Pierluigi Strippoli

List of Publications by Year
in descending order

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72 papers	2,713 citations	236925 25 h-index	197818 49 g-index
73 all docs	73 docs citations	73 times ranked	3741 citing authors

#	Article	IF	Citations
1	An estimation of the number of cells in the human body. Annals of Human Biology, 2013, 40, 463-471.	1.0	757
2	Renaming the DSCR1 / Adapt78 gene family as RCAN : regulators of calcineurin. FASEB Journal, 2007, 21, 3023-3028.	0.5	157
3	On the length, weight and GC content of the human genome. BMC Research Notes, 2019, 12, 106.	1.4	125
4	Human protein-coding genes and gene feature statistics in 2019. BMC Research Notes, 2019, 12, 315.	1.4	106
5	Plasma and urinary metabolomic profiles of Down syndrome correlate with alteration of mitochondrial metabolism. Scientific Reports, 2018, 8, 2977.	3.3	80
6	Identification of housekeeping genes suitable for gene expression analysis in the zebrafish. Gene Expression Patterns, 2011, 11, 271-276.	0.8	78
7	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.	2.9	74
8	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.	2.9	73
9	Systematic identification of human housekeeping genes possibly useful as references in gene expression studies. Molecular Medicine Reports, 2017, 16, 2397-2410.	2.4	71
10	Identification of minimal eukaryotic introns through GeneBase, a user-friendly tool for parsing the NCBI Gene databank. DNA Research, 2015, 22, 495-503.	3.4	60
11	Mutations of the Fanconi Anemia Group A Gene (FAA) in Italian Patients. American Journal of Human Genetics, 1997, 61, 1246-1253.	6.2	55
12	Systematic large-scale meta-analysis identifies a panel of two mRNAs as blood biomarkers for colorectal cancer detection. Oncotarget, 2016, 7, 30295-30306.	1.8	48
13	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.	3.8	46
14	TRAM (Transcriptome Mapper): database-driven creation and analysis of transcriptome maps from multiple sources. BMC Genomics, 2011, 12, 121.	2.8	45
15	Integrated Quantitative Transcriptome Maps of Human Trisomy 21 Tissues and Cells. Frontiers in Genetics, 2018, 9, 125.	2.3	38
16	Integrated differential transcriptome maps of Acute Megakaryoblastic Leukemia (AMKL) in children with or without Down Syndrome (DS). BMC Medical Genomics, 2014, 7, 63.	1.5	37
17	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.	2.5	35
18	UniGene Tabulator: a full parser for the UniGene format. Bioinformatics, 2006, 22, 2570-2571.	4.1	35

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19	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.	2.9	34
20	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.	2.9	33
21	A quantitative transcriptome reference map of the normal human brain. Neurogenetics, 2014, 15, 267-287.	1.4	33
22	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.	4.0	28
23	A quantitative transcriptome reference map of the normal human hippocampus. Hippocampus, 2016, 26, 13-26.	1.9	28
24	Partial trisomy 21 map: Ten cases further supporting the highly restricted Down syndrome critical region (HRâ€ÐSCR) on human chromosome 21. Molecular Genetics & Genomic Medicine, 2019, 7, e797.	1.2	28
25	Genotype-phenotype correlation for congenital heart disease in Down syndrome through analysis of partial trisomy 21 cases. Genomics, 2017, 109, 391-400.	2.9	27
26	A molecular view of the normal human thyroid structure and function reconstructed from its reference transcriptome map. BMC Genomics, 2017, 18, 739.	2.8	27
27	The murine DSCR1-like (Down Syndrome Candidate Region 1) gene family: conserved synteny with the human orthologous genes. Gene, 2000, 257, 223-232.	2.2	24
28	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.	2.6	24
29	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.	2.3	24
30	LACK OF MUTATIONS OF TYPE 1 11Î²-HYDROXYSTEROID DEHYDROGENASE GENE IN PATIENTS WITH ABDOMINAL OBESITY. Endocrine Research, 2001, 27, 47-61.	1.2	23
31	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.	2.6	23
32	Plasma metabolome and cognitive skills in Down syndrome. Scientific Reports, 2020, 10, 10491.	3.3	23
33	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.	4.0	22
34	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
35	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.	2.5	19
36	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.	2.2	18

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37	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.	0.4	16
38	Segmental paralogy in the human genome: a large-scale triplication on 1p, 6p, and 21q. Mammalian Genome, 2002, 13, 456-462.	2.2	16
39	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.	2.2	16
40	Sequence, "subtle" alternative splicing and expression of the CYYR1 (cysteine/tyrosine-rich 1) mRNA in human neuroendocrine tumors. BMC Cancer, 2007, 7, 66.	2.6	16
41	One-carbon pathway and cognitive skills in children with Down syndrome. Scientific Reports, 2021, 11, 4225.	3.3	15
42	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.	2.6	15
43	Hereditary Thrombocytopenia due to Reduced Platelet Production. Thrombosis and Haemostasis, 2000, 83, 931-936.	3.4	14
44	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.	2.2	14
45	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.	3.3	14
46	MTHFR C677T polymorphism analysis: A simple, effective restriction enzymeâ€based method improving previous protocols. Molecular Genetics & Genomic Medicine, 2019, 7, e628.	1.2	14
47	Is the Age of Developmental Milestones a Predictor for Future Development in Down Syndrome?. Brain Sciences, 2021, 11, 655.	2.3	14
48	Cytofluorimetric and Functional Analysis of C-Kit Receptor in Acute Leukemia. Leukemia and Lymphoma, 1995, 18, 451-455.	1.3	13
49	Uncertainty principle of genetic information in a living cell. Theoretical Biology and Medical Modelling, 2005, 2, 40.	2.1	13
50	Identification and analysis of human RCAN3 (DSCR1L2) mRNA and protein isoforms. Gene, 2008, 407, 159-168.	2.2	13
51	The transcriptome profile of human trisomy 21 blood cells. Human Genomics, 2021, 15, 25.	2.9	13
52	Complexity of Bidirectional Transcription and Alternative Splicing at Human RCAN3 Locus. PLoS ONE, 2011, 6, e24508.	2.5	12
53	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.	4.1	12
54	Genome-scale analysis of human mRNA 5â€² coding sequences based on expressed sequence tag (EST) database. Genomics, 2012, 100, 125-130.	2.9	11

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55	Production of stem cell factor and expression of c-kit in human rhabdomyosarcoma cells: Lack of autocrine growth modulation. , 1998, 78, 441-445.		10
56	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.	3.2	8
57	Sequence analysis of ADARB1 gene in patients with familial bipolar disorder. Journal of Affective Disorders, 2004, 81, 79-85.	4.1	8
58	Search for epithelial-specific mRNAs in peripheral blood of patients with colon cancer by RT-PCR. International Journal of Oncology, 2004, 25, 1049-56.	3.3	8
59	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.	2.3	8
60	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.	3.2	7
61	Characterization of human gene locus CYYR1: a complex multi-transcript system. Molecular Biology Reports, 2014, 41, 6025-6038.	2.3	7
62	Genetics and genomics of Down syndrome. International Review of Research in Developmental Disabilities, 2019, , 1-39.	0.8	6
63	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.	3.2	5
64	Systematic analysis of mRNA 5' coding sequence incompleteness in Danio rerio: an automated EST-based approach. Biology Direct, 2007, 2, 34.	4.6	4
65	Improving mRNA 5â€² coding sequence determination in the mouse genome. Mammalian Genome, 2014, 25, 149-159.	2.2	4
66	A reassessment of Jacksonâ€™s checklist and identification of two Down syndrome sub-phenotypes. Scientific Reports, 2022, 12, 3104.	3.3	3
67	Expression of T cell receptor alpha gene (TCRA) in human rhabdomyosarcoma and other musculo-skeletal sarcomas. Gene, 2005, 353, 16-22.	2.2	2
68	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.	1.0	2
69	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
70	Reference quantitative transcriptome dataset for adult Caenorhabditis elegans. Data in Brief, 2019, 25, 104152.	1.0	1
71	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.	3.0	0
72	Letter to the Editor: On osteocytes density in the human body. Bone, 2016, 93, 222.	2.9	0