

# Vijay S Reddy

## List of Publications by Citations

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36  
papers

1,323  
citations

14  
h-index

36  
g-index

38  
ext. papers

1,495  
ext. citations

7.9  
avg, IF

4.48  
L-index

#	Paper	IF	Citations
36	VIPERdb2: an enhanced and web API enabled relational database for structural virology. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D436-42	20.1	317
35	Crystal structure of human adenovirus at 3.5 Å resolution. <i>Science</i> , <b>2010</b> , 329, 1071-5	33.3	186
34	Virus Particle Explorer (VIPER), a website for virus capsid structures and their computational analyses. <i>Journal of Virology</i> , <b>2001</b> , 75, 11943-7	6.6	163
33	VIPERdb: a relational database for structural virology. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D386-9	20.1	108
32	Crystallographically identical virus capsids display different properties in solution. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 114-6		75
31	Structures and organization of adenovirus cement proteins provide insights into the role of capsid maturation in virus entry and infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 11715-20	11.5	73
30	Adenovirus composition, proteolysis, and disassembly studied by in-depth qualitative and quantitative proteomics. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 11421-11430	5.4	67
29	Cryo-EM structure of human adenovirus D26 reveals the conservation of structural organization among human adenoviruses. <i>Science Advances</i> , <b>2017</b> , 3, e1602670	14.3	48
28	Characterization of polymorphism displayed by the coat protein mutants of tomato bushy stunt virus. <i>Virology</i> , <b>2006</b> , 349, 222-9	3.6	35
27	Structure-derived insights into virus assembly. <i>Advances in Virus Research</i> , <b>2005</b> , 64, 45-68	10.7	28
26	The cleaved N-terminus of pVI binds peripentonal hexons in mature adenovirus. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 1971-9	6.5	23
25	VIPERdb: A Tool for Virus Research. <i>Annual Review of Virology</i> , <b>2018</b> , 5, 477-488	14.6	20
24	Crystal Structure and Proteomics Analysis of Empty Virus-like Particles of Cowpea Mosaic Virus. <i>Structure</i> , <b>2016</b> , 24, 567-575	5.2	18
23	Localized reconstruction in Scipion expedites the analysis of symmetry mismatches in cryo-EM data. <i>Progress in Biophysics and Molecular Biology</i> , <b>2021</b> , 160, 43-52	4.7	17
22	Revised Crystal Structure of Human Adenovirus Reveals the Limits on Protein IX Quasi-Equivalence and on Analyzing Large Macromolecular Complexes. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 4132-4141	6.5	14
21	Isolation and Characterization of Metallosphaera Turreted Icosahedral Virus, a Founding Member of a New Family of Archaeal Viruses. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	14
20	Molecular characterization of a plant mitochondrial chaperone GrpE. <i>Plant Molecular Biology</i> , <b>1999</b> , 39, 871-81	4.6	13

19	Data to knowledge: how to get meaning from your result. <i>IUCrJ</i> , <b>2015</b> , 2, 45-58	4.7	10
18	Structure-based assessment of protein-protein interactions and accessibility of protein IX in adenoviruses with implications for antigen display. <i>Virology</i> , <b>2018</b> , 516, 102-107	3.6	10
17	A novel method to map and compare protein-protein interactions in spherical viral capsids. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 73, 644-55	4.2	10
16	Unravelling the Stability and Capsid Dynamics of the Three Virions of Brome Mosaic Virus Assembled Autonomously. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	10
15	The Role of Hexon Protein as a Molecular Mold in Patterning the Protein IX Organization in Human Adenoviruses. <i>Journal of Molecular Biology</i> , <b>2017</b> , 429, 2747-2751	6.5	9
14	Rapid increase of near atomic resolution virus capsid structures determined by cryo-electron microscopy. <i>Journal of Structural Biology</i> , <b>2018</b> , 201, 1-4	3.4	8
13	Proline-rich domain of human ALIX contains multiple TSG101-UEV interaction sites and forms phosphorylation-mediated reversible amyloids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 24274-24284	11.5	8
12	VIPERdb v3.0: a structure-based data analytics platform for viral capsids. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D809-D816	20.1	7
11	Reply to Campos: Revised structures of adenovirus cement proteins represent a consensus model for understanding virus assembly and disassembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E4544-5	11.5	6
10	Extent of protein-protein interactions and quasi-equivalence in viral capsids. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 58, 472-7	4.2	6
9	Structural Organization and Protein-Protein Interactions in Human Adenovirus Capsid. <i>Sub-Cellular Biochemistry</i> , <b>2021</b> , 96, 503-518	5.5	5
8	CapsidMaps: protein-protein interaction pattern discovery platform for the structural analysis of virus capsids using Google Maps. <i>Journal of Structural Biology</i> , <b>2015</b> , 190, 47-55	3.4	4
7	Structure based sequence analysis of viral and cellular protein assemblies. <i>Journal of Structural Biology</i> , <b>2016</b> , 196, 299-308	3.4	4
6	The Architecture of a Water-Selective Pore in the Lipid Bilayer Visualized by Electron Crystallography in Vitreous Ice. <i>Novartis Foundation Symposium</i> , <b>2008</b> , 33-50		3
5	and CD46 Receptor Utilization by Species D Human Adenovirus Serotype 26 (HAdV26). <i>Journal of Virology</i> , <b>2021</b> , JVI0082621	6.6	2
4	Application of the phase extension method in virus crystallography. <i>Crystallography Reviews</i> , <b>2016</b> , 22, 128-140	1.3	1
3	Structure of a Cell Entry Defective Human Adenovirus Provides Insights into Precursor Proteins and Capsid Maturation. <i>Journal of Molecular Biology</i> , <b>2021</b> , 434, 167350	6.5	1
2	Epitope-Analyzer: A structure-based webtool to analyze broadly neutralizing epitopes.. <i>Journal of Structural Biology</i> , <b>2022</b> , 214, 107839	3.4	0

1 Insights Derived from the Structure of Human Adenovirus. *FASEB Journal*, **2011**, 25, lb161

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