

# Coral del Val

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

2,039  
citations

279798

23  
h-index

254184

43  
g-index

60  
all docs

60  
docs citations

60  
times ranked

3037  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of genetic networks for human creativity. <i>Molecular Psychiatry</i> , 2022, 27, 354-376.	7.9	36
2	Identification of novel prostate cancer genes in patients stratified by Gleason classification: Role of antitumoral genes. <i>International Journal of Cancer</i> , 2022, 151, 255-264.	5.1	6
3	Three geneticâ€“environmental networks for human personality. <i>Molecular Psychiatry</i> , 2021, 26, 3858-3875.	7.9	58
4	Uncovering the complex genetics of human character. <i>Molecular Psychiatry</i> , 2020, 25, 2295-2312.	7.9	77
5	Uncovering the complex genetics of human temperament. <i>Molecular Psychiatry</i> , 2020, 25, 2275-2294.	7.9	72
6	Uncovering the complex genetics of human personality: response from authors on the PGMRA Model. <i>Molecular Psychiatry</i> , 2020, 25, 2210-2213.	7.9	17
7	Low endogenous NO levels in roots and antioxidant systems are determinants for the resistance of <i>Arabidopsis</i> seedlings grown in Cd. <i>Environmental Pollution</i> , 2020, 256, 113411.	7.5	14
8	A graph-based approach identifies dynamic H-bond communication networks in spike protein S of SARS-CoV-2. <i>Journal of Structural Biology</i> , 2020, 212, 107617.	2.8	26
9	Uncovering Tumour Heterogeneity through PKR and nc886 Analysis in Metastatic Colon Cancer Patients Treated with 5-FU-Based Chemotherapy. <i>Cancers</i> , 2020, 12, 379.	3.7	12
10	miRNAs as radioâ€“response biomarkers for breast cancer stem cells. <i>Molecular Oncology</i> , 2020, 14, 556-570.	4.6	31
11	Diversity and sequence motifs of the bacterial SecA protein motor. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183319.	2.6	3
12	Role of nitric oxide in plant responses to heavy metal stress: exogenous application versus endogenous production. <i>Journal of Experimental Botany</i> , 2019, 70, 4477-4488.	4.8	87
13	Charged groups at binding interfaces of the PsbO subunit of photosystem II: A combined bioinformatics and simulation study. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 432-441.	1.0	15
14	High throughput sequencing analysis of <i>Trypanosoma brucei</i> DRBD3/PTB1-bound mRNAs. <i>Molecular and Biochemical Parasitology</i> , 2015, 199, 1-4.	1.1	27
15	Membrane Protein Structure, Function, and Dynamics: a Perspective from Experiments and Theory. <i>Journal of Membrane Biology</i> , 2015, 248, 611-640.	2.1	157
16	Identification, sequencing and comparative analysis of pBp15.S plasmid from the newly described entomopathogen <i>Bacillus pumilus</i> 15.1. <i>Plasmid</i> , 2015, 82, 17-27.	1.4	4
17	Uncovering the Hidden Risk Architecture of the Schizophrenias: Confirmation in Three Independent Genome-Wide Association Studies. <i>American Journal of Psychiatry</i> , 2015, 172, 139-153.	7.2	204
18	Coupling between inter-helical hydrogen bonding and water dynamics in a proton transporter. <i>Journal of Structural Biology</i> , 2014, 186, 95-111.	2.8	36

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19	Channelrhodopsins: A bioinformatics perspective. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 643-655.	1.0	11
20	A multiobjective method for robust identification of bacterial small non-coding RNAs. <i>Bioinformatics</i> , 2014, 30, 2875-2882.	4.1	10
21	Proton-Coupled Water and Hydrogen-Bond Dynamics in Channelrhodopsin. <i>Biophysical Journal</i> , 2014, 106, 16a-17a.	0.5	0
22	PGMRA: a web server for (phenotype x genotype) many-to-many relation analysis in GWAS. <i>Nucleic Acids Research</i> , 2013, 41, W142-W149.	14.5	28
23	A survey of sRNA families in $\hat{\pm}$ -proteobacteria. <i>RNA Biology</i> , 2012, 9, 119-129.	3.1	32
24	Ser/Thr Motifs in Transmembrane Proteins: Conservation Patterns and Effects on Local Protein Structure and Dynamics. <i>Journal of Membrane Biology</i> , 2012, 245, 717-730.	2.1	30
25	Kinetics of Proton Release and Uptake by Channelrhodopsin-2. <i>Biophysical Journal</i> , 2012, 102, 575a.	0.5	0
26	Kinetics of proton release and uptake by channelrhodopsinâ€². <i>FEBS Letters</i> , 2012, 586, 1344-1348.	2.8	27
27	Finding promoter profiles with multiobjective identification of cis-regulatory modules based on constraints. , 2011, , .		0
28	Integrating network motifs into a genetic network: A case of study based on the Phop/PhoQ two-component system. , 2011, , .		0
29	PromoterSweep: a tool for identification of transcription factor binding sites. <i>Theoretical Chemistry Accounts</i> , 2010, 125, 583-591.	1.4	5
30	Optimization of multi-classifiers for computational biology: application to gene finding and expression. <i>Theoretical Chemistry Accounts</i> , 2010, 125, 599-611.	1.4	7
31	TissueDistributionDBs: a repository of organism-specific tissue-distribution profiles. <i>Theoretical Chemistry Accounts</i> , 2010, 125, 651-658.	1.4	17
32	Dynamics of SecY Translocons with Translocation-Defective Mutations. <i>Structure</i> , 2010, 18, 847-857.	3.3	47
33	The transcriptome of the colonial marine hydroid <i>Hydractiniaâ€¢fechinata</i> . <i>FEBS Journal</i> , 2010, 277, 197-209.	4.7	25
34	Rhomboid Protease Dynamics and Lipid Interactions. <i>Structure</i> , 2009, 17, 395-405.	3.3	101
35	Profile analysis and prediction of tissue-specific CpG island methylation classes. <i>BMC Bioinformatics</i> , 2009, 10, 116.	2.6	28
36	Identifying promoter features of co-regulated genes with similar network motifs. <i>BMC Bioinformatics</i> , 2009, 10, S1.	2.6	10

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37	Optimization of Multi-classifiers for Computational Biology: Application to the Gene Finding Problem. , 2009, , .		0
38	Metabolic and bacterial diversity in soils historically contaminated by heavy metals and hydrocarbons. Journal of Environmental Monitoring, 2008, 10, 1287.	2.1	42
39	Onto-CC: a web server for identifying Gene Ontology conceptual clusters. Nucleic Acids Research, 2008, 36, W352-W357.	14.5	8
40	Mining and Predicting CpG islands. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	2
41	ProtSweep, 2Dsweep and DomainSweep: protein analysis suite at DKFZ. Nucleic Acids Research, 2007, 35, W444-W450.	14.5	14
42	Identification of differentially expressed small non-coding RNAs in the legume endosymbiont <i>Sinorhizobium meliloti</i> by comparative genomics. Molecular Microbiology, 2007, 66, 1080-1091.	2.5	106
43	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
44	GOPET: a tool for automated predictions of Gene Ontology terms. BMC Bioinformatics, 2006, 7, 161.	2.6	44
45	CAFTAN: a tool for fast mapping, and quality assessment of cDNAs. BMC Bioinformatics, 2006, 7, 473.	2.6	0
46	Lentiviral vector integration sites in human NOD/SCID repopulating cells. Journal of Gene Medicine, 2006, 8, 1197-1207.	2.8	46
47	The LIFEdb database in 2006. Nucleic Acids Research, 2006, 34, D415-D418.	14.5	36
48	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
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	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
52	High-throughput protein analysis integrating bioinformatics and experimental assays. Nucleic Acids Research, 2004, 32, 742-748.	14.5	17
53	Multiple Myeloma: Global Expression Profiling (GEP) Indicates Upregulation of the Ribosomal Machinery in Hyperdiploid Clones.. Blood, 2004, 104, 1421-1421.	1.4	0
54	cDNA2Genome: a tool for mapping and annotating cDNAs. BMC Bioinformatics, 2003, 4, 39.	2.6	12

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55	PATH: a task for the inference of phylogenies. <i>Bioinformatics</i> , 2002, 18, 646-647.	4.1	7
56	Diversity of Arbuscular Mycorrhizal Fungus Populations in Heavy-Metal-Contaminated Soils. <i>Applied and Environmental Microbiology</i> , 1999, 65, 718-723.	3.1	280
57	Assessing the tolerance to heavy metals of arbuscular mycorrhizal fungi isolated from sewage sludge-contaminated soils. <i>Applied Soil Ecology</i> , 1999, 11, 261-269.	4.3	120
58	Deep Learning in Omics Data Analysis and Precision Medicine. , 0, , 37-53.		30