

Henry A Gabb

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6944620/publications.pdf>

Version: 2024-02-01

15
papers

1,572
citations

1040056

9
h-index

1199594

12
g-index

15
all docs

15
docs citations

15
times ranked

1440
citing authors

#	ARTICLE	IF	CITATIONS
1	Modelling protein docking using shape complementarity, electrostatics and biochemical information 1 Edited by J. Thornton. Journal of Molecular Biology, 1997, 272, 106-120.	4.2	779
2	Use of pair potentials across protein interfaces in screening predicted docked complexes. Proteins: Structure, Function and Bioinformatics, 1999, 35, 364-373.	2.6	245
3	Rapid refinement of protein interfaces incorporating solvation: application to the docking problem. Journal of Molecular Biology, 1998, 276, 265-285.	4.2	230
4	Predictive docking of protein-protein and protein-DNA complexes. Current Opinion in Structural Biology, 1998, 8, 250-256.	5.7	113
5	Modelling repressor proteins docking to DNA. , 1998, 33, 535-549.		48
6	Dual-Level Parallel Analysis of Harbor Wave Response Using MPI and OpenMP. International Journal of High Performance Computing Applications, 2000, 14, 49-64.	3.7	31
7	Conformational transitions in potential and free energy space for furanoses and 2'-deoxynucleosides. Journal of the American Chemical Society, 1993, 115, 4218-4227.	13.7	27
8	Finding and visualizing nucleic acid base stacking. Journal of Molecular Graphics, 1996, 14, 6-11.	1.1	26
9	Parallel programming with message passing and directives. Computing in Science and Engineering, 2001, 3, 22-37.	1.2	21
10	Protein-Protein Docking: Generation and Filtering of Complexes. , 2000, 143, 399-415.		19
11	Modeling large nucleic acids. Current Opinion in Structural Biology, 1993, 3, 241-246.	5.7	18
12	A small intraexonic deletion within the dystrophin gene suggests a possible mechanism of mutagenesis. Human Genetics, 1997, 99, 658-662.	3.8	9
13	Algorithm 821. ACM Transactions on Mathematical Software, 2002, 28, 354-371.	2.9	3
14	Use of pair potentials across protein interfaces in screening predicted docked complexes. Proteins: Structure, Function and Bioinformatics, 1999, 35, 364-373.	2.6	3
15	Using a Fortran Interface to Posix Threads. IFIP Advances in Information and Communication Technology, 2001, , 257-272.	0.7	0