Wentian Li

List of Publications by Year
in descending order

153 papers	8,303 citations	76196 40 h-index	49773 87 g-index
163 all docs	163 docs citations	163 times ranked	9838 citing authors

#	ARTICLE	IF	CITATIONS
1	*STAT4* and the Risk of Rheumatoid Arthritis and Systemic Lupus Erythematosus. New England Journal of Medicine, 2007, 357, 977-986.	13.9	914
2	*TRAF1–C5* as a Risk Locus for Rheumatoid Arthritis — A Genomewide Study. New England Journal of Medicine, 2007, 357, 1199-1209.	13.9	729
3	Analysis of Families in the Multiple Autoimmune Disease Genetics Consortium (MADGC) Collection: the PTPN22 620W Allele Associates with Multiple Autoimmune Phenotypes. American Journal of Human Genetics, 2005, 76, 561-571.	2.6	528
4	Mutual information functions versus correlation functions. Journal of Statistical Physics, 1990, 60, 823-837.	0.5	355
5	Random texts exhibit Zipf's-law-like word frequency distribution. IEEE Transactions on Information Theory, 1992, 38, 1842-1845.	1.5	322
6	Elevated Serum Levels of Interferon-Regulated Chemokines Are Biomarkers for Active Human Systemic Lupus Erythematosus. PLoS Medicine, 2006, 3, e491.	3.9	262
7	The study of correlation structures of DNA sequences: a critical review. Computers & Chemistry, 1997, 21, 257-271.	1.2	214
8	A Complete Enumeration and Classification of Two-Locus Disease Models. Human Heredity, 2000, 50, 334-349.	0.4	205
9	Genome-Wide Association Scan Identifies Candidate Polymorphisms Associated with Differential Response to Anti-TNF Treatment in Rheumatoid Arthritis. Molecular Medicine, 2008, 14, 575-581.	1.9	199
10	Regulation of anti-cyclic citrullinated peptide antibodies in rheumatoid arthritis: Contrasting effects of HLA-DR3 and the shared epitope alleles. Arthritis and Rheumatism, 2005, 52, 3813-3818.	6.7	194
11	Dissecting the Genetic Complexity of the Association between Human Leukocyte Antigens and Rheumatoid Arthritis. American Journal of Human Genetics, 2002, 71, 585-594.	2.6	183
12	Gene Discovery in Bladder Cancer Progression using cDNA Microarrays. American Journal of Pathology, 2003, 163, 505-516.	1.9	177
13	The PTPN22 R620W polymorphism associates with RF positive rheumatoid arthritis in a dose-dependent manner but not with HLA-SE status. Genes and Immunity, 2005, 6, 129-133.	2.2	173
14	Peripheral blood gene expression profiling in rheumatoid arthritis. Genes and Immunity, 2005, 6, 388-397.	2.2	161
15	VOLCANO PLOTS IN ANALYZING DIFFERENTIAL EXPRESSIONS WITH mRNA MICROARRAYS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1231003.	0.3	152
16	Application of t-SNE to human genetic data. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750017.	0.3	149
17	Intraclonal Complexity in Chronic Lymphocytic Leukemia: Fractions Enriched in Recently Born/Divided and Older/Quiescent Cells. Molecular Medicine, 2011, 17, 1374-1382.	1.9	140
18	Understanding long-range correlations in DNA sequences. Physica D: Nonlinear Phenomena, 1994, 75, 392-416.	1.3	132

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19	Transition phenomena in cellular automata rule space. Physica D: Nonlinear Phenomena, 1990, 45, 77-94.	1.3	122
20	High-density SNP analysis of 642 Caucasian families with rheumatoid arthritis identifies two new linkage regions on 11p12 and 2q33. Genes and Immunity, 2006, 7, 277-286.	2.2	119
21	Microarray Analyses of Peripheral Blood Cells Identifies Unique Gene Expression Signature in Psoriatic Arthritis. Molecular Medicine, 2005, 11, 21-29.	1.9	113
22	Identification of outcome-correlated cytokine clusters in chronic lymphocytic leukemia. Blood, 2011, 118, 5201-5210.	0.6	110
23	Expansion-modification systems: A model for spatial 1/f spectra. Physical Review A, 1991, 43, 5240-5260.	1.0	104
24	Blood autoantibody and cytokine profiles predict response to anti-tumor necrosis factor therapy in rheumatoid arthritis. Arthritis Research and Therapy, 2009, 11, R76.	1.6	99
25	Overlapping Probabilities of Top Ranking Gene Lists, Hypergeometric Distribution, and Stringency of Gene Selection Criterion. , 2006, 2006, 5531-4.		91
26	GENERATING NONTRIVIAL LONG-RANGE CORRELATIONS AND 1/f SPECTRA BY REPLICATION AND MUTATION. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 1992, 02, 137-154.	0.7	88
27	Distinctions among Circulating Antibody-Secreting Cell Populations, Including B-1 Cells, in Human Adult Peripheral Blood. Journal of Immunology, 2016, 196, 1060-1069.	0.4	86
28	Several Regions in the Major Histocompatibility Complex Confer Risk for Anti-CCP-Antibody Positive Rheumatoid Arthritis, Independent of the DRB1 Locus. Molecular Medicine, 2008, 14, 293-300.	1.9	83
29	Applications of recursive segmentation to the analysis of DNA sequences. Computers & Chemistry, 2002, 26, 491-510.	1.2	74
30	Compositional Heterogeneity within, and Uniformity between, DNA Sequences of Yeast Chromosomes. Genome Research, 1998, 8, 916-928.	2.4	66
31	The Role of Genetics in Advancing Precision Medicine for Alzheimer's Disease—A Narrative Review. Frontiers in Medicine, 2018, 5, 108.	1.2	61
32	Marker Selection by Akaike Information Criterion and Bayesian Information Criterion. Genetic Epidemiology, 2001, 21, S272-7.	0.6	60
33	Universal $1/f$ noise, crossovers of scaling exponents, and chromosome-specific patterns of guanine-cytosine content in DNA sequences of the human genome. Physical Review E, 2005, 71, 041910.	0.8	57
34	Zipf's Law in Importance of Genes for Cancer Classification Using Microarray Data. Journal of Theoretical Biology, 2002, 219, 539-551.	0.8	55
35	How Many Genes are Needed for a Discriminant Microarray Data Analysis. , 2002, , 137-149.		54
36	Absolute pitch exhibits phenotypic and genetic overlap with synesthesia. Human Molecular Genetics, 2013, 22, 2097-2104.	1.4	52

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37	The complexity of DNA. Complexity, 1997, 3, 33-38.	0.9	51
38	New Stopping Criteria for Segmenting DNA Sequences. Physical Review Letters, 2001, 86, 5815-5818.	2.9	51
39	Spatial 1/f Spectra in Open Dynamical Systems. Europhysics Letters, 1989, 10, 395-400.	0.7	50
40	Fitting Ranked Linguistic Data with Two-Parameter Functions. Entropy, 2010, 12, 1743-1764.	1.1	47
41	Isochores merit the prefix â€˜isoâ€™. Computational Biology and Chemistry, 2003, 27, 5-10.	1.1	45
42	DNA correlations. Nature, 1992, 360, 635-636.	13.7	43
43	Delineating relative homogeneous G+C domains in DNA sequences. Gene, 2001, 276, 57-72.	1.0	43
44	Menzerath's law at the geneâ€“exon level in the human genome. Complexity, 2012, 17, 49-53.	0.9	41
45	Phenomenology of nonlocal cellular automata. Journal of Statistical Physics, 1992, 68, 829-882.	0.5	40
46	Diminishing return for increased Mappability with longer sequencing reads: implications of the k-mer distributions in the human genome. BMC Bioinformatics, 2014, 15, 2.	1.2	39
47	Candidate genes involved in cardiovascular risk factors by a family-based association study on the island of Kosrae, Federated States of Micronesia. American Journal of Medical Genetics Part A, 2002, 110, 234-242.	2.4	38
48	Mappability and read length. Frontiers in Genetics, 2014, 5, 381.	1.1	38
49	Characterization of structurally defined epitopes recognized by monoclonal antibodies produced by chronic lymphocytic leukemia B cells. Blood, 2009, 114, 3615-3624.	0.6	37
50	Three lectures on case control genetic association analysis. Briefings in Bioinformatics, 2007, 9, 1-13.	3.2	35
51	Autoimmune Diseaseâ€"Associated Haplotypes of BLK Exhibit Lowered Thresholds for B Cell Activation and Expansion of Ig Classâ€"Switched B Cells. Arthritis and Rheumatology, 2015, 67, 2866-2876.	2.9	35
52	Are isochore sequences homogeneous?. Gene, 2002, 300, 129-139.	1.0	34
53	DNA segmentation as a model selection process. , 2001, , .		32
54	Identification of two novel female-specific non-major histocompatibility complex loci regulating collagen-induced arthritis severity and chronicity, and evidence of epistasis. Arthritis and Rheumatism, 2004, 50, 2695-2705.	6.7	31

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55	Partial correlation analysis indicates causal relationships between GC-content, exon density and recombination rate in the human genome. BMC Bioinformatics, 2009, 10, S66.	1.2	29
56	Fractal Dimension of Cantori. Physical Review Letters, 1986, 57, 655-658.	2.9	28
57	Statistical properties of open reading frames in complete genome sequences. Computers & Chemistry, 1999, 23, 283-301.	1.2	27
58	Two-parameter characterization of chromosome-scale recombination rate. Genome Research, 2009, 19, 2300-2307.	2.4	25
59	Extreme Value Distribution Based Gene Selection Criteria for Discriminant Microarray Data Analysis Using Logistic Regression. Journal of Computational Biology, 2004, 11, 215-226.	0.8	23
60	Inferring causal relationships among intermediate phenotypes and biomarkers: a case study of rheumatoid arthritis. Bioinformatics, 2006, 22, 1503-1507.	1.8	23
61	Cia5d regulates a new fibroblast-like synoviocyte invasion-associated gene expression signature. Arthritis Research and Therapy, 2008, 10, R92.	1.6	23
62	On parameters of the human genome. Journal of Theoretical Biology, 2011, 288, 92-104.	0.8	23
63	Using volcano plots and regularized-chi statistics in genetic association studies. Computational Biology and Chemistry, 2014, 48, 77-83.	1.1	22
64	Low-Order Polynomial Trends of Female-to-Male Map Distance Ratios along Human Chromosomes. Human Heredity, 1998, 48, 266-270.	0.4	21
65	Fitting Ranked English and Spanish Letter Frequency Distribution in US and Mexican Presidential Speeches. Journal of Quantitative Linguistics, 2011, 18, 359-380.	0.7	21
66	Comparing single-nucleotide polymorphism marker-based and microsatellite marker-based linkage analyses. BMC Genetics, 2005, 6, S13.	2.7	20
67	The osteopontin transgenic mouse is a new model for Sjögren's syndrome. Clinical Immunology, 2015, 157, 30-42.	1.4	20
68	Arg206Cys substitution in *DNASE1L3* causes a defect in DNASE1L3 protein secretion that confers risk of systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2021, 80, 782-787.	0.5	19
69	A seven-gene expression panel distinguishing clonal expansions of pre-leukemic and chronic lymphocytic leukemia B cells from normal B lymphocytes. Immunologic Research, 2015, 63, 90-100.	1.3	18
70	Effective sample size: Quick estimation of the effect of related samples in genetic case–control association analyses. Computational Biology and Chemistry, 2011, 35, 40-49.	1.1	17
71	Comparison of two–phase analyses for case–control genetic association studies. Statistics in Medicine, 2008, 27, 5054-5075.	0.8	16
72	Characterizing regions in the human genome unmappable by next-generation-sequencing at the read length of 1000 bases. Computational Biology and Chemistry, 2014, 53, 108-117.	1.1	16

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73	Enrichment of Genetic Variants for Rheumatoid Arthritis within T-Cell and NK-Cell Enhancer Regions. Molecular Medicine, 2015, 21, 180-184.	1.9	16
74	Copy-number-variation and copy-number-alteration region detection by cumulative plots. BMC Bioinformatics, 2009, 10, S67.	1.2	14
75	Analyses of baby name popularity distribution in U.S. for the last 131 years. Complexity, 2012, 18, 44-50.	0.9	14
76	Human B-1 cells are not preplasmablasts: analysis of microarray data and other issues. Blood, 2013, 122, 3691-3693.	0.6	14
77	Beyond Zipfâ€™s Law: The Lavalette Rank Function and Its Properties. PLoS ONE, 2016, 11, e0163241.	1.1	14
78	Empirical design of a variant quality control pipeline for whole genome sequencing data using replicate discordance. Scientific Reports, 2019, 9, 16156.	1.6	14
79	Alignment-free approaches for predicting novel Nuclear Mitochondrial Segments (NUMTs) in the human genome. Gene, 2019, 691, 141-152.	1.0	14
80	Complex patterns generated by next nearest neighbors cellular automata. Computers and Graphics, 1989, 13, 531-537.	1.4	13
81	Simplifying the mosaic description of DNA sequences. Physical Review E, 2002, 66, 031913.	0.8	13
82	Locus category based analysis of a large genome-wide association study of rheumatoid arthritis. Human Molecular Genetics, 2010, 19, 3863-3872.	1.4	13
83	Entropic fluctuations in DNA sequences. Physica A: Statistical Mechanics and Its Applications, 2018, 493, 444-457.	1.2	13
84	Design of artificial neural network and its applications to the analysis of alcoholism data. Genetic Epidemiology, 1999, 17, S223-8.	0.6	12
85	The-more-the-better and the-less-the-better. Bioinformatics, 2006, 22, 2187-2188.	1.8	12
86	Transient behavior of cellular automaton rule 110. Physics Letters, Section A: General, Atomic and Solid State Physics, 1992, 166, 335-339.	0.9	11
87	SPECTRAL ANALYSIS OF GUANINE AND CYTOSINE FLUCTUATIONS OF MOUSE GENOMIC DNA. Fluctuation and Noise Letters, 2004, 04, L453-L464.	1.0	11
88	Monoclonal antibody classification based on epitope-binding using differential antigen disruption. Journal of Immunological Methods, 2006, 314, 9-20.	0.6	11
89	Rapid self-organized criticality: Fractal evolution in extreme environments. Physical Review E, 2004, 70, 036118.	0.8	10
90	Principles for the organization of gene-sets. Computational Biology and Chemistry, 2015, 59, 139-149.	1.1	10

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91	Predicting functional regulatory SNPs in the human antimicrobial peptide genes DEFB1 and CAMP in tuberculosis and HIV/AIDS. Computational Biology and Chemistry, 2015, 59, 117-125.	1.1	10
92	Differential burden of rare protein truncating variants in Alzheimerâ€™s disease patients compared to centenarians. Human Molecular Genetics, 2016, 25, ddw150.	1.4	10
93	A Study on Factors Impacting Length of Hospital Stay of COVID-19 Inpatients. Journal of Contemporary Medicine, 2021, 11, 396-404.	0.1	10
94	Beyond standard pipeline and pâ€¯<â€¯0.05 in pathway enrichment analyses. Computational Biology and Chemistry, 2021, 92, 107455.	1.1	10
95	Alpha variant (B.1.1.7) of SARS-CoV-2 increases fatality-rate for patients under age of 70 years and hospitalization risk overall. Acta Microbiologica Et Immunologica Hungarica, 2021, , .	0.4	10
96	Affected-sib-pair analyses of bipolar disorder using data on chromosome 18. Genetic Epidemiology, 1997, 14, 641-646.	0.6	9
97	Increased synovial expression of nuclear receptors correlates with protection in pristane-induced arthritis: A possible novel genetically regulated homeostatic mechanism. Arthritis and Rheumatism, 2011, 63, 2918-2929.	6.7	9
98	Fitting Chinese syllable-to-character mapping spectrum by the beta rank function. Physica A: Statistical Mechanics and Its Applications, 2012, 391, 1515-1518.	1.2	9
99	Population patterns in Worldâ€™s administrative units. Royal Society Open Science, 2017, 4, 170281.	1.1	9
100	Mechanism for IL-15â€"Driven B Cell Chronic Lymphocytic Leukemia Cycling: Roles for AKT and STAT5 in Modulating Cyclin D2 and DNA Damage Response Proteins. Journal of Immunology, 2019, 202, 2924-2944.	0.4	9
101	Correlation between quantitative traits and correlation between corresponding LOD scores: detection of pleiotropic effects. BMC Genetics, 2003, 4, S60.	2.7	8
102	Reply to Henthorn and Deutsch: Ethnicity versus early environment: Comment on â€˜Early Childhood Music Education and Predisposition to Absolute Pitch: Teasing Apart Genes and Environmentâ€™ by Peter K. Gregersen, Elena Kowalsky, Nina Kohn, and Elizabeth West Marvin [2000]. American Journal of Medical Genetics, Part A, 2007, 143A, 104-105.	0.7	8
103	Bacterial genomes lacking long-range correlations may not be modeled by low-order Markov chains: The role of mixing statistics and frame shift of neighboring genes. Computational Biology and Chemistry, 2014, 53, 15-25.	1.1	8
104	Glomerulocapillary miRNA response to HLA-class I antibody in vitro and in vivo. Scientific Reports, 2017, 7, 14554.	1.6	8
105	An unusual 500,000 bases long oscillation of guanine and cytosine content in human chromosome 21. Computational Biology and Chemistry, 2004, 28, 393-399.	1.1	7
106	Large-scale oscillation of structure-related DNA sequence features in human chromosome 21. Physical Review E, 2006, 74, 021912.	0.8	7
107	Periodic Distribution of a Putative Nucleosome Positioning Motif in Human, Nonhuman Primates, and Archaea: Mutual Information Analysis. International Journal of Genomics, 2013, 2013, 1-13.	0.8	7
108	Editorial: Complexity in genomes. Computational Biology and Chemistry, 2014, 53, 1-4.	1.1	7

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109	Evaluation of the capacities of mouse TCR profiling from short read RNA-seq data. PLoS ONE, 2018, 13, e0207020.	1.1	7
110	Psychotropic Medication Use Is Associated With Greater 1-Year Incidence of Dementia After COVID-19 Hospitalization. Frontiers in Medicine, 2022, 9, 841326.	1.2	7
111	Characterizing Ranked Chinese Syllable-to-Character Mapping Spectrum: A Bridge between the Spoken and Written Chinese Language. Journal of Quantitative Linguistics, 2013, 20, 153-167.	0.7	6
112	Combining Expression of Hypervariably Expressed Genes with IGHV Mutation Status Is a More Robust Prognostic Indicator Than Mutation Status Alone in Chronic Lymphocytic Leukemia. Blood, 2011, 118, 1774-1774.	0.6	6
113	Does Logarithm Transformation of Microarray Data Affect Ranking Order of Differentially Expressed Genes?. , 2006, Suppl, 6593-6.		5
114	Size distribution of function-based human gene sets and the splitâ€"merge model. Royal Society Open Science, 2016, 3, 160275.	1.1	5
115	Genotype analysis of theNF1 gene in the French Canadians from the Quï¿½bec population. American Journal of Medical Genetics Part A, 2001, 104, 189-198.	2.4	4
116	Exploring caseâ€"control genetic association tests using phase diagrams. Computational Biology and Chemistry, 2008, 32, 391-399.	1.1	4
117	Localization of Type 1 Diabetes susceptibility in the ancestral haplotype 18.2 by high density SNP mapping. Genomics, 2009, 94, 228-232.	1.3	4
118	Human repetitive sequence densities are mostly negatively correlated with R/Y-based nucleosome-positioning motifs and positively correlated with W/S-based motifs. Genomics, 2013, 101, 125-133.	1.3	4
119	Human Î²â€defensin 1 (<i>DEFB1</i>) allele and genotype frequencies probably impact on ethnic susceptibility to atopic dermatitis. International Journal of Dermatology, 2013, 52, 115-117.	0.5	4
120	Influence of genetic copy number variants of the human GLUT3 glucose transporter gene SLC2A3 on protein expression, glycolysis and rheumatoid arthritis risk: A genetic replication study. Molecular Genetics and Metabolism Reports, 2019, 19, 100470.	0.4	4
121	Survival Analyses of COVID-19 Patients in a Turkish Cohort: Comparison between Using Time to Death and Time to Release. SciMedicine Journal, 0, 3, 1-9.	1.5	4
122	COVID-19 outpatients and surviving inpatients exhibit comparable blood test results that are distinct from non-surviving inpatients. Journal of Health Sciences and Medicine, 2021, 4, 306-313.	0.0	4
123	Genome-Wide Association Study. , 2013, , 834-834.		4
124	GENOTYPE-BASED CASE-CONTROL ANALYSIS, VIOLATION OF HARDY-WEINBERG EQUILIBRIUM, AND PHASE DIAGRAMS. , 2007, , .		4
125	Linkage disequilibrium and founder effect analysis of the NF1 gene in French Canadians from the Quebec population. Annales De GÃ©nÃ©tique, 2002, 45, 39-44.	0.4	3
126	A mathematical framework for examining whether a minimum number of chiasmata is required per metacentric chromosome or chromosome arm in human. Genomics, 2011, 97, 186-192.	1.3	3

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127	Multi-Parameter Phenotypic Analysis of Members of Chronic Lymphocytic Leukemia Clones Identifies Distinct Proliferative and Resting/Re-Entry Compartments with Discrete Gene Expression Profiles.. Blood, 2009, 114, 668-668.	0.6	3
128	A composite ranking of risk factors for COVID-19 time-to-event data from a Turkish cohort. Computational Biology and Chemistry, 2022, 98, 107681.	1.1	3
129	Reconstructing haplotypes in pedigrees: Importance of parental information. American Journal of Medical Genetics Part A, 2004, 124A, 107-109.	2.4	2
130	A survey of disease connections for CD4+ T cell master genes and their directly linked genes. Computational Biology and Chemistry, 2015, 59, 78-90.	1.1	2
131	Beta rank function: A smooth double-Pareto-like distribution. Communications in Statistics - Theory and Methods, 2022, 51, 3645-3668.	0.6	2
132	Genetic Marker. , 2013, , 821-824.		2
133	Expression Levels of a Single Gene, Lymphoid Enhancer Binding Factor 1, Discriminates CLL B-Cells from Other B-Cell Malignancies.. Blood, 2007, 110, 1113-1113.	0.6	2
134	Identification of Distinct Cytokine and Chemokine Clusters That Correlate with Outcome In B-Cell Chronic Lymphocytic Leukemia: Implications for Disease Pathogenesis. Blood, 2010, 116, 1368-1368.	0.6	2
135	A comparison of founder-only and all-pedigree-members genotype-expression association by regression analysis. BMC Proceedings, 2007, 1, S8.	1.8	1
136	FRACTAL CHARACTERIZATIONS OF MAX STATISTICAL DISTRIBUTION IN GENETIC ASSOCIATION STUDIES. International Journal of Modeling, Simulation, and Scientific Computing, 2009, 12, 513-531.	0.9	1
137	Editorial. Computational Biology and Chemistry, 2014, 48, A1.	1.1	1
138	Quantifying local randomness in human DNA and RNA sequences using ErdÃ¶s motifs. Journal of Theoretical Biology, 2019, 461, 41-50.	0.8	1
139	Investigations into SCAMP5, a candidate lupus risk gene expressed in plasmacytoid dendritic cells. Lupus Science and Medicine, 2021, 8, e000567.	1.1	1
140	Isochores Merit the Prefix 'Iso'. Genome Biology, 2002, 3, preprint0009.1.	13.9	0
141	Comments on ?linguistic features in eukaryotic genomes?. Complexity, 2004, 9, 10-11.	0.9	0
142	Effective Sample Size: Quick Estimation of the Effect of Related Samples in Genetic Case-Control Association Analyses. Nature Precedings, 2007, , .	0.1	0
143	Editorial. Computational Biology and Chemistry, 2013, 47, vii.	1.1	0
144	Advances in systems biology â€" New trends and perspectives. Computational Biology and Chemistry, 2015, 59, 1-2.	1.1	0

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145	Editorial. Computational Biology and Chemistry, 2016, 64, vii-viii.	1.1	0
146	Editorial. Computational Biology and Chemistry, 2020, 89, 107373.	1.1	0
147	Differential Expression Genes of CLL Subgroups Defined by Ki67 Expression Level Which Correlated with Clinical Outcome. Blood, 2010, 116, 2435-2435.	0.6	0
148	Gene Set Enrichment Analysis of Ki-67high CLL Clones Suggests Complex Interactions of B-Cell Receptor Signaling and Normal Cell Interactions in the Disease. Blood, 2011, 118, 2833-2833.	0.6	0
149	Gene Expression Profiles Document That Recently- and Previously-Divided CLL Fractions Represent a Continuum but Suggest Differing Modes of Activation for These Fractions in U-CLL and M-CLL. Blood, 2012, 120, 317-317.	0.6	0
150	Can We Understand Parameter Values in the Human Genome?. Springer Proceedings in Complexity, 2013, , 1071-1076.	0.2	0
151	Apparent Involvement Of The Interferon, RNA Processing, and Wnt Signaling Pathways In Monoclonal B Lymphocytosis. Blood, 2013, 122, 4157-4157.	0.6	0
152	Revisiting the neutral dynamics derived limiting guanine-cytosine content using human de novo point mutation data. Meta Gene, 2022, 31, 100994.	0.3	0
153	Noether's Theorem as a Metaphor for Chargaff's 2nd Parity Rule in Genomics. Journal of Molecular Evolution, 2022, 90, 231-238.	0.8	0