

# Renuka Kadirvelraj

## List of Publications by Year in descending order

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Version: 2024-02-01

15  
papers

474  
citations

840585

11  
h-index

1058333

14  
g-index

16  
all docs

16  
docs citations

16  
times ranked

852  
citing authors

#	ARTICLE	IF	CITATIONS
1	The entropic force generated by intrinsically disordered segments tunes protein function. <i>Nature</i> , 2018, 563, 584-588.	13.7	113
2	Involvement of Water in Carbohydrate-Protein Binding: Concanavalin A Revisited. <i>Journal of the American Chemical Society</i> , 2008, 130, 16933-16942.	6.6	89
3	Cascade chemistry in azacryptand cages: bridging carbonates and methylcarbonates Electronic supplementary information (ESI) available: magnetic data. See <a href="http://www.rsc.org/suppdata/dt/b1/b110449g/">http://www.rsc.org/suppdata/dt/b1/b110449g/</a> . <i>Dalton Transactions RSC</i> , 2002, , 1704-1713.	2.3	68
4	Human <i>N</i> -acetylglucosaminyltransferase II substrate recognition uses a modular architecture that includes a convergent exosite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4637-4642.	3.3	37
5	Role of Packing Defects in the Evolution of Allostery and Induced Fit in Human UDP-Glucose Dehydrogenase. <i>Biochemistry</i> , 2011, 50, 5780-5789.	1.2	32
6	Crystal and Molecular Structure of Sclerophytin F Methyl Ether from the Soft Coral <i>Cladiella krempfi</i> . <i>Journal of Natural Products</i> , 1993, 56, 1977-1980.	1.5	28
7	Hysteresis and Negative Cooperativity in Human UDP-Glucose Dehydrogenase. <i>Biochemistry</i> , 2013, 52, 1456-1465.	1.2	20
8	Characterizing human $\alpha$ -1,6-fucosyltransferase (FUT8) substrate specificity and structural similarities with related fucosyltransferases. <i>Journal of Biological Chemistry</i> , 2020, 295, 17027-17045.	1.6	19
9	Systematic Crystallographic Investigation of Hydrogen-Bonded Networks Involving Monohydrogen Tartrate-Amine Complexes: A Potential Materials for Nonlinear Optics-. <i>Chemistry of Materials</i> , 1996, 8, 2313-2323.	3.2	18
10	Comparison of human poly-N-acetyl-lactosamine synthase structure with GT-A fold glycosyltransferases supports a modular assembly of catalytic subsites. <i>Journal of Biological Chemistry</i> , 2021, 296, 100110.	1.6	15
11	A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. <i>Science Signaling</i> , 2020, 13, .	1.6	12
12	Hysteresis in Human UDP-Glucose Dehydrogenase Is Due to a Restrained Hexameric Structure That Favors Feedback Inhibition. <i>Biochemistry</i> , 2014, 53, 8043-8051.	1.2	9
13	Title is missing!. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 1998, 30, 321-330.	1.6	8
14	Exceptionally long crystal formation from 4-(3-bromopropoxy)salicylaldehyde. X-Ray crystallographic investigation. <i>Chemical Communications</i> , 1996, , 2725.	2.2	6
15	The role of intrinsic disorder in human UDP-glucose dehydrogenase. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a173-a173.	0.0	0