

# Joke Reumers

## List of Publications by Year in descending order

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35  
papers

3,547  
citations

270111

25  
h-index

406436

35  
g-index

36  
all docs

36  
docs citations

36  
times ranked

8820  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetically Engineered iPSC-Derived FTDP-17 MAPT Neurons Display Mutation-Specific Neurodegenerative and Neurodevelopmental Phenotypes. <i>Stem Cell Reports</i> , 2018, 11, 363-379.	2.3	43
2	A random effects model for the identification of differential splicing (REIDS) using exon and HTA arrays. <i>BMC Bioinformatics</i> , 2017, 18, 273.	1.2	2
3	Identification of cis-regulatory mutations generating de novo edges in personalized cancer gene regulatory networks. <i>Genome Medicine</i> , 2017, 9, 80.	3.6	17
4	Halvade-RNA: Parallel variant calling from transcriptomic data using MapReduce. <i>PLoS ONE</i> , 2017, 12, e0174575.	1.1	17
5	Performance Analysis of a Parallel, Multi-node Pipeline for DNA Sequencing. <i>Lecture Notes in Computer Science</i> , 2016, , 233-242.	1.0	2
6	elPrep: High-Performance Preparation of Sequence Alignment/Map Files for Variant Calling. <i>PLoS ONE</i> , 2015, 10, e0132868.	1.1	22
7	Halvade: scalable sequence analysis with MapReduce. <i>Bioinformatics</i> , 2015, 31, 2482-2488.	1.8	69
8	QQ-SNV: single nucleotide variant detection at low frequency by comparing the quality quantiles. <i>BMC Bioinformatics</i> , 2015, 16, 379.	1.2	3
9	ViVaMBC: estimating viral sequence variation in complex populations from illumina deep-sequencing data using model-based clustering. <i>BMC Bioinformatics</i> , 2015, 16, 59.	1.2	12
10	Performance assessment of the Illumina massively parallel sequencing platform for deep sequencing analysis of viral minority variants. <i>Journal of Virological Methods</i> , 2015, 221, 29-38.	1.0	26
11	VirVarSeq: a low-frequency virus variant detection pipeline for Illumina sequencing using adaptive base-calling accuracy filtering. <i>Bioinformatics</i> , 2015, 31, 94-101.	1.8	47
12	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. <i>Nature Communications</i> , 2014, 5, 4767.	5.8	421
13	Mismatch repair deficiency endows tumors with a unique mutation signature and sensitivity to DNA double-strand breaks. <i>ELife</i> , 2014, 3, e02725.	2.8	71
14	Efficiency of whole genome amplification of single circulating tumor cells enriched by CellSearch and sorted by FACS. <i>Genome Medicine</i> , 2013, 5, 106.	3.6	79
15	Pipit: visualizing functional impacts of structural variations. <i>Bioinformatics</i> , 2013, 29, 2206-2207.	1.8	1
16	Whole-genome sequencing reveals a coding non-pathogenic variant tagging a non-coding pathogenic hexanucleotide repeat expansion in C9orf72 as cause of amyotrophic lateral sclerosis. <i>Human Molecular Genetics</i> , 2012, 21, 2412-2419.	1.4	33
17	Optimized filtering reduces the error rate in detecting genomic variants by short-read sequencing. <i>Nature Biotechnology</i> , 2012, 30, 61-68.	9.4	211
18	VEGF pathway genetic variants as biomarkers of treatment outcome with bevacizumab: an analysis of data from the AVITA and AVOREN randomised trials. <i>Lancet Oncology</i> , The, 2012, 13, 724-733.	5.1	174

#	ARTICLE	IF	CITATIONS
19	SNPeffect 4.0: on-line prediction of molecular and structural effects of protein-coding variants. <i>Nucleic Acids Research</i> , 2012, 40, D935-D939.	6.5	235
20	Î±-Galactosidase Aggregation Is a Determinant of Pharmacological Chaperone Efficacy on Fabry Disease Mutants. <i>Journal of Biological Chemistry</i> , 2012, 287, 28386-28397.	1.6	31
21	Gain of function of mutant p53 by coaggregation with multiple tumor suppressors. <i>Nature Chemical Biology</i> , 2011, 7, 285-295.	3.9	450
22	An Evolutionary Trade-Off between Protein Turnover Rate and Protein Aggregation Favors a Higher Aggregation Propensity in Fast Degrading Proteins. <i>PLoS Computational Biology</i> , 2011, 7, e1002090.	1.5	50
23	Sequencing of DISC1 Pathway Genes Reveals Increased Burden of Rare Missense Variants in Schizophrenia Patients from a Northern Swedish Population. <i>PLoS ONE</i> , 2011, 6, e23450.	1.1	46
24	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. <i>Breast Cancer Research</i> , 2010, 12, R110.	2.2	82
25	Exploring the sequence determinants of amyloid structure using position-specific scoring matrices. <i>Nature Methods</i> , 2010, 7, 237-242.	9.0	566
26	PepX: a structural database of non-redundant protein-peptide complexes. <i>Nucleic Acids Research</i> , 2010, 38, D545-D551.	6.5	102
27	Multiple Evolutionary Mechanisms Reduce Protein Aggregation~!2009-04-21~!2009-07-09~!2010-01-02~!. <i>The Open Biology Journal</i> , 2010, 2, 176-184.	0.5	7
28	Using structural bioinformatics to investigate the impact of non synonymous SNPs and disease mutations: scope and limitations. <i>BMC Bioinformatics</i> , 2009, 10, S9.	1.2	22
29	Protein sequences encode safeguards against aggregation. <i>Human Mutation</i> , 2009, 30, 431-437.	1.1	86
30	Genetic variability in the mitochondrial serine protease<i>HTRA2</i> contributes to risk for Parkinson disease. <i>Human Mutation</i> , 2008, 29, 832-840.	1.1	107
31	Joint annotation of coding and non-coding single nucleotide polymorphisms and mutations in the SNPeffect and PupaSuite databases. <i>Nucleic Acids Research</i> , 2008, 36, D825-D829.	6.5	60
32	Reconstruction of Protein Backbones from the BriX Collection of Canonical Protein Fragments. <i>PLoS Computational Biology</i> , 2008, 4, e1000083.	1.5	42
33	SNPeffect v2.0: a new step in investigating the molecular phenotypic effects of human non-synonymous SNPs. <i>Bioinformatics</i> , 2006, 22, 2183-2185.	1.8	80
34	PupaSuite: finding functional single nucleotide polymorphisms for large-scale genotyping purposes. <i>Nucleic Acids Research</i> , 2006, 34, W621-W625.	6.5	194
35	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. <i>Nucleic Acids Research</i> , 2004, 33, D527-D532.	6.5	136