Birte HÃ¶cker

List of Publications by Year
in descending order

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63	2,325	236925	233421
papers	citations	25 h-index	45 g-index

76	76	76	2209
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Modular peptide bindersÂâ€“ development of a predictive technology as alternative for reagent antibodies. Biological Chemistry, 2022, 403, 535-543.	2.5	4
2	Dreaming ideal protein structures. Nature Biotechnology, 2022, , .	17.5	2
3	Protein engineering & design: hitting new heights. Biological Chemistry, 2022, 403, 453-453.	2.5	0
4	A newly introduced salt bridge cluster improves structural and biophysical properties of de novo<scp>TIM</scp> barrels. Protein Science, 2022, 31, 513-527.	7.6	8
5	Controllable protein design with language models. Nature Machine Intelligence, 2022, 4, 521-532.	16.0	76
6	De novo designed peptides for cellular delivery and subcellular localisation. Nature Chemical Biology, 2022, 18, 999-1004.	8.0	16
7	A versatile assay platform for enzymatic poly(ethylene-terephthalate) degradation. Protein Engineering, Design and Selection, 2021, 34, .	2.1	2
8	An Artificial Cofactor Catalyzing the Baylisâ€Hillman Reaction with Designed Streptavidin as Protein Host**. ChemBioChem, 2021, 22, 1573-1577.	2.6	7
9	Extension of a de novo TIM barrel with a rationally designed secondary structure element. Protein Science, 2021, 30, 982-989.	7.6	9
10	A biosensor for the direct visualization of auxin. Nature, 2021, 592, 768-772.	27.8	88
11	Protlego: a Python package for the analysis and design of chimeric proteins. Bioinformatics, 2021, 37, 3182-3189.	4.1	13
12	A comprehensive binding study illustrates ligand recognition in the periplasmic binding protein PotF. Structure, 2021, 29, 433-443.e4.	3.3	9
13	ProteinTools: a toolkit to analyze protein structures. Nucleic Acids Research, 2021, 49, W559-W566.	14.5	49
14	Evolution, folding, and design of TIM barrels and related proteins. Current Opinion in Structural Biology, 2021, 68, 94-104.	5.7	34
15	Fuzzle 2.0: Ligand Binding in Natural Protein Building Blocks. Frontiers in Molecular Biosciences, 2021, 8, 715972.	3.5	6
16	The Stability Landscape of de novo TIM Barrels Explored by a Modular Design Approach. Journal of Molecular Biology, 2021, 433, 167153.	4.2	15
17	Computational design and experimental characterization of a photo-controlled mRNA-cap guanine-N7 methyltransferase. RSC Chemical Biology, 2021, 2, 1484-1490.	4.1	2
18	Fine-tuning spermidine binding modes in the putrescine binding protein PotF. Journal of Biological Chemistry, 2021, 297, 101419.	3.4	2

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19	Impact of Enzymatic Degradation on the Material Properties of Poly(Ethylene Terephthalate). Polymers, 2021, 13, 3885.	4.5	7
20	The Bacteroidetes Aequorivita sp. and Kaistella jeonii Produce Promiscuous Esterases With PET-Hydrolyzing Activity. Frontiers in Microbiology, 2021, 12, 803896.	3.5	21
21	Synthetic biology approaches to dissecting linear motor protein function: towards the design and synthesis of artificial autonomous protein walkers. Biophysical Reviews, 2020, 12, 1041-1054.	3.2	12
22	Identification and Analysis of Natural Building Blocks for Evolution-Guided Fragment-Based Protein Design. Journal of Molecular Biology, 2020, 432, 3898-3914.	4.2	34
23	Reconstructing the Remote Origins of a Fold Singleton from a Flavodoxin-Like Ancestor. Biochemistry, 2019, 58, 4790-4793.	2.5	9
24	Redesign of LAOBP to bind novel <scp>l</scp>â€amino acid ligands. Protein Science, 2018, 27, 957-968.	7.6	19
25	Strategies for designing non-natural enzymes and binders. Current Opinion in Chemical Biology, 2018, 47, 67-76.	6.1	46
26	Engineering an AB5 Protein Carrier. Scientific Reports, 2018, 8, 12643.	3.3	1
27	Editorial overview: A perspective on protein evolution. Current Opinion in Structural Biology, 2018, 48, viii-ix.	5.7	0
28	Highlight issue: protein design. Biological Chemistry, 2017, 398, 1-2.	2.5	2
29	PocketOptimizer and the Design of Ligand Binding Sites. Methods in Molecular Biology, 2016, 1414, 63-75.	0.9	10
30	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. Nature Chemical Biology, 2016, 12, 29-34.	8.0	214
31	Identification of Protein Scaffolds for Enzyme Design Using Scaffold Selection. Methods in Molecular Biology, 2014, 1216, 183-196.	0.9	3
32	Designing protein function â€“ Macromolecular design. Journal of Structural Biology, 2014, 185, 135.	2.8	0
33	Change in protein-ligand specificity through binding pocket grafting. Journal of Structural Biology, 2014, 185, 186-192.	2.8	20
34	Evolutionary relationship of two ancient protein superfolds. Nature Chemical Biology, 2014, 10, 710-715.	8.0	68
35	Design of proteins from smaller fragmentsâ€”learning from evolution. Current Opinion in Structural Biology, 2014, 27, 56-62.	5.7	49
36	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

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37	Computational protein design of ligand binding and catalysis. Current Opinion in Chemical Biology, 2013, 17, 929-933.	6.1	44
38	Design of Chimeric Proteins by Combination of Subdomain-Sized Fragments. Methods in Enzymology, 2013, 523, 389-405.	1.0	8
39	Engineering chimaeric proteins from fold fragments: â€˜hopeful monstersâ€™ in protein design. Biochemical Society Transactions, 2013, 41, 1137-1140.	3.4	5
40	A toolbox for protein design. Nature, 2012, 491, 204-205.	27.8	7
41	A highly stable protein chimera built from fragments of different folds. Protein Engineering, Design and Selection, 2012, 25, 699-703.	2.1	26
42	A metalloenzyme reloaded. Nature Chemical Biology, 2012, 8, 224-225.	8.0	3
43	Potential of Fragment Recombination for Rational Design of Proteins. Journal of the American Chemical Society, 2012, 134, 4019-4022.	13.7	40
44	Einblicke in die Mechanismen der Evolution durch Protein Design. Akademie Der Wissenschaften Zu Goettingen Jahrbuch, 2012, 2011, 183-187.	0.0	0
45	Binding Pocket Optimization by Computational Protein Design. PLoS ONE, 2012, 7, e52505.	2.5	39
46	Metals Make Proteins Stick. Chemistry and Biology, 2010, 17, 103-104.	6.0	1
47	Evolutionary mechanism as a template for protein engineering. Journal of Peptide Science, 2010, 16, 538-544.	1.4	20
48	Engineering the Enolase Magnesium II Binding Site: Implications for Its Evolution. Biochemistry, 2010, 49, 7582-7589.	2.5	21
49	Computational design of ligand binding is not a solved problem. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18491-18496.	7.1	92
50	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
51	Automated scaffold selection for enzyme design. Proteins: Structure, Function and Bioinformatics, 2009, 77, 74-83.	2.6	45
52	High-Resolution Crystal Structure of an Artificial (Î²Î±)8-Barrel Protein Designed from Identical Half-Barrels. Biochemistry, 2009, 48, 1145-1147.	2.5	36
53	A Robust Protein Host for Anchoring Chelating Ligands and Organocatalysts. ChemBioChem, 2008, 9, 552-564.	2.6	67
54	A Î²Î±-barrel built by the combination of fragments from different folds. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9942-9947.	7.1	61

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55	Structureâ€based design of robust glucose biosensors using a Thermotoga maritima periplasmic glucoseâ€binding protein. Protein Science, 2007, 16, 2240-2250.	7.6	39
56	Directed evolution of (Î²Î±)8-barrel enzymes. New Biotechnology, 2005, 22, 31-38.	2.7	24
57	Catalytic Versatility, Stability, and Evolution of the (Î²Î±)8-Barrel Enzyme Fold. Chemical Reviews, 2005, 105, 4038-4055.	47.7	181
58	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
59	A common evolutionary origin of two elementary enzyme folds. FEBS Letters, 2002, 510, 133-135.	2.8	36
60	Identification of residues important for NAD+binding by theThermotoga maritimaÎ±-glucosidase AglA, a member of glycoside hydrolase family 4. FEBS Letters, 2002, 517, 267-271.	2.8	26
61	Stability, catalytic versatility and evolution of the (Î²Î±)8-barrel fold. Current Opinion in Biotechnology, 2001, 12, 376-381.	6.6	83
62	Dissection of a (betaalpha)8-barrel enzyme into two folded halves. Nature Structural Biology, 2001, 8, 32-36.	9.7	134
63	Oxygen-Insensitive Nitroreductases: Analysis of the Roles of nfsA and nfsB in Development of Resistance to 5-Nitrofuran Derivatives in Escherichia coli. Journal of Bacteriology, 1998, 180, 5529-5539.	2.2	190