

Neil David Rawlings

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

16,351
citations

53794

45
h-index

69250

77
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99
all docs

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docs citations

99
times ranked

22654
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199. | 14.5 | 1,358 |
| 2 | InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360. | 14.5 | 1,291 |
| 3 | 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. | 14.5 | 1,234 |
| 4 | MEROPS: the database of proteolytic enzymes, their substrates and inhibitors. <i>Nucleic Acids Research</i> , 2012, 40, D343-D350. | 14.5 | 1,047 |
| 5 | MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2010, 38, D227-D233. | 14.5 | 786 |
| 6 | <i>MEROPS</i> : the database of proteolytic enzymes, their substrates and inhibitors. <i>Nucleic Acids Research</i> , 2014, 42, D503-D509. | 14.5 | 782 |
| 7 | [13] Evolutionary families of metallopeptidases. <i>Methods in Enzymology</i> , 1995, 248, 183-228. | 1.0 | 707 |
| 8 | Twenty years of the <i>MEROPS</i> database of proteolytic enzymes, their substrates and inhibitors. <i>Nucleic Acids Research</i> , 2016, 44, D343-D350. | 14.5 | 648 |
| 9 | New mini- zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. <i>BMC Bioinformatics</i> , 2014, 15, 1. | 2.6 | 541 |
| 10 | Evolutionary families of peptidase inhibitors. <i>Biochemical Journal</i> , 2004, 378, 705-716. | 3.7 | 528 |
| 11 | [2] Families of serine peptidases. <i>Methods in Enzymology</i> , 1994, 244, 19-61. | 1.0 | 506 |
| 12 | MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2007, 36, D320-D325. | 14.5 | 497 |
| 13 | MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2006, 34, D270-D272. | 14.5 | 477 |
| 14 | MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 1999, 27, 325-331. | 14.5 | 421 |
| 15 | MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2004, 32, 160D-164. | 14.5 | 355 |
| 16 | Cloning, Isolation, and Characterization of Mammalian Legumain, an Asparaginyl Endopeptidase. <i>Journal of Biological Chemistry</i> , 1997, 272, 8090-8098. | 3.4 | 314 |
| 17 | [32] Families of cysteine peptidases. <i>Methods in Enzymology</i> , 1994, 244, 461-486. | 1.0 | 311 |
| 18 | Genome of the Host-Cell Transforming Parasite <i>Theileria annulata</i> Compared with <i>T. parva</i> . <i>Science</i> , 2005, 309, 131-133. | 12.6 | 285 |

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|----|---|------|-----------|
| 19 | Evolution of proteins of the cystatin superfamily. <i>Journal of Molecular Evolution</i> , 1990, 30, 60-71. | 1.8 | 277 |
| 20 | Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386. | 12.6 | 254 |
| 21 | The CHAP domain: a large family of amidases including GSP amidase and peptidoglycan hydrolases. <i>Trends in Biochemical Sciences</i> , 2003, 28, 234-237. | 7.5 | 209 |
| 22 | Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015, 4, e06974. | 6.0 | 198 |
| 23 | 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, 361-365. | 2.8 | 197 |
| 24 | MEROPS: the protease database. <i>Nucleic Acids Research</i> , 2002, 30, 343-346. | 14.5 | 190 |
| 25 | Evolutionary Lines of Cysteine Peptidases. <i>Biological Chemistry</i> , 2001, 382, 727-33. | 2.5 | 179 |
| 26 | Families and Clans of Serine Peptidases. <i>Archives of Biochemistry and Biophysics</i> , 1995, 318, 247-250. | 3.0 | 177 |
| 27 | Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685. | 5.5 | 176 |
| 28 | 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. | 6.5 | 166 |
| 29 | A Primitive Enzyme for a Primitive Cell: The Protease Required for Excystation of <i>Giardia</i> . <i>Cell</i> , 1997, 89, 437-444. | 28.9 | 146 |
| 30 | [7] Families of aspartic peptidases, and those of unknown catalytic mechanism. <i>Methods in Enzymology</i> , 1995, 248, 105-120. | 1.0 | 131 |
| 31 | Stem bromelain: Amino acid sequence and implications for weak binding of cystatin. <i>FEBS Letters</i> , 1989, 247, 419-424. | 2.8 | 129 |
| 32 | The MEROPS Database as a Protease Information System. <i>Journal of Structural Biology</i> , 2001, 134, 95-102. | 2.8 | 124 |
| 33 | MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2000, 28, 323-325. | 14.5 | 109 |
| 34 | [32] Thimet oligopeptidase and oligopeptidase M or neurolysin. <i>Methods in Enzymology</i> , 1995, 248, 529-556. | 1.0 | 92 |
| 35 | 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. | 2.1 | 89 |
| 36 | Asparagine Peptide Lyases. <i>Journal of Biological Chemistry</i> , 2011, 286, 38321-38328. | 3.4 | 89 |

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|----|---|------|-----------|
| 37 | Oligopeptidases, and the Emergence of the Prolyl Oligopeptidase Family. <i>Biological Chemistry Hoppe-Seyler</i> , 1992, 373, 353-360. | 1.4 | 86 |
| 38 | Structure of membrane glutamate carboxypeptidase. <i>BBA - Proteins and Proteomics</i> , 1997, 1339, 247-252. | 2.1 | 79 |
| 39 | Peptidase inhibitors in the MEROPS database. <i>Biochimie</i> , 2010, 92, 1463-1483. | 2.6 | 74 |
| 40 | 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. | 6.5 | 70 |
| 41 | The PepSY domain: a regulator of peptidase activity in the microbial environment?. <i>Trends in Biochemical Sciences</i> , 2004, 29, 169-172. | 7.5 | 68 |
| 42 | The MEROPS batch BLAST: A tool to detect peptidases and their non-peptidase homologues in a genome. <i>Biochimie</i> , 2008, 90, 243-259. | 2.6 | 68 |
| 43 | Families and clans of cysteine peptidases. <i>Journal of Computer - Aided Molecular Design</i> , 1996, 6, 1-11. | 1.0 | 54 |
| 44 | 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. | 2.6 | 54 |
| 45 | Prokaryote-derived protein inhibitors of peptidases: A sketchy occurrence and mostly unknown function. <i>Biochimie</i> , 2010, 92, 1644-1656. | 2.6 | 47 |
| 46 | How to use the <sc><i>MEROPS</i></sc> database and website to help understand peptidase specificity. <i>Protein Science</i> , 2021, 30, 83-92. | 7.6 | 44 |
| 47 | The Baculovirus<i>Autographa californica</i> Nuclear Polyhedrosis Virus Genome Includes a Papain-Like Sequence. <i>Biological Chemistry Hoppe-Seyler</i> , 1992, 373, 1211-1216. | 1.4 | 43 |
| 48 | Papaya proteinase IV amino acid sequence. <i>FEBS Letters</i> , 1989, 258, 109-112. | 2.8 | 41 |
| 49 | Using the MEROPS Database for Proteolytic Enzymes and Their Inhibitors and Substrates. <i>Current Protocols in Bioinformatics</i> , 2014, 48, 1.25.1-33. | 25.8 | 39 |
| 50 | 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-bap015. | 3.0 | 37 |
| 51 | Types and families of endopeptidases. <i>Biochemical Society Transactions</i> , 1991, 19, 707-715. | 3.4 | 36 |
| 52 | Managing Peptidases in the Genomic Era. <i>Biological Chemistry</i> , 2003, 384, 873-82. | 2.5 | 36 |
| 53 | â€Speciesâ€™ of peptidases. <i>Biological Chemistry</i> , 2007, 388, 1151-7. | 2.5 | 32 |
| 54 | Introduction: metallopeptidases and their clans. , 2004, , 231-267. | | 31 |

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|----|---|------|-----------|
| 55 | Pepsin homologues in bacteria. BMC Genomics, 2009, 10, 437. | 2.8 | 30 |
| 56 | Origins of peptidases. Biochimie, 2019, 166, 4-18. | 2.6 | 30 |
| 57 | Genome properties in 2019: a new companion database to InterPro for the inference of complete functional attributes. Nucleic Acids Research, 2019, 47, D564-D572. | 14.5 | 27 |
| 58 | Structural Analysis of Papain-Like NlpC/P60 Superfamily Enzymes with a Circularly Permuted Topology Reveals Potential Lipid Binding Sites. PLoS ONE, 2011, 6, e22013. | 2.5 | 22 |
| 59 | FLUSYS: a software package for the collection and analysis of kinetic and scanning data from Perkin-Elmer fluorimeters. Bioinformatics, 1990, 6, 118-119. | 4.1 | 19 |
| 60 | Fxna, a novel gene differentially expressed in the rat ovary at the time of folliculogenesis, is required for normal ovarian histogenesis. Development (Cambridge), 2007, 134, 945-957. | 2.5 | 18 |
| 61 | Twenty-five years of nomenclature and classification of proteolytic enzymes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140345. | 2.3 | 18 |
| 62 | Dipeptidyl-peptidase II is related to lysosomal Pro-X carboxypeptidase. BBA - Proteins and Proteomics, 1996, 1298, 1-3. | 2.1 | 17 |
| 63 | Structural and Sequence Analysis of Imelysin-Like Proteins Implicated in Bacterial Iron Uptake. PLoS ONE, 2011, 6, e21875. | 2.5 | 17 |
| 64 | A novel RCE1 isoform is required for H-Ras plasma membrane localization and is regulated by USP17. Biochemical Journal, 2014, 457, 289-300. | 3.7 | 16 |
| 65 | Bacterial calpains and the evolution of the calpain (C2) family of peptidases. Biology Direct, 2015, 10, 66. | 4.6 | 15 |
| 66 | Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013. | 2.6 | 13 |
| 67 | An Introduction to Peptidases and the Merops Database. , 2007, , 161-179. | | 10 |
| 68 | Introduction: aspartic peptidases and their clans. , 2004, , 3-12. | | 10 |
| 69 | Unusual phyletic distribution of peptidases as a tool for identifying potential drug targets. Biochemical Journal, 2007, 401, e5-7. | 3.7 | 8 |
| 70 | LUD, a new protein domain associated with lactate utilization. BMC Bioinformatics, 2013, 14, 341. | 2.6 | 8 |
| 71 | Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063. | 3.0 | 8 |
| 72 | A comparison of Pfam and MEROPS: two databases, one comprehensive, and one specialised. BMC Bioinformatics, 2003, 4, 17. | 2.6 | 7 |

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|----|---|-----|-----------|
| 73 | Identification and prioritization of novel uncharacterized peptidases for biochemical characterization. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat022. | 3.0 | 6 |
| 74 | Thimet oligopeptidase: site-directed mutagenesis disproves previous assumptions about the nature of the catalytic site. FEBS Letters, 1998, 435, 16-20. | 2.8 | 5 |
| 75 | Potential metal ligands in the insulinase superfamily of endopeptidases. Biochemical Society Transactions, 1991, 19, 289S-289S. | 3.4 | 4 |
| 76 | Using the MEROPS Database for Investigation of Lysosomal Peptidases, Their Inhibitors, and Substrates. Methods in Molecular Biology, 2017, 1594, 213-226. | 0.9 | 4 |
| 77 | Evolution of the Thermopsin Peptidase Family (A5). PLoS ONE, 2013, 8, e78998. | 2.5 | 4 |
| 78 | The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. F1000Research, 2013, 2, 154. | 1.6 | 3 |
| 79 | The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. F1000Research, 2013, 2, 154. | 1.6 | 2 |
| 80 | 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. BMC Bioinformatics, 2014, 15, 75. | 2.6 | 1 |
| 81 | Peptidases, families, and clans. , 2005, , . | | 0 |
| 82 | Antarease. , 2013, , 1079-1081. | | 0 |
| 83 | Bacteriophage T4 Prohead Endopeptidase. , 2013, , 3560-3562. | | 0 |
| 84 | Nonviral Peptidases. , 2021, , 1-17. | | 0 |
| 85 | ADAM15 Peptidase. , 2013, , 1122-1125. | | 0 |
| 86 | Nonviral Peptidases. , 2021, , 1152-1169. | | 0 |
| 87 | Non-viral Peptidases. , 2008, , 876-883. | | 0 |