

François Stricher

List of Publications by Year in descending order

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32
papers

5,635
citations

236612

25
h-index

433756

31
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32
all docs

32
docs citations

32
times ranked

8668
citing authors

#	ARTICLE	IF	CITATIONS
1	Directed evolution of prenylated FMN-dependent Fdc supports efficient in vivo isobutene production. Nature Communications, 2021, 12, 5300.	5.8	11
2	Production of unstable proteins through the formation of stable core complexes. Nature Communications, 2016, 7, 10932.	5.8	9
3	Engineering of weak helper interactions for high-efficiency FRET probes. Nature Methods, 2013, 10, 1021-1027.	9.0	62
4	HSPA8/HSC70 chaperone protein. Autophagy, 2013, 9, 1937-1954.	4.3	307
5	E-Cadherin Destabilization Accounts for the Pathogenicity of Missense Mutations in Hereditary Diffuse Gastric Cancer. PLoS ONE, 2012, 7, e33783.	1.1	53
6	Analysis of Disease-Linked Rhodopsin Mutations Based on Structure, Function, and Protein Stability Calculations. Journal of Molecular Biology, 2011, 405, 584-606.	2.0	86
7	Molecular basis of engineered meganuclease targeting of the endogenous human RAG1 locus. Nucleic Acids Research, 2011, 39, 729-743.	6.5	63
8	A graphical interface for the FoldX forcefield. Bioinformatics, 2011, 27, 1711-1712.	1.8	288
9	BriX: a database of protein building blocks for structural analysis, modeling and design. Nucleic Acids Research, 2011, 39, D435-D442.	6.5	48
10	Modeling protein-peptide interactions using protein fragments: fitting the pieces?. BMC Bioinformatics, 2010, 11, .	1.2	1
11	Using protein design algorithms to understand the molecular basis of disease caused by protein-DNA interactions: the Pax6 example. Nucleic Acids Research, 2010, 38, 7422-7431.	6.5	55
12	PepX: a structural database of non-redundant protein-peptide complexes. Nucleic Acids Research, 2010, 38, D545-D551.	6.5	102
13	T-RMSD: A Fine-grained, Structure-based Classification Method and its Application to the Functional Characterization of TNF Receptors. Journal of Molecular Biology, 2010, 400, 605-617.	2.0	5
14	Protein-Peptide Interactions Adopt the Same Structural Motifs as Monomeric Protein Folds. Structure, 2009, 17, 1128-1136.	1.6	79
15	Protein design in biological networks: from manipulating the input to modifying the output. Protein Engineering, Design and Selection, 2009, 22, 537-542.	1.0	24
16	Quantifying information transfer by protein domains: Analysis of the Fyn SH2 domain structure. BMC Structural Biology, 2008, 8, 43.	2.3	33
17	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. Nature, 2008, 456, 107-111.	13.7	150
18	Combinatorial Optimization of a CD4-Mimetic Miniprotein and Cocrystal Structures with HIV-1 gp120 Envelope Glycoprotein. Journal of Molecular Biology, 2008, 382, 510-524.	2.0	54

#	ARTICLE	IF	CITATIONS
19	Computer design of obligate heterodimer meganucleases allows efficient cutting of custom DNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, 2163-2173.	6.5	49
20	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. <i>PLoS Computational Biology</i> , 2008, 4, e1000052.	1.5	39
21	Reconstruction of Protein Backbones from the BriX Collection of Canonical Protein Fragments. <i>PLoS Computational Biology</i> , 2008, 4, e1000083.	1.5	42
22	How Protein Stability and New Functions Trade Off. <i>PLoS Computational Biology</i> , 2008, 4, e1000002.	1.5	468
23	The Stability Effects of Protein Mutations Appear to be Universally Distributed. <i>Journal of Molecular Biology</i> , 2007, 369, 1318-1332.	2.0	396
24	Predicted Effects of Missense Mutations on Native-State Stability Account for Phenotypic Outcome in Phenylketonuria, a Paradigm of Misfolding Diseases. <i>American Journal of Human Genetics</i> , 2007, 81, 1006-1024.	2.6	157
25	Engineering of Large Numbers of Highly Specific Homing Endonucleases that Induce Recombination on Novel DNA Targets. <i>Journal of Molecular Biology</i> , 2006, 355, 443-458.	2.0	175
26	Design of Miniproteins by the Transfer of Active Sites Onto Small-Size Scaffolds. , 2006, 340, 113-150.		7
27	A high-throughput fluorescence polarization assay specific to the CD4 binding site of HIV-1 glycoproteins based on a fluorescein-labelled CD4 mimic. <i>Biochemical Journal</i> , 2005, 390, 29-39.	1.7	22
28	Scorpion-Toxin Mimics of CD4 in Complex with Human Immunodeficiency Virus gp120. <i>Structure</i> , 2005, 13, 755-768.	1.6	107
29	Prediction of water and metal binding sites and their affinities by using the Fold-X force field. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10147-10152.	3.3	315
30	The FoldX web server: an online force field. <i>Nucleic Acids Research</i> , 2005, 33, W382-W388.	6.5	2,110
31	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. <i>Nucleic Acids Research</i> , 2004, 33, D527-D532.	6.5	136
32	Rational design of a CD4 mimic that inhibits HIV-1 entry and exposes cryptic neutralization epitopes. <i>Nature Biotechnology</i> , 2003, 21, 71-76.	9.4	182