

Sridhar Govindarajan

List of Publications by Year in descending order

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34
papers

4,255
citations

270111

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488211

31
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34
all docs

34
docs citations

34
times ranked

5675
citing authors

#	ARTICLE	IF	CITATIONS
1	Site and Mutation-Specific Predictions Enable Minimal Directed Evolution Libraries. ACS Synthetic Biology, 2018, 7, 1730-1741.	1.9	23
2	Exploring sequence-function space of a poplar glutathione transferase using designed information-rich gene variants. Protein Engineering, Design and Selection, 2017, 30, 543-549.	1.0	15
3	Mapping of Amino Acid Substitutions Conferring Herbicide Resistance in Wheat Glutathione Transferase. ACS Synthetic Biology, 2015, 4, 221-227.	1.9	32
4	Redesigning and characterizing the substrate specificity and activity of Vibrio fluvialis aminotransferase for the synthesis of imigabalin. Protein Engineering, Design and Selection, 2013, 26, 25-33.	1.0	113
5	Engineering genes for predictable protein expression. Protein Expression and Purification, 2012, 83, 37-46.	0.6	144
6	Analysis of the Ketosynthase-Chain Length Factor Heterodimer from the Fredericamycin Polyketide Synthase. Chemistry and Biology, 2011, 18, 1021-1031.	6.2	16
7	Reconstructed evolutionary adaptive paths give polymerases accepting reversible terminators for sequencing and SNP detection. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1948-1953.	3.3	71
8	A family of thermostable fungal cellulases created by structure-guided recombination. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5610-5615.	3.3	244
9	Engineering the <i>Salmonella</i> type III secretion system to export spider silk monomers. Molecular Systems Biology, 2009, 5, 309.	3.2	130
10	SCHEMA Recombination of a Fungal Cellulase Uncovers a Single Mutation That Contributes Markedly to Stability. Journal of Biological Chemistry, 2009, 284, 26229-26233.	1.6	108
11	Design Parameters to Control Synthetic Gene Expression in Escherichia coli. PLoS ONE, 2009, 4, e7002.	1.1	298
12	Palaeotemperature trend for Precambrian life inferred from resurrected proteins. Nature, 2008, 451, 704-707.	13.7	338
13	Protein engineering of improved prolyl endopeptidases for celiac sprue therapy. Protein Engineering, Design and Selection, 2008, 21, 699-707.	1.0	80
14	Directed evolution of gene-shuffled IFN- α molecules with activity profiles tailored for treatment of chronic viral diseases. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8269-8274.	3.3	32
15	Engineering proteinase K using machine learning and synthetic genes. BMC Biotechnology, 2007, 7, 16.	1.7	88
16	Gene Designer: a synthetic biology tool for constructing artificial DNA segments. BMC Bioinformatics, 2006, 7, 285.	1.2	302
17	Empirical Biocatalyst Engineering: Escaping the Tyranny of High-Throughput Screening. ACS Symposium Series, 2005, , 37-50.	0.5	4
18	Predicting enzyme function from protein sequence. Current Opinion in Chemical Biology, 2005, 9, 202-209.	2.8	31

#	ARTICLE	IF	CITATIONS
19	Codon bias and heterologous protein expression. Trends in Biotechnology, 2004, 22, 346-353.	4.9	1,045
20	Engineered protein function by selective amino acid diversification. Methods, 2004, 32, 416-427.	1.9	13
21	Putting engineering back into protein engineering: bioinformatic approaches to catalyst design. Current Opinion in Biotechnology, 2003, 14, 366-370.	3.3	31
22	Evolutionary Potential of (Î²/Î±)8-Barrels:Â Functional Promiscuity Produced by Single Substitutions in the Enolase Superfamily. Biochemistry, 2003, 42, 8387-8393.	1.2	171
23	Systematic Variation of Amino Acid Substitutions for Stringent Assessment of Pairwise Covariation. Journal of Molecular Biology, 2003, 328, 1061-1069.	2.0	42
24	Optimizing the search algorithm for protein engineering by directed evolution. Protein Engineering, Design and Selection, 2003, 16, 589-597.	1.0	59
25	Synthetic shuffling expands functional protein diversity by allowing amino acids to recombine independently. Nature Biotechnology, 2002, 20, 1251-1255.	9.4	189
26	The adaptive evolution database (TAED). Genome Biology, 2001, 2, research0028.1.	13.9	35
27	Advances in directed protein evolution by recursive genetic recombination: applications to therapeutic proteins. Current Opinion in Biotechnology, 2001, 12, 361-370.	3.3	111
28	Exploration of sequence space for protein engineering. Journal of Molecular Recognition, 2001, 14, 308-314.	1.1	12
29	Functional inferences from reconstructed evolutionary biology involving rectified databases “ an evolutionarily grounded approach to functional genomics. Research in Microbiology, 2000, 151, 97-106.	1.0	58
30	Estimating the total number of protein folds. , 1999, 35, 408-414.		131
31	Evolution of model proteins on a foldability landscape. , 1997, 29, 461-466.		86
32	The foldability landscape of model proteins. , 1997, 42, 427-438.		65
33	Searching for foldable protein structures using optimized energy functions. Biopolymers, 1995, 36, 43-51.	1.2	72
34	Optimal local propensities for model proteins. Proteins: Structure, Function and Bioinformatics, 1995, 22, 413-418.	1.5	66