Marie-Dominique Devignes

List of Publications by Year
in descending order

71 papers	2,789 citations	331670 21 h-index	189892 50 g-index
74 all docs	74 docs citations	74 times ranked	4413 citing authors

#	Article	IF	Citations
1	HexServer: an FFT-based protein docking server powered by graphics processors. Nucleic Acids Research, 2010, 38, W445-W449.	14.5	529
2	Application of Artificial Intelligence to Gastroenterology and Hepatology. Gastroenterology, 2020, 158, 76-94.e2.	1.3	335
3	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
4	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
5	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
6	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
7	Protein docking using caseâ€based reasoning. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2150-2158.	2.6	98
8	IntelliGO: a new vector-based semantic similarity measure including annotation origin. BMC Bioinformatics, 2010, 11, 588.	2.6	80
9	New Insights into the Classification and Integration Specificity of Streptococcus Integrative Conjugative Elements through Extensive Genome Exploration. Frontiers in Microbiology, 2015, 6, 1483.	3.5	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. Genome Research, 1999, 9, 1313-1320.	5.5	55
11	Activation of Peroxisome Proliferator-Activated Receptor Gamma by Human Cytomegalovirus for *De Novo* Replication Impairs Migration and Invasiveness of Cytotrophoblasts from Early Placentas. Journal of Virology, 2010, 84, 2946-2954.	3.4	55
12	The Genexpress IMAGE Knowledge Base of the Human Brain Transcriptome: A Prototype Integrated Resource for Functional and Computational Genomics. Genome Research, 1999, 9, 195-209.	5.5	52
13	Integrative relational machine-learning for understanding drug side-effect profiles. BMC Bioinformatics, 2013, 14, 207.	2.6	48
14	Codon context effect in virus translational readthrough A study in vitro of the determinants of TMV and Mo-MuLV amber suppression. FEBS Letters, 1992, 306, 133-139.	2.8	37
15	Spatial clustering of protein binding sites for template based protein docking. Bioinformatics, 2011, 27, 2820-2827.	4.1	36
16	A Glimpse into the World of Integrative and Mobilizable Elements in Streptococci Reveals an Unexpected Diversity and Novel Families of Mobilization Proteins. Frontiers in Microbiology, 2017, 8, 443.	3.5	33
17	KBDOCK 2013: a spatial classification of 3D protein domain family interactions. Nucleic Acids Research, 2014, 42, D389-D395.	14.5	31
18	Extended spectrum of MBD5 mutations in neurodevelopmental disorders. European Journal of Human Genetics, 2013, 21, 1457-1461.	2.8	30

#	ARTICLE	IF	CITATIONS
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). Biomarkers, 2020, 25, 201-211.	1.9	26
20	Prediction of Monomer Isomery in Florine: A Workflow Dedicated to Nonribosomal Peptide Discovery. PLoS ONE, 2014, 9, e85667.	2.5	25
21	The human semaphorin 6B gene is down regulated by PPARs. Genomics, 2004, 83, 1141-1150.	2.9	24
22	Rapid and high efficiency site-directed mutagenesis by improvement of the homologous recombination technique. Nucleic Acids Research, 1995, 23, 1642-1643.	14.5	23
23	ECDomainMiner: discovering hidden associations between enzyme commission numbers and Pfam domains. BMC Bioinformatics, 2017, 18, 107.	2.6	22
24	Gene–disease relationship discovery based on model-driven data integration and database view definition. Bioinformatics, 2009, 25, 230-236.	4.1	21
25	Extended persistence of antiphospholipid antibodies beyond the 12-week time interval: Association with baseline antiphospholipid antibodies titres. International Journal of Laboratory Hematology, 2019, 41, 726-730.	1.3	20
26	Plasma protein biomarkers and their association with mutually exclusive cardiovascular phenotypes: the FIBRO-TARGETS case–control analyses. Clinical Research in Cardiology, 2020, 109, 22-33.	3.3	19
27	Multiple-step virtual screening using VSM-G: overview and validation of fast geometrical matching enrichment. Journal of Molecular Modeling, 2008, 14, 135-148.	1.8	18
28	Characterization of a relaxase belonging to the MOBT family, a widespread family in Firmicutes mediating the transfer of ICEs. Mobile DNA, 2019, 10, 18.	3.6	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. Genomics, 1994, 24, 69-77.	2.9	16
30	Querying a Bioinformatic Data Sources Registry with Concept Lattices. Lecture Notes in Computer Science, 2005, , 323-336.	1.3	16
31	Screening of subtle copy number changes in Aicardi syndrome patients with a high resolution X chromosome array-CGH. European Journal of Medical Genetics, 2007, 50, 386-391.	1.3	16
32	Ontology-guided data preparation for discovering genotype-phenotype relationships. BMC Bioinformatics, 2008, 9, S3.	2.6	16
33	Suggested Ontology for Pharmacogenomics (SO-Pharm): Modular Construction and Preliminary Testing. Lecture Notes in Computer Science, 2006, , 648-657.	1.3	14
34	PGxCorpus, a manually annotated corpus for pharmacogenomics. Scientific Data, 2020, 7, 3.	5.3	13
35	The Complete cDNA Sequence Encoding Dog Gastric Lipase:Short Communication. DNA Sequence, 1998, 8, 257-262.	0.7	12
36	A transgenic mouse model engineered to investigate human brain-derived neurotrophic factor in vivo. Transgenic Research, 2007, 16, 223-237.	2.4	12

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37	Discovering associations between adverse drug events using pattern structures and ontologies. Journal of Biomedical Semantics, 2017, 8, 29.	1.6	12
38	Sex differences in circulating proteins in heart failure with preserved ejection fraction. Biology of Sex Differences, 2020, 11, 47.	4.1	12
39	Chicken Tyrosine Hydroxylase Gene: Isolation and Functional Characterization of the 5â€² Flanking Region. Journal of Neurochemistry, 1993, 61, 2215-2224.	3.9	11
40	Comparison of Three Preprocessing Filters Efficiency in Virtual Screening: Identification of New Putative LXRÎ² Regulators As a Test Case. Journal of Chemical Information and Modeling, 2010, 50, 701-715.	5.4	10
41	PPIDomainMiner: Inferring domain-domain interactions from multiple sources of protein-protein interactions. PLoS Computational Biology, 2021, 17, e1008844.	3.2	10
42	Regional assignment of 68 new human gene transcripts on chromosome 11.. Genome Research, 1995, 5, 60-70.	5.5	9
43	Low-Dose Alkylphenol Exposure Promotes Mammary Epithelium Alterations and Transgenerational Developmental Defects, But Does Not Enhance Tumorigenic Behavior of Breast Cancer Cells. Frontiers in Endocrinology, 2017, 8, 272.	3.5	9
44	SNP-Converter: An Ontology-Based Solution to Reconcile Heterogeneous SNP Descriptions for Pharmacogenomic Studies. Lecture Notes in Computer Science, 2006, , 82-93.	1.3	8
45	Cloning and mapping of 5â€² exons from the gene encoding chicken beta nerve growth factor. Gene, 1992, 116, 173-179.	2.2	7
46	Detailed transcript map of a 810-kb region at 11p14 involving identification of 10 novel human 3â€² exons. European Journal of Human Genetics, 1999, 7, 487-495.	2.8	7
47	Circulating plasma proteins and new-onset diabetes in a population-based study: proteomic and genomic insights from the STANISLAS cohort. European Journal of Endocrinology, 2020, 183, 285-295.	3.7	7
48	Characterization of tissue expression and full-length coding sequence of a novel human gene mapping at 3q12.1 and transcribed in oligodendrocytes. Gene, 2002, 289, 119-129.	2.2	6
49	Alternative usage of 5â€² exons in the chicken nerve growth factor gene: refined characterization of a weakly expressed gene. Gene, 2004, 334, 83-97.	2.2	6
50	Integrated Physical, Genetic, and Genic Map Covering 3 Mb Around the Human NGF Gene (NGFB) at 1p13. Genomics, 1996, 31, 80-89.	2.9	5
51	BioRegistry: A Structured Metadata Repository for Bioinformatic Databases. Lecture Notes in Computer Science, 2005, , 46-56.	1.3	5
52	A Structure-Based Classification and Analysis of Protein Domain Family Binding Sites and Their Interactions. Biology, 2015, 4, 327-343.	2.8	5
53	Insulin-like growth factor binding protein 2: A prognostic biomarker for heart failure hardly redundant with natriuretic peptides. International Journal of Cardiology, 2020, 300, 252-254.	1.7	5
54	Ontology-Based Knowledge Discovery in Pharmacogenomics. Advances in Experimental Medicine and Biology, 2011, 696, 357-366.	1.6	5

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55	Immunoselection and characterization of a human genomic PPAR binding fragment located within POTE genes. Biochimie, 2007, 89, 329-336.	2.6	4
56	BioRegistry: Automatic extraction of metadata for biological database retrieval and discovery. International Journal of Metadata, Semantics and Ontologies, 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. International Journal of Computational Biology and Drug Design, 2012, 5, 245.	0.3	4
58	Classification and Exploration of 3D Protein Domain Interactions Using Kbdock. Methods in Molecular Biology, 2016, 1415, 91-105.	0.9	4
59	ECCB 2014: The 13th European Conference on Computational Biology. Bioinformatics, 2014, 30, i345-i348.	4.1	3
60	Computational discovery of direct associations between GO terms and protein domains. BMC Bioinformatics, 2018, 19, 413.	2.6	3
61	Treillis de concepts et ontologies pour interroger l'annuaire de sources de donnÃ©es biologiques BioRegistry. Ingenierie Des Systemes D'Information, 2006, 11, 39-60.	0.7	3
62	INCONSISTENCIES BETWEEN MAPS OF HUMAN CHROMOSOME 22 CORRELATE WITH INCREASED FREQUENCY OF DISEASE-RELATED LOCI. Journal of Biological Systems, 2002, 10, 303-317.	1.4	2
63	Modeling and minimizing CAPRI round 30 symmetrical protein complexes from CASPâ€‘11 structural models. Proteins: Structure, Function and Bioinformatics, 2017, 85, 463-469.	2.6	2
64	Steps towards causal Formal Concept Analysis. International Journal of Approximate Reasoning, 2022, 142, 338-348.	3.3	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. Lecture Notes in Computer Science, 2017, , 127-138.	1.3	1
68	Extending Attribute Dependencies for Lattice-Based Querying and Navigation. Lecture Notes in Computer Science, 2008, , 189-202.	1.3	1
69	On the design of a similarity function for sparse binary data with application on protein function annotation. Knowledge-Based Systems, 2022, 238, 107863.	7.1	1
70	ILP Characterization of 3D Protein-Binding Sites and FCA-Based Interpretation. Communications in Computer and Information Science, 2013, , 84-100.	0.5	0
71	Mining Linked Open Data: A Case Study with Genes Responsible for Intellectual Disability. Lecture Notes in Computer Science, 2014, , 16-31.	1.3	0