence Reconstruction using FireProt^{ASR}. Current Protocols, 2021, 1, e30.	2.9	12
20	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
21	The tetrameric structure of the novel haloalkane dehalogenase DpaA from Paraglaciecola agarilytica NO2. Acta Crystallographica Section D: Structural Biology, 2021, 77, 347-356.	2.3	5
22	Computational design of enzymes for biotechnological applications. Biotechnology Advances, 2021, 47, 107696.	11.7	51
23	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
24	Promiscuous Dehalogenase Activity of the Epoxide Hydrolase CorEH from Corynebacterium sp. C12. ACS Catalysis, 2021, 11, 6113-6120.	11.2	5
25	Engineering theÂprotein dynamics of anÂancestral luciferase. Nature Communications, 2021, 12, 3616.	12.8	54
26	Structure-activity relationships of dually-acting acetylcholinesterase inhibitors derived from tacrine on N-methyl-d-Aspartate receptors. European Journal of Medicinal Chemistry, 2021, 219, 113434.	5.5	9
27	Web-based tools for computational enzyme design. Current Opinion in Structural Biology, 2021, 69, 19-34.	5.7	38
28	Stabilization of Haloalkane Dehalogenase Structure by Interfacial Interaction with Ionic Liquids. Crystals, 2021, 11, 1052.	2.2	4
29	Screening of world approved drugs against highly dynamical spike glycoprotein of SARS-CoV-2 using CaverDock and machine learning. Computational and Structural Biotechnology Journal, 2021, 19, 3187-3197.	4.1	11
30	SoluProt: prediction of soluble protein expression in Escherichia coli. Bioinformatics, 2021, 37, 23-28.	4.1	66
31	Computational Enzyme Stabilization Can Affect Folding Energy Landscapes and Lead to Catalytically Enhanced Domain-Swapped Dimers. ACS Catalysis, 2021, 11, 12864-12885.	11.2	10
32	Description of Transport Tunnel in Haloalkane Dehalogenase Variant LinB D147C+L177C from Sphingobium japonicum. Catalysts, 2021, 11, 5.	3.5	1
33	Structural Analysis of the Ancestral Haloalkane Dehalogenase AncLinB-DmbA. International Journal of Molecular Sciences, 2021, 22, 11992.	4.1	0
34	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
35	Machine Learning in Enzyme Engineering. ACS Catalysis, 2020, 10, 1210-1223.	11.2	250
36	An Ultrasensitive Fluorescence Assay for the Detection of Halides and Enzymatic Dehalogenation. ChemCatChem, 2020, 12, 2032-2039.	3.7	9

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37	Structures of hyperstable ancestral haloalkane dehalogenases show restricted conformational dynamics. Computational and Structural Biotechnology Journal, 2020, 18, 1497-1508.	4.1	10
38	Decoding the intricate network of molecular interactions of a hyperstable engineered biocatalyst. Chemical Science, 2020, 11, 11162-11178.	7.4	13
39	EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities. Nucleic Acids Research, 2020, 48, W104-W109.	14.5	51
40	Structural and catalytic effects of surface loop-helix transplantation within haloalkane dehalogenase family. Computational and Structural Biotechnology Journal, 2020, 18, 1352-1362.	4.1	2
41	A Haloalkane Dehalogenase from Saccharomonospora viridis Strain DSM 43017, a Compost Bacterium with Unusual Catalytic Residues, Unique (S)-Enantiopreference, and High Thermostability. Applied and Environmental Microbiology, 2020, 86, .	3.1	7
42	DockVis: Visual Analysis of Molecular Docking Trajectories. Computer Graphics Forum, 2020, 39, 452-464.	3.0	2
43	Exploration of enzyme diversity: High-throughput techniques for protein production and microscale biochemical characterization. Methods in Enzymology, 2020, 643, 51-85.	1.0	5
44	Fluorescent substrates for haloalkane dehalogenases: Novel probes for mechanistic studies and protein labeling. Computational and Structural Biotechnology Journal, 2020, 18, 922-932.	4.1	9
45	The impact of tunnel mutations on enzymatic catalysis depends on the tunnel-substrate complementarity and the rate-limiting step. Computational and Structural Biotechnology Journal, 2020, 18, 805-813.	4.1	14
46	Development of Fluorescent Assay for Monitoring of Dehalogenase Activity. Biotechnology Journal, 2019, 14, 1800144.	3.5	7
47	Analysis of Long Molecular Dynamics Simulations Using Interactive Focus+Context Visualization. Computer Graphics Forum, 2019, 38, 441-453.	3.0	11
48	Structural Biology and Protein Engineering of Thrombolytics. Computational and Structural Biotechnology Journal, 2019, 17, 917-938.	4.1	45
49	Crystallization and Crystallographic Analysis of a Bradyrhizobium Elkanii USDA94 Haloalkane Dehalogenase Variant with an Eliminated Halide-Binding Site. Crystals, 2019, 9, 375.	2.2	3
50	Controlled Oil/Water Partitioning of Hydrophobic Substrates Extending the Bioanalytical Applications of Droplet-Based Microfluidics. Analytical Chemistry, 2019, 91, 10008-10015.	6.5	20
51	Deciphering the Structural Basis of High Thermostability of Dehalogenase from Psychrophilic Bacterium Marinobacter sp. ELB17. Microorganisms, 2019, 7, 498.	3.6	18
52	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
53	Crystal structure of the cold-adapted haloalkane dehalogenase DpcA fromPsychrobacter cryohalolentisK5. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 324-331.	0.8	5
54	CaverDock: a molecular docking-based tool to analyse ligand transport through protein tunnels and channels. Bioinformatics, 2019, 35, 4986-4993.	4.1	51

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55	Engineering enzyme access tunnels. Biotechnology Advances, 2019, 37, 107386.	11.7	128
56	Light-Emitting Dehalogenases: Reconstruction of Multifunctional Biocatalysts. ACS Catalysis, 2019, 9, 4810-4823.	11.2	33
57	Structure-Function Relationships and Engineering of Haloalkane Dehalogenases. , 2019, , 367-387.		3
58	Transhalogenation Catalysed by Haloalkane Dehalogenases Engineered to Stop Natural Pathway at Intermediate. Advanced Synthesis and Catalysis, 2019, 361, 2438.	4.3	4
59	Fluorescent pH Indicators for Neutral to Near-Alkaline Conditions Based on 9-Iminopyronin Derivatives. ACS Omega, 2019, 4, 5479-5485.	3.5	17
60	Surface-enhanced Raman Spectroscopy in Microfluidic Chips for Directed Evolution of Enzymes and Environmental Monitoring. , 2019, , .		0
61	Computational Modelling of Metabolic Burden and Substrate Toxicity in Escherichia coli Carrying a Synthetic Metabolic Pathway. Microorganisms, 2019, 7, 553.	3.6	9
62	Fast Screening of Inhibitor Binding/Unbinding Using Novel Software Tool CaverDock. Frontiers in Chemistry, 2019, 7, 709.	3.6	19
63	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
64	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
65	Computational Design of Stable and Soluble Biocatalysts. ACS Catalysis, 2019, 9, 1033-1054.	11.2	87
66	Differences in crystallization of several selected haloalkane dehalogenases and their mutation variants. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e126-e126.	0.1	0
67	Impact of the access tunnel engineering on catalysis is strictly ligandâ€specific. FEBS Journal, 2018, 285, 1456-1476.	4.7	50
68	Exploration of Enzyme Diversity by Integrating Bioinformatics with Expression Analysis and Biochemical Characterization. ACS Catalysis, 2018, 8, 2402-2412.	11.2	58
69	Computerâ€assisted engineering of hyperstable fibroblast growth factor 2. Biotechnology and Bioengineering, 2018, 115, 850-862.	3.3	49
70	Gram-scale production of recombinant microbial enzymes in shake flasks. FEMS Microbiology Letters, 2018, 365, .	1.8	5
71	Computational Analysis of Protein Tunnels and Channels. Methods in Molecular Biology, 2018, 1685, 25-42.	0.9	23
72	A Haloalkane Dehalogenase from a Marine Microbial Consortium Possessing Exceptionally Broad Substrate Specificity. Applied and Environmental Microbiology, 2018, 84, .	3.1	12

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73	Molecular Gating of an Engineered Enzyme Captured in Real Time. Journal of the American Chemical Society, 2018, 140, 17999-18008.	13.7	25
74	Detection of Chloroalkanes by Surface-Enhanced Raman Spectroscopy in Microfluidic Chips. Sensors, 2018, 18, 3212.	3.8	6
75	Sensitive operation of enzyme-based biodevices by advanced signal processing. PLoS ONE, 2018, 13, e0198913.	2.5	2
76	Evolutionary Analysis As a Powerful Complement to Energy Calculations for Protein Stabilization. ACS Catalysis, 2018, 8, 9420-9428.	11.2	20
77	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
78	CalFitter: a web server for analysis of protein thermal denaturation data. Nucleic Acids Research, 2018, 46, W344-W349.	14.5	30
79	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
80	Conformational changes allow processing of bulky substrates by a haloalkane dehalogenase with a small and buried active site. Journal of Biological Chemistry, 2018, 293, 11505-11512.	3.4	11
81	Haloalkane Dehalogenases From Marine Organisms. Methods in Enzymology, 2018, 605, 203-251.	1.0	15
82	Computational Study of Protein-Ligand Unbinding for Enzyme Engineering. Frontiers in Chemistry, 2018, 6, 650.	3.6	35
83	Structural characterization and comparison of crystallization behaviour of selected haloalkane dehalogenases. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e185-e185.	0.1	0
84	Surface-enhanced Raman spectroscopy of chloroalkanes in microfluidic chips. , 2018, , .		0
85	Different Structural Origins of the Enantioselectivity of Haloalkane Dehalogenases toward Linear Î²â€Haloalkanes: Openâ€“Solvated versus Occludedâ€“Desolvated Active Sites. Angewandte Chemie, 2017, 129, 4797-4801.	2.0	0
86	Ancestral Haloalkane Dehalogenases Show Robustness and Unique Substrate Specificity. ChemBioChem, 2017, 18, 1448-1456.	2.6	45
87	NewProt â€“ a protein engineering portal. Protein Engineering, Design and Selection, 2017, 30, 441-447.	2.1	11
88	FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research, 2017, 45, W393-W399.	14.5	104
89	Different Structural Origins of the Enantioselectivity of Haloalkane Dehalogenases toward Linear Î²â€Haloalkanes: Openâ€“Solvated versus Occludedâ€“Desolvated Active Sites. Angewandte Chemie - International Edition, 2017, 56, 4719-4723.	13.8	15
90	Enzyme Tunnels and Gates As Relevant Targets in Drug Design. Medicinal Research Reviews, 2017, 37, 1095-1139.	10.5	65

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91	Bioremediation 3.0: Engineering pollutant-removing bacteria in the times of systemic biology. Biotechnology Advances, 2017, 35, 845-866.	11.7	240
92	Exploration of Protein Unfolding by Modelling Calorimetry Data from Reheating. Scientific Reports, 2017, 7, 16321.	3.3	39
93	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
94	Metagenome-derived haloalkane dehalogenases with novel catalytic properties. Applied Microbiology and Biotechnology, 2017, 101, 6385-6397.	3.6	8
95	Kinetics of binding of fluorescent ligands to enzymes with engineered access tunnels. FEBS Journal, 2017, 284, 134-148.	4.7	12
96	Wedelolactone Acts as Proteasome Inhibitor in Breast Cancer Cells. International Journal of Molecular Sciences, 2017, 18, 729.	4.1	25
97	Structure-Function Relationships and Engineering of Haloalkane Dehalogenases. , 2017, , 1-21.		0
98	Haloalkane dehalogenases as a subject for crystallographic studies. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C155-C155.	0.1	0
99	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
100	Suppression of protein inactivation during freezing by minimizing pH changes using ionic cryoprotectants. International Journal of Pharmaceutics, 2016, 509, 41-49.	5.2	44
101	Enzyme-Based Test Strips for Visual or Photographic Detection and Quantitation of Gaseous Sulfur Mustard. Analytical Chemistry, 2016, 88, 6044-6049.	6.5	36
102	Engineering a de Novo Transport Tunnel. ACS Catalysis, 2016, 6, 7597-7610.	11.2	84
103	Discovery of Novel Haloalkane Dehalogenase Inhibitors. Applied and Environmental Microbiology, 2016, 82, 1958-1965.	3.1	9
104	Fluorescence-based biosensor for monitoring of environmental pollutants: From concept to field application. Biosensors and Bioelectronics, 2016, 84, 97-105.	10.1	58
105	CAVER: Algorithms for Analyzing Dynamics of Tunnels in Macromolecules. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 505-517.	3.0	108
106	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
107	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
108	Structure-functional relationships of a novel haloalkane dehalogenase with two halide-binding sites. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s218-s218.	0.1	0

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109	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
110	Balancing the Stabilityâ€“Activity Tradeâ€Off by Fineâ€Tuning Dehalogenase Access Tunnels. ChemCatChem, 2015, 7, 648-659.	3.7	39
111	Instability restricts signaling of multiple fibroblast growth factors. Cellular and Molecular Life Sciences, 2015, 72, 2445-2459.	5.4	48
112	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
113	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
114	FireProt: Energy- and Evolution-Based Computational Design of Thermostable Multiple-Point Mutants. PLoS Computational Biology, 2015, 11, e1004556.	3.2	144
115	PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology, 2014, 10, e1003440.	3.2	593
116	Stepwise enhancement of catalytic performance of haloalkane dehalogenase LinB towards Î²-hexachlorocyclohexane. AMB Express, 2014, 4, 72.	3.0	11
117	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
118	Dynamics and hydration explain failed functional transformation in dehalogenase design. Nature Chemical Biology, 2014, 10, 428-430.	8.0	52
119	Microscopic monitoring provides information on structure and properties during biocatalyst immobilization. Biotechnology Journal, 2014, 9, 852-860.	3.5	11
120	Computational tools for designing and engineering enzymes. Current Opinion in Chemical Biology, 2014, 19, 8-16.	6.1	185
121	A Pseudomonas putida Strain Genetically Engineered for 1,2,3-Trichloropropane Bioremediation. Applied and Environmental Microbiology, 2014, 80, 5467-5476.	3.1	42
122	Maximizing the Efficiency of Multienzyme Process by Stoichiometry Optimization. ChemBioChem, 2014, 15, 1891-1895.	2.6	31
123	Comparison of catalysis by haloalkane dehalogenases in aqueous solutions of deep eutectic and organic solvents. Green Chemistry, 2014, 16, 2754-2761.	9.0	28
124	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
125	Immobilized Synthetic Pathway for Biodegradation of Toxic Recalcitrant Pollutant 1,2,3-Trichloropropane. Environmental Science & Technology, 2014, 48, 6859-6866.	10.0	54
126	Computer-Assisted Engineering of the Synthetic Pathway for Biodegradation of a Toxic Persistent Pollutant. ACS Synthetic Biology, 2014, 3, 172-181.	3.8	39

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127	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
128	Crystallographic analysis of 1,2,3-trichloropropane biodegradation by the haloalkane dehalogenase DhaA31. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 209-217.	2.5	10
129	Computational Tools for Designing Smart Libraries. Methods in Molecular Biology, 2014, 1179, 291-314.	0.9	21
130	Online Monitoring of Biodegradation Processes Using Enzymatic Biosensors. , 2014, , 155-179.		1
131	Crystal structure of the novel haloalkane dehalogenases. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1678-C1678.	0.1	1
132	Sphingobium baderi sp. nov., isolated from a hexachlorocyclohexane dump site. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 673-678.	1.7	29
133	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
134	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
135	Strategies for Stabilization of Enzymes in Organic Solvents. ACS Catalysis, 2013, 3, 2823-2836.	11.2	514
136	Novosphingobium barchaimii sp. nov., isolated from hexachlorocyclohexane-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 667-672.	1.7	46
137	Organic coâ€solvents affect activity, stability and enantioselectivity of haloalkane dehalogenases. Biotechnology Journal, 2013, 8, 719-729.	3.5	36
138	Software tools for identification, visualization and analysis of protein tunnels and channels. Biotechnology Advances, 2013, 31, 38-49.	11.7	74
139	DspA from Strongylocentrotus purpuratus: The first biochemically characterized haloalkane dehalogenase of non-microbial origin. Biochimie, 2013, 95, 2091-2096.	2.6	26
140	Gates of Enzymes. Chemical Reviews, 2013, 113, 5871-5923.	47.7	216
141	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
142	Interaction of organic solvents with protein structures at protein-solvent interface. Journal of Molecular Modeling, 2013, 19, 4701-4711.	1.8	33
143	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
144	Varenicline and nicotine enhance GABAergic synaptic transmission in rat CA1 hippocampal and medial septum/diagonal band neurons. Life Sciences, 2013, 92, 337-344.	4.3	15

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145	Expansion of Access Tunnels and Activeâ€Site Cavities Influence Activity of Haloalkane Dehalogenases in Organic Cosolvents. ChemBioChem, 2013, 14, 890-897.	2.6	33
146	Are Time-Dependent Fluorescence Shifts at the Tunnel Mouth of Haloalkane Dehalogenase Enzymes Dependent on the Choice of the Chromophore?. Journal of Physical Chemistry B, 2013, 117, 7898-7906.	2.6	14
147	Release of Halide Ions from the Buried Active Site of the Haloalkane Dehalogenase LinB Revealed by Stopped-Flow Fluorescence Analysis and Free Energy Calculations. Journal of Physical Chemistry B, 2013, 117, 14329-14335.	2.6	4
148	Haloalkane dehalogenases: Biotechnological applications. Biotechnology Journal, 2013, 8, 32-45.	3.5	126
149	Sphingobium czechense sp. nov., isolated from a hexachlorocyclohexane dump site. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 723-728.	1.7	18
150	Differences in crystallization of two LinB variants fromSphingobium japonicumUT26. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 284-287.	0.7	5
151	Crystallographic analysis of new psychrophilic haloalkane dehalogenases: DpcA fromPsychrobacter cryohalolentisK5 and DmxA fromMarinobactersp. ELB17. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 683-688.	0.7	8
152	Lincomycin Biosynthesis Involves a Tyrosine Hydroxylating Heme Protein of an Unusual Enzyme Family. PLoS ONE, 2013, 8, e79974.	2.5	24
153	The PCNA Interaction Protein Box Sequence in Rad54 Is an Integral Part of Its ATPase Domain and Is Required for Efficient DNA Repair and Recombination. PLoS ONE, 2013, 8, e82630.	2.5	9
154	CAVER 3.0: A Tool for the Analysis of Transport Pathways in Dynamic Protein Structures. PLoS Computational Biology, 2012, 8, e1002708.	3.2	991
155	Effects of developmental nicotine exposure in rats on decision-making in adulthood. Behavioural Pharmacology, 2012, 23, 34-42.	1.7	29
156	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
157	Biochemical Characterization of a Novel Haloalkane Dehalogenase from a Cold-Adapted Bacterium. Applied and Environmental Microbiology, 2012, 78, 4995-4998.	3.1	33
158	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
159	Characterization of Protein Glycosylation in Francisella tularensis subsp. holarctica. Molecular and Cellular Proteomics, 2012, 11, M111.015016-1-M111.015016-12.	3.8	36
160	Rad52 SUMOylation affects the efficiency of the DNA repair. Nucleic Acids Research, 2012, 40, 3775-3775.	14.5	0
161	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
162	Analyzer for fluorescent biosensing application. , 2011, , .		0

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163	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
164	Development of a Crystallization Protocol for the DbeA1 Variant of Novel Haloalkane Dehalogenase fromBradyrhizobium elkaniUSDA94. Crystal Growth and Design, 2011, 11, 516-519.	3.0	3
165	The new platinum-based anticancer agent LA-12 induces retinol binding protein 4 in vivo. Proteome Science, 2011, 9, 68.	1.7	23
166	Crystallization and preliminary X-ray diffraction analysis of the wild-type haloalkane dehalogenase DhaA and its variant DhaA13 complexed with different ligands. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 253-257.	0.7	5
167	Crystallization and crystallographic analysis of theRhodococcus rhodochrousNCIMB 13064 DhaA mutant DhaA31 and its complex with 1,2,3-trichloropropane. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 397-400.	0.7	4
168	Elicitinâ€“membrane interaction is driven by a positive charge on the protein surface: Role of Lys13 residue in lipids loading and resistance induction. Plant Physiology and Biochemistry, 2011, 49, 321-328.	5.8	15
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