Noam Shomron

List of Publications by Year
in descending order

208	8,541	41344	56724
papers	citations	49 h-index	83 g-index

225	225	225	14992
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Canalization of development by microRNAs. Nature Genetics, 2006, 38, S20-S24.	21.4	535
2	The Birth of an Alternatively Spliced Exon: 3' Splice-Site Selection in Alu Exons. Science, 2003, 300, 1288-1291.	12.6	394
3	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. Rna, 2007, 13, 1894-1910.	3.5	333
4	Machine learning-based prediction of COVID-19 diagnosis based on symptoms. Npj Digital Medicine, 2021, 4, 3.	10.9	324
5	Desmoglein 1 deficiency results in severe dermatitis, multiple allergies and metabolic wasting. Nature Genetics, 2013, 45, 1244-1248.	21.4	289
6	Familial Pityriasis Rubra Pilaris Is Caused by Mutations in CARD14. American Journal of Human Genetics, 2012, 91, 163-170.	6.2	220
7	Identification of Let-7â€“Regulated Oncofetal Genes. Cancer Research, 2008, 68, 2587-2591.	0.9	195
8	Targeted genomic capture and massively parallel sequencing to identify genes for hereditary hearing loss in middle eastern families. Genome Biology, 2011, 12, R89.	9.6	183
9	MicroRNAs are essential for development and function of inner ear hair cells in vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7915-7920.	7.1	169
10	Systematic identification of edited microRNAs in the human brain. Genome Research, 2012, 22, 1533-1540.	5.5	163
11	Pharmaco-miR: linking microRNAs and drug effects. Briefings in Bioinformatics, 2014, 15, 648-659.	6.5	131
12	Local microRNA delivery targets Palladin and prevents metastatic breast cancer. Nature Communications, 2016, 7, 12868.	12.8	127
13	MicroRNA pharmacogenomics: Post-transcriptional regulation of drug response. Trends in Molecular Medicine, 2011, 17, 412-423.	6.7	112
14	Exosomal microRNAs derived from colorectal cancer-associated fibroblasts: role in driving cancer progression. Aging, 2017, 9, 2666-2694.	3.1	112
15	Emergence and Transmission of Arbovirus Evolutionary Intermediates with Epidemic Potential. Cell Host and Microbe, 2014, 15, 706-716.	11.0	107
16	Group Selection and Contribution of Minority Variants during Virus Adaptation Determines Virus Fitness and Phenotype. PLoS Pathogens, 2015, 11, e1004838.	4.7	106
17	Variant PADI3 in Central Centrifugal Cicatricial Alopecia. New England Journal of Medicine, 2019, 380, 833-841.	27.0	102
18	Hsa-mir-125b-2 is highly expressed in childhood ETV6/RUNX1 (TEL/AML1) leukemias and confers survival advantage to growth inhibitory signals independent of p53. Leukemia, 2010, 24, 89-96.	7.2	100

#	Article	IF	Citations
19	Whole-Genome Sequencing Analysis from the Chikungunya Virus Caribbean Outbreak Reveals Novel Evolutionary Genomic Elements. PLoS Neglected Tropical Diseases, 2016, 10, e0004402.	3.0	96
20	The Involvement of MicroRNAs in Major Depression, Suicidal Behavior, and Related Disorders: A Focus on miR-185 and miR-491-3p. Cellular and Molecular Neurobiology, 2014, 34, 17-30.	3.3	92
21	Pax6 Regulates Gene Expression in the Vertebrate Lens through miR-204. PLoS Genetics, 2013, 9, e1003357.	3.5	86
22	miRNAkey: a software for microRNA deep sequencing analysis. Bioinformatics, 2010, 26, 2615-2616.	4.1	85
23	Downregulation of Mir-31, Mir-155, and Mir-564 in Chronic Myeloid Leukemia Cells. PLoS ONE, 2012, 7, e35501.	2.5	79
24	Regulation of Cancer Aggressive Features in Melanoma Cells by MicroRNAs. PLoS ONE, 2011, 6, e18936.	2.5	77
25	Interplay between pre-mRNA splicing and microRNA biogenesis within the supraspliceosome. Nucleic Acids Research, 2014, 42, 4640-4651.	14.5	77
26	Early diagnosis of gestational diabetes mellitus using circulating microRNAs. European Journal of Endocrinology, 2019, 181, 565-577.	3.7	77
27	MicroRNA-Biogenesis and Pre-mRNA Splicing Crosstalk. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-6.	3.0	76
28	MiR-30e induces apoptosis and sensitizes K562 cells to imatinib treatment via regulation of the BCRâ€“ABL protein. Cancer Letters, 2015, 356, 597-605.	7.2	75
29	A nationwide genetic analysis of inherited retinal diseases in Israel as assessed by the Israeli inherited retinal disease consortium (IIRDC). Human Mutation, 2020, 41, 140-149.	2.5	75
30	miRNAminer: A tool for homologous microRNA gene search. BMC Bioinformatics, 2008, 9, 39.	2.6	73
31	Species-specific microRNA roles elucidated following astrocyte activation. Nucleic Acids Research, 2011, 39, 3710-3723.	14.5	73
32	Feed-Forward Microprocessing and Splicing Activities at a MicroRNAâ€“Containing Intron. PLoS Genetics, 2011, 7, e1002330.	3.5	73
33	Insulin-like Growth Factor-I Receptor (IGF-IR) Translocates to Nucleus and Autoregulates IGF-IR Gene Expression in Breast Cancer Cells. Journal of Biological Chemistry, 2012, 287, 2766-2776.	3.4	73
34	Opposing actions of environmental enrichment and Alzheimerâ€™s disease on the expression of hippocampal microRNAs in mouse models. Translational Psychiatry, 2013, 3, e304-e304.	4.8	73
35	Phylogenetic and Genome-Wide Deep-Sequencing Analyses of Canine Parvovirus Reveal Co-Infection with Field Variants and Emergence of a Recent Recombinant Strain. PLoS ONE, 2014, 9, e111779.	2.5	73
36	Inference of Splicing Regulatory Activities by Sequence Neighborhood Analysis. PLoS Genetics, 2006, 2, e191.	3.5	71

#	Article	IF	Citations
37	Analysis of insertion-deletion from deep-sequencing data: software evaluation for optimal detection. Briefings in Bioinformatics, 2013, 14, 46-55.	6.5	71
38	Axonal TDP-43 condensates drive neuromuscular junction disruption through inhibition of local synthesis of nuclear encoded mitochondrial proteins. Nature Communications, 2021, 12, 6914.	12.8	67
39	miRviewer: a multispecies microRNA homologous viewer. BMC Research Notes, 2012, 5, 92.	1.4	66
40	Identification of Dormancy-Associated MicroRNAs for the Design of Osteosarcoma-Targeted Dendritic Polyglycerol Nanopolyplexes. ACS Nano, 2016, 10, 2028-2045.	14.6	64
41	Pathogen detection using short-RNA deep sequencing subtraction and assembly. Bioinformatics, 2011, 27, 2027-2030.	4.1	63
42	MicroRNAs and pharmacogenomics. Pharmacogenomics, 2010, 11, 629-632.	1.3	62
43	Deep sequencing analysis of viral infection and evolution allows rapid and detailed characterization of viral mutant spectrum. Bioinformatics, 2015, 31, 2141-2150.	4.1	62
44	Characterization of Coding Synonymous and Non-Synonymous Variants in ADAMTS13 Using Ex Vivo and In Silico Approaches. PLoS ONE, 2012, 7, e38864.	2.5	61
45	Genome-wide expression profiling of human lymphoblastoid cell lines implicates integrin beta-3 in the mode of action of antidepressants. Translational Psychiatry, 2013, 3, e313-e313.	4.8	60
46	Genome-wide miRNA expression profiling of human lymphoblastoid cell lines identifies tentative SSRI antidepressant response biomarkers. Pharmacogenomics, 2012, 13, 1129-1139.	1.3	57
47	microRNA-125a-3p reduces cells proliferation and migration by targeting Fyn. Journal of Cell Science, 2013, 126, 2867-76.	2.0	57
48	Mutations in Coronavirus Nonstructural Protein 10 Decrease Virus Replication Fidelity. Journal of Virology, 2015, 89, 6418-6426.	3.4	56
49	Stress alters the subcellular distribution of hSlu7 and thus modulates alternative splicing. Journal of Cell Science, 2005, 118, 1151-1159.	2.0	55
50	MicroRNA-382 expression is elevated in the olfactory neuroepithelium of schizophrenia patients. Neurobiology of Disease, 2013, 55, 1-10.	4.4	55
51	Restoration of miR-424 suppresses BCRâ€“ABL activity and sensitizes CML cells to imatinib treatment. Cancer Letters, 2015, 360, 245-256.	7.2	55
52	Bioactivation of carbamate-based 20(S)-camptothecin prodrugs. Bioorganic and Medicinal Chemistry, 2004, 12, 1859-1866.	3.0	51
53	MicroRNA regulation of p21 and TASK1 cellular restriction-factors enhances HIV-1 infection. Journal of Cell Science, 2015, 128, 1607-16.	2.0	51
54	RNA-Binding Protein PTB and MicroRNA-221 Coregulate AdipoR1 Translation and Adiponectin Signaling. Diabetes, 2014, 63, 433-445.	0.6	50

#	Article	IF	Citations
55	MicroRNA miR-125a-3p modulates molecular pathway of motility and migration in prostate cancer cells. Oncoscience, 2014, 1, 250-261.	2.2	50
56	Non-syndromic retinitis pigmentosa due to mutations in the mucopolysaccharidosis type IIIC gene, heparan-alpha-glucosaminide N-acetyltransferase (HGSNAT). Human Molecular Genetics, 2015, 24, 3742-51.	2.9	47
57	Next-generation sequencing of small RNAs from inner ear sensory epithelium identifies microRNAs and defines regulatory pathways. BMC Genomics, 2014, 15, 484.	2.8	46
58	Early Detection of Preeclampsia Using Circulating Small non-coding RNA. Scientific Reports, 2018, 8, 3401.	3.3	46
59	An Evolutionary Perspective of Animal MicroRNAs and Their Targets. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-9.	3.0	45
60	Weak definition ofIKBKAPexon 20 leads to aberrant splicing in familial dysautonomia. Human Mutation, 2007, 28, 41-53.	2.5	44
61	Ethnic differences in alphaâ€1 antitrypsin deficiency allele frequencies may partially explain national differences in COVIDâ€19 fatality rates. FASEB Journal, 2020, 34, 14160-14165.	0.5	43
62	The U1 snRNP Base Pairs with the 5â€² Splice Site within a Penta-snRNP Complex. Molecular and Cellular Biology, 2003, 23, 3442-3455.	2.3	42
63	Cole Disease Results from Mutations in ENPP1. American Journal of Human Genetics, 2013, 93, 752-757.	6.2	41
64	MicroRNA Editing Facilitates Immune Elimination of HCMV Infected Cells. PLoS Pathogens, 2014, 10, e1003963.	4.7	40
65	Versatility of MicroRNA Biogenesis. PLoS ONE, 2011, 6, e19391.	2.5	39
66	MicroRNAs in the growth plate are responsive to nutritional cues: association between miR-140 and SIRT1. Journal of Nutritional Biochemistry, 2012, 23, 1474-1481.	4.2	39
67	Speciesâ€specific micro<scp>RNA</scp> regulation influences phenotypic variability. BioEssays, 2013, 35, 881-888.	2.5	37
68	miR-192 Directly Binds and Regulates Dicer1 Expression in Neuroblastoma. PLoS ONE, 2013, 8, e78713.	2.5	37
69	Filaggrin 2 Deficiency Results in Abnormal Cell-Cell Adhesion in the Cornified Cell Layers and Causes Peeling Skin Syndrome Type A. Journal of Investigative Dermatology, 2018, 138, 1736-1743.	0.7	37
70	Comparison of breast cancer metastasis models reveals a possible mechanism of tumor aggressiveness. Cell Death and Disease, 2018, 9, 1040.	6.3	36
71	The microRNA Transcriptome of Human Cytomegalovirus (HCMV). The Open Virology Journal, 2012, 6, 38-48.	1.8	36
72	Insulin-like Growth Factor 1 Differentially Affects Lithium Sensitivity of Lymphoblastoid Cell Lines from Lithium Responder and Non-responder Bipolar Disorder Patients. Journal of Molecular Neuroscience, 2015, 56, 681-687.	2.3	35

#	Article	IF	Citations
73	Neuro-Epigenetic Indications of Acute Stress Response in Humans: The Case of MicroRNA-29c. PLoS ONE, 2016, 11, e0146236.	2.5	34
74	Distinctive pattern of let-7 family microRNAs in aggressive carcinoma of the oral tongue in young patients. Oncology Letters, 2016, 12, 1729-1736.	1.8	34
75	Molecular Risk Factors for Schizophrenia. Trends in Molecular Medicine, 2016, 22, 242-253.	6.7	34
76	Circulating MicroRNAs: a Potential Biomarker for Cardiac Damage, Inflammatory Response, and Left Ventricular Function Recovery in Pediatric Viral Myocarditis. Journal of Cardiovascular Translational Research, 2018, 11, 319-328.	2.4	34
77	Novel ADNP Syndrome Mice Reveal Dramatic Sex-Specific Peripheral Gene Expression With Brain Synaptic and Tau Pathologies. Biological Psychiatry, 2022, 92, 81-95.	1.3	32
78	Mutations in TSPEAR, Encoding a Regulator of Notch Signaling, Affect Tooth and Hair Follicle Morphogenesis. PLoS Genetics, 2016, 12, e1006369.	3.5	32
79	MicroRNA regulation of progesterone receptor in breast cancer. Oncotarget, 2017, 8, 25963-25976.	1.8	32
80	Bayesian-based noninvasive prenatal diagnosis of single-gene disorders. Genome Research, 2019, 29, 428-438.	5.5	31
81	Proteogenomics of glioblastoma associates molecular patterns with survival. Cell Reports, 2021, 34, 108787.	6.4	31
82	The possible involvement of microRNAs in preeclampsia and gestational diabetes mellitus. Best Practice and Research in Clinical Obstetrics and Gynaecology, 2015, 29, 176-182.	2.8	30
83	Exploring the longitudinal glioma microenvironment landscape uncovers reprogrammed pro-tumorigenic neutrophils in the bone marrow. Cell Reports, 2021, 36, 109480.	6.4	30
84	Involvement of IGF-1R regulation by miR-515-5p modifies breast cancer risk among BRCA1 carriers. Breast Cancer Research and Treatment, 2013, 138, 753-760.	2.5	29
85	Pharmacogenomics genes show varying perceptibility to microRNA regulation. Pharmacogenetics and Genomics, 2011, 21, 251-262.	1.5	28
86	Differential effects of chronic stress in young-adult and old female mice: cognitive-behavioral manifestations and neurobiological correlates. Molecular Psychiatry, 2018, 23, 1432-1445.	7.9	28
87	Seasonal Genetic Drift of Human Influenza A Virus Quasispecies Revealed by Deep Sequencing. Frontiers in Microbiology, 2018, 9, 2596.	3.5	27
88	The autism-mutated ADNP plays a key role in stress response. Translational Psychiatry, 2019, 9, 235.	4.8	27
89	Boric acid reversibly inhibits the second step of pre-mRNA splicing. FEBS Letters, 2003, 552, 219-224.	2.8	26
90	MicroRNA 10b promotes abnormal expression of the proto-oncogene c-Jun in metastatic breast cancer cells. Oncotarget, 2016, 7, 59932-59944.	1.8	26

#	Article	IF	Citations
91	Biased hosting of intronic microRNA genes. Bioinformatics, 2010, 26, 992-995.	4.1	24
92	Vaccinia virus infection suppresses the cell microRNA machinery. Archives of Virology, 2012, 157, 1719-1727.	2.1	23
93	RGS2 expression predicts amyloid-Î² sensitivity, MCI and Alzheimerâ€™s disease: genome-wide transcriptomic profiling and bioinformatics data mining. Translational Psychiatry, 2016, 6, e909-e909.	4.8	23
94	Analysis of microRNAs in familial Mediterranean fever. PLoS ONE, 2018, 13, e0197829.	2.5	22
95	HIV-1 infection increases microRNAs that inhibit Dicer1, HRB and HIV-EP2, thereby reducing viral replication. PLoS ONE, 2019, 14, e0211111.	2.5	22
96	Variant in SCYL1 gene causes aberrant splicing in a family with cerebellar ataxia, recurrent episodes of liver failure, and growth retardation. European Journal of Human Genetics, 2019, 27, 263-268.	2.8	22
97	Genome-wide noninvasive prenatal diagnosis of monogenic disorders: Current and future trends. Computational and Structural Biotechnology Journal, 2020, 18, 2463-2470.	4.1	22
98	The pathogenicity of SLC38A8 in five families with foveal hypoplasia and congenital nystagmus. Experimental Eye Research, 2020, 193, 107958.	2.6	22
99	Does base-pairing strength play a role in microRNA repression?. Rna, 2012, 18, 1947-1956.	3.5	21
100	Intensified vmPFC surveillance over PTSS under perturbed microRNA-608/AChE interaction. Translational Psychiatry, 2016, 6, e801-e801.	4.8	21
101	Intercellular transfer of small RNAs from astrocytes to lung tumor cells induces resistance to chemotherapy. Oncotarget, 2016, 7, 12489-12504.	1.8	21
102	MicroRNA-Mediated Regulation of ITGB3 and CHL1 Is Implicated in SSRI Action. Frontiers in Molecular Neuroscience, 2017, 10, 355.	2.9	20
103	Teratogen-induced alterations in microRNA-34, microRNA-125b and microRNA-155 expression: correlation with embryonic p53 genotype and limb phenotype. BMC Developmental Biology, 2010, 10, 20.	2.1	19
104	Rare genetic variants in Tunisian Jewish patients suffering from age-related macular degeneration. Journal of Medical Genetics, 2015, 52, 484-492.	3.2	19
105	MicroRNAs Expression in the Ileal Pouch of Patients with Ulcerative Colitis Is Robustly Up-Regulated and Correlates with Disease Phenotypes. PLoS ONE, 2016, 11, e0159956.	2.5	19
106	Calpain 12 Function Revealed through the Study of an Atypical Case of Autosomal Recessive Congenital Ichthyosis. Journal of Investigative Dermatology, 2017, 137, 385-393.	0.7	19
107	Loss of Protocadherinâ€12<scp>L</scp>eads to <scp>D</scp>iencephalicâ€<scp>M</scp>esencephalic <scp>J</scp>unction <scp>D</scp>ysplasia <scp>S</scp>yndrome. Annals of Neurology, 2018, 84, 638-647.	5.3	19
108	Transcriptional Profiling of Mouse Eosinophils Identifies Distinct Gene Signatures Following Cellular Activation. Frontiers in Immunology, 2021, 12, 802839.	4.8	19

#	Article	IF	Citations
109	Exome Sequencing Analysis: A Guide to Disease Variant Detection. Methods in Molecular Biology, 2013, 1038, 137-158.	0.9	18
110	Reversible inhibition of the second step of splicing suggests a possible role of zinc in the second step of splicing. Nucleic Acids Research, 2002, 30, 4127-4137.	14.5	17
111	Novel insight into the non-coding repertoire through deep sequencing analysis. Nucleic Acids Research, 2012, 40, e86-e86.	14.5	17
112	<scp>RBM</scp>28, a protein deficient in <scp>ANE</scp> syndrome, regulates hair follicle growth via miRâ€203 and p63. Experimental Dermatology, 2015, 24, 618-622.	2.9	17
113	Regulation of Complement-Dependent Cytotoxicity by MicroRNAs miR-200b, miR-200c, and miR-217. Journal of Immunology, 2016, 196, 5156-5165.	0.8	17
114	A rare variant in the FHL1 gene associated with X-linked recessive hypoparathyroidism. Human Genetics, 2017, 136, 835-845.	3.8	17
115	Regulation of transcription of the RNA splicing factor hSlu7 by Elk-1 and Sp1 affects alternative splicing. Rna, 2007, 13, 1988-1999.	3.5	15
116	Spectrum of genes for inherited hearing loss in the Israeli Jewish population, including the novel human deafness gene <scp>ATOH1</scp>. Clinical Genetics, 2020, 98, 353-364.	2.0	15
117	Ab initio identification of functionally interacting pairs of cis-regulatory elements. Genome Research, 2008, 18, 1643-1651.	5.5	14
118	A splice variant of ADAMTS13 is expressed in human hepatic stellate cells and cancerous tissues. Thrombosis and Haemostasis, 2010, 104, 531-533.	3.4	14
119	MicroRNAs and Developmental Robustness: A New Layer Is Revealed. PLoS Biology, 2010, 8, e1000397.	5.6	14
120	Crowdfunding Effort Identifies the Causative Mutation in a Patient with Nystagmus, Microcephaly, Dystonia and Hypomyelination. Journal of Genetics and Genomics, 2015, 42, 79-81.	3.9	14
121	Biomaterials for Abrogating Metastasis: Bridging the Gap between Basic and Translational Research. Advanced Healthcare Materials, 2016, 5, 2312-2319.	7.6	14
122	Novel WWOX deleterious variants cause early infantile epileptic encephalopathy, severe developmental delay and dysmorphism among Yemenite Jews. European Journal of Paediatric Neurology, 2019, 23, 418-426.	1.6	14
123	Loss-of-Function Variants in SERPINA12 Underlie Autosomal Recessive Palmoplantar Keratoderma. Journal of Investigative Dermatology, 2020, 140, 2178-2187.	0.7	14
124	Processing and Analysis of RNA-seq Data from Public Resources. Methods in Molecular Biology, 2021, 2243, 81-94.	0.9	14
125	Decreased sensitivity to paroxetine-induced inhibition of peripheral blood mononuclear cell growth in depressed and antidepressant treatment-resistant patients. Translational Psychiatry, 2016, 6, e827-e827.	4.8	13
126	Whole-exome sequencing in individuals with multiple cardiovascular risk factors and normal coronary arteries. Coronary Artery Disease, 2016, 27, 257-266.	0.7	13

#	Article	IF	Citations
127	MicroRNAs as predictors for CNS relapse of systemic diffuse large B-cell lymphoma. Oncotarget, 2017, 8, 86020-86030.	1.8	13
128	Fluid consumption and taste novelty determines transcription temporal dynamics in the gustatory cortex. Molecular Brain, 2016, 9, 13.	2.6	12
129	Evaluation of optimization techniques for variable selection in logistic regression applied to diagnosis of myocardial infarction. Bioinformation, 2009, 3, 311-313.	0.5	12
130	Splicing Factor hSlu7 Contains a Unique Functional Domain Required to Retain the Protein within the Nucleus. Molecular Biology of the Cell, 2004, 15, 3782-3795.	2.1	11
131	Missense mutation in the MEN1 gene discovered through whole exome sequencing co-segregates with familial hyperparathyroidism. Genetical Research, 2013, 95, 114-120.	0.9	11
132	Epidermolytic Ichthyosis Sine Epidermolysis. American Journal of Dermatopathology, 2017, 39, 440-444.	0.6	11
133	Dual inhibition of ABCE1 and LCP1 by microRNA-96 results in an additive effect in breast cancer mouse model. Oncotarget, 2019, 10, 2086-2094.	1.8	11
134	Toxicogenomic analysis of a sustained release local anesthetic delivery system. Biomaterials, 2012, 33, 3586-3593.	11.4	10
135	Privacy, anonymity and subjectivity in genomic research. Genetical Research, 2016, 98, e2.	0.9	10
136	MicroRNAs Affect Complement Regulator Expression and Mitochondrial Activity to Modulate Cell Resistance to Complement-Dependent Cytotoxicity. Cancer Immunology Research, 2019, 7, 1970-1983.	3.4	10
137	Molecular epidemiology of nonâ€syndromic autosomal recessive congenital ichthyosis in a Middleâ€Eastern population. Experimental Dermatology, 2021, 30, 1290-1297.	2.9	10
138	MicroRNAs in ascending thoracic aortic aneurysms. Bioscience Reports, 2020, 40, .	2.4	10
139	Predicting bloodstream infection outcome using machine learning. Scientific Reports, 2021, 11, 20101.	3.3	10
140	Modulation of RNA Splicing by Oligonucleotides: Mechanisms of Action and Therapeutic Implications. Nucleic Acid Therapeutics, 2022, 32, 123-138.	3.6	10
141	MULTIPLE ways to correct for MULTIPLE comparisons in MULTIPLE types of studies. British Journal of Dermatology, 2021, 185, 1081-1083.	1.5	10
142	Genome-wide transcriptomic variations of human lymphoblastoid cell lines: insights from pairwise gene-expression correlations. Pharmacogenomics, 2012, 13, 1893-1904.	1.3	9
143	Behavioral aspects and neurobiological properties underlying medical cannabis treatment in Shank3 mouse model of autism spectrum disorder. Translational Psychiatry, 2021, 11, 524.	4.8	9
144	A novel intronic mutation of is a major cause of autosomal recessive retinitis pigmentosa among Caucasus Jews. Molecular Vision, 2019, 25, 155-164.	1.1	9

#	Article	IF	Citations
145	Characterization of MicroRNA and Gene Expression Profiles Following Ricin Intoxication. Toxins, 2019, 11, 250.	3.4	8
146	The black sheep of the family- whole-exome sequencing in family of lithium response discordant bipolar monozygotic twins. European Neuropsychopharmacology, 2020, 34, 19-27.	0.7	8
147	Heterozygous APC germline mutations impart predisposition to colorectal cancer. Scientific Reports, 2021, 11, 5113.	3.3	8
148	Overcoming Interpretability in Deep Learning Cancer Classification. Methods in Molecular Biology, 2021, 2243, 297-309.	0.9	8
149	Altered White Matter and microRNA Expression in a Murine Model Related to Williams Syndrome Suggests That miR-34b/c Affects Brain Development via Ptpru and Dcx Modulation. Cells, 2022, 11, 158.	4.1	8
150	TWIST1 methylation by SETD6 selectively antagonizes LINC-PINT expression in glioma. Nucleic Acids Research, 2022, 50, 6903-6918.	14.5	8
151	MicroRNA-34a is dispensable for p53 function as teratogenesis inducer. Archives of Toxicology, 2014, 88, 1749-1763.	4.2	7
152	Actionable clinical decisions based on comprehensive genomic evaluation in asymptomatic adults. Molecular Genetics & Genomic Medicine, 2015, 3, 433-439.	1.2	7
153	Differential analysis of mutations in the Jewish population and their implications for diseases. Genetical Research, 2017, 99, e3.	0.9	7
154	<scp>SMYD</scp>1 is the underlying gene for the AnWjâ€negative blood group phenotype. European Journal of Haematology, 2018, 101, 496-501.	2.2	7
155	Rare Genetic Variants in Jewish Patients Suffering from Age-Related Macular Degeneration. Genes, 2019, 10, 825.	2.4	7
156	Continuous Remote Patient Monitoring Shows Early Cardiovascular Changes in COVID-19 Patients. Journal of Clinical Medicine, 2021, 10, 4218.	2.4	7
157	Population differences in antibody response to SARSâ€CoVâ€2 infection and BNT162b2 vaccination. FASEB Journal, 2022, 36, e22223.	0.5	7
158	LY6S, a New IFN-Inducible Human Member of the Ly6a Subfamily Expressed by Spleen Cells and Associated with Inflammation and Viral Resistance. ImmunoHorizons, 2022, 6, 253-272.	1.8	7
159	MicroRNAs and their antagonists as novel therapeutics. European Journal of Cancer, 2009, 45, 388-390.	2.8	6
160	MicroRNAs: fundamental regulators of gene expression in major affective disorders and suicidal behavior?. Frontiers in Cellular Neuroscience, 2013, 7, 208.	3.7	6
161	X-linked elliptocytosis with impaired growth is related to mutated AMMECR1. Gene, 2017, 606, 47-52.	2.2	6
162	Autophagy is induced and modulated by cholesterol depletion through transcription of autophagy-related genes and attenuation of flux. Cell Death Discovery, 2021, 7, 320.	4.7	6

#	Article	IF	Citations
163	Adaptive sequencing using nanopores and deep learning of mitochondrial DNA. Briefings in Bioinformatics, 2022, 23, .	6.5	6
164	Prioritizing personalized medicine. Genetical Research, 2014, 96, e007.	0.9	5
165	Somatic Mosaicism for a â€œLethalâ€•<scp>GJB</scp>2 Mutation Results in a Patterned Form of Spiny Hyperkeratosis without Eccrine Involvement. Pediatric Dermatology, 2016, 33, 322-326.	0.9	5
166	Punctate palmoplantar keratoderma: an unusual mutation causing an unusual phenotype. British Journal of Dermatology, 2018, 178, 1455-1457.	1.5	5
167	The Contribution of MicroRNAs to the Inflammatory and Neoplastic Characteristics of Erdheimâ€“Chester Disease. Cancers, 2020, 12, 3240.	3.7	5
168	Palmoplantar keratoderma caused by a missense variant in CTSB encoding cathepsin B. Clinical and Experimental Dermatology, 2021, 46, 103-108.	1.3	5
169	Synergy of oxytocin and citalopram in modulating Itgb3/Chl1 interplay: Relevance to sensitivity to SSRI therapy. Psychoneuroendocrinology, 2021, 129, 105234.	2.7	5
170	PNPT1, MYO15A, PTPRQ, and SLC12A2â€associated genetic and phenotypic heterogeneity among hearing impaired assortative mating families in Southern India. Annals of Human Genetics, 2022, 86, 1-13.	0.8	5
171	Blood transcriptional response to treatment-resistant depression during electroconvulsive therapy. Journal of Psychiatric Research, 2021, 141, 92-103.	3.1	5
172	Microdeletion of 16q24.1â€“q24.2â€”A unique etiology of Lymphedemaâ€“Distichiasis syndrome and neurodevelopmental disorder. American Journal of Medical Genetics, Part A, 2022, 188, 1990-1996.	1.2	5
173	<scp>DYRK1B</scp> haploinsufficiency in a family with metabolic syndrome and abnormal cognition. Clinical Genetics, 2022, 101, 265-266.	2.0	4
174	Promoter-Associated RNAs Regulate HSPC152 Gene Expression in Malignant Melanoma. Non-coding RNA, 2016, 2, 7.	2.6	3
175	Deep Learning Applied on Next Generation Sequencing Data Analysis. Methods in Molecular Biology, 2021, 2243, 169-182.	0.9	3
176	Single-Cell Transcriptome Profiling. Methods in Molecular Biology, 2021, 2243, 311-325.	0.9	3
177	Analysis of microRNA Regulation in Single Cells. Methods in Molecular Biology, 2021, 2243, 339-354.	0.9	3
178	Reâ€evaluating the pathogenicity of the c.783+2T>C BAP1 germline variant. Human Mutation, 2021, 42, 592-599.	2.5	3
179	Slow Transcription of the 99a/let-7c/125b-2 Cluster Results in Differential MiRNA Expression and Promotes Melanoma Phenotypic Plasticity. Journal of Investigative Dermatology, 2021, 141, 2944-2956.e6.	0.7	3
180	MicroRNA-15a-5p acts as a tumor suppressor in histiocytosis by mediating CXCL10-ERK-LIN28a-let-7 axis. Leukemia, 2021, , .	7.2	3

#	Article	IF	Citations
181	Sequencing your genome: your future is here, but are you sure you want to know it?. Genetical Research, 2014, 96, e006.	0.9	2
182	Influence of population diversity on neurovirulence potential of plaque purified L-Zagreb variants. Vaccine, 2016, 34, 2383-2389.	3.8	2
183	381 Epidermolytic ichthyosis sine epidermolysis. Journal of Investigative Dermatology, 2016, 136, S67.	0.7	2
184	Phenotypic suppression of acral peeling skin syndrome in a patient with autosomal recessive congenital ichthyosis. Experimental Dermatology, 2020, 29, 742-748.	2.9	2
185	Genome-Wide Noninvasive Prenatal Diagnosis of De Novo Mutations. Methods in Molecular Biology, 2021, 2243, 249-269.	0.9	2
186	Two intronic cisâ€acting variants in both alleles of the POLR3A gene cause progressive spastic ataxia with hypodontia. Clinical Genetics, 2021, 99, 713-718.	2.0	2
187	Genome wide analysis implicates upregulation of proteasome pathway in major depressive disorder. Translational Psychiatry, 2021, 11, 409.	4.8	2
188	MicroRNAs and Their Antagonists as Novel Therapeutics. RNA Technologies, 2012, , 503-523.	0.3	2
189	Structure-function conservation between the methyltransferases SETD3 and SETD6. Biochimie, 2022, 200, 27-35.	2.6	2
190	Genetics research: jumping into the deep end of the pool. Genetical Research, 2013, 95, 1-3.	0.9	1
191	The ABC of reporting statistical analyses in theBJD: Always Be Clear. British Journal of Dermatology, 2018, 179, 3-5.	1.5	1
192	Improved noninvasive fetal variant calling using standardized benchmarking approaches. Computational and Structural Biotechnology Journal, 2021, 19, 509-517.	4.1	1
193	Association of Variants in TMEM45A With Keratoglobus. JAMA Ophthalmology, 2021, 139, 1089.	2.5	1
194	Involvement of microRNA in the regulation of progesterone receptor in breast cancer.. Journal of Clinical Oncology, 2013, 31, 578-578.	1.6	1
195	The Role of microRNAs in the Pathogenesis of Erdheim-Chester Disease and Their Potential Use As Biomarkers for Diagnosis and Prognosis of the Disease. Blood, 2018, 132, 2397-2397.	1.4	1
196	Marginal Contribution Feature Importance - an Axiomatic Approach for Explaining Data. Proceedings of Machine Learning Research, 2021, 139, 1324-1335.	0.3	1
197	Breast cancer genomics in the deep sequencing era. Israel Medical Association Journal, 2014, 16, 783-4.	0.1	1
198	Olfactory cells aid in the understanding of neurodegenerative disorders. Human Mutation, 2012, 33, 5-5.	2.5	0

#	Article	IF	Citations
199	A personal perspective on personalized medicine. Genetical Research, 2013, 95, 51-51.	0.9	0
200	Prizing the development of a personalized medicine diagnostic test. Genetical Research, 2013, 95, 52-52.	0.9	0
201	Cancer Therapy: Biomaterials for Abrogating Metastasis: Bridging the Gap between Basic and Translational Research (Adv. Healthcare Mater. 18/2016). Advanced Healthcare Materials, 2016, 5, 2452-2452.	7.6	0
202	774 Focal facial dermal dysplasia type I caused by a duplication on 1p36.22. Journal of Investigative Dermatology, 2018, 138, S131.	0.7	0
203	Genome-Wide Noninvasive Prenatal Diagnosis of SNPs and Indels. Methods in Molecular Biology, 2021, 2243, 227-248.	0.9	0
204	DNA Data Collection and Analysis in the Forensic Arena. Methods in Molecular Biology, 2021, 2243, 355-368.	0.9	0
205	Assessing the involvement of the placental microbiome and virome in preeclampsia using non coding RNA sequencing. Journal of Perinatal Medicine, 2021, 49, 1071-1083.	1.4	0
206	Human Hepatic Stellate Cells Carry a New Splice Variant of the Human ADAMTS13. Blood, 2008, 112, 4085-4085.	1.4	0
207	microRNAs and the expression of the progesterone receptor in breast cancer.. Journal of Clinical Oncology, 2014, 32, e11529-e11529.	1.6	0
208	P.0061 Ketamine affects expression of Itgb3, Itgav, Chl1 and Sirt1 in the prefrontal cortex of rats in a depressive-like behaviour model. European Neuropsychopharmacology, 2021, 53, S44-S45.	0.7	0