

Justin B Siegel

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,293
citations

840776

11
h-index

677142

22
g-index

27
all docs

27
docs citations

27
times ranked

1930
citing authors

#	ARTICLE	IF	CITATIONS
1	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
2	Computational protein design enables a novel one-carbon assimilation pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3704-3709.	7.1	286
3	Impact of scaffold rigidity on the design and evolution of an artificial Diels-Alderase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8013-8018.	7.1	111
4	Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. <i>Bioinformatics</i> , 2017, 33, 2765-2767.	4.1	77
5	Engineering a nicotinamide mononucleotide redox cofactor system for biocatalysis. <i>Nature Chemical Biology</i> , 2020, 16, 87-94.	8.0	64
6	Comparative analyses of ubiquitin-like <i>ATG8</i> and cysteine protease <i>ATG4</i> autophagy genes in the plant lineage and cross-kingdom processing of ATG8 by ATG4. <i>Autophagy</i> , 2016, 12, 2054-2068.	9.1	50
7	Mechanistic Analysis of an Engineered Enzyme that Catalyzes the Formose Reaction. <i>ChemBioChem</i> , 2015, 16, 1950-1954.	2.6	39
8	Discovery of a natural cyan blue: A unique food-sourced anthocyanin could replace synthetic brilliant blue. <i>Science Advances</i> , 2021, 7, .	10.3	34
9	Computer-Aided Drug Design for Undergraduates. <i>Journal of Chemical Education</i> , 2019, 96, 920-925.	2.3	21
10	Molecular annotation of food " Towards personalized diet and precision health. <i>Trends in Food Science and Technology</i> , 2019, 91, 675-680.	15.1	17
11	Changing Face: A Key Residue for the Addition of Water by Sclareol Synthase. <i>ACS Catalysis</i> , 2018, 8, 3133-3137.	11.2	14
12	Discovery, Design, and Structural Characterization of Alkane-Producing Enzymes across the Ferritin-like Superfamily. <i>Biochemistry</i> , 2020, 59, 3834-3843.	2.5	11
13	Improvement of a Potential Anthrax Therapeutic by Computational Protein Design. <i>Journal of Biological Chemistry</i> , 2011, 286, 32586-32592.	3.4	10
14	β -Glucosidase Discovery and Design for the Degradation of Oleuropein. <i>ACS Omega</i> , 2018, 3, 15754-15762.	3.5	8
15	High-throughput mutagenesis reveals unique structural features of human ADAR1. <i>Nature Communications</i> , 2020, 11, 5130.	12.8	8
16	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. <i>The Biophysicist</i> , 2021, 2, 108-122.	0.3	8
17	Engineering Embden-Meyerhof-Parnas Glycolysis to Generate Noncanonical Reducing Power. <i>ACS Catalysis</i> , 2022, 12, 8582-8592.	11.2	5
18	Assessing Alkene Reactivity toward Cytochrome P450-Mediated Epoxidation through Localized Descriptors and Regression Modeling. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1979-1987.	5.4	4

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19	Systematic Functional Analysis of Active-Site Residues in <i>Thermoplasma volcanium</i> -Threonine Dehydrogenase from <i>Thermoplasma volcanium</i> . ACS Omega, 2017, 2, 3308-3314.	3.5	3
20	The pyruvate decarboxylase activity of IpdC is a limitation for isobutanol production by <i>Klebsiella pneumoniae</i> . , 2022, 15, 41.		3
21	Regression Modeling for the Prediction of Hydrogen Atom Transfer Barriers in Cytochrome P450 from Semiempirically Derived Descriptors. Chemistry Methods, 2022, 2, .	3.8	2
22	A Benchmark for Homomeric Enzyme Active Site Structure Prediction Highlights the Importance of Accurate Modeling of Protein Symmetry. ACS Omega, 2019, 4, 22356-22362.	3.5	1
23	Treatment of experimental anthrax with pegylated circularly permuted capsule depolymerase. Science Translational Medicine, 2021, 13, eabh1682.	12.4	1