## Coral del Val

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3454610/publications.pdf

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		279798	254184
58	2,039	23	43
papers	citations	h-index	g-index
60	60	60	3037
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Diversity of Arbuscular Mycorrhizal Fungus Populations in Heavy-Metal-Contaminated Soils. Applied and Environmental Microbiology, 1999, 65, 718-723.	3.1	280
2	Uncovering the Hidden Risk Architecture of the Schizophrenias: Confirmation in Three Independent Genome-Wide Association Studies. American Journal of Psychiatry, 2015, 172, 139-153.	7.2	204
3	Membrane Protein Structure, Function, and Dynamics: a Perspective from Experiments and Theory. Journal of Membrane Biology, 2015, 248, 611-640.	2.1	157
4	Assessing the tolerance to heavy metals of arbuscular mycorrhizal fungi isolated from sewage sludge-contaminated soils. Applied Soil Ecology, 1999, 11, 261-269.	4.3	120
5	Identification of differentially expressed small nonâ€coding RNAs in the legume endosymbiont <i>Sinorhizobium meliloti</i> by comparative genomics. Molecular Microbiology, 2007, 66, 1080-1091.	2.5	106
6	Rhomboid Protease Dynamics and Lipid Interactions. Structure, 2009, 17, 395-405.	3.3	101
7	Role of nitric oxide in plant responses to heavy metal stress: exogenous application versus endogenous production. Journal of Experimental Botany, 2019, 70, 4477-4488.	4.8	87
8	Uncovering the complex genetics of human character. Molecular Psychiatry, 2020, 25, 2295-2312.	7.9	77
9	Uncovering the complex genetics of human temperament. Molecular Psychiatry, 2020, 25, 2275-2294.	7.9	72
10	Three genetic–environmental networks for human personality. Molecular Psychiatry, 2021, 26, 3858-3875.	7.9	58
11	Dynamics of SecY Translocons with Translocation-Defective Mutations. Structure, 2010, 18, 847-857.	3.3	47
12	Lentiviral vector integration sites in human NOD/SCID repopulating cells. Journal of Gene Medicine, 2006, 8, 1197-1207.	2.8	46
13	GOPET: a tool for automated predictions of Gene Ontology terms. BMC Bioinformatics, 2006, 7, 161.	2.6	44
14	Metabolic and bacterial diversity in soils historically contaminated by heavy metals and hydrocarbons. Journal of Environmental Monitoring, 2008, 10, 1287.	2.1	42
15	The LIFEdb database in 2006. Nucleic Acids Research, 2006, 34, D415-D418.	14.5	36
16	Coupling between inter-helical hydrogen bonding and water dynamics in a proton transporter. Journal of Structural Biology, 2014, 186, 95-111.	2.8	36
17	Evolution of genetic networks for human creativity. Molecular Psychiatry, 2022, 27, 354-376.	7.9	36
18	A survey of sRNA families in α-proteobacteria. RNA Biology, 2012, 9, 119-129.	3.1	32

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19	miRNAs as radioâ€response biomarkers for breast cancer stem cells. Molecular Oncology, 2020, 14, 556-570.	4.6	31
20	Ser/Thr Motifs in Transmembrane Proteins: Conservation Patterns and Effects on Local Protein Structure and Dynamics. Journal of Membrane Biology, 2012, 245, 717-730.	2.1	30
21	Deep Learning in Omics Data Analysis and Precision Medicine. , 0, , 37-53.		30
22	Profile analysis and prediction of tissue-specific CpG island methylation classes. BMC Bioinformatics, 2009, 10, 116.	2.6	28
23	PGMRA: a web server for (phenotype x genotype) many-to-many relation analysis in GWAS. Nucleic Acids Research, 2013, 41, W142-W149.	14.5	28
24	Kinetics of proton release and uptake by channelrhodopsinâ€2. FEBS Letters, 2012, 586, 1344-1348.	2.8	27
25	High throughput sequencing analysis of Trypanosoma brucei DRBD3/PTB1-bound mRNAs. Molecular and Biochemical Parasitology, 2015, 199, 1-4.	1.1	27
26	A graph-based approach identifies dynamic H-bond communication networks in spike protein S of SARS-CoV-2. Journal of Structural Biology, 2020, 212, 107617.	2.8	26
27	The transcriptome of the colonial marine hydroid <i>Hydractinia echinata</i> . FEBS Journal, 2010, 277, 197-209.	4.7	25
28	High-throughput protein analysis integrating bioinformatics and experimental assays. Nucleic Acids Research, 2004, 32, 742-748.	14.5	17
29	TissueDistributionDBs: a repository of organism-specific tissue-distribution profiles. Theoretical Chemistry Accounts, 2010, 125, 651-658.	1.4	17
30	Uncovering the complex genetics of human personality: response from authors on the PGMRA Model. Molecular Psychiatry, 2020, 25, 2210-2213.	7.9	17
31	Charged groups at binding interfaces of the PsbO subunit of photosystem II: A combined bioinformatics and simulation study. Biochimica Et Biophysica Acta - Bioenergetics, 2017, 1858, 432-441.	1.0	15
32	ProtSweep, 2Dsweep and DomainSweep: protein analysis suite at DKFZ. Nucleic Acids Research, 2007, 35, W444-W450.	14.5	14
33	Low endogenous NO levels in roots and antioxidant systems are determinants for the resistance of Arabidopsis seedlings grown in Cd. Environmental Pollution, 2020, 256, 113411.	7.5	14
34	cDNA2Genome: a tool for mapping and annotating cDNAs. BMC Bioinformatics, 2003, 4, 39.	2.6	12
35	Uncovering Tumour Heterogeneity through PKR and nc886 Analysis in Metastatic Colon Cancer Patients Treated with 5-FU-Based Chemotherapy. Cancers, 2020, 12, 379.	3.7	12
36	Channelrhodopsins: A bioinformatics perspective. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 643-655.	1.0	11

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37	Identifying promoter features of co-regulated genes with similar network motifs. BMC Bioinformatics, 2009, 10, S1.	2.6	10
38	A multiobjective method for robust identification of bacterial small non-coding RNAs. Bioinformatics, 2014, 30, 2875-2882.	4.1	10
39	Onto-CC: a web server for identifying Gene Ontology conceptual clusters. Nucleic Acids Research, 2008, 36, W352-W357.	14.5	8
40	PATH: a task for the inference of phylogenies. Bioinformatics, 2002, 18, 646-647.	4.1	7
41	Optimization of multi-classifiers for computational biology: application to gene finding and expression. Theoretical Chemistry Accounts, 2010, 125, 599-611.	1.4	7
42	Retroviral vector insertions in T-lymphocytes used for suicide gene therapy occur in gene groups with specific molecular functions. Bone Marrow Transplantation, 2006, 38, 229-235.	2.4	6
43	Identification of novel prostate cancer genes in patients stratified by Gleason classification: Role of antitumoral genes. International Journal of Cancer, 2022, 151, 255-264.	5.1	6
44	PromoterSweep: a tool for identification of transcription factor binding sites. Theoretical Chemistry Accounts, 2010, 125, 583-591.	1.4	5
45	Identification, sequencing and comparative analysis of pBp15.S plasmid from the newly described entomopathogen Bacillus pumilus 15.1. Plasmid, 2015, 82, 17-27.	1.4	4
46	Molecular Classification of Multiple Myeloma (MM) Based on Gene Expression Profiling (GEP) and Fluorescence In Situ Hybridisation (FISH) Is an Independent Predictor for Event Free Survival (EFS) Blood, 2005, 106, 507-507.	1.4	4
47	Diversity and sequence motifs of the bacterial SecA protein motor. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183319.	2.6	3
48	Mining and Predicting CpG islands. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	2
49	Optimal Selection of Microarray Analysis Methods Using a Conceptual Clustering Algorithm. Lecture Notes in Computer Science, 2006, , 172-183.	1.3	2
50	Decision Making Association Rules for Recognition of Differential Gene Expression Profiles. Lecture Notes in Computer Science, 2006, , 1137-1149.	1.3	1
51	CAFTAN: a tool for fast mapping, and quality assessment of cDNAs. BMC Bioinformatics, 2006, 7, 473.	2.6	0
52	769. Genes Encoding Receptors, Signal Transducers and Transcription Regulators Are Preferred Targets of Retroviral Vector Integration in T-Lymphocytes In Vitro and In Vivo. Molecular Therapy, 2006, 13, S297-S298.	8.2	0
53	Optimization of Multi-classifiers for Computational Biology: Application to the Gene Finding Problem. , 2009, , .		0
54	Finding promoter profiles with multiobjective identification of cis-regulatory modules based on constraints, , $2011$ , , .		0

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55	Integrating network motifs into a genetic network: A case of study based on the Phop/PhoQ two-component system. , $2011,\ldots$		0
56	Kinetics of Proton Release and Uptake by Channelrhodopsin-2. Biophysical Journal, 2012, 102, 575a.	0.5	0
57	Proton-Coupled Water and Hydrogen-Bond Dynamics in Channelrhodopsin. Biophysical Journal, 2014, 106, 16a-17a.	0.5	O
58	Multiple Myeloma: Global Expression Profiling (GEP) Indicates Upregulation of the Ribosomal Machinery in Hyperdiploid Clones Blood, 2004, 104, 1421-1421.	1.4	0