

# Blaz Zupan

## List of Publications by Year in descending order

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Version: 2024-02-01

109  
papers

7,569  
citations

81900

39  
h-index

58581

82  
g-index

115  
all docs

115  
docs citations

115  
times ranked

10057  
citing authors

#	ARTICLE	IF	CITATIONS
1	iCLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 909-915.	8.2	1,026
2	Characterizing the RNA targets and position-dependent splicing regulation by TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 452-458.	14.8	956
3	Predictive data mining in clinical medicine: Current issues and guidelines. <i>International Journal of Medical Informatics</i> , 2008, 77, 81-97.	3.3	653
4	From hype to reality: data science enabling personalized medicine. <i>BMC Medicine</i> , 2018, 16, 150.	5.5	278
5	Widespread binding of FUS along nascent RNA regulates alternative splicing in the brain. <i>Scientific Reports</i> , 2012, 2, 603.	3.3	231
6	iCLIP Predicts the Dual Splicing Effects of TIA-RNA Interactions. <i>PLoS Biology</i> , 2010, 8, e1000530.	5.6	226
7	Polymorphic Members of the lag Gene Family Mediate Kin Discrimination in <i>Dictyostelium</i> . <i>Current Biology</i> , 2009, 19, 567-572.	3.9	204
8	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. <i>Genome Research</i> , 2011, 21, 1572-1582.	5.5	199
9	Analysis of CLIP and iCLIP methods for nucleotide-resolution studies of protein-RNA interactions. <i>Genome Biology</i> , 2012, 13, R67.	9.6	195
10	Orange: From Experimental Machine Learning to Interactive Data Mining. <i>Lecture Notes in Computer Science</i> , 2004, , 537-539.	1.3	174
11	iCLIP - Transcriptome-wide Mapping of Protein-RNA Interactions with Individual Nucleotide Resolution. <i>Journal of Visualized Experiments</i> , 2011, , .	0.3	168
12	Data Fusion by Matrix Factorization. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2015, 37, 41-53.	13.9	166
13	Conserved developmental transcriptomes in evolutionarily divergent species. <i>Genome Biology</i> , 2010, 11, R35.	9.6	164
14	Microarray data mining with visual programming. <i>Bioinformatics</i> , 2005, 21, 396-398.	4.1	131
15	A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family. <i>Nature Communications</i> , 2017, 8, 1541.	12.8	124
16	Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins. <i>Bioinformatics</i> , 2016, 32, 1527-1535.	4.1	108
17	Machine learning for survival analysis: a case study on recurrence of prostate cancer. <i>Artificial Intelligence in Medicine</i> , 2000, 20, 59-75.	6.5	107
18	Epistasis analysis with global transcriptional phenotypes. <i>Nature Genetics</i> , 2005, 37, 471-477.	21.4	100

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19	Discovering disease-disease associations by fusing systems-level molecular data. <i>Scientific Reports</i> , 2013, 3, 3202.	3.3	96
20	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. <i>RNA Biology</i> , 2014, 11, 146-155.	3.1	82
21	miR669a and miR669q prevent skeletal muscle differentiation in postnatal cardiac progenitors. <i>Journal of Cell Biology</i> , 2011, 193, 1197-1212.	5.2	77
22	dictyBase—a Dictyostelium bioinformatics resource update. <i>Nucleic Acids Research</i> , 2009, 37, D515-D519.	14.5	71
23	Towards knowledge-based gene expression data mining. <i>Journal of Biomedical Informatics</i> , 2007, 40, 787-802.	4.3	70
24	VizRank: Data Visualization Guided by Machine Learning. <i>Data Mining and Knowledge Discovery</i> , 2006, 13, 119-136.	3.7	69
25	Bacterial Discrimination by Dictyostelid Amoebae Reveals the Complexity of Ancient Interspecies Interactions. <i>Current Biology</i> , 2013, 23, 862-872.	3.9	69
26	Applications of qualitative multi-attribute decision models in health care. <i>International Journal of Medical Informatics</i> , 2000, 58-59, 191-205.	3.3	67
27	Visualization-based cancer microarray data classification analysis. <i>Bioinformatics</i> , 2007, 23, 2147-2154.	4.1	67
28	Nomograms for Visualization of Naive Bayesian Classifier. <i>Lecture Notes in Computer Science</i> , 2004, , 337-348.	1.3	63
29	dictyExpress: a Dictyostelium discoideum gene expression database with an explorative data analysis web-based interface. <i>BMC Bioinformatics</i> , 2009, 10, 265.	2.6	63
30	Developmentally Regulated DNA Methylation in Dictyostelium discoideum. <i>Eukaryotic Cell</i> , 2006, 5, 18-25.	3.4	61
31	Leaps and lulls in the developmental transcriptome of Dictyostelium discoideum. <i>BMC Genomics</i> , 2015, 16, 294.	2.8	61
32	VizRank: finding informative data projections in functional genomics by machine learning. <i>Bioinformatics</i> , 2005, 21, 413-414.	4.1	58
33	Learning by discovering concept hierarchies. <i>Artificial Intelligence</i> , 1999, 109, 211-242.	5.8	56
34	Nomograms for visualizing support vector machines. , 2005, , .		55
35	GenePath: a system for automated construction of genetic networks from mutant data. <i>Bioinformatics</i> , 2003, 19, 383-389.	4.1	54
36	FreeViz—An intelligent multivariate visualization approach to explorative analysis of biomedical data. <i>Journal of Biomedical Informatics</i> , 2007, 40, 661-671.	4.3	54

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37	A function-decomposition method for development of hierarchical multi-attribute decision models. <i>Decision Support Systems</i> , 2004, 36, 215-233.	5.9	47
38	Assessment of Machine Learning Reliability Methods for Quantifying the Applicability Domain of QSAR Regression Models. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 431-441.	5.4	46
39	Democratized image analytics by visual programming through integration of deep models and small-scale machine learning. <i>Nature Communications</i> , 2019, 10, 4551.	12.8	44
40	Predictive model for survival at the conclusion of a damage control laparotomy. <i>American Journal of Surgery</i> , 2000, 180, 540-545.	1.8	42
41	Feature mining and predictive model construction from severe trauma patient's data. <i>International Journal of Medical Informatics</i> , 2001, 63, 41-50.	3.3	39
42	SNPsyn: detection and exploration of SNP-SNP interactions. <i>Nucleic Acids Research</i> , 2011, 39, W444-W449.	14.5	35
43	Gene network inference by fusing data from diverse distributions. <i>Bioinformatics</i> , 2015, 31, i230-i239.	4.1	34
44	Hands-on training about overfitting. <i>PLoS Computational Biology</i> , 2021, 17, e1008671.	3.2	34
45	dictyExpress: a web-based platform for sequence data management and analytics in <i>Dictyostelium</i> and beyond. <i>BMC Bioinformatics</i> , 2017, 18, 291.	2.6	29
46	Open-Source Tools for Data Mining. <i>Clinics in Laboratory Medicine</i> , 2008, 28, 37-54.	1.4	28
47	Computational approaches for the genetic and phenotypic characterization of a <i>Saccharomyces cerevisiae</i> wine yeast collection. <i>Yeast</i> , 2009, 26, 675-692.	1.7	25
48	Jumping across biomedical contexts using compressive data fusion. <i>Bioinformatics</i> , 2016, 32, i90-i100.	4.1	24
49	Gene discovery by chemical mutagenesis and whole-genome sequencing in <i>Dictyostelium</i> . <i>Genome Research</i> , 2016, 26, 1268-1276.	5.5	23
50	Data Mining in Medicine. , 2009, , 1111-1136.		23
51	Optimization of rule-based systems using state space graphs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 1998, 10, 238-254.	5.7	22
52	TA-clustering: Cluster analysis of gene expression profiles through Temporal Abstractions. <i>International Journal of Medical Informatics</i> , 2005, 74, 505-517.	3.3	22
53	Gene Prioritization by Compressive Data Fusion and Chaining. <i>PLoS Computational Biology</i> , 2015, 11, e1004552.	3.2	22
54	GenePath: a system for inference of genetic networks and proposal of genetic experiments. <i>Artificial Intelligence in Medicine</i> , 2003, 29, 107-130.	6.5	21

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55	Computational Models for Prediction of Yeast Strain Potential for Winemaking from Phenotypic Profiles. PLoS ONE, 2013, 8, e66523.	2.5	21
56	Computational models reveal genotype–phenotype associations in <i>Saccharomyces cerevisiae</i> . Yeast, 2014, 31, 265-277.	1.7	20
57	Modelling impacts of cropping systems: Demands and solutions for DEX methodology. European Journal of Operational Research, 2008, 189, 594-608.	5.7	19
58	BzpF is a CREB-like transcription factor that regulates spore maturation and stability in Dictyostelium. Developmental Biology, 2011, 358, 137-146.	2.0	19
59	Stage prediction of embryonic stem cell differentiation from genome-wide expression data. Bioinformatics, 2011, 27, 2546-2553.	4.1	18
60	Transcriptional Profiling of Dictyostelium with RNA Sequencing. Methods in Molecular Biology, 2013, 983, 139-171.	0.9	17
61	Heterogeneous computing architecture for fast detection of SNP-SNP interactions. BMC Bioinformatics, 2014, 15, 216.	2.6	17
62	Seroprevalence of severe acute respiratory syndrome coronavirus 2 in Slovenia: results of two rounds of a nationwide population study on a probability-based sample, challenges and lessons learned. Clinical Microbiology and Infection, 2021, 27, 1039.e1-1039.e7.	6.0	17
63	proDEX – A DSS tool for environmental decision-making. Environmental Modelling and Software, 2006, 21, 1514-1516.	4.5	16
64	Knowledge-based data analysis and interpretation. Artificial Intelligence in Medicine, 2006, 37, 163-165.	6.5	16
65	OCT4 and the acquisition of oocyte developmental competence during folliculogenesis. International Journal of Developmental Biology, 2012, 56, 853-858.	0.6	16
66	GenePath: from mutations to genetic networks and back. Nucleic Acids Research, 2005, 33, W749-W752.	14.5	15
67	Subgroup discovery in data sets with multi-dimensional responses. Intelligent Data Analysis, 2011, 15, 533-549.	0.9	14
68	ABC Transporters in Dictyostelium discoideum Development. PLoS ONE, 2013, 8, e70040.	2.5	14
69	Matrix factorization-based data fusion for gene function prediction in baker's yeast and slime mold. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 400-11.	0.7	14
70	Predictive Model for Estimating Risk of Crush Syndrome: A Data Mining Approach. Journal of Trauma, 2007, 62, 940-945.	2.3	13
71	Matrix factorization-based data fusion for drug-induced liver injury prediction. Systems Biomedicine (Austin, Tex ), 2014, 2, 16-22.	0.7	13
72	COLLECTIVE PAIRWISE CLASSIFICATION FOR MULTI-WAY ANALYSIS OF DISEASE AND DRUG DATA. , 2016, , .		13

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73	Genome Sequence of a Lethal Strain of Xylem-Invading <i>Verticillium nonalfalfae</i> . Genome Announcements, 2018, 6, .	0.8	13
74	Fast optimization of non-negative matrix tri-factorization. PLoS ONE, 2019, 14, e0217994.	2.5	12
75	Data Imputation in Epistatic MAPs by Network-Guided Matrix Completion. Journal of Computational Biology, 2015, 22, 595-608.	1.6	11
76	Transcriptional milestones in <i>Dictyostelium</i> development. Genome Research, 2021, 31, 1498-1511.	5.5	11
77	COLLECTIVE PAIRWISE CLASSIFICATION FOR MULTI-WAY ANALYSIS OF DISEASE AND DRUG DATA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 81-92.	0.7	11
78	New components of the <i>Dictyostelium</i> PKA pathway revealed by Bayesian analysis of expression data. BMC Bioinformatics, 2010, 11, 163.	2.6	10
79	Embedding to reference t-SNE space addresses batch effects in single-cell classification. Machine Learning, 2023, 112, 721-740.	5.4	10
80	Relating clinical and neurophysiological assessment of spasticity by machine learning. International Journal of Medical Informatics, 1998, 49, 243-251.	3.3	9
81	Data Mining in Medicine. , 2005, , 1107-1137.		9
82	Textual features for corpus visualization using correspondence analysis. Intelligent Data Analysis, 2009, 13, 795-813.	0.9	9
83	scOrange—a tool for hands-on training of concepts from single-cell data analytics. Bioinformatics, 2019, 35, i4-i12.	4.1	8
84	Machine Learning for Survival Analysis: A Case Study on Recurrence of Prostate Cancer. Lecture Notes in Computer Science, 1999, , 346-355.	1.3	8
85	Acquiring background knowledge for machine learning using function decomposition: a case study in rheumatology. Artificial Intelligence in Medicine, 1998, 14, 101-117.	6.5	7
86	Subgroup Discovery in Data Sets with Multi-dimensional Responses: A Method and a Case Study in Traumatology. Lecture Notes in Computer Science, 2009, , 265-274.	1.3	7
87	Scalable non-negative matrix tri-factorization. BioData Mining, 2017, 10, 41.	4.0	7
88	Supporting Regenerative Medicine by Integrative Dimensionality Reduction. Methods of Information in Medicine, 2012, 51, 341-347.	1.2	5
89	Discovery of Genetic Networks Through Abduction and Qualitative Simulation. Lecture Notes in Computer Science, 2007, , 228-247.	1.3	5
90	Does replication groups scoring reduce false positive rate in SNP interaction discovery?. BMC Genomics, 2010, 11, 58.	2.8	4

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91	Embedding to Reference t-SNE Space Addresses Batch Effects in Single-Cell Classification. Lecture Notes in Computer Science, 2019, , 246-260.	1.3	4
92	Inference of the Molecular Mechanism of Action from Genetic Interaction and Gene Expression Data. OMICS A Journal of Integrative Biology, 2010, 14, 357-367.	2.0	3
93	Survival regression by data fusion. Systems Biomedicine (Austin, Tex ), 2014, 2, 47-53.	0.7	3
94	Gene network inference by probabilistic scoring of relationships from a factorized model of interactions. Bioinformatics, 2014, 30, i246-i254.	4.1	3
95	On Quality of Different Annotation Sources for Gene Expression Analysis. Lecture Notes in Computer Science, 2009, , 421-425.	1.3	3
96	Rule-based Clustering for Gene Promoter Structure Discovery. Methods of Information in Medicine, 2009, 48, 229-235.	1.2	3
97	FragViz: visualization of fragmented networks. BMC Bioinformatics, 2010, 11, 475.	2.6	2
98	RICERCANDO: Data mining toolkit for mobile broadband measurements. Computer Networks, 2020, 177, 107294.	5.1	2
99	Simple and effective visual models for gene expression cancer diagnostics. , 2005, , .		1
100	Concurrent software architectures for exploratory data analysis. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2015, 5, 165-180.	6.8	1
101	Integrative Clustering by Nonnegative Matrix Factorization Can Reveal Coherent Functional Groups From Gene Profile Data. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 698-708.	6.3	1
102	A Data Mining Library for miRNA Annotation and Analysis. Lecture Notes in Computer Science, 2011, , 80-84.	1.3	1
103	Ranking and 1-Dimensional Projection of Cell Development Transcription Profiles. Lecture Notes in Computer Science, 2011, , 85-89.	1.3	1
104	Knowledge-based bioinformatics for the study of mammalian oocytes. International Journal of Developmental Biology, 2012, 56, 859-866.	0.6	1
105	Predicting patient's long-term clinical status after hip arthroplasty using hierarchical decision modelling and data mining. Methods of Information in Medicine, 2001, 40, 25-31.	1.2	1
106	Bioinformatic approaches for the genetic and phenotypic characterization of a Saccharomyces cerevisiae wine yeast collection. Nature Precedings, 2008, , .	0.1	0
107	Finding Patterns in Class-Labeled Data Using Data Visualization. , 2008, , 106-123.		0
108	Data-Driven Revision of Decision Models. , 2009, , 617-623.		0

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109	Similarity of Transcription Profiles for Genes in Gene Sets. Lecture Notes in Computer Science, 2011, , 393-399.	1.3	0