

# Marie-Dominique Devignes

## List of Publications by Year in descending order

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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	On the design of a similarity function for sparse binary data with application on protein function annotation. Knowledge-Based Systems, 2022, 238, 107863.	4.0	1
2	Steps towards causal Formal Concept Analysis. International Journal of Approximate Reasoning, 2022, 142, 338-348.	1.9	2
3	PPIDomainMiner: Inferring domain-domain interactions from multiple sources of protein-protein interactions. PLoS Computational Biology, 2021, 17, e1008844.	1.5	10
4	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.	1.5	19
5	Application of Artificial Intelligence to Gastroenterology and Hepatology. Gastroenterology, 2020, 158, 76-94.e2.	0.6	335
6	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.	0.8	5
7	PGxCorpus, a manually annotated corpus for pharmacogenomics. Scientific Data, 2020, 7, 3.	2.4	13
8	Sex differences in circulating proteins in heart failure with preserved ejection fraction. Biology of Sex Differences, 2020, 11, 47.	1.8	12
9	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.	0.9	26
10	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.	1.9	7
11	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
12	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.	0.7	20
13	Characterization of a relaxase belonging to the MOB family, a widespread family in Firmicutes mediating the transfer of ICEs. Mobile DNA, 2019, 10, 18.	1.3	17
14	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
15	Computational discovery of direct associations between GO terms and protein domains. BMC Bioinformatics, 2018, 19, 413.	1.2	3
16	ECDomainMiner: discovering hidden associations between enzyme commission numbers and Pfam domains. BMC Bioinformatics, 2017, 18, 107.	1.2	22
17	Associating Gene Ontology Terms with Pfam Protein Domains. Lecture Notes in Computer Science, 2017, , 127-138.	1.0	1
18	Modeling and minimizing CAPRI round 30 symmetrical protein complexes from CASP11 structural models. Proteins: Structure, Function and Bioinformatics, 2017, 85, 463-469.	1.5	2

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19	Discovering associations between adverse drug events using pattern structures and ontologies. <i>Journal of Biomedical Semantics</i> , 2017, 8, 29.	0.9	12
20	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
21	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
22	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
23	Classification and Exploration of 3D Protein Domain Interactions Using Kbdock. <i>Methods in Molecular Biology</i> , 2016, 1415, 91-105.	0.4	4
24	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
25	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
26	Prediction of Monomer Isomery in Florine: A Workflow Dedicated to Nonribosomal Peptide Discovery. <i>PLoS ONE</i> , 2014, 9, e85667.	1.1	25
27	ECCB 2014: The 13th European Conference on Computational Biology. <i>Bioinformatics</i> , 2014, 30, i345-i348.	1.8	3
28	KBDOCK 2013: a spatial classification of 3D protein domain family interactions. <i>Nucleic Acids Research</i> , 2014, 42, D389-D395.	6.5	31
29	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
30	Integrative relational machine-learning for understanding drug side-effect profiles. <i>BMC Bioinformatics</i> , 2013, 14, 207.	1.2	48
31	Protein docking using case-based reasoning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2150-2158.	1.5	98
32	Extended spectrum of MBD5 mutations in neurodevelopmental disorders. <i>European Journal of Human Genetics</i> , 2013, 21, 1457-1461.	1.4	30
33	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
34	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
35	Ontology-based functional classification of genes: Evaluation with reference sets and overlap analysis. , 2011, , .		1
36	Spatial clustering of protein binding sites for template based protein docking. <i>Bioinformatics</i> , 2011, 27, 2820-2827.	1.8	36

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37	Ontology-Based Knowledge Discovery in Pharmacogenomics. <i>Advances in Experimental Medicine and Biology</i> , 2011, 696, 357-366.	0.8	5
38	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
39	IntelliGO: a new vector-based semantic similarity measure including annotation origin. <i>BMC Bioinformatics</i> , 2010, 11, 588.	1.2	80
40	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
41	Comparison of Three Preprocessing Filters Efficiency in Virtual Screening: Identification of New Putative LXRI <sup>2</sup> Regulators As a Test Case. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 701-715.	2.5	10
42	HexServer: an FFT-based protein docking server powered by graphics processors. <i>Nucleic Acids Research</i> , 2010, 38, W445-W449.	6.5	529
43	Gene-disease relationship discovery based on model-driven data integration and database view definition. <i>Bioinformatics</i> , 2009, 25, 230-236.	1.8	21
44	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
45	Ontology-guided data preparation for discovering genotype-phenotype relationships. <i>BMC Bioinformatics</i> , 2008, 9, S3.	1.2	16
46	Extending Attribute Dependencies for Lattice-Based Querying and Navigation. <i>Lecture Notes in Computer Science</i> , 2008, , 189-202.	1.0	1
47	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
48	Immunoselection and characterization of a human genomic PPAR binding fragment located within POTE genes. <i>Biochimie</i> , 2007, 89, 329-336.	1.3	4
49	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
50	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
51	Suggested Ontology for Pharmacogenomics (SO-Pharm): Modular Construction and Preliminary Testing. <i>Lecture Notes in Computer Science</i> , 2006, , 648-657.	1.0	14
52	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
53	Querying a Bioinformatic Data Sources Registry with Concept Lattices. <i>Lecture Notes in Computer Science</i> , 2005, , 323-336.	1.0	16
54	BioRegistry: A Structured Metadata Repository for Bioinformatic Databases. <i>Lecture Notes in Computer Science</i> , 2005, , 46-56.	1.0	5

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55	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
56	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
57	The human semaphorin 6B gene is down regulated by PPARs. <i>Genomics</i> , 2004, 83, 1141-1150.	1.3	24
58	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
59	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
60	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
61	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
62	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
63	Fibre-fluorescence in situ hybridization directly performed from fresh biological samples: novel perspectives for genetic diagnosis. , 1998, 6, 501-503.		1
64	The Complete cDNA Sequence Encoding Dog Gastric Lipase:Short Communication. <i>DNA Sequence</i> , 1998, 8, 257-262.	0.7	12
65	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
66	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
67	Regional assignment of 68 new human gene transcripts on chromosome 11.. <i>Genome Research</i> , 1995, 5, 60-70.	2.4	9
68	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
69	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
70	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
71	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