Jan Maciej Komorowski

List of Publications by Citations

Source: https://exaly.com/author-pdf/2762055/jan-maciej-komorowski-publications-by-citations.pdf

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

164
papers10,084
citations33
h-index99
g-index184
ext. papers11,303
ext. citations5.9
avg, IF5.19
L-index

#	Paper	IF	Citations
164	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
163	Kcnq1ot1 antisense noncoding RNA mediates lineage-specific transcriptional silencing through chromatin-level regulation. <i>Molecular Cell</i> , 2008 , 32, 232-46	17.6	961
162	A literature network of human genes for high-throughput analysis of gene expression. <i>Nature Genetics</i> , 2001 , 28, 21-8	36.3	590
161	Phenotypically concordant and discordant monozygotic twins display different DNA copy-number-variation profiles. <i>American Journal of Human Genetics</i> , 2008 , 82, 763-71	11	437
160	Markers of adenocarcinoma characteristic of the site of origin: development of a diagnostic algorithm. <i>Clinical Cancer Research</i> , 2005 , 11, 3766-72	12.9	251
159	Nucleosomes are well positioned in exons and carry characteristic histone modifications. <i>Genome Research</i> , 2009 , 19, 1732-41	9.7	242
158	. Nature Genetics, 2001 , 28, 21-28	36.3	227
157	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
156	Somatic mosaicism for copy number variation in differentiated human tissues. <i>Human Mutation</i> , 2008 , 29, 1118-24	4.7	172
155	Monte Carlo feature selection for supervised classification. <i>Bioinformatics</i> , 2008 , 24, 110-7	7.2	155
154	The signal transducers Stat1 and Stat3 and their novel target Jmjd3 drive the expression of inflammatory genes in microglia. <i>Journal of Molecular Medicine</i> , 2014 , 92, 239-54	5.5	124
153	Butyrate mediates decrease of histone acetylation centered on transcription start sites and down-regulation of associated genes. <i>Genome Research</i> , 2007 , 17, 708-19	9.7	106
152	Endocan is a VEGF-A and PI3K regulated gene with increased expression in human renal cancer. <i>Experimental Cell Research</i> , 2007 , 313, 1285-94	4.2	100
151	Predicting gene ontology biological process from temporal gene expression patterns. <i>Genome Research</i> , 2003 , 13, 965-79	9.7	76
150	Whole-genome maps of USF1 and USF2 binding and histone H3 acetylation reveal new aspects of promoter structure and candidate genes for common human disorders. <i>Genome Research</i> , 2008 , 18, 380	o- 9 2	72
149	Combinatorial control of gene expression by the three yeast repressors Mig1, Mig2 and Mig3. <i>BMC Genomics</i> , 2008 , 9, 601	4.5	71
148	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. <i>Human Molecular Genetics</i> , 2005 , 14, 3435-47	7 ^{5.6}	66

(2009-2003)

147	Learning rule-based models of biological process from gene expression time profiles using gene ontology. <i>Bioinformatics</i> , 2003 , 19, 1116-23	7.2	65	
146	Modelling prognostic power of cardiac tests using rough sets. <i>Artificial Intelligence in Medicine</i> , 1999 , 15, 167-91	7.4	59	
145	Differential binding and co-binding pattern of FOXA1 and FOXA3 and their relation to H3K4me3 in HepG2 cells revealed by ChIP-seq. <i>Genome Biology</i> , 2009 , 10, R129	18.3	57	•
144	Molecular interactions between HNF4a, FOXA2 and GABP identified at regulatory DNA elements through ChIP-sequencing. <i>Nucleic Acids Research</i> , 2009 , 37, 7498-508	20.1	51	
143	Effect of thalidomide affecting VEGF secretion, cell migration, adhesion and capillary tube formation of human endothelial EA.hy 926 cells. <i>Life Sciences</i> , 2006 , 78, 2558-63	6.8	48	
142	Matrix metalloproteinases, tissue inhibitors of matrix metalloproteinases and angiogenic cytokines in peripheral blood of patients with thyroid cancer. <i>Thyroid</i> , 2002 , 12, 655-62	6.2	47	
141	Focal amplifications are associated with high grade and recurrences in stage Ta bladder carcinoma. <i>International Journal of Cancer</i> , 2010 , 126, 1390-402	7.5	45	
140	Resistin increases with obesity and atherosclerotic risk factors in patients with myocardial infarction. <i>Metabolism: Clinical and Experimental</i> , 2008 , 57, 488-93	12.7	43	
139	Profiling of copy number variations (CNVs) in healthy individuals from three ethnic groups using a human genome 32 K BAC-clone-based array. <i>Human Mutation</i> , 2008 , 29, 398-408	4.7	43	
138	Computational proteomics analysis of HIV-1 protease interactome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 305-12	4.2	42	
137	Decreased 1-25 dihydroxyvitamin D3 concentration in peripheral blood serum of patients with thyroid cancer. <i>Archives of Medical Research</i> , 2010 , 41, 190-4	6.6	40	
136	A previously unrecognized microdeletion syndrome on chromosome 22 band q11.2 encompassing the BCR gene. <i>American Journal of Medical Genetics, Part A</i> , 2007 , 143A, 2178-84	2.5	40	
135	Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 568-79	4.2	38	
134	Generalized proteochemometric model of multiple cytochrome p450 enzymes and their inhibitors. Journal of Chemical Information and Modeling, 2008 , 48, 1840-50	6.1	35	
133	The LCB Data Warehouse. <i>Bioinformatics</i> , 2006 , 22, 1024-6	7.2	34	
132	Discovering regulatory binding-site modules using rule-based learning. <i>Genome Research</i> , 2005 , 15, 850	5-6 6 7	34	
131	Cytokines locally produced by lymphocytes removed from the hypertrophic nasopharyngeal and palatine tonsils. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2005 , 69, 937-41	1.7	33	
130	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. <i>Neuro-Oncology</i> , 2009 , 11, 803-18	1	32	

129	Liver gene expression in rats in response to the peroxisome proliferator-activated receptor-alpha agonist ciprofibrate. <i>Physiological Genomics</i> , 2003 , 15, 9-19	3.6	32
128	FirueRnull allele detection in microsatellite loci: a comparison of methods, assessment of difficulties and survey of possible improvements. <i>Molecular Ecology Resources</i> , 2015 , 15, 477-88	8.4	31
127	Biochemical deficiencies of coenzyme Q10 in HIV-infection and exploratory treatment. <i>Biochemical and Biophysical Research Communications</i> , 1988 , 153, 888-96	3.4	31
126	Combinations of histone modifications mark exon inclusion levels. <i>PLoS ONE</i> , 2012 , 7, e29911	3.7	29
125	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. <i>Experimental and Molecular Medicine</i> , 2010 , 42, 484-502	12.8	29
124	A comprehensive analysis of the structure-function relationship in proteins based on local structure similarity. <i>PLoS ONE</i> , 2009 , 4, e6266	3.7	29
123	Identification of candidate regulatory SNPs by combination of transcription-factor-binding site prediction, SNP genotyping and haploChIP. <i>Nucleic Acids Research</i> , 2009 , 37, e85	20.1	29
122	Gis1 and Rph1 regulate glycerol and acetate metabolism in glucose depleted yeast cells. <i>PLoS ONE</i> , 2012 , 7, e31577	3.7	28
121	A segmental maximum a posteriori approach to genome-wide copy number profiling. <i>Bioinformatics</i> , 2008 , 24, 751-8	7.2	28
120	A Significant Regulatory Mutation Burden at a High-Affinity Position of the CTCF Motif in Gastrointestinal Cancers. <i>Human Mutation</i> , 2016 , 37, 904-13	4.7	28
119	Cancer associated epigenetic transitions identified by genome-wide histone methylation binding profiles in human colorectal cancer samples and paired normal mucosa. <i>BMC Cancer</i> , 2011 , 11, 450	4.8	27
118	Angiopoietin 1 (Ang-1), angiopoietin 2 (Ang-2) and Tie-2 (a receptor tyrosine kinase) concentrations in peripheral blood of patients with thyroid cancers. <i>Cytokine</i> , 2006 , 36, 291-5	4	27
117	Recurrent genomic alterations in benign and malignant pheochromocytomas and paragangliomas revealed by whole-genome array comparative genomic hybridization analysis. <i>Endocrine-Related Cancer</i> , 2010 , 17, 561-79	5.7	26
116	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. <i>Epigenetics</i> , 2009 , 4, 107-13	5.7	24
115	Gene expression based classification of gastric carcinoma. <i>Cancer Letters</i> , 2004 , 210, 227-37	9.9	24
114	Rough set-based proteochemometrics modeling of G-protein-coupled receptor-ligand interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 24-34	4.2	23
113	Evaluation of the levels of bFGF, VEGF, sICAM-1, and sVCAM-1 in serum of patients with thyroid cancer. <i>Recent Results in Cancer Research</i> , 2003 , 162, 189-94	1.5	22
112	Hypothalamic-pituitary-thyroid axis and the immune system. <i>NeuroImmunoModulation</i> , 1994 , 1, 149-52	2.5	22

111	Long-term impact of vertical banded gastroplasty (VBG) on plasma concentration of leptin, soluble leptin receptor, ghrelin, omentin-1, obestatin, and retinol binding protein 4 (RBP4) in patients with severe obesity. <i>Cytokine</i> , 2013 , 64, 490-3	4	21	
110	A look inside HIV resistance through retroviral protease interaction maps. <i>PLoS Computational Biology</i> , 2007 , 3, e48	5	21	
109	Different distribution of histone modifications in genes with unidirectional and bidirectional transcription and a role of CTCF and cohesin in directing transcription. <i>BMC Genomics</i> , 2015 , 16, 300	4.5	20	
108	Aetiology-specific patterns in end-stage heart failure patients identified by functional annotation and classification of microarray data. <i>European Journal of Heart Failure</i> , 2006 , 8, 381-9	12.3	20	
107	A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins. <i>Bioinformatics</i> , 2003 , 19 Suppl 2, ii81-91	7.2	20	
106	An introduction to partial deduction. <i>Lecture Notes in Computer Science</i> , 1992 , 49-69	0.9	20	
105	Systemic blood osteopontin, endostatin, and E-selectin concentrations after vertical banding surgery in severely obese adults. <i>Cytokine</i> , 2011 , 55, 56-61	4	19	
104	A Rough Set-Based Model of HIV-1 Reverse Transcriptase Resistome. <i>Bioinformatics and Biology Insights</i> , 2009 , 3, 109-27	5.3	19	
103	Growth hormone replacement decreases plasma levels of matrix metalloproteinases (2 and 9) and vascular endothelial growth factor in growth hormone-deficient individuals. <i>Circulation</i> , 2004 , 109, 240	05 ⁻¹ 60 ⁷	19	
102	Intra- and inter-individual metabolic profiling highlights carnitine and lysophosphatidylcholine pathways as key molecular defects in type 2 diabetes. <i>Scientific Reports</i> , 2019 , 9, 9653	4.9	18	
101	Monoclonal anti-TNFalpha antibody (infliximab) in the treatment of patient with thyroid associated ophthalmopathy. <i>Klinika Oczna</i> , 2007 , 109, 457-60	0.5	17	
100	Ciruvis: a web-based tool for rule networks and interaction detection using rule-based classifiers. <i>BMC Bioinformatics</i> , 2014 , 15, 139	3.6	15	
99	Cytokines serum levels as the markers of thyroid activation in GravesRdisease. <i>Immunology Letters</i> , 1998 , 60, 143-8	4.1	15	
98	Genome-scale study of the importance of binding site context for transcription factor binding and gene regulation. <i>BMC Bioinformatics</i> , 2008 , 9, 484	3.6	15	
97	Proteochemometric analysis of small cyclic peptides Rinteraction with wild-type and chimeric melanocortin receptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 83-96	4.2	15	
96	Effect of hyperprolactinaemia on Toxoplasma gondii prevalence in humans. <i>Parasitology Research</i> , 2008 , 102, 723-9	2.4	15	
95	Novel genes in cell cycle control and lipid metabolism with dynamically regulated binding sites for sterol regulatory element-binding protein 1 and RNA polymerase II in HepG2 cells detected by chromatin immunoprecipitation with microarray detection. <i>FEBS Journal</i> , 2009 , 276, 1878-90	5.7	14	
94	Effects of hCG and beta-hCG on IL-2 and sIL-2R secretion from human peripheral blood mononuclear cells: a dose-response study in vitro. <i>Immunology Letters</i> , 1997 , 59, 29-33	4.1	14	

93	Rule-based models of the interplay between genetic and environmental factors in childhood allergy. <i>PLoS ONE</i> , 2013 , 8, e80080	3.7	14
92	Alteration in the serum concentrations of FGF19, FGFR4 and Klotho in patients with thyroid cancer. <i>Cytokine</i> , 2018 , 105, 32-36	4	13
91	Nitrogen depletion in the fission yeast Schizosaccharomyces pombe causes nucleosome loss in both promoters and coding regions of activated genes. <i>Genome Research</i> , 2010 , 20, 361-71	9.7	13
90	A Statistical Method for Determining Importance of Variables in an Information System. <i>Lecture Notes in Computer Science</i> , 2006 , 557-566	0.9	13
89	Proteochemometrics mapping of the interaction space for retroviral proteases and their substrates. <i>Bioorganic and Medicinal Chemistry</i> , 2009 , 17, 5229-37	3.4	12
88	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
87	Allele specific chromatin signals, 3D interactions, and motif predictions for immune and B cell related diseases. <i>Scientific Reports</i> , 2019 , 9, 2695	4.9	12
86	Integration of genome-wide of Stat3 binding and epigenetic modification mapping with transcriptome reveals novel Stat3 target genes in glioma cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014 , 1839, 1341-50	6	11
85	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. <i>OMICS A Journal of Integrative Biology</i> , 2020 , 24, 180-2	1948	10
84	Combinatorial identification of DNA methylation patterns over age in the human brain. <i>BMC Bioinformatics</i> , 2016 , 17, 393	3.6	10
83	Monte Carlo feature selection and rule-based models to predict Alzheimer disease in mild cognitive impairment. <i>Journal of Neural Transmission</i> , 2012 , 119, 821-31	4.3	10
82	Peak Finder Metaserver - a novel application for finding peaks in ChIP-seq data. <i>BMC Bioinformatics</i> , 2013 , 14, 280	3.6	10
81	The place of somatostatin analogs in the diagnosis and treatment of the neuoroendocrine glands tumors. <i>Recent Patents on Anti-Cancer Drug Discovery</i> , 2006 , 1, 237-54	2.6	10
80	Increased interleukin-2 level in patients with primary hypothyroidism. <i>Clinical Immunology and Immunopathology</i> , 1992 , 63, 200-2		10
79	Monte Carlo Feature Selection and Interdependency Discovery in Supervised Classification. <i>Studies in Computational Intelligence</i> , 2010 , 371-385	0.8	10
78	Somatostatin Analogs and Tumor Localization Do Not Influence Vitamin D Concentration in Patients with Neuroendocrine Tumors. <i>Nutrition and Cancer</i> , 2016 , 68, 428-34	2.8	10
77	Risk stratification in cervical cancer screening by complete screening history: Applying bioinformatics to a general screening population. <i>International Journal of Cancer</i> , 2017 , 141, 200-209	7.5	9
76	Elevated Concentrations of SERPINE2/Protease Nexin-1 and Secretory Leukocyte Protease Inhibitor in the Serum of Patients with Papillary Thyroid Cancer. <i>Disease Markers</i> , 2017 , 2017, 4962137	3.2	9

(2014-2013)

75	Random Reducts: A Monte Carlo Rough Set-based Method for Feature Selection in Large Datasets. <i>Fundamenta Informaticae</i> , 2013 , 127, 273-288	1	9	
74	Stimulatory effect of growth hormone-releasing hormone (GHRH(1-29)NH2) on the proliferation, VEGF and chromogranin A secretion by human neuroendocrine tumor cell line NCI-H727 in vitro. <i>Neuropeptides</i> , 2009 , 43, 397-400	3.3	9	
73	Elevated peripheral blood plasma concentrations of tie-2 and angiopoietin 2 in patients with neuroendocrine tumors. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 1444-60	6.3	9	
72	SICTIN: Rapid footprinting of massively parallel sequencing data. <i>BioData Mining</i> , 2010 , 3, 4	4.3	9	
71	Influence of granulocyte-macrophage colony stimulating factor on pituitary-adrenal axis (PAA) in rats in vivo. <i>Pituitary</i> , 1999 , 2, 211-6	4.3	9	
70	A Rough Set Framework for Learning in a Directed Acyclic Graph. <i>Lecture Notes in Computer Science</i> , 2002 , 144-155	0.9	9	
69	ChIP-seq in steatohepatitis and normal liver tissue identifies candidate disease mechanisms related to progression to cancer. <i>BMC Medical Genomics</i> , 2013 , 6, 50	3.7	8	
68	Towards a Rough Mereology-Based Logic for Approximate Solution Synthesis. Part 1. <i>Studia Logica</i> , 1997 , 58, 143-184	0.7	8	
67	Using local gene expression similarities to discover regulatory binding site modules. <i>BMC Bioinformatics</i> , 2006 , 7, 505	3.6	8	
66	Classification of Gene Expression Data in an Ontology. Lecture Notes in Computer Science, 2001, 186-19	40.9	8	
65	Analyzing DNA methylation patterns in subjects diagnosed with schizophrenia using machine learning methods. <i>Journal of Psychiatric Research</i> , 2019 , 114, 41-47	5.2	7	
64	A complete map of potential pathogenicity markers of avian influenza virus subtype H5 predicted from 11 expressed proteins. <i>BMC Microbiology</i> , 2015 , 15, 128	4.5	7	
63	Reduced plasma level of diazepam-binding inhibitor (DBI) in patients with morbid obesity. <i>Endocrine</i> , 2015 , 49, 859-62	4	7	
62	Unveiling new interdependencies between significant DNA methylation sites, gene expression profiles and glioma patients survival. <i>Scientific Reports</i> , 2018 , 8, 4390	4.9	7	
61	Antineoplastic action of growth hormone-releasing hormone (GHRH) antagonists. <i>Recent Patents on Anti-Cancer Drug Discovery</i> , 2012 , 7, 56-63	2.6	7	
60	Discovering Networks of Interdependent Features in High-Dimensional Problems. <i>Studies in Big Data</i> , 2016 , 285-304	0.9	7	
59	Maps of context-dependent putative regulatory regions and genomic signal interactions. <i>Nucleic Acids Research</i> , 2016 , 44, 9110-9120	20.1	7	
58	Nucleosome regulatory dynamics in response to TGFII <i>Nucleic Acids Research</i> , 2014 , 42, 6921-34	20.1	6	

57	Revealing cell cycle control by combining model-based detection of periodic expression with novel cis-regulatory descriptors. <i>BMC Systems Biology</i> , 2007 , 1, 45	3.5	6
56	Taming Large Rule Models in Rough Set Approaches. Lecture Notes in Computer Science, 1999 , 193-203	0.9	6
55	Ultrafiltration - an alternative method to polyethylene glycol precipitation for macroprolactin detection. <i>Archives of Medical Science</i> , 2015 , 11, 1001-7	2.9	6
54	Usefulness of PTH measurements in FNAB washouts in the identification of pathological parathyroidsanalysis of the factors that influence the effectiveness of this method. <i>Endokrynologia Polska</i> , 2014 , 65, 25-32	1.1	6
53	Macrophage-associated wound healing contributes to African green monkey SIV pathogenesis control. <i>Nature Communications</i> , 2019 , 10, 5101	17.4	5
52	Computational Analysis of Molecular Interaction Networks Underlying Change of HIV-1 Resistance to Selected Reverse Transcriptase Inhibitors. <i>Bioinformatics and Biology Insights</i> , 2010 , 4, 137-46	5.3	5
51	Gene expression trends and protein features effectively complement each other in gene function prediction. <i>Bioinformatics</i> , 2009 , 25, 322-30	7.2	5
50	Inhibition of proliferation, VEGF secretion of human neuroendocrine tumor cell line NCI-H727 by an antagonist of growth hormone-releasing hormone (GH-RH) in vitro. <i>Cancer Letters</i> , 2008 , 268, 120-8	9.9	5
49	Overlapping phenotype of Wolf-Hirschhorn and Beckwith-Wiedemann syndromes in a girl with der(4)t(4;11)(pter;pter). <i>American Journal of Medical Genetics, Part A</i> , 2007 , 143A, 1760-6	2.5	5
48	Efficacy and safety of high-dose long-acting repeatable octreotide as monotherapy or in combination with pegvisomant or cabergoline in patients with acromegaly not adequately controlled by conventional regimens: results of an open-label, multicentre study. <i>Endokrynologia</i>	1.1	5
47	Rough Sets in Bioinformatics 2007 , 225-243		5
46	R.ROSETTA: an interpretable machine learning framework. <i>BMC Bioinformatics</i> , 2021 , 22, 110	3.6	5
45	Decreased serum level of IL-7 in patients with active GravesRdisease. <i>Cytokine</i> , 2015 , 75, 373-9	4	4
44	Selection of Significant Features Using Monte Carlo Feature Selection. <i>Studies in Computational Intelligence</i> , 2016 , 25-38	0.8	4
43	A strand specific high resolution normalization method for chip-sequencing data employing multiple experimental control measurements. <i>Algorithms for Molecular Biology</i> , 2012 , 7, 2	1.8	4
42	Logic programming and rapid prototyping. Science of Computer Programming, 1987, 9, 179-205	1.1	4
41	Feature Synthesis and Extraction for the Construction of Generalized Properties of Amino Acids. <i>Lecture Notes in Computer Science</i> , 2004 , 786-791	0.9	4
40	A Prolegomenon to Partial Deduction. <i>Fundamenta Informaticae</i> , 1993 , 18, 41-64	1	4

39	Interleukin-15 response signature predicts RhCMV/SIV vaccine efficacy. PLoS Pathogens, 2021, 17, e100	9,288	4
38	Genomic characterization of relapsed acute myeloid leukemia reveals novel putative therapeutic targets. <i>Blood Advances</i> , 2021 , 5, 900-912	7.8	4
37	PiiL: visualization of DNA methylation and gene expression data in gene pathways. <i>BMC Genomics</i> , 2017 , 18, 571	4.5	3
36	Serum concentrations of TNF land its soluble receptors in patients with adrenal tumors treated by surgery. <i>International Journal of Molecular Sciences</i> , 2010 , 11, 2281-90	6.3	3
35	Partial Structural Synthesis of Programs. Fundamenta Informaticae, 1997 , 31, 125-144	1	3
34	Diagnosing Acute Appendicitis with Very Simple Classification Rules. <i>Lecture Notes in Computer Science</i> , 1999 , 462-467	0.9	3
33	Multifaceted regulation of hepatic lipid metabolism by YY1. Life Science Alliance, 2021, 4,	5.8	3
32	Identification of combinatorial host-specific signatures with a potential to affect host adaptation in influenza A H1N1 and H3N2 subtypes. <i>BMC Genomics</i> , 2016 , 17, 529	4.5	3
31	Interpretable Machine Learning Reveals Dissimilarities Between Subtypes of Autism Spectrum Disorder. <i>Frontiers in Genetics</i> , 2021 , 12, 618277	4.5	3
30	({mathcal R}o{mathcal S}y): A Rough Knowledge Base System. <i>Lecture Notes in Computer Science</i> , 2005 , 48-58	0.9	3
29	Towards refinement of definite logic programs. Lecture Notes in Computer Science, 1994, 315-325	0.9	3
28	Rough sets for data mining and knowledge discovery. Lecture Notes in Computer Science, 1997, 393-393	0.9	3
27	Relation of C-reactive protein to obesity, adipose tissue hormones and cardiovascular risk factors in men treated with early percutaneous intervention in course of acute myocardial infarction. Neuroendocrinology Letters, 2007, 28, 427-32	0.3	3
26	Studies of liver tissue identify functional gene regulatory elements associated to gene expression, type 2 diabetes, and other metabolic diseases. <i>Human Genomics</i> , 2019 , 13, 20	6.8	2
25	Integration of whole-body [F]FDG PET/MRI with non-targeted metabolomics can provide new insights on tissue-specific insulin resistance in type 2 diabetes. <i>Scientific Reports</i> , 2020 , 10, 8343	4.9	2
24	Some Heuristics for Default Knowledge Discovery. <i>Lecture Notes in Computer Science</i> , 1998 , 373-380	0.9	2
23	Inhibitory effect of thalidomide on the growth, secretory function and angiogenesis of estrogen-induced prolactinoma in Fischer 344 rats. <i>Life Sciences</i> , 2006 , 79, 1741-8	6.8	2
22	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021 , 12, 3621	17.4	2

21	Angiogenic and anti-angiogenic factors in adrenal tumours. <i>Endokrynologia Polska</i> , 2006 , 57, 633-40	1.1	2
20	Estimation of vitamin D status in patients with secondary and primary hypothyroidism of different etiology. <i>Neuroendocrinology Letters</i> , 2018 , 38, 565-564	0.3	2
19	Serum vascular endothelial growth factor (VEGF) is elevated in GH deficient adults. <i>Growth Hormone and IGF Research</i> , 2011 , 21, 96-101	2	1
18	Differential gene expression in the olfactory bulb following exposure to the olfactory toxicant 2,6-dichlorophenyl methylsulphone and its 2,5-dichlorinated isomer in mice. <i>NeuroToxicology</i> , 2007 , 28, 1120-8	4.4	1
17	A study on Monte Carlo Gene Screening 2005 , 349-356		1
16	R.ROSETTA: an interpretable machine learning framework		1
15	funMotifs: Tissue-specific transcription factor motifs		1
14	Partial deduction in the framework of structural synthesis of programs. <i>Lecture Notes in Computer Science</i> , 1997 , 239-255	0.9	1
13	Visualization of Rules in Rule-Based Classifiers. Smart Innovation, Systems and Technologies, 2012, 329-	33:2 5	1
12	Organ-specific metabolic pathways distinguish prediabetes, type 2 diabetes and normal tissues		1
11	Sustained IL-15 response signature predicts RhCMV/SIV vaccine efficacy		1
10	Soft Computing Approach to the Analysis of the Amino Acid Similarity Matrices 2005 , 663-670		1
9	Peripheral blood concentrations of vascular endothelial growth factor and its soluble receptors (R1 and R2) in patients with adrenal cortex tumours treated by surgery. <i>Endokrynologia Polska</i> , 2009 , 60, 9-13	1.1	1
8	Nucleolar rDNA folds into condensed foci with a specific combination of epigenetic marks. <i>Plant Journal</i> , 2021 , 105, 1534-1548	6.9	O
7	Interpretable machine learning identifies paediatric Systemic Lupus Erythematosus subtypes based on gene expression data <i>Scientific Reports</i> , 2022 , 12, 7433	4.9	О
6	The relationship between features of metabolic syndrome and blood adipocytokine concentrations in the morbid obese patients during dynamic weight loss. <i>Open Medicine (Poland)</i> , 2006 , 1, 136-147	2.2	
5	Interleukins in GravesRDisease 2001 , 251-261		
4	-ROSETTA. Lecture Notes in Computer Science, 2020 , 8-25	0.9	

LIST OF PUBLICATIONS

Construction of Rough Set-Based Classifiers for Predicting HIV Resistance to Nucleoside Reverse Transcriptase Inhibitors **2008**, 249-258

2	Towards Knowledge Discovery from cDNA Microarray Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2000 , 470-475	0.9
1	A non-coding cancer mutation disrupting an HNF4lbinding motif affects an enhancer regulating genes associated to the progression of liver cancer. <i>Experimental Oncology</i> , 2021 , 43, 2-6	0.8