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1	279	Rahul Agarwal, Matthew Kent, Eli Grindflek, Maren Van Son and Sigbjørn Lien. Whole-Genome Resequencing Identifies Variants Within QTL Regions for Boar Taint
2	299	Nikita Alexeev. Random matrix approach and Combinatorial topology approach to Sorting by transpositions
3	307	Arnald Alonso, Sara Marsal and Antonio Julià. CNStream2: a fast and highly accurate tool for SNP and CNV genotyping with Illumina microarrays
4	309	Sonja Althammer, Amadis Pages and Eduardo Eyras. Models of regulatory genomics
5	304	Tomasz Arodz and Przemyslaw Plonka. Uncovering the Distribution of Protein Structure Change Magnitudes upon Single Amino Acid Substitutions
6	275	Çiğdem Sevim Bayrak and Burak Erman. Predicting the Most Probable Conformations of a Given Peptide Sequence in the Random Coil State
7	260	Mahdi Belcaid, Anne Bergeron, Aida Ouangraoua, Philippe Lavoie-Mongrain, Nicolas Massoulier and Guylaine Poisson. Duplications in tape measure proteins
8	296	Biter Bilen and Mihaela Zavolan. Probabilistic framework to identify crosslinked positions in RNA-binding protein crosslinking and immune-precipitation data
9	301	Thomas Bonfert, Gergely Csaba, Ralf Zimmer and Caroline C. Friedel. A context-based approach to identify the most likely mapping for RNA-seq experiments
10	298	Jascha Casadio, Oriol Fornés, Elena Hidalgo, José Ayté, Isabel Calvo Arnedo, Patricia Garcia and Baldo Oliva. A computational analysis of the regulation of oxidative stress genes in S. pombe by Pap1 and Prr1
11	257	Chih-Hung Chang, Hsiang-Iu Wang, Hsiang-Chia Lu, Hong-Hwa Chen, Chuan Yi Tang and Hsin-Hung Yeh. A hierarchical screening strategy for gene functional analysis using RNA interference
12	244	Sean Chun-Chang Chen, Feng-Chi Chen and Wen-Hsiung Li. Distinct evolutionary rates of phosphorylated and nonphosphoryalted amino acid residues in mammals
13	261	Shih-Yi Chao and A-Mei Huang. Metastatic Pathway Identification – a case study of prostate cancer
14	291	Danielle Hyun-Jin Choi and Brett Tyler. Mathematical Modeling of Phytophthora sojae Effector Gene Evolution
15	252	Gwo-Yu Chuang, Jeffrey Boyington, Michael Joyce, Jiang Zhu, Gary Nabel, Peter Kwong and Ivelin Georgiev. Bioinformatics Prediction Of N-linked Glycosylation Incorporating Structural Properties and Patterns
16	285	Joao Curado, Hagen Tilgner and Roderic Guigo. Modeling splicing from chromatin
17	249	Noah Daniels, Raghavendra Hosur, Bonnie Berger and Lenore Cowen. SMURFLite: combining simplified Markov random fields with simulated evolution improves remote homology detection for beta-structural proteins
18	290	Ines de Santiago, Tom Carroll and Ana Pombo. SeqGI: Sequence Read Enrichment at Genomic Intervals
19	286	Juliane C. Dohm, Andre E. Minoche, Daniela Holtgraewe, Thomas Rosleff Sörensen, Richard Reinhardt, Hans Lehrach, Bernd Weisshaar and Heinz Himmelbauer. Drafting a large genome at high quality: Multi-platform sequence assembly and integration with genetic and physical maps of sugar beet (Beta vulgaris)
20	287	Sumeet Dua and Afolabi Olomola. Functional Model Discovery from Gene Expression Time Series using Markov Models
21	284	Ionas Erb, Juan Ramon González-Vallinas, Giovanni Bussotti, Enrique Blanco, Eduardo Eyras and Notredame Cedric. Use of ChiP-Seq data for the design of a multiple promoter-alignment method
22	259	Mario Fasold, David Langenberger, Hans Binder, Peter F. Stadler and Steve Hoffmann. DARIO: A ncRNA detection and analysis tool for next-generation sequencing experiments
23	258	Oscar Flores and Modesto Orozco. Automatic annotation of nucleosome positions: from peaks to reads

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25	302	Santi González, Bàrbara Montserrat-Sentís, Friman Sánchez, Montserrat Puiggròs, Enrique Blanco, Laura Martinez, Alex Ramirez and David Torrents. Prediction of regulatory regions using ReLA
26	282	Mar Gonzàlez-Porta, Miquel Calvo, Michael Sammeth and Roderic Guigó. Estimation of alternative splicing variability in human populations
27	306	Juan González-Vallinas and Eduardo Eyras. Predicting and characterizing active enhancers in cancer using high-throughput sequencing data
28	268	Lydia Hopp, Henry Wirth, Mario Fasold, Markus Loeffler and Hans Binder. Portraying the expression landscapes of cancer subtypes
29	276	Thibaut Hourlier, Daniel Barrell, Susan Fairley, Magali Ruffier, Carlos Garcia Giron, Rishi Nag, Simon White, Andreas Kähäri, Amonida Zadissa, Bronwen Aken, Stephen Searle and Tim Hubbard. Ensembl and RNA-Seq: towards better genome annotation!
30	289	Md Jamiul Jahid and Jianhua Ruan. A randomized Steiner-tree approach for biomarker discovery and classification for breast cancer metastasis
31	303	Daeyong Jin and Hyunju Lee. A computational approach to identifying gene-microRNA regulatory modules in cancer
32	262	Yan Jing, Ping Han and Xiaofeng Song. Intracellular protein stability correlated with the features of the solvent accessible surface
33	280	Kwang Su Jung and Kiejung Park. An aCGH-based Tool for Detecting Genomic Variation
34	267	Sangcheol Kim, Seulji Lee, Byungwook Lee, Sanghyuk Lee, Sungwon Kwon and Johan Lim. Stouffer's Test in a Large Scale Simultaneous Hypothesis Testing
35	292	Youn-Jae Kim, Jong-Eun Lee, Heon Yoo, Seung-Hoon Lee and Jong Bae Park. Lung cancer brain metastasis-specific mutations identified by exome sequencing
36	247	David Knox and Robin Dowell. Automated Generation of Stochastic Model Rules for Single Cell Simulation of Transcriptional Regulation Mechanisms
37	273	Byungwook Lee. Quantification of transcriptome from RNA-Seq data by effective length normalization
38	246	Ana Paula Leite, Maxim N. Artyomov, Fadi Towfic and Aviv Regev. Systematic identification of topologically essential interactions in regulatory networks
39	297	José Ignacio Lucas Lledó and Mario Cáceres. Detection of chromosomal inversions with paired-end sequencing
40	248	Serghei Mangul, Adrian Caciula, Nicholas Mancuso, Ion Mandoiu and Alex Zelikovsky. Poster : An Integer Programming Approach to Novel Transcript Reconstruction from Paired-End RNA-Seq Reads
41	325	Marta Mele, Roderic Guigó and Tomàs Marquès. Studying lncRNAs in great ape evolution
42	288	Fernando Meyer, Stefan Kurtz and Michael Beckstette. Fast and flexible approximate database search for RNA sequence-structure patterns
43	250	Andre E. Minoche, Juliane C. Dohm and Heinz Himmelbauer. Errors and biases in Illumina second generation sequencing data
44	295	Jae Yong Nam, Seung Gu Park and Sun Shim Choi. Analysis of evolutionary characteristics of protein secondary structural units
45	270	Asif Naqvi, Shaymaa Bahnassy, Kuldeep Uchadia, Rinkesh Goyal, Luccky Sharma and Aruna Devi. Study to test the inhibitory activity of THC- Δ9-tetrahydrocannabinol and its derivatives on Acetylcholinesterase (AChe) enzyme: A Molecular Modeling Study
46	255	Leonid Nazarov, Yan Stirmanov, Sergey Larionov, Sergey Rybalko, Eugene Ryadchenko and Alexander Loskutov. The Nature of Extremophiles Genomes Clusterization by Detrended Fluctuation Analysis

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48	251	Eva Maria Novoa, Mariana Pavon-Eternod, Tao Pan and Lluis Ribas de Pouplana. A role for tRNA modifications in genome structure and codon usage
49	243	Hatice Osmanbeyoglu and Xinghua Lu. Investigating Mechanisms of Estrogen-Mediated Repression of ERα Target Genes in Breast Cancer Cell Lines
50	256	Aida Ouangraoua, Krister Swenson and Anne Bergeron. On the comparison of sets of alternative transcripts
51	294	Seung Gu Park and Sun Shim Choi. Evolutionary non-random flow of synonymous codon usage in multiple organisms
52	293	Yuri Pritykin and Mona Singh. Confirmation of Date and Party Hubs across Organisms
53	263	Florian Rasche, Kerstin Scheubert, Franziska Hufsky, Marco Kai, Ales Svatos and Sebastian Böcker. Characterisation of unknown metabolites by tandem mass spectrometry
54	264	Tobias Rausch, Thomas Zichner, Andreas Schlattl, Adrian Stütz, Vladimir Benes and Jan Korbel. DELLY: Structural variant discovery at single-nucleotide resolution
55	265	Rocio Rebollido-Rios, Stanislav Jakuschev and Daniel Hoffmann. HOW DOES THE CALCIUM BINDING COULD AFFECT THE SUSPECTED PROTEASE ACTIVITY OF SONIC HEDGEHOG?
56	308	Jairo Rocha and Ricardo Alberich. The Significance of the ProtDeform Score for Structure Prediction and Alignment
57	254	Sayed Mohammad Ebrahim Sahraeian and Byung-Jun Yoon. NAPAbench: a comprehensive network alignment benchmark
58	245	David Sankoff, Chunfang Zheng and Baoyong Wang. A model for biased fractionation after whole genome duplication
59	277	Melanie Schirmer, Christopher Quince, William T. Sloan and David Taylor. Benchmarking of Viral Haplotype Reconstruction Programs
60	274	Matthias Scholz. A missing data approach to validate nonlinear PCA
61	278	H.M.Mahadeva Swamy, Ramasamy Asokan and Riaz Mahmood. Bacillus thuringiensis Cry1I and Cry3A Coleopteran-active insecticidal crystal Proteins: Homology-based 3D Modelling and Implications for Toxin Activity
62	300	Fahad Syed, Mikko Arvas, Marja Ilmen and Tiina Nakari-Setala. Comparison of Bacterial Genomes
63	305	Oznur Tastan, Yanjun Qi, Jaime G. Carbonell and Judith Klein-Seetharaman. Refining Literature Curated HIV-1, Human Protein-Protein Interactions Using Expert Opinions
64	283	Marie Trussart, Davide Bau, Marc A. Marti-Renom, Eva Yus Najera and Luis Serrano Pubul. The three-dimensional genome conformation of Mycoplasma pneumoniae
65	253	Chan-Shuo Wu, Chun-Ying Yu, Ching-Yu Chuang, Hung-Chih Kuo and Trees-Juen Chuang. Identification and analysis of trans-splicing in human embryonic stem cells by transcriptome sequencing

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67	328	Catarina Allegue, Óscar Campuzano, Lucía Quintana, Carles Ferrer, Sergio Castillo, Eduardo Salas, Mónica Bayés, Simon Heath, Anna María Iglesias, Mónica Coll and Ramon Brugada. VALIDATION OF A NGS STRATEGY FOR GENETIC SCREENING OF SUDDEN CARDIAC DEATH
68	347	Derya Aydın, Meltem Muftuoglu and Burak Erman. Identifying small molecule inhibitors targeting base excision repair enzymes DNA polymerase γ and β to increase the effects of cancer treatment
69	339	Paweł Bednarz, Agnieszka Podsiadło, Joanna Giemza, Norbert Dojer and Bartek Wilczynski. BNFinder2: efficient software for learning Bayesian networks
70	338	Evrim Besray Unal, Maria Lluch, Eva Yus, Yogi Jaeger and Luis Serrano. Reverse Engineering of Mycoplasma pneumoniae Gene Regulatory Network
71	375	Nathan Boley. Integrative De Novo Transcriptome Assembly in Fruit Fly
72	313	Sílvia Bonàs, Josep M. Mercader and David Torrents. Empirical evaluation of different modern reference panels for imputation and their implication for Genome Wide Association Studies.
73	320	Orion Buske, Ashokkumar Manickaraj, Seema Mital and Michael Brudno. Identification of deleterious synonymous variants in human genomes
74	377	Alejandro Caceres, Suzanne Sindi, Benjamin Raphael, Mario Caceres and Juan Gonzalez. Identification of Polymorphic Inversions from Genotypes
75	337	Sònia Casillas, Can Alkan, Evan E Eichler and Mario Cáceres. Calling inversions from Next-Generation Sequencing Paired-End Mapping data with GRIAL
76	336	Nikolay Chekanov, Egor Prokhortchouk, Artem Artemov, Artem Nedoluzhko, Eugenia Bulygina, Sergey Rastorguev, Svetlana Tsygankova, Natalia Gruzdeva and Konstantin Skryabin. A family study of early-onset Alzheimer's disease
77	374	Myungguen Chung and Kie-Jung Park. Automated analysis support system for Imputed Genotype based Case-Control Study with a Disease by using next-generation sequencing data
78	367	Ornella Cominetti, David Smith, Nick Jones, Radek Erban, Philip Maini and Climent Casals-Pascual. Identification of new pathobiological clusters in severe malaria using unsupervised methods
79	351	Oliver Drechsel, Rubayte Rahman and Stephan Ossowski. Clinical application and computational analyses of Exome-seq for disease studies
80	342	Prerna Dua, Chaitanya Pinnamaneni, Pradeep Chowriappa and Walter Lukiw. A Co-expression Network Based Approach for Gene Expression Analysis in Alzheimer's' Disease Progression
81	349	David Dufour and Marc A. Marti-Renom. RNA structure prediction by knowledge-based statistical potentials and Selective 2′-Hydroxyl Acylation and Primer Extension (SHAPE)
82	362	Matthew Edwards and David Gifford. High-resolution genetic mapping with pooled sequencing
83	266	Nadia El-Mabrouk, Yves Gagnon and Mathieu Blanchette. Ancestral Genome Reconstruction based on Gapped Adjacencies
84	340	Cemal Erdem, Alper Demir, Ahmet Gül and Burak Erman. Mathematical Modeling of a Human Immune-Mediated Auto-Inflammatory Disease
85	346	Sinan Erten, Salim A. Chowdhury, Xiaowei Guan, Rod K. Nibbe, Jill S. Barnholtz-Sloan, Mark R. Chance and Mehmet Koyuturk. Identifying stage-specific protein subnetworks for colorectal cancer
86	319	Jennifer Fang, Siddarth Selvaraj, Jesse Dixon, Feng Yue, Ming Hu, Ke Deng, Zhaohui Qin, Yixin Zhu, Jun Liu and Bing Ren. 3D Chromosome Structure Visualization from Hi-C Data
87	317	Itrat Fatima and Shaneen Singh. Computational Analysis of GRAM domains in the model plant Arabidopsis thaliana.
88	315	Boris Fedorov, Leonid Zaslavsky, Vyacheslav Chetvernin, Stacy Ciufo, Boris Kiryutin, Kathleeen O'Neill, Alexandre Souvorov, Igor Tolstoy and Tatiana Tatusova. Integrated system for bacterial pan-genome analysis

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90	360	Oriol Fornes and Baldo Oliva. Prediction of DNA-binding specificities using statistical potentials
91	359	Marc Friedländer, Esther Lizano, Eulàlia Martí and Xavier Estivill. NATA: a combined wetlab and drylab method for naïve transcriptome analysis
92	355	Jon Hallander, Petter Lindgren, Pär Larsson and Andreas Sjödin. A microbial forensic approach using Ultra-Deep Sequencing (UDS) for analysis of haplotype spectra in clonal bacterial strains
93	363	Joseph Herman, Ádám Novák, Rune Lyngsø and Jotun Hein. A probabilistic framework for incorporating alignment uncertainty into multiple sequence analysis
94	318	Irina Khrebtukova, Ryan Kelley, Shujun Luo, Tim Hill, Patrick Lau, Jennifer Chiniquy, Kathryn Stephens, Semyon Kruglyak and Gary P Schroth. Automated workflow for RNA-Seq analysis: application and testing with various types of RNA-Seq protocols
95	334	Baeksoo Kim and Hyunju Lee. A cancer text ranking algorithm based on cancer-related terms
96	327	Jeongkyun Kim, Hee-Jin Lee, Jong C. Park and Hyunju Lee. A search engine for recommending cancer-related genes based on literature evidence
97	361	Eva König, Lars Feuerbach, Barbara Hutter, Matthias Schlesner, Qi Wang, Benedikt Brors and Thomas Lengauer. Improving loss of heterozygosity identification by tumor purity estimation
98	311	Paweł P. Łabaj and David P. Kreil. Improving RNA-Seq precision with MapAl
99	314	Hayan Lee and Michael Schatz. Genomic Dark Matter: The reliability of short read mapping illustrated by the Genome Mappability Score
100	316	Miler Lee, Ariel Bazzini, Polloneal Ocbina, Carter Takacs and Antonio Giraldez. Computational analysis of ribosome profiling data to characterize translational dynamics in Zebrafish
101	335	Andreas Leha, Tim Beißbarth and Klaus Jung. Predicting Ordinal Response in High-Dimensional Datasets
102	376	Manway Liu, Haozhi Lin, Anupama Reddy, Alan Huang, Giordano Caponigro and Joseph Lehar. Network Analysis of Pharmacologic, Genomic, and Transcriptomic Assays in Cancer Cell Lines
103	324	Ray Marin and Jiri Vanicek. PACCMIT: Prediction of ACcessible and/or Conserved MIcroRNA Targets
104	312	Tobias Marschall, Ivan Gesteira Costa, Stefan Canzar, Markus Bauer, Gunnar W. Klau, Alexander Schliep and Alexander Schoenhuth. CLEVER: Clique-Enumerating Variant Finder
105	343	Alexander Martinez Fundichely, Meritxell Oliva Pavia, Juan Ramon Gonzalez Ruiz, Sònia Casillas and Mario Cáceres. Accurate prediction of inversions in the human genome from paired-end mapping data with the GRIAL algorithm.
106	331	John R. .Mcpherson, Yingting Wu, Patrick Tan and Steve Rozen. Identifying Genomic Copy Number Alteration and Loss of Heterozygosity in Next-Generation Sequence Data
107	364	Abhishek Mitra and Maga Rowicka. Instant-Seq:- an integrated tool with web interface for fast analysis of ChIP-Seq data
108	321	James Morton, Patricia Abrudan, Chun Liang and John Karro. Tools for Cleaning NGS Transciptome Data
109	366	Sana Ben Mustapha, Hend Ben Tamarzizst, Ghada Baraket and Amel Salhi Hannachi. SSR markers and sequences of the trnL intron to study polymorphism in Tunisian plum
110	344	Layla Oesper, Anna Ritz, Sarah Aerni, Ryan Drebin and Ben Raphael. Reconstructing Cancer Genomes from Paired-end Sequencing Data
111	326	Merja Oja, Paula Jouhten, Eija Rintala, Mervi Toivari, Marilyn Wiebe, Laura Ruohonen and Merja Penttilä. Systems biology for studying the physiology of acid producing yeast

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113	368	Anna Ritz, Suzanne Sindi, Ali Bashir and Benjamin Raphael. A Probabilistic Method for Structural Variant Prediction from Strobe Sequencing Data
114	373	Maga Rowicka, Nicola Crosetto, Abhishek Mitra, Maria Joao Silva, Magda Bienko, Philippe Pasero and Ivan Dikic. BLESS: mapping DNA double-strand breaks by next-generation sequencing
115	354	Matthew Ruffalo, Mehmet Koyuturk, Soumya Ray and Thomas Laframboise. Accurate Estimation of Short Read Mapping Quality for Second-Generation Genome Sequencing
116	365	Dhany Saputra, Thomas Sicheritz Pontén and Ole Lund. Reads2Type: An Online Tool for Rapid Bacterial Typing
117	310	Ole Schulz-Trieglaff, Elizabeth Murchison, Zemin Ning and Anthony Cox. The devil is in the detail: mining and annotating genomic variants in the Tasmanian Devil facial tumour genome
118	332	Teppei Shimamura, Seiya Imoto, Atsushi Niida and Satoru Miyano. Identification of key methylated genes from patient-specific gene networks
119	323	Jeeyoung Shin, Minkyu Shin and Yangseok Kim. Association Investigator: The intelligent for investigating the relationship between genomics data and clinical variables
120	356	Yuichi Shiraishi, Yusuke Sato, Aiko Sato-Otsubo, Yusuke Okuno, Shigekatsu Maekawa, Hidewaki Nakagawa, Seishi Ogawa and Satoru Miyano. Fusion gene detection by using soft clipping information
121	379	Jeanre Smit, Misha Le Grange, Phelelani Mpangase, Michal Szolkiewicz and Fourie Joubert. Discovery: a resource for the rational selection of drug target proteins and leads for the malaria parasite, Plasmodium falciparum
122	341	Ian Streeter, David Thybert, Klara Stefflova, Laura Clarke, Duncan Odom and Paul Flicek. A comparison of read-mapping and de novo assembly methods for calling inter-species variants between Mus caroli and Mus musculus
123	371	Jon Sveinbjornsson and Bjarni Halldorsson. BAM Region Viewer: A Viewer Application For BAM
124	269	Krister Swenson and Nadia El-Mabrouk. Correcting Errors in Reconciliation
125	330	Juan Ramon Tejedor, Panagiotis Papasaikas and Juan Valcarcel. Reconstruction of a Splicing Regulatory Circuitry Involved in Cell Proliferation and Apoptosis.
126	352	Kalliopi Tsafou, Damian Plichta, Branka Radić, Uwe Rix, Giulio Superti-Furga, Irene Kouskoumvekaki and Ramneek Gupta. Investigating the Genomic Landscape of Ewing Sarcoma
127	322	Andreas Untergasser, Ioana Cutcutache, Triinu Koressaar, Jian Ye, Brant C. Faircloth, Maido Remm and Steve Rozen. Primer3 - New Capabilities and Interfaces
128	370	Fabio Vandin, Hsin-Ta Wu, Eli Upfal and Ben Raphael. Algorithms to Find Mutated Pathways in Cancer
129	357	Juris Viksna, Karlis Freivalds and Paulis Kikusts. Application of graph clustering and visualization methods for detection of evolutionary related groups of proteins
130	369	Anne Wenzel, Erdinc Akbasli and Jan Gorodkin. RIsearch: fast yet accurate RNA-RNA interaction search
131	333	Agata Wesołowska, Louise Borst, Marlene Dalgaard, Louise Helt, Hans Madsen, Hanne Marquart, Peder Wehner, Morten Rasmussen, Eske Willerslev, Thomas Gilbert, Søren Brunak, Kjeld Schmiegelow and Ramneek Gupta. Relating genomic variation to drug response in childhood acute lymphoblastic leukemia
132	348	Rachita Yadav, Klaus Bønnelykke, Thomas Nordahl Petersen, Anne Mølgaard, Hans Bisgaard and Ramneek Gupta. Machine learning risk prediction of childhood asthma.
133	378	Jin Zhang, Jiayin Wang and Yufeng Wu. Calling Structural Variations with Low-coverage Sequencing Data by Mapping to Focal Region