

Tanja Kunej

List of Publications by Year in Descending Order

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

101
papers

2,233
citations

23
h-index

45
g-index

110
ext. papers

2,627
ext. citations

4.1
avg. IF

5.42
L-index

#	Paper	IF	Citations
101	Transcriptomics of receptive endometrium in women with sonographic features of adenomyosis.. <i>Reproductive Biology and Endocrinology</i> , 2022 , 20, 2	5	0
100	Genetic variants of the hypoxia-inducible factor 3 alpha subunit (Hif3a) gene in the Fat and Lean mouse selection lines.. <i>Molecular Biology Reports</i> , 2022 , 1	2.8	0
99	Top Trends in Multiomics Research: Evaluation of 52 Published Studies and New Ways of Thinking Terminology and Visual Displays. <i>OMICS A Journal of Integrative Biology</i> , 2021 , 25, 681-692	3.8	2
98	Integration and Visualization of Regulatory Elements and Variations of the Gene in Human. <i>Genes</i> , 2021 , 12,	4.2	1
97	Erythrocytosis: genes and pathways involved in disease development. <i>Blood Transfusion</i> , 2021 , 19, 518-532	3.8	4
96	Interview: Prof. Tanja Kunej, a Pioneer of Multiomics, on 21st Century Systems Science Prospects and Challenges. <i>OMICS A Journal of Integrative Biology</i> , 2021 , 25, 136-138	3.8	
95	Thanatechnology and the Living Dead: New Concepts in Digital Transformation and Human-Computer Interaction. <i>OMICS A Journal of Integrative Biology</i> , 2021 , 25, 401-407	3.8	2
94	Molecular Dynamics Simulations Reveal Interactions of an IgG1 Antibody With Selected Fc Receptors. <i>Frontiers in Chemistry</i> , 2021 , 9, 705931	5	3
93	De novo mutations in idiopathic male infertility-A pilot study. <i>Andrology</i> , 2021 , 9, 212-220	4.2	5
92	CaNDis: a web server for investigation of causal relationships between diseases, drugs and drug targets. <i>Bioinformatics</i> , 2021 , 37, 885-887	7.2	2
91	A Multi-Omics Analysis of PON1 Lactonase Activity in Relation to Human Health and Disease. <i>OMICS A Journal of Integrative Biology</i> , 2021 , 25, 38-51	3.8	2
90	Genetic analysis of 39 erythrocytosis and hereditary hemochromatosis-associated genes in the Slovenian family with idiopathic erythrocytosis. <i>Journal of Clinical Laboratory Analysis</i> , 2021 , 35, e23715 ³		2
89	Identification of Variants Associated With Rare Hematological Disorder Erythrocytosis Using Targeted Next-Generation Sequencing Analysis. <i>Frontiers in Genetics</i> , 2021 , 12, 689868	4.5	2
88	Systematic Search for Novel Circulating Biomarkers Associated with Extracellular Vesicles in Alzheimer's Disease: Combining Literature Screening and Database Mining Approaches. <i>Journal of Personalized Medicine</i> , 2021 , 11,	3.6	1
87	Integrative Map of Regulatory Elements and Variations. <i>Genes</i> , 2021 , 12,	4.2	2
86	Molecular signature of eutopic endometrium in endometriosis based on the multi-omics integrative synthesis. <i>Journal of Assisted Reproduction and Genetics</i> , 2020 , 37, 1593-1611	3.4	5
85	Association of Peroxisome Proliferator-Activated Receptors (PPARs) with Diabetic Retinopathy in Human and Animal Models: Analysis of the Literature and Genome Browsers. <i>PPAR Research</i> , 2020 , 2020, 1783564	4.3	4

84	Digging Deeper into Precision/Personalized Medicine: Cracking the Sugar Code, the Third Alphabet of Life, and Sociomateriality of the Cell. <i>OMICS A Journal of Integrative Biology</i> , 2020 , 24, 62-80	3.8	11
83	Genetic variability of serotonin pathway associated with schizophrenia onset, progression, and treatment. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020 , 183, 113-127	3.5	3
82	Determining the Molecular Background of Endometrial Receptivity in Adenomyosis. <i>Biomolecules</i> , 2020 , 10,	5.9	2
81	Molecular sexing assays in 114 mammalian species: In silico sequence reanalysis and a unified graphical visualization of diagnostic tests. <i>Ecology and Evolution</i> , 2019 , 9, 5018-5028	2.8	4
80	A Map of the microRNA Regulatory Networks Identified by Experimentally Validated microRNA-Target Interactions in Five Domestic Animals: Cattle, Pig, Sheep, Dog, and Chicken. <i>OMICS A Journal of Integrative Biology</i> , 2019 , 23, 448-456	3.8	4
79	Genetic variability of hypoxia-inducible factor alpha (HIFA) genes in familial erythrocytosis: Analysis of the literature and genome databases. <i>European Journal of Haematology</i> , 2019 , 103, 287-299	3.8	9
78	Genetic Variations of Ultraconserved Elements in the Human Genome. <i>OMICS A Journal of Integrative Biology</i> , 2019 , 23, 549-559	3.8	6
77	Rise of Systems Glycobiology and Personalized Glycomedicine: Why and How to Integrate Glycomics with Multiomics Science?. <i>OMICS A Journal of Integrative Biology</i> , 2019 , 23, 615-622	3.8	13
76	Vascular endothelial growth factor (VEGF)-related polymorphisms rs10738760 and rs6921438 are not risk factors for proliferative diabetic retinopathy (PDR) in patients with type 2 diabetes mellitus (T2DM). <i>Bosnian Journal of Basic Medical Sciences</i> , 2019 , 19, 94-100	3.3	6
75	The role of circadian rhythm in male reproduction. <i>Current Opinion in Endocrinology, Diabetes and Obesity</i> , 2019 , 26, 313-316	4	7
74	Genetic variants of erythropoietin (EPO) and EPO receptor genes in familial erythrocytosis. <i>International Journal of Laboratory Hematology</i> , 2019 , 41, 162-167	2.5	17
73	Sarcoidosis Related Novel Candidate Genes Identified by Multi-Omics Integrative Analyses. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 322-331	3.8	8
72	Insights from Ion Binding Site Network Analysis into Evolution and Functions of Proteins. <i>Molecular Informatics</i> , 2018 , 37, e1700144	3.8	4
71	Classification of heterogeneous genetic variations of microRNA regulome in cancer. <i>Cancer Letters</i> , 2018 , 419, 128-138	9.9	5
70	Genetic sex determination assays in 53 mammalian species: Literature analysis and guidelines for reporting standardization. <i>Ecology and Evolution</i> , 2018 , 8, 1009-1018	2.8	11
69	From Genomics to Omics Landscapes of Parkinson Disease: Revealing the Molecular Mechanisms. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 1-16	3.8	26
68	Classification of miRNA-related sequence variations. <i>Epigenomics</i> , 2018 , 10, 463-481	4.4	28
67	Genome-wide screening for smallest regions of overlaps in cryptorchidism. <i>Reproductive BioMedicine Online</i> , 2018 , 37, 85-99	4	3

66	Multiomics Data Triangulation for Asthma Candidate Biomarkers and Precision Medicine. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 392-409	3.8	10
65	To Genotype or Phenotype for Drug and Food Safety? Exiting the Technology Echo Chambers. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 525-527	3.8	
64	Harnessing Omics Big Data in Nine Vertebrate Species by Genome-Wide Prioritization of Sequence Variants with the Highest Predicted Deleterious Effect on Protein Function. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 410-421	3.8	5
63	Asthma MicroRNA Regulome Development Using Validated miRNA-Target Interaction Visualization. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 607-615	3.8	6
62	Molecular Mechanisms of Syndromic Cryptorchidism: Data Synthesis of 50 Studies and Visualization of Gene-Disease Network. <i>Frontiers in Endocrinology</i> , 2018 , 9, 425	5.7	8
61	PPAR γ Gene and Atherosclerosis: Genetic Polymorphisms, Epigenetics and Therapeutic Implications. <i>Balkan Journal of Medical Genetics</i> , 2018 , 21, 39-46	0.9	4
60	The microRNA gene <i>bta-mir-2313</i> in cattle: an atlas of regulatory elements and an association analysis with growth and carcass traits in the Slovenian Simental cattle breed. <i>Archives Animal Breeding</i> , 2018 , 61, 271-278	1.6	2
59	MicroRNA-Target Interactions Reloaded: Identification of Potentially Functional Sequence Variants Within Validated MicroRNA-Target Interactions. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 700-708	3.8	4
58	An Updated Taxonomy and a Graphical Summary Tool for Optimal Classification and Comprehension of Omics Research. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 337-353	3.8	8
57	Toward a Taxonomy for Multi-Omics Science? Terminology Development for Whole Genome Study Approaches by Omics Technology and Hierarchy. <i>OMICS A Journal of Integrative Biology</i> , 2017 , 21, 1-16	3.8	38
56	HIF1A gene polymorphisms and human diseases: Graphical review of 97 association studies. <i>Genes Chromosomes and Cancer</i> , 2017 , 56, 439-452	5	20
55	Identification of Sequence Variants within Experimentally Validated Protein Interaction Sites Provides New Insights into Molecular Mechanisms of Disease Development. <i>Molecular Informatics</i> , 2017 , 36, 1700017	3.8	4
54	Minimal Standards for Reporting microRNA:Target Interactions. <i>OMICS A Journal of Integrative Biology</i> , 2017 , 21, 197-206	3.8	20
53	Stop the Spam! Conference Ethics and Decoding the Subtext in Post-Truth Science. What Would Denis Diderot Say?. <i>OMICS A Journal of Integrative Biology</i> , 2017 , 21, 658-664	3.8	1
52	GenProBiS: web server for mapping of sequence variants to protein binding sites. <i>Nucleic Acids Research</i> , 2017 , 45, W253-W259	20.1	8
51	Initiative for standardization of reporting genetics of male infertility. <i>Systems Biology in Reproductive Medicine</i> , 2017 , 63, 58-66	2.9	12
50	Drug repositioning: computational approaches and research examples classified according to the evidence level. <i>Discoveries</i> , 2017 , 5, e75	3.7	2
49	MicroRNA epigenetic signatures in human disease. <i>Archives of Toxicology</i> , 2016 , 90, 2405-19	5.8	187

48	Transcription factor HIF1A: downstream targets, associated pathways, polymorphic hypoxia response element (HRE) sites, and initiative for standardization of reporting in scientific literature. <i>Tumor Biology</i> , 2016 , 37, 14851-14861	2.9	45
47	RASopathies: Presentation at the Genome, Interactome, and Phenome Levels. <i>Molecular Syndromology</i> , 2016 , 7, 72-9	1.5	9
46	In silico screening of the chicken genome for overlaps between genomic regions: microRNA genes, coding and non-coding transcriptional units, QTL, and genetic variations. <i>Chromosome Research</i> , 2016 , 24, 225-30	4.4	2
45	Construction of an integrative regulatory element and variation map of the murine Tst locus. <i>BMC Genetics</i> , 2016 , 17, 77	2.6	1
44	FTO gene variants are associated with growth and carcass traits in cattle. <i>Animal Genetics</i> , 2016 , 47, 219-23	2.3	7
43	Computational identification of non-synonymous polymorphisms within regions corresponding to protein interaction sites. <i>Computers in Biology and Medicine</i> , 2016 , 79, 30-35	7	5
42	Molecular mechanisms of cryptorchidism development: update of the database, disease comorbidity, and initiative for standardization of reporting in scientific literature. <i>Andrology</i> , 2016 , 4, 894-902	4.2	15
41	Catalog of genetic variants within mature microRNA seed regions in chicken. <i>Poultry Science</i> , 2015 , 94, 2037-40	3.9	4
40	Genetic variability of microRNA regulome in human. <i>Molecular Genetics & Genomic Medicine</i> , 2015 , 3, 30-9	2.3	17
39	Micro RNA research in cattle, pig, sheep, and chicken. <i>Acta Agriculturae Slovenica</i> , 2015 , 13-20	1.3	
38	Genetic Variability of MicroRNA Genes in 15 Animal Species. <i>Journal of Genomics</i> , 2015 , 3, 51-6	0.9	23
37	MicroRNA Silencing by DNA Methylation in Human Cancer: a Literature Analysis. <i>Non-coding RNA</i> , 2015 , 1, 44-52	7.1	24
36	MicroRNA Polymorphisms in Cancer: A Literature Analysis. <i>Cancers</i> , 2015 , 7, 1806-14	6.6	25
35	An updated h-index measures both the primary and total scientific output of a researcher. <i>Discoveries</i> , 2015 , 3,	3.7	9
34	Development of Integrative Map of MicroRNA Gene Regulatory Elements. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2015 , 4, 205-8	2.9	4
33	The decalog of long non-coding RNA involvement in cancer diagnosis and monitoring. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2014 , 51, 344-57	9.4	76
32	Data integration of 104 studies related with microRNA epigenetics revealed that miR-34 gene family is silenced by DNA methylation in the highest number of cancer types. <i>Discoveries</i> , 2014 , 2, e18	3.7	9
31	Pivotal role of the muscle-contraction pathway in cryptorchidism and evidence for genomic connections with cardiomyopathy pathways in RASopathies. <i>BMC Medical Genomics</i> , 2013 , 6, 5	3.7	27

30	HINCUTs in cancer: hypoxia-induced noncoding ultraconserved transcripts. <i>Cell Death and Differentiation</i> , 2013 , 20, 1675-87	12.7	85
29	Genome-wide in silico screening for microRNA genetic variability in livestock species. <i>Animal Genetics</i> , 2013 , 44, 669-77	2.5	27
28	The MicroRNA Decalogue of Cancer Involvement 2013 , 199-221		
27	Obesity gene atlas in mammals. <i>Journal of Genomics</i> , 2013 , 1, 45-55	0.9	42
26	Genome-wide and species-wide in silico screening for intragenic MicroRNAs in human, mouse and chicken. <i>PLoS ONE</i> , 2013 , 8, e65165	3.7	60
25	Catalog of microRNA seed polymorphisms in vertebrates. <i>PLoS ONE</i> , 2012 , 7, e30737	3.7	57
24	Cross talk between microRNA and coding cancer genes. <i>Cancer Journal (Sudbury, Mass)</i> , 2012 , 18, 223-31	1.2	67
23	Comparative genomics approach to identify candidate genetic loci for male fertility. <i>Reproduction in Domestic Animals</i> , 2011 , 46, 229-39	1.6	18
22	Epigenetic regulation of microRNAs in cancer: an integrated review of literature. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2011 , 717, 77-84	3.3	164
21	Polymorphisms in microRNA targets: a source of new molecular markers for male reproduction. <i>Asian Journal of Andrology</i> , 2011 , 13, 505-8	2.8	7
20	Non-coding RNAs: identification of cancer-associated microRNAs by gene profiling. <i>Technology in Cancer Research and Treatment</i> , 2010 , 9, 123-38	2.7	59
19	Single-nucleotide polymorphisms inside microRNA target sites influence tumor susceptibility. <i>Cancer Research</i> , 2010 , 70, 2789-98	10.1	314
18	Genetics and Genomics of Reproductive Disorders 2010 , 67-97		1
17	The glypican 3-hosted murine mir717 gene: sequence conservation, seed region polymorphisms and putative targets. <i>International Journal of Biological Sciences</i> , 2010 , 6, 769-72	11.2	13
16	Database of cattle candidate genes and genetic markers for milk production and mastitis. <i>Animal Genetics</i> , 2009 , 40, 832-51	2.5	148
15	Discovery of novel genetic networks associated with 19 economically important traits in beef cattle. <i>International Journal of Biological Sciences</i> , 2009 , 5, 528-42	11.2	46
14	Polymorphisms in the kappa casein (CSN3) gene in horse and comparative analysis of its promoter and coding region. <i>Animal Genetics</i> , 2008 , 39, 520-30	2.5	14
13	Functional UQCRC1 polymorphisms affect promoter activity and body lipid accumulation. <i>Obesity</i> , 2007 , 15, 2896-901	8	25

12	Analysis of the CAG repeat number in exon 1 of the androgen receptor gene in Slovene men with idiopathic azoospermia and oligoasthenoteratozoospermia. <i>Asian Journal of Andrology</i> , 2007 , 9, 280-2	2.8	6
11	A novel type of sequence variation: multiple-nucleotide length polymorphisms discovered in the bovine genome. <i>Genetics</i> , 2007 , 176, 403-7	4	6
10	Association between the apolipoprotein B signal peptide gene insertion/deletion polymorphism and male infertility. <i>Molecular Human Reproduction</i> , 2006 , 12, 777-9	4.4	14
9	Analysis of the hemochromatosis mutations C282Y and H63D in infertile men. <i>Fertility and Sterility</i> , 2006 , 86, 1796-8	4.8	5
8	Cross species association examination of UCN3 and CRHR2 as potential pharmacological targets for antiobesity drugs. <i>PLoS ONE</i> , 2006 , 1, e80	3.7	16
7	Significant associations of the mitochondrial transcription factor A promoter polymorphisms with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 334, 516-23	3.4	44
6	Frequency distribution of a Cys430Ser polymorphism in peroxisome proliferator-activated receptor-gamma coactivator-1 (PPARGC1) gene sequence in Chinese and Western pig breeds. <i>Journal of Animal Breeding and Genetics</i> , 2005 , 122, 7-11	2.9	17
5	Gly482Ser polymorphism of the peroxisome proliferator-activated receptor-gamma coactivator-1 gene might be a risk factor for diabetic retinopathy in Slovene population (Caucasians) with type 2 diabetes and the Pro12Ala polymorphism of the PPARgamma gene is not. <i>Diabetes/Metabolism Research and Reviews</i> , 2005 , 21, 470-4	7.5	23
4	CTG amplification in the DM1PK gene is not associated with idiopathic male subfertility. <i>Human Reproduction</i> , 2004 , 19, 2084-7	5.7	9
3	Diagnostic test for Y chromosome microdeletion screening in male infertility. <i>Genetic Testing and Molecular Biomarkers</i> , 2004 , 8, 45-9		10
2	Y chromosome microdeletions in infertile men with cryptorchidism. <i>Fertility and Sterility</i> , 2003 , 79 Suppl 3, 1559-65	4.8	15
1	Screening for Y chromosome microdeletions in 226 Slovenian subfertile men. <i>Human Reproduction</i> , 2002 , 17, 17-24	5.7	67