

# Ruth Y Eberhardt

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/551374/publications.pdf>

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	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
2	The contribution of X-linked coding variation to severe developmental disorders. <i>Nature Communications</i> , 2021, 12, 627.	5.8	33
3	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
4	Evidence for 28 genetic disorders discovered by combining healthcare and research data. <i>Nature</i> , 2020, 586, 757-762.	13.7	343
5	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
6	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	6.5	5,391
7	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	6.5	1,000
8	Rfam: Annotating Families of Non-Coding RNA Sequences. <i>Methods in Molecular Biology</i> , 2015, 1269, 349-363.	0.4	35
9	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
10	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	6.5	5,425
11	New mini-zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. <i>BMC Bioinformatics</i> , 2014, 15, 1.	1.2	541
12	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
13	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
14	Filling out the structural map of the NTF2-like superfamily. <i>BMC Bioinformatics</i> , 2013, 14, 327.	1.2	74
15	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
16	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232.	6.5	745
17	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
18	The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. <i>F1000Research</i> , 2013, 2, 154.	0.8	2

#	ARTICLE	IF	CITATIONS
19	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. PLoS ONE, 2013, 8, e57848.	1.1	6
20	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	1.4	38
21	The UniProt-GO Annotation database in 2011. Nucleic Acids Research, 2012, 40, D565-D570.	6.5	349
22	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	6.5	3,306
23	EMBL Nucleotide Sequence Database in 2006. Nucleic Acids Research, 2007, 35, D16-D20.	6.5	136
24	Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. Nucleic Acids Research, 2007, 36, D5-D12.	6.5	46
25	The EMBL Nucleotide Sequence Database. Nucleic Acids Research, 2004, 33, D29-D33.	6.5	269
26	Characterization of a cellulosome dockerin domain from the anaerobic fungus Piromyces equi. Nature Structural Biology, 2001, 8, 775-778.	9.7	44
27	Development and evaluation of ELISA procedures to detect antibodies against the major envelope protein (GL) of equine arteritis virus. Journal of Virological Methods, 2000, 90, 167-183.	1.0	35
28	Primary sequence and enzymic properties of two modular endoglucanases, Cel5A and Cel45A, from the anaerobic fungus Piromyces equi The EMBL accession numbers for the sequences reported in this paper are AJ277482 and AJ277483.. Microbiology (United Kingdom), 2000, 146, 1999-2008.	0.7	43