

# 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	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
2	Evolution of Complex Regulation for Cell-Cycle Control. Genome Biology and Evolution, 2022, 14, .	1.1	4
3	The spread of the first introns in proto-eukaryotic paralogs. Communications Biology, 2022, 5, 476.	2.0	7
4	Benchmarking orthology methods using phylogenetic patterns defined at the base of Eukaryotes. Briefings in Bioinformatics, 2021, 22, .	3.2	24
5	Timing the origin of eukaryotic cellular complexity with ancient duplications. Nature Ecology and Evolution, 2021, 5, 92-100.	3.4	61
6	Chromosomal instability by mutations in the novel minor spliceosome component <i>CENATAC</i> . EMBO Journal, 2021, 40, e106536.	3.5	26
7	Recurrent sequence evolution after independent gene duplication. BMC Evolutionary Biology, 2020, 20, 98.	3.2	8
8	Evolutionary Dynamics of the Spindle Assembly Checkpoint in Eukaryotes. Current Biology, 2020, 30, R589-R602.	1.8	55
9	Measuring the impact of gene prediction on gene loss estimates in Eukaryotes by quantifying falsely inferred absences. PLoS Computational Biology, 2019, 15, e1007301.	1.5	43
10	The molecular basis of monopolin recruitment to the kinetochore. Chromosoma, 2019, 128, 331-354.	1.0	17
11	Mosaic origin of the eukaryotic kinetochore. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12873-12882.	3.3	76
12	Epigenetics and transcription regulation during eukaryotic diversification: the saga of TFIID. Genes and Development, 2019, 33, 888-902.	2.7	29
13	Inferring the Evolutionary History of Your Favorite Protein: A Guide for Molecular Biologists. BioEssays, 2019, 41, 1900006.	1.2	14
14	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> . Rna, 2019, 25, 292-304.	1.6	33
15	The Arabidopsis bZIP transcription factor family "an update. Current Opinion in Plant Biology, 2018, 45, 36-49.	3.5	294
16	Extensive translational regulation during seed germination revealed by polysomal profiling. New Phytologist, 2017, 214, 233-244.	3.5	69
17	Unique Phylogenetic Distributions of the Ska and Dam1 Complexes Support Functional Analogy and Suggest Multiple Parallel Displacements of Ska by Dam1. Genome Biology and Evolution, 2017, 9, 1295-1303.	1.1	50
18	Evolutionary dynamics of the kinetochore network in eukaryotes as revealed by comparative genomics. EMBO Reports, 2017, 18, 1559-1571.	2.0	206

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19	Domestication of self-splicing introns during eukaryogenesis: the rise of the complex spliceosomal machinery. <i>Biology Direct</i> , 2017, 12, 30.	1.9	37
20	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
21	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
22	The PLETHORA Gene Regulatory Network Guides Growth and Cell Differentiation in Arabidopsis Roots. <i>Plant Cell</i> , 2016, 28, 2937-2951.	3.1	127
23	<scp>DOWNY MILDEW RESISTANT</scp> 6 and <scp>DMR</scp>6 are <scp>LIKE OXYGENASE</scp> 1 are partially redundant but distinct suppressors of immunity in Arabidopsis. <i>Plant Journal</i> , 2015, 81, 210-222.	2.8	168
24	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
25	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
26	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
27	Genesis of Chromatin and Transcription Dynamics in the Origin of Species. <i>Cell</i> , 2015, 161, 724-736.	13.5	64
28	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
29	Evolutionary Acquisition of Cysteines Determines FOXO Paralog-Specific Redox Signaling. <i>Antioxidants and Redox Signaling</i> , 2015, 22, 15-28.	2.5	61
30	Small Homologous Blocks in Phytophthora Genomes Do Not Point to an Ancient Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2014, 6, 1079-1085.	1.1	9
31	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, 572-579.	1.1	10
32	Increased sucrose levels mediate selective mRNA translation in Arabidopsis. <i>BMC Plant Biology</i> , 2014, 14, 306.	1.6	26
33	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
34	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
35	Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors. <i>Cell</i> , 2014, 157, 740-752.	13.5	248
36	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

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37	ABI4: versatile activator and repressor. <i>Trends in Plant Science</i> , 2013, 18, 125-132.	4.3	142
38	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.	1.5	221
39	Shared Protein Complex Subunits Contribute to Explaining Disrupted Co-occurrence. <i>PLoS Computational Biology</i> , 2013, 9, e1003124.	1.5	10
40	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
41	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
42	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
43	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
44	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
45	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
46	The R-spondin protein family. <i>Genome Biology</i> , 2012, 13, 242.	13.9	236
47	The Vertebrate Mitotic Checkpoint Protein BUBR1 Is an Unusual Pseudokinase. <i>Developmental Cell</i> , 2012, 22, 1321-1329.	3.1	116
48	Gene duplications contribute to the overrepresentation of interactions between proteins of a similar age. <i>BMC Evolutionary Biology</i> , 2012, 12, 99.	3.2	6
49	Evolution and Function of the Mitotic Checkpoint. <i>Developmental Cell</i> , 2012, 23, 239-250.	3.1	126
50	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
51	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
52	Tyrosine Phosphorylation Profiling in FGF-2 Stimulated Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2011, 6, e17538.	1.1	58
53	Evaluating Experimental Bias and Completeness in Comparative Phosphoproteomics Analysis. <i>PLoS ONE</i> , 2011, 6, e23276.	1.1	12
54	<i>Arabidopsis</i> PLETHORA Transcription Factors Control Phyllotaxis. <i>Current Biology</i> , 2011, 21, 1123-1128.	1.8	124

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55	Evolution of the TOR Pathway. <i>Journal of Molecular Evolution</i> , 2011, 73, 209-220.	0.8	118
56	Evolution of the Ras-like small GTPases and their regulators. <i>Small GTPases</i> , 2011, 2, 4-16.	0.7	54
57	A Domain-Centric Analysis of Oomycete Plant Pathogen Genomes Reveals Unique Protein Organization. <i>Plant Physiology</i> , 2011, 155, 628-644.	2.3	79
58	Enrichment of homologs in insignificant BLAST hits by co-complex network alignment. <i>BMC Bioinformatics</i> , 2010, 11, 86.	1.2	8
59	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.	2.5	155
60	SOMBRERO, BEARSKIN1, and BEARSKIN2 Regulate Root Cap Maturation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010, 22, 640-654.	3.1	163
61	Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. <i>Cell</i> , 2010, 143, 991-1004.	13.5	123
62	Cohesive versus Flexible Evolution of Functional Modules in Eukaryotes. <i>PLoS Computational Biology</i> , 2009, 5, e1000276.	1.5	19
63	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
64	Complex fate of paralogs. <i>BMC Evolutionary Biology</i> , 2008, 8, 337.	3.2	21
65	Comparative phosphoproteomics reveals evolutionary and functional conservation of phosphorylation across eukaryotes. <i>Genome Biology</i> , 2008, 9, R144.	13.9	75
66	Coevolution of gene families in prokaryotes. <i>Genome Research</i> , 2008, 18, 462-468.	2.4	21
67	Protein Complex Evolution Does Not Involve Extensive Network Rewiring. <i>PLoS Computational Biology</i> , 2008, 4, e1000132.	1.5	50
68	Signature Genes as a Phylogenomic Tool. <i>Molecular Biology and Evolution</i> , 2008, 25, 1659-1667.	3.5	72
69	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007, 35, D358-D362.	6.5	568
70	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. <i>Genome Biology</i> , 2007, 8, R197.	13.9	3
71	Identification of homologs in insignificant blast hits by exploiting extrinsic gene properties. <i>BMC Bioinformatics</i> , 2007, 8, 356.	1.2	33
72	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , 2007, 8, 83.	1.2	117

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73	Origin and evolution of the peroxisomal proteome. <i>Biology Direct</i> , 2006, 1, 8.	1.9	152
74	Conflicting phylogenetic position of <i>Schizosaccharomyces pombe</i> . <i>Genomics</i> , 2006, 88, 387-393.	1.3	22
75	Phylogenomics reveal a robust fungal tree of life. <i>FEMS Yeast Research</i> , 2006, 6, 1213-1220.	1.1	66
76	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	13.7	1,075
77	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. <i>Science</i> , 2006, 311, 1283-1287.	6.0	1,435
78	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
79	Predicting disease genes using protein-protein interactions. <i>Journal of Medical Genetics</i> , 2006, 43, 691-698.	1.5	518
80	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005, 33, 7176-7176.	6.5	0
81	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005, 33, 6164-6171.	6.5	38
82	GENOME TREES AND THE NATURE OF GENOME EVOLUTION. <i>Annual Review of Microbiology</i> , 2005, 59, 191-209.	2.9	184
83	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
84	Variation and evolution of biomolecular systems: Searching for functional relevance. <i>FEBS Letters</i> , 2005, 579, 1839-1845.	1.3	14
85	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
86	Quantifying Modularity in the Evolution of Biomolecular Systems. <i>Genome Research</i> , 2004, 14, 391-397.	2.4	91
87	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
88	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, 280-284.	2.0	228
89	Comparative genomics for reliable protein-function prediction from genomic data. <i>Trends in Genetics</i> , 2004, 20, 340-344.	2.9	20
90	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

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91	Function prediction and protein networks. <i>Current Opinion in Cell Biology</i> , 2003, 15, 191-198.	2.6	133
92	Predicting gene function by conserved co-expression. <i>Trends in Genetics</i> , 2003, 19, 238-242.	2.9	175
93	Systematic discovery of analogous enzymes in thiamin biosynthesis. <i>Nature Biotechnology</i> , 2003, 21, 790-795.	9.4	121
94	STRING: a database of predicted functional associations between proteins. <i>Nucleic Acids Research</i> , 2003, 31, 258-261.	6.5	1,897
95	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
96	Genomes in Flux: The Evolution of Archaeal and Proteobacterial Gene Content. <i>Genome Research</i> , 2002, 12, 17-25.	2.4	305
97	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
98	Comparative Genome Analysis of the Mollicutes. , 2002, , 255-278.		18
99	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 407-410.	4.9	111
100	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 410.	4.9	5
101	SHOT: a web server for the construction of genome phylogenies. <i>Trends in Genetics</i> , 2002, 18, 158-162.	2.9	193
102	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002, 417, 399-403.	13.7	2,137
103	Inversions and the dynamics of eukaryotic gene order. <i>Trends in Genetics</i> , 2001, 17, 304-306.	2.9	63
104	The phylogenetic distribution of frataxin indicates a role in iron-sulfur cluster protein assembly. <i>Human Molecular Genetics</i> , 2001, 10, 2463-2468.	1.4	139
105	Exploitation of gene context. <i>Current Opinion in Structural Biology</i> , 2000, 10, 366-370.	2.6	80
106	Gene context conservation of a higher order than operons. <i>Trends in Biochemical Sciences</i> , 2000, 25, 474-479.	3.7	187
107	Genome evolution. <i>Trends in Genetics</i> , 2000, 16, 9-11.	2.9	170
108	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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109	Predicting Protein Function by Genomic Context: Quantitative Evaluation and Qualitative Inferences. <i>Genome Research</i> , 2000, 10, 1204-1210.	2.4	453
110	Gene and context: Integrative approaches to genome analysis. <i>Advances in Protein Chemistry</i> , 2000, 54, 345-379.	4.4	67
111	Comparative Genome Analysis: Exploiting the Context of Genes to Infer Evolution and Predict Function. <i>Computational Biology</i> , 2000, , 281-294.	0.1	7
112	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
113	Lateral Gene Transfer, Genome Surveys, and the Phylogeny of Prokaryotes. <i>Science</i> , 1999, 286, 1443a-1443.	6.0	52
114	Genome phylogeny based on gene content. <i>Nature Genetics</i> , 1999, 21, 108-110.	9.4	658
115	Domains in plexins: links to integrins and transcription factors. <i>Trends in Biochemical Sciences</i> , 1999, 24, 261-263.	3.7	180
116	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , 1999, 343, 115-124.	1.7	208
117	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , 1999, 343, 115.	1.7	83
118	Conservation of gene order: a fingerprint of proteins that physically interact. <i>Trends in Biochemical Sciences</i> , 1998, 23, 324-328.	3.7	991