

# Alfonso Valencia

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
360	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , <b>2012</b> , 22, 1760-74	9.7	3142
359	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
358	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , <b>2011</b> , 475, 101-5	50.4	1206
357	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , <b>2011</b> , 44, 47-52	36.3	752
356	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D452-5	20.1	670
355	Correlated mutations and residue contacts in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1994</b> , 18, 309-17	4.2	662
354	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , <b>2016</b> , 167, 1415-1429.e19	56.2	637
353	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , <b>2015</b> , 526, 519-24	50.4	565
352	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 10522-7	11.5	563
351	The ras protein family: evolutionary tree and role of conserved amino acids. <i>Biochemistry</i> , <b>1991</b> , 30, 4637-48	3.48	517
350	A hierarchical unsupervised growing neural network for clustering gene expression patterns. <i>Bioinformatics</i> , <b>2001</b> , 17, 126-36	7.2	465
349	Correlated mutations contain information about protein-protein interaction. <i>Journal of Molecular Biology</i> , <b>1997</b> , 271, 511-23	6.5	443
348	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , <b>2012</b> , 44, 1236-42	36.3	422
347	Emerging methods in protein co-evolution. <i>Nature Reviews Genetics</i> , <b>2013</b> , 14, 249-61	30.1	415
346	Reductive genome evolution in <i>Buchnera aphidicola</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 581-6	11.5	404
345	Multiple evidence strands suggest that there may be as few as 19,000 human protein-coding genes. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 5866-78	5.6	385

344	A gene network for navigating the literature. <i>Nature Genetics</i> , <b>2004</b> , 36, 664	36.3	373
343	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , <b>2016</b> , 167, 1398-1414	56.2	232
342	Similarity of phylogenetic trees as indicator of protein-protein interaction. <i>Protein Engineering, Design and Selection</i> , <b>2001</b> , 14, 609-14	1.9	337
341	A method to predict functional residues in proteins. <i>Nature Structural and Molecular Biology</i> , <b>1995</b> , 2, 171-8	17.6	329
340	Convergent evolution of similar enzymatic function on different protein folds: the hexokinase, ribokinase, and galactokinase families of sugar kinases. <i>Protein Science</i> , <b>1993</b> , 2, 31-40	6.3	307
339	Computational methods for the prediction of protein interactions. <i>Current Opinion in Structural Biology</i> , <b>2002</b> , 12, 368-73	8.1	274
338	Practical limits of function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2000</b> , 41, 98-107	4.2	266
337	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 224-6	44.5	261
336	The Ras protein superfamily: evolutionary tree and role of conserved amino acids. <i>Journal of Cell Biology</i> , <b>2012</b> , 196, 189-201	7.3	247
335	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , <b>2015</b> , 12, 615-621	21.6	235
334	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
333	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , <b>2016</b> , 17, 184	18.3	218
332	In silico two-hybrid system for the selection of physically interacting protein pairs. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 47, 219-27	4.2	214
331	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , <b>2015</b> , 47, 746-56	36.3	209
330	EnrichNet: network-based gene set enrichment analysis. <i>Bioinformatics</i> , <b>2012</b> , 28, i451-i457	7.2	204
329	Prediction of protein-protein interaction sites in heterocomplexes with neural networks. <i>FEBS Journal</i> , <b>2002</b> , 269, 1356-61		191
328	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. <i>Nature Genetics</i> , <b>2013</b> , 45, 1464-9	36.3	186
327	Alternative Splicing May Not Be the Key to Proteome Complexity. <i>Trends in Biochemical Sciences</i> , <b>2017</b> , 42, 98-110	10.3	180

326	Automatic methods for predicting functionally important residues. <i>Journal of Molecular Biology</i> , <b>2003</b> , 326, 1289-302	6.5	179
325	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> , <b>2007</b> , 104, 5495-500	11.5	177
324	MARVEL: a conserved domain involved in membrane apposition events. <i>Trends in Biochemical Sciences</i> , <b>2002</b> , 27, 599-601	10.3	170
323	Identification of amino acid residues crucial for chemokine receptor dimerization. <i>Nature Immunology</i> , <b>2004</b> , 5, 216-23	19.1	166
322	Improving contact predictions by the combination of correlated mutations and other sources of sequence information. <i>Folding &amp; Design</i> , <b>1997</b> , 2, S25-32		161
321	Overview of the protein-protein interaction annotation extraction task of BioCreative II. <i>Genome Biology</i> , <b>2008</b> , 9 Suppl 2, S4	18.3	157
320	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> , <b>2016</b> , 18, 325-32	8.1	153
319	Text-mining and information-retrieval services for molecular biology. <i>Genome Biology</i> , <b>2005</b> , 6, 224	18.3	151
318	Filamin-A regulates actin-dependent clustering of HIV receptors. <i>Nature Cell Biology</i> , <b>2007</b> , 9, 838-46	23.4	146
317	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , <b>2014</b> , 24, 212-26	9.7	143
316	Effective use of sequence correlation and conservation in fold recognition. <i>Journal of Molecular Biology</i> , <b>1999</b> , 293, 1221-39	6.5	142
315	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> , <b>2008</b> , 105, 934-9	11.5	138
314	Implementing the iHOP concept for navigation of biomedical literature. <i>Bioinformatics</i> , <b>2005</b> , 21 Suppl 2, ii252-8	7.2	137
313	Conserved clusters of functionally related genes in two bacterial genomes. <i>Journal of Molecular Evolution</i> , <b>1997</b> , 44, 66-73	3.1	136
312	Prediction of contact maps with neural networks and correlated mutations. <i>Protein Engineering, Design and Selection</i> , <b>2001</b> , 14, 835-43	1.9	133
311	Protein co-evolution, co-adaptation and interactions. <i>EMBO Journal</i> , <b>2008</b> , 27, 2648-55	13	132
310	Linking genes to literature: text mining, information extraction, and retrieval applications for biology. <i>Genome Biology</i> , <b>2008</b> , 9 Suppl 2, S8	18.3	131
309	EVA: Evaluation of protein structure prediction servers. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3311-5	20.1	131

308	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , <b>2013</b> , 10, 723-9	21.6	129
307	APPRIS: annotation of principal and alternative splice isoforms. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D110-7	20.1	128
306	Evaluation of text-mining systems for biology: overview of the Second BioCreative community challenge. <i>Genome Biology</i> , <b>2008</b> , 9 Suppl 2, S1	18.3	127
305	Eukaryotic translation elongation factor 1 gamma contains a glutathione transferase domain--study of a diverse, ancient protein superfamily using motif search and structural modeling. <i>Protein Science</i> , <b>1994</b> , 3, 2045-54	6.3	127
304	Information Retrieval and Text Mining Technologies for Chemistry. <i>Chemical Reviews</i> , <b>2017</b> , 117, 7673-7761	11	124
303	CHEMDNER: The drugs and chemical names extraction challenge. <i>Journal of Cheminformatics</i> , <b>2015</b> , 7, S1	8.6	120
302	Integrated next-generation sequencing and avatar mouse models for personalized cancer treatment. <i>Clinical Cancer Research</i> , <b>2014</b> , 20, 2476-84	12.9	118
301	Molecular evidence for the inverse comorbidity between central nervous system disorders and cancers detected by transcriptomic meta-analyses. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004173	6	116
300	Progress and challenges in predicting protein-protein interaction sites. <i>Briefings in Bioinformatics</i> , <b>2009</b> , 10, 233-46	13.4	116
299	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> , <b>2014</b> , 83, 89-105	9.4	113
298	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> , <b>1994</b> , 1, 95-101	17.6	109
297	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> , <b>2010</b> , 107, 1995-2000	11.5	108
296	Text mining for the biocuration workflow. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2012</b> , 2012, bas020	5	108
295	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 8, S3	3.6	104
294	No paradox, no progress: inverse cancer comorbidity in people with other complex diseases. <i>Lancet Oncology</i> , <b>2011</b> , 12, 604-8	21.7	103
293	Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , <b>2012</b> , 22, 1231-42	9.7	101
292	Text-mining approaches in molecular biology and biomedicine. <i>Drug Discovery Today</i> , <b>2005</b> , 10, 439-45	8.8	101
291	BioC: a minimalist approach to interoperability for biomedical text processing. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat064	5	100

290	Mosaic uniparental disomies and aneuploidies as large structural variants of the human genome. <i>American Journal of Human Genetics</i> , <b>2010</b> , 87, 129-38	11	100
289	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , <b>2015</b> , 7, S2	8.6	98
288	iHOP web services. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W21-6	20.1	96
287	Automatic annotation of protein function. <i>Current Opinion in Structural Biology</i> , <b>2005</b> , 15, 267-74	8.1	96
286	Assessment of predictions submitted for the CASP6 comparative modeling category. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61 Suppl 7, 27-45	4.2	95
285	CAFASP2: the second critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , Suppl 5, 171-83	4.2	93
284	Bringing gene order into bacterial shape. <i>Trends in Genetics</i> , <b>2001</b> , 17, 124-6	8.5	90
283	Analyzing the first drafts of the human proteome. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 3854-5	5.6	88
282	Towards the prediction of protein interaction partners using physical docking. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 469	12.2	88
281	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> , <b>2015</b> , 112, 13567-72	11.5	87
280	The pseudo GTPase CENP-M drives human kinetochore assembly. <i>ELife</i> , <b>2014</b> , 3, e02978	8.9	86
279	Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. <i>Npj Digital Medicine</i> , <b>2020</b> , 3, 81	15.7	85
278	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , <b>2016</b> , 17, 251	18.3	85
277	firestar--prediction of functionally important residues using structural templates and alignment reliability. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W573-7	20.1	83
276	Evaluation of BioCreAtIvE assessment of task 2. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 1, S16	3.6	82
275	The small GTP-binding protein, Rhes, regulates signal transduction from G protein-coupled receptors. <i>Oncogene</i> , <b>2004</b> , 23, 559-68	9.2	81
274	Towards a detailed atlas of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , <b>2013</b> , 23, 929-40	8.1	80
273	Most highly expressed protein-coding genes have a single dominant isoform. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 1880-7	5.6	78

272	Progress in predicting inter-residue contacts of proteins with neural networks and correlated mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , Suppl 5, 157-62	4.2	78
271	Overview of the BioCreative III Workshop. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 8, S1	3.6	77
270	A new ATP-binding fold in actin, hexokinase and Hsc70. <i>Trends in Cell Biology</i> , <b>1993</b> , 3, 53-9	18.3	76
269	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. <i>Gastroenterology</i> , <b>2015</b> , 149, 563-6	13.3	75
268	An Overview of BioCreative II.5. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2010</b> , 7, 385-99	3	74
267	Three-dimensional view of the surface motif associated with the P-loop structure: cis and trans cases of convergent evolution. <i>Journal of Molecular Biology</i> , <b>2000</b> , 303, 455-65	6.5	73
266	CASP6 assessment of contact prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61 Suppl 7, 214-24	4.2	72
265	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , <b>2020</b> , 7, 136	8.2	71
264	The BLUEPRINT Data Analysis Portal. <i>Cell Systems</i> , <b>2016</b> , 3, 491-495.e5	10.6	71
263	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , <b>2017</b> , 18, 18	18.3	70
262	APPRIS 2017: principal isoforms for multiple gene sets. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D213-D217	20.1	70
261	A la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. <i>Molecular Microbiology</i> , <b>2001</b> , 42, 47-59	4.1	70
260	Big data analytics for personalized medicine. <i>Current Opinion in Biotechnology</i> , <b>2019</b> , 58, 161-167	11.4	69
259	Effector recognition by the small GTP-binding proteins Ras and Ral. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 17763-70	5.4	66
258	Assessment of intramolecular contact predictions for CASP7. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69 Suppl 8, 152-8	4.2	65
257	NOTCH pathway inactivation promotes bladder cancer progression. <i>Journal of Clinical Investigation</i> , <b>2015</b> , 125, 824-30	15.9	64
256	Comparative proteomics reveals a significant bias toward alternative protein isoforms with conserved structure and function. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2265-83	8.3	64
255	How does the switch II region of G-domains work?. <i>FEBS Letters</i> , <b>1993</b> , 320, 1-6	3.8	64

254	Information extraction in molecular biology. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 154-65	13.4	61
253	Analysis of biological processes and diseases using text mining approaches. <i>Methods in Molecular Biology</i> , <b>2010</b> , 593, 341-82	1.4	61
252	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. <i>BMC Genomics</i> , <b>2015</b> , 16, 403	4.5	59
251	Text mining for biology--the way forward: opinions from leading scientists. <i>Genome Biology</i> , <b>2008</b> , 9 Suppl 2, S7	18.3	59
250	Identification of conserved amino acid residues in rat liver carnitine palmitoyltransferase I critical for malonyl-CoA inhibition. Mutation of methionine 593 abolishes malonyl-CoA inhibition. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 9058-63	5.4	58
249	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , <b>2003</b> , 19, 717-26	7.2	58
248	The organization of the microbial biodegradation network from a systems-biology perspective. <i>EMBO Reports</i> , <b>2003</b> , 4, 994-9	6.5	56
247	Towards FAIR principles for 'research' software. <i>Data Science</i> , <b>2020</b> , 3, 37-59	2.2	56
246	Phylogeny-independent detection of functional residues. <i>Bioinformatics</i> , <b>2006</b> , 22, 1440-8	7.2	55
245	Proteomics studies confirm the presence of alternative protein isoforms on a large scale. <i>Genome Biology</i> , <b>2008</b> , 9, R162	18.3	54
244	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , <b>2018</b> , 24, 2784-2794	10.6	54
243	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. <i>Molecular Informatics</i> , <b>2011</b> , 30, 506-19	3.8	53
242	MetaRouter: bioinformatics for bioremediation. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D588-92	20.1	52
241	Life cycles of successful genes. <i>Trends in Genetics</i> , <b>2003</b> , 19, 79-81	8.5	52
240	Predicting reliable regions in protein alignments from sequence profiles. <i>Journal of Molecular Biology</i> , <b>2003</b> , 330, 705-18	6.5	52
239	Mining functional information associated with expression arrays. <i>Functional and Integrative Genomics</i> , <b>2001</b> , 1, 256-68	3.8	52
238	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , <b>2017</b> , 14, 782-788	21.6	51
237	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , <b>2012</b> , 7, e28213	3.7	51



236	Structural model for family 32 of glycosyl-hydrolase enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1998</b> , 33, 383-95	4.2	51
235	Text mining for metabolic pathways, signaling cascades, and protein networks. <i>Science Signaling</i> , <b>2005</b> , 2005, pe21	8.8	51
234	Clustering of proximal sequence space for the identification of protein families. <i>Bioinformatics</i> , <b>2002</b> , 18, 908-21	7.2	50
233	Model of the ran-RCC1 interaction using biochemical and docking experiments. <i>Journal of Molecular Biology</i> , <b>1999</b> , 289, 1119-30	6.5	50
232	Defining functional distances over gene ontology. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 50	3.6	49
231	Introducing meta-services for biomedical information extraction. <i>Genome Biology</i> , <b>2008</b> , 9 Suppl 2, S6	18.3	49
230	Assessment of predictions submitted for the CASP7 function prediction category. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69 Suppl 8, 165-74	4.2	49
229	TopoGSA: network topological gene set analysis. <i>Bioinformatics</i> , <b>2010</b> , 26, 1271-2	7.2	48
228	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , <b>2009</b> , 10, 206	18.3	48
227	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004325	5	47
226	MidA is a putative methyltransferase that is required for mitochondrial complex I function. <i>Journal of Cell Science</i> , <b>2010</b> , 123, 1674-83	5.3	47
225	Systemic approaches to biodegradation. <i>FEMS Microbiology Reviews</i> , <b>2009</b> , 33, 98-108	15.1	47
224	Most Alternative Isoforms Are Not Functionally Important. <i>Trends in Biochemical Sciences</i> , <b>2017</b> , 42, 408-410	4.9	46
223	A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimer's Disease, Glioblastoma and Lung cancer. <i>Scientific Reports</i> , <b>2017</b> , 7, 4474	4.9	45
222	Distribution and functional diversification of the ras superfamily in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , <b>1998</b> , 434, 219-25	3.8	45
221	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. <i>Journal of Biotechnology</i> , <b>2002</b> , 98, 269-83	3.7	44
220	Identifying ELIXIR Core Data Resources. <i>F1000Research</i> , <b>2016</b> , 5,	3.6	44
219	Subfunctionalization via adaptive evolution influenced by genomic context: the case of histone chaperones ASF1a and ASF1b. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1853-66	8.3	42

218	Automated alphabet reduction for protein datasets. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 6	3.6	41
217	firestar--advances in the prediction of functionally important residues. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W235-41	20.1	41
216	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , <b>2018</b> , 40, 1700148	4.1	40
215	Classification of protein families and detection of the determinant residues with an improved self-organizing map. <i>Biological Cybernetics</i> , <b>1997</b> , 76, 441-50	2.8	40
214	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D142-51	20.1	39
213	Automatic annotation of protein function based on family identification. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53, 683-92	4.2	39
212	Structural model of the catalytic core of carnitine palmitoyltransferase I and carnitine octanoyltransferase (COT): mutation of CPT I histidine 473 and alanine 381 and COT alanine 238 impairs the catalytic activity. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 45001-8	5.4	39
211	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , <b>2020</b> , 11, 729	17.4	38
210	Long-range epigenetic silencing associates with deregulation of Ikaros targets in colorectal cancer cells. <i>Molecular Cancer Research</i> , <b>2011</b> , 9, 1139-51	6.6	38
209	The environmental fate of organic pollutants through the global microbial metabolism. <i>Molecular Systems Biology</i> , <b>2007</b> , 3, 114	12.2	38
208	Legacy data sharing to improve drug safety assessment: the eTOX project. <i>Nature Reviews Drug Discovery</i> , <b>2017</b> , 16, 811-812	64.1	37
207	A text-mining perspective on the requirements for electronically annotated abstracts. <i>FEBS Letters</i> , <b>2008</b> , 582, 1178-81	3.8	37
206	Scoring docking models with evolutionary information. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 60, 275-80	4.2	37
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