Alfonso Valencia

List of Publications by Year in Descending Order

361 papers	34,543 citations	85 h-index	180 g-index
393 ext. papers	40,280 ext. citations	10.3 avg, IF	6.89 L-index

#	Paper	IF	Citations
361	The structural coverage of the human proteome before and after AlphaFold.. *PLoS Computational Biology*, **2022**, 18, e1009818	5	9
360	Patient-specific Boolean models of signalling networks guide personalised treatments.. *ELife*, **2022**, 11,	8.9	4
359	Optimizing Dosage-Specific Treatments in a Multi-Scale Model of a Tumor Growth.. *Frontiers in Molecular Biosciences*, **2022**, 9, 836794	5.6	0
358	Mortality in Persons With Autism Spectrum Disorder or Attention-Deficit/Hyperactivity Disorder: A Systematic Review and Meta-analysis.. *JAMA Pediatrics*, **2022**, e216401	8.3	4
357	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	3	
356	Sex and gender bias in natural language processing **2022**, 113-132		0
355	COVID-19 Flow-Maps an open geographic information system on COVID-19 and human mobility for Spain. *Scientific Data*, **2021**, 8, 310	8.2	2
354	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. *Molecular Systems Biology*, **2021**, 17, e10387	12.2	9
353	The gene regulation knowledge commons: the action area of GREEKC. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1865, 194768	6	1
352	The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. *Pharmaceuticals*, **2021**, 14,	5.2	5
351	Artificial Intelligence-Aided Precision Medicine for COVID-19: Strategic Areas of Research and Development. *Journal of Medical Internet Research*, **2021**, 23, e22453	7.6	8
350	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. *Leukemia*, **2021**, 35, 2002-2016	10.7	3
349	Transcriptomic and Genetic Associations between Alzheimer's Disease, Parkinson's Disease, and Cancer. *Cancers*, **2021**, 13,	6.6	6
348	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	3.7	4
347	STAG2 loss-of-function affects short-range genomic contacts and modulates the basal-luminal transcriptional program of bladder cancer cells. *Nucleic Acids Research*, **2021**, 49, 11005-11021	20.1	2
346	BioFVM-X: An MPI+OpenMP 3-D Simulator for Biological Systems. *Lecture Notes in Computer Science*, **2021**, 266-279	0.9	2
345	Simulating SARS-CoV-2 epidemics by region-specific variables and modeling contact tracing app containment. *Npj Digital Medicine*, **2021**, 4, 9	15.7	12

344	Unraveling the molecular basis of host cell receptor usage in SARS-CoV-2 and other human pathogenic CoVs. *Computational and Structural Biotechnology Journal*, **2021**, 19, 759-766	6.8	1
343	ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. *EMBO Journal*, **2021**, 40, e107409	13	11
342	Artificial intelligence in cancer research: learning at different levels of data granularity. *Molecular Oncology*, **2021**, 15, 817-829	7.9	5
341	Systems biology at the giga-scale: Large multiscale models of complex, heterogeneous multicellular systems. *Current Opinion in Systems Biology*, **2021**, 28, 100385	3.2	4
340	Assessing the accuracy of contact and distance predictions in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1888-1900	4.2	4
339	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. *Scientific Data*, **2020**, 7, 136	8.2	71
338	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. *Nature Communications*, **2020**, 11, 2854	17.4	7
337	Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. *Npj Digital Medicine*, **2020**, 3, 81	15.7	85
336	A user guide for the online exploration and visualization of PCAWG data. *Nature Communications*, **2020**, 11, 3400	17.4	7
335	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
334	Understanding oncogenicity of cancer driver genes and mutations in the cancer genomics era. *FEBS Letters*, **2020**, 594, 4233-4246	3.8	6
333	GOPHER, an HPC Framework for Large Scale Graph Exploration and Inference. *Lecture Notes in Computer Science*, **2020**, 211-222	0.9	
332	ECCB2020: the 19th European Conference on Computational Biology. *Bioinformatics*, **2020**, 36, i569-i572	7.2	1
331	On the inconsistent treatment of gene-protein-reaction rules in context-specific metabolic models. *Bioinformatics*, **2020**, 36, 1986-1988	7.2	1
330	Towards FAIR principles for´research´software. *Data Science*, **2020**, 3, 37-59	2.2	56
329	Leveraging European infrastructures to access 1 million human genomes by 2022. *Nature Reviews Genetics*, **2019**, 20, 693-701	30.1	36
328	Intronic CNVs and gene expression variation in human populations. *PLoS Genetics*, **2019**, 15, e1007902	6	30
327	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	6

326	Association of Anorexia Nervosa With Risk of Cancer: A Systematic Review and Meta-analysis. *JAMA Network Open*, **2019**, 2, e195313	10.4	6
325	vulcanSpot: a tool to prioritize therapeutic vulnerabilities in cancer. *Bioinformatics*, **2019**, 35, 4846-4848	7.2	4
324	Interactive Extreme-Scale Analytics: Towards Battling Cancer. *IEEE Technology and Society Magazine* , **2019**, 38, 54-61	0.8	1
323	Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. *Molecular Autism*, **2019**, 10, 17	6.5	13
322	Big data analytics for personalized medicine. *Current Opinion in Biotechnology*, **2019**, 58, 161-167	11.4	69
321	The bio.tools registry of software tools and data resources for the life sciences. *Genome Biology*, **2019**, 20, 164	18.3	19
320	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. *Journal of Cheminformatics*, **2019**, 11, 42	8.6	4
319	Patient Dossier: Healthcare queries over distributed resources. *PLoS Computational Biology*, **2019**, 15, e1007291	5	2
318	DNA methylation profiling of hepatosplenic T-cell lymphoma. *Haematologica*, **2019**, 104, e104-e107	6.6	7
317	Precision medicine needs pioneering clinical bioinformaticians. *Briefings in Bioinformatics*, **2019**, 20, 752-766	7.4	25
316	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. *BioEssays*, **2018**, 40, 1700148	4.1	40
315	APPRIS 2017: principal isoforms for multiple gene sets. *Nucleic Acids Research*, **2018**, 46, D213-D217	20.1	70
314	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	13.3	25
313	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. *Genome Medicine*, **2018**, 10, 41	14.4	35
312	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	4.7	6
311	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. *Cell Reports*, **2018**, 24, 2784-2794	10.6	54
310	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. *Genome Biology*, **2017**, 18, 18	18.3	70
309	Most Alternative Isoforms Are Not Functionally Important. *Trends in Biochemical Sciences*, **2017**, 42, 408-410	11.3	46

308	Anna Tramontano 1957-2017. *Nature Structural and Molecular Biology*, **2017**, 24, 431-432	17.6	2
307	Information Retrieval and Text Mining Technologies for Chemistry. *Chemical Reviews*, **2017**, 117, 7673-7761	60.1	124
306	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	20.1	24
305	ChiPPI: a novel method for mapping chimeric protein-protein interactions uncovers selection principles of protein fusion events in cancer. *Nucleic Acids Research*, **2017**, 45, 7094-7105	20.1	24
304	Elucidating the molecular basis of MSH2-deficient tumors by combined germline and somatic analysis. *International Journal of Cancer*, **2017**, 141, 1365-1380	7.5	18
303	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	3	13
302	Legacy data sharing to improve drug safety assessment: the eTOX project. *Nature Reviews Drug Discovery*, **2017**, 16, 811-812	64.1	37
301	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. *Nucleic Acids Research*, **2017**, 45, 9244-9259	20.1	10
300	Anorexia nervosa and cancer: a protocol for a systematic review and meta-analysis of observational studies. *Systematic Reviews*, **2017**, 6, 137	3	4
299	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	3	8
298	Comparison of algorithms for the detection of cancer drivers at subgene resolution. *Nature Methods*, **2017**, 14, 782-788	21.6	51
297	A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimer's Disease, Glioblastoma and Lung cancer. *Scientific Reports*, **2017**, 7, 4474	4.9	45
296	Alternative Splicing May Not Be the Key to Proteome Complexity. *Trends in Biochemical Sciences*, **2017**, 42, 98-110	10.3	180
295	MIB2 variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with Mirrier-like gastropathy. *Human Molecular Genetics*, **2017**, 26, 33-43	5.6	7
294	ISCB's initial reaction to New England Journal of Medicine editorial on data sharing. *Bioinformatics*, **2017**, 33, 2968	7.2	1
293	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, 325-32	8.1	153
292	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	5.6	6
291	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. *Genome Biology*, **2016**, 17, 152	18.3	26

290	The BLUEPRINT Data Analysis Portal. *Cell Systems*, **2016**, 3, 491-495.e5	10.6	71
289	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
288	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
287	CD8 T Cells from Human Neonates Are Biased toward an Innate Immune Response. *Cell Reports*, **2016**, 17, 2151-2160	10.6	34
286	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	56.2	339
285	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. *BMC Genomics*, **2016**, 17 Suppl 2, 396	4.5	7
284	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,	5	8
283	Chromatin Regulators as a Guide for Cancer Treatment Choice. *Molecular Cancer Therapeutics*, **2016**, 15, 1768-77	6.1	15
282	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. *Human Mutation*, **2016**, 37, 36-42	4.7	7
281	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	10.6	30
280	ISCB's initial reaction to New England Journal of Medicine editorial on data sharing. *F1000Research*, **2016**, 5,	3.6	1
279	Identifying ELIXIR Core Data Resources. *F1000Research*, **2016**, 5,	3.6	44
278	ISCB's Initial Reaction to The New England Journal of Medicine Editorial on Data Sharing. *PLoS Computational Biology*, **2016**, 12, e1004816	5	9
277	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. *Genome Biology*, **2016**, 17, 251	18.3	85
276	Conservation of coevolving protein interfaces bridges prokaryote-eukaryote homologies in the twilight zone. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 15018-15023	11.5	26
275	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
274	FUN-L: gene prioritization for RNAi screens. *Bioinformatics*, **2015**, 31, 2052-3	7.2	8
273	Summary of the BioLINK SIG 2013 meeting at ISMB/ECCB 2013. *Bioinformatics*, **2015**, 31, 297-8	7.2	1

272	Non-coding recurrent mutations in chronic lymphocytic leukaemia. *Nature*, **2015**, 526, 519-24	50.4	565
271	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. *Gastroenterology*, **2015**, 149, 563-6	13.3	75
270	Pathway and network analysis of cancer genomes. *Nature Methods*, **2015**, 12, 615-621	21.6	235
269	Detection of significant protein coevolution. *Bioinformatics*, **2015**, 31, 2166-73	7.2	17
268	Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. *Genome Medicine*, **2015**, 7, 8	14.4	29
267	Most highly expressed protein-coding genes have a single dominant isoform. *Journal of Proteome Research*, **2015**, 14, 1880-7	5.6	78
266	The potential clinical impact of the release of two drafts of the human proteome. *Expert Review of Proteomics*, **2015**, 12, 579-93	4.2	23
265	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, 13567-72	11.5	87
264	The evolutionary fate of alternatively spliced homologous exons after gene duplication. *Genome Biology and Evolution*, **2015**, 7, 1392-403	3.9	22
263	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. *BMC Genomics*, **2015**, 16, 403	4.5	59
262	CHEMDNER: The drugs and chemical names extraction challenge. *Journal of Cheminformatics*, **2015**, 7, S1	8.6	120
261	The CHEMDNER corpus of chemicals and drugs and its annotation principles. *Journal of Cheminformatics*, **2015**, 7, S2	8.6	98
260	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. *PLoS Computational Biology*, **2015**, 11, e1004325	5	47
259	NOTCH pathway inactivation promotes bladder cancer progression. *Journal of Clinical Investigation*, **2015**, 125, 824-30	15.9	64
258	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. *Nature Genetics*, **2015**, 47, 746-56	36.3	209
257	ChiTaRS 2.1--an improved database of the chimeric transcripts and RNA-seq data with novel sense-antisense chimeric RNA transcripts. *Nucleic Acids Research*, **2015**, 43, D68-75	20.1	22
256	Alternative splicing and co-option of transposable elements: the case of TMPO/LAP2 and ZNF451 in mammals. *Bioinformatics*, **2015**, 31, 2257-61	7.2	26
255	Structure-PPi: a module for the annotation of cancer-related single-nucleotide variants at protein-protein interfaces. *Bioinformatics*, **2015**, 31, 2397-9	7.2	31

254	APPRIS WebServer and WebServices. *Nucleic Acids Research*, **2015**, 43, W455-9	20.1	15
253	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. *Genome Research*, **2014**, 24, 212-26	9.7	143
252	Colorectal cancer classification based on gene expression is not associated with FOLFIRI response. *Nature Medicine*, **2014**, 20, 1230-1	50.5	8
251	Analyzing the first drafts of the human proteome. *Journal of Proteome Research*, **2014**, 13, 3854-5	5.6	88
250	Bioinformatics Analysis of Pancreas Cancer Genome in High-Throughput Genomic Technologies **2014**, 93-131		1
249	Transcriptional dissection of pancreatic tumors engrafted in mice. *Genome Medicine*, **2014**, 6, 27	14.4	30
248	Integrated next-generation sequencing and avatar mouse models for personalized cancer treatment. *Clinical Cancer Research*, **2014**, 20, 2476-84	12.9	118
247	Multiple evidence strands suggest that there may be as few as 19,000 human protein-coding genes. *Human Molecular Genetics*, **2014**, 23, 5866-78	5.6	385
246	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, 2522-36	3.5	36
245	Alzheimer's disease and cancer: current epidemiological evidence for a mutual protection. *Neuroepidemiology*, **2014**, 42, 121-2	5.4	21
244	CheNER: chemical named entity recognizer. *Bioinformatics*, **2014**, 30, 1039-40	7.2	13
243	Molecular evidence for the inverse comorbidity between central nervous system disorders and cancers detected by transcriptomic meta-analyses. *PLoS Genetics*, **2014**, 10, e1004173	6	116
242	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, 753-65	3	2
241	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	9.4	113
240	FireDB: a compendium of biological and pharmacologically relevant ligands. *Nucleic Acids Research*, **2014**, 42, D267-72	20.1	7
239	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 103-18	4.2	2
238	The pseudo GTPase CENP-M drives human kinetochore assembly. *ELife*, **2014**, 3, e02978	8.9	86
237	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	0.4	2

236	Evolution of the Ras Superfamily of GTPases **2014**, 3-23		
235	Computational approaches to identify functional genetic variants in cancer genomes. *Nature Methods*, **2013**, 10, 723-9	21.6	129
234	Subfunctionalization via adaptive evolution influenced by genomic context: the case of histone chaperones ASF1a and ASF1b. *Molecular Biology and Evolution*, **2013**, 30, 1853-66	8.3	42
233	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. *Nature Genetics*, **2013**, 45, 1464-9	36.3	186
232	wKinMut: an integrated tool for the analysis and interpretation of mutations in human protein kinases. *BMC Bioinformatics*, **2013**, 14, 345	3.6	5
231	Towards a detailed atlas of protein-protein interactions. *Current Opinion in Structural Biology*, **2013**, 23, 929-40	8.1	80
230	The Functional Genomics Network in the evolution of biological text mining over the past decade. *New Biotechnology*, **2013**, 30, 278-85	6.4	10
229	Emerging methods in protein co-evolution. *Nature Reviews Genetics*, **2013**, 14, 249-61	30.1	415
228	Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions. *Molecular BioSystems*, **2013**, 9, 70-6		5
227	Late-replicating CNVs as a source of new genes. *Biology Open*, **2013**, 2, 1402-11	2.2	6
226	APPRIS: annotation of principal and alternative splice isoforms. *Nucleic Acids Research*, **2013**, 41, D110-7	20.1	128
225	RUbioSeq: a suite of parallelized pipelines to automate exome variation and bisulfite-seq analyses. *Bioinformatics*, **2013**, 29, 1687-9	7.2	35
224	BioC: a minimalist approach to interoperability for biomedical text processing. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat064	5	100
223	An epistatic interaction between the PAX8 and STK17B genes in papillary thyroid cancer susceptibility. *PLoS ONE*, **2013**, 8, e74765	3.7	8
222	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. *Nucleic Acids Research*, **2013**, 41, D142-51	20.1	39
221	EnrichNet: network-based gene set enrichment analysis. *Bioinformatics*, **2012**, 28, i451-i457	7.2	204
220	Prioritization of pathogenic mutations in the protein kinase superfamily. *BMC Genomics*, **2012**, 13 Suppl 4, S3	4.5	21
219	The Ras protein superfamily: evolutionary tree and role of conserved amino acids. *Journal of Cell Biology*, **2012**, 196, 189-201	7.3	247

218	GENCODE: the reference human genome annotation for The ENCODE Project. *Genome Research*, **2012**, 22, 1760-74	9.7	3142
217	Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. *Genome Research*, **2012**, 22, 1231-42	9.7	101
216	MyMiner: a web application for computer-assisted biocuration and text annotation. *Bioinformatics*, **2012**, 28, 2285-7	7.2	34
215	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. *Nature Genetics*, **2012**, 44, 1236-42	36.3	422
214	Genome-wide analysis of Pax8 binding provides new insights into thyroid functions. *BMC Genomics*, **2012**, 13, 147	4.5	31
213	Uncovering the molecular machinery of the human spindle--an integration of wet and dry systems biology. *PLoS ONE*, **2012**, 7, e31813	3.7	11
212	Evidence for transcript networks composed of chimeric RNAs in human cells. *PLoS ONE*, **2012**, 7, e28213	3.7	51
211	Distinct DNA methylomes of newborns and centenarians. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 10522-7	11.5	563
210	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
209	Chapter 14: Cancer genome analysis. *PLoS Computational Biology*, **2012**, 8, e1002824	5	12
208	Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. *Frontiers in Physiology*, **2012**, 3, 323	4.6	7
207	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	5	25
206	JDet: interactive calculation and visualization of function-related conservation patterns in multiple sequence alignments and structures. *Bioinformatics*, **2012**, 28, 584-6	7.2	16
205	Comparative proteomics reveals a significant bias toward alternative protein isoforms with conserved structure and function. *Molecular Biology and Evolution*, **2012**, 29, 2265-83	8.3	64
204	Text mining for the biocuration workflow. *Database: the Journal of Biological Databases and Curation*, **2012**, 2012, bas020	5	108
203	Mirroring co-evolving trees in the light of their topologies. *Bioinformatics*, **2012**, 28, 1202-8	7.2	2
202	Novel domain combinations in proteins encoded by chimeric transcripts. *Bioinformatics*, **2012**, 28, i67-74	7.2	32
201	The Ras protein superfamily: Evolutionary tree and role of conserved amino acids. *Journal of Cell Biology*, **2012**, 196, 545-545	7.3	6

200	Getting personalized cancer genome analysis into the clinic: the challenges in bioinformatics. *Genome Medicine*, **2012**, 4, 61	14.4	22
199	iHOP Web Services Family. *Lecture Notes in Computer Science*, **2012**, 102-107	0.9	4
198	Bioinformatic Software Developments in Spain. *Lecture Notes in Computer Science*, **2012**, 108-120	0.9	
197	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. *Nature Genetics*, **2011**, 44, 47-52	36.3	752
196	Selection of organisms for the co-evolution-based study of protein interactions. *BMC Bioinformatics* , **2011**, 12, 363	3.6	13
195	No paradox, no progress: inverse cancer comorbidity in people with other complex diseases. *Lancet Oncology, The*, **2011**, 12, 604-8	21.7	103
194	Characterization of pathogenic germline mutations in human protein kinases. *BMC Bioinformatics*, **2011**, 12 Suppl 4, S1	3.6	10
193	Overview of the BioCreative III Workshop. *BMC Bioinformatics*, **2011**, 12 Suppl 8, S1	3.6	77
192	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. *BMC Bioinformatics*, **2011**, 12 Suppl 8, S3	3.6	104
191	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. *Molecular Informatics*, **2011**, 30, 506-19	3.8	53
190	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. *Nature* , **2011**, 475, 101-5	50.4	1206
189	Towards the prediction of protein interaction partners using physical docking. *Molecular Systems Biology*, **2011**, 7, 469	12.2	88
188	Long-range epigenetic silencing associates with deregulation of Ikaros targets in colorectal cancer cells. *Molecular Cancer Research*, **2011**, 9, 1139-51	6.6	38
187	firestar--advances in the prediction of functionally important residues. *Nucleic Acids Research*, **2011**, 39, W235-41	20.1	41
186	Education and Research Infrastructures **2011**, 165-181		2
185	Mutated genes, pathways and processes in tumours. *EMBO Reports*, **2010**, 11, 805-10	6.5	27
184	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
183	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. *Nature Biotechnology*, **2010**, 28, 897-9	44.5	33

182	FragKB: structural and literature annotation resource of conserved peptide fragments and residues. *PLoS ONE*, **2010**, 5, e9679	3.7	6
181	Inference of functional relations in predicted protein networks with a machine learning approach. *PLoS ONE*, **2010**, 5, e9969	3.7	8
180	MidA is a putative methyltransferase that is required for mitochondrial complex I function. *Journal of Cell Science*, **2010**, 123, 1674-83	5.3	47
179	Protein interactions and ligand binding: from protein subfamilies to functional specificity. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 1995-2000	11.5	108
178	An Overview of BioCreative II.5. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* , **2010**, 7, 385-99	3	74
177	TopoGSA: network topological gene set analysis. *Bioinformatics*, **2010**, 26, 1271-2	7.2	48
176	Mosaic uniparental disomies and aneuploidies as large structural variants of the human genome. *American Journal of Human Genetics*, **2010**, 87, 129-38	11	100
175	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. *BMC Bioinformatics*, **2010**, 11, 597	3.6	34
174	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,	3.6	3
173	Predicted residue-residue contacts can help the scoring of 3D models. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1980-91	4.2	28
172	Analysis of biological processes and diseases using text mining approaches. *Methods in Molecular Biology*, **2010**, 593, 341-82	1.4	61
171	Overview of the Ninth Annual Meeting of the BioLINK SIG at ISMB: Linking Literature, Information and Knowledge for Biology. *Lecture Notes in Computer Science*, **2010**, 1-7	0.9	1
170	Bionemo: molecular information on biodegradation metabolism. *Nucleic Acids Research*, **2009**, 37, D598-602	20.1	36
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8	Lessons Learned: Recommendations for Establishing Critical Periodic Scientific Benchmarking		12
7	COVID-19 Disease Map, a computational knowledge repository of SARS-CoV-2 virus-host interaction mechanisms		4
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5	Pathway and network analysis of more than 2,500 whole cancer genomes		4
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