

# Reinhard Sterner

## List of Publications by Year in descending order

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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	Structural Evidence for Evolution of the beta /alpha Barrel Scaffold by Gene Duplication and Fusion. <i>Science</i> , 2000, 289, 1546-1550.	12.6	310
2	2.0 Å structure of indole-3-glycerol phosphate synthase from the hyperthermophile <i>Sulfolobus solfataricus</i> : possible determinants of protein stability. <i>Structure</i> , 1995, 3, 1295-1306.	3.3	241
3	Catalytic Versatility, Stability, and Evolution of the (β/α) <sub>8</sub> -Barrel Enzyme Fold. <i>Chemical Reviews</i> , 2005, 105, 4038-4055.	47.7	181
4	Dissection of a (β/α) <sub>8</sub> -barrel enzyme into two folded halves. <i>Nature Structural Biology</i> , 2001, 8, 32-36.	9.7	134
5	Ancestral protein reconstruction: techniques and applications. <i>Biological Chemistry</i> , 2016, 397, 1-21.	2.5	121
6	Structural Evidence for Ammonia Tunneling across the (β/α) <sub>8</sub> Barrel of the Imidazole Glycerol Phosphate Synthase Bifunctional Complex. <i>Structure</i> , 2002, 10, 185-193.	3.3	109
7	Crystal Structure at 2.0 Å Resolution of Phosphoribosyl Anthranilate Isomerase from the Hyperthermophile <i>Thermotoga maritima</i> : Possible Determinants of Protein Stability. <i>Biochemistry</i> , 1997, 36, 6009-6016.	2.5	100
8	Mimicking enzyme evolution by generating new (β/α) <sub>8</sub> -barrels from (β/α) <sub>4</sub> -half-barrels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16448-16453.	7.1	97
9	Structure and function of mutationally generated monomers of dimeric phosphoribosylanthranilate isomerase from <i>Thermotoga maritima</i> . <i>Structure</i> , 2000, 8, 265-276.	3.3	92
10	Imidazole Glycerol Phosphate Synthase from <i>Thermotoga maritima</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 20387-20396.	3.4	86
11	Stability, catalytic versatility and evolution of the (β/α) <sub>8</sub> -barrel fold. <i>Current Opinion in Biotechnology</i> , 2001, 12, 376-381.	6.6	83
12	Phosphoribosyl anthranilate isomerase from <i>Thermotoga maritima</i> is an extremely stable and active homodimer. <i>Protein Science</i> , 1996, 5, 2000-2008.	7.6	75
13	Two (β/α) <sub>8</sub> -Barrel Enzymes of Histidine and Tryptophan Biosynthesis Have Similar Reaction Mechanisms and Common Strategies for Protecting Their Labile Substrates. <i>Biochemistry</i> , 2002, 41, 12032-12042.	2.5	68
14	A Robust Protein Host for Anchoring Chelating Ligands and Organocatalysts. <i>ChemBioChem</i> , 2008, 9, 552-564.	2.6	67
15	Establishing wild-type levels of catalytic activity on natural and artificial (β/α) <sub>8</sub> -barrel protein scaffolds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3704-3709.	7.1	65
16	Exploiting Protein Symmetry To Design Light-Controllable Enzyme Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 595-598.	13.8	61
17	Computational and Experimental Evidence for the Evolution of a (β/α) <sub>8</sub> -Barrel Protein from an Ancestral Quarter-Barrel Stabilised by Disulfide Bonds. <i>Journal of Molecular Biology</i> , 2010, 398, 763-773.	4.2	54
18	Molecular Engineering of Organophosphate Hydrolysis Activity from a Weak Promiscuous Lactonase Template. <i>Journal of the American Chemical Society</i> , 2013, 135, 11670-11677.	13.7	53

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19	Evidence for the Existence of Elaborate Enzyme Complexes in the Paleoproterozoic Era. <i>Journal of the American Chemical Society</i> , 2014, 136, 122-129.	13.7	51
20	Enhancing the Stability and Solubility of the Glucocorticoid Receptor Ligand-Binding Domain by High-Throughput Library Screening. <i>Journal of Molecular Biology</i> , 2010, 403, 562-577.	4.2	46
21	Stabilisation of a ( $\beta$ )-Barrel Protein Designed from Identical Half Barrels. <i>Journal of Molecular Biology</i> , 2007, 372, 114-129.	4.2	44
22	Interconverting the Catalytic Activities of ( $\beta$ )-barrel Enzymes from Different Metabolic Pathways: Sequence Requirements and Molecular Analysis. <i>Journal of Molecular Biology</i> , 2004, 337, 871-879.	4.2	43
23	Rosetta:MSF: a modular framework for multi-state computational protein design. <i>PLoS Computational Biology</i> , 2017, 13, e1005600.	3.2	43
24	Catalysis Uncoupling in a Glutamine Amidotransferase Bifunctional Enzyme by Unblocking the Glutaminase Active Site. <i>Chemistry and Biology</i> , 2012, 19, 1589-1599.	6.0	40
25	A common evolutionary origin of two elementary enzyme folds. <i>FEBS Letters</i> , 2002, 510, 133-135.	2.8	36
26	High-Resolution Crystal Structure of an Artificial ( $\beta$ )-Barrel Protein Designed from Identical Half-Barrels. <i>Biochemistry</i> , 2009, 48, 1145-1147.	2.5	36
27	Extreme thermostability of tarantula hemocyanin. <i>FEBS Letters</i> , 1995, 364, 9-12.	2.8	33
28	Ancestral Tryptophan Synthase Reveals Functional Sophistication of Primordial Enzyme Complexes. <i>Cell Chemical Biology</i> , 2016, 23, 709-715.	5.2	31
29	<i>In Silico</i> Identification and Experimental Validation of Distal Activity-Enhancing Mutations in Tryptophan Synthase. <i>ACS Catalysis</i> , 2021, 11, 13733-13743.	11.2	30
30	Photochromic coenzyme Q derivatives: switching redox potentials with light. <i>Chemical Science</i> , 2017, 8, 6474-6483.	7.4	27
31	Analysis of allosteric communication in a multienzyme complex by ancestral sequence reconstruction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 346-354.	7.1	26
32	Small-angle X-ray scattering reveals differences between the quaternary structures of oxygenated and deoxygenated tarantula hemocyanin. <i>FEBS Letters</i> , 1996, 393, 226-230.	2.8	25
33	Light Regulation of Enzyme Allostery through Photo-responsive Unnatural Amino Acids. <i>Cell Chemical Biology</i> , 2019, 26, 1501-1514.e9.	5.2	25
34	Computational Design of Enzymes. <i>Chemistry and Biology</i> , 2008, 15, 421-423.	6.0	24
35	Structural and Mutational Analysis of Substrate Complexation by Anthranilate Phosphoribosyltransferase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 21410-21421.	3.4	23
36	A comprehensive analysis of the geranylgeranylgeranyl phosphate synthase enzyme family identifies novel members and reveals mechanisms of substrate specificity and quaternary structure organization. <i>Molecular Microbiology</i> , 2014, 92, 885-899.	2.5	23

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37	A Rationally Designed Monomeric Variant of Anthranilate Phosphoribosyltransferase from <i>Sulfolobus solfataricus</i> is as Active as the Dimeric Wild-type Enzyme but Less Thermostable. <i>Journal of Molecular Biology</i> , 2008, 376, 506-516.	4.2	22
38	Reconstruction of ancestral enzymes. <i>Perspectives in Science</i> , 2016, 9, 17-23.	0.6	22
39	Evolutionary diversification of protein-protein interactions by interface add-ons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8333-E8342.	7.1	22
40	Molecular basis for the allosteric activation mechanism of the heterodimeric imidazole glycerol phosphate synthase complex. <i>Nature Communications</i> , 2021, 12, 2748.	12.8	22
41	Role of the N-Terminal Extension of the (Î²Î±)8-Barrel Enzyme Indole-3-glycerol Phosphate Synthase for Its Fold, Stability, and Catalytic Activity. <i>Biochemistry</i> , 2005, 44, 16405-16412.	2.5	21
42	Conservation of the Folding Mechanism between Designed Primordial (Î²Î±)8-Barrel Proteins and Their Modern Descendant. <i>Journal of the American Chemical Society</i> , 2012, 134, 12786-12791.	13.7	21
43	Related (Î²Î±)8-Barrel Proteins in Histidine and Tryptophan Biosynthesis: A Paradigm to Study Enzyme Evolution. <i>ChemBioChem</i> , 2011, 12, 1487-1494.	2.6	20
44	Artificial Light Regulation of an Allosteric Bienenzyme Complex by a Photosensitive Ligand. <i>ChemBioChem</i> , 2018, 19, 1750-1757.	2.6	19
45	Prediction of quaternary structure by analysis of hot spot residues in protein-protein interfaces: the case of anthranilate phosphoribosyltransferases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 815-825.	2.6	18
46	Long-Term Persistence of Bi-functionality Contributes to the Robustness of Microbial Life through Exaptation. <i>PLoS Genetics</i> , 2016, 12, e1005836.	3.5	18
47	Directed evolution of (Î±Î±)8-barrel enzymes: establishing phosphoribosylanthranilate isomerisation activity on the scaffold of the tryptophan synthase Î±-subunit. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 285-293.	2.1	17
48	Standardized cloning vectors for protein production and generation of large gene libraries in <i>Escherichia coli</i> . <i>BioTechniques</i> , 2018, 64, 24-26.	1.8	17
49	Functional characterisation of two Î³ <sup>12</sup> -desaturases demonstrates targeted production of linoleic acid as pheromone precursor in <i>Nasonia</i> . <i>Journal of Experimental Biology</i> , 2019, 222, .	1.7	16
50	Epimerisation of chiral hydroxylactones by short-chain dehydrogenases/reductases accounts for sex pheromone evolution in <i>Nasonia</i> . <i>Scientific Reports</i> , 2016, 6, 34697.	3.3	15
51	Significance of the Protein Interface Configuration for Allostery in Imidazole Glycerol Phosphate Synthase. <i>Biochemistry</i> , 2020, 59, 2729-2742.	2.5	15
52	BIOCHEMISTRY: De Novo Design of an Enzyme. <i>Science</i> , 2004, 304, 1916-1917.	12.6	14
53	Kinetic Mechanism of Indole-3-glycerol Phosphate Synthase. <i>Biochemistry</i> , 2013, 52, 132-142.	2.5	14
54	Conversion of Anthranilate Synthase into Isochorismate Synthase: Implications for the Evolution of Chorismate-utilizing Enzymes. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 11270-11274.	13.8	14

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55	Improving thermal and detergent stability of <i>Bacillus stearothermophilus</i> neopullulanase by rational enzyme design. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 147-151.	2.1	14
56	Combining ancestral sequence reconstruction with protein design to identify an interface hotspot in a key metabolic enzyme complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 312-321.	2.6	14
57	Experimental Assessment of the Importance of Amino Acid Positions Identified by an Entropy-Based Correlation Analysis of Multiple-Sequence Alignments. <i>Biochemistry</i> , 2012, 51, 5633-5641.	2.5	12
58	Relationship of Catalysis and Active Site Loop Dynamics in the (Î²Î±) <sub>8</sub> -Barrel Enzyme Indole-3-glycerol Phosphate Synthase. <i>Biochemistry</i> , 2018, 57, 3265-3277.	2.5	12
59	Activation of Anthranilate Phosphoribosyltransferase from <i>Sulfolobus solfataricus</i> by Removal of Magnesium Inhibition and Acceleration of Product Release. <i>Biochemistry</i> , 2009, 48, 5199-5209.	2.5	11
60	Mapping the Allosteric Communication Network of Aminodeoxychorismate Synthase. <i>Journal of Molecular Biology</i> , 2019, 431, 2718-2728.	4.2	11
61	Towards Photochromic Azobenzene-Based Inhibitors for Tryptophan Synthase. <i>Chemistry - A European Journal</i> , 2021, 27, 2439-2451.	3.3	11
62	Stabilization of a Metabolic Enzyme by Library Selection in <i>Thermus thermophilus</i> . <i>ChemBioChem</i> , 2011, 12, 1581-1588.	2.6	10
63	A Fast and Precise Approach for Computational Saturation Mutagenesis and its Experimental Validation by Using an Artificial (Î²Î±) <sub>8</sub> -Barrel Protein. <i>ChemBioChem</i> , 2011, 12, 1544-1550.	2.6	10
64	Folding Mechanism of an Extremely Thermostable (Î²Î±) <sub>8</sub> -Barrel Enzyme: A High Kinetic Barrier Protects the Protein from Denaturation. <i>Biochemistry</i> , 2012, 51, 3420-3432.	2.5	10
65	Hexamerization of Geranylgeranylglyceryl Phosphate Synthase Ensures Structural Integrity and Catalytic Activity at High Temperatures. <i>Biochemistry</i> , 2018, 57, 2335-2348.	2.5	10
66	A Fold-Independent Interface Residue Is Crucial for Complex Formation and Allosteric Signaling in Class I Glutamine Amidotransferases. <i>Biochemistry</i> , 2019, 58, 2584-2588.	2.5	10
67	Establishing catalytic activity on an artificial (Î²Î±) <sub>8</sub> -barrel protein designed from identical half-barrels. <i>FEBS Letters</i> , 2013, 587, 2798-2805.	2.8	9
68	Protein Design at the Crossroads of Biotechnology, Chemistry, Theory, and Evolution. <i>Angewandte Chemie - International Edition</i> , 2003, 42, 140-142.	13.8	8
69	TransCent: Computational enzyme design by transferring active sites and considering constraints relevant for catalysis. <i>BMC Bioinformatics</i> , 2009, 10, 54.	2.6	8
70	Light-Regulation of Tryptophan Synthase by Combining Protein Design and Enzymology. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5106.	4.1	8
71	A sugar isomerization reaction established on various (Î²Î±) <sub>8</sub> -barrel scaffolds is based on substrate-assisted catalysis. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 751-760.	2.1	7
72	Dimerization Determines Substrate Specificity of a Bacterial Prenyltransferase. <i>ChemBioChem</i> , 2012, 13, 1297-1303.	2.6	6

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73	Identification and Characterization of Heptaprenylglyceryl Phosphate Processing Enzymes in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 14861-14870.	3.4	6
74	Evolutionary Morphing of Tryptophan Synthase: Functional Mechanisms for the Enzymatic Channeling of Indole. <i>Journal of Molecular Biology</i> , 2018, 430, 5066-5079.	4.2	6
75	Activation of a Chimeric Rpb5/RpoH Subunit Using Library Selection. <i>PLoS ONE</i> , 2014, 9, e87485.	2.5	6
76	Generation of a Stand-Alone Tryptophan Synthase $\beta$ -Subunit by Mimicking an Evolutionary Blueprint. <i>ChemBioChem</i> , 2019, 20, 2747-2751.	2.6	4
77	Quaternary Structure of the Tryptophan Synthase $\beta$ -Subunit Homolog BX1 from <i>Zea mays</i> . <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 227-233.	2.8	4
78	Editorial: Directed Evolution: A Powerful Approach to Optimising and Understanding Enzymes. <i>ChemBioChem</i> , 2011, 12, 1439-1440.	2.6	3
79	Mapping key amino acid residues for the epimerase efficiency and stereospecificity of the sex pheromone biosynthetic short-chain dehydrogenases/reductases of <i>Nasonia</i> . <i>Scientific Reports</i> , 2019, 9, 330.	3.3	3
80	Reprogramming the Specificity of a Protein Interface by Computational and Data-Driven Design. <i>Structure</i> , 2021, 29, 292-304.e3.	3.3	2
81	Photoswitching of Feedback Inhibition by Tryptophan in Anthranilate Synthase. <i>ACS Synthetic Biology</i> , 2022, 11, 2846-2856.	3.8	2
82	The Structure of Carbamoylphosphate Synthetase Unravels Central Functional Features of a Key Metabolic Multienzyme Complex. <i>Biochemistry</i> , 2021, 60, 3422-3423.	2.5	1
83	Library Selection with a Randomized Repertoire of $(\beta\text{-barrel})_8$ -Barrel Enzymes Results in Unexpected Induction of Gene Expression. <i>Biochemistry</i> , 2019, 58, 4207-4217.	2.5	0
84	Substrate Specificity and Quaternary Structure of a Novel Class of Tryptophan Synthases. <i>FASEB Journal</i> , 2015, 29, 573.5.	0.5	0
85	Library Generation and Auxotrophic Selection Assays in <i>Escherichia coli</i> and <i>Thermus thermophilus</i> . <i>Methods in Molecular Biology</i> , 2018, 1685, 333-345.	0.9	0