

Mario Albrecht

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3881784/publications.pdf>

Version: 2024-02-01

89
papers

12,396
citations

44042

48
h-index

48277

88
g-index

92
all docs

92
docs citations

92
times ranked

19049
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide association scan of nonsynonymous SNPs identifies a susceptibility variant for Crohn disease in ATG16L1. <i>Nature Genetics</i> , 2007, 39, 207-211.	9.4	1,712
2	Computing topological parameters of biological networks. <i>Bioinformatics</i> , 2008, 24, 282-284.	1.8	1,601
3	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. <i>Nature Genetics</i> , 2008, 40, 1319-1323.	9.4	534
4	Sarcoidosis is associated with a truncating splice site mutation in BTNL2. <i>Nature Genetics</i> , 2005, 37, 357-364.	9.4	451
5	Topological analysis and interactive visualization of biological networks and protein structures. <i>Nature Protocols</i> , 2012, 7, 670-685.	5.5	445
6	Genetic variation in DLC5 is associated with inflammatory bowel disease. <i>Nature Genetics</i> , 2004, 36, 476-480.	9.4	443
7	Recruitment and Activation of a Lipid Kinase by Hepatitis C Virus NS5A Is Essential for Integrity of the Membranous Replication Compartment. <i>Cell Host and Microbe</i> , 2011, 9, 32-45.	5.1	435
8	Resistance proteins: molecular switches of plant defence. <i>Current Opinion in Plant Biology</i> , 2006, 9, 383-390.	3.5	360
9	Structure-function analysis of the NB-ARC domain of plant disease resistance proteins. <i>Journal of Experimental Botany</i> , 2008, 59, 1383-1397.	2.4	358
10	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. <i>Nature Genetics</i> , 2013, 45, 670-675.	9.4	339
11	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. <i>Nature Genetics</i> , 2010, 42, 991-995.	9.4	331
12	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , 2010, 38, W755-W762.	6.5	310
13	Genetics of Crohn disease, an archetypal inflammatory barrier disease. <i>Nature Reviews Genetics</i> , 2005, 6, 376-388.	7.7	290
14	Mutations in the NB-ARC Domain of I-2 That Impair ATP Hydrolysis Cause Autoactivation. <i>Plant Physiology</i> , 2006, 140, 1233-1245.	2.3	276
15	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274
16	Analyzing and visualizing residue networks of protein structures. <i>Trends in Biochemical Sciences</i> , 2011, 36, 179-182.	3.7	244
17	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	3.3	206
18	Dissection of the Inflammatory Bowel Disease Transcriptome Using Genome-Wide cDNA Microarrays. <i>PLoS Medicine</i> , 2005, 2, e199.	3.9	179

#	ARTICLE	IF	CITATIONS
19	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). <i>Nature Genetics</i> , 2010, 42, 292-294.	9.4	177
20	Variants in a Novel Epidermal Collagen Gene (COL29A1) Are Associated with Atopic Dermatitis. <i>PLoS Biology</i> , 2007, 5, e242.	2.6	153
21	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. <i>Gastroenterology</i> , 2013, 145, 339-347.	0.6	149
22	An arginine/lysine-rich motif is crucial for VCP/p97-mediated modulation of ataxin-3 fibrillogenesis. <i>EMBO Journal</i> , 2006, 25, 1547-1558.	3.5	142
23	Specificity of Linear Motifs That Bind to a Common Mitogen-Activated Protein Kinase Docking Groove. <i>Science Signaling</i> , 2012, 5, ra74.	1.6	140
24	An Integrative Approach to Gain Insights into the Cellular Function of Human Ataxin-2. <i>Journal of Molecular Biology</i> , 2005, 346, 203-214.	2.0	132
25	Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. <i>PLoS ONE</i> , 2007, 2, e691.	1.1	123
26	Structural and functional analysis of ataxin-2 and ataxin-3. <i>FEBS Journal</i> , 2004, 271, 3155-3170.	0.2	118
27	Improving disease gene prioritization using the semantic similarity of Gene Ontology terms. <i>Bioinformatics</i> , 2010, 26, i561-i567.	1.8	104
28	Diversity and functional plasticity of eukaryotic selenoproteins: Identification and characterization of the SelJ family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16188-16193.	3.3	94
29	Ataxin-2 and huntingtin interact with endophilin-A complexes to function in plastin-associated pathways. <i>Human Molecular Genetics</i> , 2005, 14, 2893-2909.	1.4	93
30	Survey on the PABC recognition motif PAM2. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 129-138.	1.0	87
31	Integrating biological data into the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008, 9, S3.	1.2	87
32	A FYVE zinc finger domain protein specifically links mRNA transport to endosome trafficking. <i>ELife</i> , 2015, 4, .	2.8	86
33	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , 2010, 7, 419-420.	9.0	84
34	Deciphering the Molecular Profile of Plaques, Memory Decline and Neuron Loss in Two Mouse Models for Alzheimer's Disease by Deep Sequencing. <i>Frontiers in Aging Neuroscience</i> , 2014, 6, 75.	1.7	78
35	Novel Sm-like proteins with long C-terminal tails and associated methyltransferases. <i>FEBS Letters</i> , 2004, 569, 18-26.	1.3	76
36	Intragenic allele pyramiding combines different specificities of wheat Pm3 resistance alleles. <i>Plant Journal</i> , 2010, 64, 433-445.	2.8	76

#	ARTICLE	IF	CITATIONS
37	Molecular basis of telaprevir resistance due to V36 and T54 mutations in the NS3-4A protease of the hepatitis C virus. <i>Genome Biology</i> , 2008, 9, R16.	13.9	74
38	A new CARD15 mutation in Blau syndrome. <i>European Journal of Human Genetics</i> , 2005, 13, 742-747.	1.4	72
39	The HIN domain of IFI-200 proteins consists of two OB folds. <i>Biochemical and Biophysical Research Communications</i> , 2005, 327, 679-687.	1.0	71
40	FunSimMat: a comprehensive functional similarity database. <i>Nucleic Acids Research</i> , 2007, 36, D434-D439.	6.5	70
41	Computational analysis of human protein interaction networks. <i>Proteomics</i> , 2007, 7, 2541-2552.	1.3	70
42	Transcomplementation, but not Physical Association of the CC-NB-ARC and LRR Domains of Tomato R Protein Mi-1.2 is Altered by Mutations in the ARC2 Subdomain. <i>Molecular Plant</i> , 2008, 1, 401-410.	3.9	67
43	Simple consensus procedures are effective and sufficient in secondary structure prediction. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 459-462.	1.0	63
44	Update on the domain architectures of NLRs and R proteins. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 459-462.	1.0	62
45	Mutations in the MutS \pm interaction interface of MLH1 can abolish DNA mismatch repair. <i>Nucleic Acids Research</i> , 2006, 34, 6574-6586.	6.5	61
46	Recent approaches to the prioritization of candidate disease genes. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 429-442.	6.6	59
47	Identification of HNRNPK as Regulator of Hepatitis C Virus Particle Production. <i>PLoS Pathogens</i> , 2015, 11, e1004573.	2.1	56
48	Identification of PatL1, a human homolog to yeast P body component Pat1. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2007, 1773, 1786-1792.	1.9	54
49	Characterization of the EGFR interactome reveals associated protein complex networks and intracellular receptor dynamics. <i>Proteomics</i> , 2013, 13, 3131-3144.	1.3	54
50	Structural localization of disease-associated sequence variations in the NACHT and LRR domains of PYPAF1 and NOD2. <i>FEBS Letters</i> , 2003, 554, 520-528.	1.3	50
51	Comprehensive cluster analysis with Transitivity Clustering. <i>Nature Protocols</i> , 2011, 6, 285-295.	5.5	47
52	Functional evaluation of domain domain interactions and human protein interaction networks. <i>Bioinformatics</i> , 2007, 23, 859-865.	1.8	41
53	Abundant Genetic Overlap between Blood Lipids and Immune-Mediated Diseases Indicates Shared Molecular Genetic Mechanisms. <i>PLoS ONE</i> , 2015, 10, e0123057.	1.1	40
54	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. <i>PLoS ONE</i> , 2013, 8, e78648.	1.1	38

#	ARTICLE	IF	CITATIONS
55	NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. <i>Bioinformatics</i> , 2013, 29, 1471-1473.	1.8	35
56	Mining GO Annotations for Improving Annotation Consistency. <i>PLoS ONE</i> , 2012, 7, e40519.	1.1	33
57	Structural modeling of ataxin-3 reveals distant homology to adaptins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 50, 355-370.	1.5	31
58	Tissue-Specific Proteins and Functional Implications. <i>Journal of Proteome Research</i> , 2011, 10, 1893-1903.	1.8	31
59	CytoGEDEVO – global alignment of biological networks with Cytoscape. <i>Bioinformatics</i> , 2016, 32, 1259-1261.	1.8	31
60	Structural and functional comparison of the non-structural protein 4B in flaviviridae. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 546-557.	1.3	29
61	FunSimMat update: new features for exploring functional similarity. <i>Nucleic Acids Research</i> , 2010, 38, D244-D248.	6.5	25
62	Pyranose oxidase identified as a member of the GMC oxidoreductase family. <i>Bioinformatics</i> , 2003, 19, 1216-1220.	1.8	24
63	A Network-based Analysis of Polyanion-binding Proteins Utilizing Human Protein Arrays. <i>Journal of Biological Chemistry</i> , 2007, 282, 10153-10163.	1.6	24
64	Disease-associated variants in PYPAF1 and NOD2 result in similar alterations of conserved sequence. <i>Bioinformatics</i> , 2003, 19, 2171-2175.	1.8	22
65	Clinical Significance of In Vitro Replication – Enhancing Mutations of the Hepatitis C Virus (HCV) Replicon in Patients with Chronic HCV Infection. <i>Journal of Infectious Diseases</i> , 2005, 192, 1710-1719.	1.9	21
66	GOTax: investigating biological processes and biochemical activities along the taxonomic tree. <i>Genome Biology</i> , 2007, 8, R33.	13.9	20
67	Decomposing protein networks into domain-domain interactions. <i>Bioinformatics</i> , 2005, 21, ii220-ii221.	1.8	19
68	Color blindness. <i>Nature Methods</i> , 2010, 7, 775-775.	9.0	17
69	Inferring Physical Protein Contacts from Large-Scale Purification Data of Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004929.	2.5	16
70	Structural and functional analysis of a novel mutation of CYP21B in a heterozygote carrier of 21-hydroxylase deficiency. <i>Human Genetics</i> , 2005, 117, 558-564.	1.8	15
71	A Network-based Analysis of Polyanion-binding Proteins Utilizing Yeast Protein Arrays. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2263-2278.	2.5	15
72	An integrative approach for predicting interactions of protein regions. <i>Bioinformatics</i> , 2008, 24, i35-i41.	1.8	15

#	ARTICLE	IF	CITATIONS
73	DASMI: exchanging, annotating and assessing molecular interaction data. <i>Bioinformatics</i> , 2009, 25, 1321-1328.	1.8	15
74	setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149.	0.8	14
75	Finding scaffold proteins in interactomes. <i>Trends in Cell Biology</i> , 2010, 20, 2-4.	3.6	13
76	Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014, 8, S2.	1.8	13
77	Dimerization of the hepatitis C virus nonstructural protein 4B depends on the integrity of an aminoterminal basic leucine zipper. <i>Protein Science</i> , 2010, 19, 1327-1336.	3.1	11
78	Identification of mammalian orthologs associates PYPAF5 with distinct functional roles. <i>FEBS Letters</i> , 2003, 538, 173-177.	1.3	10
79	Novel search method for the discovery of functional relationships. <i>Bioinformatics</i> , 2012, 28, 269-276.	1.8	10
80	Integrating expression data with domain interaction networks. <i>Bioinformatics</i> , 2008, 24, 2546-2548.	1.8	9
81	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149.	0.8	8
82	Structure Collisions between Interacting Proteins. <i>PLoS ONE</i> , 2011, 6, e19581.	1.1	3
83	Near-Neighbor Interactions in the NS3-4A Protease of HCV Impact Replicative Fitness of Drug-Resistant Viral Variants. <i>Journal of Molecular Biology</i> , 2019, 431, 2354-2368.	2.0	3
84	DASMIweb: online integration, analysis and assessment of distributed protein interaction data. <i>Nucleic Acids Research</i> , 2009, 37, W122-W128.	6.5	2
85	Integrative visual analysis of the effects of alternative splicing on protein domain interaction networks. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	2
86	Visualizing Domain Interaction Networks and the Impact of Alternative Splicing Events. , 2008, , .		1
87	Integrative Visual Analysis of the Effects of Alternative Splicing on Protein Domain Interaction Networks. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	1
88	Functional Characterization of Human Genes from Exon Expression and RNA Interference Results. <i>Methods in Molecular Biology</i> , 2012, 910, 33-53.	0.4	0
89	PSIScore (Quality Scoring of Protein Interactions). , 2013, , 1801-1802.		0