

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 | The Immune Epitope Database (IEDB): 2018 update. <i>Nucleic Acids Research</i> , 2019, 47, D339-D343. | 14.5 | 1,329 |
| 2 | 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 |
| 3 | IEDB-AR: immune epitope database analysis resource in 2019. <i>Nucleic Acids Research</i> , 2019, 47, W502-W506. | 14.5 | 247 |
| 4 | A short survey on protein blocks. <i>Biophysical Reviews</i> , 2010, 2, 137-145. | 3.2 | 107 |
| 5 | Antibody Specific B-Cell Epitope Predictions: Leveraging Information From Antibody-Antigen Protein Complexes. <i>Frontiers in Immunology</i> , 2019, 10, 298. | 4.8 | 101 |
| 6 | 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 |
| 7 | 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 |
| 8 | TCRpMHCmodels: Structural modelling of TCR-pMHC class I complexes. <i>Scientific Reports</i> , 2019, 9, 14530. | 3.3 | 41 |
| 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 | 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 |
| 11 | 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 |
| 12 | Jumping between protein conformers using normal modes. <i>Journal of Computational Chemistry</i> , 2017, 38, 1622-1630. | 3.3 | 13 |
| 13 | Benchmark datasets of immune receptor-epitope structural complexes. <i>BMC Bioinformatics</i> , 2019, 20, 490. | 2.6 | 12 |
| 14 | Knowledge-based prediction of protein backbone conformation using a structural alphabet. <i>PLoS ONE</i> , 2017, 12, e0186215. | 2.5 | 12 |
| 15 | 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 |
| 16 | Use of a structural alphabet to find compatible folds for amino acid sequences. <i>Protein Science</i> , 2015, 24, 145-153. | 7.6 | 9 |
| 17 | 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 |
| 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 | DoSA: Database of Structural Alignments. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat048-bat048. | 3.0 | 2 |