

# Takayuki Amemiya

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3401651/publications.pdf>

Version: 2024-02-01

13  
papers

330  
citations

1307594

7  
h-index

1372567

10  
g-index

13  
all docs

13  
docs citations

13  
times ranked

425  
citing authors

#	ARTICLE	IF	CITATIONS
1	IDEAL in 2014 illustrates interaction networks composed of intrinsically disordered proteins and their binding partners. <i>Nucleic Acids Research</i> , 2014, 42, D320-D325.	14.5	88
2	IDEAL: Intrinsically Disordered proteins with Extensive Annotations and Literature. <i>Nucleic Acids Research</i> , 2012, 40, D507-D511.	14.5	84
3	PSCDB: a database for protein structural change upon ligand binding. <i>Nucleic Acids Research</i> , 2012, 40, D554-D558.	14.5	45
4	Classification and Annotation of the Relationship between Protein Structural Change and Ligand Binding. <i>Journal of Molecular Biology</i> , 2011, 408, 568-584.	4.2	43
5	An assignment of intrinsically disordered regions of proteins based on NMR structures. <i>Journal of Structural Biology</i> , 2013, 181, 29-36.	2.8	26
6	Protein Structural Change upon Ligand Binding Correlates with Enzymatic Reaction Mechanism. <i>Journal of Molecular Biology</i> , 2008, 379, 397-401.	4.2	23
7	SAHG, a comprehensive database of predicted structures of all human proteins. <i>Nucleic Acids Research</i> , 2011, 39, D487-D493.	14.5	12
8	Interface property responsible for effective interactions of protean segments: Intrinsically disordered regions that undergo disorder-to-order transitions upon binding. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 123-127.	2.1	5
9	Structural changes of homodimers in the PDB. <i>Journal of Structural Biology</i> , 2018, 202, 42-50.	2.8	3
10	Substrate shielding and hydrolytic reaction in hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 926-932.	2.6	1
11	3P-018 Development of an exhaustive comparative simulation system(Protein:Structure,The 47th) Tj ETQq1 1 0.784314 rgBT <sub>0</sub> /Overlock	0.1	0
12	111436 Computational analysis of protean segments (ProSs) in intrinsically disordered proteins (IDPs)(Bioinformatics & Bioengineering,Oral Presentation,The 50th Annual Meeting of the) Tj ETQq0 0 0 rgBT <sub>0</sub> /Overlock d0 Tf 50 29	0.1	0
13	Classification and Annotation of the Protein Structural Change upon Ligand Binding. <i>Seibutsu Butsuri</i> , 2012, 52, 194-195.	0.1	0