Jaina Mistry

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21 papers	23,146 citations	16 h-index	21 g-index
21 ext. papers	29,717 ext. citations	14.4 avg, IF	6.52 L-index

#	Paper	IF	Citations
21	Pfam: the protein families database. *Nucleic Acids Research*, **2014**, 42, D222-30	20.1	3975
20	The Pfam protein families database: towards a more sustainable future. *Nucleic Acids Research*, **2016**, 44, D279-85	20.1	3678
19	The Pfam protein families database. *Nucleic Acids Research*, **2012**, 40, D290-301	20.1	2844
18	The Pfam protein families database. *Nucleic Acids Research*, **2010**, 38, D211-22	20.1	2467
17	The Pfam protein families database in 2019. *Nucleic Acids Research*, **2019**, 47, D427-D432	20.1	2298
16	The Pfam protein families database. *Nucleic Acids Research*, **2008**, 36, D281-8	20.1	1806
15	Pfam: clans, web tools and services. *Nucleic Acids Research*, **2006**, 34, D247-51	20.1	1784
14	InterPro: the integrative protein signature database. *Nucleic Acids Research*, **2009**, 37, D211-5	20.1	1379
13	InterPro in 2017-beyond protein family and domain annotations. *Nucleic Acids Research*, **2017**, 45, D190-D199	20.1	970
12	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. *Nucleic Acids Research*, **2013**, 41, e121	20.1	629
11	Pfam: The protein families database in 2021. *Nucleic Acids Research*, **2021**, 49, D412-D419	20.1	620
10	New developments in the InterPro database. *Nucleic Acids Research*, **2007**, 35, D224-8	20.1	397
9	Predicting active site residue annotations in the Pfam database. *BMC Bioinformatics*, **2007**, 8, 298	3.6	124
8	A rapid computational filter for cytochrome P450 1A2 inhibition potential of compound libraries. *Journal of Medicinal Chemistry*, **2005**, 48, 5154-61	8.3	72
7	Pfam: a domain-centric method for analyzing proteins and proteomes. *Methods in Molecular Biology* , **2007**, 396, 43-58	1.4	34
6	Genome3D: exploiting structure to help users understand their sequences. *Nucleic Acids Research*, **2015**, 43, D382-6	20.1	33
5	The challenge of increasing Pfam coverage of the human proteome. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat023	5	16

4	An estimated 5% of new protein structures solved today represent a new Pfam family. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2186-93		11
3	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. *Briefings in Bioinformatics*, **2015**, 16, 865-72	13.4	5
2	The challenge of increasing Pfam coverage of the human proteome. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013,	5	4
1	Homology-Based Annotation of Large Protein Datasets. *Methods in Molecular Biology*, **2016**, 1415, 153-76	1.4	