

# Anita Sarkar

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

1,746  
citations

471371

17  
h-index

610775

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

2577  
citing authors

#	ARTICLE	IF	CITATIONS
1	A V<sub>H</sub> 1-69 antibody lineage from an infected Chinese donor potentially neutralizes HIV-1 by targeting the V3 glycan supersite. <i>Science Advances</i> , 2020, 6, .	4.7	19
2	Structure and immunogenicity of a stabilized HIV-1 envelope trimer based on a group-M consensus sequence. <i>Nature Communications</i> , 2019, 10, 2355.	5.8	116
3	Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. <i>Cell Host and Microbe</i> , 2019, 25, 873-883.e5.	5.1	42
4	Capturing the inherent structural dynamics of the HIV-1 envelope glycoprotein fusion peptide. <i>Nature Communications</i> , 2019, 10, 763.	5.8	30
5	HIV-1 vaccine design through minimizing envelope metastability. <i>Science Advances</i> , 2018, 4, eaau6769.	4.7	75
6	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. <i>Nature Communications</i> , 2018, 9, 1956.	5.8	50
7	The human naive B cell repertoire contains distinct subclasses for a germline-targeting HIV-1 vaccine immunogen. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	113
8	Glyco3D: A Suite of Interlinked Databases of 3D Structures of Complex Carbohydrates, Lectins, Antibodies, and Glycosyltransferases. , 2017, , 133-161.		3
9	T cells control the generation of nanomolar-affinity anti-glycan antibodies. <i>Journal of Clinical Investigation</i> , 2017, 127, 1491-1504.	3.9	63
10	Lipid interactions and angle of approach to the HIV-1 viral membrane of broadly neutralizing antibody 10E8: Insights for vaccine and therapeutic design. <i>PLoS Pathogens</i> , 2017, 13, e1006212.	2.1	58
11	Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. <i>PLoS Pathogens</i> , 2016, 12, e1005815.	2.1	104
12	Tailored Immunogens Direct Affinity Maturation toward HIV Neutralizing Antibodies. <i>Cell</i> , 2016, 166, 1459-1470.e11.	13.5	230
13	A Prominent Site of Antibody Vulnerability on HIV Envelope Incorporates a Motif Associated with CCR5 Binding and Its Camouflaging Glycans. <i>Immunity</i> , 2016, 45, 31-45.	6.6	129
14	HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. <i>Science</i> , 2016, 351, 1458-1463.	6.0	382
15	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. <i>Immunity</i> , 2016, 44, 21-31.	6.6	87
16	Databases of Conformations and NMR Structures of Glycan Determinants. <i>Glycobiology</i> , 2015, 25, 1480-1490.	1.3	15
17	Glyco3D: A Portal for Structural Glycosciences. <i>Methods in Molecular Biology</i> , 2015, 1273, 241-258.	0.4	77
18	Glycoinformatics and Glycosciences. , 2015, , 414-425.		0

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19	Conformational Preferences of the O-Antigen Polysaccharides of <i>Escherichia coli</i> O5ac and O5ab Using NMR Spectroscopy and Molecular Modeling. <i>Biomacromolecules</i> , 2013, 14, 2215-2224.	2.6	11
20	Deciphering the Glycan Preference of Bacterial Lectins by Glycan Array and Molecular Docking with Validation by Microcalorimetry and Crystallography. <i>PLoS ONE</i> , 2013, 8, e71149.	1.1	25
21	Protein Aggregation in Neurodegenerative Diseases: Insights from Computational Analyses. <i>Current Bioinformatics</i> , 2012, 7, 87-95.	0.7	6
22	PolySac3DB: an annotated data base of 3 dimensional structures of polysaccharides. <i>BMC Bioinformatics</i> , 2012, 13, 302.	1.2	32
23	The G protein-coupled receptors in the pufferfish <i>Takifugu rubripes</i> . <i>BMC Bioinformatics</i> , 2011, 12, S3.	1.2	37
24	Analysis and Prediction of DNA-Recognition by Zinc Finger Proteins. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2011, , 303-317.	0.2	0
25	ZiF-Predict: A Web Tool for Predicting DNA-Binding Specificity in C2H2 Zinc Finger Proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 122-126.	3.0	20
26	Controlling aggregation propensity in A53T mutant of alpha-synuclein causing Parkinson's disease. <i>Biochemical and Biophysical Research Communications</i> , 2009, 387, 305-309.	1.0	15