

# Jan Maciej Komorowski

## List of Publications by Year in descending order

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165  
papers

12,396  
citations

116194

36  
h-index

30277

107  
g-index

184  
all docs

184  
docs citations

184  
times ranked

21103  
citing authors

#	ARTICLE	IF	CITATIONS
1	A non-coding cancer mutation disrupting an HNF4 $\beta$ binding motif affects an enhancer regulating genes associated to the progression of liver cancer. <i>Experimental Oncology</i> , 2023, 43, 2-6.	0.4	2
2	Transcriptomic analysis reveals proinflammatory signatures associated with acute myeloid leukemia progression. <i>Blood Advances</i> , 2022, 6, 152-164.	2.5	11
3	Machine Learning-Based Analysis of Glioma Grades Reveals Co-Enrichment. <i>Cancers</i> , 2022, 14, 1014.	1.7	2
4	Interpretable machine learning identifies paediatric Systemic Lupus Erythematosus subtypes based on gene expression data. <i>Scientific Reports</i> , 2022, 12, 7433.	1.6	7
5	Nucleolar rDNA folds into condensed foci with a specific combination of epigenetic marks. <i>Plant Journal</i> , 2021, 105, 1534-1548.	2.8	7
6	Genomic characterization of relapsed acute myeloid leukemia reveals novel putative therapeutic targets. <i>Blood Advances</i> , 2021, 5, 900-912.	2.5	30
7	Interpretable Machine Learning Reveals Dissimilarities Between Subtypes of Autism Spectrum Disorder. <i>Frontiers in Genetics</i> , 2021, 12, 618277.	1.1	7
8	R.ROSETTA: an interpretable machine learning framework. <i>BMC Bioinformatics</i> , 2021, 22, 110.	1.2	16
9	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021, 12, 3621.	5.8	22
10	Multifaceted regulation of hepatic lipid metabolism by YY1. <i>Life Science Alliance</i> , 2021, 4, e202000928.	1.3	13
11	Functional annotation of noncoding mutations in cancer. <i>Life Science Alliance</i> , 2021, 4, e201900523.	1.3	3
12	Interleukin-15 response signature predicts RhCMV/SIV vaccine efficacy. <i>PLoS Pathogens</i> , 2021, 17, e1009278.	2.1	18
13	MetaFetchR: An R Package for Complete Mapping of Small-Compound Data. <i>Metabolites</i> , 2021, 11, 743.	1.3	0
14	Integration of whole-body [18F]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.	1.6	5
15	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, 180-194.	1.0	26
16	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
17	-ROSETTA. <i>Lecture Notes in Computer Science</i> , 2020, , 8-25.	1.0	0
18	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.	1.6	32

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19	Macrophage-associated wound healing contributes to African green monkey SIV pathogenesis control. <i>Nature Communications</i> , 2019, 10, 5101.	5.8	17
20	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.	1.4	5
21	Analyzing DNA methylation patterns in subjects diagnosed with schizophrenia using machine learning methods. <i>Journal of Psychiatric Research</i> , 2019, 114, 41-47.	1.5	19
22	Allele specific chromatin signals, 3D interactions, and motif predictions for immune and B cell related diseases. <i>Scientific Reports</i> , 2019, 9, 2695.	1.6	24
23	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 Polska</i> , 2019, 70, 305-312.	0.3	10
24	Alteration in the serum concentrations of FGF19, FGFR4 and $\beta$ 2Klotho in patients with thyroid cancer. <i>Cytokine</i> , 2018, 105, 32-36.	1.4	18
25	Unveiling new interdependencies between significant DNA methylation sites, gene expression profiles and glioma patients survival. <i>Scientific Reports</i> , 2018, 8, 4390.	1.6	13
26	Stratifying Cervical Cancer Risk with Registry Data. , 2018, , .		1
27	Special Issue Introduction: The Wonders and Mysteries Next Generation Sequencing Technologies Help Reveal. <i>Genes</i> , 2018, 9, 505.	1.0	0
28	Estimation of vitamin D status in patients with secondary and primary hypothyroidism of different etiology. <i>Neuroendocrinology Letters</i> , 2018, 38, 565-564.	0.2	2
29	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.	2.3	12
30	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, 1-5.	0.6	18
31	Piil: visualization of DNA methylation and gene expression data in gene pathways. <i>BMC Genomics</i> , 2017, 18, 571.	1.2	3
32	A Significant Regulatory Mutation Burden at a High-Affinity Position of the CTCF Motif in Gastrointestinal Cancers. <i>Human Mutation</i> , 2016, 37, 904-913.	1.1	37
33	Somatostatin Analogs and Tumor Localization Do Not Influence Vitamin D Concentration in Patients with Neuroendocrine Tumors. <i>Nutrition and Cancer</i> , 2016, 68, 428-434.	0.9	14
34	Maps of context-dependent putative regulatory regions and genomic signal interactions. <i>Nucleic Acids Research</i> , 2016, 44, gkw800.	6.5	10
35	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.	1.2	6
36	Combinatorial identification of DNA methylation patterns over age in the human brain. <i>BMC Bioinformatics</i> , 2016, 17, 393.	1.2	13

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37	Selection of Significant Features Using Monte Carlo Feature Selection. <i>Studies in Computational Intelligence</i> , 2016, , 25-38.	0.7	4
38	Discovering Networks of Interdependent Features in High-Dimensional Problems. <i>Studies in Big Data</i> , 2016, , 285-304.	0.8	7
39	Decreased serum level of IL-7 in patients with active Graves' disease. <i>Cytokine</i> , 2015, 75, 373-379.	1.4	5
40	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.	1.3	9
41	Reduced plasma level of diazepam-binding inhibitor (DBI) in patients with morbid obesity. <i>Endocrine</i> , 2015, 49, 859-862.	1.1	8
42	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.	1.2	25
43	True null allele detection in microsatellite loci: a comparison of methods, assessment of difficulties and survey of possible improvements. <i>Molecular Ecology Resources</i> , 2015, 15, 477-488.	2.2	43
44	Ultrafiltration - an alternative method to polyethylene glycol precipitation for macroprolactin detection. <i>Archives of Medical Science</i> , 2015, 11, 1001-7.	0.4	7
45	Nucleosome regulatory dynamics in response to TGF $\beta$ . <i>Nucleic Acids Research</i> , 2014, 42, 6921-6934.	6.5	6
46	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, 239-254.	1.7	158
47	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, 1341-1350.	0.9	13
48	Ciruviz: a web-based tool for rule networks and interaction detection using rule-based classifiers. <i>BMC Bioinformatics</i> , 2014, 15, 139.	1.2	21
49	Przydatność oznaczania stężenia PTH w poprzecznych do biopsji aspiracyjnej cienkoigłowej w identyfikowaniu patologicznych przystarczyc – analiza czynników wpływających na skuteczność tej metody. <i>Endokrynologia Polska</i> , 2014, 65, 25-32.	0.3	9
50	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.	0.7	8
51	Long-term impact of vertical banded gastroplasty (VBC) 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, 490-493.	1.4	24
52	Peak Finder Metaserver - a novel application for finding peaks in ChIP-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 280.	1.2	13
53	Random Reducts: A Monte Carlo Rough Set-based Method for Feature Selection in Large Datasets. <i>Fundamenta Informaticae</i> , 2013, 127, 273-288.	0.3	9
54	Rule-Based Models of the Interplay between Genetic and Environmental Factors in Childhood Allergy. <i>PLoS ONE</i> , 2013, 8, e80080.	1.1	18

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55	Elevated Peripheral Blood Plasma Concentrations of Tie-2 and Angiotensin II in Patients with Neuroendocrine Tumors. <i>International Journal of Molecular Sciences</i> , 2012, 13, 1444-1460.	1.8	17
56	Antineoplastic Action of Growth Hormone-Releasing Hormone (GHRH) Antagonists. <i>Recent Patents on Anti-Cancer Drug Discovery</i> , 2012, 7, 56-63.	0.8	8
57	Combinations of Histone Modifications Mark Exon Inclusion Levels. <i>PLoS ONE</i> , 2012, 7, e29911.	1.1	38
58	Gis1 and Rph1 Regulate Glycerol and Acetate Metabolism in Glucose Depleted Yeast Cells. <i>PLoS ONE</i> , 2012, 7, e31577.	1.1	32
59	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.	0.3	4
60	Monte Carlo feature selection and rule-based models to predict Alzheimer's disease in mild cognitive impairment. <i>Journal of Neural Transmission</i> , 2012, 119, 821-831.	1.4	13
61	Visualization of Rules in Rule-Based Classifiers. <i>Smart Innovation, Systems and Technologies</i> , 2012, , 329-338.	0.5	2
62	Systemic blood osteopontin, endostatin, and E-selectin concentrations after vertical banding surgery in severely obese adults. <i>Cytokine</i> , 2011, 55, 56-61.	1.4	23
63	Serum vascular endothelial growth factor (VEGF) is elevated in GH deficient adults. <i>Growth Hormone and IGF Research</i> , 2011, 21, 96-101.	0.5	1
64	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.	1.1	30
65	The Place of Somatostatin Analogs in the Diagnosis and Treatment of the Neuroendocrine Glands Tumors. , 2011, , 241-272.		0
66	Focal amplifications are associated with high grade and recurrences in stage Ta bladder carcinoma. <i>International Journal of Cancer</i> , 2010, 126, 1390-1402.	2.3	54
67	Decreased 1-25 Dihydroxyvitamin D3 Concentration in Peripheral Blood Serum of Patients with Thyroid Cancer. <i>Archives of Medical Research</i> , 2010, 41, 190-194.	1.5	47
68	SICTIN: Rapid footprinting of massively parallel sequencing data. <i>BioData Mining</i> , 2010, 3, 4.	2.2	10
69	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, BBI.S6247.	1.0	5
70	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, 561-579.	1.6	29
71	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. <i>Experimental and Molecular Medicine</i> , 2010, 42, 484.	3.2	32
72	Serum Concentrations of TNF $\alpha$ and Its Soluble Receptors in Patients with Adrenal Tumors Treated by Surgery. <i>International Journal of Molecular Sciences</i> , 2010, 11, 2281-2290.	1.8	3

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73	Nitrogen depletion in the fission yeast <i>Schizosaccharomyces pombe</i> causes nucleosome loss in both promoters and coding regions of activated genes. <i>Genome Research</i> , 2010, 20, 361-371.	2.4	16
74	Monte Carlo Feature Selection and Interdependency Discovery in Supervised Classification. <i>Studies in Computational Intelligence</i> , 2010, , 371-385.	0.7	12
75	A Rough Set-Based Model of HIV-1 Reverse Transcriptase Resistome. <i>Bioinformatics and Biology Insights</i> , 2009, 3, BBI.S3382.	1.0	20
76	A Comprehensive Analysis of the Structure-Function Relationship in Proteins Based on Local Structure Similarity. <i>PLoS ONE</i> , 2009, 4, e6266.	1.1	37
77	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-e85.	6.5	34
78	Molecular interactions between HNF4a, FOXA2 and GABP identified at regulatory DNA elements through ChIP-sequencing. <i>Nucleic Acids Research</i> , 2009, 37, 7498-7508.	6.5	63
79	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. <i>Epigenetics</i> , 2009, 4, 107-113.	1.3	25
80	Gene expression trends and protein features effectively complement each other in gene function prediction. <i>Bioinformatics</i> , 2009, 25, 322-330.	1.8	5
81	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. <i>Neuro-Oncology</i> , 2009, 11, 803-818.	0.6	43
82	Stimulatory effect of growth hormone-releasing hormone (GHRH(1-29)NH <sub>2</sub> ) 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.	0.9	10
83	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, 1878-1890.	2.2	22
84	Proteochemometrics mapping of the interaction space for retroviral proteases and their substrates. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 5229-5237.	1.4	13
85	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.	13.9	64
86	Nucleosomes are well positioned in exons and carry characteristic histone modifications. <i>Genome Research</i> , 2009, 19, 1732-1741.	2.4	274
87	Peripheral blood concentrations of vascular endothelial growth factor and its soluble receptors (R1) Tj ETQq1 1 0.784314 rgBT /Overlaid 9-13.	0.3	1
88	Effect of hyperprolactinaemia on <i>Toxoplasma gondii</i> prevalence in humans. <i>Parasitology Research</i> , 2008, 102, 723-729.	0.6	16
89	Profiling of copy number variations (CNVs) in healthy individuals from three ethnic groups using a human genome 32K BAC-clone-based array. <i>Human Mutation</i> , 2008, 29, 398-408.	1.1	46
90	Somatic mosaicism for copy number variation in differentiated human tissues. <i>Human Mutation</i> , 2008, 29, 1118-1124.	1.1	184

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91	Phenotypically Concordant and Discordant Monozygotic Twins Display Different DNA Copy-Number-Variation Profiles. <i>American Journal of Human Genetics</i> , 2008, 82, 763-771.	2.6	533
92	Genome-scale study of the importance of binding site context for transcription factor binding and gene regulation. <i>BMC Bioinformatics</i> , 2008, 9, 484.	1.2	17
93	Combinatorial control of gene expression by the three yeast repressors Mig1, Mig2 and Mig3. <i>BMC Genomics</i> , 2008, 9, 601.	1.2	86
94	Resistin increases with obesity and atherosclerotic risk factors in patients with myocardial infarction. <i>Metabolism: Clinical and Experimental</i> , 2008, 57, 488-493.	1.5	48
95	Kcnq1ot1 Antisense Noncoding RNA Mediates Lineage-Specific Transcriptional Silencing through Chromatin-Level Regulation. <i>Molecular Cell</i> , 2008, 32, 232-246.	4.5	1,114
96	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, 120-128.	3.2	8
97	Generalized Proteochemometric Model of Multiple Cytochrome P450 Enzymes and Their Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1840-1850.	2.5	37
98	A segmental maximum a posteriori approach to genome-wide copy number profiling. <i>Bioinformatics</i> , 2008, 24, 751-758.	1.8	29
99	Monte Carlo feature selection for supervised classification. <i>Bioinformatics</i> , 2008, 24, 110-117.	1.8	262
100	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, 380-392.	2.4	85
101	Construction of Rough Set-Based Classifiers for Predicting HIV Resistance to Nucleoside Reverse Transcriptase Inhibitors. , 2008, , 249-258.		0
102	A Look Inside HIV Resistance through Retroviral Protease Interaction Maps. <i>PLoS Computational Biology</i> , 2007, 3, e48.	1.5	23
103	Butyrate mediates decrease of histone acetylation centered on transcription start sites and down-regulation of associated genes. <i>Genome Research</i> , 2007, 17, 708-719.	2.4	130
104	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, 1120-1128.	1.4	1
105	Overlapping phenotype of Wolfâ€™s Hirschhorn and Beckwithâ€™s Wiedemann syndromes in a girl with der(4)t(4;11)(pter;pter). <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 1760-1766.	0.7	5
106	A previously unrecognized microdeletion syndrome on chromosome 22 band q11.2 encompassing the <i>BCR</i> gene. <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 2178-2184.	0.7	42
107	Computational proteomics analysis of HIV-1 protease interactome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 305-312.	1.5	50
108	Proteochemometric analysis of small cyclic peptides' interaction with wild-type and chimeric melanocortin receptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 83-96.	1.5	15

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109	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
110	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.	3.0	8
111	Endocan is a VEGF-A and PI3K regulated gene with increased expression in human renal cancer. <i>Experimental Cell Research</i> , 2007, 313, 1285-1294.	1.2	112
112	Rough Sets in Bioinformatics. , 2007, , 225-243.		10
113	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. <i>Neuroendocrinology Letters</i> , 2007, 28, 427-32.	0.2	3
114	Monoclonal anti-TNFalpha antibody (infliximab) in the treatment of patient with thyroid associated ophthalmopathy. <i>Klinika Oczna</i> , 2007, 109, 457-60.	0.0	21
115	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, 291-295.	1.4	32
116	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, 2558-2563.	2.0	62
117	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, 1741-1748.	2.0	2
118	The Place of Somatostatin Analogs in the Diagnosis and Treatment of the Neuroendocrine Glands Tumors. <i>Recent Patents on Anti-Cancer Drug Discovery</i> , 2006, 1, 237-254.	0.8	13
119	Rough set-based proteochemometrics modeling of G-protein-coupled receptor-ligand interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 24-34.	1.5	26
120	Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 568-579.	1.5	38
121	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.	0.6	0
122	Using local gene expression similarities to discover regulatory binding site modules. <i>BMC Bioinformatics</i> , 2006, 7, 505.	1.2	12
123	The LCB Data Warehouse. <i>Bioinformatics</i> , 2006, 22, 1024-1026.	1.8	34
124	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, 381-389.	2.9	21
125	A Statistical Method for Determining Importance of Variables in an Information System. <i>Lecture Notes in Computer Science</i> , 2006, , 557-566.	1.0	17
126	Angiogenic and anti-angiogenic factors in adrenal tumours. <i>Endokrynologia Polska</i> , 2006, 57, 633-40.	0.3	2



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127	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, 3435-3447.	1.4	71
128	Discovering regulatory binding-site modules using rule-based learning. <i>Genome Research</i> , 2005, 15, 856-866.	2.4	41
129	Markers of Adenocarcinoma Characteristic of the Site of Origin: Development of a Diagnostic Algorithm. <i>Clinical Cancer Research</i> , 2005, 11, 3766-3772.	3.2	296
130	Cytokines locally produced by lymphocytes removed from the hypertrophic nasopharyngeal and palatine tonsils. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2005, 69, 937-941.	0.4	40
131	$R_{\mathcal{S}}$ : A Rough Knowledge Base System. <i>Lecture Notes in Computer Science</i> , 2005, , 48-58.	1.0	4
132	Soft Computing Approach to the Analysis of the Amino Acid Similarity Matrices. , 2005, , 663-670.		1
133	A study on Monte Carlo Gene Screening. , 2005, , 349-356.		3
134	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, 2405-2410.	1.6	27
135	Gene expression based classification of gastric carcinoma. <i>Cancer Letters</i> , 2004, 210, 227-237.	3.2	26
136	Feature Synthesis and Extraction for the Construction of Generalized Properties of Amino Acids. <i>Lecture Notes in Computer Science</i> , 2004, , 786-791.	1.0	5
137	Predicting Gene Ontology Biological Process From Temporal Gene Expression Patterns. <i>Genome Research</i> , 2003, 13, 965-979.	2.4	88
138	Learning rule-based models of biological process from gene expression time profiles using Gene Ontology. <i>Bioinformatics</i> , 2003, 19, 1116-1123.	1.8	81
139	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, 189-194.	1.8	27
140	A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins. <i>Bioinformatics</i> , 2003, 19, ii81-ii91.	1.8	25
141	Liver gene expression in rats in response to the peroxisome proliferator-activated receptor- $\alpha$ agonist ciprofibrate. <i>Physiological Genomics</i> , 2003, 15, 9-19.	1.0	38
142	Matrix Metalloproteinases, Tissue Inhibitors of Matrix Metalloproteinases and Angiogenic Cytokines in Peripheral Blood of Patients with Thyroid Cancer. <i>Thyroid</i> , 2002, 12, 655-662.	2.4	54
143	Modelling Biological Phenomena with Rough Sets. <i>Lecture Notes in Computer Science</i> , 2002, , 13-13.	1.0	3
144	A Rough Set Framework for Learning in a Directed Acyclic Graph. <i>Lecture Notes in Computer Science</i> , 2002, , 144-155.	1.0	12

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145	Interleukins in Graves' Disease. , 2001, , 251-261.		0
146	A literature network of human genes for high-throughput analysis of gene expression. Nature Genetics, 2001, 28, 21-28.	9.4	655
147	Title is missing!. Nature Genetics, 2001, 28, 21-28.	9.4	482
148	Classification of Gene Expression Data in an Ontology. Lecture Notes in Computer Science, 2001, , 186-194.	1.0	12
149	Towards Knowledge Discovery from cDNA Microarray Gene Expression Data. Lecture Notes in Computer Science, 2000, , 470-475.	1.0	0
150	Taming Large Rule Models in Rough Set Approaches. Lecture Notes in Computer Science, 1999, , 193-203.	1.0	10
151	Influence of granulocyte-macrophage colony stimulating factor on pituitary-adrenal axis (PAA) in rats in vivo. Pituitary, 1999, 2, 211-216.	1.6	9
152	Modelling prognostic power of cardiac tests using rough sets. Artificial Intelligence in Medicine, 1999, 15, 167-191.	3.8	76
153	Cytokines serum levels as the markers of thyroid activation in Graves' disease. Immunology Letters, 1998, 60, 143-148.	1.1	18
154	Some Heuristics for Default Knowledge Discovery. Lecture Notes in Computer Science, 1998, , 373-380.	1.0	3
155	Partial Structural Synthesis of Programs. Fundamenta Informaticae, 1997, 31, 125-144.	0.3	5
156	Towards a Rough Mereology-Based Logic for Approximate Solution Synthesis. Part 1. Studia Logica, 1997, 58, 143-184.	0.4	10
157	Effects of hCG and $\hat{I}^2$ -hCG on IL-2 and sIL-2R secretion from human peripheral blood mononuclear cells: A dose-response study in vitro. Immunology Letters, 1997, 59, 29-33.	1.1	16
158	Partial deduction in the framework of structural synthesis of programs. Lecture Notes in Computer Science, 1997, , 239-255.	1.0	1
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