

# Stefan A Rensing

## List of Publications by Year in descending order

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127  
papers

14,000  
citations

34105

52  
h-index

22832

112  
g-index

138  
all docs

138  
docs citations

138  
times ranked

12710  
citing authors

#	ARTICLE	IF	CITATIONS
1	An overview of bioinformatics, genomics, and transcriptomics resources for bryophytes. <i>Journal of Experimental Botany</i> , 2022, 73, 4291-4305.	4.8	11
2	Unveiling the nature of a miniature world: a horizon scan of fundamental questions in bryology. <i>Journal of Bryology</i> , 2022, 44, 1-34.	1.2	12
3	The greening ashore. <i>Trends in Plant Science</i> , 2022, 27, 847-857.	8.8	9
4	Comparative transcriptomics identifies candidate genes involved in the evolutionary transition from dehiscent to indehiscent fruits in <i>Lepidium</i> (Brassicaceae). <i>BMC Plant Biology</i> , 2022, 22, .	3.6	3
5	<i>Aethionema arabicum</i> genome annotation using PacBio full-length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. <i>Plant Journal</i> , 2021, 106, 275-293.	5.7	20
6	HAG1 and SWI3A/B control of male germ line development in <i>P. patens</i> suggests conservation of epigenetic reproductive control across land plants. <i>Plant Reproduction</i> , 2021, 34, 149-173.	2.2	9
7	The EpiDiverse Plant Epigenome-Wide Association Studies (EWAS) Pipeline. <i>Epigenomes</i> , 2021, 5, 12.	1.8	6
8	Editorial: Highlights of IAB IMOSS SEB 2019 Joint Conference. <i>Frontiers in Plant Science</i> , 2021, 12, 694765.	3.6	0
9	A tale of two morphs: developmental patterns and mechanisms of seed coat differentiation in the dimorphic diaspore model <i>Aethionema arabicum</i> (Brassicaceae). <i>Plant Journal</i> , 2021, 107, 166-181.	5.7	8
10	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
11	Polyploidization within the Funariaceae—a key principle behind speciation, sporophyte reduction and the high variance of spore diameters?. <i>Bryophyte Diversity and Evolution</i> , 2021, 43, .	1.1	9
12	Coregulation of gene expression by White collar 1 and phytochrome in <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2021, 152, 103570.	2.1	3
13	Signatures of Transcription Factor Evolution and the Secondary Gain of Red Algae Complexity. <i>Genes</i> , 2021, 12, 1055.	2.4	9
14	Flowering plant embryos: How did we end up here?. <i>Plant Reproduction</i> , 2021, 34, 365-371.	2.2	5
15	A vertically transmitted amalgavirus is present in certain accessions of the bryophyte <i>Physcomitrium patens</i> . <i>Plant Journal</i> , 2021, 108, 1786-1797.	5.7	5
16	Molecular biology of mosses. <i>Plant Molecular Biology</i> , 2021, 107, 209-211.	3.9	0
17	EpiDiverse Toolkit: a pipeline suite for the analysis of bisulfite sequencing data in ecological plant epigenetics. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab106.	3.2	7
18	Gene gains paved the path to land. <i>Nature Plants</i> , 2020, 6, 7-8.	9.3	11

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19	DEK1 displays a strong subcellular polarity during <i>Physcomitrella patens</i> 3D growth. <i>New Phytologist</i> , 2020, 226, 1029-1041.	7.3	20
20	PEATmoss ( <i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	5.7	74
21	Multi-omics reveals mechanisms of total resistance to extreme illumination of a desert alga. <i>Nature Plants</i> , 2020, 6, 1031-1043.	9.3	33
22	How Plants Conquered Land. <i>Cell</i> , 2020, 181, 964-966.	28.9	27
23	A blind and independent benchmark study for detecting differentially methylated regions in plants. <i>Bioinformatics</i> , 2020, 36, 3314-3321.	4.1	7
24	The Moss <i>Physcomitrium</i> ( <i>Physcomitrella</i> ) <i>patens</i> : A Model Organism for Non-Seed Plants. <i>Plant Cell</i> , 2020, 32, 1361-1376.	6.6	188
25	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	9.3	225
26	Are fungi-derived genomic regions related to antagonism towards fungi in mosses?. <i>New Phytologist</i> , 2020, 228, 1169-1175.	7.3	8
27	Single Nucleotide Polymorphism Charting of <i>P. patens</i> Reveals Accumulation of Somatic Mutations During in vitro Culture on the Scale of Natural Variation by Selfing. <i>Frontiers in Plant Science</i> , 2020, 11, 813.	3.6	22
28	Characterisation of evolutionarily conserved key players affecting eukaryotic flagellar motility and fertility using a moss model. <i>New Phytologist</i> , 2020, 227, 440-454.	7.3	26
29	Rocket Science: The Effect of Spaceflight on Germination Physiology, Ageing, and Transcriptome of <i>Eruca sativa</i> Seeds. <i>Life</i> , 2020, 10, 49.	2.4	19
30	<i>Physcomitrella patens</i> Reute mC herry as a tool for efficient crossing within and between ecotypes. <i>Plant Biology</i> , 2019, 21, 143-149.	3.8	17
31	Reconstructing trait evolution in plant evo“devo studies. <i>Current Biology</i> , 2019, 29, R1110-R1118.	3.9	47
32	Analysis of the Localization of Fluorescent PpROP1 and PpROP-GEF4 Fusion Proteins in Moss Protonemata Based on Genomic “Knock-In” and Estradiol-Titratable Expression. <i>Frontiers in Plant Science</i> , 2019, 10, 456.	3.6	13
33	Usability of reference-free transcriptome assemblies for detection of differential expression: a case study on <i>Aethionema arabicum</i> dimorphic seeds. <i>BMC Genomics</i> , 2019, 20, 95.	2.8	18
34	Characterization of <i>spa</i> mutants in the moss <i>Physcomitrella</i> provides evidence for functional divergence of <i>SPA</i> genes during the evolution of land plants. <i>New Phytologist</i> , 2019, 224, 1613-1626.	7.3	17
35	The intracellular distribution of the components of the GET system in vascular plants. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 1650-1662.	4.1	8
36	<i>Aethionema arabicum</i> : a novel model plant to study the light control of seed germination. <i>Journal of Experimental Botany</i> , 2019, 70, 3313-3328.	4.8	31

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37	ABA-Induced Vegetative Diaspore Formation in <i>Physcomitrella patens</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 315.	3.6	30
38	Genome Improvement and Genetic Map Construction for <i>Aethionema arabicum</i> , the First Divergent Branch in the Brassicaceae Family. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3521-3530.	1.8	17
39	A kiwellin disarms the metabolic activity of a secreted fungal virulence factor. <i>Nature</i> , 2019, 565, 650-653.	27.8	48
40	Great moments in evolution: the conquest of land by plants. <i>Current Opinion in Plant Biology</i> , 2018, 42, 49-54.	7.1	153
41	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , 2018, 95, 168-182.	5.7	115
42	The Biotrophic Development of <i>Ustilago maydis</i> Studied by RNA-Seq Analysis. <i>Plant Cell</i> , 2018, 30, 300-323.	6.6	186
43	When the BRANCHED network bears fruit: how carpic dominance causes fruit dimorphism in <i>Aethionema</i> . <i>Plant Journal</i> , 2018, 94, 352-371.	5.7	20
44	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	406
45	Evolution of the Symbiosis-Specific GRAS Regulatory Network in Bryophytes. <i>Frontiers in Plant Science</i> , 2018, 9, 1621.	3.6	17
46	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5.	3.9	134
47	Detection of somatic epigenetic variation in Norway spruce via targeted bisulfite sequencing. <i>Ecology and Evolution</i> , 2018, 8, 9672-9682.	1.9	16
48	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
49	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
50	Iron-Sulfur Cluster Biosynthesis in Algae with Complex Plastids. <i>Genome Biology and Evolution</i> , 2018, 10, 2061-2071.	2.5	9
51	Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017, 90, 447-465.	5.7	97
52	Characterization of Phytochrome Interacting Factors from the Moss <i>Physcomitrella patens</i> Illustrates Conservation of Phytochrome Signaling Modules in Land Plants. <i>Plant Cell</i> , 2017, 29, 310-330.	6.6	61
53	Three rings for the evolution of plastid shape: a tale of land plant FtsZ. <i>Protoplasma</i> , 2017, 254, 1879-1885.	2.1	28
54	Sexual reproduction, sporophyte development and molecular variation in the model moss <i>Physcomitrella patens</i> : introducing the ecotype Reute. <i>Plant Journal</i> , 2017, 90, 606-620.	5.7	56

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55	Why we need more nonâ€seed plant models. <i>New Phytologist</i> , 2017, 216, 355-360.	7.3	90
56	Ecological plant epigenetics: Evidence from model and nonâ€model species, and the way forward. <i>Ecology Letters</i> , 2017, 20, 1576-1590.	6.4	279
57	Massive Protein Import into the Early-Evolutionary-Stage Photosynthetic Organelle of the Amoeba <i>Paulinella chromatophora</i> . <i>Current Biology</i> , 2017, 27, 2763-2773.e5.	3.9	91
58	A Single-Target Mitochondrial RNA Editing Factor of <i>Funaria hygrometrica</i> Can Fully Reconstitute RNA Editing at Two Sites in <i>Physcomitrella patens</i> . <i>Plant and Cell Physiology</i> , 2017, 58, 496-507.	3.1	13
59	Selfing in Haploid Plants and Efficacy of Selection: Codon Usage Bias in the Model Moss <i>Physcomitrella patens</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1528-1546.	2.5	21
60	Comprehensive Genome-Wide Classification Reveals That Many Plant-Specific Transcription Factors Evolved in Streptophyte Algae. <i>Genome Biology and Evolution</i> , 2017, 9, 3384-3397.	2.5	95
61	Combination of the Endogenous <i>lhcsr1</i> Promoter and Codon Usage Optimization Boosts Protein Expression in the Moss <i>Physcomitrella patens</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1842.	3.6	8
62	Plant Evoâ€Devo: How Tip Growth Evolved. <i>Current Biology</i> , 2016, 26, R1228-R1230.	3.9	2
63	The DEK1 calpain Linker functions in three-dimensional body patterning in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2016, 172, pp.00925.2016.	4.8	17
64	Developmental Control and Plasticity of Fruit and Seed Dimorphism in <i>Aethionema arabicum</i> . <i>Plant Physiology</i> , 2016, 172, 1691-1707.	4.8	59
65	Structural basis for the CsrA-dependent modulation of translation initiation by an ancient regulatory protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10168-10173.	7.1	41
66	Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.	6.6	98
67	Phytochromes: More Than Meets the Eye. <i>Trends in Plant Science</i> , 2016, 21, 543-546.	8.8	29
68	Detection of SNPs based on transcriptome sequencing in Norway spruce ( <i>Picea abies</i> (L.) Karst). <i>Conservation Genetics Resources</i> , 2016, 8, 105-107.	0.8	12
69	(Why) Does Evolution Favour Embryogenesis?. <i>Trends in Plant Science</i> , 2016, 21, 562-573.	8.8	37
70	Localization and Evolution of Putative Triose Phosphate Translocators in the Diatom <i>Phaeodactylum tricorutum</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 2955-2969.	2.5	53
71	Means to optimize protein expression in transgenic plants. <i>Current Opinion in Biotechnology</i> , 2015, 32, 61-67.	6.6	27
72	The evolution of eukaryotic cells from the perspective of peroxisomes. <i>BioEssays</i> , 2015, 37, 195-203.	2.5	47

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73	<i>De novo</i> assembly and comparative analysis of the <i>sc</i>C</i>eratodon purpureus</i> transcriptome. <i>Molecular Ecology Resources</i> , 2015, 15, 203-215.	4.8	43
74	The Evolution of Transcriptional Regulation in the Viridiplantae and its Correlation with Morphological Complexity. <i>Advances in Marine Genomics</i> , 2015, , 301-333.	1.2	23
75	ppdb: plant promoter database version 3.0. <i>Nucleic Acids Research</i> , 2014, 42, D1188-D1192.	14.5	61
76	Functional analysis of COP1 and SPA orthologs from <i>Physcomitrella</i> and rice during photomorphogenesis of transgenic <i>Arabidopsis</i> reveals distinct evolutionary conservation. <i>BMC Plant Biology</i> , 2014, 14, 178.	3.6	44
77	Molecular evidence for convergent evolution and allopolyploid speciation within the <i>Physcomitrium-Physcomitrella</i> species complex. <i>BMC Evolutionary Biology</i> , 2014, 14, 158.	3.2	48
78	<i>WOX13</i>-<i>like</i> genes are required for reprogramming of leaf and protoplast cells into stem cells in the moss <i>Physcomitrella patens</i>. <i>Development (Cambridge)</i> , 2014, 141, 1660-1670.	2.5	136
79	Gene duplication as a driver of plant morphogenetic evolution. <i>Current Opinion in Plant Biology</i> , 2014, 17, 43-48.	7.1	191
80	The chromatin landscape of the moss <i>Physcomitrella patens</i> and its dynamics during development and drought stress. <i>Plant Journal</i> , 2014, 79, 67-81.	5.7	91
81	Large-scale gene expression profiling data for the model moss <i>sc</i>P</i>hyscomitrella patens</i> aid understanding of developmental progression, culture and stress conditions. <i>Plant Journal</i> , 2014, 79, 530-539.	5.7	82
82	Reannotation and extended community resources for the genome of the non-seed plant <i>Physcomitrella patens</i> provide insights into the evolution of plant gene structures and functions. <i>BMC Genomics</i> , 2013, 14, 498.	2.8	170
83	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	7.1	307
84	Evolutionary Importance of Generative Polyploidy for Genome Evolution of Haploid-Dominant Land Plants. , 2013, , 295-305.		14
85	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	12.6	439
86	Origin and evolution of PIN auxin transporters in the green lineage. <i>Trends in Plant Science</i> , 2013, 18, 5-10.	8.8	109
87	Green Targeting Predictor and Ambiguous Targeting Predictor 2: the pitfalls of plant protein targeting prediction and of transient protein expression in heterologous systems. <i>New Phytologist</i> , 2013, 200, 1022-1033.	7.3	29
88	Network Theory Inspired Analysis of Time-Resolved Expression Data Reveals Key Players Guiding <i>P. patens</i> Stem Cell Development. <i>PLoS ONE</i> , 2013, 8, e60494.	2.5	27
89	Polyphenol oxidases in <i>Physcomitrella</i> : functional PPO1 knockout modulates cytokinin-dependent development in the moss <i>Physcomitrella patens</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 5121-5135.	4.8	29
90	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377

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91	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	12.6	371
92	The Ectocarpus Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18
93	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	12.6	794
94	Assigning DYW-type PPR proteins to RNA editing sites in the funariid mosses <i>Physcomitrella patens</i> and <i>Funaria hygrometrica</i> . <i>Plant Journal</i> , 2011, 67, 370-380.	5.7	46
95	Generation-Biased Gene Expression in a Bryophyte Model System. <i>Molecular Biology and Evolution</i> , 2011, 28, 803-812.	8.9	49
96	Prediction and Validation of Promoters Involved in the Abscisic Acid Response in <i>Physcomitrella patens</i> . <i>Molecular Plant</i> , 2011, 4, 713-729.	8.3	30
97	Genome-Wide Phylogenetic Comparative Analysis of Plant Transcriptional Regulation: A Timeline of Loss, Gain, Expansion, and Correlation with Complexity. <i>Genome Biology and Evolution</i> , 2010, 2, 488-503.	2.5	174
98	Microarray analysis of the moss <i>Physcomitrella patens</i> reveals evolutionarily conserved transcriptional regulation of salt stress and abscisic acid signalling. <i>Plant Molecular Biology</i> , 2010, 72, 27-45.	3.9	110
99	Identification and characterization of NAGNAG alternative splicing in the moss <i>Physcomitrella patens</i> . <i>BMC Plant Biology</i> , 2010, 10, 76.	3.6	13
100	THE SPECIATION HISTORY OF THE <i>PHYSCOMITRIUM-PHYSCOMITRELLA</i> SPECIES COMPLEX. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 217-231.	2.3	59
101	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
102	The Molecular and Physiological Responses of <i>Physcomitrella patens</i> to Ultraviolet-B Radiation Å. <i>Plant Physiology</i> , 2010, 153, 1123-1134.	4.8	152
103	PlnTFDB: updated content and new features of the plant transcription factor database. <i>Nucleic Acids Research</i> , 2010, 38, D822-D827.	14.5	635
104	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . <i>Science</i> , 2010, 329, 223-226.	12.6	536
105	Regulation of stem cell maintenance by the Polycomb protein FIE has been conserved during land plant evolution. <i>Development (Cambridge)</i> , 2009, 136, 2433-2444.	2.5	133
106	The evolution of nuclear auxin signalling. <i>BMC Evolutionary Biology</i> , 2009, 9, 126.	3.2	115
107	RNA editing: only eleven sites are present in the <i>Physcomitrella patens</i> mitochondrial transcriptome and a universal nomenclature proposal. <i>Molecular Genetics and Genomics</i> , 2009, 281, 473-481.	2.1	103
108	Prediction of dual protein targeting to plant organelles. <i>New Phytologist</i> , 2009, 183, 224-236.	7.3	73

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109	The WUS homeobox-containing (WOX) protein family. <i>Genome Biology</i> , 2009, 10, 248.	9.6	354
110	Complex chloroplast RNA metabolism: just debugging the genetic programme?. <i>BMC Biology</i> , 2008, 6, 36.	3.8	87
111	Exploring plant biodiversity: the <i>Physcomitrella</i> genome and beyond. <i>Trends in Plant Science</i> , 2008, 13, 542-549.	8.8	132
112	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	12.6	1,712
113	A sequence-anchored genetic linkage map for the moss, <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2008, 56, 855-866.	5.7	42
114	PlanTAPDB, a Phylogeny-Based Resource of Plant Transcription-Associated Proteins. <i>Plant Physiology</i> , 2007, 143, 1452-1466.	4.8	79
115	An ancient genome duplication contributed to the abundance of metabolic genes in the moss <i>Physcomitrella patens</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 130.	3.2	171
116	Identification of genic moss SSR markers and a comparative analysis of twenty-four algal and plant gene indices reveal species-specific rather than group-specific characteristics of microsatellites. <i>BMC Plant Biology</i> , 2006, 6, 9.	3.6	78
117	The mechanism of gene targeting in <i>Physcomitrella patens</i> : homologous recombination, concatenation and multiple integration. <i>Nucleic Acids Research</i> , 2006, 34, 6205-6214.	14.5	126
118	Representation and High-Quality Annotation of the <i>Physcomitrella patens</i> Transcriptome Demonstrates a High Proportion of Proteins Involved in Metabolism in Mosses. <i>Plant Biology</i> , 2005, 7, 238-250.	3.8	96
119	Large-scale Analysis of 73 329 <i>Physcomitrella</i> Plants Transformed with Different Gene Disruption Libraries: Production Parameters and Mutant Phenotypes. <i>Plant Biology</i> , 2005, 7, 228-237.	3.8	45
120	Protein encoding genes in an ancient plant: analysis of codon usage, retained genes and splice sites in a moss, <i>Physcomitrella patens</i> . <i>BMC Genomics</i> , 2005, 6, 43.	2.8	56
121	EST Sequencing from Embryogenic <i>Cyclamen persicum</i> Cell Cultures Identifies a High Proportion of Transcripts Homologous to Plant Genes Involved in Somatic Embryogenesis. <i>Journal of Plant Growth Regulation</i> , 2005, 24, 102-115.	5.1	37
122	Diversification of fts Z During Early Land Plant Evolution. <i>Journal of Molecular Evolution</i> , 2004, 58, 154-162.	1.8	33
123	Moss transcriptome and beyond. <i>Trends in Plant Science</i> , 2002, 7, 535-538.	8.8	102
124	Day Length and Temperature Strongly Influence Sexual Reproduction and Expression of a Novel MADS-Box Gene in the Moss <i>Physcomitrella patens</i> . <i>Plant Biology</i> , 2002, 4, 595-602.	3.8	105
125	Visualization of a Cytoskeleton-like Ftsz Network in Chloroplasts. <i>Journal of Cell Biology</i> , 2000, 151, 945-950.	5.2	102
126	Characterization of a maize ribosomal P2 protein cDNA and phylogenetic analysis of the P1/P2 family of ribosomal proteins. <i>Plant Molecular Biology</i> , 1996, 30, 655-658.	3.9	5

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127	Comparative Genomics. , 0, , 42-75.		4