

# Berend Snel

## List of Publications by Year in descending order

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118  
papers

21,516  
citations

22099

59  
h-index

20900

115  
g-index

131  
all docs

131  
docs citations

131  
times ranked

25133  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002, 417, 399-403.	13.7	2,137
2	STRING: a database of predicted functional associations between proteins. <i>Nucleic Acids Research</i> , 2003, 31, 258-261.	6.5	1,897
3	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. <i>Science</i> , 2006, 311, 1283-1287.	6.0	1,435
4	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. <i>Nucleic Acids Research</i> , 2004, 33, D433-D437.	6.5	1,418
5	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	13.7	1,075
6	Conservation of gene order: a fingerprint of proteins that physically interact. <i>Trends in Biochemical Sciences</i> , 1998, 23, 324-328.	3.7	991
7	STRING: a web-server to retrieve and display the repeatedly occurring neighbourhood of a gene. <i>Nucleic Acids Research</i> , 2000, 28, 3442-3444.	6.5	976
8	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, 14422-14427.	3.3	874
9	Genome phylogeny based on gene content. <i>Nature Genetics</i> , 1999, 21, 108-110.	9.4	658
10	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007, 35, D358-D362.	6.5	568
11	Predicting disease genes using protein-protein interactions. <i>Journal of Medical Genetics</i> , 2006, 43, 691-698.	1.5	518
12	Predicting Protein Function by Genomic Context: Quantitative Evaluation and Qualitative Inferences. <i>Genome Research</i> , 2000, 10, 1204-1210.	2.4	453
13	Genomes in Flux: The Evolution of Archaeal and Proteobacterial Gene Content. <i>Genome Research</i> , 2002, 12, 17-25.	2.4	305
14	The Arabidopsis bZIP transcription factor family—an update. <i>Current Opinion in Plant Biology</i> , 2018, 45, 36-49.	3.5	294
15	Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors. <i>Cell</i> , 2014, 157, 740-752.	13.5	248
16	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, 5890-5895.	3.3	238
17	The R-spondin protein family. <i>Genome Biology</i> , 2012, 13, 242.	13.9	236
18	Re-annotating the <i>Mycoplasma pneumoniae</i> genome sequence: adding value, function and reading frames. <i>Nucleic Acids Research</i> , 2000, 28, 3278-3288.	6.5	228

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19	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
20	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . PLoS Genetics, 2013, 9, e1003272.	1.5	221
21	Pathway alignment: application to the comparative analysis of glycolytic enzymes. Biochemical Journal, 1999, 343, 115-124.	1.7	208
22	Evolutionary dynamics of the kinetochore network in eukaryotes as revealed by comparative genomics. EMBO Reports, 2017, 18, 1559-1571.	2.0	206
23	SHOT: a web server for the construction of genome phylogenies. Trends in Genetics, 2002, 18, 158-162.	2.9	193
24	Gene context conservation of a higher order than operons. Trends in Biochemical Sciences, 2000, 25, 474-479.	3.7	187
25	GENOME TREES AND THE NATURE OF GENOME EVOLUTION. Annual Review of Microbiology, 2005, 59, 191-209.	2.9	184
26	Domains in plexins: links to integrins and transcription factors. Trends in Biochemical Sciences, 1999, 24, 261-263.	3.7	180
27	Predicting gene function by conserved co-expression. Trends in Genetics, 2003, 19, 238-242.	2.9	175
28	Genome evolution. Trends in Genetics, 2000, 16, 9-11.	2.9	170
29	<scp>DOWNY MILDEW RESISTANT</scp> 6 and <scp>DMR</scp>6â€<scp>LIKE OXYGENASE</scp> 1 are partially redundant but distinct suppressors of immunity in Arabidopsis. Plant Journal, 2015, 81, 210-222.	2.8	168
30	SOMBRERO, BEARSKIN1, and BEARSKIN2 Regulate Root Cap Maturation in<i>Arabidopsis</i>. Plant Cell, 2010, 22, 640-654.	3.1	163
31	In-depth Qualitative and Quantitative Profiling of Tyrosine Phosphorylation Using a Combination of Phosphopeptide Immunoaffinity Purification and Stable Isotope Dimethyl Labeling. Molecular and Cellular Proteomics, 2010, 9, 84-99.	2.5	155
32	Origin and evolution of the peroxisomal proteome. Biology Direct, 2006, 1, 8.	1.9	152
33	ABI4: versatile activator and repressor. Trends in Plant Science, 2013, 18, 125-132.	4.3	142
34	The phylogenetic distribution of frataxin indicates a role in iron-sulfur cluster protein assembly. Human Molecular Genetics, 2001, 10, 2463-2468.	1.4	139
35	Function prediction and protein networks. Current Opinion in Cell Biology, 2003, 15, 191-198.	2.6	133
36	The PLETHORA Gene Regulatory Network Guides Growth and Cell Differentiation in Arabidopsis Roots. Plant Cell, 2016, 28, 2937-2951.	3.1	127

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37	Evolution and Function of the Mitotic Checkpoint. <i>Developmental Cell</i> , 2012, 23, 239-250.	3.1	126
38	Arrayed BUB recruitment modules in the kinetochore scaffold KNL1 promote accurate chromosome segregation. <i>Journal of Cell Biology</i> , 2013, 203, 943-955.	2.3	125
39	<i>Arabidopsis</i> PLETHORA Transcription Factors Control Phyllotaxis. <i>Current Biology</i> , 2011, 21, 1123-1128.	1.8	124
40	Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. <i>Cell</i> , 2010, 143, 991-1004.	13.5	123
41	Systematic discovery of analogous enzymes in thiamin biosynthesis. <i>Nature Biotechnology</i> , 2003, 21, 790-795.	9.4	121
42	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, 217-231.	2.3	119
43	Evolution of the TOR Pathway. <i>Journal of Molecular Evolution</i> , 2011, 73, 209-220.	0.8	118
44	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , 2007, 8, 83.	1.2	117
45	The Vertebrate Mitotic Checkpoint Protein BUBR1 Is an Unusual Pseudokinase. <i>Developmental Cell</i> , 2012, 22, 1321-1329.	3.1	116
46	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 407-410.	4.9	111
47	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. <i>Nucleic Acids Research</i> , 2004, 32, 4725-4731.	6.5	99
48	Quantifying Modularity in the Evolution of Biomolecular Systems. <i>Genome Research</i> , 2004, 14, 391-397.	2.4	91
49	The Consistent Phylogenetic Signal in Genome Trees Revealed by Reducing the Impact of Noise. <i>Journal of Molecular Evolution</i> , 2004, 58, 527-539.	0.8	88
50	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , 1999, 343, 115.	1.7	83
51	Exploitation of gene context. <i>Current Opinion in Structural Biology</i> , 2000, 10, 366-370.	2.6	80
52	A Domain-Centric Analysis of Oomycete Plant Pathogen Genomes Reveals Unique Protein Organization. <i>Plant Physiology</i> , 2011, 155, 628-644.	2.3	79
53	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.	3.3	76
54	Comparative phosphoproteomics reveals evolutionary and functional conservation of phosphorylation across eukaryotes. <i>Genome Biology</i> , 2008, 9, R144.	13.9	75

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55	Combining data from genomes, Y2H and 3D structure indicates that BolA is a reductase interacting with a glutaredoxin. <i>FEBS Letters</i> , 2005, 579, 591-596.	1.3	73
56	Signature Genes as a Phylogenomic Tool. <i>Molecular Biology and Evolution</i> , 2008, 25, 1659-1667.	3.5	72
57	Extensive translational regulation during seed germination revealed by polysomal profiling. <i>New Phytologist</i> , 2017, 214, 233-244.	3.5	69
58	Gene and context: Integrative approaches to genome analysis. <i>Advances in Protein Chemistry</i> , 2000, 54, 345-379.	4.4	67
59	Phylogenomics reveal a robust fungal tree of life. <i>FEMS Yeast Research</i> , 2006, 6, 1213-1220.	1.1	66
60	Genesis of Chromatin and Transcription Dynamics in the Origin of Species. <i>Cell</i> , 2015, 161, 724-736.	13.5	64
61	Inversions and the dynamics of eukaryotic gene order. <i>Trends in Genetics</i> , 2001, 17, 304-306.	2.9	63
62	Evolutionary Acquisition of Cysteines Determines FOXO Paralog-Specific Redox Signaling. <i>Antioxidants and Redox Signaling</i> , 2015, 22, 15-28.	2.5	61
63	Timing the origin of eukaryotic cellular complexity with ancient duplications. <i>Nature Ecology and Evolution</i> , 2021, 5, 92-100.	3.4	61
64	Tyrosine Phosphorylation Profiling in FGF-2 Stimulated Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2011, 6, e17538.	1.1	58
65	Evolutionary Dynamics of the Spindle Assembly Checkpoint in Eukaryotes. <i>Current Biology</i> , 2020, 30, R589-R602.	1.8	55
66	Evolution of the Ras-like small GTPases and their regulators. <i>Small GTPases</i> , 2011, 2, 4-16.	0.7	54
67	Lateral Gene Transfer, Genome Surveys, and the Phylogeny of Prokaryotes. <i>Science</i> , 1999, 286, 1443a-1443.	6.0	52
68	Effector identification in the lettuce downy mildew <i>Bremia lactucae</i> by massively parallel transcriptome sequencing. <i>Molecular Plant Pathology</i> , 2012, 13, 719-731.	2.0	52
69	Protein Complex Evolution Does Not Involve Extensive Network Rewiring. <i>PLoS Computational Biology</i> , 2008, 4, e1000132.	1.5	50
70	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.	1.1	50
71	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.	1.1	44
72	Targeted Quantitative Phosphoproteomics Approach for the Detection of Phospho-tyrosine Signaling in Plants. <i>Journal of Proteome Research</i> , 2012, 11, 438-448.	1.8	44

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73	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.	1.5	43
74	Widespread Recurrent Patterns of Rapid Repeat Evolution in the Kinetochores Scaffold KNL1. <i>Genome Biology and Evolution</i> , 2015, 7, 2383-2393.	1.1	40
75	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005, 33, 6164-6171.	6.5	38
76	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, 227-237.	2.3	37
77	Domestication of self-splicing introns during eukaryogenesis: the rise of the complex spliceosomal machinery. <i>Biology Direct</i> , 2017, 12, 30.	1.9	37
78	Identification of homologs in insignificant blast hits by exploiting extrinsic gene properties. <i>BMC Bioinformatics</i> , 2007, 8, 356.	1.2	33
79	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, 160315.	1.5	33
80	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>Arabidopsis thaliana</i> . <i>Rna</i> , 2019, 25, 292-304.	1.6	33
81	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.	3.2	30
82	Epigenetics and transcription regulation during eukaryotic diversification: the saga of TFIID. <i>Genes and Development</i> , 2019, 33, 888-902.	2.7	29
83	A global definition of expression context is conserved between orthologs, but does not correlate with sequence conservation. <i>BMC Genomics</i> , 2006, 7, 10.	1.2	28
84	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.	1.6	27
85	Increased sucrose levels mediate selective mRNA translation in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2014, 14, 306.	1.6	26
86	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, 1848-1859.	1.8	26
87	Chromosomal instability by mutations in the novel minor spliceosome component <i>CENATAC</i> . <i>EMBO Journal</i> , 2021, 40, e106536.	3.5	26
88	Benchmarking orthology methods using phylogenetic patterns defined at the base of Eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
89	Conflicting phylogenetic position of <i>Schizosaccharomyces pombe</i> . <i>Genomics</i> , 2006, 88, 387-393.	1.3	22
90	Complex fate of paralogs. <i>BMC Evolutionary Biology</i> , 2008, 8, 337.	3.2	21

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91	Coevolution of gene families in prokaryotes. <i>Genome Research</i> , 2008, 18, 462-468.	2.4	21
92	Phylogeny of the CDC25 homology domain reveals rapid differentiation of Ras pathways between early animals and fungi. <i>Cellular Signalling</i> , 2009, 21, 1579-1585.	1.7	21
93	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.	1.7	21
94	Comparative genomics for reliable protein-function prediction from genomic data. <i>Trends in Genetics</i> , 2004, 20, 340-344.	2.9	20
95	Contribution of the epigenetic mark H3K27me3 to functional divergence after whole genome duplication in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2012, 13, R94.	13.9	20
96	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.	1.2	20
97	Cohesive versus Flexible Evolution of Functional Modules in Eukaryotes. <i>PLoS Computational Biology</i> , 2009, 5, e1000276.	1.5	19
98	Comparative Genome Analysis of the Mollicutes. , 2002, , 255-278.		18
99	The molecular basis of monopolin recruitment to the kinetochore. <i>Chromosoma</i> , 2019, 128, 331-354.	1.0	17
100	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. <i>Journal of Proteome Research</i> , 2015, 14, 2976-2987.	1.8	16
101	Variation and evolution of biomolecular systems: Searching for functional relevance. <i>FEBS Letters</i> , 2005, 579, 1839-1845.	1.3	14
102	Inferring the Evolutionary History of Your Favorite Protein: A Guide for Molecular Biologists. <i>BioEssays</i> , 2019, 41, 1900006.	1.2	14
103	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, 407-412.	3.3	13
104	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.	1.1	13
105	Evaluating Experimental Bias and Completeness in Comparative Phosphoproteomics Analysis. <i>PLoS ONE</i> , 2011, 6, e23276.	1.1	12
106	Shared Protein Complex Subunits Contribute to Explaining Disrupted Co-occurrence. <i>PLoS Computational Biology</i> , 2013, 9, e1003124.	1.5	10
107	The Histone Modification H3K27me3 Is Retained after Gene Duplication and Correlates with Conserved Noncoding Sequences in <i>Arabidopsis</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 572-579.	1.1	10
108	Small Homologous Blocks in <i>Phytophthora</i> Genomes Do Not Point to an Ancient Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2014, 6, 1079-1085.	1.1	9

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109	Enrichment of homologs in insignificant BLAST hits by co-complex network alignment. BMC Bioinformatics, 2010, 11, 86.	1.2	8
110	Recurrent sequence evolution after independent gene duplication. BMC Evolutionary Biology, 2020, 20, 98.	3.2	8
111	Comparative Genome Analysis: Exploiting the Context of Genes to Infer Evolution and Predict Function. Computational Biology, 2000, , 281-294.	0.1	7
112	The spread of the first introns in proto-eukaryotic paralogs. Communications Biology, 2022, 5, 476.	2.0	7
113	Gene duplications contribute to the overrepresentation of interactions between proteins of a similar age. BMC Evolutionary Biology, 2012, 12, 99.	3.2	6
114	Conservation of gene co-regulation in prokaryotes and eukaryotes. Trends in Biotechnology, 2002, 20, 410.	4.9	5
115	Evolution of Complex Regulation for Cell-Cycle Control. Genome Biology and Evolution, 2022, 14, .	1.1	4
116	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. Genome Biology, 2007, 8, R197.	13.9	3
117	Correlation between sequence conservation and the genomic context after gene duplication. Nucleic Acids Research, 2005, 33, 7176-7176.	6.5	0
118	Phylogenetic profiling in eukaryotes: The effect of species, orthologous group, and interactome selection on protein interaction prediction. PLoS ONE, 2022, 17, e0251833.	1.1	0