

# Fabrizio FerrÃ

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

3,279  
citations

304743

22  
h-index

233421

45  
g-index

48  
all docs

48  
docs citations

48  
times ranked

5742  
citing authors

#	ARTICLE	IF	CITATIONS
1	Relative Information Gain: Shannon entropy-based measure of the relative structural conservation in RNA alignments. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab007.	3.2	3
2	Modeling cancer drug response through drug-specific informative genes. <i>Scientific Reports</i> , 2019, 9, 15222.	3.3	42
3	Over-Expression of UV-Damage DNA Repair Genes and Ribonucleic Acid Persistence Contribute to the Resilience of Dried Biofilms of the Desert Cyanobacterium <i>Chroococcidiopsis</i> Exposed to Mars-Like UV Flux and Long-Term Desiccation. <i>Frontiers in Microbiology</i> , 2019, 10, 2312.	3.5	19
4	The rs17084733 variant in the <i>KIT</i> 3' UTR disrupts a miR-221/222 binding site in gastrointestinal stromal tumour: a sponge-like mechanism conferring disease susceptibility. <i>Epigenetics</i> , 2019, 14, 545-557.	2.7	10
5	Discovering sequence and structure landscapes in RNA interaction motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4958-4969.	14.5	17
6	Axitinib exposure triggers endothelial cells senescence through ROS accumulation and ATM activation. <i>Oncogene</i> , 2019, 38, 5413-5424.	5.9	28
7	BEAM web server: a tool for structural RNA motif discovery. <i>Bioinformatics</i> , 2018, 34, 1058-1060.	4.1	10
8	Genome assembly and transcriptome resource for river buffalo, <i>Bubalus bubalis</i> (2n = 50). <i>GigaScience</i> , 2017, 6, 1-6.	6.4	55
9	Caspase-8 contributes to angiogenesis and chemotherapy resistance in glioblastoma. <i>ELife</i> , 2017, 6, .	6.0	47
10	c-MYC inhibition impairs hypoxia response in glioblastoma multiforme. <i>Oncotarget</i> , 2016, 7, 33257-33271.	1.8	24
11	Transcriptomic investigation of meat tenderness in two Italian cattle breeds. <i>Animal Genetics</i> , 2016, 47, 273-287.	1.7	37
12	Genome-wide methylation analysis demonstrates that 5-aza-2-deoxycytidine treatment does not cause random DNA demethylation in fragile X syndrome cells. <i>Epigenetics and Chromatin</i> , 2016, 9, 12.	3.9	28
13	Skeletal muscle transcriptional profiles in two Italian beef breeds, Chianina and Maremmana, reveal breed specific variation. <i>Molecular Biology Reports</i> , 2016, 43, 253-268.	2.3	16
14	A novel method for the identification of conserved structural patterns in RNA: From small scale to high-throughput applications. <i>Nucleic Acids Research</i> , 2016, 44, 8600-8609.	14.5	19
15	The human rs1050286 polymorphism alters <i>LOX1</i> expression through modifying miR-24 binding. <i>Journal of Cellular and Molecular Medicine</i> , 2016, 20, 181-187.	3.6	19
16	Next Generation Sequencing and Linkage Analysis for the Molecular Diagnosis of a Novel Overlapping Syndrome Characterized by Hypertrophic Cardiomyopathy and Typical Electrical Instability of Brugada Syndrome. <i>Circulation Journal</i> , 2016, 80, 938-949.	1.6	21
17	RNA-Sequencing for profiling goat milk transcriptome in colostrum and mature milk. <i>BMC Veterinary Research</i> , 2016, 12, 264.	1.9	71
18	Revealing protein-lncRNA interaction. <i>Briefings in Bioinformatics</i> , 2016, 17, 106-116.	6.5	536

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19	Web-Beagle: a web server for the alignment of RNA secondary structures: Figure 1.. Nucleic Acids Research, 2015, 43, W493-W497.	14.5	29
20	A Simple Protocol for the Inference of RNA Global Pairwise Alignments. Methods in Molecular Biology, 2015, 1269, 39-47.	0.9	1
21	Exploiting holistic approaches to model specificity in protein phosphorylation. Frontiers in Genetics, 2014, 5, 315.	2.3	14
22	Computational methods for analysis and inference of kinase/inhibitor relationships. Frontiers in Genetics, 2014, 5, 196.	2.3	16
23	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. Molecular and Cellular Proteomics, 2014, 13, 2198-2212.	3.8	5
24	A novel approach to represent and compare RNA secondary structures. Nucleic Acids Research, 2014, 42, 6146-6157.	14.5	43
25	Performances of Bioinformatics Pipelines for the Identification of Pathogens in Clinical Samples with the De Novo Assembly Approaches: Focus on 2009 Pandemic Influenza A (H1N1). Open Bioinformatics Journal, 2014, 8, 1-5.	1.0	0
26	Alternative splicing tends to avoid partial removals of protein-protein interaction sites. BMC Genomics, 2013, 14, 379.	2.8	4
27	DBATE: database of alternative transcripts expression. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat050.	3.0	11
28	webPDBinder: a server for the identification of ligand binding sites on protein structures. Nucleic Acids Research, 2013, 41, W308-W313.	14.5	5
29	Role of CTCF Protein in Regulating FMR1 Locus Transcription. PLoS Genetics, 2013, 9, e1003601.	3.5	38
30	Nucleos: a web server for the identification of nucleotide-binding sites in protein structures. Nucleic Acids Research, 2013, 41, W281-W285.	14.5	7
31	Functional characterization and expression analysis of novel alternative splicing isoforms of Olr1 gene during mouse embryogenesis. Gene, 2012, 491, 5-12.	2.2	5
32	Specific tagging of the egress-related osmiophilic bodies in the gametocytes of Plasmodium falciparum. Malaria Journal, 2012, 11, 88.	2.3	6
33	Identification of Nucleotide-Binding Sites in Protein Structures: A Novel Approach Based on Nucleotide Modularity. PLoS ONE, 2012, 7, e50240.	2.5	6
34	Coding potential of the products of alternative splicing in human. Genome Biology, 2011, 12, R9.	8.8	38
35	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. Nature, 2011, 471, 513-517.	27.8	506
36	DIAL: a web server for the pairwise alignment of two RNA three-dimensional structures using nucleotide, dihedral angle and base-pairing similarities. Nucleic Acids Research, 2007, 35, W659-W668.	14.5	55

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37	DiANNA 1.1: an extension of the DiANNA web server for ternary cysteine classification. <i>Nucleic Acids Research</i> , 2006, 34, W182-W185.	14.5	179
38	BTW: a web server for Boltzmann time warping of gene expression time series. <i>Nucleic Acids Research</i> , 2006, 34, W482-W485.	14.5	6
39	Integrated bioinformatics software at NCBI. , 2005, , .		0
40	Functional annotation by identification of local surface similarities: a novel tool for structural genomics. <i>BMC Bioinformatics</i> , 2005, 6, 194.	2.6	27
41	Disulfide connectivity prediction using secondary structure information and diresidue frequencies. <i>Bioinformatics</i> , 2005, 21, 2336-2346.	4.1	93
42	Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency. <i>Rna</i> , 2005, 11, 578-591.	3.5	178
43	DiANNA: a web server for disulfide connectivity prediction. <i>Nucleic Acids Research</i> , 2005, 33, W230-W232.	14.5	312
44	SURFACE: a database of protein surface regions for functional annotation. <i>Nucleic Acids Research</i> , 2004, 32, 240D-244.	14.5	59
45	Development of Computational Tools for the Inference of Protein Interaction Specificity Rules and Functional Annotation Using Structural Information. <i>Comparative and Functional Genomics</i> , 2003, 4, 416-419.	2.0	1
46	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	14.5	555
47	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