

# Stephen F Altschul

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

94,749  
citations

159585

30  
h-index

233421

45  
g-index

57  
all docs

57  
docs citations

57  
times ranked

96626  
citing authors

#	ARTICLE	IF	CITATIONS
1	Basic local alignment search tool. <i>Journal of Molecular Biology</i> , 1990, 215, 403-410.	4.2	82,180
2	Identification of FAP Locus Genes from Chromosome 5q21. <i>Science</i> , 1991, 253, 661-665.	12.6	2,257
3	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903.	7.1	1,610
4	A workbench for multiple alignment construction and analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 9, 180-190.	2.6	1,012
5	Protein database searches using compositionally adjusted substitution matrices. <i>FEBS Journal</i> , 2005, 272, 5101-5109.	4.7	881
6	Issues in searching molecular sequence databases. <i>Nature Genetics</i> , 1994, 6, 119-129.	21.4	770
7	Domain enhanced lookup time accelerated BLAST. <i>Biology Direct</i> , 2012, 7, 12.	4.6	705
8	A superfamily of conserved domains in DNA damage-responsive cell cycle checkpoint proteins. <i>FASEB Journal</i> , 1997, 11, 68-76.	0.5	684
9	Iterated profile searches with PSI-BLAST—a tool for discovery in protein databases. <i>Trends in Biochemical Sciences</i> , 1998, 23, 444-447.	7.5	674
10	[27] Local alignment statistics. <i>Methods in Enzymology</i> , 1996, 266, 460-480.	1.0	609
11	Amino acid substitution matrices from an information theoretic perspective. <i>Journal of Molecular Biology</i> , 1991, 219, 555-565.	4.2	538
12	Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. <i>BMC Biology</i> , 2006, 4, 41.	3.8	420
13	SAGEmap: A Public Gene Expression Resource. <i>Genome Research</i> , 2000, 10, 1051-1060.	5.5	367
14	Functional motifs. <i>Nature Genetics</i> , 1996, 13, 266-268.	21.4	362
15	Optimal sequence alignment using affine gap costs. <i>Bulletin of Mathematical Biology</i> , 1986, 48, 603-616.	1.9	166
16	Weights for data related by a tree. <i>Journal of Molecular Biology</i> , 1989, 207, 647-653.	4.2	157
17	Eukaryotic translation elongation factor 1 <sup>β</sup> contains a glutathione transferase domain—Study of a diverse, ancient protein super family using motif search and structural modeling. <i>Protein Science</i> , 1994, 3, 2045-2055.	7.6	140
18	A protein alignment scoring system sensitive at all evolutionary distances. <i>Journal of Molecular Evolution</i> , 1993, 36, 290-300.	1.8	139

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19	Trees, Stars, and Multiple Biological Sequence Alignment. <i>SIAM Journal on Applied Mathematics</i> , 1989, 49, 197-209.	1.8	129
20	PSI-BLAST pseudocounts and the minimum description length principle. <i>Nucleic Acids Research</i> , 2009, 37, 815-824.	14.5	120
21	Gap costs for multiple sequence alignment. <i>Journal of Theoretical Biology</i> , 1989, 138, 297-309.	1.7	112
22	Characterization of Gene Expression in Resting and Activated Mast Cells. <i>Journal of Experimental Medicine</i> , 1998, 188, 1657-1668.	8.5	105
23	The compositional adjustment of amino acid substitution matrices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15688-15693.	7.1	79
24	Generalized affine gap costs for protein sequence alignment. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 32, 88-96.	2.6	67
25	The Construction and Use of Log-Odds Substitution Scores for Multiple Sequence Alignment. <i>PLoS Computational Biology</i> , 2010, 6, e1000852.	3.2	58
26	Retrieval accuracy, statistical significance and compositional similarity in protein sequence database searches. <i>Nucleic Acids Research</i> , 2006, 34, 5966-5973.	14.5	53
27	A nonlinear measure of subalignment similarity and its significance levels. <i>Bulletin of Mathematical Biology</i> , 1986, 48, 617-632.	1.9	50
28	Equal animals. <i>Nature</i> , 1990, 348, 493-494.	27.8	37
29	Locally optimal subalignments using nonlinear similarity functions. <i>Bulletin of Mathematical Biology</i> , 1986, 48, 633-660.	1.9	34
30	Expression of a recombinant IRP-like <i>Plasmodium falciparum</i> protein that specifically binds putative plasmodial IREs. <i>Molecular and Biochemical Parasitology</i> , 2003, 126, 231-238.	1.1	31
31	Dirichlet Mixtures, the Dirichlet Process, and the Structure of Protein Space. <i>Journal of Computational Biology</i> , 2013, 20, 1-18.	1.6	27
32	The anatomy of successful computational biology software. <i>Nature Biotechnology</i> , 2013, 31, 894-897.	17.5	25
33	Significance levels for biological sequence comparison using non-linear similarity functions. <i>Bulletin of Mathematical Biology</i> , 1988, 50, 77-92.	1.9	17
34	Bayesian Top-Down Protein Sequence Alignment with Inferred Position-Specific Gap Penalties. <i>PLoS Computational Biology</i> , 2016, 12, e1004936.	3.2	17
35	Log-odds sequence logos. <i>Bioinformatics</i> , 2015, 31, 324-331.	4.1	14
36	Inferring joint sequence-structural determinants of protein functional specificity. <i>ELife</i> , 2018, 7, .	6.0	14

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37	Outlier detection in BLAST hits. <i>Algorithms for Molecular Biology</i> , 2018, 13, 7.	1.2	14
38	Deep Analysis of Residue Constraints (DARC): identifying determinants of protein functional specificity. <i>Scientific Reports</i> , 2020, 10, 1691.	3.3	12
39	Compositional Adjustment of Dirichlet Mixture Priors. <i>Journal of Computational Biology</i> , 2010, 17, 1607-1620.	1.6	9
40	Inference of Functionally-Relevant N-acetyltransferase Residues Based on Statistical Correlations. <i>PLoS Computational Biology</i> , 2016, 12, e1005294.	3.2	9
41	Statistical investigations of protein residue direct couplings. <i>PLoS Computational Biology</i> , 2018, 14, e1006237.	3.2	8
42	Initial Cluster Analysis. <i>Journal of Computational Biology</i> , 2018, 25, 121-129.	1.6	7
43	Leaf Pairs and Tree Dissections. <i>SIAM Journal on Discrete Mathematics</i> , 1989, 2, 293-299.	0.8	6
44	On the Inference of Dirichlet Mixture Priors for Protein Sequence Comparison. <i>Journal of Computational Biology</i> , 2011, 18, 941-954.	1.6	5
45	The Complexity of the Dirichlet Model for Multiple Alignment Data. <i>Journal of Computational Biology</i> , 2011, 18, 925-939.	1.6	3
46	eCOMPASS: evaluative comparison of multiple protein alignments by statistical score. <i>Bioinformatics</i> , 2021, 37, 3456-3463.	4.1	0