Reinhard Sterner

List of Publications by Year
in descending order

85 papers	3,173 citations	201674 27 h-index	168389 53 g-index
167 all docs	167 docs citations	167 times ranked	2619 citing authors

#	Article	IF	Citations
1	Photoswitching of Feedback Inhibition by Tryptophan in Anthranilate Synthase. ACS Synthetic Biology, 2022, 11, 2846-2856.	3.8	2
2	Towards Photochromic Azobenzeneâ€Based Inhibitors for Tryptophan Synthase. Chemistry - A European Journal, 2021, 27, 2439-2451.	3.3	11
3	Reprogramming the Specificity of a Protein Interface by Computational and Data-Driven Design. Structure, 2021, 29, 292-304.e3.	3.3	2
4	The Structure of Carbamoylphosphate Synthetase Unravels Central Functional Features of a Key Metabolic Multienzyme Complex. Biochemistry, 2021, 60, 3422-3423.	2.5	1
5	Molecular basis for the allosteric activation mechanism of the heterodimeric imidazole glycerol phosphate synthase complex. Nature Communications, 2021, 12, 2748.	12.8	22
6	<i>In Silico</i> Identification and Experimental Validation of Distal Activity-Enhancing Mutations in Tryptophan Synthase. ACS Catalysis, 2021, 11, 13733-13743.	11.2	30
7	Analysis of allosteric communication in a multienzyme complex by ancestral sequence reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 346-354.	7.1	26
8	Significance of the Protein Interface Configuration for Allostery in Imidazole Glycerol Phosphate Synthase. Biochemistry, 2020, 59, 2729-2742.	2.5	15
9	Quaternary Structure of the Tryptophan Synthase Î±-Subunit Homolog BX1 from <i>Zea mays</i>. Journal of the American Society for Mass Spectrometry, 2020, 31, 227-233.	2.8	4
10	Light-Regulation of Tryptophan Synthase by Combining Protein Design and Enzymology. International Journal of Molecular Sciences, 2019, 20, 5106.	4.1	8
11	Light Regulation of Enzyme Allostery through Photo-responsive Unnatural Amino Acids. Cell Chemical Biology, 2019, 26, 1501-1514.e9.	5.2	25
12	Library Selection with a Randomized Repertoire of (Î²Î±)₈-Barrel Enzymes Results in Unexpected Induction of Gene Expression. Biochemistry, 2019, 58, 4207-4217.	2.5	0
13	Mapping key amino acid residues for the epimerase efficiency and stereospecificity of the sex pheromone biosynthetic short-chain dehydrogenases/reductases of Nasonia. Scientific Reports, 2019, 9, 330.	3.3	3
14	A Fold-Independent Interface Residue Is Crucial for Complex Formation and Allosteric Signaling in Class I Glutamine Amidotransferases. Biochemistry, 2019, 58, 2584-2588.	2.5	10
15	Generation of a Standâ€Alone Tryptophan Synthase Î±â€Subunit by Mimicking an Evolutionary Blueprint. ChemBioChem, 2019, 20, 2747-2751.	2.6	4
16	Prediction of quaternary structure by analysis of hot spot residues in proteinâ€protein interfaces: the case of anthranilate phosphoribosyltransferases. Proteins: Structure, Function and Bioinformatics, 2019, 87, 815-825.	2.6	18
17	Mapping the Allosteric Communication Network of Aminodeoxychorismate Synthase. Journal of Molecular Biology, 2019, 431, 2718-2728.	4.2	11
18	Functional characterisation of two Î”12-desaturases demonstrates targeted production of linoleic acid as pheromone precursor in<i>Nasonia</i>. Journal of Experimental Biology, 2019, 222, .	1.7	16

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19	Relationship of Catalysis and Active Site Loop Dynamics in the (Î²Î±)₈-Barrel Enzyme Indole-3-glycerol Phosphate Synthase. Biochemistry, 2018, 57, 3265-3277.	2.5	12
20	Standardized cloning vectors for protein production and generation of large gene libraries in <i>Escherichia coli</i>. BioTechniques, 2018, 64, 24-26.	1.8	17
21	Hexamerization of Geranylgeranylglyceryl Phosphate Synthase Ensures Structural Integrity and Catalytic Activity at High Temperatures. Biochemistry, 2018, 57, 2335-2348.	2.5	10
22	Evolutionary Morphing of Tryptophan Synthase: Functional Mechanisms for the Enzymatic Channeling of Indole. Journal of Molecular Biology, 2018, 430, 5066-5079.	4.2	6
23	Artificial Light Regulation of an Allosteric Bienzyme Complex by a Photosensitive Ligand. ChemBioChem, 2018, 19, 1750-1757.	2.6	19
24	Library Generation and Auxotrophic Selection Assays in Escherichia coli and Thermus thermophilus. Methods in Molecular Biology, 2018, 1685, 333-345.	0.9	0
25	Combining ancestral sequence reconstruction with protein design to identify an interface hotspot in a key metabolic enzyme complex. Proteins: Structure, Function and Bioinformatics, 2017, 85, 312-321.	2.6	14
26	Evolutionary diversification of proteinâ€“protein interactions by interface add-ons. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8333-E8342.	7.1	22
27	Photochromic coenzyme Q derivatives: switching redox potentials with light. Chemical Science, 2017, 8, 6474-6483.	7.4	27
28	Rosetta:MSF: a modular framework for multi-state computational protein design. PLoS Computational Biology, 2017, 13, e1005600.	3.2	43
29	Identification and Characterization of Heptaprenylglyceryl Phosphate Processing Enzymes in Bacillus subtilis. Journal of Biological Chemistry, 2016, 291, 14861-14870.	3.4	6
30	Epimerisation of chiral hydroxylactones by short-chain dehydrogenases/reductases accounts for sex pheromone evolution in Nasonia. Scientific Reports, 2016, 6, 34697.	3.3	15
31	Reconstruction of ancestral enzymes. Perspectives in Science, 2016, 9, 17-23.	0.6	22
32	Ancestral Tryptophan Synthase Reveals Functional Sophistication of Primordial Enzyme Complexes. Cell Chemical Biology, 2016, 23, 709-715.	5.2	31
33	Ancestral protein reconstruction: techniques and applications. Biological Chemistry, 2016, 397, 1-21.	2.5	121
34	Long-Term Persistence of Bi-functionality Contributes to the Robustness of Microbial Life through Exaptation. PLoS Genetics, 2016, 12, e1005836.	3.5	18
35	Conversion of Anthranilate Synthase into Isochorismate Synthase: Implications for the Evolution of Chorismateâ€Utilizing Enzymes. Angewandte Chemie - International Edition, 2015, 54, 11270-11274.	13.8	14
36	Improving thermal and detergent stability of Bacillus stearothermophilus neopullulanase by rational enzyme design. Protein Engineering, Design and Selection, 2015, 28, 147-151.	2.1	14

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37	Substrate Specifity and Quaternary Structure of a Novel Class of Tryptophan Synthases. FASEB Journal, 2015, 29, 573.5.	0.5	0
38	A comprehensive analysis of the geranylgeranylglyceryl phosphate synthase enzyme family identifies novel members and reveals mechanisms of substrate specificity and quaternary structure organization. Molecular Microbiology, 2014, 92, 885-899.	2.5	23
39	Evidence for the Existence of Elaborate Enzyme Complexes in the Paleoarchean Era. Journal of the American Chemical Society, 2014, 136, 122-129.	13.7	51
40	Exploiting Protein Symmetry To Design Lightâ€Controllable Enzyme Inhibitors. Angewandte Chemie - International Edition, 2014, 53, 595-598.	13.8	61
41	Activation of a Chimeric Rpb5/RpoH Subunit Using Library Selection. PLoS ONE, 2014, 9, e87485.	2.5	6
42	Molecular Engineering of Organophosphate Hydrolysis Activity from a Weak Promiscuous Lactonase Template. Journal of the American Chemical Society, 2013, 135, 11670-11677.	13.7	53
43	Establishing catalytic activity on an artificial (Î²Î±)₈â€barrel protein designed from identical halfâ€barrels. FEBS Letters, 2013, 587, 2798-2805.	2.8	9
44	Kinetic Mechanism of Indole-3-glycerol Phosphate Synthase. Biochemistry, 2013, 52, 132-142.	2.5	14
45	Directed evolution of (ÂÂ)8-barrel enzymes: establishing phosphoribosylanthranilate isomerisation activity on the scaffold of the tryptophan synthase Â-subunit. Protein Engineering, Design and Selection, 2012, 25, 285-293.	2.1	17
46	A sugar isomerization reaction established on various (ÂÂ)8-barrel scaffolds is based on substrate-assisted catalysis. Protein Engineering, Design and Selection, 2012, 25, 751-760.	2.1	7
47	Catalysis Uncoupling in a Glutamine Amidotransferase Bienzyme by Unblocking the Glutaminase Active Site. Chemistry and Biology, 2012, 19, 1589-1599.	6.0	40
48	Experimental Assessment of the Importance of Amino Acid Positions Identified by an Entropy-Based Correlation Analysis of Multiple-Sequence Alignments. Biochemistry, 2012, 51, 5633-5641.	2.5	12
49	Folding Mechanism of an Extremely Thermostable (Î²Î±)₈-Barrel Enzyme: A High Kinetic Barrier Protects the Protein from Denaturation. Biochemistry, 2012, 51, 3420-3432.	2.5	10
50	Conservation of the Folding Mechanism between Designed Primordial (Î²Î±)₈-Barrel Proteins and Their Modern Descendant. Journal of the American Chemical Society, 2012, 134, 12786-12791.	13.7	21
51	Dimerization Determines Substrate Specificity of a Bacterial Prenyltransferase. ChemBioChem, 2012, 13, 1297-1303.	2.6	6
52	Stabilization of a Metabolic Enzyme by Library Selection in <i>Thermus thermophilus</i>. ChemBioChem, 2011, 12, 1581-1588.	2.6	10
53	A Fast and Precise Approach for Computational Saturation Mutagenesis and its Experimental Validation by Using an Artificial (Î²Î±)₈â€Barrel Protein. ChemBioChem, 2011, 12, 1544-1550.	2.6	10
54	Related (Î²Î±)₈â€Barrel Proteins in Histidine and Tryptophan Biosynthesis: A Paradigm to Study Enzyme Evolution. ChemBioChem, 2011, 12, 1487-1494.	2.6	20

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55	Editorial: Directed Evolution: A Powerful Approach to Optimising and Understanding Enzymes. ChemBioChem, 2011, 12, 1439-1440.	2.6	3
56	Computational and Experimental Evidence for the Evolution of a (Î²Î±)8-Barrel Protein from an Ancestral Quarter-Barrel Stabilised by Disulfide Bonds. Journal of Molecular Biology, 2010, 398, 763-773.	4.2	54
57	Enhancing the Stability and Solubility of the Glucocorticoid Receptor Ligand-Binding Domain by High-Throughput Library Screening. Journal of Molecular Biology, 2010, 403, 562-577.	4.2	46
58	Establishing wild-type levels of catalytic activity on natural and artificial (Î²Î±) ₈ -barrel protein scaffolds. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3704-3709.	7.1	65
59	TransCent: Computational enzyme design by transferring active sites and considering constraints relevant for catalysis. BMC Bioinformatics, 2009, 10, 54.	2.6	8
60	High-Resolution Crystal Structure of an Artificial (Î²Î±)8-Barrel Protein Designed from Identical Half-Barrels. Biochemistry, 2009, 48, 1145-1147.	2.5	36
61	Activation of Anthranilate Phosphoribosyltransferase from Sulfolobus solfataricus by Removal of Magnesium Inhibition and Acceleration of Product Release,. Biochemistry, 2009, 48, 5199-5209.	2.5	11
62	A Robust Protein Host for Anchoring Chelating Ligands and Organocatalysts. ChemBioChem, 2008, 9, 552-564.	2.6	67
63	Computational Design of Enzymes. Chemistry and Biology, 2008, 15, 421-423.	6.0	24
64	A Rationally Designed Monomeric Variant of Anthranilate Phosphoribosyltransferase from Sulfolobus solfataricus is as Active as the Dimeric Wild-type Enzyme but Less Thermostable. Journal of Molecular Biology, 2008, 376, 506-516.	4.2	22
65	Stabilisation of a (Î²Î±)8-Barrel Protein Designed from Identical Half Barrels. Journal of Molecular Biology, 2007, 372, 114-129.	4.2	44
66	Structural and Mutational Analysis of Substrate Complexation by Anthranilate Phosphoribosyltransferase from Sulfolobus solfataricus. Journal of Biological Chemistry, 2006, 281, 21410-21421.	3.4	23
67	Role of the N-Terminal Extension of the (Î²Î±)8-Barrel Enzyme Indole-3-glycerol Phosphate Synthase for Its Fold, Stability, and Catalytic Activityâ€,â€¡. Biochemistry, 2005, 44, 16405-16412.	2.5	21
68	Catalytic Versatility, Stability, and Evolution of the (Î²Î±)8-Barrel Enzyme Fold. Chemical Reviews, 2005, 105, 4038-4055.	47.7	181
69	Mimicking enzyme evolution by generating new (ÂÂ)8-barrels from (ÂÂ)4-half-barrels. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16448-16453.	7.1	97
70	BIOCHEMISTRY: De Novo Design of an Enzyme. Science, 2004, 304, 1916-1917.	12.6	14
71	Interconverting the Catalytic Activities of (Î²Î±)8-barrel Enzymes from Different Metabolic Pathways: Sequence Requirements and Molecular Analysis. Journal of Molecular Biology, 2004, 337, 871-879.	4.2	43
72	Protein Design at the Crossroads of Biotechnology, Chemistry, Theory, and Evolution. Angewandte Chemie - International Edition, 2003, 42, 140-142.	13.8	8

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73	Two (Î²Î±)8-Barrel Enzymes of Histidine and Tryptophan Biosynthesis Have Similar Reaction Mechanisms and Common Strategies for Protecting Their Labile Substrates,. Biochemistry, 2002, 41, 12032-12042.	2.5	68
74	A common evolutionary origin of two elementary enzyme folds. FEBS Letters, 2002, 510, 133-135.	2.8	36
75	Structural Evidence for Ammonia Tunneling across the (Î²Î±)8 Barrel of the Imidazole Glycerol Phosphate Synthase Bienzyme Complex. Structure, 2002, 10, 185-193.	3.3	109
76	Stability, catalytic versatility and evolution of the (Î²Î±)8-barrel fold. Current Opinion in Biotechnology, 2001, 12, 376-381.	6.6	83
77	Dissection of a (betaalpha)8-barrel enzyme into two folded halves. Nature Structural Biology, 2001, 8, 32-36.	9.7	134
78	Imidazole Glycerol Phosphate Synthase fromThermotoga maritima. Journal of Biological Chemistry, 2001, 276, 20387-20396.	3.4	86
79	Structure and function of mutationally generated monomers of dimeric phosphoribosylanthranilate isomerase from Thermotoga maritima. Structure, 2000, 8, 265-276.	3.3	92
80	Structural Evidence for Evolution of the beta /alpha Barrel Scaffold by Gene Duplication and Fusion. Science, 2000, 289, 1546-1550.	12.6	310
81	Crystal Structure at 2.0 Ã… Resolution of Phosphoribosyl Anthranilate Isomerase from the HyperthermophileThermotoga maritima:Â Possible Determinants of Protein Stabilityâ€,#. Biochemistry, 1997, 36, 6009-6016.	2.5	100
82	Small-angle X-ray scattering reveals differences between the quaternary structures of oxygenated and deoxygenated tarantula hemocyanin. FEBS Letters, 1996, 393, 226-230.	2.8	25
83	Phosphoribosyl anthranilate isomerase from <i>Thermotoga maritima</i> is an extremely stable and active homodimer. Protein Science, 1996, 5, 2000-2008.	7.6	75
84	2.0 Ã¥ structure of indole-3-glycerol phosphate synthase from the hyperthermophile Sulfolobus solfataricus: possible determinants of protein stability. Structure, 1995, 3, 1295-1306.	3.3	241
85	Extreme thermostability of tarantula hemocyanin. FEBS Letters, 1995, 364, 9-12.	2.8	33