Lewis Y Geer

List of Publications by Year
in descending order

45	23,502	87888 38	233421 45
papers	citations	h-index	g-index

46	46	46	37466
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CDD: NCBI's conserved domain database. Nucleic Acids Research, 2015, 43, D222-D226.	14.5	3,022
2	CDD: a Conserved Domain Database for the functional annotation of proteins. Nucleic Acids Research, 2011, 39, D225-D229.	14.5	2,727
3	CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. Nucleic Acids Research, 2017, 45, D200-D203.	14.5	2,402
4	Open Mass Spectrometry Search Algorithm. Journal of Proteome Research, 2004, 3, 958-964.	3.7	1,350
5	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2018, 46, D8-D13.	14.5	1,291
6	CDD: a Conserved Domain Database for protein classification. Nucleic Acids Research, 2004, 33, D192-D196.	14.5	976
7	CDD: specific functional annotation with the Conserved Domain Database. Nucleic Acids Research, 2009, 37, D205-D210.	14.5	935
8	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2009, 37, D5-D15.	14.5	797
9	CDD: conserved domains and protein three-dimensional structure. Nucleic Acids Research, 2012, 41, D348-D352.	14.5	766
10	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2007, 36, D13-D21.	14.5	757
11	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2007, 35, D5-D12.	14.5	757
12	RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Research, 2018, 46, D851-D860.	14.5	749
13	The NCBI BioSystems database. Nucleic Acids Research, 2010, 38, D492-D496.	14.5	706
14	CDD: a curated Entrez database of conserved domain alignments. Nucleic Acids Research, 2003, 31, 383-387.	14.5	673
15	CDART: Protein Homology by Domain Architecture. Genome Research, 2002, 12, 1619-1623.	5.5	622
16	CDD: a database of conserved domain alignments with links to domain three-dimensional structure. Nucleic Acids Research, 2002, 30, 281-283.	14.5	609
17	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2011, 39, D38-D51.	14.5	582
18	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

#	Article	IF	Citations
19	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2012, 40, D13-D25.	14.5	510
20	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2006, 34, D173-D180.	14.5	435
21	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2010, 38, D5-D16.	14.5	417
22	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2014, 42, D7-D17.	14.5	349
23	Cn3D: sequence and structure views for Entrez. Trends in Biochemical Sciences, 2000, 25, 300-302.	7.5	271
24	MMDB: Entrez's 3D-structure database. Nucleic Acids Research, 2003, 31, 474-477.	14.5	137
25	iCn3D, a web-based 3D viewer for sharing 1D/2D/3D representations of biomolecular structures. Bioinformatics, 2020, 36, 131-135.	4.1	113
26	Modeling the Evolution of Protein Domain Architectures Using Maximum Parsimony. Journal of Molecular Biology, 2007, 366, 307-315.	4.2	104
27	DBParser:â€‰ Web-Based Software for Shotgun Proteomic Data Analyses. Journal of Proteome Research, 2004, 3, 1002-1008.	3.7	97
28	MMDB: 3D structures and macromolecular interactions. Nucleic Acids Research, 2012, 40, D461-D464.	14.5	96
29	MMDB: annotating protein sequences with Entrez's 3D-structure database. Nucleic Acids Research, 2007, 35, D298-D300.	14.5	92
30	MMDB: Entrez's 3D-structure database. Nucleic Acids Research, 2002, 30, 249-252.	14.5	87
31	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
32	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
33	Portal dose images II: Patient dose estimation. International Journal of Radiation Oncology Biology Physics, 1990, 18, 1465-1475.	0.8	57
34	Analysis of the Acidic Proteome with Negative Electron-Transfer Dissociation Mass Spectrometry. Analytical Chemistry, 2012, 84, 2875-2882.	6.5	57
35	MMDB: Entrez's 3D structure database. Nucleic Acids Research, 1999, 27, 240-243.	14.5	43
36	MMDB: 3D structure data in Entrez. Nucleic Acids Research, 2000, 28, 243-245.	14.5	43

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37	Charge-changing fragmentation of 10.6 GeV/nucleonAu197nuclei. Physical Review C, 1995, 52, 334-345.	2.9	42
38	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
39	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
40	Charge-pickup by heavy relativistic nuclei. Physical Review C, 1994, 50, 1065-1076.	2.9	23
41	Interactions of 10.6 gold nuclei in targets from 1H to 82Pb. Nuclear Physics A, 1994, 566, 427-430.	1.5	19
42	Target enhanced 2D similarity search by using explicit biological activity annotations and profiles. Journal of Cheminformatics, 2015, 7, 55.	6.1	10
43	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
44	Automated annotation of chemical names in the literature with tunable accuracy. Journal of Cheminformatics, 2011, 3, 52.	6.1	4
45	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