

Sean R Eddy

List of Publications by Year in Descending Order

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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	Constructing benchmark test sets for biological sequence analysis using independent set algorithms.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009492	5	1
131	A computational screen for alternative genetic codes in over 250,000 genomes. <i>ELife</i> , 2021 , 10,	8.9	4
130	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021 , 49, D192-D200	20.1	108
129	Estimating the power of sequence covariation for detecting conserved RNA structure. <i>Bioinformatics</i> , 2020 , 36, 3072-3076	7.2	37
128	Many, but not all, lineage-specific genes can be explained by homology detection failure. <i>PLoS Biology</i> , 2020 , 18, e3000862	9.7	26
127	Remote homology search with hidden Potts models. <i>PLoS Computational Biology</i> , 2020 , 16, e1008085	5	9
126	A genetic, genomic, and computational resource for exploring neural circuit function. <i>ELife</i> , 2020 , 9,	8.9	78
125	Many, but not all, lineage-specific genes can be explained by homology detection failure 2020 , 18, e3000862		
124	Many, but not all, lineage-specific genes can be explained by homology detection failure 2020 , 18, e3000862		
123	Many, but not all, lineage-specific genes can be explained by homology detection failure 2020 , 18, e3000862		
122	Many, but not all, lineage-specific genes can be explained by homology detection failure 2020 , 18, e3000862		
121	Many, but not all, lineage-specific genes can be explained by homology detection failure 2020 , 18, e3000862		
120	Many, but not all, lineage-specific genes can be explained by homology detection failure 2020 , 18, e3000862		
119	Remote homology search with hidden Potts models 2020 , 16, e1008085		
118	Remote homology search with hidden Potts models 2020 , 16, e1008085		
117	Remote homology search with hidden Potts models 2020 , 16, e1008085		
116	Remote homology search with hidden Potts models 2020 , 16, e1008085		

115	Free circular introns with an unusual branchpoint in neuronal projections. <i>ELife</i> , 2019 , 8,	8.9	7
114	Representation learning of genomic sequence motifs with convolutional neural networks. <i>PLoS Computational Biology</i> , 2019 , 15, e1007560	5	24
113	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D427-D432	20.1	2298
112	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. <i>Nucleic Acids Research</i> , 2018 , 46, D335-D342	20.1	533
111	HMMER web server: 2018 update. <i>Nucleic Acids Research</i> , 2018 , 46, W200-W204	20.1	596
110	Group I introns are widespread in archaea. <i>Nucleic Acids Research</i> , 2018 , 46, 7970-7976	20.1	13
109	Identification and Characterization of a Class of MALAT1-like Genomic Loci. <i>Cell Reports</i> , 2017 , 19, 1723-1738	10.38	41
108	Gene Evolution: Getting Something from Nothing. <i>Current Biology</i> , 2017 , 27, R661-R663	6.3	15
107	A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs. <i>Nature Methods</i> , 2017 , 14, 45-48	21.6	191
106	The Dfam database of repetitive DNA families. <i>Nucleic Acids Research</i> , 2016 , 44, D81-9	20.1	295
105	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016 , 44, D279-85	20.1	3678
104	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016 , 5, e11613	8.9	83
103	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015 , 86, 1369-84	13.9	430
102	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015 , 43, D130-7	20.1	723
101	Parameterizing sequence alignment with an explicit evolutionary model. <i>BMC Bioinformatics</i> , 2015 , 16, 406	3.6	17
100	HMMER web server: 2015 update. <i>Nucleic Acids Research</i> , 2015 , 43, W30-8	20.1	590
99	Combinatorial DNA Rearrangement Facilitates the Origin of New Genes in Ciliates. <i>Genome Biology and Evolution</i> , 2015 , 7, 2859-70	3.9	19
98	Homology searches for structural RNAs: from proof of principle to practical use. <i>Rna</i> , 2015 , 21, 605-7	5.8	3

97	Computational analysis of conserved RNA secondary structure in transcriptomes and genomes. <i>Annual Review of Biophysics</i> , 2014 , 43, 433-56	21.1	85
96	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014 , 42, D222-30	20.1	3975
95	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , 2013 , 41, D70-82	20.1	147
94	The ENCODE project: missteps overshadowing a success. <i>Current Biology</i> , 2013 , 23, R259-61	6.3	67
93	nhmmer: DNA homology search with profile HMMs. <i>Bioinformatics</i> , 2013 , 29, 2487-9	7.2	366
92	The <i>Oxytricha trifallax</i> macronuclear genome: a complex eukaryotic genome with 16,000 tiny chromosomes. <i>PLoS Biology</i> , 2013 , 11, e1001473	9.7	145
91	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013 , 41, D226-32	20.1	596
90	Infernal 1.1: 100-fold faster RNA homology searches. <i>Bioinformatics</i> , 2013 , 29, 2933-5	7.2	1252
89	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013 , 41, e121	20.1	629
88	Computational identification of functional RNA homologs in metagenomic data. <i>RNA Biology</i> , 2013 , 10, 1170-9	4.8	33
87	Transcription factors that convert adult cell identity are differentially polycomb repressed. <i>PLoS ONE</i> , 2013 , 8, e63407	3.7	16
86	The C-value paradox, junk DNA and ENCODE. <i>Current Biology</i> , 2012 , 22, R898-9	6.3	118
85	Cell type-specific genomics of <i>Drosophila</i> neurons. <i>Nucleic Acids Research</i> , 2012 , 40, 9691-704	20.1	114
84	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	5.8	62
83	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012 , 40, D290-301	20.1	2844
82	HMMER web server: interactive sequence similarity searching. <i>Nucleic Acids Research</i> , 2011 , 39, W29-37	20.1	2917
81	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011 , 39, D141-5	20.1	321
80	Fast filtering for RNA homology search. <i>Bioinformatics</i> , 2011 , 27, 3102-9	7.2	26

79	Exploiting <i>Oxytricha trifallax</i> nanochromosomes to screen for non-coding RNA genes. <i>Nucleic Acids Research</i> , 2011 , 39, 7529-47	20.1	10
78	Accelerated Profile HMM Searches. <i>PLoS Computational Biology</i> , 2011 , 7, e1002195	5	3068
77	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010 , 38, D211-22	20.1	2467
76	Hidden Markov model speed heuristic and iterative HMM search procedure. <i>BMC Bioinformatics</i> , 2010 , 11, 431	3.6	546
75	A survey of nematode SmY RNAs. <i>RNA Biology</i> , 2009 , 6, 5-8	4.8	19
74	A NEW GENERATION OF HOMOLOGY SEARCH TOOLS BASED ON PROBABILISTIC INFERENCE 2009 ,		255
73	Infernal 1.0: inference of RNA alignments. <i>Bioinformatics</i> , 2009 , 25, 1335-7	7.2	1001
72	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009 , 37, D136-40	20.1	652
71	Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70	50.4	197
70	Local RNA structure alignment with incomplete sequence. <i>Bioinformatics</i> , 2009 , 25, 1236-43	7.2	14
69	A new generation of homology search tools based on probabilistic inference. <i>Genome Informatics</i> , 2009 , 23, 205-11		636
68	Probabilistic phylogenetic inference with insertions and deletions. <i>PLoS Computational Biology</i> , 2008 , 4, e1000172	5	46
67	A probabilistic model of local sequence alignment that simplifies statistical significance estimation. <i>PLoS Computational Biology</i> , 2008 , 4, e1000069	5	225
66	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2008 , 36, D281-8	20.1	1806
65	Query-dependent banding (QDB) for faster RNA similarity searches. <i>PLoS Computational Biology</i> , 2007 , 3, e56	5	234
64	Efficient pairwise RNA structure prediction and alignment using sequence alignment constraints. <i>BMC Bioinformatics</i> , 2006 , 7, 400	3.6	92
63	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
62	Genetics. Total information awareness for worm genetics. <i>Science</i> , 2006 , 311, 1381-2	33.3	5

61	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , 2005 , 33, D121-4	20.1	990
60	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005 , 434, 724-31	50.4	61
59	A model of the statistical power of comparative genome sequence analysis. <i>PLoS Biology</i> , 2005 , 3, e10	9.7	94
58	Kissing complex RNAs mediate interaction between the Fragile-X mental retardation protein KH2 domain and brain polyribosomes. <i>Genes and Development</i> , 2005 , 19, 903-18	12.6	208
57	"Antedisciplinary" science. <i>PLoS Computational Biology</i> , 2005 , 1, e6	5	26
56	C. elegans noncoding RNA genes. <i>WormBook</i> , 2005 , 1-7		28
55	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, 14097-101	11.5	38
54	What is dynamic programming?. <i>Nature Biotechnology</i> , 2004 , 22, 909-10	44.5	79
53	Where did the BLOSUM62 alignment score matrix come from?. <i>Nature Biotechnology</i> , 2004 , 22, 1035-6	44.5	164
52	What is Bayesian statistics?. <i>Nature Biotechnology</i> , 2004 , 22, 1177-8	44.5	79
51	What is a hidden Markov model?. <i>Nature Biotechnology</i> , 2004 , 22, 1315-6	44.5	258
50	How do RNA folding algorithms work?. <i>Nature Biotechnology</i> , 2004 , 22, 1457-8	44.5	100
49	Pack-MULE transposable elements mediate gene evolution in plants. <i>Nature</i> , 2004 , 431, 569-73	50.4	433
48	Evaluation of several lightweight stochastic context-free grammars for RNA secondary structure prediction. <i>BMC Bioinformatics</i> , 2004 , 5, 71	3.6	165
47	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
46	RSEARCH: finding homologs of single structured RNA sequences. <i>BMC Bioinformatics</i> , 2003 , 4, 44	3.6	178
45	An active DNA transposon family in rice. <i>Nature</i> , 2003 , 421, 163-7	50.4	371
44	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003 , 424, 157-64	50.4	202

43	A uniform system for microRNA annotation. <i>Rna</i> , 2003 , 9, 277-9	5.8	1332
42	Rfam: an RNA family database. <i>Nucleic Acids Research</i> , 2003 , 31, 439-41	20.1	970
41	Computational identification of non-coding RNAs in <i>Saccharomyces cerevisiae</i> by comparative genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 4119-28	20.1	70
40	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. <i>BMC Bioinformatics</i> , 2002 , 3, 14	3.6	140
39	A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure. <i>BMC Bioinformatics</i> , 2002 , 3, 18	3.6	163
38	Archaeal guide RNAs function in rRNA modification in the eukaryotic nucleus. <i>Current Biology</i> , 2002 , 12, 199-203	6.3	19
37	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
36	Automated de novo identification of repeat sequence families in sequenced genomes. <i>Genome Research</i> , 2002 , 12, 1269-76	9.7	499
35	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, 7542-7	11.5	142
34	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2002 , 30, 276-80	20.1	1839
33	Computational genomics of noncoding RNA genes. <i>Cell</i> , 2002 , 109, 137-40	56.2	192
32	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
31	Non-coding RNA genes and the modern RNA world. <i>Nature Reviews Genetics</i> , 2001 , 2, 919-29	30.1	1012
30	Computational identification of noncoding RNAs in <i>E. coli</i> by comparative genomics. <i>Current Biology</i> , 2001 , 11, 1369-73	6.3	327
29	Noncoding RNA gene detection using comparative sequence analysis. <i>BMC Bioinformatics</i> , 2001 , 2, 8	3.6	342
28	ATV: display and manipulation of annotated phylogenetic trees. <i>Bioinformatics</i> , 2001 , 17, 383-4	7.2	234
27	Changes in gene expression associated with developmental arrest and longevity in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2001 , 11, 1346-52	9.7	186
26	Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs. <i>Bioinformatics</i> , 2000 , 16, 583-605	7.2	220

25	Homologs of small nucleolar RNAs in Archaea. <i>Science</i> , 2000 , 288, 517-22	33.3	289
24	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2000 , 28, 263-6	20.1	1074
23	A computational screen for methylation guide snoRNAs in yeast. <i>Science</i> , 1999 , 283, 1168-71	33.3	398
22	Noncoding RNA genes. <i>Current Opinion in Genetics and Development</i> , 1999 , 9, 695-9	4.9	113
21	A dynamic programming algorithm for RNA structure prediction including pseudoknots. <i>Journal of Molecular Biology</i> , 1999 , 285, 2053-68	6.5	511
20	Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids 1998 ,		2271
19	tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. <i>Nucleic Acids Research</i> , 1997 , 25, 955-64	20.1	7694
18	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. <i>Nucleic Acids Research</i> , 1997 , 25, 0955-964	20.1	3624
17	A member of the immunoglobulin superfamily in bacteriophage T4. <i>Virus Genes</i> , 1997 , 14, 163-5	2.3	24
16	Pfam: a comprehensive database of protein domain families based on seed alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 28, 405-20	4.2	841
15	Hidden Markov models. <i>Current Opinion in Structural Biology</i> , 1996 , 6, 361-5	8.1	847
14	Members of the immunoglobulin superfamily in bacteria. <i>Protein Science</i> , 1996 , 5, 1939-41	6.3	57
13	Is the Pope the Pope?. <i>Nature</i> , 1996 , 382, 490-490	50.4	0
12	RNA structure alignment on a massively parallel computer. <i>Lecture Notes in Computer Science</i> , 1995 , 502, 507		
11	Maximum discrimination hidden Markov models of sequence consensus. <i>Journal of Computational Biology</i> , 1995 , 2, 9-23	1.7	167
10	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, 402-4	10.3	133
9	RNA sequence analysis using covariance models. <i>Nucleic Acids Research</i> , 1994 , 22, 2079-88	20.1	586
8	Autogenous translational operator recognized by bacteriophage T4 DNA polymerase. <i>Journal of Molecular Biology</i> , 1990 , 213, 749-61	6.5	74

7	Mixing genome annotation methods in a comparative analysis inflates the apparent number of lineage-specific genes		1
6	Many but not all lineage-specific genes can be explained by homology detection failure		5
5	A Genetic, Genomic, and Computational Resource for Exploring Neural Circuit Function. <i>SSRN Electronic Journal</i> ,	1	2
4	Estimating the power of sequence covariation for detecting conserved RNA structure		2
3	Remote homology search with hidden Potts models		2
2	A genetic, genomic, and computational resource for exploring neural circuit function		14
1	A computational screen for alternative genetic codes in over 250,000 genomes		1