Neil David Rawlings

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/266729/neil-david-rawlings-publications-by-year.pdf

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

88
papers
12,232
citations
43
p-index
99
g-index

99
ext. papers
90
g-index

6.6
L-index

#	Paper	IF	Citations
88	Nonviral Peptidases 2021 , 1152-1169		
87	How to use the MEROPS database and website to help understand peptidase specificity. <i>Protein Science</i> , 2021 , 30, 83-92	6.3	14
86	Twenty-five years of nomenclature and classification of proteolytic enzymes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020 , 1868, 140345	4	8
85	Origins of peptidases. <i>Biochimie</i> , 2019 , 166, 4-18	4.6	13
84	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2150-2166	13.4	48
83	Genome properties in 2019: a new companion database to InterPro for the inference of complete functional attributes. <i>Nucleic Acids Research</i> , 2019 , 47, D564-D572	20.1	15
82	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019 , 47, D351-D360	20.1	835
81	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. <i>Briefings in Bioinformatics</i> , 2019 , 20, 638-658	13.4	124
80	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. <i>Nucleic Acids Research</i> , 2018 , 46, D624-D632	20.1	643
79	Using the MEROPS Database for Investigation of Lysosomal Peptidases, Their Inhibitors, and Substrates. <i>Methods in Molecular Biology</i> , 2017 , 1594, 213-226	1.4	3
78	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-	- D 199	970
77	Peptidase specificity from the substrate cleavage collection in the MEROPS database and a tool to measure cleavage site conservation. <i>Biochimie</i> , 2016 , 122, 5-30	4.6	43
76	Twenty years of the MEROPS database of proteolytic enzymes, their substrates and inhibitors. <i>Nucleic Acids Research</i> , 2016 , 44, D343-50	20.1	489
75	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav063	5	5
74	Bacterial calpains and the evolution of the calpain (C2) family of peptidases. <i>Biology Direct</i> , 2015 , 10, 66	7.2	11
73	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015 , 4, e06974	8.9	138
7 2	Genome sequence of the tsetse fly (Glossina morsitans): vector of African trypanosomiasis. <i>Science</i> , 2014 , 344, 380-6	33.3	192

(2013-2014)

71	Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. <i>BMC Bioinformatics</i> , 2014 , 15, 75	3.6	1
70	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014 , 24, 1676-85	9.7	121
69	MEROPS: the database of proteolytic enzymes, their substrates and inhibitors. <i>Nucleic Acids Research</i> , 2014 , 42, D503-9	20.1	602
68	A novel RCE1 isoform is required for H-Ras plasma membrane localization and is regulated by USP17. <i>Biochemical Journal</i> , 2014 , 457, 289-300	3.8	13
67	Peptidases 2014 ,		2
66	Using the MEROPS Database for Proteolytic Enzymes and Their Inhibitors and Substrates. <i>Current Protocols in Bioinformatics</i> , 2014 , 48, 1.25.1-33	24.2	33
65	New mini- zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. <i>BMC Bioinformatics</i> , 2014 , 15, 1	3.6	225
64	Antarease 2013 , 1079-1081		
63	Introduction: The Clans and Families of Cysteine Peptidases 2013 , 1743-1773		11
62	Introduction: Metallopeptidases and Their Clans 2013 , 325-370		10
62 61	Introduction: Metallopeptidases and Their Clans 2013 , 325-370 LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341	3.6	10
		3.6	,
61	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341	3.6 5	,
61 60	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341 Unusual Species Distribution and Horizontal Transfer of Peptidases 2013 , 285-314 Identification and prioritization of novel uncharacterized peptidases for biochemical		6
61 60 59	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341 Unusual Species Distribution and Horizontal Transfer of Peptidases 2013 , 285-314 Identification and prioritization of novel uncharacterized peptidases for biochemical characterization. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat022		6
61 60 59 58	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341 Unusual Species Distribution and Horizontal Transfer of Peptidases 2013 , 285-314 Identification and prioritization of novel uncharacterized peptidases for biochemical characterization. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat022 Bacteriophage T4 Prohead Endopeptidase 2013 , 3560-3562 The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> ,	5	2
61 60 59 58 57	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341 Unusual Species Distribution and Horizontal Transfer of Peptidases 2013 , 285-314 Identification and prioritization of novel uncharacterized peptidases for biochemical characterization. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat022 Bacteriophage T4 Prohead Endopeptidase 2013 , 3560-3562 The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013 , 2, 154	5 3.6	2

53	MEROPS: the database of proteolytic enzymes, their substrates and inhibitors. <i>Nucleic Acids Research</i> , 2012 , 40, D343-50	20.1	686
52	Structural and sequence analysis of imelysin-like proteins implicated in bacterial iron uptake. <i>PLoS ONE</i> , 2011 , 6, e21875	3.7	15
51	Asparagine peptide lyases: a seventh catalytic type of proteolytic enzymes. <i>Journal of Biological Chemistry</i> , 2011 , 286, 38321-38328	5.4	65
50	Structural analysis of papain-like NlpC/P60 superfamily enzymes with a circularly permuted topology reveals potential lipid binding sites. <i>PLoS ONE</i> , 2011 , 6, e22013	3.7	19
49	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2010 , 38, D227-33	20.1	670
48	Peptidase inhibitors in the MEROPS database. <i>Biochimie</i> , 2010 , 92, 1463-83	4.6	52
47	Prokaryote-derived protein inhibitors of peptidases: A sketchy occurrence and mostly unknown function. <i>Biochimie</i> , 2010 , 92, 1644-56	4.6	41
46	A large and accurate collection of peptidase cleavages in the MEROPS database. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap015	5	33
45	Pepsin homologues in bacteria. <i>BMC Genomics</i> , 2009 , 10, 437	4.5	27
44	The MEROPS batch BLAST: a tool to detect peptidases and their non-peptidase homologues in a genome. <i>Biochimie</i> , 2008 , 90, 243-59	4.6	61
43	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2008 , 36, D320-5	20.1	453
42	SpeciesVof peptidases. <i>Biological Chemistry</i> , 2007 , 388, 1151-7	4.5	31
41	Unusual phyletic distribution of peptidases as a tool for identifying potential drug targets. <i>Biochemical Journal</i> , 2007 , 401, e5-7	3.8	6
40	Fxna, a novel gene differentially expressed in the rat ovary at the time of folliculogenesis, is required for normal ovarian histogenesis. <i>Development (Cambridge)</i> , 2007 , 134, 945-57	6.6	15
39	An Introduction to Peptidases and the Merops Database 2007 , 161-179		6
38	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2006 , 34, D270-2	20.1	455
37	Genome of the host-cell transforming parasite Theileria annulata compared with T. parva. <i>Science</i> , 2005 , 309, 131-3	33.3	235
36	Introduction: metallopeptidases and their clans 2004 , 231-267		24

35	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2004 , 32, D160-4	20.1	325
34	The PepSY domain: a regulator of peptidase activity in the microbial environment?. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 169-72	10.3	55
33	Evolutionary families of peptidase inhibitors. <i>Biochemical Journal</i> , 2004 , 378, 705-16	3.8	459
32	Introduction: aspartic peptidases and their clans 2004 , 3-12		6
31	Managing peptidases in the genomic era. <i>Biological Chemistry</i> , 2003 , 384, 873-82	4.5	33
30	The CHAP domain: a large family of amidases including GSP amidase and peptidoglycan hydrolases. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 234-7	10.3	182
29	A comparison of Pfam and MEROPS: two databases, one comprehensive, and one specialised. <i>BMC Bioinformatics</i> , 2003 , 4, 17	3.6	6
28	MEROPS: the protease database. <i>Nucleic Acids Research</i> , 2002 , 30, 343-6	20.1	160
27	Evolutionary lines of cysteine peptidases. <i>Biological Chemistry</i> , 2001 , 382, 727-33	4.5	145
26	The MEROPS database as a protease information system. <i>Journal of Structural Biology</i> , 2001 , 134, 95-1	023.4	106
26 25	The MEROPS database as a protease information system. <i>Journal of Structural Biology</i> , 2001 , 134, 95-1 MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000 , 28, 323-5	20.1	
		· ·	
25	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000 , 28, 323-5 Tripeptidyl-peptidase I is apparently the CLN2 protein absent in classical late-infantile neuronal	· ·	97
25 24	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000 , 28, 323-5 Tripeptidyl-peptidase I is apparently the CLN2 protein absent in classical late-infantile neuronal ceroid lipofuscinosis. <i>BBA - Proteins and Proteomics</i> , 1999 , 1429, 496-500	20.1	97
25 24 23	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000 , 28, 323-5 Tripeptidyl-peptidase I is apparently the CLN2 protein absent in classical late-infantile neuronal ceroid lipofuscinosis. <i>BBA - Proteins and Proteomics</i> , 1999 , 1429, 496-500 MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 1999 , 27, 325-31 Thimet oligopeptidase: site-directed mutagenesis disproves previous assumptions about the	20.1	97 74 187
25 24 23 22	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000 , 28, 323-5 Tripeptidyl-peptidase I is apparently the CLN2 protein absent in classical late-infantile neuronal ceroid lipofuscinosis. <i>BBA - Proteins and Proteomics</i> , 1999 , 1429, 496-500 MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 1999 , 27, 325-31 Thimet oligopeptidase: site-directed mutagenesis disproves previous assumptions about the nature of the catalytic site. <i>FEBS Letters</i> , 1998 , 435, 16-20 Identification of the active site of legumain links it to caspases, clostripain and gingipains in a new	20.1	97 74 187 5
25 24 23 22 21	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000 , 28, 323-5 Tripeptidyl-peptidase I is apparently the CLN2 protein absent in classical late-infantile neuronal ceroid lipofuscinosis. <i>BBA - Proteins and Proteomics</i> , 1999 , 1429, 496-500 MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 1999 , 27, 325-31 Thimet oligopeptidase: site-directed mutagenesis disproves previous assumptions about the nature of the catalytic site. <i>FEBS Letters</i> , 1998 , 435, 16-20 Identification of the active site of legumain links it to caspases, clostripain and gingipains in a new clan of cysteine endopeptidases. <i>FEBS Letters</i> , 1998 , 441, 361-5 Cloning, isolation, and characterization of mammalian legumain, an asparaginyl endopeptidase.	20.1 20.1 3.8 5.4	97 74 187 5 169

17	Families and clans of cysteine peptidases. <i>Journal of Computer - Aided Molecular Design</i> , 1996 , 6, 1-11		35
16	Dipeptidyl-peptidase II is related to lysosomal Pro-X carboxypeptidase. <i>BBA - Proteins and Proteomics</i> , 1996 , 1298, 1-3		16
15	Families of aspartic peptidases, and those of unknown catalytic mechanism. <i>Methods in Enzymology</i> , 1995 , 248, 105-20	1.7	114
14	Thimet oligopeptidase and oligopeptidase M or neurolysin. <i>Methods in Enzymology</i> , 1995 , 248, 529-56	1.7	85
13	Families and clans of serine peptidases. Archives of Biochemistry and Biophysics, 1995, 318, 247-50	4.1	152
12	Evolutionary families of metallopeptidases. <i>Methods in Enzymology</i> , 1995 , 248, 183-228	1.7	601
11	Families of cysteine peptidases. <i>Methods in Enzymology</i> , 1994 , 244, 461-86	1.7	261
10	Families of serine peptidases. <i>Methods in Enzymology</i> , 1994 , 244, 19-61	1.7	423
9	Oligopeptidases, and the emergence of the prolyl oligopeptidase family. <i>Biological Chemistry Hoppe-Seyler</i> , 1992 , 373, 353-60		74
8	The baculovirus Autographa californica nuclear polyhedrosis virus genome includes a papain-like sequence. <i>Biological Chemistry Hoppe-Seyler</i> , 1992 , 373, 1211-5		34
7	Types and families of endopeptidases. <i>Biochemical Society Transactions</i> , 1991 , 19, 707-15	5.1	28
6	Potential metal ligands in the insulinase superfamily of endopeptidases. <i>Biochemical Society Transactions</i> , 1991 , 19, 289S	5.1	4
5	Evolution of proteins of the cystatin superfamily. <i>Journal of Molecular Evolution</i> , 1990 , 30, 60-71	3.1	251
4	FLUSYS: a software package for the collection and analysis of kinetic and scanning data from Perkin-Elmer fluorimeters. <i>Bioinformatics</i> , 1990 , 6, 118-9	7.2	18
3	Stem bromelain: amino acid sequence and implications for weak binding of cystatin. <i>FEBS Letters</i> , 1989 , 247, 419-24	3.8	108
2	Papaya proteinase IV amino acid sequence. <i>FEBS Letters</i> , 1989 , 258, 109-12	3.8	37

1 Peptidases2, 86-94