

# Werner G Krebs

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8691376/publications.pdf>

Version: 2024-02-01

13  
papers

2,224  
citations

1163117

8  
h-index

1281871

11  
g-index

14  
all docs

14  
docs citations

14  
times ranked

2425  
citing authors

#	ARTICLE	IF	CITATIONS
1	Scientific workflow management and the Kepler system. <i>Concurrency Computation Practice and Experience</i> , 2006, 18, 1039-1065.	2.2	1,333
2	A database of macromolecular motions. <i>Nucleic Acids Research</i> , 1998, 26, 4280-4290.	14.5	333
3	Normal mode analysis of macromolecular motions in a database framework: Developing mode concentration as a useful classifying statistic. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 682-695.	2.6	248
4	SURVEY AND SUMMARY: The morph server: a standardized system for analyzing and visualizing macromolecular motions in a database framework. <i>Nucleic Acids Research</i> , 2000, 28, 1665-1675.	14.5	219
5	PartsList: a web-based system for dynamically ranking protein folds based on disparate attributes, including whole-genome expression and interaction information. <i>Nucleic Acids Research</i> , 2001, 29, 1750-1764.	14.5	45
6	Tools and Databases to Analyze Protein Flexibility; Approaches to Mapping Implied Features onto Sequences. <i>Methods in Enzymology</i> , 2003, 374, 544-584.	1.0	14
7	Con-Struct Map: a comparative contact map analysis tool. <i>Bioinformatics</i> , 2007, 23, 2491-2492.	4.1	12
8	Statistically rigorous automated protein annotation. <i>Bioinformatics</i> , 2004, 20, 1066-1073.	4.1	10
9	Studying Macromolecular Motions in a Database Framework: From Structure to Sequence. , 2002, , 401-420.		5
10	STATISTICAL AND VISUAL MORPH MOVIE ANALYSIS OF CRYSTALLOGRAPHIC MUTANT SELECTION BIAS IN PROTEIN MUTATION RESOURCE DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 61-75.	0.8	2
11	Detecting botnet signals using process mining. <i>Computational and Mathematical Organization Theory</i> , 2021, 27, 161-178.	2.0	2
12	Carbohydrates and glycoconjugates Biophysical methods. <i>Current Opinion in Structural Biology</i> , 2002, 12, 565-566.	5.7	1
13	A Review of the Morph Server and the Macromolecular Motions Database: A Standardized System for Analyzing and Visualizing Macromolecular Motions in a Database Framework. , 2003, , 29-42.		0