

Berend Snel

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

121
papers

16,680
citations

55
h-index

129
g-index

131
ext. papers

19,709
ext. citations

10.9
avg, IF

6.38
L-index

#	Paper	IF	Citations
121	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002 , 417, 399-403	40.3	1856
120	Toward automatic reconstruction of a highly resolved tree of life. <i>Science</i> , 2006 , 311, 1283-7	33.3	1197
119	STRING: a database of predicted functional associations between proteins. <i>Nucleic Acids Research</i> , 2003 , 31, 258-61	20.1	1182
118	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. <i>Nucleic Acids Research</i> , 2005 , 33, D433-7	20.1	953
117	Conservation of gene order: a fingerprint of proteins that physically interact. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 324-8	10.3	865
116	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006 , 440, 790-4	50.4	861
115	The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 14422-7	11.5	778
114	STRING: a web-server to retrieve and display the repeatedly occurring neighbourhood of a gene. <i>Nucleic Acids Research</i> , 2000 , 28, 3442-4	20.1	651
113	Genome phylogeny based on gene content. <i>Nature Genetics</i> , 1999 , 21, 108-10	36.3	556
112	STRING 7--recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007 , 35, D358-62	20.1	503
111	Predicting disease genes using protein-protein interactions. <i>Journal of Medical Genetics</i> , 2006 , 43, 691-8	5.8	393
110	Predicting protein function by genomic context: quantitative evaluation and qualitative inferences. <i>Genome Research</i> , 2000 , 10, 1204-10	9.7	351
109	Genomes in flux: the evolution of archaeal and proteobacterial gene content. <i>Genome Research</i> , 2002 , 12, 17-25	9.7	257
108	The identification of functional modules from the genomic association of genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5890-5	11.5	213
107	Re-annotating the <i>Mycoplasma pneumoniae</i> genome sequence: adding value, function and reading frames. <i>Nucleic Acids Research</i> , 2000 , 28, 3278-88	20.1	194
106	The yeast coexpression network has a small-world, scale-free architecture and can be explained by a simple model. <i>EMBO Reports</i> , 2004 , 5, 280-4	6.5	186
105	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , 1999 , 343, 115-124	3.8	185

104	The R-spondin protein family. <i>Genome Biology</i> , 2012 , 13, 242	18.3	182
103	Gene context conservation of a higher order than operons. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 474-80.3	8.3	164
102	Large-scale genetic perturbations reveal regulatory networks and an abundance of gene-specific repressors. <i>Cell</i> , 2014 , 157, 740-52	56.2	160
101	SHOT: a web server for the construction of genome phylogenies. <i>Trends in Genetics</i> , 2002 , 18, 158-62	8.5	156
100	Predicting gene function by conserved co-expression. <i>Trends in Genetics</i> , 2003 , 19, 238-42	8.5	156
99	Domains in plexins: links to integrins and transcription factors. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 261-3	10.3	156
98	Genome trees and the nature of genome evolution. <i>Annual Review of Microbiology</i> , 2005 , 59, 191-209	17.5	151
97	In-depth qualitative and quantitative profiling of tyrosine phosphorylation using a combination of phosphopeptide immunoaffinity purification and stable isotope dimethyl labeling. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 84-99	7.6	142
96	Genome evolution. Gene fusion versus gene fission. <i>Trends in Genetics</i> , 2000 , 16, 9-11	8.5	136
95	Origin and evolution of the peroxisomal proteome. <i>Biology Direct</i> , 2006 , 1, 8	7.2	132
94	Distinctive expansion of potential virulence genes in the genome of the oomycete fish pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003272	6	130
93	Evolutionary dynamics of the kinetochore network in eukaryotes as revealed by comparative genomics. <i>EMBO Reports</i> , 2017 , 18, 1559-1571	6.5	128
92	SOMBRERO, BEARSKIN1, and BEARSKIN2 regulate root cap maturation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010 , 22, 640-54	11.6	124
91	The <i>Arabidopsis</i> bZIP transcription factor family-an update. <i>Current Opinion in Plant Biology</i> , 2018 , 45, 36-49	9.9	120
90	Function prediction and protein networks. <i>Current Opinion in Cell Biology</i> , 2003 , 15, 191-8	9	118
89	The phylogenetic distribution of frataxin indicates a role in iron-sulfur cluster protein assembly. <i>Human Molecular Genetics</i> , 2001 , 10, 2463-8	5.6	114
88	ABI4: versatile activator and repressor. <i>Trends in Plant Science</i> , 2013 , 18, 125-32	13.1	110
87	Systematic discovery of analogous enzymes in thiamin biosynthesis. <i>Nature Biotechnology</i> , 2003 , 21, 790-5	44.5	109

86	Functional overlap and regulatory links shape genetic interactions between signaling pathways. <i>Cell</i> , 2010 , 143, 991-1004	56.2	105
85	Evolution and function of the mitotic checkpoint. <i>Developmental Cell</i> , 2012 , 23, 239-50	10.2	103
84	DOWNY MILDEW RESISTANT 6 and DMR6-LIKE OXYGENASE 1 are partially redundant but distinct suppressors of immunity in Arabidopsis. <i>Plant Journal</i> , 2015 , 81, 210-22	6.9	100
83	A TPR domain-containing N-terminal module of MPS1 is required for its kinetochore localization by Aurora B. <i>Journal of Cell Biology</i> , 2013 , 201, 217-31	7.3	100
82	The vertebrate mitotic checkpoint protein BUBR1 is an unusual pseudokinase. <i>Developmental Cell</i> , 2012 , 22, 1321-9	10.2	98
81	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , 2007 , 8, 83	3.6	97
80	Arabidopsis PLETHORA transcription factors control phyllotaxis. <i>Current Biology</i> , 2011 , 21, 1123-8	6.3	96
79	Arrayed BUB recruitment modules in the kinetochore scaffold KNL1 promote accurate chromosome segregation. <i>Journal of Cell Biology</i> , 2013 , 203, 943-55	7.3	92
78	Evolution of the TOR pathway. <i>Journal of Molecular Evolution</i> , 2011 , 73, 209-20	3.1	90
77	Quantifying modularity in the evolution of biomolecular systems. <i>Genome Research</i> , 2004 , 14, 391-7	9.7	81
76	The PLETHORA Gene Regulatory Network Guides Growth and Cell Differentiation in Arabidopsis Roots. <i>Plant Cell</i> , 2016 , 28, 2937-2951	11.6	81
75	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002 , 20, 407-10; discussion 410	15.1	79
74	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005 , 33, 7176-7176	20.1	78
73	Exploitation of gene context. <i>Current Opinion in Structural Biology</i> , 2000 , 10, 366-70	8.1	77
72	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , 1999 , 343, 115	3.8	75
71	Comparative phosphoproteomics reveals evolutionary and functional conservation of phosphorylation across eukaryotes. <i>Genome Biology</i> , 2008 , 9, R144	18.3	64
70	Combining data from genomes, Y2H and 3D structure indicates that BolA is a reductase interacting with a glutaredoxin. <i>FEBS Letters</i> , 2005 , 579, 591-6	3.8	64
69	The consistent phylogenetic signal in genome trees revealed by reducing the impact of noise. <i>Journal of Molecular Evolution</i> , 2004 , 58, 527-39	3.1	60

68	A domain-centric analysis of oomycete plant pathogen genomes reveals unique protein organization. <i>Plant Physiology</i> , 2011 , 155, 628-44	6.6	59
67	Phylogenomics reveal a robust fungal tree of life. <i>FEMS Yeast Research</i> , 2006 , 6, 1213-20	3.1	57
66	Inversions and the dynamics of eukaryotic gene order. <i>Trends in Genetics</i> , 2001 , 17, 304-6	8.5	54
65	Genesis of chromatin and transcription dynamics in the origin of species. <i>Cell</i> , 2015 , 161, 724-36	56.2	53
64	Tyrosine phosphorylation profiling in FGF-2 stimulated human embryonic stem cells. <i>PLoS ONE</i> , 2011 , 6, e17538	3.7	53
63	Signature genes as a phylogenomic tool. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1659-67	8.3	53
62	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. <i>Nucleic Acids Research</i> , 2004 , 32, 4725-31	20.1	51
61	Gene and context: integrative approaches to genome analysis. <i>Advances in Protein Chemistry</i> , 2000 , 54, 345-79		49
60	Extensive translational regulation during seed germination revealed by polysomal profiling. <i>New Phytologist</i> , 2017 , 214, 233-244	9.8	46
59	Evolutionary acquisition of cysteines determines FOXO paralog-specific redox signaling. <i>Antioxidants and Redox Signaling</i> , 2015 , 22, 15-28	8.4	44
58	Evolution of the Ras-like small GTPases and their regulators. <i>Small GTPases</i> , 2011 , 2, 4-16	2.7	44
57	Effector identification in the lettuce downy mildew <i>Bremia lactucae</i> by massively parallel transcriptome sequencing. <i>Molecular Plant Pathology</i> , 2012 , 13, 719-31	5.7	39
56	Targeted quantitative phosphoproteomics approach for the detection of phospho-tyrosine signaling in plants. <i>Journal of Proteome Research</i> , 2012 , 11, 438-48	5.6	39
55	Lateral Gene Transfer, Genome Surveys, and the Phylogeny of Prokaryotes. <i>Science</i> , 1999 , 286, 1443a-1443	4.33	39
54	Mosaic origin of the eukaryotic kinetochore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 12873-12882	11.5	38
53	Reconstruction of oomycete genome evolution identifies differences in evolutionary trajectories leading to present-day large gene families. <i>Genome Biology and Evolution</i> , 2012 , 4, 199-211	3.9	38
52	Protein complex evolution does not involve extensive network rewiring. <i>PLoS Computational Biology</i> , 2008 , 4, e1000132	5	38
51	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005 , 33, 6164-71	20.1	37

50	A subfamily of putative cytokinin receptors is revealed by an analysis of the evolution of the two-component signaling system of plants. <i>Plant Physiology</i> , 2014 , 165, 227-37	6.6	33
49	Unique Phylogenetic Distributions of the Ska and Dam1 Complexes Support Functional Analogy and Suggest Multiple Parallel Displacements of Ska by Dam1. <i>Genome Biology and Evolution</i> , 2017 , 9, 1295-1303	3.9	32
48	Identification of homologs in insignificant blast hits by exploiting extrinsic gene properties. <i>BMC Bioinformatics</i> , 2007 , 8, 356	3.6	25
47	A global definition of expression context is conserved between orthologs, but does not correlate with sequence conservation. <i>BMC Genomics</i> , 2006 , 7, 10	4.5	25
46	The plant Polycomb repressive complex 1 (PRC1) existed in the ancestor of seed plants and has a complex duplication history. <i>BMC Evolutionary Biology</i> , 2015 , 15, 44	3	23
45	Widespread Recurrent Patterns of Rapid Repeat Evolution in the Kinetochores Scaffold KNL1. <i>Genome Biology and Evolution</i> , 2015 , 7, 2383-93	3.9	23
44	Phylogenomics-guided discovery of a novel conserved cassette of short linear motifs in BubR1 essential for the spindle checkpoint. <i>Open Biology</i> , 2016 , 6,	7	23
43	Measuring the impact of gene prediction on gene loss estimates in Eukaryotes by quantifying falsely inferred absences. <i>PLoS Computational Biology</i> , 2019 , 15, e1007301	5	22
42	Epigenetics and transcription regulation during eukaryotic diversification: the saga of TFIID. <i>Genes and Development</i> , 2019 , 33, 888-902	12.6	21
41	Coevolution of gene families in prokaryotes. <i>Genome Research</i> , 2008 , 18, 462-8	9.7	20
40	Domestication of self-splicing introns during eukaryogenesis: the rise of the complex spliceosomal machinery. <i>Biology Direct</i> , 2017 , 12, 30	7.2	19
39	Quantitative label-free phosphoproteomics of six different life stages of the late blight pathogen <i>Phytophthora infestans</i> reveals abundant phosphorylation of members of the CRN effector family. <i>Journal of Proteome Research</i> , 2014 , 13, 1848-59	5.6	19
38	Contribution of the epigenetic mark H3K27me3 to functional divergence after whole genome duplication in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2012 , 13, R94	18.3	19
37	Comparative genomics for reliable protein-function prediction from genomic data. <i>Trends in Genetics</i> , 2004 , 20, 340-4	8.5	19
36	Novel pipeline identifies new upstream ORFs and non-AUG initiating main ORFs with conserved amino acid sequences in the 5' leader of mRNAs in. <i>Rna</i> , 2019 , 25, 292-304	5.8	19
35	Conflicting phylogenetic position of <i>Schizosaccharomyces pombe</i> . <i>Genomics</i> , 2006 , 88, 387-93	4.3	18
34	Phylogeny of the CDC25 homology domain reveals rapid differentiation of Ras pathways between early animals and fungi. <i>Cellular Signalling</i> , 2009 , 21, 1579-85	4.9	17
33	The phylogeny of C/S1 bZIP transcription factors reveals a shared algal ancestry and the pre-angiosperm translational regulation of S1 transcripts. <i>Scientific Reports</i> , 2016 , 6, 30444	4.9	17

32	Timing the origin of eukaryotic cellular complexity with ancient duplications. <i>Nature Ecology and Evolution</i> , 2021 , 5, 92-100	12.3	17
31	Increased sucrose levels mediate selective mRNA translation in Arabidopsis. <i>BMC Plant Biology</i> , 2014 , 14, 306	5.3	16
30	Cohesive versus flexible evolution of functional modules in eukaryotes. <i>PLoS Computational Biology</i> , 2009 , 5, e1000276	5	15
29	Complex fate of paralogs. <i>BMC Evolutionary Biology</i> , 2008 , 8, 337	3	15
28	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. <i>Journal of Proteome Research</i> , 2015 , 14, 2976-87	5.6	13
27	Evolutionary Dynamics of the Spindle Assembly Checkpoint in Eukaryotes. <i>Current Biology</i> , 2020 , 30, R589-R602	6.3	13
26	The molecular basis of monopolin recruitment to the kinetochore. <i>Chromosoma</i> , 2019 , 128, 331-354	2.8	12
25	Database independent proteomics analysis of the ostrich and human proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 407-12	11.5	12
24	Variation and evolution of biomolecular systems: searching for functional relevance. <i>FEBS Letters</i> , 2005 , 579, 1839-45	3.8	12
23	Comparative Genome Analysis of the Mollicutes 2002 , 255-278		12
22	A high-resolution gene expression atlas of epistasis between gene-specific transcription factors exposes potential mechanisms for genetic interactions. <i>BMC Biology</i> , 2015 , 13, 112	7.3	11
21	Evaluating experimental bias and completeness in comparative phosphoproteomics analysis. <i>PLoS ONE</i> , 2011 , 6, e23276	3.7	11
20	Shared protein complex subunits contribute to explaining disrupted co-occurrence. <i>PLoS Computational Biology</i> , 2013 , 9, e1003124	5	10
19	Inferring the Evolutionary History of Your Favorite Protein: A Guide for Molecular Biologists. <i>BioEssays</i> , 2019 , 41, e1900006	4.1	8
18	A predicted functional gene network for the plant pathogen <i>Phytophthora infestans</i> as a framework for genomic biology. <i>BMC Genomics</i> , 2013 , 14, 483	4.5	8
17	The histone modification H3K27me3 is retained after gene duplication and correlates with conserved noncoding sequences in Arabidopsis. <i>Genome Biology and Evolution</i> , 2014 , 6, 572-9	3.9	8
16	Enrichment of homologs in insignificant BLAST hits by co-complex network alignment. <i>BMC Bioinformatics</i> , 2010 , 11, 86	3.6	8
15	Small homologous blocks in phytophthora genomes do not point to an ancient whole-genome duplication. <i>Genome Biology and Evolution</i> , 2014 , 6, 1079-85	3.9	7

14	Gene duplications contribute to the overrepresentation of interactions between proteins of a similar age. <i>BMC Evolutionary Biology</i> , 2012 , 12, 99	3	6
13	Bioinformatic inference of specific and general transcription factor binding sites in the plant pathogen <i>Phytophthora infestans</i> . <i>PLoS ONE</i> , 2012 , 7, e51295	3.7	6
12	Comparative Genome Analysis: Exploiting the Context of Genes to Infer Evolution and Predict Function. <i>Computational Biology</i> , 2000 , 281-294	0.7	6
11	Benchmarking orthology methods using phylogenetic patterns defined at the base of Eukaryotes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
10	Chromosomal instability by mutations in the novel minor spliceosome component CENATAC. <i>EMBO Journal</i> , 2021 , 40, e106536	13	4
9	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. <i>Genome Biology</i> , 2007 , 8, R197	18.3	3
8	The first eukaryotic kinome tree illuminates the dynamic history of present-day kinases		3
7	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002 , 20, 410	15.1	2
6	Chromosomal instability by mutations in a novel specificity factor of the minor spliceosome		1
5	Timing the origin of eukaryotic cellular complexity with ancient duplications		1
4	Recurrent sequence evolution after independent gene duplication. <i>BMC Evolutionary Biology</i> , 2020 , 20, 98	3	1
3	The spread of the first introns in proto-eukaryotic paralogs.. <i>Communications Biology</i> , 2022 , 5, 476	6.7	0
2	Reliable and Specific Protein Function Prediction by Combining Homology with Genomic(s) Context 2006 , 13-29		
1	Phylogenetic profiling in eukaryotes: The effect of species, orthologous group, and interactome selection on protein interaction prediction.. <i>PLoS ONE</i> , 2022 , 17, e0251833	3.7	