Sean R Eddy

List of Publications by Year
in descending order

128 papers	123,708 citations	6613 79 h-index	22161 113 g-index
144 all docs	144 docs citations	144 times ranked	99377 citing authors

#	Article	IF	Citations
1	Constructing benchmark test sets for biological sequence analysis using independent set algorithms. PLoS Computational Biology, 2022, 18, e1009492.	3.2	10
2	Mixing genome annotation methods in a comparative analysis inflates the apparent number of lineage-specific genes. Current Biology, 2022, 32, 2632-2639.e2.	3.9	36
3	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. Nucleic Acids Research, 2021, 49, D192-D200.	14.5	475
4	A computational screen for alternative genetic codes in over 250,000 genomes. ELife, 2021, 10, .	6.0	30
5	Estimating the power of sequence covariation for detecting conserved RNA structure. Bioinformatics, 2020, 36, 3072-3076.	4.1	69
6	Many, but not all, lineage-specific genes can be explained by homology detection failure. PLoS Biology, 2020, 18, e3000862.	5.6	113
7	Remote homology search with hidden Potts models. PLoS Computational Biology, 2020, 16, e1008085.	3.2	21
8	A genetic, genomic, and computational resource for exploring neural circuit function. ELife, 2020, 9, .	6.0	159
9	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
10	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
11	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
12	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
13	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
14	Many, but not all, lineage-specific genes can be explained by homology detection failure. , 2020, 18, e3000862.		0
15	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0
16	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0
17	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0
18	Remote homology search with hidden Potts models. , 2020, 16, e1008085.		0

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19	Representation learning of genomic sequence motifs with convolutional neural networks. PLoS Computational Biology, 2019, 15, e1007560.	3.2	72
20	The Pfam protein families database in 2019. Nucleic Acids Research, 2019, 47, D427-D432.	14.5	3,937
21	Free circular introns with an unusual branchpoint in neuronal projections. ELife, 2019, 8, .	6.0	14
22	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. Nucleic Acids Research, 2018, 46, D335-D342.	14.5	819
23	Group I introns are widespread in archaea. Nucleic Acids Research, 2018, 46, 7970-7976.	14.5	20
24	HMMER web server: 2018 update. Nucleic Acids Research, 2018, 46, W200-W204.	14.5	1,432
25	Identification and Characterization of a Class of MALAT1-like Genomic Loci. Cell Reports, 2017, 19, 1723-1738.	6.4	55
26	Gene Evolution: Getting Something from Nothing. Current Biology, 2017, 27, R661-R663.	3.9	23
27	A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs. Nature Methods, 2017, 14, 45-48.	19.0	300
28	The Dfam database of repetitive DNA families. Nucleic Acids Research, 2016, 44, D81-D89.	14.5	543
29	The Pfam protein families database: towards a more sustainable future. Nucleic Acids Research, 2016, 44, D279-D285.	14.5	5,391
30	Epigenomic landscapes of retinal rods and cones. ELife, 2016, 5, e11613.	6.0	106
31	Parameterizing sequence alignment with an explicit evolutionary model. BMC Bioinformatics, 2015, 16, 406.	2.6	26
32	HMMER web server: 2015 update. Nucleic Acids Research, 2015, 43, W30-W38.	14.5	849
33	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. Genome Biology and Evolution, 2015, 7, evv172.	2.5	22
34	Homology searches for structural RNAs: from proof of principle to practical use. Rna, 2015, 21, 605-607.	3.5	3
35	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. Neuron, 2015, 86, 1369-1384.	8.1	640
36	Rfam 12.0: updates to the RNA families database. Nucleic Acids Research, 2015, 43, D130-D137.	14.5	1,000

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37	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	14.5	5,425
38	Computational Analysis of Conserved RNA Secondary Structure in Transcriptomes and Genomes. Annual Review of Biophysics, 2014, 43, 433-456.	10.0	118
39	The ENCODE project: Missteps overshadowing a success. Current Biology, 2013, 23, R259-R261.	3.9	86
40	nhmmer: DNA homology search with profile HMMs. Bioinformatics, 2013, 29, 2487-2489.	4.1	735
41	The Oxytricha trifallax Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. PLoS Biology, 2013, 11, e1001473.	5.6	198
42	Rfam 11.0: 10 years of RNA families. Nucleic Acids Research, 2013, 41, D226-D232.	14.5	745
43	Infernal 1.1: 100-fold faster RNA homology searches. Bioinformatics, 2013, 29, 2933-2935.	4.1	2,281
44	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. Nucleic Acids Research, 2013, 41, e121-e121.	14.5	1,214
45	Computational identification of functional RNA homologs in metagenomic data. RNA Biology, 2013, 10, 1170-1179.	3.1	56
46	Transcription Factors That Convert Adult Cell Identity Are Differentially Polycomb Repressed. PLoS ONE, 2013, 8, e63407.	2.5	16
47	Cell type–specific genomics of Drosophila neurons. Nucleic Acids Research, 2012, 40, 9691-9704.	14.5	138
48	A range of complex probabilistic models for RNA secondary structure prediction that includes the nearest-neighbor model and more. Rna, 2012, 18, 193-212.	3.5	103
49	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	14.5	3,306
50	The C-value paradox, junk DNA and ENCODE. Current Biology, 2012, 22, R898-R899.	3.9	155
51	Dfam: a database of repetitive DNA based on profile hidden Markov models. Nucleic Acids Research, 2012, 41, D70-D82.	14.5	243
52	HMMER web server: interactive sequence similarity searching. Nucleic Acids Research, 2011, 39, W29-W37.	14.5	4,492
53	Rfam: Wikipedia, clans and the "decimal" release. Nucleic Acids Research, 2011, 39, D141-D145.	14.5	355
54	Fast filtering for RNA homology search. Bioinformatics, 2011, 27, 3102-3109.	4.1	39

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55	Exploiting Oxytricha trifallax nanochromosomes to screen for non-coding RNA genes. Nucleic Acids Research, 2011, 39, 7529-7547.	14.5	11
56	Accelerated Profile HMM Searches. PLoS Computational Biology, 2011, 7, e1002195.	3.2	5,076
57	Hidden Markov model speed heuristic and iterative HMM search procedure. BMC Bioinformatics, 2010, 11, 431.	2.6	966
58	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	14.5	2,693
59	Broadening Pfam Protein Sequence Annotations. Nature Precedings, 2009, , .	0.1	0
60	A survey of nematode SmY RNAs. RNA Biology, 2009, 6, 5-8.	3.1	21
61	A NEW GENERATION OF HOMOLOGY SEARCH TOOLS BASED ON PROBABILISTIC INFERENCE. , 2009, , .		403
62	Infernal 1.0: inference of RNA alignments. Bioinformatics, 2009, 25, 1335-1337.	4.1	1,293
63	Rfam: updates to the RNA families database. Nucleic Acids Research, 2009, 37, D136-D140.	14.5	820
64	Prepublication data sharing. Nature, 2009, 461, 168-170.	27.8	243
65	Local RNA structure alignment with incomplete sequence. Bioinformatics, 2009, 25, 1236-1243.	4.1	17
66	A new generation of homology search tools based on probabilistic inference. Genome Informatics, 2009, 23, 205-11.	0.4	699
67	Probabilistic Phylogenetic Inference with Insertions and Deletions. PLoS Computational Biology, 2008, 4, e1000172.	3.2	51
68	A Probabilistic Model of Local Sequence Alignment That Simplifies Statistical Significance Estimation. PLoS Computational Biology, 2008, 4, e1000069.	3.2	287
69	Query-Dependent Banding (QDB) for Faster RNA Similarity Searches. PLoS Computational Biology, 2007, 3, e56.	3.2	259
70	The Pfam protein families database. Nucleic Acids Research, 2007, 36, D281-D288.	14.5	6,372
71	Efficient pairwise RNA structure prediction and alignment using sequence alignment constraints. BMC Bioinformatics, 2006, 7, 400.	2.6	110
72	Pfam: clans, web tools and services. Nucleic Acids Research, 2006, 34, D247-D251.	14.5	2,030

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73	GENETICS: Total Information Awareness for Worm Genetics. Science, 2006, 311, 1381-1382.	12.6	6
74	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	27.8	85
75	A Model of the Statistical Power of Comparative Genome Sequence Analysis. PLoS Biology, 2005, 3, e10.	5.6	103
76	Kissing complex RNAs mediate interaction between the Fragile-X mental retardation protein KH2 domain and brain polyribosomes. Genes and Development, 2005, 19, 903-918.	5.9	243
77	â€œAntedisciplinaryâ€•Science. PLoS Computational Biology, 2005, 1, e6.	3.2	30
78	C. elegans noncoding RNA genes. WormBook, 2005, , 1-7.	5.3	34
79	Circular box C/D RNAs in Pyrococcus furiosus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14097-14101.	7.1	46
80	What is dynamic programming?. Nature Biotechnology, 2004, 22, 909-910.	17.5	116
81	Where did the BLOSUM62 alignment score matrix come from?. Nature Biotechnology, 2004, 22, 1035-1036.	17.5	227
82	What is Bayesian statistics?. Nature Biotechnology, 2004, 22, 1177-1178.	17.5	105
83	What is a hidden Markov model?. Nature Biotechnology, 2004, 22, 1315-1316.	17.5	403
84	How do RNA folding algorithms work?. Nature Biotechnology, 2004, 22, 1457-1458.	17.5	117
85	Pack-MULE transposable elements mediate gene evolution in plants. Nature, 2004, 431, 569-573.	27.8	495
86	Evaluation of several lightweight stochastic context-free grammars for RNA secondary structure prediction. BMC Bioinformatics, 2004, 5, 71.	2.6	207
87	Rfam: annotating non-coding RNAs in complete genomes. Nucleic Acids Research, 2004, 33, D121-D124.	14.5	1,255
88	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	14.5	3,084
89	RSEARCH: finding homologs of single structured RNA sequences. BMC Bioinformatics, 2003, 4, 44.	2.6	224
90	An active DNA transposon family in rice. Nature, 2003, 421, 163-167.	27.8	415

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91	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	27.8	236
92	A uniform system for microRNA annotation. Rna, 2003, 9, 277-279.	3.5	1,620
93	Rfam: an RNA family database. Nucleic Acids Research, 2003, 31, 439-441.	14.5	1,296
94	Computational identification of non-coding RNAs in Saccharomyces cerevisiae by comparative genomics. Nucleic Acids Research, 2003, 31, 4119-4128.	14.5	79
95	Automated De Novo Identification of Repeat Sequence Families in Sequenced Genomes. Genome Research, 2002, 12, 1269-1276.	5.5	776
96	Noncoding RNA genes identified in AT-rich hyperthermophiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7542-7547.	7.1	154
97	The Pfam Protein Families Database. Nucleic Acids Research, 2002, 30, 276-280.	14.5	2,067
98	Computational Genomics of Noncoding RNA Genes. Cell, 2002, 109, 137-140.	28.9	221
99	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. BMC Bioinformatics, 2002, 3, 14.	2.6	160
100	A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure. BMC Bioinformatics, 2002, 3, 18.	2.6	206
101	Archaeal Guide RNAs Function in rRNA Modification in the Eukaryotic Nucleus. Current Biology, 2002, 12, 199-203.	3.9	19
102	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
103	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
104	Non‑coding RNA genes and the modern RNA world. Nature Reviews Genetics, 2001, 2, 919-929.	16.3	1,235
105	Computational identification of noncoding RNAs in E. coli by comparative genomics. Current Biology, 2001, 11, 1369-1373.	3.9	363
106	Noncoding RNA gene detection using comparative sequence analysis. BMC Bioinformatics, 2001, 2, 8.	2.6	402
107	ATV: display and manipulation of annotated phylogenetic trees. Bioinformatics, 2001, 17, 383-384.	4.1	251
108	Changes in Gene Expression Associated with Developmental Arrest and Longevity in Caenorhabditis elegans. Genome Research, 2001, 11, 1346-1352.	5.5	202

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109	Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs. Bioinformatics, 2000, 16, 583-605.	4.1	267
110	Homologs of Small Nucleolar RNAs in Archaea. Science, 2000, 288, 517-522.	12.6	324
111	The Pfam Protein Families Database. Nucleic Acids Research, 2000, 28, 263-266.	14.5	1,173
112	A Computational Screen for Methylation Guide snoRNAs in Yeast. Science, 1999, 283, 1168-1171.	12.6	444
113	Noncoding RNA genes. Current Opinion in Genetics and Development, 1999, 9, 695-699.	3.3	135
114	A dynamic programming algorithm for RNA structure prediction including pseudoknots 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1999, 285, 2053-2068.	4.2	649
115	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. Nucleic Acids Research, 1997, 25, 955-964.	14.5	9,417
116	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. Nucleic Acids Research, 1997, 25, 0955-964.	14.5	3,970
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	A member of the immunoglobulin superfamily in bacteriophage T4. Virus Genes, 1997, 14, 163-165.	1.6	28
119	Pfam: A comprehensive database of protein domain families based on seed alignments. Proteins: Structure, Function and Bioinformatics, 1997, 28, 405-420.	2.6	1,036
120	Hidden Markov models. Current Opinion in Structural Biology, 1996, 6, 361-365.	5.7	1,118
121	Members of the immunoglobulin superfamily in bacteria. Protein Science, 1996, 5, 1939-1941.	7.6	66
122	Is the Pope the Pope?. Nature, 1996, 382, 490-490.	27.8	2
123	RNA structure alignment on a massively parallel computer. Lecture Notes in Computer Science, 1995, , 502-507.	1.3	0
124	Maximum Discrimination Hidden Markov Models of Sequence Consensus. Journal of Computational Biology, 1995, 2, 9-23.	1.6	218
125	Amino acid sequence motif of group I intron endonucleases is conserved in open reading frames of group II introns. Trends in Biochemical Sciences, 1994, 19, 402-404.	7.5	142
126	RNA sequence analysis using covariance models. Nucleic Acids Research, 1994, 22, 2079-2088.	14.5	727

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127	Autogenous translational operator recognized by bacteriophage T4 DNA polymerase. Journal of Molecular Biology, 1990, 213, 749-761.	4.2	84
128	A Genetic, Genomic, and Computational Resource for Exploring Neural Circuit Function. SSRN Electronic Journal, 0, , .	0.4	6