Pierluigi Strippoli

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1806352/publications.pdf

Version: 2024-02-01

72	2,713	270111	223390
papers	citations	25 h-index	49 g-index

73	73	73	4103
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A reassessment of Jacksonâ€™s checklist and identification of two Down syndrome sub-phenotypes. Scientific Reports, 2022, 12, 3104.	1.6	3
2	One-carbon pathway and cognitive skills in children with Down syndrome. Scientific Reports, 2021, 11, 4225.	1.6	15
3	Is the Age of Developmental Milestones a Predictor for Future Development in Down Syndrome?. Brain Sciences, 2021, 11, 655.	1.1	14
4	The transcriptome profile of human trisomy 21 blood cells. Human Genomics, 2021, 15, 25.	1.4	13
5	Structural Characterization of the Highly Restricted Down Syndrome Critical Region on 21q22.13: New KCNJ6 and DSCR4 Transcript Isoforms. Frontiers in Genetics, 2021, 12, 770359.	1.1	8
6	Plasma metabolome and cognitive skills in Down syndrome. Scientific Reports, 2020, 10, 10491.	1.6	23
7	Genetics and genomics of Down syndrome. International Review of Research in Developmental Disabilities, 2019, , 1-39.	0.6	6
8	Reference quantitative transcriptome dataset for adult Caenorhabditis elegans. Data in Brief, 2019, 25, 104152.	0.5	1
9	Human trisomy 21 fibroblasts rescue methotrexate toxic effect after treatment with 5â€methylâ€tetrahydrofolate and 5â€formylâ€tetrahydrofolate. Journal of Cellular Physiology, 2019, 234, 15010-15024.	2.0	12
10	Partial trisomy 21 map: Ten cases further supporting the highly restricted Down syndrome critical region (HRâ€DSCR) on human chromosome 21. Molecular Genetics & Genomic Medicine, 2019, 7, e797.	0.6	28
11	Human protein-coding genes and gene feature statistics in 2019. BMC Research Notes, 2019, 12, 315.	0.6	106
12	Dataset of differential gene expression between total normal human thyroid and histologically normal thyroid adjacent to papillary thyroid carcinoma. Data in Brief, 2019, 24, 103835.	0.5	2
13	On the length, weight and GC content of the human genome. BMC Research Notes, 2019, 12, 106.	0.6	125
14	MTHFR C677T polymorphism analysis: A simple, effective restriction enzymeâ€based method improving previous protocols. Molecular Genetics & Genomic Medicine, 2019, 7, e628.	0.6	14
15	Plasma and urinary metabolomic profiles of Down syndrome correlate with alteration of mitochondrial metabolism. Scientific Reports, 2018, 8, 2977.	1.6	80
16	LGALS4, CEACAM6, TSPAN8, and COL1A2: Blood Markers for Colorectal Cancerâ€”Validation in a Cohort of Subjects With Positive Fecal Immunochemical Test Result. Clinical Colorectal Cancer, 2018, 17, e217-e228.	1.0	24
17	Integrated Quantitative Transcriptome Maps of Human Trisomy 21 Tissues and Cells. Frontiers in Genetics, 2018, 9, 125.	1.1	38
18	Systematic identification of human housekeeping genes possibly useful as references in gene expression studies. Molecular Medicine Reports, 2017, 16, 2397-2410.	1.1	71

#	Article	IF	Citations
19	Genotype-phenotype correlation for congenital heart disease in Down syndrome through analysis of partial trisomy 21 cases. Genomics, 2017, 109, 391-400.	1.3	27
20	A molecular view of the normal human thyroid structure and function reconstructed from its reference transcriptome map. BMC Genomics, 2017, 18, 739.	1.2	27
21	Systematic reanalysis of partial trisomy 21 cases with or without Down syndrome suggests a small region on 21q22.13 as critical to the phenotype. Human Molecular Genetics, 2016, 25, ddw116.	1.4	74
22	Letter to the Editor: On osteocytes density in the human body. Bone, 2016, 93, 222.	1.4	0
23	A quantitative transcriptome reference map of the normal human hippocampus. Hippocampus, 2016, 26, 13-26.	0.9	28
24	Systematic large-scale meta-analysis identifies a panel of two mRNAs as blood biomarkers for colorectal cancer detection. Oncotarget, 2016, 7, 30295-30306.	0.8	48
25	Identification of minimal eukaryotic introns through GeneBase, a user-friendly tool for parsing the NCBI Gene databank. DNA Research, 2015, 22, 495-503.	1.5	60
26	Trisomy 21: research for a cure and rediscovery of the thought of JÃ©rÃ´me Lejeune. Journal of Medicine and the Person, 2014, 12, 104-110.	0.1	1
27	Integrated differential transcriptome maps of Acute Megakaryoblastic Leukemia (AMKL) in children with or without Down Syndrome (DS). BMC Medical Genomics, 2014, 7, 63.	0.7	37
28	Improving mRNA 5â€² coding sequence determination in the mouse genome. Mammalian Genome, 2014, 25, 149-159.	1.0	4
29	A quantitative transcriptome reference map of the normal human brain. Neurogenetics, 2014, 15, 267-287.	0.7	33
30	Characterization of human gene locus CYYR1: a complex multi-transcript system. Molecular Biology Reports, 2014, 41, 6025-6038.	1.0	7
31	An estimation of the number of cells in the human body. Annals of Human Biology, 2013, 40, 463-471.	0.4	757
32	Universal tight correlation of codon bias and pool of RNA codons (codonome): The genome is optimized to allow any distribution of gene expression values in the transcriptome from bacteria to humans. Genomics, 2013, 101, 282-289.	1.3	34
33	An integrated route to identifying new pathogenesis-based therapeutic approaches for trisomy 21 (Down Syndrome) following the thought of JÃ©rÃ´me Lejeune. Science Postprint, 2013, 1, .	0.3	20
34	Genome-scale analysis of human mRNA 5â€² coding sequences based on expressed sequence tag (EST) database. Genomics, 2012, 100, 125-130.	1.3	11
35	Complexity of Bidirectional Transcription and Alternative Splicing at Human RCAN3 Locus. PLoS ONE, 2011, 6, e24508.	1.1	12
36	Identification of housekeeping genes suitable for gene expression analysis in the zebrafish. Gene Expression Patterns, 2011, 11, 271-276.	0.3	78

#	Article	IF	Citations
37	TRAM (Transcriptome Mapper): database-driven creation and analysis of transcriptome maps from multiple sources. BMC Genomics, 2011, 12, 121.	1.2	45
38	IL23R, NOD2/CARD15, ATG16L1 and PHOX2B polymorphisms in a group of patients with Crohn's disease and correlation with sub-phenotypes. International Journal of Molecular Medicine, 2011, 27, 469-77.	1.8	28
39	Identification by a Digital Gene Expression Displayer (DGED) and test by RT-PCR analysis of new mRNA candidate markers for colorectal cancer in peripheral blood. International Journal of Oncology, 2010, 37, 519-25.	1.4	14
40	Displayed correlation between gene expression profiles and submicroscopic alterations in response to cetuximab, gefitinib and EGF in human colon cancer cell lines. BMC Cancer, 2008, 8, 227.	1.1	24
41	Identification and analysis of human RCAN3 (DSCR1L2) mRNA and protein isoforms. Gene, 2008, 407, 159-168.	1.0	13
42	Renaming the DSCR1 / Adapt78 gene family as RCAN : regulators of calcineurin. FASEB Journal, 2007, 21, 3023-3028.	0.2	157
43	Systematic analysis of mRNA 5' coding sequence incompleteness in Danio rerio: an automated EST-based approach. Biology Direct, 2007, 2, 34.	1.9	4
44	Sequence, "subtle" alternative splicing and expression of the CYYR1 (cysteine/tyrosine-rich 1) mRNA in human neuroendocrine tumors. BMC Cancer, 2007, 7, 66.	1.1	16
45	Proteins encoded by human Down syndrome critical region gene 1-like 2 (DSCR1L2) mRNA and by a novel DSCR1L2 mRNA isoform interact with cardiac troponin I (TNNI3). Gene, 2006, 372, 128-136.	1.0	14
46	Microarray-based identification and RT-PCR test screening for epithelial-specific mRNAs in peripheral blood of patients with colon cancer. BMC Cancer, 2006, 6, 250.	1.1	23
47	UniGene Tabulator: a full parser for the UniGene format. Bioinformatics, 2006, 22, 2570-2571.	1.8	35
48	Differential expression of alternatively spliced mRNA forms of the insulin-like growth factor 1 receptor in human neuroendocrine tumors. Oncology Reports, 2006, 15, 1249-56.	1.2	15
49	Uncertainty principle of genetic information in a living cell. Theoretical Biology and Medical Modelling, 2005, 2, 40.	2.1	13
50	Expression of T cell receptor alpha gene (TCRA) in human rhabdomyosarcoma and other musculo-skeletal sarcomas. Gene, 2005, 353, 16-22.	1.0	2
51	Sequence analysis of ADARB1 gene in patients with familial bipolar disorder. Journal of Affective Disorders, 2004, 81, 79-85.	2.0	8
52	Identification of candidate genes involved in the reversal of malignant phenotype of osteosarcoma cells transfected with the liver/bone/kidney alkaline phosphatase gene. Bone, 2004, 34, 672-679.	1.4	33
53	Search for epithelial-specific mRNAs in peripheral blood of patients with colon cancer by RT-PCR. International Journal of Oncology, 2004, 25, 1049-56.	1.4	8
54	mRNA 5â€² region sequence incompleteness: a potential source of systematic errors in translation initiation codon assignment in human mRNAs. Gene, 2003, 321, 185-193.	1.0	16

#	Article	IF	Citations
55	Sequence and Expression Analysis Of The Î²-2-Microglobulin Gene In Dialysis Patients. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2002, 9, 212-215.	1.4	0
56	Cysteine and tyrosine-rich 1 (CYYR1), a novel unpredicted gene on human chromosome 21 (21q21.2), encodes a cysteine and tyrosine-rich protein and defines a new family of highly conserved vertebrate-specific genes. Gene, 2002, 290, 141-151.	1.0	18
57	Segmental paralogy in the human genome: a large-scale triplication on 1p, 6p, and 21q. Mammalian Genome, 2002, 13, 456-462.	1.0	16
58	LACK OF MUTATIONS OF TYPE 1 11Î²-HYDROXYSTEROID DEHYDROGENASE GENE IN PATIENTS WITH ABDOMINAL OBESITY. Endocrine Research, 2001, 27, 47-61.	0.6	23
59	Compound heterozygosity for two different amino-acid substitution mutations in the thrombopoietin receptor (c-mpl gene) in congenital amegakaryocytic thrombocytopenia (CAMT). Human Genetics, 2000, 107, 225-233.	1.8	46
60	Hereditary Thrombocytopenia due to Reduced Platelet Production. Thrombosis and Haemostasis, 2000, 83, 931-936.	1.8	14
61	A New Gene Family Including DSCR1 (Down Syndrome Candidate Region 1) and ZAKI-4: Characterization from Yeast to Human and Identification of DSCR1-like 2, a Novel Human Member (DSCR1L2). Genomics, 2000, 64, 252-263.	1.3	73
62	The murine DSCR1-like (Down Syndrome Candidate Region 1) gene family: conserved synteny with the human orthologous genes. Gene, 2000, 257, 223-232.	1.0	24
63	Thrombopoietin and interleukin 11 have different modulatory effects on cell cycle and programmed cell death in primary acute myeloid leukemia cells. Experimental Hematology, 1999, 27, 1255-1263.	0.2	16
64	Regioselective synthesis and biological profiling of butyric and phenylalkylcarboxylic esters derivated from D-mannose and xylitol: influence of alkyl chain length on acute toxicity. European Journal of Pharmaceutical Sciences, 1999, 7, 93-106.	1.9	22
65	Production of stem cell factor and expression of c-kit in human rhabdomyosarcoma cells: Lack of autocrine growth modulation. , 1998, 78, 441-445.		10
66	Mutational screening of thrombopoietin receptor gene (c-mpl) in patients with congenital thrombocytopenia and absent radii (TAR). British Journal of Haematology, 1998, 103, 311-314.	1.2	35
67	Mutations of the Fanconi Anemia Group A Gene (FAA) in Italian Patients. American Journal of Human Genetics, 1997, 61, 1246-1253.	2.6	55
68	An erythroid and megakaryocytic common precursor cell line (B1647) expressing both câ€mpl and erythropoietin receptor (Epoâ€R) proliferates and modifies globin chain synthesis in response to megakaryocyte growth and development factor (MGDF) but not to erythropoietin (Epo). British Journal of Haematology, 1997, 98, 549-559.	1.2	19
69	Production of interleukin 6, leukemia inhibitory factor and granulocyte-macrophage colony stimulating factor by peripheral blood mononuclear cells in fanconi's anemia. Stem Cells, 1996, 11, 137-143.	1.4	8
70	Cytofluorimetric and Functional Analysis of C-Kit Receptor in Acute Leukemia. Leukemia and Lymphoma, 1995, 18, 451-455.	0.6	13
71	Clinical implications of the heterogeneity of hematopoietic progenitors elicited in peripheral blood by anticancer therapy with cyclophosphamide and cytokine(s). Stem Cells, 1993, 11, 72-75.	1.4	5
72	M-07e cell bioassay detects stromal cell production of granulocyte-macrophage colony stimulating factor and stem cell factor in normal and in diamond-blackfan anemia bone marrow. Stem Cells, 1993, 11, 131-136.	1.4	7