Justin B Siegel

List of Publications by Year
in descending order

23	1,293	840776 11	677142 22
papers	citations	h-index	g-index

27	27	27	1930
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Assessing Alkene Reactivity toward Cytochrome P450-Mediated Epoxidation through Localized Descriptors and Regression Modeling. Journal of Chemical Information and Modeling, 2022, 62, 1979-1987.	5.4	4
2	The pyruvate decarboxylase activity of IpdC is a limitation for isobutanol production by Klebsiella pneumoniae. , 2022, 15, 41.		3
3	Regression Modeling for the Prediction of Hydrogen Atom Transfer Barriers in Cytochrome P450 from Semiâ€empirically Derived Descriptors. Chemistry Methods, 2022, 2, .	3.8	2
4	Engineering Embdenâ€“Meyerhofâ€“Parnas Glycolysis to Generate Noncanonical Reducing Power. ACS Catalysis, 2022, 12, 8582-8592.	11.2	5
5	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
6	Discovery of a natural cyan blue: A unique food-sourced anthocyanin could replace synthetic brilliant blue. Science Advances, 2021, 7, .	10.3	34
7	Treatment of experimental anthrax with pegylated circularly permuted capsule depolymerase. Science Translational Medicine, 2021, 13, eabh1682.	12.4	1
8	Engineering a nicotinamide mononucleotide redox cofactor system for biocatalysis. Nature Chemical Biology, 2020, 16, 87-94.	8.0	64
9	High-throughput mutagenesis reveals unique structural features of human ADAR1. Nature Communications, 2020, 11, 5130.	12.8	8
10	Discovery, Design, and Structural Characterization of Alkane-Producing Enzymes across the Ferritin-like Superfamily. Biochemistry, 2020, 59, 3834-3843.	2.5	11
11	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
12	Molecular annotation of food â€“ Towards personalized diet and precision health. Trends in Food Science and Technology, 2019, 91, 675-680.	15.1	17
13	Computer-Aided Drug Design for Undergraduates. Journal of Chemical Education, 2019, 96, 920-925.	2.3	21
14	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
15	Changing Face: A Key Residue for the Addition of Water by Sclareol Synthase. ACS Catalysis, 2018, 8, 3133-3137.	11.2	14
16	Î²-Glucosidase Discovery and Design for the Degradation of Oleuropein. ACS Omega, 2018, 3, 15754-15762.	3.5	8
17	Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. Bioinformatics, 2017, 33, 2765-2767.	4.1	77
18	Systematic Functional Analysis of Active-Site Residues in <scp>l</scp>-Threonine Dehydrogenase from Thermoplasma volcanium. ACS Omega, 2017, 2, 3308-3314.	3.5	3

#	Article	IF	Citations
19	Comparative analyses of ubiquitin-like ATG8 and cysteine protease ATG4 autophagy genes in the plant lineage and cross-kingdom processing of ATG8 by ATG4. Autophagy, 2016, 12, 2054-2068.	9.1	50
20	Mechanistic Analysis of an Engineered Enzyme that Catalyzes the Formose Reaction. ChemBioChem, 2015, 16, 1950-1954.	2.6	39
21	Computational protein design enables a novel one-carbon assimilation pathway. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3704-3709.	7.1	286
22	Impact of scaffold rigidity on the design and evolution of an artificial Diels-Alderase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8013-8018.	7.1	111
23	Improvement of a Potential Anthrax Therapeutic by Computational Protein Design. Journal of Biological Chemistry, 2011, 286, 32586-32592.	3.4	10