

Pavel A Pevzner

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.

124
papers

26,018
citations

50
h-index

132
g-index

132
ext. papers

37,410
ext. citations

12.2
avg, IF

7.11
L-index

#	Paper	IF	Citations
124	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities.. <i>Nature Biotechnology</i> , 2022 ,	44.5	13
123	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads.. <i>Nature Biotechnology</i> , 2022 ,	44.5	5
122	viralFlye: assembling viruses and identifying their hosts from long-read metagenomics data.. <i>Genome Biology</i> , 2022 , 23, 57	18.3	1
121	Complete genomic and epigenetic maps of human centromeres.. <i>Science</i> , 2022 , 376, eabl4178	33.3	19
120	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
119	Automated annotation of human centromeres with HORmon.. <i>Genome Research</i> , 2022 ,	9.7	1
118	Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. <i>Nature Communications</i> , 2021 , 12, 1044	17.4	20
117	Thousands of previously unknown phages discovered in whole-community human gut metagenomes. <i>Microbiome</i> , 2021 , 9, 78	16.6	19
116	Integrating genomics and metabolomics for scalable non-ribosomal peptide discovery. <i>Nature Communications</i> , 2021 , 12, 3225	17.4	8
115	ORFograph: search for novel insecticidal protein genes in genomic and metagenomic assembly graphs. <i>Microbiome</i> , 2021 , 9, 149	16.6	1
114	Trace Reconstruction Problems in Computational Biology. <i>IEEE Transactions on Information Theory</i> , 2021 , 67, 3295-3314	2.8	5
113	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021 , 19,	6	6
112	CentromereArchitect: inference and analysis of the architecture of centromeres. <i>Bioinformatics</i> , 2021 , 37, i196-i204	7.2	6
111	Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. <i>Genome Research</i> , 2020 , 30, 898-909	9.7	15
110	Metaviral SPAdes: assembly of viruses from metagenomic data. <i>Bioinformatics</i> , 2020 , 36, 4126-4129	7.2	44
109	Automated analysis of immunosequencing datasets reveals novel immunoglobulin D genes across diverse species. <i>PLoS Computational Biology</i> , 2020 , 16, e1007837	5	4
108	MosaicFlye: Resolving Long Mosaic Repeats Using Long Reads. <i>Lecture Notes in Computer Science</i> , 2020 , 226-228	0.9	1

107	De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. <i>Cell Systems</i> , 2020 , 10, 99-108.e5	10.6	16
106	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020 , 17, 1103-1110	21.6	101
105	Automated assembly of centromeres from ultra-long error-prone reads. <i>Nature Biotechnology</i> , 2020 , 38, 1309-1316	44.5	24
104	TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. <i>Bioinformatics</i> , 2020 , 36, i75-i83	7.2	21
103	The string decomposition problem and its applications to centromere analysis and assembly. <i>Bioinformatics</i> , 2020 , 36, i93-i101	7.2	13
102	V(DD)J recombination is an important and evolutionarily conserved mechanism for generating antibodies with unusually long CDR3s. <i>Genome Research</i> , 2020 , 30, 1547-1558	9.7	3
101	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020 , 585, 79-84	50.4	269
100	Inference of Diversity Genes and Analysis of Non-canonical V(DD)J Recombination in Immunoglobulins. <i>Frontiers in Immunology</i> , 2019 , 10, 987	8.4	14
99	BiosyntheticSPAdes: reconstructing biosynthetic gene clusters from assembly graphs. <i>Genome Research</i> , 2019 , 29, 1352-1362	9.7	26
98	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , 2019 , 29, 961-968	9.7	48
97	How bioinformatics and open data can boost basic science in countries and universities with limited resources. <i>Nature Biotechnology</i> , 2019 , 37, 324-326	44.5	11
96	Assembly of long, error-prone reads using repeat graphs. <i>Nature Biotechnology</i> , 2019 , 37, 540-546	44.5	897
95	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019 , 9, 600-608.e4	10.6	26
94	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019 , 20, 226	18.3	24
93	Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. <i>Nature Microbiology</i> , 2018 , 3, 319-327	26.6	49
92	A family of small, cyclic peptides buried in preproalbumin since the Eocene epoch. <i>Plant Direct</i> , 2018 , 2, e00042	3.3	21
91	Joint Analysis of Long and Short Reads Enables Accurate Estimates of Microbiome Complexity. <i>Cell Systems</i> , 2018 , 7, 192-200.e3	10.6	5
90	Detection and analysis of ancient segmental duplications in mammalian genomes. <i>Genome Research</i> , 2018 , 28, 901-909	9.7	23

89	Dereplication of microbial metabolites through database search of mass spectra. <i>Nature Communications</i> , 2018 , 9, 4035	17.4	109
88	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
87	Top-down analysis of immunoglobulin G isotypes 1 and 2 with electron transfer dissociation on a high-field Orbitrap mass spectrometer. <i>Journal of Proteomics</i> , 2017 , 159, 67-76	3.9	36
86	metaSPAdes: a new versatile metagenomic assembler. <i>Genome Research</i> , 2017 , 27, 824-834	9.7	1305
85	The Antibody Repertoire of Colorectal Cancer. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 2111-2124	7.6	3
84	Single-molecule protein identification by sub-nanopore sensors. <i>PLoS Computational Biology</i> , 2017 , 13, e1005356	5	40
83	Dereplication of peptidic natural products through database search of mass spectra. <i>Nature Chemical Biology</i> , 2017 , 13, 30-37	11.7	131
82	Reconstructing Antibody Repertoires from Error-Prone Immunosequencing Reads. <i>Journal of Immunology</i> , 2017 , 199, 3369-3380	5.3	21
81	Immunoglobulin Classification Using the Colored Antibody Graph. <i>Journal of Computational Biology</i> , 2016 , 23, 483-94	1.7	4
80	TruSPAdes: barcode assembly of TruSeq synthetic long reads. <i>Nature Methods</i> , 2016 , 13, 248-50	21.6	32
79	SpectroGene: A Tool for Proteogenomic Annotations Using Top-Down Spectra. <i>Journal of Proteome Research</i> , 2016 , 15, 144-51	5.6	12
78	hybridSPAdes: an algorithm for hybrid assembly of short and long reads. <i>Bioinformatics</i> , 2016 , 32, 1009-152	15.2	292
77	Dereplication, sequencing and identification of peptidic natural products: from genome mining to peptidogenomics to spectral networks. <i>Natural Product Reports</i> , 2016 , 33, 73-86	15.1	54
76	Spatial Molecular Architecture of the Microbial Community of a Lichen. <i>MSystems</i> , 2016 , 1,	7.6	22
75	Assembly of long error-prone reads using de Bruijn graphs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E8396-E8405	11.5	120
74	Top-down analysis of protein samples by de novo sequencing techniques. <i>Bioinformatics</i> , 2016 , 32, 2753-92	9.2	12
73	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016 , 34, 828-837	44.5	1566
72	plasmidSPAdes: assembling plasmids from whole genome sequencing data. <i>Bioinformatics</i> , 2016 , 32, 3380-3387	7.2	233

71	IgRepertoireConstructor: a novel algorithm for antibody repertoire construction and immunoproteogenomics analysis. <i>Bioinformatics</i> , 2015 , 31, i53-61	7.2	27
70	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. <i>Journal of Proteome Research</i> , 2015 , 14, 3555-67	5.6	22
69	De Novo Sequencing of Peptides from Top-Down Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2015 , 14, 4450-62	5.6	28
68	Single cells within the Puerto Rico trench suggest hadal adaptation of microbial lineages. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 8265-76	4.8	34
67	Assembling short reads from jumping libraries with large insert sizes. <i>Bioinformatics</i> , 2015 , 31, 3262-8	7.2	28
66	MS-GF+ makes progress towards a universal database search tool for proteomics. <i>Nature Communications</i> , 2014 , 5, 5277	17.4	633
65	Manifold de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2014 , 296-310	0.9	5
64	Automated genome mining of ribosomal peptide natural products. <i>ACS Chemical Biology</i> , 2014 , 9, 1545-51	4.9	114
63	NRPquest: Coupling Mass Spectrometry and Genome Mining for Nonribosomal Peptide Discovery. <i>Journal of Natural Products</i> , 2014 , 77, 1902-9	4.9	64
62	What is the difference between the breakpoint graph and the de Bruijn graph?. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S6	4.5	11
61	Characterization of cyanobacterial hydrocarbon composition and distribution of biosynthetic pathways. <i>PLoS ONE</i> , 2014 , 9, e85140	3.7	114
60	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014 , 30, i293-301	7.2	80
59	Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. <i>Journal of Computational Biology</i> , 2013 , 20, 714-37	1.7	815
58	Pathset graphs: a novel approach for comprehensive utilization of paired reads in genome assembly. <i>Journal of Computational Biology</i> , 2013 , 20, 359-71	1.7	11
57	A new approach to evaluating statistical significance of spectral identifications. <i>Journal of Proteome Research</i> , 2013 , 12, 1560-8	5.6	16
56	From de Bruijn Graphs to Rectangle Graphs for Genome Assembly. <i>Lecture Notes in Computer Science</i> , 2012 , 249-261	0.9	7
55	SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. <i>Journal of Computational Biology</i> , 2012 , 19, 455-77	1.7	11958
54	SEQuel: improving the accuracy of genome assemblies. <i>Bioinformatics</i> , 2012 , 28, i188-96	7.2	46

53	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. <i>Lecture Notes in Computer Science</i> , 2012 , 200-212	0.9	3
52	How to apply de Bruijn graphs to genome assembly. <i>Nature Biotechnology</i> , 2011 , 29, 987-91	44.5	341
51	Multiplex de novo sequencing of peptide antibiotics. <i>Journal of Computational Biology</i> , 2011 , 18, 1371-81.	7	36
50	Cycloquest: identification of cyclopeptides via database search of their mass spectra against genome databases. <i>Journal of Proteome Research</i> , 2011 , 10, 4505-12	5.6	33
49	Spectral archives: extending spectral libraries to analyze both identified and unidentified spectra. <i>Nature Methods</i> , 2011 , 8, 587-91	21.6	67
48	Paired de bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers. <i>Journal of Computational Biology</i> , 2011 , 18, 1625-34	1.7	50
47	Paired de Bruijn Graphs: A Novel Approach for Incorporating Mate Pair Information into Genome Assemblers. <i>Lecture Notes in Computer Science</i> , 2011 , 238-251	0.9	12
46	Sequencing cyclic peptides by multistage mass spectrometry. <i>Proteomics</i> , 2011 , 11, 3642-50	4.8	32
45	Preface: 2nd Satellite Meeting on Bioinformatics Education, Research in Computational Molecular Biology (RECOMB-BE 2010). <i>Journal of Computational Biology</i> , 2011 , 18, 865	1.7	
44	Imaging mass spectrometry of intraspecies metabolic exchange revealed the cannibalistic factors of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 16286-90	11.5	155
43	DRIMM-Synten: decomposing genomes into evolutionary conserved segments. <i>Bioinformatics</i> , 2010 , 26, 2509-16	7.2	65
42	Identifying protease cleavage sites by label-free mass spectrometry. <i>FASEB Journal</i> , 2010 , 24, 905.4	0.9	
41	Dereplication and de novo sequencing of nonribosomal peptides. <i>Nature Methods</i> , 2009 , 6, 596-9	21.6	75
40	Computing has changed biology--biology education must catch up. <i>Science</i> , 2009 , 325, 541-2	33.3	61
39	De novo fragment assembly with short mate-paired reads: Does the read length matter?. <i>Genome Research</i> , 2009 , 19, 336-46	9.7	199
38	Automated de novo protein sequencing of monoclonal antibodies. <i>Nature Biotechnology</i> , 2008 , 26, 1336-8.	41.5	100
37	Short read fragment assembly of bacterial genomes. <i>Genome Research</i> , 2008 , 18, 324-30	9.7	332
36	Interpreting top-down mass spectra using spectral alignment. <i>Analytical Chemistry</i> , 2008 , 80, 2499-505	7.8	65

35	Spectral probabilities and generating functions of tandem mass spectra: a strike against decoy databases. <i>Journal of Proteome Research</i> , 2008 , 7, 3354-63	5.6	341
34	Clustering millions of tandem mass spectra. <i>Journal of Proteome Research</i> , 2008 , 7, 113-22	5.6	187
33	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. <i>Bioinformatics</i> , 2008 , 24, i416-23	7.2	25
32	Comment on "Protein sequences from mastodon and Tyrannosaurus rex revealed by mass spectrometry". <i>Science</i> , 2008 , 321, 1040; author reply 1040	33.3	51
31	Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. <i>Nature Genetics</i> , 2007 , 39, 1361-8	36.3	162
30	Protein identification by spectral networks analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 6140-5	11.5	133
29	Shotgun protein sequencing: assembly of peptide tandem mass spectra from mixtures of modified proteins. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1123-34	7.6	71
28	Educating Biologists in the 21st Century: Bioinformatics Scientists versus Bioinformatics Technicians 2007 , 1-5		
27	InsPecT: identification of posttranslationally modified peptides from tandem mass spectra. <i>Analytical Chemistry</i> , 2005 , 77, 4626-39	7.8	502
26	PepNovo: de novo peptide sequencing via probabilistic network modeling. <i>Analytical Chemistry</i> , 2005 , 77, 964-73	7.8	506
25	Identification of post-translational modifications by blind search of mass spectra. <i>Nature Biotechnology</i> , 2005 , 23, 1562-7	44.5	231
24	Are There Rearrangement Hotspots in the Human Genome?. <i>PLoS Computational Biology</i> , 2005 , preprint, e209	5	
23	De novo repeat classification and fragment assembly 2004 ,		12
22	De novo repeat classification and fragment assembly. <i>Genome Research</i> , 2004 , 14, 1786-96	9.7	157
21	Fragment assembly with short reads. <i>Bioinformatics</i> , 2004 , 20, 2067-74	7.2	134
20	Whole-genome analysis of Alu repeat elements reveals complex evolutionary history. <i>Genome Research</i> , 2004 , 14, 2245-52	9.7	146
19	Genome rearrangements in mammalian evolution: lessons from human and mouse genomes. <i>Genome Research</i> , 2003 , 13, 37-45	9.7	244
18	Human and mouse genomic sequences reveal extensive breakpoint reuse in mammalian evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 7672-7	11.5	290

17	GENOME-WIDE ANALYSIS OF BACTERIAL PROMOTER REGIONS 2002 ,		5
16	Fragment assembly with double-barreled data. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S225-33	7.2	79
15	Mutation-tolerant protein identification by mass spectrometry. <i>Journal of Computational Biology</i> , 2000 , 7, 777-87	1.7	107
14	De novo peptide sequencing via tandem mass spectrometry. <i>Journal of Computational Biology</i> , 1999 , 6, 327-42	1.7	434
13	1-Tuple DNA sequencing: computer analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 1989 , 7, 63-73	3.6	188
12	HORmon: automated annotation of human centromeres		2
11	MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides		1
10	TandemMapper and TandemQUAST: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats		3
9	mosaicFlye: Resolving long mosaic repeats using long error-prone reads		5
8	Thousands of previously unknown phages discovered in whole-community human gut metagenomes		3
7	Assembly of Long Error-Prone Reads Using Repeat Graphs		28
6	metaFlye: scalable long-read metagenome assembly using repeat graphs		14
5	Telomere-to-telomere assembly of a complete human X chromosome		45
4	centroFlye: Assembling Centromeres with Long Error-Prone Reads		9
3	The complete sequence of a human genome		58
2	Generation of lineage-resolved complete metagenome-assembled genomes by precision phasing		2
1	Complete genomic and epigenetic maps of human centromeres		8