

Hein J Wijma

List of Publications by Year in descending order

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39
papers

1,695
citations

279798

23
h-index

302126

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docs citations

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times ranked

2029
citing authors

#	ARTICLE	IF	CITATIONS
1	Computationally designed libraries for rapid enzyme stabilization. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 49-58.	2.1	205
2	Structure- and sequence-analysis inspired engineering of proteins for enhanced thermostability. <i>Current Opinion in Structural Biology</i> , 2013, 23, 588-594.	5.7	161
3	Computational redesign of enzymes for regio- and enantioselective hydroamination. <i>Nature Chemical Biology</i> , 2018, 14, 664-670.	8.0	137
4	Enantioselective Enzymes by Computational Design and In Silico Screening. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 3726-3730.	13.8	119
5	Real-Time Conformational Changes and Controlled Orientation of Native Proteins Inside a Protein Nanoreactor. <i>Journal of the American Chemical Society</i> , 2017, 139, 18640-18646.	13.7	83
6	A Random-sequential Mechanism for Nitrite Binding and Active Site Reduction in Copper-containing Nitrite Reductase*. <i>Journal of Biological Chemistry</i> , 2006, 281, 16340-16346.	3.4	72
7	Computational Library Design for Increasing Haloalkane Dehalogenase Stability. <i>ChemBioChem</i> , 2014, 15, 1660-1672.	2.6	68
8	Versatile Peptide C-Terminal Functionalization via a Computationally Engineered Peptide Amidase. <i>ACS Catalysis</i> , 2016, 6, 5405-5414.	11.2	60
9	Bidirectional Catalysis by Copper-Containing Nitrite Reductase. <i>Biochemistry</i> , 2004, 43, 10467-10474.	2.5	59
10	Stabilization of cyclohexanone monooxygenase by a computationally designed disulfide bond spanning only one residue. <i>FEBS Open Bio</i> , 2014, 4, 168-174.	2.3	59
11	Computational design gains momentum in enzyme catalysis engineering. <i>FEBS Journal</i> , 2013, 280, 2948-2960.	4.7	58
12	Directed Evolution Strategies for Enantiocomplementary Haloalkane Dehalogenases: From Chemical Waste to Enantiopure Building Blocks. <i>ChemBioChem</i> , 2012, 13, 137-148.	2.6	55
13	Protein Film Voltammetry of Copper-Containing Nitrite Reductase Reveals Reversible Inactivation. <i>Journal of the American Chemical Society</i> , 2007, 129, 8557-8565.	13.7	45
14	Biocatalytic and Structural Properties of a Highly Engineered Halohydrin Dehalogenase. <i>ChemBioChem</i> , 2013, 14, 870-881.	2.6	44
15	Computationally Efficient and Accurate Enantioselectivity Modeling by Clusters of Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 2079-2092.	5.4	44
16	Reconstitution of the Type-1 Active Site of the H145G/A Variants of Nitrite Reductase by Ligand Insertion. <i>Biochemistry</i> , 2003, 42, 4075-4083.	2.5	37
17	Kinetic Resolution of α -Bromoamides: Experimental and Theoretical Investigation of Highly Enantioselective Reactions Catalyzed by Haloalkane Dehalogenases. <i>Advanced Synthesis and Catalysis</i> , 2011, 353, 931-944.	4.3	35
18	Exploring the gating mechanisms of aquaporin-3: new clues for the design of inhibitors?. <i>Molecular BioSystems</i> , 2016, 12, 1564-1573.	2.9	32

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19	Sensing Nitrite through a Pseudoazurin-Nitrite Reductase Electron Transfer Relay. <i>ChemPhysChem</i> , 2005, 6, 1114-1120.	2.1	29
20	Biochemical Properties and Crystal Structure of a \hat{I}^2 -Phenylalanine Aminotransferase from <i>Variovorax paradoxus</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 185-195.	3.1	29
21	Computational Redesign of an \hat{I}° -Transaminase from <i>Pseudomonas jessenii</i> for Asymmetric Synthesis of Enantiopure Bulky Amines. <i>ACS Catalysis</i> , 2021, 11, 10733-10747.	11.2	28
22	Effect of the Methionine Ligand on the Reorganization Energy of the Type-1 Copper Site of Nitrite Reductase. <i>Journal of the American Chemical Society</i> , 2007, 129, 519-525.	13.7	25
23	Engineering of an enantioselective tyrosine aminomutase by mutation of a single active site residue in phenylalanine aminomutase. <i>Chemical Communications</i> , 2010, 46, 8157.	4.1	23
24	A robust cosolvent-compatible halohydrin dehalogenase by computational library design. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 173-187.	2.1	23
25	Hot or not? Discovery and characterization of a thermostable alditol oxidase from <i>Acidothermus cellulolyticus</i> 11B. <i>Applied Microbiology and Biotechnology</i> , 2012, 95, 389-403.	3.6	20
26	Calorimetric and spectroscopic investigations of the thermal denaturation of wild type nitrite reductase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1752, 47-55.	2.3	19
27	X-ray crystallographic validation of structure predictions used in computational design for protein stabilization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 940-951.	2.6	17
28	Computational Prediction of \hat{I}° -Transaminase Specificity by a Combination of Docking and Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5569-5580.	5.4	17
29	The Substrate-Bound Type 2 Copper Site of Nitrite Reductase: The Nitrogen Hyperfine Coupling of Nitrite Revealed by Pulsed EPR. <i>Biochemistry</i> , 2005, 44, 15193-15202.	2.5	15
30	Computational Design of Enantiocomplementary Epoxide Hydrolases for Asymmetric Synthesis of Aliphatic and Aromatic Diols. <i>ChemBioChem</i> , 2020, 21, 1893-1904.	2.6	15
31	A Rearranging Ligand Enables Allosteric Control of Catalytic Activity in Copper-containing Nitrite Reductase. <i>Journal of Molecular Biology</i> , 2006, 358, 1081-1093.	4.2	12
32	Asymmetric Synthesis of Optically Pure Aliphatic Amines with an Engineered Robust \hat{I}° -Transaminase. <i>Catalysts</i> , 2020, 10, 1310.	3.5	10
33	Aminoacyl-coenzyme A synthesis catalyzed by a CoA ligase from <i>Penicillium chrysogenum</i> . <i>FEBS Letters</i> , 2011, 585, 893-898.	2.8	8
34	A Systematic Study of the Influence of Peptide Modification of a Gold Electrode on the Cyclic Voltammetry of Pseudoazurin from <i>Alcaligenes faecalis</i> Strain S-6. <i>Electroanalysis</i> , 2004, 16, 1155-1165.	2.9	7
35	Stabilizing Aqdc, a <i>Pseudomonas</i> Quinolone Signal-Cleaving Dioxygenase from <i>Mycobacteria</i> , by FRESCO-Based Protein Engineering. <i>ChemBioChem</i> , 2021, 22, 733-742.	2.6	7
36	Thermodynamics Determine the Diastereochemical Outcome of Catalytic Reactions. <i>ChemCatChem</i> , 2021, 13, 2530-2536.	3.7	7

#	ARTICLE	IF	CITATIONS
37	Catalytic and structural properties of ATP -dependent caprolactamase from <i>Pseudomonas jessenii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1079-1098.	2.6	6
38	Thermal stability effects of removing the type-2 copper ligand His306 at the interface of nitrite reductase subunits. <i>European Biophysics Journal</i> , 2007, 36, 805-813.	2.2	3
39	Metabolism of β -valine via a CoA-dependent ammonia lyase pathway. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8987-8998.	3.6	2