

Ruth Y Eberhardt

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

18,442
citations

361296

20
h-index

501076

28
g-index

32
all docs

32
docs citations

32
times ranked

34210
citing authors

#	ARTICLE	IF	CITATIONS
1	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	6.5	5,425
2	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	6.5	5,391
3	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012, 40, D290-D301.	6.5	3,306
4	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	6.5	1,000
5	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232.	6.5	745
6	New mini- zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. <i>BMC Bioinformatics</i> , 2014, 15, 1.	1.2	541
7	Prenatal exome sequencing analysis in fetal structural anomalies detected by ultrasonography (PAGE): a cohort study. <i>Lancet, The</i> , 2019, 393, 747-757.	6.3	443
8	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , 2012, 40, D565-D570.	6.5	349
9	Evidence for 28 genetic disorders discovered by combining healthcare and research data. <i>Nature</i> , 2020, 586, 757-762.	13.7	343
10	The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2004, 33, D29-D33.	6.5	269
11	EMBL Nucleotide Sequence Database in 2006. <i>Nucleic Acids Research</i> , 2007, 35, D16-D20.	6.5	136
12	Filling out the structural map of the NTF2-like superfamily. <i>BMC Bioinformatics</i> , 2013, 14, 327.	1.2	74
13	Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2007, 36, D5-D12.	6.5	46
14	Characterization of a cellulosome dockerin domain from the anaerobic fungus <i>Piromyces equi</i> . <i>Nature Structural Biology</i> , 2001, 8, 775-778.	9.7	44
15	Primary sequence and enzymic properties of two modular endoglucanases, Cel5A and Cel45A, from the anaerobic fungus <i>Piromyces equi</i> The EMBL accession numbers for the sequences reported in this paper are AJ277482 and AJ277483.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1999-2008.	0.7	43
16	Non-coding region variants upstream of MEF2C cause severe developmental disorder through three distinct loss-of-function mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 1083-1094.	2.6	42
17	AntiFam: a tool to help identify spurious ORFs in protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas003-bas003.	1.4	38
18	Development and evaluation of ELISA procedures to detect antibodies against the major envelope protein (GL) of equine arteritis virus. <i>Journal of Virological Methods</i> , 2000, 90, 167-183.	1.0	35

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19	Rfam: Annotating Families of Non-Coding RNA Sequences. <i>Methods in Molecular Biology</i> , 2015, 1269, 349-363.	0.4	35
20	The contribution of X-linked coding variation to severe developmental disorders. <i>Nature Communications</i> , 2021, 12, 627.	5.8	33
21	The challenge of increasing Pfam coverage of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat023.	1.4	22
22	Structural genomics analysis of uncharacterized protein families overrepresented in human gut bacteria identifies a novel glycoside hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 112.	1.2	13
23	Detecting cryptic clinically relevant structural variation in exome-sequencing data increases diagnostic yield for developmental disorders. <i>American Journal of Human Genetics</i> , 2021, 108, 2186-2194.	2.6	12
24	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
25	Structure- and context-based analysis of the GxGYxYP family reveals a new putative class of Glycoside Hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 196.	1.2	8
26	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. <i>PLoS ONE</i> , 2013, 8, e57848.	1.1	6
27	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from <i>Legionella pneumophila</i> . <i>BMC Bioinformatics</i> , 2013, 14, 265.	1.2	3
28	The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013, 2, 154.	0.8	2