FranÃ§ois Stricher

List of Publications by Year
in descending order

32	5,635	236612	433756
papers	citations	25	31
		h-index	g-index

32	32	32	8668
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The FoldX web server: an online force field. Nucleic Acids Research, 2005, 33, W382-W388.	6.5	2,110
2	How Protein Stability and New Functions Trade Off. PLoS Computational Biology, 2008, 4, e1000002.	1.5	468
3	The Stability Effects of Protein Mutations Appear to be Universally Distributed. Journal of Molecular Biology, 2007, 369, 1318-1332.	2.0	396
4	Prediction of water and metal binding sites and their affinities by using the Fold-X force field. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10147-10152.	3.3	315
5	HSPA8/HSC70 chaperone protein. Autophagy, 2013, 9, 1937-1954.	4.3	307
6	A graphical interface for the FoldX forcefield. Bioinformatics, 2011, 27, 1711-1712.	1.8	288
7	Rational design of a CD4 mimic that inhibits HIV-1 entry and exposes cryptic neutralization epitopes. Nature Biotechnology, 2003, 21, 71-76.	9.4	182
8	Engineering of Large Numbers of Highly Specific Homing Endonucleases that Induce Recombination on Novel DNA Targets. Journal of Molecular Biology, 2006, 355, 443-458.	2.0	175
9	Predicted Effects of Missense Mutations on Native-State Stability Account for Phenotypic Outcome in Phenylketonuria, a Paradigm of Misfolding Diseases. American Journal of Human Genetics, 2007, 81, 1006-1024.	2.6	157
10	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. Nature, 2008, 456, 107-111.	13.7	150
11	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. Nucleic Acids Research, 2004, 33, D527-D532.	6.5	136
12	Scorpion-Toxin Mimics of CD4 in Complex with Human Immunodeficiency Virus gp120. Structure, 2005, 13, 755-768.	1.6	107
13	PepX: a structural database of non-redundant proteinâ€"peptide complexes. Nucleic Acids Research, 2010, 38, D545-D551.	6.5	102
14	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
15	Protein-Peptide Interactions Adopt the Same Structural Motifs as Monomeric Protein Folds. Structure, 2009, 17, 1128-1136.	1.6	79
16	Molecular basis of engineered meganuclease targeting of the endogenous human RAG1 locus. Nucleic Acids Research, 2011, 39, 729-743.	6.5	63
17	Engineering of weak helper interactions for high-efficiency FRET probes. Nature Methods, 2013, 10, 1021-1027.	9.0	62
18	Using protein design algorithms to understand the molecular basis of disease caused by proteinâ€"DNA interactions: the Pax6 example. Nucleic Acids Research, 2010, 38, 7422-7431.	6.5	55

#	Article	IF	Citations
19	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
20	E-Cadherin Destabilization Accounts for the Pathogenicity of Missense Mutations in Hereditary Diffuse Gastric Cancer. PLoS ONE, 2012, 7, e33783.	1.1	53
21	Computer design of obligate heterodimer meganucleases allows efficient cutting of custom DNA sequences. Nucleic Acids Research, 2008, 36, 2163-2173.	6.5	49
22	BriX: a database of protein building blocks for structural analysis, modeling and design. Nucleic Acids Research, 2011, 39, D435-D442.	6.5	48
23	Reconstruction of Protein Backbones from the BriX Collection of Canonical Protein Fragments. PLoS Computational Biology, 2008, 4, e1000083.	1.5	42
24	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. PLoS Computational Biology, 2008, 4, e1000052.	1.5	39
25	Quantifying information transfer by protein domains: Analysis of the Fyn SH2 domain structure. BMC Structural Biology, 2008, 8, 43.	2.3	33
26	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
27	A high-throughput fluorescence polarization assay specific to the CD4 binding site of HIV-1 glycoproteins based on a fluorescein-labelled CD4 mimic. Biochemical Journal, 2005, 390, 29-39.	1.7	22
28	Directed evolution of prenylated FMN-dependent Fdc supports efficient in vivo isobutene production. Nature Communications, 2021, 12, 5300.	5.8	11
29	Production of unstable proteins through the formation of stable core complexes. Nature Communications, 2016, 7, 10932.	5.8	9
30	Design of Miniproteins by the Transfer of Active Sites Onto Small-Size Scaffolds. , 2006, 340, 113-150.		7
31	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
32	Modeling protein-peptide interactions using protein fragments: fitting the pieces?. BMC Bioinformatics, 2010, 11, .	1.2	1