

# Alfonso Valencia

## List of Publications by Year in descending order

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356  
papers

44,213  
citations

3334

91  
h-index

2629

194  
g-index

393  
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393  
docs citations

393  
times ranked

57933  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
2	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	5.5	4,217
3	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
4	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	27.8	1,364
5	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	28.9	1,052
6	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	21.4	893
7	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	14.5	864
8	Correlated mutations and residue contacts in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 18, 309-317.	2.6	801
9	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	27.8	749
10	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527.	7.1	687
11	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	28.9	573
12	A hierarchical unsupervised growing neural network for clustering gene expression patterns. <i>Bioinformatics</i> , 2001, 17, 126-136.	4.1	562
13	The ras protein family: evolutionary tree and role of conserved amino acids. <i>Biochemistry</i> , 1991, 30, 4637-4648.	2.5	561
14	Emerging methods in protein co-evolution. <i>Nature Reviews Genetics</i> , 2013, 14, 249-261.	16.3	553
15	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 1236-1242.	21.4	525
16	Correlated mutations contain information about protein-protein interaction 1 1Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1997, 271, 511-523.	4.2	498
17	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. <i>Human Molecular Genetics</i> , 2014, 23, 5866-5878.	2.9	463
18	Reductive genome evolution in <i>Buchnera aphidicola</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 581-586.	7.1	461

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19	A gene network for navigating the literature. <i>Nature Genetics</i> , 2004, 36, 664-664.	21.4	432
20	Similarity of phylogenetic trees as indicator of protein-protein interaction. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 609-614.	2.1	425
21	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
22	A method to predict functional residues in proteins. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 171-178.	8.2	385
23	Convergent evolution of similar enzymatic function on different protein folds: The hexokinase, ribokinase, and galactokinase families of sugar kinases. <i>Protein Science</i> , 1993, 2, 31-40.	7.6	353
24	Computational methods for the prediction of protein interactions. <i>Current Opinion in Structural Biology</i> , 2002, 12, 368-373.	5.7	330
25	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	17.5	323
26	The Ras protein superfamily: Evolutionary tree and role of conserved amino acids. <i>Journal of Cell Biology</i> , 2012, 196, 189-201.	5.2	321
27	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
28	Practical limits of function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 98-107.	2.6	306
29	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	19.0	297
30	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	21.4	278
31	Alternative Splicing May Not Be the Key to Proteome Complexity. <i>Trends in Biochemical Sciences</i> , 2017, 42, 98-110.	7.5	277
32	EnrichNet: network-based gene set enrichment analysis. <i>Bioinformatics</i> , 2012, 28, i451-i457.	4.1	269
33	In silico two-hybrid system for the selection of physically interacting protein pairs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 219-227.	2.6	241
34	Prediction of protein-protein interaction sites in heterocomplexes with neural networks. <i>FEBS Journal</i> , 2002, 269, 1356-1361.	0.2	225
35	Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. <i>Npj Digital Medicine</i> , 2020, 3, 81.	10.9	225
36	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. <i>Nature Genetics</i> , 2013, 45, 1464-1469.	21.4	224

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37	POLE and POLD1 mutations in 529 kindred with familial colorectal cancer and/or polyposis: review of reported cases and recommendations for genetic testing and surveillance. <i>Genetics in Medicine</i> , 2016, 18, 325-332.	2.4	209
38	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	7.1	206
39	APPRIS: annotation of principal and alternative splice isoforms. <i>Nucleic Acids Research</i> , 2013, 41, D110-D117.	14.5	205
40	MARVEL: a conserved domain involved in membrane apposition events. <i>Trends in Biochemical Sciences</i> , 2002, 27, 599-601.	7.5	199
41	Overview of the protein-protein interaction annotation extraction task of BioCreative II. <i>Genome Biology</i> , 2008, 9, S4.	9.6	195
42	Information Retrieval and Text Mining Technologies for Chemistry. <i>Chemical Reviews</i> , 2017, 117, 7673-7761.	47.7	195
43	Automatic Methods for Predicting Functionally Important Residues. <i>Journal of Molecular Biology</i> , 2003, 326, 1289-1302.	4.2	194
44	Improving contact predictions by the combination of correlated mutations and other sources of sequence information. <i>Folding &amp; Design</i> , 1997, 2, S25-S32.	4.5	184
45	Linking genes to literature: text mining, information extraction, and retrieval applications for biology. <i>Genome Biology</i> , 2008, 9, S8.	8.8	181
46	Text-mining and information-retrieval services for molecular biology. <i>Genome Biology</i> , 2005, 6, 224.	9.6	180
47	CHEMDNER: The drugs and chemical names extraction challenge. <i>Journal of Cheminformatics</i> , 2015, 7, S1.	6.1	179
48	Implementing the iHOP concept for navigation of biomedical literature. <i>Bioinformatics</i> , 2005, 21, ii252-ii258.	4.1	177
49	Identification of amino acid residues crucial for chemokine receptor dimerization. <i>Nature Immunology</i> , 2004, 5, 216-223.	14.5	176
50	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
51	Prediction of contact maps with neural networks and correlated mutations. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 835-843.	2.1	172
52	High-confidence prediction of global interactomes based on genome-wide coevolutionary networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 934-939.	7.1	172
53	Filamin-A regulates actin-dependent clustering of HIV receptors. <i>Nature Cell Biology</i> , 2007, 9, 838-846.	10.3	167
54	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2.	6.1	166

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55	Molecular Evidence for the Inverse Comorbidity between Central Nervous System Disorders and Cancers Detected by Transcriptomic Meta-analyses. <i>PLoS Genetics</i> , 2014, 10, e1004173.	3.5	165
56	Inverse and Direct Cancer Comorbidity in People with Central Nervous System Disorders: A Meta-Analysis of Cancer Incidence in 577,013 Participants of 50 Observational Studies. <i>Psychotherapy and Psychosomatics</i> , 2014, 83, 89-105.	8.8	164
57	Conserved Clusters of Functionally Related Genes in Two Bacterial Genomes. <i>Journal of Molecular Evolution</i> , 1997, 44, 66-73.	1.8	163
58	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	19.0	161
59	Evaluation of text-mining systems for biology: overview of the Second BioCreative community challenge. <i>Genome Biology</i> , 2008, 9, S1.	9.6	159
60	Effective use of sequence correlation and conservation in fold recognition 1 Edited by J. M. Thornton. <i>Journal of Molecular Biology</i> , 1999, 293, 1221-1239.	4.2	157
61	EVA: evaluation of protein structure prediction servers. <i>Nucleic Acids Research</i> , 2003, 31, 3311-3315.	14.5	154
62	Big data analytics for personalized medicine. <i>Current Opinion in Biotechnology</i> , 2019, 58, 161-167.	6.6	152
63	Protein co-evolution, co-adaptation and interactions. <i>EMBO Journal</i> , 2008, 27, 2648-2655.	7.8	151
64	Progress and challenges in predicting protein-protein interaction sites. <i>Briefings in Bioinformatics</i> , 2008, 10, 233-246.	6.5	145
65	Towards FAIR principles for research software. <i>Data Science</i> , 2020, 3, 37-59.	0.9	144
66	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242.	5.5	143
67	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
68	Integrated Next-Generation Sequencing and Avatar Mouse Models for Personalized Cancer Treatment. <i>Clinical Cancer Research</i> , 2014, 20, 2476-2484.	7.0	140
69	APPRIS 2017: principal isoforms for multiple gene sets. <i>Nucleic Acids Research</i> , 2018, 46, D213-D217.	14.5	134
70	Protein interactions and ligand binding: From protein subfamilies to functional specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1995-2000.	7.1	132
71	Text mining for the biocuration workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas020-bas020.	3.0	132
72	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	8.8	131

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73	CAFASP2: The second critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 171-183.	2.6	130
74	A conserved loop in the ATPase domain of the DnaK chaperone is essential for stable binding of GrpE. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 95-101.	8.2	124
75	BioC: a minimalist approach to interoperability for biomedical text processing. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat064-bat064.	3.0	123
76	The BLUEPRINT Data Analysis Portal. <i>Cell Systems</i> , 2016, 3, 491-495.e5.	6.2	123
77	No paradox, no progress: inverse cancer comorbidity in people with other complex diseases. <i>Lancet Oncology</i> , The, 2011, 12, 604-608.	10.7	122
78	Text-mining approaches in molecular biology and biomedicine. <i>Drug Discovery Today</i> , 2005, 10, 439-445.	6.4	121
79	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. <i>BMC Bioinformatics</i> , 2011, 12, S3.	2.6	121
80	From residue coevolution to protein conformational ensembles and functional dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13567-13572.	7.1	116
81	Bringing gene order into bacterial shape. <i>Trends in Genetics</i> , 2001, 17, 124-126.	6.7	111
82	Mosaic Uniparental Disomies and Aneuploidies as Large Structural Variants of the Human Genome. <i>American Journal of Human Genetics</i> , 2010, 87, 129-138.	6.2	111
83	Evaluation of BioCreAtIvE assessment of task 2. <i>BMC Bioinformatics</i> , 2005, 6, S16.	2.6	108
84	Automatic annotation of protein function. <i>Current Opinion in Structural Biology</i> , 2005, 15, 267-274.	5.7	107
85	The pseudo GTPase CENP-M drives human kinetochore assembly. <i>ELife</i> , 2014, 3, e02978.	6.0	107
86	iHOP web services. <i>Nucleic Acids Research</i> , 2007, 35, W21-W26.	14.5	106
87	Most Highly Expressed Protein-Coding Genes Have a Single Dominant Isoform. <i>Journal of Proteome Research</i> , 2015, 14, 1880-1887.	3.7	106
88	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.4	104
89	Towards the prediction of protein interaction partners using physical docking. <i>Molecular Systems Biology</i> , 2011, 7, 469.	7.2	102
90	Assessment of predictions submitted for the CASP6 comparative modeling category. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 27-45.	2.6	101

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91	Analyzing the First Drafts of the Human Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 3854-3855.	3.7	101
92	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	5.3	99
93	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	8.8	97
94	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. <i>Gastroenterology</i> , 2015, 149, 563-566.	1.3	94
95	The small GTP-binding protein, Rhes, regulates signal transduction from G protein-coupled receptors. <i>Oncogene</i> , 2004, 23, 559-568.	5.9	93
96	Towards a detailed atlas of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 929-940.	5.7	92
97	A new ATP-binding fold in actin, hexokinase and Hsc70. <i>Trends in Cell Biology</i> , 1993, 3, 53-59.	7.9	91
98	firestar-prediction of functionally important residues using structural templates and alignment reliability. <i>Nucleic Acids Research</i> , 2007, 35, W573-W577.	14.5	91
99	Overview of the BioCreative III Workshop. <i>BMC Bioinformatics</i> , 2011, 12, S1.	2.6	88
100	Progress in predicting inter-residue contacts of proteins with neural networks and correlated mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 157-162.	2.6	86
101	CASP6 assessment of contact prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 214-224.	2.6	86
102	NOTCH pathway inactivation promotes bladder cancer progression. <i>Journal of Clinical Investigation</i> , 2015, 125, 824-830.	8.2	86
103	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. <i>BMC Genomics</i> , 2015, 16, 403.	2.8	86
104	Information extraction in molecular biology. <i>Briefings in Bioinformatics</i> , 2002, 3, 154-165.	6.5	85
105	A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimer's Disease, Glioblastoma and Lung cancer. <i>Scientific Reports</i> , 2017, 7, 4474.	3.3	85
106	An Overview of BioCreative II.5. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 385-399.	3.0	83
107	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. <i>PLoS Computational Biology</i> , 2015, 11, e1004325.	3.2	80
108	Three-dimensional view of the surface motif associated with the P-loop structure: cis and trans cases of convergent evolution 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2000, 303, 455-465.	4.2	78

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109	Effector Recognition by the Small GTP-binding Proteins Ras and Ral. <i>Journal of Biological Chemistry</i> , 1999, 274, 17763-17770.	3.4	76
110	How does the switch II region of G-domains work?. <i>FEBS Letters</i> , 1993, 320, 1-6.	2.8	75
111	Text mining for biology - the way forward: opinions from leading scientists. <i>Genome Biology</i> , 2008, 9, S7.	9.6	74
112	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	12.8	73
113	Analysis of Biological Processes and Diseases Using Text Mining Approaches. <i>Methods in Molecular Biology</i> , 2010, 593, 341-382.	0.9	73
114	Assessment of intramolecular contact predictions for CASP7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 152-158.	2.6	72
115	À la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. <i>Molecular Microbiology</i> , 2008, 42, 47-59.	2.5	72
116	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , 2017, 14, 782-788.	19.0	72
117	The structural coverage of the human proteome before and after AlphaFold. <i>PLoS Computational Biology</i> , 2022, 18, e1009818.	3.2	72
118	Comparative Proteomics Reveals a Significant Bias Toward Alternative Protein Isoforms with Conserved Structure and Function. <i>Molecular Biology and Evolution</i> , 2012, 29, 2265-2283.	8.9	71
119	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , 2018, 40, 1700148.	2.5	71
120	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	16.3	69
121	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. <i>Molecular Informatics</i> , 2011, 30, 506-519.	2.5	66
122	Most Alternative Isoforms Are Not Functionally Important. <i>Trends in Biochemical Sciences</i> , 2017, 42, 408-410.	7.5	66
123	Identification of Conserved Amino Acid Residues in Rat Liver Carnitine Palmitoyltransferase I Critical for Malonyl-CoA Inhibition. <i>Journal of Biological Chemistry</i> , 2003, 278, 9058-9063.	3.4	65
124	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	4.1	65
125	Mining functional information associated with expression arrays. <i>Functional and Integrative Genomics</i> , 2001, 1, 256-268.	3.5	64
126	MetaRouter: bioinformatics for bioremediation. <i>Nucleic Acids Research</i> , 2004, 33, D588-D592.	14.5	64



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127	Text Mining for Metabolic Pathways, Signaling Cascades, and Protein Networks. <i>Science Signaling</i> , 2005, 2005, pe21-pe21.	3.6	64
128	CD8 + T Cells from Human Neonates Are Biased toward an Innate Immune Response. <i>Cell Reports</i> , 2016, 17, 2151-2160.	6.4	64
129	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. <i>Genome Medicine</i> , 2018, 10, 41.	8.2	63
130	The organization of the microbial biodegradation network from a systems biology perspective. <i>EMBO Reports</i> , 2003, 4, 994-999.	4.5	62
131	Life cycles of successful genes. <i>Trends in Genetics</i> , 2003, 19, 79-81.	6.7	61
132	Introducing meta-services for biomedical information extraction. <i>Genome Biology</i> , 2008, 9, S6.	8.8	61
133	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.5	61
134	Intronic CNVs and gene expression variation in human populations. <i>PLoS Genetics</i> , 2019, 15, e1007902.	3.5	61
135	Phylogeny-independent detection of functional residues. <i>Bioinformatics</i> , 2006, 22, 1440-1448.	4.1	60
136	Subfunctionalization via Adaptive Evolution Influenced by Genomic Context: The Case of Histone Chaperones ASF1a and ASF1b. <i>Molecular Biology and Evolution</i> , 2013, 30, 1853-1866.	8.9	60
137	Structural model for family 32 of glycosyl-hydrolase enzymes. , 1998, 33, 383-395.		59
138	Clustering of proximal sequence space for the identification of protein families. <i>Bioinformatics</i> , 2002, 18, 908-921.	4.1	58
139	TopoGSA: network topological gene set analysis. <i>Bioinformatics</i> , 2010, 26, 1271-1272.	4.1	58
140	Distribution and functional diversification of the ras superfamily in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1998, 434, 219-225.	2.8	57
141	Systemic approaches to biodegradation. <i>FEMS Microbiology Reviews</i> , 2009, 33, 98-108.	8.6	57
142	Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. <i>Genome Medicine</i> , 2015, 7, 8.	8.2	57
143	Proteomics studies confirm the presence of alternative protein isoforms on a large scale. <i>Genome Biology</i> , 2008, 9, R162.	9.6	56
144	Legacy data sharing to improve drug safety assessment: the eTOX project. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 811-812.	46.4	56

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145	Defining functional distances over Gene Ontology. BMC Bioinformatics, 2008, 9, 50.	2.6	55
146	Predicting Reliable Regions in Protein Alignments from Sequence Profiles. Journal of Molecular Biology, 2003, 330, 705-718.	4.2	54
147	Assessment of predictions submitted for the CASP7 function prediction category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 165-174.	2.6	54
148	Automated Alphabet Reduction for Protein Datasets. BMC Bioinformatics, 2009, 10, 6.	2.6	54
149	Model of the Ran-RCC1 Interaction using Biochemical and Docking Experiments. Journal of Molecular Biology, 1999, 289, 1119-1130.	4.2	53
150	Structural Model of the Catalytic Core of Carnitine Palmitoyltransferase I and Carnitine Octanoyltransferase (COT). Journal of Biological Chemistry, 2001, 276, 45001-45008.	3.4	53
151	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	9.6	53
152	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
153	Can Bibliographic Pointers for Known Biological Data Be Found Automatically? Protein Interactions as a Case Study. Comparative and Functional Genomics, 2001, 2, 196-206.	2.0	52
154	Bionemo: molecular information on biodegradation metabolism. Nucleic Acids Research, 2009, 37, D598-D602.	14.5	52
155	firestar - advances in the prediction of functionally important residues. Nucleic Acids Research, 2011, 39, W235-W241.	14.5	52
156	Identifying ELIXIR Core Data Resources. F1000Research, 2016, 5, 2422.	1.6	52
157	Automatic annotation of protein function based on family identification. Proteins: Structure, Function and Bioinformatics, 2003, 53, 683-692.	2.6	51
158	MidA is a putative methyltransferase that is required for mitochondrial complex I function. Journal of Cell Science, 2010, 123, 1674-1683.	2.0	49
159	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. Journal of Biotechnology, 2002, 98, 269-283.	3.8	48
160	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	3.4	47
161	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. Nucleic Acids Research, 2012, 41, D142-D151.	14.5	47
162	Classification of protein families and detection of the determinant residues with an improved self-organizing map. Biological Cybernetics, 1997, 76, 441-450.	1.3	46

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163	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. <i>Genome Biology</i> , 2016, 17, 152.	8.8	46
164	A textâ€œmining perspective on the requirements for electronically annotated abstracts. <i>FEBS Letters</i> , 2008, 582, 1178-1181.	2.8	45
165	MyMiner: a web application for computer-assisted biocuration and text annotation. <i>Bioinformatics</i> , 2012, 28, 2285-2287.	4.1	44
166	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. <i>Molecular Biology of the Cell</i> , 2014, 25, 2522-2536.	2.1	44
167	Mortality in Persons With Autism Spectrum Disorder or Attention-Deficit/Hyperactivity Disorder. <i>JAMA Pediatrics</i> , 2022, 176, e216401.	6.2	44
168	The environmental fate of organic pollutants through the global microbial metabolism. <i>Molecular Systems Biology</i> , 2007, 3, 114.	7.2	43
169	BioCreative-IV virtual issue. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau039-bau039.	3.0	43
170	The success (or not) of HUGO nomenclature. <i>Genome Biology</i> , 2006, 7, 402.	9.6	42
171	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. <i>Nature Biotechnology</i> , 2010, 28, 897-899.	17.5	42
172	Pitfalls of protein sequence analysis. <i>Current Opinion in Biotechnology</i> , 1996, 7, 457-461.	6.6	41
173	Scoring docking models with evolutionary information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 275-280.	2.6	41
174	Transcriptional dissection of pancreatic tumors engrafted in mice. <i>Genome Medicine</i> , 2014, 6, 27.	8.2	41
175	LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes. <i>Nucleic Acids Research</i> , 2017, 45, W484-W489.	14.5	41
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