

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