

# Swapnil Mahajan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5500492/publications.pdf>

Version: 2024-02-01

19  
papers

2,563  
citations

759233

12  
h-index

794594

19  
g-index

22  
all docs

22  
docs citations

22  
times ranked

3767  
citing authors

#	ARTICLE	IF	CITATIONS
1	TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. <i>Frontiers in Immunology</i> , 2021, 12, 640725.	4.8	64
2	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	6.2	19
3	TCRpMHCmodels: Structural modelling of TCR-pMHC class I complexes. <i>Scientific Reports</i> , 2019, 9, 14530.	3.3	41
4	Benchmark datasets of immune receptor-epitope structural complexes. <i>BMC Bioinformatics</i> , 2019, 20, 490.	2.6	12
5	A survey of known immune epitopes in the enteroviruses strains associated with acute flaccid myelitis. <i>Human Immunology</i> , 2019, 80, 923-929.	2.4	11
6	IEDB-AR: immune epitope database analysis resource in 2019. <i>Nucleic Acids Research</i> , 2019, 47, W502-W506.	14.5	247
7	Antibody Specific B-Cell Epitope Predictions: Leveraging Information From Antibody-Antigen Protein Complexes. <i>Frontiers in Immunology</i> , 2019, 10, 298.	4.8	101
8	The Immune Epitope Database (IEDB): 2018 update. <i>Nucleic Acids Research</i> , 2019, 47, D339-D343.	14.5	1,329
9	Epitope Specific Antibodies and T Cell Receptors in the Immune Epitope Database. <i>Frontiers in Immunology</i> , 2018, 9, 2688.	4.8	39
10	Jumping between protein conformers using normal modes. <i>Journal of Computational Chemistry</i> , 2017, 38, 1622-1630.	3.3	13
11	The Immune Epitope Database and Analysis Resource in Epitope Discovery and Synthetic Vaccine Design. <i>Frontiers in Immunology</i> , 2017, 8, 278.	4.8	369
12	Knowledge-based prediction of protein backbone conformation using a structural alphabet. <i>PLoS ONE</i> , 2017, 12, e0186215.	2.5	12
13	On the relationship between low-frequency normal modes and the large-scale conformational changes of proteins. <i>Archives of Biochemistry and Biophysics</i> , 2015, 567, 59-65.	3.0	75
14	Use of a structural alphabet to find compatible folds for amino acid sequences. <i>Protein Science</i> , 2015, 24, 145-153.	7.6	9
15	Correlation between local structural dynamics of proteins inferred from NMR ensembles and evolutionary dynamics of homologues of known structure. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 751-758.	3.5	6
16	DoSA: Database of Structural Alignments. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat048-bat048.	3.0	2
17	Comparison of tertiary structures of proteins in protein-protein complexes with unbound forms suggests prevalence of allostery in signalling proteins. <i>BMC Structural Biology</i> , 2012, 12, 6.	2.3	19
18	Identification of Local Conformational Similarity in Structurally Variable Regions of Homologous Proteins Using Protein Blocks. <i>PLoS ONE</i> , 2011, 6, e17826.	2.5	6

#	ARTICLE	IF	CITATIONS
19	A short survey on protein blocks. Biophysical Reviews, 2010, 2, 137-145.	3.2	107