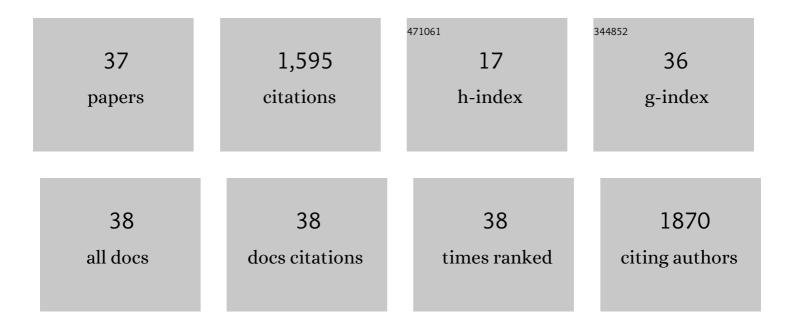
Vijay S Reddy

List of Publications by Year in descending order

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VIIAV S REDDV

#	Article	IF	CITATIONS
1	VIPERdb2: an enhanced and web API enabled relational database for structural virology. Nucleic Acids Research, 2009, 37, D436-D442.	6.5	348
2	Crystal Structure of Human Adenovirus at 3.5 Ã Resolution. Science, 2010, 329, 1071-1075.	6.0	206
3	Virus Particle Explorer (VIPER), a Website for Virus Capsid Structures and Their Computational Analyses. Journal of Virology, 2001, 75, 11943-11947.	1.5	174
4	VIPERdb: a relational database for structural virology. Nucleic Acids Research, 2006, 34, D386-D389.	6.5	115
5	Structures and organization of adenovirus cement proteins provide insights into the role of capsid maturation in virus entry and infection. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11715-11720.	3.3	90
6	Crystallographically identical virus capsids display different properties in solution. Nature Structural Biology, 1999, 6, 114-116.	9.7	86
7	Adenovirus Composition, Proteolysis, and Disassembly Studied by In-depth Qualitative and Quantitative Proteomics. Journal of Biological Chemistry, 2014, 289, 11421-11430.	1.6	81
8	Cryo-EM structure of human adenovirus D26 reveals the conservation of structural organization among human adenoviruses. Science Advances, 2017, 3, e1602670.	4.7	64
9	Characterization of polymorphism displayed by the coat protein mutants of tomato bushy stunt virus. Virology, 2006, 349, 222-229.	1.1	38
10	VIPERdb v3.0: a structure-based data analytics platform for viral capsids. Nucleic Acids Research, 2021, 49, D809-D816.	6.5	35
11	Localized reconstruction in Scipion expedites the analysis of symmetry mismatches in cryo-EM data. Progress in Biophysics and Molecular Biology, 2021, 160, 43-52.	1.4	33
12	VIPERdb: A Tool for Virus Research. Annual Review of Virology, 2018, 5, 477-488.	3.0	32
13	Structureâ€Đerived Insights into Virus Assembly. Advances in Virus Research, 2005, 64, 45-68.	0.9	30
14	The Cleaved N-Terminus of pVI Binds Peripentonal Hexons in Mature Adenovirus. Journal of Molecular Biology, 2014, 426, 1971-1979.	2.0	25
15	Crystal Structure and Proteomics Analysis of Empty Virus-like Particles of Cowpea Mosaic Virus. Structure, 2016, 24, 567-575.	1.6	22
16	Proline-rich domain of human ALIX contains multiple TSG101-UEV interaction sites and forms phosphorylation-mediated reversible amyloids. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24274-24284.	3.3	21
17	Revised Crystal Structure of Human Adenovirus Reveals the Limits on Protein IX Quasi-Equivalence and on Analyzing Large Macromolecular Complexes. Journal of Molecular Biology, 2018, 430, 4132-4141.	2.0	20
18	Isolation and Characterization of Metallosphaera Turreted Icosahedral Virus, a Founding Member of a New Family of Archaeal Viruses. Journal of Virology, 2017, 91, .	1.5	19

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#	Article	IF	CITATIONS
19	Molecular characterization of a plant mitochondrial chaperone GrpE. Plant Molecular Biology, 1999, 39, 871-881.	2.0	16
20	Unravelling the Stability and Capsid Dynamics of the Three Virions of Brome Mosaic Virus Assembled Autonomously <i>In Vivo</i> . Journal of Virology, 2020, 94, .	1.5	15
21	A novel method to map and compare protein–protein interactions in spherical viral capsids. Proteins: Structure, Function and Bioinformatics, 2008, 73, 644-655.	1.5	13
22	The Role of Hexon Protein as a Molecular Mold in Patterning the Protein IX Organization in Human Adenoviruses. Journal of Molecular Biology, 2017, 429, 2747-2751.	2.0	13
23	Structure-based assessment of protein-protein interactions and accessibility of protein IX in adenoviruses with implications for antigen display. Virology, 2018, 516, 102-107.	1.1	13
24	Data to knowledge: how to get meaning from your result. IUCrJ, 2015, 2, 45-58.	1.0	12
25	Rapid increase of near atomic resolution virus capsid structures determined by cryo-electron microscopy. Journal of Structural Biology, 2018, 201, 1-4.	1.3	10
26	Structural Organization and Protein-Protein Interactions in Human Adenovirus Capsid. Sub-Cellular Biochemistry, 2021, 96, 503-518.	1.0	10
27	CapsidMaps: Protein–protein interaction pattern discovery platform for the structural analysis of virus capsids using Google Maps. Journal of Structural Biology, 2015, 190, 47-55.	1.3	9
28	<i>Ex Vivo</i> and <i>In Vivo</i> CD46 Receptor Utilization by Species D Human Adenovirus Serotype 26 (HAdV26). Journal of Virology, 2022, 96, JV10082621.	1.5	9
29	Epitope-Analyzer: A structure-based webtool to analyze broadly neutralizing epitopes. Journal of Structural Biology, 2022, 214, 107839.	1.3	8
30	Reply to Campos: Revised structures of adenovirus cement proteins represent a consensus model for understanding virus assembly and disassembly. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4544-5.	3.3	7
31	Extent of protein-protein interactions and quasi-equivalence in viral capsids. Proteins: Structure, Function and Bioinformatics, 2004, 58, 472-477.	1.5	6
32	Structure based sequence analysis of viral and cellular protein assemblies. Journal of Structural Biology, 2016, 196, 299-308.	1.3	5
33	The Architecture of a Water-Selective Pore in the Lipid Bilayer Visualized by Electron Crystallography in Vitreous Ice. Novartis Foundation Symposium, 2008, , 33-50.	1.2	4
34	Structure of a Cell Entry Defective Human Adenovirus Provides Insights into Precursor Proteins and Capsid Maturation. Journal of Molecular Biology, 2022, 434, 167350.	2.0	4
35	Application of the phase extension method in virus crystallography. Crystallography Reviews, 2016, 22, 128-140.	0.4	1
36	Refined Capsid Structure of Human Adenovirus D26 at 3.4 Ã Resolution. Viruses, 2022, 14, 414.	1.5	1

#	Article	IF	CITATIONS
37	Insights Derived from the Structure of Human Adenovirus. FASEB Journal, 2011, 25, lb161.	0.2	Ο