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 all docs	393 docs citations	393 times ranked	57933 citing authors

#	Article	IF	Citations
1	The gene regulation knowledge commons: the action area of GREEKC. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194768.	1.9	3
2	The structural coverage of the human proteome before and after AlphaFold. PLoS Computational Biology, 2022, 18, e1009818.	3.2	72
3	Patient-specific Boolean models of signalling networks guide personalised treatments. ELife, 2022, 11, .	6.0	38
4	Parallel model exploration for tumor treatment simulations. Computational Intelligence, 2022, 38, 1379-1401.	3.2	9
5	Optimizing Dosage-Specific Treatments in a Multi-Scale Model of a Tumor Growth. Frontiers in Molecular Biosciences, 2022, 9, 836794.	3.5	6
6	Mortality in Persons With Autism Spectrum Disorder or Attention-Deficit/Hyperactivity Disorder. JAMA Pediatrics, 2022, 176, e216401.	6.2	44
7	Design and methodological characteristics of studies using observational routinely collected health data for investigating the link between cancer and neurodegenerative diseases: protocol for a meta-research study. BMJ Open, 2022, 12, e058738.	1.9	1
8	Sex and gender bias in natural language processing. , 2022, , 113-132.		2
9	Evaluating the policy of closing bars and restaurants in CataluÃ±a and its effects on mobility and COVID19 incidence. Scientific Reports, 2022, 12, .	3.3	6
10	OUP accepted manuscript. Nucleic Acids Research, 2021, 49, 11005-11021.	14.5	14
11	BioFVM-X: An MPI+OpenMP 3-D Simulator for Biological Systems. Lecture Notes in Computer Science, 2021, , 266-279.	1.3	8
12	Simulating SARS-CoV-2 epidemics by region-specific variables and modeling contact tracing app containment. Npj Digital Medicine, 2021, 4, 9.	10.9	25
13	Unraveling the molecular basis of host cell receptor usage in SARS-CoV-2 and other human pathogenic Î²-CoVs. Computational and Structural Biotechnology Journal, 2021, 19, 759-766.	4.1	5
14	ELIXIRâ€EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	7.8	18
15	Artificial intelligence in cancer research: learning at different levels of data granularity. Molecular Oncology, 2021, 15, 817-829.	4.6	15
16	The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. Pharmaceuticals, 2021, 14, 237.	3.8	17
17	Artificial Intelligenceâ€"Aided Precision Medicine for COVID-19: Strategic Areas of Research and Development. Journal of Medical Internet Research, 2021, 23, e22453.	4.3	21
18	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34

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19	Transcriptomic and Genetic Associations between Alzheimerâ€™s Disease, Parkinsonâ€™s Disease, and Cancer. Cancers, 2021, 13, 2990.	3.7	26
20	Computational analysis of sense-antisense chimeric transcripts reveals their potential regulatory features and the landscape of expression in human cells. NAR Genomics and Bioinformatics, 2021, 3, lqab074.	3.2	12
21	Systems biology at the giga-scale: Large multiscale models of complex, heterogeneous multicellular systems. Current Opinion in Systems Biology, 2021, 28, 100385.	2.6	25
22	Assessing the accuracy of contact and distance predictions in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1888-1900.	2.6	15
23	COVID19 Disease Map, a computational knowledge repository of virusâ€“host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
24	COVID-19 Flow-Maps an open geographic information system on COVID-19 and human mobility for Spain. Scientific Data, 2021, 8, 310.	5.3	11
25	On the inconsistent treatment of gene-protein-reaction rules in context-specific metabolic models. Bioinformatics, 2020, 36, 1986-1988.	4.1	5
26	Towards FAIR principles forÂresearchÂsoftware. Data Science, 2020, 3, 37-59.	0.9	144
27	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
28	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. Nature Communications, 2020, 11, 2854.	12.8	20
29	Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. Npj Digital Medicine, 2020, 3, 81.	10.9	225
30	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, 3400.	12.8	23
31	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	12.8	73
32	Understanding oncogenicity of cancer driver genes and mutations in the cancer genomics era. FEBS Letters, 2020, 594, 4233-4246.	2.8	20
33	ECCB2020: the 19th European Conference on Computational Biology. Bioinformatics, 2020, 36, i569-i572.	4.1	1
34	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	39
35	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. Journal of Cheminformatics, 2019, 11, 42.	6.1	4
36	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69

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37	Intronic CNVs and gene expression variation in human populations. PLoS Genetics, 2019, 15, e1007902.	3.5	61
38	Molecular Inverse Comorbidity between Alzheimerâ€™s Disease and Lung Cancer: New Insights from Matrix Factorization. International Journal of Molecular Sciences, 2019, 20, 3114.	4.1	11
39	Association of Anorexia Nervosa With Risk of Cancer. JAMA Network Open, 2019, 2, e195313.	5.9	10
40	vulcanSpot: a tool to prioritize therapeutic vulnerabilities in cancer. Bioinformatics, 2019, 35, 4846-4848.	4.1	10
41	Interactive Extreme-Scale Analytics: Towards Battling Cancer. IEEE Technology and Society Magazine, 2019, 38, 54-61.	0.8	3
42	Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. Molecular Autism, 2019, 10, 17.	4.9	30
43	Big data analytics for personalized medicine. Current Opinion in Biotechnology, 2019, 58, 161-167.	6.6	152
44	Patient Dossier: Healthcare queries over distributed resources. PLoS Computational Biology, 2019, 15, e1007291.	3.2	2
45	DNA methylation profiling of hepatosplenic T-cell lymphoma. Haematologica, 2019, 104, e104-e107.	3.5	11
46	Precision medicine needs pioneering clinical bioinformaticians. Briefings in Bioinformatics, 2019, 20, 752-766.	6.5	40
47	Alternative Splicing. , 2019, , 1-8.		0
48	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. BioEssays, 2018, 40, 1700148.	2.5	71
49	APPRIS 2017: principal isoforms for multiple gene sets. Nucleic Acids Research, 2018, 46, D213-D217.	14.5	134
50	Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. Gastroenterology, 2018, 154, 181-194.e20.	1.3	32
51	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	6.4	104
52	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. Genome Medicine, 2018, 10, 41.	8.2	63
53	Germline variation in the oxidative DNA repair genes NUDT1 and OGG1 is not associated with hereditary colorectal cancer or polyposis. Human Mutation, 2018, 39, 1214-1225.	2.5	10
54	ISCBâ€™s initial reaction to New England Journal of Medicine editorial on data sharing. Bioinformatics, 2017, 33, 2968-2968.	4.1	1

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55	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
56	Most Alternative Isoforms Are Not Functionally Important. Trends in Biochemical Sciences, 2017, 42, 408-410.	7.5	66
57	Anna Tramontano 1957â€“2017. Nature Structural and Molecular Biology, 2017, 24, 431-432.	8.2	2
58	Information Retrieval and Text Mining Technologies for Chemistry. Chemical Reviews, 2017, 117, 7673-7761.	47.7	195
59	LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes. Nucleic Acids Research, 2017, 45, W484-W489.	14.5	41
60	ChiPPI: a novel method for mapping chimeric proteinâ€“protein interactions uncovers selection principles of protein fusion events in cancer. Nucleic Acids Research, 2017, 45, 7094-7105.	14.5	33
61	Elucidating the molecular basis of MSH2â€deficient tumors by combined germline and somatic analysis. International Journal of Cancer, 2017, 141, 1365-1380.	5.1	26
62	Cancer and central nervous system disorders: protocol for an umbrella review of systematic reviews and updated meta-analyses of observational studies. Systematic Reviews, 2017, 6, 69.	5.3	24
63	Legacy data sharing to improve drug safety assessment: the eTOX project. Nature Reviews Drug Discovery, 2017, 16, 811-812.	46.4	56
64	Comparison of algorithms for the detection of cancer drivers at subgene resolution. Nature Methods, 2017, 14, 782-788.	19.0	72
65	A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimerâ€™s Disease, Glioblastoma and Lung cancer. Scientific Reports, 2017, 7, 4474.	3.3	85
66	Alternative Splicing May Not Be the Key to Proteome Complexity. Trends in Biochemical Sciences, 2017, 42, 98-110.	7.5	277
67	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. Nucleic Acids Research, 2017, 45, 9244-9259.	14.5	19
68	Anorexia nervosa and cancer: a protocol for a systematic review and meta-analysis of observational studies. Systematic Reviews, 2017, 6, 137.	5.3	6
69	Risk of mortality among children, adolescents, and adults with autism spectrum disorder or attention deficit hyperactivity disorder and their first-degree relatives: a protocol for a systematic review and meta-analysis of observational studies. Systematic Reviews, 2017, 6, 189.	5.3	11
70	MIB2variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with MÃ©nÃ©trier-like gastropathy. Human Molecular Genetics, 2016, 26, ddw365.	2.9	7
71	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
72	Conservation of coevolving protein interfaces bridges prokaryoteâ€“eukaryote homologies in the twilight zone. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15018-15023.	7.1	40

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73	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
74	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. Genome Biology, 2016, 17, 152.	8.8	46
75	The BLUEPRINT Data Analysis Portal. Cell Systems, 2016, 3, 491-495.e5.	6.2	123
76	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
77	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
78	CD8 + T Cells from Human Neonates Are Biased toward an Innate Immune Response. Cell Reports, 2016, 17, 2151-2160.	6.4	64
79	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
80	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. BMC Genomics, 2016, 17, 396.	2.8	11
81	The Markyt visualisation, prediction and benchmark platform for chemical and gene entity recognition at BioCreative/CHEMDNER challenge. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw120.	3.0	10
82	Chromatin Regulators as a Guide for Cancer Treatment Choice. Molecular Cancer Therapeutics, 2016, 15, 1768-1777.	4.1	18
83	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. Human Mutation, 2016, 37, 36-42.	2.5	10
84	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. Cell Reports, 2016, 14, 1246-1257.	6.4	38
85	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. Genetics in Medicine, 2016, 18, 325-332.	2.4	209
86	A computational approach inspired by simulated annealing to study the stability of protein interaction networks in cancer and neurological disorders. Data Mining and Knowledge Discovery, 2016, 30, 226-242.	3.7	7
87	ISCBâ€™s initial reaction to New England Journal of Medicine editorial on data sharing. F1000Research, 2016, 5, 157.	1.6	1
88	Identifying ELIXIR Core Data Resources. F1000Research, 2016, 5, 2422.	1.6	52
89	ISCBâ€™s Initial Reaction to The New England Journal of Medicine Editorial on Data Sharing. PLoS Computational Biology, 2016, 12, e1004816.	3.2	12
90	CHEMDNER: The drugs and chemical names extraction challenge. Journal of Cheminformatics, 2015, 7, S1.	6.1	179

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91	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	6.1	166
92	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. PLoS Computational Biology, 2015, 11, e1004325.	3.2	80
93	NOTCH pathway inactivation promotes bladder cancer progression. Journal of Clinical Investigation, 2015, 125, 824-830.	8.2	86
94	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
95	ChiTaRS 2.1â€"an improved database of the chimeric transcripts and RNA-seq data with novel senseâ€"antisense chimeric RNA transcripts. Nucleic Acids Research, 2015, 43, D68-D75.	14.5	26
96	Alternative splicing and co-option of transposable elements: the case of TMPO/LAP2Î± and ZNF451 in mammals. Bioinformatics, 2015, 31, 2257-2261.	4.1	33
97	Structure-PPi: a module for the annotation of cancer-related single-nucleotide variants at proteinâ€"protein interfaces. Bioinformatics, 2015, 31, 2397-2399.	4.1	38
98	APPRIS WebServer and WebServices. Nucleic Acids Research, 2015, 43, W455-W459.	14.5	19
99	FUN-L: gene prioritization for RNAi screens: Fig. 1.. Bioinformatics, 2015, 31, 2052-2053.	4.1	9
100	Summary of the BioLINK SIG 2013 meeting at ISMB/ECCB 2013. Bioinformatics, 2015, 31, 297-298.	4.1	1
101	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	27.8	749
102	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. Gastroenterology, 2015, 149, 563-566.	1.3	94
103	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
104	Detection of significant protein coevolution. Bioinformatics, 2015, 31, 2166-2173.	4.1	32
105	Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. Genome Medicine, 2015, 7, 8.	8.2	57
106	Most Highly Expressed Protein-Coding Genes Have a Single Dominant Isoform. Journal of Proteome Research, 2015, 14, 1880-1887.	3.7	106
107	The potential clinical impact of the release of two drafts of the human proteome. Expert Review of Proteomics, 2015, 12, 579-593.	3.0	26
108	From residue coevolution to protein conformational ensembles and functional dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13567-13572.	7.1	116

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109	The Evolutionary Fate of Alternatively Spliced Homologous Exons after Gene Duplication. Genome Biology and Evolution, 2015, 7, 1392-1403.	2.5	31
110	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. BMC Genomics, 2015, 16, 403.	2.8	86
111	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. Molecular Biology of the Cell, 2014, 25, 2522-2536.	2.1	44
112	Alzheimer's Disease and Cancer: Current Epidemiological Evidence for a Mutual Protection. Neuroepidemiology, 2014, 42, 121-122.	2.3	23
113	CheNER: chemical named entity recognizer. Bioinformatics, 2014, 30, 1039-1040.	4.1	15
114	Molecular Evidence for the Inverse Comorbidity between Central Nervous System Disorders and Cancers Detected by Transcriptomic Meta-analyses. PLoS Genetics, 2014, 10, e1004173.	3.5	165
115	Predicting Protein Relationships to Human Pathways through a Relational Learning Approach Based on Simple Sequence Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 753-765.	3.0	3
116	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. Psychotherapy and Psychosomatics, 2014, 83, 89-105.	8.8	164
117	FireDB: a compendium of biological and pharmacologically relevant ligands. Nucleic Acids Research, 2014, 42, D267-D272.	14.5	21
118	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. Proteins: Structure, Function and Bioinformatics, 2014, 82, 103-118.	2.6	3
119	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	5.5	175
120	Colorectal cancer classification based on gene expression is not associated with FOLFIRI response. Nature Medicine, 2014, 20, 1230-1231.	30.7	8
121	Analyzing the First Drafts of the Human Proteome. Journal of Proteome Research, 2014, 13, 3854-3855.	3.7	101
122	Bioinformatics Analysis of Pancreas Cancer Genome in High-Throughput Genomic Technologies. , 2014, , 93-131.		1
123	Transcriptional dissection of pancreatic tumors engrafted in mice. Genome Medicine, 2014, 6, 27.	8.2	41
124	Integrated Next-Generation Sequencing and Avatar Mouse Models for Personalized Cancer Treatment. Clinical Cancer Research, 2014, 20, 2476-2484.	7.0	140
125	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. Human Molecular Genetics, 2014, 23, 5866-5878.	2.9	463
126	BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039.	3.0	43

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127	Retrieval and Discovery of Cell Cycle Literature and Proteins by Means of Machine Learning, Text Mining and Network Analysis. Advances in Intelligent Systems and Computing, 2014, , 285-292.	0.6	2
128	The pseudo GTPase CENP-M drives human kinetochore assembly. ELife, 2014, 3, e02978.	6.0	107
129	Evolution of the Ras Superfamily of GTPases. , 2014, , 3-23.		0
130	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
131	Subfunctionalization via Adaptive Evolution Influenced by Genomic Context: The Case of Histone Chaperones ASF1a and ASF1b. Molecular Biology and Evolution, 2013, 30, 1853-1866.	8.9	60
132	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. Nature Genetics, 2013, 45, 1464-1469.	21.4	224
133	wKinMut: An integrated tool for the analysis and interpretation of mutations in human protein kinases. BMC Bioinformatics, 2013, 14, 345.	2.6	5
134	Towards a detailed atlas of proteinâ€“protein interactions. Current Opinion in Structural Biology, 2013, 23, 929-940.	5.7	92
135	The Functional Genomics Network in the evolution of biological text mining over the past decade. New Biotechnology, 2013, 30, 278-285.	4.4	10
136	Emerging methods in protein co-evolution. Nature Reviews Genetics, 2013, 14, 249-261.	16.3	553
137	Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions. Molecular BioSystems, 2013, 9, 70-76.	2.9	8
138	Late-replicating CNVs as a source of new genes. Biology Open, 2013, 2, 1402-1411.	1.2	9
139	APPRIS: annotation of principal and alternative splice isoforms. Nucleic Acids Research, 2013, 41, D110-D117.	14.5	205
140	RUbioSeq: a suite of parallelized pipelines to automate exome variation and bisulfite-seq analyses. Bioinformatics, 2013, 29, 1687-1689.	4.1	37
141	BioC: a minimalist approach to interoperability for biomedical text processing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat064-bat064.	3.0	123
142	An Epistatic Interaction between the PAX8 and STK17B Genes in Papillary Thyroid Cancer Susceptibility. PLoS ONE, 2013, 8, e74765.	2.5	9
143	Chapter 14: Cancer Genome Analysis. PLoS Computational Biology, 2012, 8, e1002824.	3.2	14
144	Interpretation of the Consequences of Mutations in Protein Kinases: Combined Use of Bioinformatics and Text Mining. Frontiers in Physiology, 2012, 3, 323.	2.8	9

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145	How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas017-bas017.	3.0	27
146	JDet: interactive calculation and visualization of function-related conservation patterns in multiple sequence alignments and structures. Bioinformatics, 2012, 28, 584-586.	4.1	20
147	Comparative Proteomics Reveals a Significant Bias Toward Alternative Protein Isoforms with Conserved Structure and Function. Molecular Biology and Evolution, 2012, 29, 2265-2283.	8.9	71
148	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
149	Text mining for the biocuration workflow. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas020-bas020.	3.0	132
150	Mirroring co-evolving trees in the light of their topologies. Bioinformatics, 2012, 28, 1202-1208.	4.1	4
151	Novel domain combinations in proteins encoded by chimeric transcripts. Bioinformatics, 2012, 28, i67-i74.	4.1	35
152	BioCreative-2012 Virtual Issue. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas049-bas049.	3.0	19
153	Getting personalized cancer genome analysis into the clinic: the challenges in bioinformatics. Genome Medicine, 2012, 13, 61.	8.2	23
154	EnrichNet: network-based gene set enrichment analysis. Bioinformatics, 2012, 28, i451-i457.	4.1	269
155	Prioritization of pathogenic mutations in the protein kinase superfamily. BMC Genomics, 2012, 13, S3.	2.8	21
156	The Ras protein superfamily: Evolutionary tree and role of conserved amino acids. Journal of Cell Biology, 2012, 196, 189-201.	5.2	321
157	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
158	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. Genome Research, 2012, 22, 1231-1242.	5.5	143
159	MyMiner: a web application for computer-assisted biocuration and text annotation. Bioinformatics, 2012, 28, 2285-2287.	4.1	44
160	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	21.4	525
161	Genome-wide analysis of Pax8 binding provides new insights into thyroid functions. BMC Genomics, 2012, 13, 147.	2.8	38
162	Uncovering the Molecular Machinery of the Human Spindleâ€"An Integration of Wet and Dry Systems Biology. PLoS ONE, 2012, 7, e31813.	2.5	14

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163	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	2.5	61
164	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	21.4	893
165	Distinct DNA methylomes of newborns and centenarians. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10522-10527.	7.1	687
166	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	17.5	323
167	iHOP Web Services Family. Lecture Notes in Computer Science, 2012, , 102-107.	1.3	4
168	Bioinformatic Software Developments in Spain. Lecture Notes in Computer Science, 2012, , 108-120.	1.3	0
169	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
170	Towards the prediction of protein interaction partners using physical docking. Molecular Systems Biology, 2011, 7, 469.	7.2	102
171	Selection of organisms for the co-evolution-based study of protein interactions. BMC Bioinformatics, 2011, 12, 363.	2.6	13
172	No paradox, no progress: inverse cancer comorbidity in people with other complex diseases. Lancet Oncology, The, 2011, 12, 604-608.	10.7	122
173	PathExpand: Extending biological pathways using molecular interaction networks. Nature Precedings, 2011, , .	0.1	0
174	Characterization of pathogenic germline mutations in human Protein Kinases. BMC Bioinformatics, 2011, 12, S1.	2.6	10
175	Overview of the BioCreative III Workshop. BMC Bioinformatics, 2011, 12, S1.	2.6	88
176	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. BMC Bioinformatics, 2011, 12, S3.	2.6	121
177	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. Molecular Informatics, 2011, 30, 506-519.	2.5	66
178	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	3.4	47
179	firestar â€"advances in the prediction of functionally important residues. Nucleic Acids Research, 2011, 39, W235-W241.	14.5	52
180	Education and Research Infrastructures. , 2011, , 165-181.		2

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181	Mosaic Uniparental Disomies and Aneuploidies as Large Structural Variants of the Human Genome. American Journal of Human Genetics, 2010, 87, 129-138.	6.2	111
182	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. BMC Bioinformatics, 2010, 11, 597.	2.6	40
183	The PPI affix dictionary (PPIAD) and BioMethod Lexicon: importance of affixes and tags for recognition of entity mentions and experimental protein interactions. BMC Bioinformatics, 2010, 11, .	2.6	4
184	The FEBS Letters SDA corpus: A collection of protein interaction articles with high quality annotations for the BioCreative II.5 online challenge and the text mining community. FEBS Letters, 2010, 584, 4129-4130.	2.8	8
185	Predicted residueâ€“residue contacts can help the scoring of 3D models. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1980-1991.	2.6	30
186	Mutated genes, pathways and processes in tumours. EMBO Reports, 2010, 11, 805-810.	4.5	31
187	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
188	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. Nature Biotechnology, 2010, 28, 897-899.	17.5	42
189	FragKB: Structural and Literature Annotation Resource of Conserved Peptide Fragments and Residues. PLoS ONE, 2010, 5, e9679.	2.5	7
190	Inference of Functional Relations in Predicted Protein Networks with a Machine Learning Approach. PLoS ONE, 2010, 5, e9969.	2.5	11
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