

# Kumaran Baskaran

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2594722/publications.pdf>

Version: 2024-02-01

19  
papers

1,227  
citations

759055

12  
h-index

887953

17  
g-index

19  
all docs

19  
docs citations

19  
times ranked

2166  
citing authors

#	ARTICLE	IF	CITATIONS
1	The life and times of the PDB format – looking towards the future with mmCIF. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, a193-a193.	0.0	0
2	Anomalous amide proton chemical shifts as signatures of hydrogen bonding to aromatic sidechains. <i>Magnetic Resonance</i> , 2021, 2, 765-775.	0.8	5
3	Merging NMR Data and Computation Facilitates Data-Centered Research. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 817175.	1.6	2
4	BioMagResBank (BMRB) as a Resource for Structural Biology. <i>Methods in Molecular Biology</i> , 2020, 2112, 187-218.	0.4	35
5	Structure determination using solution NMR: Is it worth the effort?. <i>Journal of Magnetic Resonance</i> , 2019, 306, 195-201.	1.2	18
6	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	1.1	46
7	NMR-STAR: comprehensive ontology for representing, archiving and exchanging data from nuclear magnetic resonance spectroscopic experiments. <i>Journal of Biomolecular NMR</i> , 2019, 73, 5-9.	1.6	32
8	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	6.5	671
9	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	45
10	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	1.6	210
11	Increasing rigor in NMR-based metabolomics through validated and open source tools. <i>Current Opinion in Biotechnology</i> , 2017, 43, 56-61.	3.3	20
12	Understanding the fabric of protein crystals: computational classification of biological interfaces and crystal contacts. <i>Bioinformatics</i> , 2016, 32, 481-489.	1.8	37
13	Analyzing protein-protein contacts at the PDB-wide level. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s274-s274.	0.0	0
14	A PDB-wide, evolution-based assessment of protein-protein interfaces. <i>BMC Structural Biology</i> , 2014, 14, 22.	2.3	54
15	An analysis of oligomerization interfaces in transmembrane proteins. <i>BMC Structural Biology</i> , 2013, 13, 21.	2.3	29
16	Stereospecific Assignment of the Asparagine and Glutamine Side Chain Amide Protons in Random-Coil Peptides by Combination of Molecular Dynamic Simulations with Relaxation Matrix Calculations. <i>Applied Magnetic Resonance</i> , 2013, 44, 319-331.	0.6	3
17	Mapping of protein structural ensembles by chemical shifts. <i>Journal of Biomolecular NMR</i> , 2010, 48, 71-83.	1.6	16
18	Chemical shift optimization in multidimensional NMR spectra by AUREMOL-SHIFTOPT. <i>Journal of Biomolecular NMR</i> , 2009, 43, 197-210.	1.6	2

#	ARTICLE	IF	CITATIONS
19	Protein structure calculation with data imputation: the use of substitute restraints. Journal of Biomolecular NMR, 2009, 45, 397-411.	1.6	2