Gunnar RÃ¤tsch

List of Publications by Year
in descending order

142 papers	31,559 citations	31976 53 h-index	16183 124 g-index
179 all docs	179 docs citations	179 times ranked	46976 citing authors

#	Article	IF	Citations
1	Lossless Indexing withÂCounting de Bruijn Graphs. Lecture Notes in Computer Science, 2022, , 374-376.	1.3	2
2	Lossless indexing with counting de Bruijn graphs. Genome Research, 2022, 32, 1754-1764.	5.5	5
3	Targeting eIF4A-Dependent Translation of KRAS Signaling Molecules. Cancer Research, 2021, 81, 2002-2014.	0.9	17
4	Identification of HIF-dependent alternative splicing in gastrointestinal cancers and characterization of a long, coding isoform of SLC35A3. Genomics, 2021, 113, 515-529.	2.9	4
5	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	16.8	71
6	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
7	Topology-based sparsification of graph annotations. Bioinformatics, 2021, 37, i169-i176.	4.1	4
8	Boosting Variational Inference With Locally Adaptive Step-Sizes. , 2021, , .		1
9	Sparse Gaussian Processes on Discrete Domains. IEEE Access, 2021, 9, 76750-76758.	4.2	1
10	Reconstructing tumor evolutionary histories and clone trees in polynomial-time with SubMARine. PLoS Computational Biology, 2021, 17, e1008400.	3.2	7
11	Communication-Efficient Jaccard similarity for High-Performance Distributed Genome Comparisons. , 2020, , .		34
12	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
13	Sparse Binary Relation Representations for Genome Graph Annotation. Journal of Computational Biology, 2020, 27, 626-639.	1.6	9
14	Early prediction of circulatory failure in the intensive care unit using machine learning. Nature Medicine, 2020, 26, 364-373.	30.7	204
15	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	27.8	280
16	SCIM: universal single-cell matching with unpaired feature sets. Bioinformatics, 2020, 36, i919-i927.	4.1	37
17	AStarix: Fast and Optimal Sequence-to-Graph Alignment. Lecture Notes in Computer Science, 2020, , 104-119.	1.3	9
18	SPHN/PHRT: Forming a Swiss-Wide Infrastructure for Data-Driven Sepsis Research. Studies in Health Technology and Informatics, 2020, 270, 1163-1167.	0.3	3

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19	Dynamic compression schemes for graph coloring. Bioinformatics, 2019, 35, 407-414.	4.1	19
20	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	28.9	144
21	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. Nature Communications, 2019, 10, 2524.	12.8	35
22	c-MYC regulates mRNA translation efficiency and start-site selection in lymphoma. Journal of Experimental Medicine, 2019, 216, 1509-1524.	8.5	32
23	HBEGF $^+$ macrophages in rheumatoid arthritis induce fibroblast invasiveness. Science Translational Medicine, 2019, 11, .	12.4	143
24	Sparse Binary Relation Representations for Genome Graph Annotation. Lecture Notes in Computer Science, 2019, , 120-135.	1.3	4
25	*EIF1AX* and *RAS* Mutations Cooperate to Drive Thyroid Tumorigenesis through ATF4 and c-MYC. Cancer Discovery, 2019, 9, 264-281.	9.4	57
26	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. PLoS Genetics, 2018, 14, e1007752.	3.5	148
27	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
28	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	2.8	33
29	Genomic Rearrangements in *Arabidopsis* Considered as Quantitative Traits. Genetics, 2017, 205, 1425-1441.	2.9	21
30	Prediction of potent shRNAs with a sequential classification algorithm. Nature Biotechnology, 2017, 35, 350-353.	17.5	129
31	RiboDiff: detecting changes of mRNA translation efficiency from ribosome footprints. Bioinformatics, 2017, 33, 139-141.	4.1	134
32	04.10â€¦Chronic inflammation regulates the mrna stabilome in rheumatoid arthritis fibroblast-like synoviocytes. , 2017, , .		0
33	Tumor Necrosis Factor dynamically regulates the mRNA stabilome in rheumatoid arthritis fibroblast-like synoviocytes. PLoS ONE, 2017, 12, e0179762.	2.5	21
34	Abstract A45: Targeting eIF4A dependent translation as therapeutics in pancreatic cancer. , 2017, , .		0
35	Abstract 389: Integrating diverse transcriptomic alterations to identify cancer-relevant genes. , 2017, , .		0
36	*SplAdder*: identification, quantification and testing of alternative splicing events from RNA-Seq data. Bioinformatics, 2016, 32, 1840-1847.	4.1	124

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37	MMR: a tool for read multi-mapper resolution. Bioinformatics, 2016, 32, 770-772.	4.1	39
38	Alternative Splicing Substantially Diversifies the Transcriptome during Early Photomorphogenesis and Correlates with the Energy Availability in Arabidopsis. Plant Cell, 2016, 28, 2715-2734.	6.6	97
39	Efficient privacy-preserving string search and an application in genomics. Bioinformatics, 2016, 32, 1652-1661.	4.1	46
40	Abstract 892: Functional characterization of EIF1AX mutations in thyroid cancer predicts for gain of function by increasing translational rate with concomitant derepression of upstream inputs from mTOR. , 2016, , .		0
41	Protein translational control and its contribution to oncogenesis revealed by computational methods. BMC Bioinformatics, 2015, 16, .	2.6	3
42	Interferon-Î³ regulates cellular metabolism and mRNA translation to potentiate macrophage activation. Nature Immunology, 2015, 16, 838-849.	14.5	239
43	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
44	Probabilistic clustering of time-evolving distance data. Machine Learning, 2015, 100, 635-654.	5.4	2
45	SVM2Motifâ€"Reconstructing Overlapping DNA Sequence Motifs by Mimicking an SVM Predictor. PLoS ONE, 2015, 10, e0144782.	2.5	5
46	DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. ELife, 2015, 4, e05255.	6.0	457
47	Abstract B23: The 5 UTR of many oncogenes and transcription factors encodes a targetable dependence on the eIF4A RNA helicase. , 2015, , .		0
48	Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 44-55.	0.7	5
49	INTEGRATIVE GENOME-WIDE ANALYSIS OF THE DETERMINANTS OF RNA SPLICING IN KIDNEY RENAL CLEAR CELL CARCINOMA. , 2014, , .		3
50	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT â€œOMICSâ€•DATA. , 2014, , .		0
51	Genome-wide analysis of alternative splicing in Volvox carteri. BMC Genomics, 2014, 15, 1117.	2.8	37
52	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. Bioinformatics, 2014, 30, 1300-1301.	4.1	12
53	Regularization-Based Multitask Learning With Applications to Genome Biology and Biological Imaging. KI - Kunstliche Intelligenz, 2014, 28, 29-33.	3.2	6
54	Species-wide Genetic Incompatibility Analysis Identifies Immune Genes as Hot Spots of Deleterious Epistasis. Cell, 2014, 159, 1341-1351.	28.9	247

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55	Graph-regularized 3D shape reconstruction from highly anisotropic and noisy images. Signal, Image and Video Processing, 2014, 8, 41-48.	2.7	3
56	RNA G-quadruplexes cause eIF4A-dependent oncogene translation in cancer. Nature, 2014, 513, 65-70.	27.8	506
57	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
58	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. Cell, 2014, 158, 1431-1443.	28.9	1,515
59	Oqtans: a multifunctional workbench for RNA-seq data analysis. BMC Bioinformatics, 2014, 15, .	2.6	0
60	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	19.0	679
61	Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191.	19.0	467
62	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
63	An Empirical Analysis of Topic Modeling for Mining Cancer Clinical Notes. , 2013, , .		20
64	Nonsense-Mediated Decay of Alternative Precursor mRNA Splicing Variants Is a Major Determinant of the <i>Arabidopsis</i> Steady State Transcriptome. Plant Cell, 2013, 25, 3726-3742.	6.6	209
65	Accurate detection of differential RNA processing. Nucleic Acids Research, 2013, 41, 5189-5198.	14.5	39
66	MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. Bioinformatics, 2013, 29, 2529-2538.	4.1	57
67	Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. PLoS Computational Biology, 2013, 9, e1003388.	3.2	487
68	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT â€œOMICSâ€•DATA- SESSION INTRODUCTION. , 2013, , .		0
69	Multiple insert size paired-end sequencing for deconvolution of complex transcriptomes. RNA Biology, 2012, 9, 596-609.	3.1	2
70	Cohesin Rings Devoid of Scc3 and Pds5 Maintain Their Stable Association with the DNA. PLoS Genetics, 2012, 8, e1002856.	3.5	50
71	Efficient Training of Graph-Regularized Multitask SVMs. Lecture Notes in Computer Science, 2012, , 633-647.	1.3	6
72	Polypyrimidine Tract Binding Protein Homologs from <i>Arabidopsis</i> Are Key Regulators of Alternative Splicing with Implications in Fundamental Developmental Processes. Plant Cell, 2012, 24, 4360-4375.	6.6	84

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73	HnRNP L and L-like cooperate in multiple-exon regulation of CD45 alternative splicing. Nucleic Acids Research, 2012, 40, 5666-5678.	14.5	45
74	A spatial and temporal map of *C. elegans* gene expression. Genome Research, 2011, 21, 325-341.	5.5	241
75	Persistence and Availability of Web Services in Computational Biology. PLoS ONE, 2011, 6, e24914.	2.5	21
76	RNA-Seq analysis in mutant zebrafish reveals role of U1C protein in alternative splicing regulation. EMBO Journal, 2011, 30, 1965-1976.	7.8	39
77	Support vector machines-based identification of alternative splicing in Arabidopsis thaliana from whole-genome tiling arrays. BMC Bioinformatics, 2011, 12, 55.	2.6	21
78	Oqtans: a Galaxy-integrated workflow for quantitative transcriptome analysis from NGS Data. BMC Bioinformatics, 2011, 12, .	2.6	2
79	Receptor-type guanylate cyclase is required for carbon dioxide sensation by *Caenorhabditis elegans*. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 254-259.	7.1	113
80	Multiple reference genomes and transcriptomes for Arabidopsis thaliana. Nature, 2011, 477, 419-423.	27.8	593
81	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. Nature Precedings, 2010, , .	0.1	13
82	Next generation genome annotation with mGene.ngs. BMC Bioinformatics, 2010, 11, .	2.6	8
83	Inferring latent task structure for Multitask Learning by Multiple Kernel Learning. BMC Bioinformatics, 2010, 11, S5.	2.6	24
84	Exploiting physico-chemical properties in string kernels. BMC Bioinformatics, 2010, 11, S7.	2.6	17
85	Global effects of the small RNA biogenesis machinery on the *Arabidopsis thaliana* transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17466-17473.	7.1	66
86	Integrative Analysis of the *Caenorhabditis elegans* Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
87	RNAâ€Seq Read Alignments with PALMapper. Current Protocols in Bioinformatics, 2010, 32, Unit 11.6.	25.8	46
88	rQuant.web: a tool for RNA-Seq-based transcript quantitation. Nucleic Acids Research, 2010, 38, W348-W351.	14.5	58
89	Leveraging Sequence Classification by Taxonomy-Based Multitask Learning. Lecture Notes in Computer Science, 2010, , 522-534.	1.3	50
90	Novel Machine Learning Methods for MHC Class I Binding Prediction. Lecture Notes in Computer Science, 2010, , 98-109.	1.3	30

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91	mGene: Accurate SVM-based gene finding with an application to nematode genomes. Genome Research, 2009, 19, 2133-2143.	5.5	79
92	KIRMES: kernel-based identification of regulatory modules in euchromatic sequences. Bioinformatics, 2009, 25, 2126-2133.	4.1	21
93	mGene.web: a web service for accurate computational gene finding. Nucleic Acids Research, 2009, 37, W312-W316.	14.5	23
94	Transcript quantification with RNA-Seq data. BMC Bioinformatics, 2009, 10, .	2.6	10
95	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. Plant Journal, 2009, 57, 184-194.	5.7	65
96	Stressâ€induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using wholeâ€genome tiling arrays. Plant Journal, 2009, 58, 1068-1082.	5.7	273
97	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12273-12278.	7.1	581
98	Prototype Classification: Insights from Machine Learning. Neural Computation, 2009, 21, 272-300.	2.2	17
99	The Feature Importance Ranking Measure. Lecture Notes in Computer Science, 2009, , 694-709.	1.3	57
100	Optimal spliced alignments of short sequence reads. BMC Bioinformatics, 2008, 9, .	2.6	21
101	Revealing sequence variation patterns in rice with machine learning methods. BMC Bioinformatics, 2008, 9, .	2.6	1
102	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in Arabidopsis thaliana. Genome Biology, 2008, 9, R112.	9.6	91
103	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8795-8800.	7.1	378
104	POIMs: positional oligomer importance matricesâ€"understanding support vector machine-based signal detectors. Bioinformatics, 2008, 24, i6-i14.	4.1	51
105	Optimal spliced alignments of short sequence reads. Bioinformatics, 2008, 24, i174-i180.	4.1	86
106	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. Genome Research, 2008, 18, 918-929.	5.5	50
107	Support Vector Machines and Kernels for Computational Biology. PLoS Computational Biology, 2008, 4, e1000173.	3.2	515
108	Transcript normalization and segmentation of tiling array data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 527-38.	0.7	8

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109	Improving the Caenorhabditis elegans Genome Annotation Using Machine Learning. PLoS Computational Biology, 2007, 3, e20.	3.2	57
110	PALMA: mRNA to genome alignments using large margin algorithms. Bioinformatics, 2007, 23, 1892-1900.	4.1	12
111	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i>. Science, 2007, 317, 338-342.	12.6	689
112	NIPS workshop on New Problems and Methods in Computational Biology. BMC Bioinformatics, 2007, 8, .	2.6	2
113	Accurate splice site prediction using support vector machines. BMC Bioinformatics, 2007, 8, S7.	2.6	135
114	TRANSCRIPT NORMALIZATION AND SEGMENTATION OF TILING ARRAY DATA. , 2007, , .		3
115	ARTS: accurate recognition of transcription starts in human. Bioinformatics, 2006, 22, e472-e480.	4.1	101
116	Learning Interpretable SVMs for Biological Sequence Classification. BMC Bioinformatics, 2006, 7, S9.	2.6	58
117	Totally corrective boosting algorithms that maximize the margin. , 2006, , .		59
118	Graph Based Semi-supervised Learning with Sharper Edges. Lecture Notes in Computer Science, 2006, , 401-412.	1.3	13
119	Solving Semi-infinite Linear Programs Using Boosting-Like Methods. Lecture Notes in Computer Science, 2006, , 10-11.	1.3	0
120	RASE: recognition of alternatively spliced exons in C.elegans. Bioinformatics, 2005, 21, i369-i377.	4.1	109
121	Image reconstruction by linear programming. IEEE Transactions on Image Processing, 2005, 14, 737-744.	9.8	17
122	Classifying â€˜Drug-likeness' with Kernel-Based Learning Methods. Journal of Chemical Information and Modeling, 2005, 45, 249-253.	5.4	90
123	Large scale genomic sequence SVM classifiers. , 2005, , .		27
124	Active Learning with Support Vector Machines in the Drug Discovery Process. Journal of Chemical Information and Computer Sciences, 2003, 43, 667-673.	2.8	281
125	Constructing descriptive and discriminative nonlinear features: rayleigh coefficients in kernel feature spaces. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2003, 25, 623-628.	13.9	158
126	An Introduction to Boosting and Leveraging. Lecture Notes in Computer Science, 2003, , 118-183.	1.3	206

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127	A New Discriminative Kernel from Probabilistic Models. Neural Computation, 2002, 14, 2397-2414.	2.2	88
128	Constructing boosting algorithms from SVMs: an application to one-class classification. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2002, 24, 1184-1199.	13.9	197
129	Sparse Regression Ensembles in Infinite and Finite Hypothesis Spaces. Machine Learning, 2002, 48, 189-218.	5.4	26
130	Maximizing the Margin with Boosting. Lecture Notes in Computer Science, 2002, , 334-350.	1.3	15
131	New Methods for Splice Site Recognition. Lecture Notes in Computer Science, 2002, , 329-336.	1.3	28
132	An introduction to kernel-based learning algorithms. IEEE Transactions on Neural Networks, 2001, 12, 181-201.	4.2	2,811
133	Soft Margins for AdaBoost. Machine Learning, 2001, 42, 287-320.	5.4	1,000
134	Learning to Predict the Leave-One-Out Error of Kernel Based Classifiers. Lecture Notes in Computer Science, 2001, , 331-338.	1.3	12
135	An Arcing algorithm with an intuitive learning control parameter. Transactions of the Japanese Society for Artificial Intelligence, 2001, 16, 417-426.	0.1	0
136	Engineering support vector machine kernels that recognize translation initiation sites. Bioinformatics, 2000, 16, 799-807.	4.1	373
137	Robust Ensemble Learning for Data Mining. Lecture Notes in Computer Science, 2000, , 341-344.	1.3	14
138	Input space versus feature space in kernel-based methods. IEEE Transactions on Neural Networks, 1999, 10, 1000-1017.	4.2	953
139	Kernel PCA Pattern Reconstruction via Approximate Pre-Images. Perspectives in Neural Computing, 1998, , 147-152.	0.1	60
140	Fisher discriminant analysis with kernels. , 0, , .		1,381
141	Experimental analysis of support vector machines with different kernels based on non-intrusive monitoring data. , 0, , .		9
142	RNA Instant Quality Check: Alignment-Free RNA-Degradation Detection. Journal of Computational Biology, 0, , .	1.6	1