

Fabio Parmeggiani

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20
papers

996
citations

14
h-index

21
g-index

21
ext. papers

1,175
ext. citations

12.5
avg, IF

3.94
L-index

#	Paper	IF	Citations
20	Repeat proteins: designing new shapes and functions for solenoid folds. <i>Current Opinion in Structural Biology</i> , 2021 , 68, 208-214	8.1	0
19	Elfin UI: A Graphical Interface for Protein Design With Modular Building Blocks. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 568318	5.8	1
18	Elfin: An algorithm for the computational design of custom three-dimensional structures from modular repeat protein building blocks. <i>Journal of Structural Biology</i> , 2018 , 201, 100-107	3.4	6
17	Extreme stability in de novo-designed repeat arrays is determined by unusually stable short-range interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 7539-7544	11.5	18
16	Designing repeat proteins: a modular approach to protein design. <i>Current Opinion in Structural Biology</i> , 2017 , 45, 116-123	8.1	27
15	Computational design of self-assembling cyclic protein homo-oligomers. <i>Nature Chemistry</i> , 2017 , 9, 353-360	36.0	78
14	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. <i>Nature Chemical Biology</i> , 2016 , 12, 29-34	11.7	151
13	Computational design of a homotrimeric metalloprotein with a trisbipyridyl core. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 15012-15017	11.5	33
12	Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. <i>Journal of Molecular Biology</i> , 2016 , 428, 4467-4489	6.5	12
11	A general computational approach for repeat protein design. <i>Journal of Molecular Biology</i> , 2015 , 427, 563-75	6.5	63
10	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015 , 528, 580-4	50.4	156
9	Rational design of helical tandem repeat proteins with closed architectures. <i>Nature</i> , 2015 , 528, 585-8	50.4	85
8	Control of repeat-protein curvature by computational protein design. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 167-74	17.6	69
7	A substitution in the fingers domain of DNA polymerase β reduces fidelity by altering nucleotide discrimination in the catalytic site. <i>Journal of Biological Chemistry</i> , 2013 , 288, 5572-80	5.4	11
6	Optimization of designed armadillo repeat proteins by molecular dynamics simulations and NMR spectroscopy. <i>Protein Science</i> , 2012 , 21, 1298-314	6.3	28
5	Designed Armadillo repeat proteins: library generation, characterization and selection of peptide binders with high specificity. <i>Journal of Molecular Biology</i> , 2012 , 424, 68-87	6.5	43
4	Engineering domain fusion chimeras from I-Onu1 family LAGLIDADG homing endonucleases. <i>Nucleic Acids Research</i> , 2012 , 40, 7985-8000	20.1	30

- 3 Designed armadillo repeat proteins as general peptide-binding scaffolds: consensus design and computational optimization of the hydrophobic core. *Journal of Molecular Biology*, **2008**, 376, 1282-304 6.5 102
- 2 Tyrosine83 is essential for the activity of E. coli galactoside transacetylase. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2007**, 1774, 243-8 4
- 1 Thermodynamic benchmark study using Biacore technology. *Analytical Biochemistry*, **2007**, 364, 67-77 3.1 83