Martijn A Huynen

List of Publications by Year in descending order

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234 papers	23,117 citations	9428 76 h-index	11282 141 g-index
253 all docs	253 docs citations	253 times ranked	30856 citing authors

#	Article	IF	Citations
1	Mitochondrial <scp>RNA</scp> processing defect caused by a <scp>SUPV3L1</scp> mutation in two siblings with a novel neurodegenerative syndrome. Journal of Inherited Metabolic Disease, 2022, 45, 292-307.	1.7	6
2	BCG-induced trained immunity enhances acellular pertussis vaccination responses in an explorative randomized clinical trial. Npj Vaccines, 2022, 7, 21.	2.9	5
3	Mitochondrial complex complexification. Science, 2022, 376, 794-795.	6.0	5
4	Targeted RNA next generation sequencing analysis of cervical smears can predict the presence of hrHPV-induced cervical lesions. BMC Medicine, 2022, 20, .	2.3	3
5	Novel insights from the Plasmodium falciparum sporozoite-specific proteome by probabilistic integration of 26 studies. PLoS Computational Biology, 2021, 17, e1008067.	1.5	6
6	Genome-wide analysis in Escherichia coli unravels a high level of genetic homoplasy associated with cefotaxime resistance. Microbial Genomics, 2021, 7, .	1.0	5
7	Stimulation of cholesterol biosynthesis in mitochondrial complex I-deficiency lowers reductive stress and improves motor function and survival in mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166062.	1.8	7
8	Composition and stage dynamics of mitochondrial complexes in Plasmodium falciparum. Nature Communications, 2021, 12, 3820.	5.8	54
9	CEDAR, an online resource for the reporting and exploration of complexome profiling data. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148411.	0.5	27
10	Differences in the number of de novo mutations between individuals are due to small family-specific effects and stochasticity. Genome Research, 2021, 31, 1513-1518.	2.4	6
11	Monoclonal antibodies block transmission of genetically diverse Plasmodium falciparum strains to mosquitoes. Npj Vaccines, 2021, 6, 101.	2.9	24
12	A Prioritized and Validated Resource of Mitochondrial Proteins in Plasmodium Identifies Unique Biology. MSphere, 2021, 6, e0061421.	1.3	16
13	Invisible leashes: The tethering VAPs from infectious diseases to neurodegeneration. Journal of Biological Chemistry, 2021, 296, 100421.	1.6	14
14	Chemokine profiling in children and adults with symptomatic and asymptomatic respiratory viral infections. Journal of Infection, 2021, 83, 709-737.	1.7	1
15	Novel high-resolution targeted sequencing of the cervicovaginal microbiome. BMC Biology, 2021, 19, 267.	1.7	11
16	RNA-based high-risk HPV genotyping and identification of high-risk HPV transcriptional activity in cervical tissues. Modern Pathology, 2020, 33, 748-757.	2.9	11
17	Diabetes is associated with genotypically drug-resistant tuberculosis. European Respiratory Journal, 2020, 55, 1901891.	3.1	13
18	Uncovering Distinct Primary Vaccination-Dependent Profiles in Human Bordetella pertussis Specific CD4+ T-Cell Responses Using a Novel Whole Blood Assay. Vaccines, 2020, 8, 225.	2.1	11

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19	Surveillance-embedded genomic outbreak resolution of methicillin-susceptible Staphylococcus aureus in a neonatal intensive care unit. Scientific Reports, 2020, 10, 2619.	1.6	15
20	Metabolic models predict bacterial passengers in colorectal cancer. Cancer & Metabolism, 2020, 8, 3.	2.4	28
21	TMEM70 functions in the assembly of complexes I and V. Biochimica Et Biophysica Acta - Bioenergetics, 2020, 1861, 148202.	0.5	31
22	Isocitrate dehydrogenase 1â€“mutated human gliomas depend on lactate and glutamate to alleviate metabolic stress. FASEB Journal, 2019, 33, 557-571.	0.2	33
23	A Combined Mass Spectrometry and Data Integration Approach to Predict the Mitochondrial Poly(A) RNA Interacting Proteome. Frontiers in Cell and Developmental Biology, 2019, 7, 283.	1.8	2
24	The Tudor protein Veneno assembles the ping-pong amplification complex that produces viral piRNAs in Aedes mosquitoes. Nucleic Acids Research, 2019, 47, 2546-2559.	6.5	35
25	Use of whole-genome sequencing to predict Mycobacterium tuberculosis drug resistance in Indonesia. Journal of Global Antimicrobial Resistance, 2019, 16, 170-177.	0.9	13
26	COmplexome Profiling ALignment (COPAL) reveals remodeling of mitochondrial protein complexes in Barth syndrome. Bioinformatics, 2019, 35, 3083-3091.	1.8	37
27	CiliaCarta: An integrated and validated compendium of ciliary genes. PLoS ONE, 2019, 14, e0216705.	1.1	104
28	Allele-specific RNA-seq expression profiling of imprinted genes in mouse isogenic pluripotent states. Epigenetics and Chromatin, 2019, 12, 14.	1.8	11
29	Molecular Profiling of Druggable Targets in Clear Cell Renal Cell Carcinoma Through Targeted RNA Sequencing. Frontiers in Oncology, 2019, 9, 117.	1.3	17
30	Mapping actionable pathways and mutations in brain tumours using targeted RNA next generation sequencing. Acta Neuropathologica Communications, 2019, 7, 185.	2.4	7
31	The assembly pathway of complex I in Arabidopsis thaliana. Plant Journal, 2019, 97, 447-459.	2.8	84
32	Probabilistic data integration identifies reliable gametocyte-specific proteins and transcripts in malaria parasites. Scientific Reports, 2018, 8, 410.	1.6	39
33	Towards predicting the environmental metabolome from metagenomics with a mechanistic model. Nature Microbiology, 2018, 3, 456-460.	5.9	79
34	Does mitochondrial DNA evolution in metazoa drive the origin of new mitochondrial proteins?. IUBMB Life, 2018, 70, 1240-1250.	1.5	13
35	Xrp1 genetically interacts with the ALS-associated FUS orthologue caz and mediates its toxicity. Journal of Cell Biology, 2018, 217, 3947-3964.	2.3	23
36	Heterozygous missense variants of LMX1A lead to nonsyndromic hearing impairment and vestibular dysfunction. Human Genetics, 2018, 137, 389-400.	1.8	32

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37	Mammalian embryo comparison identifies novel pluripotency genes associated with the naÃ¯ve or primed state. Biology Open, 2018, 7, .	0.6	32
38	Large-scale genomic analysis shows association between homoplastic genetic variation in Mycobacterium tuberculosis genes and meningeal or pulmonary tuberculosis. BMC Genomics, 2018, 19, 122.	1.2	18
39	Haemophilus is overrepresented in the nasopharynx of infants hospitalized with RSV infection and associated with increased viral load and enhanced mucosal CXCL8 responses. Microbiome, 2018, 6, 10.	4.9	49
40	A homozygousFITM2mutation causes a deafness-dystonia syndrome with motor regression and signs of ichthyosis and sensory neuropathy. DMM Disease Models and Mechanisms, 2017, 10, 105-118.	1.2	16
41	Fifteen years of research on oralâ€“facialâ€“digital syndromes: from 1 to 16 causal genes. Journal of Medical Genetics, 2017, 54, 371-380.	1.5	85
42	Identification and evolutionary analysis of tissue-specific isoforms of mitochondrial complex I subunit NDUFV3. Biochimica Et Biophysica Acta - Bioenergetics, 2017, 1858, 208-217.	0.5	33
43	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. Clinical Microbiology Reviews, 2017, 30, 1015-1063.	5.7	310
44	Interspecies differences in PTH-mediated PKA phosphorylation of the epithelial calcium channel TRPV5. Pflugers Archiv European Journal of Physiology, 2017, 469, 1301-1311.	1.3	7
45	Heterochromatic histone modifications at transposons in Xenopus tropicalis embryos. Developmental Biology, 2017, 426, 460-471.	0.9	21
46	Genome-scale detection of positive selection in nine primates predicts human-virus evolutionary conflicts. Nucleic Acids Research, 2017, 45, 10634-10648.	6.5	76
47	Modest heterologous protection after Plasmodium falciparum sporozoite immunization: a double-blind randomized controlled clinical trial. BMC Medicine, 2017, 15, 168.	2.3	78
48	Regulatory remodeling in the allo-tetraploid frog Xenopus laevis. Genome Biology, 2017, 18, 198.	3.8	34
49	The Gene Ontology of eukaryotic cilia and flagella. Cilia, 2017, 6, 10.	1.8	6
50	Immunologic defects in severe mucocutaneous HSV-2 infections: Response to IFN-Î³ therapy. Journal of Allergy and Clinical Immunology, 2016, 138, 895-898.	1.5	6
51	Proteomics of Human Dendritic Cell Subsets Reveals Subset-Specific Surface Markers and Differential Inflammasome Function. Cell Reports, 2016, 16, 2953-2966.	2.9	72
52	ATP6AP1 deficiency causes an immunodeficiency with hepatopathy, cognitive impairment and abnormal protein glycosylation. Nature Communications, 2016, 7, 11600.	5.8	110
53	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. Nature Communications, 2016, 7, 11491.	5.8	207
54	The origin of the supernumerary subunits and assembly factors of complex I: A treasure trove of pathway evolution. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 971-979.	0.5	57

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55	WeGET: predicting new genes for molecular systems by weighted co-expression. Nucleic Acids Research, 2016, 44, D567-D573.	6.5	35
56	CTCF-mediated chromatin loops enclose inducible gene regulatory domains. BMC Genomics, 2016, 17, 252.	1.2	58
57	CCDC115 Deficiency Causes a Disorder of Golgi Homeostasis with Abnormal Protein Glycosylation. American Journal of Human Genetics, 2016, 98, 310-321.	2.6	88
58	TMEM199 Deficiency Is a Disorder of Golgi Homeostasis Characterized by Elevated Aminotransferases, Alkaline Phosphatase, and Cholesterol and Abnormal Glycosylation. American Journal of Human Genetics, 2016, 98, 322-330.	2.6	73
59	OFIP/KIAA0753 forms a complex with OFD1 and FOR20 at pericentriolar satellites and centrosomes and is mutated in one individual with oral-facial-digital syndrome. Human Molecular Genetics, 2016, 25, 497-513.	1.4	42
60	Evolution and structural organization of the mitochondrial contact site (MICOS) complex and the mitochondrial intermembrane space bridging (MIB) complex. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 91-101.	1.9	150
61	Systematic Phenomics Analysis Deconvolutes Genes Mutated in Intellectual Disability into Biologically Coherent Modules. American Journal of Human Genetics, 2016, 98, 149-164.	2.6	270
62	TMEM107 recruits ciliopathy proteins to subdomains of the ciliary transition zone and causes JoubertÂsyndrome. Nature Cell Biology, 2016, 18, 122-131.	4.6	118
63	The Eukaryotic-Specific ISD11 Is a Complex-Orphan Protein with Ability to Bind the Prokaryotic IscS. PLoS ONE, 2016, 11, e0157895.	1.1	6
64	Sequence specificity between interacting and non-interacting homologs identifies interface residues â€“ a homodimer and monomer use case. BMC Bioinformatics, 2015, 16, 325.	1.2	18
65	Transcriptome analysis of complex I-deficient patients reveals distinct expression programs for subunits and assembly factors of the oxidative phosphorylation system. BMC Genomics, 2015, 16, 691.	1.2	12
66	KIAA0556 is a novel ciliary basal body component mutated in Joubert syndrome. Genome Biology, 2015, 16, 293.	3.8	56
67	The RIG-I-like helicase receptor MDA5 (IFIH1) is involved in the host defense against Candida infections. European Journal of Clinical Microbiology and Infectious Diseases, 2015, 34, 963-974.	1.3	69
68	Skeletal muscle mitochondria of NDUFS4â^'/â^' mice display normal maximal pyruvate oxidation and ATP production. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 526-533.	0.5	21
69	An siRNA-based functional genomics screen for theÂidentification of regulators of ciliogenesis and ciliopathyÂgenes. Nature Cell Biology, 2015, 17, 1074-1087.	4.6	215
70	The pros and cons of vertebrate animal models for functional and therapeutic research on inherited retinal dystrophies. Progress in Retinal and Eye Research, 2015, 48, 137-159.	7.3	81
71	Integrative Genomics-Based Discovery of Novel Regulators of the Innate Antiviral Response. PLoS Computational Biology, 2015, 11, e1004553.	1.5	25
72	Predicting Human Genetic Interactions from Cancer Genome Evolution. PLoS ONE, 2015, 10, e0125795.	1.1	22

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73	Estimating Metabolic Fluxes Using a Maximum Network Flexibility Paradigm. PLoS ONE, 2015, 10, e0139665.	1.1	4
74	optGpSampler: An Improved Tool for Uniformly Sampling the Solution-Space of Genome-Scale Metabolic Networks. PLoS ONE, 2014, 9, e86587.	1.1	137
75	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. Cell Reports, 2014, 8, 1832-1844.	2.9	192
76	MPV17L2 is required for ribosome assembly in mitochondria. Nucleic Acids Research, 2014, 42, 8500-8515.	6.5	56
77	A mutation in the human CBP4 ortholog UQCC3 impairs complex III assembly, activity and cytochrome b stability. Human Molecular Genetics, 2014, 23, 6356-6365.	1.4	69
78	The symbiotic intestinal ciliates and the evolution of their hosts. European Journal of Protistology, 2014, 50, 166-173.	0.5	49
79	The SYSCILIA gold standard (SCGSv1) of known ciliary components and its applications within a systems biology consortium. Cilia, 2013, 2, 7.	1.8	160
80	The PinkThing for analysing ChIP profiling data in their genomic context. BMC Research Notes, 2013, 6, 133.	0.6	4
81	Loss, replacement and gain of proteins at the origin of the mitochondria. Biochimica Et Biophysica Acta - Bioenergetics, 2013, 1827, 224-231.	0.5	45
82	A complex V ATP5A1 defect causes fatal neonatal mitochondrial encephalopathy. Brain, 2013, 136, 1544-1554.	3.7	80
83	Genome evolution predicts genetic interactions in protein complexes and reveals cancer drug targets. Nature Communications, 2013, 4, 2124.	5.8	42
84	Mutations in the UQCC1-Interacting Protein, UQCC2, Cause Human Complex III Deficiency Associated with Perturbed Cytochrome b Protein Expression. PLoS Genetics, 2013, 9, e1004034.	1.5	96
85	Inferring Metabolic States in Uncharacterized Environments Using Gene-Expression Measurements. PLoS Computational Biology, 2013, 9, e1002988.	1.5	39
86	Human Intellectual Disability Genes Form Conserved Functional Modules in Drosophila. PLoS Genetics, 2013, 9, e1003911.	1.5	39
87	A mutation in the FAM36A gene, the human ortholog of COX20, impairs cytochrome c oxidase assembly and is associated with ataxia and muscle hypotonia. Human Molecular Genetics, 2013, 22, 656-667.	1.4	75
88	CEP89 is required for mitochondrial metabolism and neuronal function in man and fly. Human Molecular Genetics, 2013, 22, 3138-3151.	1.4	38
89	Evolution of modular intraflagellar transport from a coatomer-like progenitor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6943-6948.	3.3	144
90	BOLA1 Is an Aerobic Protein That Prevents Mitochondrial Morphology Changes Induced by Glutathione Depletion. Antioxidants and Redox Signaling, 2013, 18, 129-138.	2.5	46

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91	ODoSE: A Webserver for Genome-Wide Calculation of Adaptive Divergence in Prokaryotes. PLoS ONE, 2013, 8, e62447.	1.1	9
92	Evolution and Diversification of the Organellar Release Factor Family. Molecular Biology and Evolution, 2012, 29, 3497-3512.	3.5	41
93	C7orf30 specifically associates with the large subunit of the mitochondrial ribosome and is involved in translation. Nucleic Acids Research, 2012, 40, 4040-4051.	6.5	46
94	Mitochondrial Protein Acetylation and Sirtuin-Mediated Deacetylation. Oxidative Stress and Disease, 2012, , 245-267.	0.3	0
95	Chromatin accessibility, p300, and histone acetylation define PML-RARÎ± and AML1-ETO binding sites in acute myeloid leukemia. Blood, 2012, 120, 3058-3068.	0.6	60
96	Iterative orthology prediction uncovers new mitochondrial proteins and identifies C12orf62 as the human ortholog of COX14, a protein involved in the assembly of cytochrome c oxidase. Genome Biology, 2012, 13, R12.	13.9	100
97	A three-dimensional topology of complex I inferred from evolutionary correlations. BMC Structural Biology, 2012, 12, 19.	2.3	9
98	Structure based hypothesis of a mitochondrial ribosome rescue mechanism. Biology Direct, 2012, 7, 14.	1.9	31
99	Analysis of genes regulated by the transcription factor LUMAN identifies ApoA4 as a target gene in dendritic cells. Molecular Immunology, 2012, 50, 66-73.	1.0	18
100	CATCHprofiles: Clustering and Alignment Tool for ChIP Profiles. PLoS ONE, 2012, 7, e28272.	1.1	10
101	Discovery of a hapE Mutation That Causes Azole Resistance in Aspergillus fumigatus through Whole Genome Sequencing and Sexual Crossing. PLoS ONE, 2012, 7, e50034.	1.1	168
102	FACIL: Fast and Accurate Genetic Code Inference and Logo. Bioinformatics, 2011, 27, 1929-1933.	1.8	42
103	Restoration of complex V deficiency caused by a novel deletion in the human TMEM70 gene normalizes mitochondrial morphology. Mitochondrion, 2011, 11, 954-963.	1.6	39
104	The Organellar Genome and Metabolic Potential of the Hydrogen-Producing Mitochondrion of Nyctotherus ovalis. Molecular Biology and Evolution, 2011, 28, 2379-2391.	3.5	82
105	NDUFB7 and NDUFA8 are located at the intermembrane surface of complex I. FEBS Letters, 2011, 585, 737-743.	1.3	57
106	A Mutation in C2orf64 Causes Impaired Cytochrome c Oxidase Assembly and Mitochondrial Cardiomyopathy. American Journal of Human Genetics, 2011, 88, 488-493.	2.6	75
107	MicroRNA genes preferentially expressed in dendritic cells contain sites for conserved transcription factor binding motifs in their promoters. BMC Genomics, 2011, 12, 330.	1.2	26
108	TEFM (c17orf42) is necessary for transcription of human mtDNA. Nucleic Acids Research, 2011, 39, 4284-4299.	6.5	142

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109	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. Briefings in Bioinformatics, 2011, 12, 442-448.	3.2	67
110	Flux Measurement Selection in Metabolic Networks. Lecture Notes in Computer Science, 2011, , 214-224.	1.0	0
111	The alpha-kinase family: an exceptional branch on the protein kinase tree. Cellular and Molecular Life Sciences, 2010, 67, 875-890.	2.4	104
112	Quantitative proteome profiling of respiratory virus-infected lung epithelial cells. Journal of Proteomics, 2010, 73, 1680-1693.	1.2	48
113	Mosaic origin of the mitochondrial proteome. Proteomics, 2010, 10, 4012-4024.	1.3	77
114	A functional peptidyl-tRNA hydrolase, ICT1, has been recruited into the human mitochondrial ribosome. EMBO Journal, 2010, 29, 1116-1125.	3.5	167
115	Measuring the physical cohesiveness of proteins using physical interaction enrichment. Bioinformatics, 2010, 26, 2737-2743.	1.8	18
116	Genome-Wide Profiling of p63 DNAâ€“Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. PLoS Genetics, 2010, 6, e1001065.	1.5	169
117	Dominant Processes during Human Dendritic Cell Maturation Revealed by Integration of Proteome and Transcriptome at the Pathway Level. Journal of Proteome Research, 2010, 9, 1727-1737.	1.8	45
118	Acyl-CoA Dehydrogenase 9 Is Required for the Biogenesis of Oxidative Phosphorylation Complex I. Cell Metabolism, 2010, 12, 283-294.	7.2	172
119	Clustering of Codons with Rare Cognate tRNAs in Human Genes Suggests an Extra Level of Expression Regulation. PLoS Genetics, 2009, 5, e1000548.	1.5	54
120	Increasing the coverage of a metapopulation consensus genome by iterative read mapping and assembly. Bioinformatics, 2009, 25, 2878-2881.	1.8	29
121	The hydrogenosomes of Psalteriomonas lanterna. BMC Evolutionary Biology, 2009, 9, 287.	3.2	29
122	The mitochondrial genomes of the ciliates Euplotes minuta and Euplotes crassus. BMC Genomics, 2009, 10, 514.	1.2	36
123	Mutations in NDUFAF3 (C3ORF60), Encoding an NDUFAF4 (C6ORF66)-Interacting Complex I Assembly Protein, Cause Fatal Neonatal Mitochondrial Disease. American Journal of Human Genetics, 2009, 84, 718-727.	2.6	155
124	The Biological Coherence of Human Phenome Databases. American Journal of Human Genetics, 2009, 85, 801-808.	2.6	37
125	Mitochondrial proteome evolution and genetic disease. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2009, 1792, 1122-1129.	1.8	29
126	Expansion of the human mitochondrial proteome by intra- and inter-compartmental protein duplication. Genome Biology, 2009, 10, R135.	13.9	23

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127	Asymmetric relationships between proteins shape genome evolution. Genome Biology, 2009, 10, R19.	13.9	39
128	Identification of Nipsnap1 as a novel auxiliary protein inhibiting TRPV6 activity. Pflugers Archiv European Journal of Physiology, 2008, 457, 91-101.	1.3	26
129	The ironâ€“sulphur protein Ind1 is required for effective complex I assembly. EMBO Journal, 2008, 27, 1736-1746.	3.5	158
130	Conserved co-expression for candidate disease gene prioritization. BMC Bioinformatics, 2008, 9, 208.	1.2	37
131	Complex fate of paralogs. BMC Evolutionary Biology, 2008, 8, 337.	3.2	21
132	Macronuclear genome structure of the ciliate Nyctotherus ovalis: Single-gene chromosomes and tiny introns. BMC Genomics, 2008, 9, 587.	1.2	33
133	Phenome connections. Trends in Genetics, 2008, 24, 103-106.	2.9	107
134	Conservation of divergent transcription in fungi. Trends in Genetics, 2008, 24, 207-211.	2.9	48
135	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. Journal of the Royal Society Interface, 2008, 5, 151-170.	1.5	97
136	Signature, a web server for taxonomic characterization of sequence samples using signature genes. Nucleic Acids Research, 2008, 36, W470-W474.	6.5	14
137	Evolution of Closely Linked Gene Pairs in Vertebrate Genomes. Molecular Biology and Evolution, 2008, 25, 1909-1921.	3.5	17
138	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. PLoS Pathogens, 2008, 4, e1000195.	2.1	191
139	Signature Genes as a Phylogenomic Tool. Molecular Biology and Evolution, 2008, 25, 1659-1667.	3.5	72
140	Molecular and Biochemical Analysis of the Plastidic ADP-glucose Transporter (ZmBT1) from Zea mays*. Journal of Biological Chemistry, 2007, 282, 22481-22491.	1.6	102
141	From Endosymbiont to Host-Controlled Organelle: The Hijacking of Mitochondrial Protein Synthesis and Metabolism. PLoS Computational Biology, 2007, 3, e219.	1.5	101
142	Assessment of phylogenomic and orthology approaches for phylogenetic inference. Bioinformatics, 2007, 23, 815-824.	1.8	87
143	Optimized design and assessment of whole genome tiling arrays. Bioinformatics, 2007, 23, i195-i204.	1.8	53
144	Reconstructing the evolution of the mitochondrial ribosomal proteome. Nucleic Acids Research, 2007, 35, 4686-4703.	6.5	168

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145	Reconstruction of ancestral proteomes. , 2007, , 128-138.		1
146	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. Genome Biology, 2007, 8, R197.	13.9	3
147	Orthology prediction at scalable resolution by phylogenetic tree analysis. BMC Bioinformatics, 2007, 8, 83.	1.2	117
148	Optimising oligonucleotide array design for ChIP-on-chip. BMC Bioinformatics, 2007, 8, .	1.2	1
149	The [FeFe] hydrogenase of Nyctotherus ovalis has a chimeric origin. BMC Evolutionary Biology, 2007, 7, 230.	3.2	34
150	Development of the first marmoset-specific DNA microarray (EUMAMA): a new genetic tool for large-scale expression profiling in a non-human primate. BMC Genomics, 2007, 8, 190.	1.2	22
151	Hydrogenosomes (and Related Organelles, Either) Are Not the Same. , 2007, , 135-159.		5
152	Benchmarking ortholog identification methods using functional genomics data. Genome Biology, 2006, 7, R31.	13.9	139
153	Origin and evolution of the peroxisomal proteome. Biology Direct, 2006, 1, 8.	1.9	152
154	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. Nature, 2006, 440, 790-794.	13.7	1,075
155	Mitochondria, hydrogenosomes and mitosomes: products of evolutionary tinkering!. Current Genetics, 2006, 50, 225-245.	0.8	73
156	Formation of peroxisomes: Present and past. Biochimica Et Biophysica Acta - Molecular Cell Research, 2006, 1763, 1647-1654.	1.9	48
157	YfhJ, a Molecular Adaptor in Iron-Sulfur Cluster Formation or a Frataxin-like Protein?. Structure, 2006, 14, 857-867.	1.6	42
158	Combinatorial gene regulation in Plasmodium falciparum. Trends in Genetics, 2006, 22, 73-78.	2.9	48
159	A global definition of expression context is conserved between orthologs, but does not correlate with sequence conservation. BMC Genomics, 2006, 7, 10.	1.2	28
160	Horizontal gene transfer from Bacteria to rumen Ciliates indicates adaptation to their anaerobic, carbohydrates-rich environment. BMC Genomics, 2006, 7, 22.	1.2	138
161	Predicting disease genes using protein-protein interactions. Journal of Medical Genetics, 2006, 43, 691-698.	1.5	518
162	An anaerobic mitochondrion that produces hydrogen. Nature, 2005, 434, 74-79.	13.7	242

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163	Lineage-specific gene loss following mitochondrial endosymbiosis and its potential for function prediction in eukaryotes. Bioinformatics, 2005, 21, ii144-ii150.	1.8	26
164	Correlation between sequence conservation and the genomic context after gene duplication. Nucleic Acids Research, 2005, 33, 7176-7176.	6.5	0
165	The properties of protein family space depend on experimental design. Bioinformatics, 2005, 21, 2618-2622.	1.8	10
166	POMT2 mutations cause Â-dystroglycan hypoglycosylation and Walker-Warburg syndrome. Journal of Medical Genetics, 2005, 42, 907-912.	1.5	374
167	Correlation between sequence conservation and the genomic context after gene duplication. Nucleic Acids Research, 2005, 33, 6164-6171.	6.5	38
168	GENOME TREES AND THE NATURE OF GENOME EVOLUTION. Annual Review of Microbiology, 2005, 59, 191-209.	2.9	184
169	Tracing the Evolution of a Large Protein Complex in the Eukaryotes, NADH:Ubiquinone Oxidoreductase (Complex I). Journal of Molecular Biology, 2005, 348, 857-870.	2.0	228
170	Combining data from genomes, Y2H and 3D structure indicates that BolA is a reductase interacting with a glutaredoxin. FEBS Letters, 2005, 579, 591-596.	1.3	73
171	Variation and evolution of biomolecular systems: Searching for functional relevance. FEBS Letters, 2005, 579, 1839-1845.	1.3	14
172	From Endosymbiont to Host-Controlled Organelle: the Hijacking of Mitochondrial Protein Synthesis and Metabolism. PLoS Computational Biology, 2005, preprint, e219.	1.5	0
173	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. Nucleic Acids Research, 2004, 32, 4725-4731.	6.5	99
174	Prokaryotic diversity of the Saccharomyces cerevisiae Atx1p-mediated copper pathway. Bioinformatics, 2004, 20, 2644-2655.	1.8	12
175	Quantifying Modularity in the Evolution of Biomolecular Systems. Genome Research, 2004, 14, 391-397.	2.4	91
176	Identification and Functional Verification of Archaeal-Type Phosphoenolpyruvate Carboxylase, a Missing Link in Archaeal Central Carbohydrate Metabolism. Journal of Bacteriology, 2004, 186, 7754-7762.	1.0	33
177	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. Nucleic Acids Research, 2004, 33, D433-D437.	6.5	1,418
178	A divergent ADP/ATP carrier in the hydrogenosomes of Trichomonas gallinae argues for an independent origin of these organelles. Molecular Microbiology, 2004, 51, 1439-1446.	1.2	49
179	The yeast coexpression network has a smallâ€world, scaleâ€free architecture and can be explained by a simple model. EMBO Reports, 2004, 5, 280-284.	2.0	228
180	Comparative genomics for reliable protein-function prediction from genomic data. Trends in Genetics, 2004, 20, 340-344.	2.9	20

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