

Birte HÃ¼cker

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

2,325
citations

236925

25
h-index

233421

45
g-index

76
all docs

76
docs citations

76
times ranked

2209
citing authors

#	ARTICLE	IF	CITATIONS
1	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. <i>Nature Chemical Biology</i> , 2016, 12, 29-34.	8.0	214
2	Oxygen-Insensitive Nitroreductases: Analysis of the Roles of <i>nfsA</i> and <i>nfsB</i> in Development of Resistance to 5-Nitrofuranyl Derivatives in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1998, 180, 5529-5539.	2.2	190
3	Catalytic Versatility, Stability, and Evolution of the (β)8-Barrel Enzyme Fold. <i>Chemical Reviews</i> , 2005, 105, 4038-4055.	47.7	181
4	Dissection of a (β)8-barrel enzyme into two folded halves. <i>Nature Structural Biology</i> , 2001, 8, 32-36.	9.7	134
5	Mimicking enzyme evolution by generating new (β)8-barrels from (β)4-half-barrels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16448-16453.	7.1	97
6	Computational design of ligand binding is not a solved problem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18491-18496.	7.1	92
7	A biosensor for the direct visualization of auxin. <i>Nature</i> , 2021, 592, 768-772.	27.8	88
8	Stability, catalytic versatility and evolution of the (β)8-barrel fold. <i>Current Opinion in Biotechnology</i> , 2001, 12, 376-381.	6.6	83
9	Controllable protein design with language models. <i>Nature Machine Intelligence</i> , 2022, 4, 521-532.	16.0	76
10	Evolutionary relationship of two ancient protein superfolds. <i>Nature Chemical Biology</i> , 2014, 10, 710-715.	8.0	68
11	A Robust Protein Host for Anchoring Chelating Ligands and Organocatalysts. <i>ChemBioChem</i> , 2008, 9, 552-564.	2.6	67
12	Establishing wild-type levels of catalytic activity on natural and artificial (β)8-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
13	A (β)8-barrel built by the combination of fragments from different folds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9942-9947.	7.1	61
14	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
15	Design of proteins from smaller fragments—learning from evolution. <i>Current Opinion in Structural Biology</i> , 2014, 27, 56-62.	5.7	49
16	ProteinTools: a toolkit to analyze protein structures. <i>Nucleic Acids Research</i> , 2021, 49, W559-W566.	14.5	49
17	Strategies for designing non-natural enzymes and binders. <i>Current Opinion in Chemical Biology</i> , 2018, 47, 67-76.	6.1	46
18	Automated scaffold selection for enzyme design. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 74-83.	2.6	45

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19	Computational protein design of ligand binding and catalysis. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 929-933.	6.1	44
20	Potential of Fragment Recombination for Rational Design of Proteins. <i>Journal of the American Chemical Society</i> , 2012, 134, 4019-4022.	13.7	40
21	Structure-based design of robust glucose biosensors using a <i>Thermotoga maritima</i> periplasmic glucose-binding protein. <i>Protein Science</i> , 2007, 16, 2240-2250.	7.6	39
22	Binding Pocket Optimization by Computational Protein Design. <i>PLoS ONE</i> , 2012, 7, e52505.	2.5	39
23	A common evolutionary origin of two elementary enzyme folds. <i>FEBS Letters</i> , 2002, 510, 133-135.	2.8	36
24	High-Resolution Crystal Structure of an Artificial (12±)8-Barrel Protein Designed from Identical Half-Barrels. <i>Biochemistry</i> , 2009, 48, 1145-1147.	2.5	36
25	Identification and Analysis of Natural Building Blocks for Evolution-Guided Fragment-Based Protein Design. <i>Journal of Molecular Biology</i> , 2020, 432, 3898-3914.	4.2	34
26	Evolution, folding, and design of TIM barrels and related proteins. <i>Current Opinion in Structural Biology</i> , 2021, 68, 94-104.	5.7	34
27	Identification of residues important for NAD ⁺ -binding by the <i>Thermotoga maritima</i> glucosidase AglA, a member of glycoside hydrolase family 4. <i>FEBS Letters</i> , 2002, 517, 267-271.	2.8	26
28	A highly stable protein chimera built from fragments of different folds. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 699-703.	2.1	26
29	Directed evolution of (12±)8-barrel enzymes. <i>New Biotechnology</i> , 2005, 22, 31-38.	2.7	24
30	Engineering the Enolase Magnesium II Binding Site: Implications for Its Evolution. <i>Biochemistry</i> , 2010, 49, 7582-7589.	2.5	21
31	The Bacteroidetes <i>Aequorivita</i> sp. and <i>Kaistella jeonii</i> Produce Promiscuous Esterases With PET-Hydrolyzing Activity. <i>Frontiers in Microbiology</i> , 2021, 12, 803896.	3.5	21
32	Evolutionary mechanism as a template for protein engineering. <i>Journal of Peptide Science</i> , 2010, 16, 538-544.	1.4	20
33	Change in protein-ligand specificity through binding pocket grafting. <i>Journal of Structural Biology</i> , 2014, 185, 186-192.	2.8	20
34	Redesign of LAOBP to bind novel amino acid ligands. <i>Protein Science</i> , 2018, 27, 957-968.	7.6	19
35	De novo designed peptides for cellular delivery and subcellular localisation. <i>Nature Chemical Biology</i> , 2022, 18, 999-1004.	8.0	16
36	The Stability Landscape of de novo TIM Barrels Explored by a Modular Design Approach. <i>Journal of Molecular Biology</i> , 2021, 433, 167153.	4.2	15

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37	Protlego: a Python package for the analysis and design of chimeric proteins. <i>Bioinformatics</i> , 2021, 37, 3182-3189.	4.1	13
38	Synthetic biology approaches to dissecting linear motor protein function: towards the design and synthesis of artificial autonomous protein walkers. <i>Biophysical Reviews</i> , 2020, 12, 1041-1054.	3.2	12
39	PocketOptimizer and the Design of Ligand Binding Sites. <i>Methods in Molecular Biology</i> , 2016, 1414, 63-75.	0.9	10
40	Reconstructing the Remote Origins of a Fold Singleton from a Flavodoxin-Like Ancestor. <i>Biochemistry</i> , 2019, 58, 4790-4793.	2.5	9
41	Extension of a <i>de novo</i> TIM barrel with a rationally designed secondary structure element. <i>Protein Science</i> , 2021, 30, 982-989.	7.6	9
42	A comprehensive binding study illustrates ligand recognition in the periplasmic binding protein PotF. <i>Structure</i> , 2021, 29, 433-443.e4.	3.3	9
43	Design of Chimeric Proteins by Combination of Subdomain-Sized Fragments. <i>Methods in Enzymology</i> , 2013, 523, 389-405.	1.0	8
44	A newly introduced salt bridge cluster improves structural and biophysical properties of <i>de novo</i> TIM barrels. <i>Protein Science</i> , 2022, 31, 513-527.	7.6	8
45	A toolbox for protein design. <i>Nature</i> , 2012, 491, 204-205.	27.8	7
46	An Artificial Cofactor Catalyzing the Baylis-Hillman Reaction with Designed Streptavidin as Protein Host**. <i>ChemBioChem</i> , 2021, 22, 1573-1577.	2.6	7
47	Impact of Enzymatic Degradation on the Material Properties of Poly(Ethylene Terephthalate). <i>Polymers</i> , 2021, 13, 3885.	4.5	7
48	Fuzzle 2.0: Ligand Binding in Natural Protein Building Blocks. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 715972.	3.5	6
49	Engineering chimaeric proteins from fold fragments: "hopeful monsters"™ in protein design. <i>Biochemical Society Transactions</i> , 2013, 41, 1137-1140.	3.4	5
50	Modular peptide binders " development of a predictive technology as alternative for reagent antibodies. <i>Biological Chemistry</i> , 2022, 403, 535-543.	2.5	4
51	A metalloenzyme reloaded. <i>Nature Chemical Biology</i> , 2012, 8, 224-225.	8.0	3
52	Identification of Protein Scaffolds for Enzyme Design Using Scaffold Selection. <i>Methods in Molecular Biology</i> , 2014, 1216, 183-196.	0.9	3
53	Highlight issue: protein design. <i>Biological Chemistry</i> , 2017, 398, 1-2.	2.5	2
54	A versatile assay platform for enzymatic poly(ethylene-terephthalate) degradation. <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	2.1	2

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55	Computational design and experimental characterization of a photo-controlled mRNA-cap guanine-N7 methyltransferase. RSC Chemical Biology, 2021, 2, 1484-1490.	4.1	2
56	Fine-tuning spermidine binding modes in the putrescine binding protein PotF. Journal of Biological Chemistry, 2021, 297, 101419.	3.4	2
57	Dreaming ideal protein structures. Nature Biotechnology, 2022, , .	17.5	2
58	Metals Make Proteins Stick. Chemistry and Biology, 2010, 17, 103-104.	6.0	1
59	Engineering an AB5 Protein Carrier. Scientific Reports, 2018, 8, 12643.	3.3	1
60	Einblicke in die Mechanismen der Evolution durch Protein Design. Akademie Der Wissenschaften Zu Goettingen Jahrbuch, 2012, 2011, 183-187.	0.0	0
61	Designing protein function " Macromolecular design. Journal of Structural Biology, 2014, 185, 135.	2.8	0
62	Editorial overview: A perspective on protein evolution. Current Opinion in Structural Biology, 2018, 48, viii-ix.	5.7	0
63	Protein engineering & design: hitting new heights. Biological Chemistry, 2022, 403, 453-453.	2.5	0