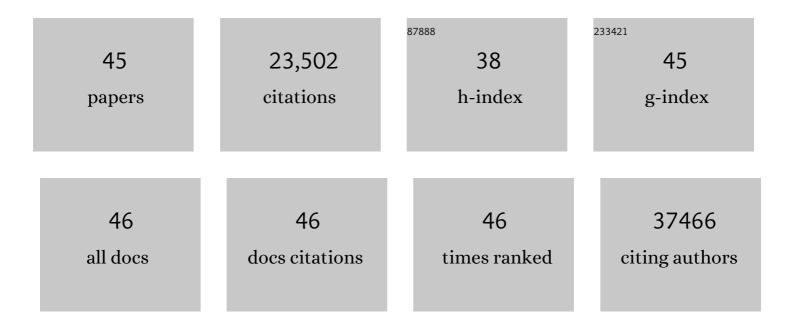
Lewis Y Geer

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	iCn3D, a web-based 3D viewer for sharing 1D/2D/3D representations of biomolecular structures. Bioinformatics, 2020, 36, 131-135.	4.1	113
2	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2018, 46, D8-D13.	14.5	1,291
3	RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Research, 2018, 46, D851-D860.	14.5	749
4	CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. Nucleic Acids Research, 2017, 45, D200-D203.	14.5	2,402
5	CDD: NCBI's conserved domain database. Nucleic Acids Research, 2015, 43, D222-D226.	14.5	3,022
6	Target enhanced 2D similarity search by using explicit biological activity annotations and profiles. Journal of Cheminformatics, 2015, 7, 55.	6.1	10
7	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2014, 42, D7-D17.	14.5	349
8	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2012, 40, D13-D25.	14.5	510
9	Analysis of the Acidic Proteome with Negative Electron-Transfer Dissociation Mass Spectrometry. Analytical Chemistry, 2012, 84, 2875-2882.	6.5	57
10	CDD: conserved domains and protein three-dimensional structure. Nucleic Acids Research, 2012, 41, D348-D352.	14.5	766
11	MMDB: 3D structures and macromolecular interactions. Nucleic Acids Research, 2012, 40, D461-D464.	14.5	96
12	Increasing peptide identifications and decreasing search times for ETD spectra by pre-processing and calculation of parent precursor charge. Proteome Science, 2012, 10, 8.	1.7	6
13	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2011, 39, D38-D51.	14.5	582
14	CDD: a Conserved Domain Database for the functional annotation of proteins. Nucleic Acids Research, 2011, 39, D225-D229.	14.5	2,727
15	Automated annotation of chemical names in the literature with tunable accuracy. Journal of Cheminformatics, 2011, 3, 52.	6.1	4
16	Automatic annotation of experimentally derived, evolutionarily conserved post-translational modifications onto multiple genomes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar019-bar019.	3.0	3
17	The NCBI BioSystems database. Nucleic Acids Research, 2010, 38, D492-D496.	14.5	706
18	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2010, 38, D5-D16.	14.5	417

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#	Article	IF	CITATIONS
19	CDD: specific functional annotation with the Conserved Domain Database. Nucleic Acids Research, 2009, 37, D205-D210.	14.5	935
20	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2009, 37, D5-D15.	14.5	797
21	MMDB: annotating protein sequences with Entrez's 3D-structure database. Nucleic Acids Research, 2007, 35, D298-D300.	14.5	92
22	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2007, 36, D13-D21.	14.5	757
23	Analysis of phosphorylation sites on proteins from Saccharomyces cerevisiae by electron transfer dissociation (ETD) mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2193-2198.	7.1	541
24	Modeling the Evolution of Protein Domain Architectures Using Maximum Parsimony. Journal of Molecular Biology, 2007, 366, 307-315.	4.2	104
25	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2007, 35, D5-D12.	14.5	757
26	Analysis of intact proteins on a chromatographic time scale by electron transfer dissociation tandem mass spectrometry. International Journal of Mass Spectrometry, 2007, 259, 197-203.	1.5	80
27	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2006, 34, D173-D180.	14.5	435
28	Assessing Data Quality of Peptide Mass Spectra Obtained by Quadrupole Ion Trap Mass Spectrometry. Journal of Proteome Research, 2005, 4, 300-305.	3.7	36
29	CDD: a Conserved Domain Database for protein classification. Nucleic Acids Research, 2004, 33, D192-D196.	14.5	976
30	Open Mass Spectrometry Search Algorithm. Journal of Proteome Research, 2004, 3, 958-964.	3.7	1,350
31	DBParser:  Web-Based Software for Shotgun Proteomic Data Analyses. Journal of Proteome Research, 2004, 3, 1002-1008.	3.7	97
32	CDD: a curated Entrez database of conserved domain alignments. Nucleic Acids Research, 2003, 31, 383-387.	14.5	673
33	MMDB: Entrez's 3D-structure database. Nucleic Acids Research, 2003, 31, 474-477.	14.5	137
34	MMDB: Entrez's 3D-structure database. Nucleic Acids Research, 2002, 30, 249-252.	14.5	87
35	CDD: a database of conserved domain alignments with links to domain three-dimensional structure. Nucleic Acids Research, 2002, 30, 281-283.	14.5	609
36	CDART: Protein Homology by Domain Architecture. Genome Research, 2002, 12, 1619-1623.	5.5	622

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37	Cn3D: sequence and structure views for Entrez. Trends in Biochemical Sciences, 2000, 25, 300-302.	7.5	271
38	MMDB: 3D structure data in Entrez. Nucleic Acids Research, 2000, 28, 243-245.	14.5	43
39	MMDB: Entrez's 3D structure database. Nucleic Acids Research, 1999, 27, 240-243.	14.5	43
40	Charge-changing fragmentation of 10.6 GeV/nucleonAu197nuclei. Physical Review C, 1995, 52, 334-345.	2.9	42
41	Charge-pickup by heavy relativistic nuclei. Physical Review C, 1994, 50, 1065-1076.	2.9	23
42	Interactions of 10.6 gold nuclei in targets from 1H to 82Pb. Nuclear Physics A, 1994, 566, 427-430.	1.5	19
43	A method to analyze 2-dimensional daily radiotherapy portal images from an on-line fiber-optic imaging system. International Journal of Radiation Oncology Biology Physics, 1991, 20, 613-619.	0.8	40
44	Portal dose images II: Patient dose estimation. International Journal of Radiation Oncology Biology Physics, 1990, 18, 1465-1475.	0.8	57
45	On-line radiotherapy imaging with an array of fiber-optic image reducers. International Journal of Radiation Oncology Biology Physics, 1990, 18, 1477-1484.	0.8	66