

# Sean R Eddy

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

132 papers	92,025 citations	79 h-index	144 g-index
144 ext. papers	109,581 ext. citations	15.9 avg, IF	8.33 L-index

#	Paper	IF	Citations
132	Initial sequencing and analysis of the human genome. <i>Nature</i> , <b>2001</b> , 409, 860-921	50.4	17366
131	tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 955-64	20.1	7694
130	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , <b>2002</b> , 420, 520-62	50.4	5376
129	Pfam: the protein families database. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D222-30	20.1	3975
128	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D279-85	20.1	3678
127	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 0955-964	20.1	3624
126	Accelerated Profile HMM Searches. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002195	5	3068
125	HMMER web server: interactive sequence similarity searching. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W29-37	20.1	2917
124	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D290-301	20.1	2844
123	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D138-41	20.1	2720
122	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D211-22	20.1	2467
121	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D427-D432	20.1	2298
120	Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids <b>1998</b> ,		2271
119	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 276-80	20.1	1839
118	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D281-8	20.1	1806
117	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D247-51	20.1	1784
116	A uniform system for microRNA annotation. <i>Rna</i> , <b>2003</b> , 9, 277-9	5.8	1332

115	Infernal 1.1: 100-fold faster RNA homology searches. <i>Bioinformatics</i> , <b>2013</b> , 29, 2933-5	7.2	1252
114	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 263-6	20.1	1074
113	Non-coding RNA genes and the modern RNA world. <i>Nature Reviews Genetics</i> , <b>2001</b> , 2, 919-29	30.1	1012
112	Infernal 1.0: inference of RNA alignments. <i>Bioinformatics</i> , <b>2009</b> , 25, 1335-7	7.2	1001
111	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D121-4	20.1	990
110	Rfam: an RNA family database. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 439-41	20.1	970
109	Hidden Markov models. <i>Current Opinion in Structural Biology</i> , <b>1996</b> , 6, 361-5	8.1	847
108	Pfam: a comprehensive database of protein domain families based on seed alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1997</b> , 28, 405-20	4.2	841
107	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D130-7	20.1	723
106	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D136-40	20.1	652
105	A new generation of homology search tools based on probabilistic inference. <i>Genome Informatics</i> , <b>2009</b> , 23, 205-11		636
104	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e121	20.1	629
103	HMMER web server: 2018 update. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W200-W204	20.1	596
102	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D226-32	20.1	596
101	HMMER web server: 2015 update. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W30-8	20.1	590
100	RNA sequence analysis using covariance models. <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 2079-88	20.1	586
99	Hidden Markov model speed heuristic and iterative HMM search procedure. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 431	3.6	546
98	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D335-D342	20.1	533

97	A dynamic programming algorithm for RNA structure prediction including pseudoknots. <i>Journal of Molecular Biology</i> , <b>1999</b> , 285, 2053-68	6.5	511
96	Automated de novo identification of repeat sequence families in sequenced genomes. <i>Genome Research</i> , <b>2002</b> , 12, 1269-76	9.7	499
95	Pack-MULE transposable elements mediate gene evolution in plants. <i>Nature</i> , <b>2004</b> , 431, 569-73	50.4	433
94	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , <b>2015</b> , 86, 1369-84	13.9	430
93	A computational screen for methylation guide snoRNAs in yeast. <i>Science</i> , <b>1999</b> , 283, 1168-71	33.3	398
92	An active DNA transposon family in rice. <i>Nature</i> , <b>2003</b> , 421, 163-7	50.4	371
91	nhmmer: DNA homology search with profile HMMs. <i>Bioinformatics</i> , <b>2013</b> , 29, 2487-9	7.2	366
90	Noncoding RNA gene detection using comparative sequence analysis. <i>BMC Bioinformatics</i> , <b>2001</b> , 2, 8	3.6	342
89	Computational identification of noncoding RNAs in E. coli by comparative genomics. <i>Current Biology</i> , <b>2001</b> , 11, 1369-73	6.3	327
88	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D141-5	20.1	321
87	The Dfam database of repetitive DNA families. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D81-9	20.1	295
86	Homologs of small nucleolar RNAs in Archaea. <i>Science</i> , <b>2000</b> , 288, 517-22	33.3	289
85	What is a hidden Markov model?. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1315-6	44.5	258
84	A NEW GENERATION OF HOMOLOGY SEARCH TOOLS BASED ON PROBABILISTIC INFERENCE <b>2009</b> ,		255
83	Query-dependent banding (QDB) for faster RNA similarity searches. <i>PLoS Computational Biology</i> , <b>2007</b> , 3, e56	5	234
82	ATV: display and manipulation of annotated phylogenetic trees. <i>Bioinformatics</i> , <b>2001</b> , 17, 383-4	7.2	234
81	A probabilistic model of local sequence alignment that simplifies statistical significance estimation. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000069	5	225
80	Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs. <i>Bioinformatics</i> , <b>2000</b> , 16, 583-605	7.2	220

79	Kissing complex RNAs mediate interaction between the Fragile-X mental retardation protein KH2 domain and brain polyribosomes. <i>Genes and Development</i> , <b>2005</b> , 19, 903-18	12.6	208
78	The DNA sequence of human chromosome 7. <i>Nature</i> , <b>2003</b> , 424, 157-64	50.4	202
77	Prepublication data sharing. <i>Nature</i> , <b>2009</b> , 461, 168-70	50.4	197
76	Computational genomics of noncoding RNA genes. <i>Cell</i> , <b>2002</b> , 109, 137-40	56.2	192
75	A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs. <i>Nature Methods</i> , <b>2017</b> , 14, 45-48	21.6	191
74	Changes in gene expression associated with developmental arrest and longevity in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , <b>2001</b> , 11, 1346-52	9.7	186
73	RSEARCH: finding homologs of single structured RNA sequences. <i>BMC Bioinformatics</i> , <b>2003</b> , 4, 44	3.6	178
72	Maximum discrimination hidden Markov models of sequence consensus. <i>Journal of Computational Biology</i> , <b>1995</b> , 2, 9-23	1.7	167
71	Evaluation of several lightweight stochastic context-free grammars for RNA secondary structure prediction. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 71	3.6	165
70	Where did the BLOSUM62 alignment score matrix come from?. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1035-6	44.5	164
69	A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure. <i>BMC Bioinformatics</i> , <b>2002</b> , 3, 18	3.6	163
68	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D70-82	20.1	147
67	The <i>Oxytricha trifallax</i> macronuclear genome: a complex eukaryotic genome with 16,000 tiny chromosomes. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001473	9.7	145
66	Noncoding RNA genes identified in AT-rich hyperthermophiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 7542-7	11.5	142
65	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. <i>BMC Bioinformatics</i> , <b>2002</b> , 3, 14	3.6	140
64	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> , <b>1994</b> , 19, 402-4	10.3	133
63	The C-value paradox, junk DNA and ENCODE. <i>Current Biology</i> , <b>2012</b> , 22, R898-9	6.3	118
62	Cell type-specific genomics of <i>Drosophila</i> neurons. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 9691-704	20.1	114

61	Noncoding RNA genes. <i>Current Opinion in Genetics and Development</i> , <b>1999</b> , 9, 695-9	4.9	113
60	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D192-D200	20.1	108
59	How do RNA folding algorithms work?. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1457-8	44.5	100
58	A model of the statistical power of comparative genome sequence analysis. <i>PLoS Biology</i> , <b>2005</b> , 3, e10	9.7	94
57	Efficient pairwise RNA structure prediction and alignment using sequence alignment constraints. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 400	3.6	92
56	Computational analysis of conserved RNA secondary structure in transcriptomes and genomes. <i>Annual Review of Biophysics</i> , <b>2014</b> , 43, 433-56	21.1	85
55	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , <b>2016</b> , 5, e11613	8.9	83
54	What is dynamic programming?. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 909-10	44.5	79
53	What is Bayesian statistics?. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1177-8	44.5	79
52	A genetic, genomic, and computational resource for exploring neural circuit function. <i>ELife</i> , <b>2020</b> , 9,	8.9	78
51	Autogenous translational operator recognized by bacteriophage T4 DNA polymerase. <i>Journal of Molecular Biology</i> , <b>1990</b> , 213, 749-61	6.5	74
50	Computational identification of non-coding RNAs in <i>Saccharomyces cerevisiae</i> by comparative genomics. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 4119-28	20.1	70
49	The ENCODE project: missteps overshadowing a success. <i>Current Biology</i> , <b>2013</b> , 23, R259-61	6.3	67
48	A range of complex probabilistic models for RNA secondary structure prediction that includes the nearest-neighbor model and more. <i>Rna</i> , <b>2012</b> , 18, 193-212	5.8	62
47	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , <b>2005</b> , 434, 724-31	50.4	61
46	Members of the immunoglobulin superfamily in bacteria. <i>Protein Science</i> , <b>1996</b> , 5, 1939-41	6.3	57
45	Probabilistic phylogenetic inference with insertions and deletions. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000172	5	46
44	Identification and Characterization of a Class of MALAT1-like Genomic Loci. <i>Cell Reports</i> , <b>2017</b> , 19, 1723-1738	17.38	41

43	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> , <b>2004</b> , 101, 14097-101	11.5	38
42	Estimating the power of sequence covariation for detecting conserved RNA structure. <i>Bioinformatics</i> , <b>2020</b> , 36, 3072-3076	7.2	37
41	Computational identification of functional RNA homologs in metagenomic data. <i>RNA Biology</i> , <b>2013</b> , 10, 1170-9	4.8	33
40	<i>C. elegans</i> noncoding RNA genes. <i>WormBook</i> , <b>2005</b> , 1-7		28
39	Fast filtering for RNA homology search. <i>Bioinformatics</i> , <b>2011</b> , 27, 3102-9	7.2	26
38	Many, but not all, lineage-specific genes can be explained by homology detection failure. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000862	9.7	26
37	"Antedisciplinary" science. <i>PLoS Computational Biology</i> , <b>2005</b> , 1, e6	5	26
36	A member of the immunoglobulin superfamily in bacteriophage T4. <i>Virus Genes</i> , <b>1997</b> , 14, 163-5	2.3	24
35	Representation learning of genomic sequence motifs with convolutional neural networks. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007560	5	24
34	Combinatorial DNA Rearrangement Facilitates the Origin of New Genes in Ciliates. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 2859-70	3.9	19
33	A survey of nematode SmY RNAs. <i>RNA Biology</i> , <b>2009</b> , 6, 5-8	4.8	19
32	Archaeal guide RNAs function in rRNA modification in the eukaryotic nucleus. <i>Current Biology</i> , <b>2002</b> , 12, 199-203	6.3	19
31	Parameterizing sequence alignment with an explicit evolutionary model. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 406	3.6	17
30	Transcription factors that convert adult cell identity are differentially polycomb repressed. <i>PLoS ONE</i> , <b>2013</b> , 8, e63407	3.7	16
29	Gene Evolution: Getting Something from Nothing. <i>Current Biology</i> , <b>2017</b> , 27, R661-R663	6.3	15
28	Local RNA structure alignment with incomplete sequence. <i>Bioinformatics</i> , <b>2009</b> , 25, 1236-43	7.2	14
27	A genetic, genomic, and computational resource for exploring neural circuit function		14
26	Group I introns are widespread in archaea. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 7970-7976	20.1	13

25	Exploiting <i>Oxytricha trifallax</i> nanochromosomes to screen for non-coding RNA genes. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 7529-47	20.1	10
24	Remote homology search with hidden Potts models. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008085	5	9
23	Free circular introns with an unusual branchpoint in neuronal projections. <i>ELife</i> , <b>2019</b> , 8,	8.9	7
22	Genetics. Total information awareness for worm genetics. <i>Science</i> , <b>2006</b> , 311, 1381-2	33.3	5
21	Many but not all lineage-specific genes can be explained by homology detection failure		5
20	A computational screen for alternative genetic codes in over 250,000 genomes. <i>ELife</i> , <b>2021</b> , 10,	8.9	4
19	Homology searches for structural RNAs: from proof of principle to practical use. <i>Rna</i> , <b>2015</b> , 21, 605-7	5.8	3
18	A Genetic, Genomic, and Computational Resource for Exploring Neural Circuit Function. <i>SSRN Electronic Journal</i> ,	1	2
17	Estimating the power of sequence covariation for detecting conserved RNA structure		2
16	Remote homology search with hidden Potts models		2
15	Mixing genome annotation methods in a comparative analysis inflates the apparent number of lineage-specific genes		1
14	A computational screen for alternative genetic codes in over 250,000 genomes		1
13	Constructing benchmark test sets for biological sequence analysis using independent set algorithms.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009492	5	1
12	Is the Pope the Pope?. <i>Nature</i> , <b>1996</b> , 382, 490-490	50.4	0
11	RNA structure alignment on a massively parallel computer. <i>Lecture Notes in Computer Science</i> , <b>1995</b> , 502-507	50.7	
10	Many, but not all, lineage-specific genes can be explained by homology detection failure <b>2020</b> , 18, e3000862		
9	Many, but not all, lineage-specific genes can be explained by homology detection failure <b>2020</b> , 18, e3000862		
8	Many, but not all, lineage-specific genes can be explained by homology detection failure <b>2020</b> , 18, e3000862		



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