

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 | 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 |
| 2 | CytoGEDEVO – global alignment of biological networks with Cytoscape. <i>Bioinformatics</i> , 2016, 32, 1259-1261. | 1.8 | 31 |
| 3 | Identification of HNRNPK as Regulator of Hepatitis C Virus Particle Production. <i>PLoS Pathogens</i> , 2015, 11, e1004573. | 2.1 | 56 |
| 4 | 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 |
| 5 | A FYVE zinc finger domain protein specifically links mRNA transport to endosome trafficking. <i>ELife</i> , 2015, 4, . | 2.8 | 86 |
| 6 | 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 |
| 7 | Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014, 8, S2. | 1.8 | 13 |
| 8 | setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149. | 0.8 | 14 |
| 9 | setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014, 3, 149. | 0.8 | 8 |
| 10 | Characterization of the EGFR interactome reveals associated protein complex networks and intracellular receptor dynamics. <i>Proteomics</i> , 2013, 13, 3131-3144. | 1.3 | 54 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. <i>PLoS ONE</i> , 2013, 8, e78648. | 1.1 | 38 |
| 15 | PSISCORE (Quality Scoring of Protein Interactions)., 2013, , 1801-1802. | | 0 |
| 16 | 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 |
| 17 | Novel search method for the discovery of functional relationships. <i>Bioinformatics</i> , 2012, 28, 269-276. | 1.8 | 10 |
| 18 | Topological analysis and interactive visualization of biological networks and protein structures. <i>Nature Protocols</i> , 2012, 7, 670-685. | 5.5 | 445 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | 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 |
| 20 | Mining GO Annotations for Improving Annotation Consistency. <i>PLoS ONE</i> , 2012, 7, e40519. | 1.1 | 33 |
| 21 | 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 |
| 22 | Tissue-Specific Proteins and Functional Implications. <i>Journal of Proteome Research</i> , 2011, 10, 1893-1903. | 1.8 | 31 |
| 23 | PSICQUIC and PSIScore: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529. | 9.0 | 274 |
| 24 | 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 |
| 25 | Structure Collisions between Interacting Proteins. <i>PLoS ONE</i> , 2011, 6, e19581. | 1.1 | 3 |
| 26 | Comprehensive cluster analysis with Transitivity Clustering. <i>Nature Protocols</i> , 2011, 6, 285-295. | 5.5 | 47 |
| 27 | Analyzing and visualizing residue networks of protein structures. <i>Trends in Biochemical Sciences</i> , 2011, 36, 179-182. | 3.7 | 244 |
| 28 | 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 |
| 29 | Finding scaffold proteins in interactomes. <i>Trends in Cell Biology</i> , 2010, 20, 2-4. | 3.6 | 13 |
| 30 | 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 |
| 31 | Intragenic allele pyramiding combines different specificities of wheat Pm3 resistance alleles. <i>Plant Journal</i> , 2010, 64, 433-445. | 2.8 | 76 |
| 32 | 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 |
| 33 | Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. <i>Nature Genetics</i> , 2010, 42, 991-995. | 9.4 | 331 |
| 34 | Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , 2010, 7, 419-420. | 9.0 | 84 |
| 35 | Color blindness. <i>Nature Methods</i> , 2010, 7, 775-775. | 9.0 | 17 |
| 36 | Improving disease gene prioritization using the semantic similarity of Gene Ontology terms. <i>Bioinformatics</i> , 2010, 26, i561-i567. | 1.8 | 104 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | FunSimMat update: new features for exploring functional similarity. <i>Nucleic Acids Research</i> , 2010, 38, D244-D248. | 6.5 | 25 |
| 38 | AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , 2010, 38, W755-W762. | 6.5 | 310 |
| 39 | DASMI: exchanging, annotating and assessing molecular interaction data. <i>Bioinformatics</i> , 2009, 25, 1321-1328. | 1.8 | 15 |
| 40 | DASMIweb: online integration, analysis and assessment of distributed protein interaction data. <i>Nucleic Acids Research</i> , 2009, 37, W122-W128. | 6.5 | 2 |
| 41 | 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 |
| 42 | Integrating biological data â€” the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008, 9, S3. | 1.2 | 87 |
| 43 | 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 |
| 44 | 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 |
| 45 | Visualizing Domain Interaction Networks and the Impact of Alternative Splicing Events. , 2008, , . | | 1 |
| 46 | Computing topological parameters of biological networks. <i>Bioinformatics</i> , 2008, 24, 282-284. | 1.8 | 1,601 |
| 47 | An integrative approach for predicting interactions of protein regions. <i>Bioinformatics</i> , 2008, 24, i35-i41. | 1.8 | 15 |
| 48 | Structureâ€™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 |
| 49 | Integrating expression data with domain interaction networks. <i>Bioinformatics</i> , 2008, 24, 2546-2548. | 1.8 | 9 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | FunSimMat: a comprehensive functional similarity database. <i>Nucleic Acids Research</i> , 2007, 36, D434-D439. | 6.5 | 70 |
| 54 | Variants in a Novel Epidermal Collagen Gene (COL29A1) Are Associated with Atopic Dermatitis. <i>PLoS Biology</i> , 2007, 5, e242. | 2.6 | 153 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 55 | Functional evaluation of domain domain interactions and human protein interaction networks. <i>Bioinformatics</i> , 2007, 23, 859-865. | 1.8 | 41 |
| 56 | 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 |
| 57 | GOTax: investigating biological processes and biochemical activities along the taxonomic tree. <i>Genome Biology</i> , 2007, 8, R33. | 13.9 | 20 |
| 58 | Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. <i>PLoS ONE</i> , 2007, 2, e691. | 1.1 | 123 |
| 59 | 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 |
| 60 | Computational analysis of human protein interaction networks. <i>Proteomics</i> , 2007, 7, 2541-2552. | 1.3 | 70 |
| 61 | 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 |
| 62 | 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 |
| 63 | Update on the domain architectures of NLRs and R proteins. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 459-462. | 1.0 | 62 |
| 64 | 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 |
| 65 | Resistance proteins: molecular switches of plant defence. <i>Current Opinion in Plant Biology</i> , 2006, 9, 383-390. | 3.5 | 360 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | Sarcoidosis is associated with a truncating splice site mutation in BTNL2. <i>Nature Genetics</i> , 2005, 37, 357-364. | 9.4 | 451 |
| 70 | Genetics of Crohn disease, an archetypal inflammatory barrier disease. <i>Nature Reviews Genetics</i> , 2005, 6, 376-388. | 7.7 | 290 |
| 71 | A new CARD15 mutation in Blau syndrome. <i>European Journal of Human Genetics</i> , 2005, 13, 742-747. | 1.4 | 72 |
| 72 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 73 | Dissection of the Inflammatory Bowel Disease Transcriptome Using Genome-Wide cDNA Microarrays. PLoS Medicine, 2005, 2, e199. | 3.9 | 179 |
| 74 | Decomposing protein networks into domain-domain interactions. Bioinformatics, 2005, 21, ii220-ii221. | 1.8 | 19 |
| 75 | Diversity and functional plasticity of eukaryotic selenoproteins: Identification and characterization of the SelJ family. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16188-16193. | 3.3 | 94 |
| 76 | Ataxin-2 and huntingtin interact with endophilin-A complexes to function in plastin-associated pathways. Human Molecular Genetics, 2005, 14, 2893-2909. | 1.4 | 93 |
| 77 | Clinical Significance of In Vitro Replication-Enhancing Mutations of the Hepatitis C Virus (HCV) Replicon in Patients with Chronic HCV Infection. Journal of Infectious Diseases, 2005, 192, 1710-1719. | 1.9 | 21 |
| 78 | An Integrative Approach to Gain Insights into the Cellular Function of Human Ataxin-2. Journal of Molecular Biology, 2005, 346, 203-214. | 2.0 | 132 |
| 79 | The HIN domain of IFI-200 proteins consists of two OB folds. Biochemical and Biophysical Research Communications, 2005, 327, 679-687. | 1.0 | 71 |
| 80 | Structural and functional analysis of ataxin-2 and ataxin-3. FEBS Journal, 2004, 271, 3155-3170. | 0.2 | 118 |
| 81 | Genetic variation in DLG5 is associated with inflammatory bowel disease. Nature Genetics, 2004, 36, 476-480. | 9.4 | 443 |
| 82 | Novel Sm-like proteins with long C-terminal tails and associated methyltransferases. FEBS Letters, 2004, 569, 18-26. | 1.3 | 76 |
| 83 | Survey on the PABC recognition motif PAM2. Biochemical and Biophysical Research Communications, 2004, 316, 129-138. | 1.0 | 87 |
| 84 | Identification of mammalian orthologs associates PYPAF5 with distinct functional roles. FEBS Letters, 2003, 538, 173-177. | 1.3 | 10 |
| 85 | Structural localization of disease-associated sequence variations in the NACHT and LRR domains of PYPAF1 and NOD2. FEBS Letters, 2003, 554, 520-528. | 1.3 | 50 |
| 86 | Simple consensus procedures are effective and sufficient in secondary structure prediction. Protein Engineering, Design and Selection, 2003, 16, 459-462. | 1.0 | 63 |
| 87 | Disease-associated variants in PYPAF1 and NOD2 result in similar alterations of conserved sequence. Bioinformatics, 2003, 19, 2171-2175. | 1.8 | 22 |
| 88 | Pyranose oxidase identified as a member of the GMC oxidoreductase family. Bioinformatics, 2003, 19, 1216-1220. | 1.8 | 24 |
| 89 | Structural modeling of ataxin-3 reveals distant homology to adaptins. Proteins: Structure, Function and Bioinformatics, 2002, 50, 355-370. | 1.5 | 31 |