

Marie-Dominique Devignes

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

2,789
citations

377584

21
h-index

214428

50
g-index

74
all docs

74
docs citations

74
times ranked

4949
citing authors

#	ARTICLE	IF	CITATIONS
1	HexServer: an FFT-based protein docking server powered by graphics processors. <i>Nucleic Acids Research</i> , 2010, 38, W445-W449.	6.5	529
2	Application of Artificial Intelligence to Gastroenterology and Hepatology. <i>Gastroenterology</i> , 2020, 158, 76-94.e2.	0.6	335
3	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
4	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
5	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	1.5	148
6	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	1.5	99
7	Protein docking using case-based reasoning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2150-2158.	1.5	98
8	IntelliGO: a new vector-based semantic similarity measure including annotation origin. <i>BMC Bioinformatics</i> , 2010, 11, 588.	1.2	80
9	New Insights into the Classification and Integration Specificity of Streptococcus Integrative Conjugative Elements through Extensive Genome Exploration. <i>Frontiers in Microbiology</i> , 2015, 6, 1483.	1.5	64
10	The Genexpress IMAGE Knowledge Base of the Human Muscle Transcriptome: A Resource of Structural, Functional, and Positional Candidate Genes for Muscle Physiology and Pathologies. <i>Genome Research</i> , 1999, 9, 1313-1320.	2.4	55
11	Activation of Peroxisome Proliferator-Activated Receptor Gamma by Human Cytomegalovirus for <i>De Novo</i> Replication Impairs Migration and Invasiveness of Cytotrophoblasts from Early Placentas. <i>Journal of Virology</i> , 2010, 84, 2946-2954.	1.5	55
12	The Genexpress IMAGE Knowledge Base of the Human Brain Transcriptome: A Prototype Integrated Resource for Functional and Computational Genomics. <i>Genome Research</i> , 1999, 9, 195-209.	2.4	52
13	Integrative relational machine-learning for understanding drug side-effect profiles. <i>BMC Bioinformatics</i> , 2013, 14, 207.	1.2	48
14	Codon context effect in virus translational readthrough A study in vitro of the determinants of TMV and Mo-MuLV amber suppression. <i>FEBS Letters</i> , 1992, 306, 133-139.	1.3	37
15	Spatial clustering of protein binding sites for template based protein docking. <i>Bioinformatics</i> , 2011, 27, 2820-2827.	1.8	36
16	A Glimpse into the World of Integrative and Mobilizable Elements in Streptococci Reveals an Unexpected Diversity and Novel Families of Mobilization Proteins. <i>Frontiers in Microbiology</i> , 2017, 8, 443.	1.5	33
17	KBDOCK 2013: a spatial classification of 3D protein domain family interactions. <i>Nucleic Acids Research</i> , 2014, 42, D389-D395.	6.5	31
18	Extended spectrum of MBD5 mutations in neurodevelopmental disorders. <i>European Journal of Human Genetics</i> , 2013, 21, 1457-1461.	1.4	30

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19	Enhanced clinical phenotyping by mechanistic bioprofiling in heart failure with preserved ejection fraction: insights from the MEDIA-DHF study (The Metabolic Road to Diastolic Heart Failure). <i>Biomarkers</i> , 2020, 25, 201-211.	0.9	26
20	Prediction of Monomer Isomery in Florine: A Workflow Dedicated to Nonribosomal Peptide Discovery. <i>PLoS ONE</i> , 2014, 9, e85667.	1.1	25
21	The human semaphorin 6B gene is down regulated by PPARs. <i>Genomics</i> , 2004, 83, 1141-1150.	1.3	24
22	Rapid and high efficiency site-directed mutagenesis by improvement of the homologous recombination technique. <i>Nucleic Acids Research</i> , 1995, 23, 1642-1643.	6.5	23
23	ECDomainMiner: discovering hidden associations between enzyme commission numbers and Pfam domains. <i>BMC Bioinformatics</i> , 2017, 18, 107.	1.2	22
24	Gene-disease relationship discovery based on model-driven data integration and database view definition. <i>Bioinformatics</i> , 2009, 25, 230-236.	1.8	21
25	Extended persistence of antiphospholipid antibodies beyond the 12-week time interval: Association with baseline antiphospholipid antibodies titres. <i>International Journal of Laboratory Hematology</i> , 2019, 41, 726-730.	0.7	20
26	Plasma protein biomarkers and their association with mutually exclusive cardiovascular phenotypes: the FIBRO-TARGETS case-control analyses. <i>Clinical Research in Cardiology</i> , 2020, 109, 22-33.	1.5	19
27	Multiple-step virtual screening using VSM-G: overview and validation of fast geometrical matching enrichment. <i>Journal of Molecular Modeling</i> , 2008, 14, 135-148.	0.8	18
28	Characterization of a relaxase belonging to the MOB family, a widespread family in Firmicutes mediating the transfer of ICEs. <i>Mobile DNA</i> , 2019, 10, 18.	1.3	17
29	A 1.7-Mb YAC Contig around the Human BDNF Gene (11p13): Integration of the Physical, Genetic, and Cytogenetic Maps in Relation to WAGR Syndrome. <i>Genomics</i> , 1994, 24, 69-77.	1.3	16
30	Querying a Bioinformatic Data Sources Registry with Concept Lattices. <i>Lecture Notes in Computer Science</i> , 2005, , 323-336.	1.0	16
31	Screening of subtle copy number changes in Aicardi syndrome patients with a high resolution X chromosome array-CGH. <i>European Journal of Medical Genetics</i> , 2007, 50, 386-391.	0.7	16
32	Ontology-guided data preparation for discovering genotype-phenotype relationships. <i>BMC Bioinformatics</i> , 2008, 9, S3.	1.2	16
33	Suggested Ontology for Pharmacogenomics (SO-Pharm): Modular Construction and Preliminary Testing. <i>Lecture Notes in Computer Science</i> , 2006, , 648-657.	1.0	14
34	PGxCorpus, a manually annotated corpus for pharmacogenomics. <i>Scientific Data</i> , 2020, 7, 3.	2.4	13
35	The Complete cDNA Sequence Encoding Dog Gastric Lipase:Short Communication. <i>DNA Sequence</i> , 1998, 8, 257-262.	0.7	12
36	A transgenic mouse model engineered to investigate human brain-derived neurotrophic factor in vivo. <i>Transgenic Research</i> , 2007, 16, 223-237.	1.3	12

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37	Discovering associations between adverse drug events using pattern structures and ontologies. <i>Journal of Biomedical Semantics</i> , 2017, 8, 29.	0.9	12
38	Sex differences in circulating proteins in heart failure with preserved ejection fraction. <i>Biology of Sex Differences</i> , 2020, 11, 47.	1.8	12
39	Chicken Tyrosine Hydroxylase Gene: Isolation and Functional Characterization of the 5' Flanking Region. <i>Journal of Neurochemistry</i> , 1993, 61, 2215-2224.	2.1	11
40	Comparison of Three Preprocessing Filters Efficiency in Virtual Screening: Identification of New Putative LXR β Regulators As a Test Case. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 701-715.	2.5	10
41	PPIDomainMiner: Inferring domain-domain interactions from multiple sources of protein-protein interactions. <i>PLoS Computational Biology</i> , 2021, 17, e1008844.	1.5	10
42	Regional assignment of 68 new human gene transcripts on chromosome 11.. <i>Genome Research</i> , 1995, 5, 60-70.	2.4	9
43	Low-Dose Alkylphenol Exposure Promotes Mammary Epithelium Alterations and Transgenerational Developmental Defects, But Does Not Enhance Tumorigenic Behavior of Breast Cancer Cells. <i>Frontiers in Endocrinology</i> , 2017, 8, 272.	1.5	9
44	SNP-Converter: An Ontology-Based Solution to Reconcile Heterogeneous SNP Descriptions for Pharmacogenomic Studies. <i>Lecture Notes in Computer Science</i> , 2006, , 82-93.	1.0	8
45	Cloning and mapping of 5' exons from the gene encoding chicken beta nerve growth factor. <i>Gene</i> , 1992, 116, 173-179.	1.0	7
46	Detailed transcript map of a 810-kb region at 11p14 involving identification of 10 novel human 3' exons. <i>European Journal of Human Genetics</i> , 1999, 7, 487-495.	1.4	7
47	Circulating plasma proteins and new-onset diabetes in a population-based study: proteomic and genomic insights from the STANISLAS cohort. <i>European Journal of Endocrinology</i> , 2020, 183, 285-295.	1.9	7
48	Characterization of tissue expression and full-length coding sequence of a novel human gene mapping at 3q12.1 and transcribed in oligodendrocytes. <i>Gene</i> , 2002, 289, 119-129.	1.0	6
49	Alternative usage of 5' exons in the chicken nerve growth factor gene: refined characterization of a weakly expressed gene. <i>Gene</i> , 2004, 334, 83-97.	1.0	6
50	Integrated Physical, Genetic, and Genic Map Covering 3 Mb Around the Human NGF Gene (NGFB) at 1p13. <i>Genomics</i> , 1996, 31, 80-89.	1.3	5
51	BioRegistry: A Structured Metadata Repository for Bioinformatic Databases. <i>Lecture Notes in Computer Science</i> , 2005, , 46-56.	1.0	5
52	A Structure-Based Classification and Analysis of Protein Domain Family Binding Sites and Their Interactions. <i>Biology</i> , 2015, 4, 327-343.	1.3	5
53	Insulin-like growth factor binding protein 2: A prognostic biomarker for heart failure hardly redundant with natriuretic peptides. <i>International Journal of Cardiology</i> , 2020, 300, 252-254.	0.8	5
54	Ontology-Based Knowledge Discovery in Pharmacogenomics. <i>Advances in Experimental Medicine and Biology</i> , 2011, 696, 357-366.	0.8	5

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55	Immunoselection and characterization of a human genomic PPAR binding fragment located within POTE genes. <i>Biochimie</i> , 2007, 89, 329-336.	1.3	4
56	BioRegistry: Automatic extraction of metadata for biological database retrieval and discovery. <i>International Journal of Metadata, Semantics and Ontologies</i> , 2010, 5, 184.	0.2	4
57	Functional classification of genes using semantic distance and fuzzy clustering approach: evaluation with reference sets and overlap analysis. <i>International Journal of Computational Biology and Drug Design</i> , 2012, 5, 245.	0.3	4
58	Classification and Exploration of 3D Protein Domain Interactions Using Kbdock. <i>Methods in Molecular Biology</i> , 2016, 1415, 91-105.	0.4	4
59	ECCB 2014: The 13th European Conference on Computational Biology. <i>Bioinformatics</i> , 2014, 30, i345-i348.	1.8	3
60	Computational discovery of direct associations between GO terms and protein domains. <i>BMC Bioinformatics</i> , 2018, 19, 413.	1.2	3
61	Treillis de concepts et ontologies pour interroger l'annuaire de sources de données biologiques BioRegistry. <i>Ingenierie Des Systemes D'Information</i> , 2006, 11, 39-60.	0.5	3
62	INCONSISTENCIES BETWEEN MAPS OF HUMAN CHROMOSOME 22 CORRELATE WITH INCREASED FREQUENCY OF DISEASE-RELATED LOCI. <i>Journal of Biological Systems</i> , 2002, 10, 303-317.	0.5	2
63	Modeling and minimizing CAPRI round 30 symmetrical protein complexes from CASP11 structural models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 463-469.	1.5	2
64	Steps towards causal Formal Concept Analysis. <i>International Journal of Approximate Reasoning</i> , 2022, 142, 338-348.	1.9	2
65	Fibre-fluorescence in situ hybridization directly performed from fresh biological samples: novel perspectives for genetic diagnosis. , 1998, 6, 501-503.		1
66	Ontology-based functional classification of genes: Evaluation with reference sets and overlap analysis. , 2011, , .		1
67	Associating Gene Ontology Terms with Pfam Protein Domains. <i>Lecture Notes in Computer Science</i> , 2017, , 127-138.	1.0	1
68	Extending Attribute Dependencies for Lattice-Based Querying and Navigation. <i>Lecture Notes in Computer Science</i> , 2008, , 189-202.	1.0	1
69	On the design of a similarity function for sparse binary data with application on protein function annotation. <i>Knowledge-Based Systems</i> , 2022, 238, 107863.	4.0	1
70	ILP Characterization of 3D Protein-Binding Sites and FCA-Based Interpretation. <i>Communications in Computer and Information Science</i> , 2013, , 84-100.	0.4	0
71	Mining Linked Open Data: A Case Study with Genes Responsible for Intellectual Disability. <i>Lecture Notes in Computer Science</i> , 2014, , 16-31.	1.0	0