

Sean R Eddy

List of Publications by Year in descending order

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128
papers

123,708
citations

6613

79
h-index

22166

113
g-index

144
all docs

144
docs citations

144
times ranked

99377
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. <i>Nucleic Acids Research</i> , 1997, 25, 955-964.	14.5	9,417
3	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2007, 36, D281-D288.	14.5	6,372
4	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,819
5	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	14.5	5,425
6	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	14.5	5,391
7	Accelerated Profile HMM Searches. <i>PLoS Computational Biology</i> , 2011, 7, e1002195.	3.2	5,076
8	HMMER web server: interactive sequence similarity searching. <i>Nucleic Acids Research</i> , 2011, 39, W29-W37.	14.5	4,492
9	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. <i>Nucleic Acids Research</i> , 1997, 25, 0955-964.	14.5	3,970
10	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D427-D432.	14.5	3,937
11	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012, 40, D290-D301.	14.5	3,306
12	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004, 32, 138D-141.	14.5	3,084
13	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010, 38, D211-D222.	14.5	2,693
14	Infernal 1.1: 100-fold faster RNA homology searches. <i>Bioinformatics</i> , 2013, 29, 2933-2935.	4.1	2,281
15	The Pfam Protein Families Database. <i>Nucleic Acids Research</i> , 2002, 30, 276-280.	14.5	2,067
16	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006, 34, D247-D251.	14.5	2,030
17	A uniform system for microRNA annotation. <i>Rna</i> , 2003, 9, 277-279.	3.5	1,620
18	HMMER web server: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W200-W204.	14.5	1,432

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19	Rfam: an RNA family database. <i>Nucleic Acids Research</i> , 2003, 31, 439-441.	14.5	1,296
20	Infernal 1.0: inference of RNA alignments. <i>Bioinformatics</i> , 2009, 25, 1335-1337.	4.1	1,293
21	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , 2004, 33, D121-D124.	14.5	1,255
22	Non-coding RNA genes and the modern RNA world. <i>Nature Reviews Genetics</i> , 2001, 2, 919-929.	16.8	1,235
23	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013, 41, e121-e121.	14.5	1,214
24	The Pfam Protein Families Database. <i>Nucleic Acids Research</i> , 2000, 28, 263-266.	14.5	1,173
25	Hidden Markov models. <i>Current Opinion in Structural Biology</i> , 1996, 6, 361-365.	5.7	1,118
26	Pfam: A comprehensive database of protein domain families based on seed alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 405-420.	2.6	1,036
27	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	14.5	1,000
28	Hidden Markov model speed heuristic and iterative HMM search procedure. <i>BMC Bioinformatics</i> , 2010, 11, 431.	2.6	966
29	HMMER web server: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, W30-W38.	14.5	849
30	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009, 37, D136-D140.	14.5	820
31	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. <i>Nucleic Acids Research</i> , 2018, 46, D335-D342.	14.5	819
32	Automated De Novo Identification of Repeat Sequence Families in Sequenced Genomes. <i>Genome Research</i> , 2002, 12, 1269-1276.	5.5	776
33	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232.	14.5	745
34	nhmmer: DNA homology search with profile HMMs. <i>Bioinformatics</i> , 2013, 29, 2487-2489.	4.1	735
35	RNA sequence analysis using covariance models. <i>Nucleic Acids Research</i> , 1994, 22, 2079-2088.	14.5	727
36	A new generation of homology search tools based on probabilistic inference. <i>Genome Informatics</i> , 2009, 23, 205-11.	0.4	699

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37	A dynamic programming algorithm for RNA structure prediction including pseudoknots 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 285, 2053-2068.	4.2	649
38	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	8.1	640
39	The Dfam database of repetitive DNA families. <i>Nucleic Acids Research</i> , 2016, 44, D81-D89.	14.5	543
40	Pack-MULE transposable elements mediate gene evolution in plants. <i>Nature</i> , 2004, 431, 569-573.	27.8	495
41	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	14.5	475
42	A Computational Screen for Methylation Guide snoRNAs in Yeast. <i>Science</i> , 1999, 283, 1168-1171.	12.6	444
43	An active DNA transposon family in rice. <i>Nature</i> , 2003, 421, 163-167.	27.8	415
44	What is a hidden Markov model?. <i>Nature Biotechnology</i> , 2004, 22, 1315-1316.	17.5	403
45	A NEW GENERATION OF HOMOLOGY SEARCH TOOLS BASED ON PROBABILISTIC INFERENCE. , 2009, , .		403
46	Noncoding RNA gene detection using comparative sequence analysis. <i>BMC Bioinformatics</i> , 2001, 2, 8.	2.6	402
47	Computational identification of noncoding RNAs in E. coli by comparative genomics. <i>Current Biology</i> , 2001, 11, 1369-1373.	3.9	363
48	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145.	14.5	355
49	Homologs of Small Nucleolar RNAs in Archaea. <i>Science</i> , 2000, 288, 517-522.	12.6	324
50	A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs. <i>Nature Methods</i> , 2017, 14, 45-48.	19.0	300
51	A Probabilistic Model of Local Sequence Alignment That Simplifies Statistical Significance Estimation. <i>PLoS Computational Biology</i> , 2008, 4, e1000069.	3.2	287
52	Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs. <i>Bioinformatics</i> , 2000, 16, 583-605.	4.1	267
53	Query-Dependent Banding (QDB) for Faster RNA Similarity Searches. <i>PLoS Computational Biology</i> , 2007, 3, e56.	3.2	259
54	ATV: display and manipulation of annotated phylogenetic trees. <i>Bioinformatics</i> , 2001, 17, 383-384.	4.1	251

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55	Kissing complex RNAs mediate interaction between the Fragile-X mental retardation protein KH2 domain and brain polyribosomes. <i>Genes and Development</i> , 2005, 19, 903-918.	5.9	243
56	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	27.8	243
57	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , 2012, 41, D70-D82.	14.5	243
58	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003, 424, 157-164.	27.8	236
59	Where did the BLOSUM62 alignment score matrix come from?. <i>Nature Biotechnology</i> , 2004, 22, 1035-1036.	17.5	227
60	RSEARCH: finding homologs of single structured RNA sequences. <i>BMC Bioinformatics</i> , 2003, 4, 44.	2.6	224
61	Computational Genomics of Noncoding RNA Genes. <i>Cell</i> , 2002, 109, 137-140.	28.9	221
62	Maximum Discrimination Hidden Markov Models of Sequence Consensus. <i>Journal of Computational Biology</i> , 1995, 2, 9-23.	1.6	218
63	Evaluation of several lightweight stochastic context-free grammars for RNA secondary structure prediction. <i>BMC Bioinformatics</i> , 2004, 5, 71.	2.6	207
64	A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure. <i>BMC Bioinformatics</i> , 2002, 3, 18.	2.6	206
65	Changes in Gene Expression Associated with Developmental Arrest and Longevity in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2001, 11, 1346-1352.	5.5	202
66	The <i>Oxytricha trifallax</i> Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. <i>PLoS Biology</i> , 2013, 11, e1001473.	5.6	198
67	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. <i>BMC Bioinformatics</i> , 2002, 3, 14.	2.6	160
68	A genetic, genomic, and computational resource for exploring neural circuit function. <i>ELife</i> , 2020, 9, .	6.0	159
69	The C-value paradox, junk DNA and ENCODE. <i>Current Biology</i> , 2012, 22, R898-R899.	3.9	155
70	Noncoding RNA genes identified in AT-rich hyperthermophiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7542-7547.	7.1	154
71	Amino acid sequence motif of group I intron endonucleases is conserved in open reading frames of group II introns. <i>Trends in Biochemical Sciences</i> , 1994, 19, 402-404.	7.5	142
72	Cell type-specific genomics of <i>Drosophila</i> neurons. <i>Nucleic Acids Research</i> , 2012, 40, 9691-9704.	14.5	138

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73	Noncoding RNA genes. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 695-699.	3.3	135
74	Computational Analysis of Conserved RNA Secondary Structure in Transcriptomes and Genomes. <i>Annual Review of Biophysics</i> , 2014, 43, 433-456.	10.0	118
75	How do RNA folding algorithms work?. <i>Nature Biotechnology</i> , 2004, 22, 1457-1458.	17.5	117
76	What is dynamic programming?. <i>Nature Biotechnology</i> , 2004, 22, 909-910.	17.5	116
77	Many, but not all, lineage-specific genes can be explained by homology detection failure. <i>PLoS Biology</i> , 2020, 18, e3000862.	5.6	113
78	Efficient pairwise RNA structure prediction and alignment using sequence alignment constraints. <i>BMC Bioinformatics</i> , 2006, 7, 400.	2.6	110
79	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	6.0	106
80	What is Bayesian statistics?. <i>Nature Biotechnology</i> , 2004, 22, 1177-1178.	17.5	105
81	A Model of the Statistical Power of Comparative Genome Sequence Analysis. <i>PLoS Biology</i> , 2005, 3, e10.	5.6	103
82	A range of complex probabilistic models for RNA secondary structure prediction that includes the nearest-neighbor model and more. <i>Rna</i> , 2012, 18, 193-212.	3.5	103
83	The ENCODE project: Missteps overshadowing a success. <i>Current Biology</i> , 2013, 23, R259-R261.	3.9	86
84	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	27.8	85
85	Autogenous translational operator recognized by bacteriophage T4 DNA polymerase. <i>Journal of Molecular Biology</i> , 1990, 213, 749-761.	4.2	84
86	Computational identification of non-coding RNAs in <i>Saccharomyces cerevisiae</i> by comparative genomics. <i>Nucleic Acids Research</i> , 2003, 31, 4119-4128.	14.5	79
87	Representation learning of genomic sequence motifs with convolutional neural networks. <i>PLoS Computational Biology</i> , 2019, 15, e1007560.	3.2	72
88	Estimating the power of sequence covariation for detecting conserved RNA structure. <i>Bioinformatics</i> , 2020, 36, 3072-3076.	4.1	69
89	Members of the immunoglobulin superfamily in bacteria. <i>Protein Science</i> , 1996, 5, 1939-1941.	7.6	66
90	Computational identification of functional RNA homologs in metagenomic data. <i>RNA Biology</i> , 2013, 10, 1170-1179.	3.1	56

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91	Identification and Characterization of a Class of MALAT1-like Genomic Loci. <i>Cell Reports</i> , 2017, 19, 1723-1738.	6.4	55
92	Probabilistic Phylogenetic Inference with Insertions and Deletions. <i>PLoS Computational Biology</i> , 2008, 4, e1000172.	3.2	51
93	Circular box C/D RNAs in <i>Pyrococcus furiosus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14097-14101.	7.1	46
94	Fast filtering for RNA homology search. <i>Bioinformatics</i> , 2011, 27, 3102-3109.	4.1	39
95	Mixing genome annotation methods in a comparative analysis inflates the apparent number of lineage-specific genes. <i>Current Biology</i> , 2022, 32, 2632-2639.e2.	3.9	36
96	<i>C. elegans</i> noncoding RNA genes. <i>WormBook</i> , 2005, , 1-7.	5.3	34
97	“Antedisciplinary” Science. <i>PLoS Computational Biology</i> , 2005, 1, e6.	3.2	30
98	A computational screen for alternative genetic codes in over 250,000 genomes. <i>ELife</i> , 2021, 10, .	6.0	30
99	A member of the immunoglobulin superfamily in bacteriophage T4. <i>Virus Genes</i> , 1997, 14, 163-165.	1.6	28
100	Parameterizing sequence alignment with an explicit evolutionary model. <i>BMC Bioinformatics</i> , 2015, 16, 406.	2.6	26
101	Gene Evolution: Getting Something from Nothing. <i>Current Biology</i> , 2017, 27, R661-R663.	3.9	23
102	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172.	2.5	22
103	A survey of nematode SmY RNAs. <i>RNA Biology</i> , 2009, 6, 5-8.	3.1	21
104	Remote homology search with hidden Potts models. <i>PLoS Computational Biology</i> , 2020, 16, e1008085.	3.2	21
105	Group I introns are widespread in archaea. <i>Nucleic Acids Research</i> , 2018, 46, 7970-7976.	14.5	20
106	Archaeal Guide RNAs Function in rRNA Modification in the Eukaryotic Nucleus. <i>Current Biology</i> , 2002, 12, 199-203.	3.9	19
107	Local RNA structure alignment with incomplete sequence. <i>Bioinformatics</i> , 2009, 25, 1236-1243.	4.1	17
108	Transcription Factors That Convert Adult Cell Identity Are Differentially Polycomb Repressed. <i>PLoS ONE</i> , 2013, 8, e63407.	2.5	16

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109	Free circular introns with an unusual branchpoint in neuronal projections. <i>ELife</i> , 2019, 8, .	6.0	14
110	Exploiting <i>Oxytricha trifallax</i> nanochromosomes to screen for non-coding RNA genes. <i>Nucleic Acids Research</i> , 2011, 39, 7529-7547.	14.5	11
111	Constructing benchmark test sets for biological sequence analysis using independent set algorithms. <i>PLoS Computational Biology</i> , 2022, 18, e1009492.	3.2	10
112	GENETICS: Total Information Awareness for Worm Genetics. <i>Science</i> , 2006, 311, 1381-1382.	12.6	6
113	A Genetic, Genomic, and Computational Resource for Exploring Neural Circuit Function. <i>SSRN Electronic Journal</i> , 0, , .	0.4	6
114	Homology searches for structural RNAs: from proof of principle to practical use. <i>Rna</i> , 2015, 21, 605-607.	3.5	3
115	Is the Pope the Pope?. <i>Nature</i> , 1996, 382, 490-490.	27.8	2
116	RNA structure alignment on a massively parallel computer. <i>Lecture Notes in Computer Science</i> , 1995, , 502-507.	1.3	0
117	Inside the black boxes Computer methods for macromolecular sequence analysis (Methods in Tj ETQq1 1 0.784314 rgBT /Overlock 1	7.5	0
118	Broadening Pfam Protein Sequence Annotations. <i>Nature Precedings</i> , 2009, , .	0.1	0
119	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
120	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
121	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
122	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
123	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
124	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
125	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0
126	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0

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127	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0
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