Larisa M Haupt

List of Publications by Year
in descending order

131	3,976	186265	144013
papers	citations	28 h-index	57 g-index

141	141	141	6626
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Development of an accurate genomic ancestry prediction strategy to enable the accounting of Australian and Japanese historical military remains. Australian Journal of Forensic Sciences, 2022, 54, 416-436.	1.2	1
2	Association of polymorphisms in ARRB2 and clinical response to methadone for pain in advanced cancer. Pharmacogenomics, 2022, 23, 281-289.	1.3	2
3	Syndecan-1 and -4 influence Wnt signaling and cell migration in human breast cancers. Biochimie, 2022, 198, 60-75.	2.6	2
4	Pedigree derived mutation rate across the entire mitochondrial genome of the Norfolk Island population. Scientific Reports, 2022, 12, 6827.	3.3	4
5	Investigation of Mitochondrial Related Variants in a Cerebral Small Vessel Disease Cohort. Molecular Neurobiology, 2022, 59, 5366-5378.	4.0	3
6	Proteoglycans, Neurogenesis and Stem Cell Differentiation. Biology of Extracellular Matrix, 2021, , 111-152.	0.3	1
7	Mini review: genome and transcriptome editing using CRISPR-cas systems for haematological malignancy gene therapy. Transgenic Research, 2021, 30, 129-141.	2.4	4
8	Three-Dimensional Human Neural Stem Cell Models to Mimic Heparan Sulfate Proteoglycans and the Neural Niche. Seminars in Thrombosis and Hemostasis, 2021, 47, 308-315.	2.7	4
9	Genetic Association Analysis Implicates Six MicroRNA-Related SNPs With Increased Risk of Breast Cancer in Australian Caucasian Women. Clinical Breast Cancer, 2021, 21, e694-e703.	2.4	6
10	A genome-wide methylation study of body fat traits in the Norfolk Island isolate. Nutrition, Metabolism and Cardiovascular Diseases, 2021, 31, 1556-1563.	2.6	4
11	The MinION as a cost-effective technology for diagnostic screening of the SCN1A gene in epilepsy patients. Epilepsy Research, 2021, 172, 106593.	1.6	1
12	Genome wide association study of response to interval and continuous exercise training: the Predict-HIIT study. Journal of Biomedical Science, 2021, 28, 37.	7.0	15
13	Metaâ€analysis of genomeâ€wide DNA methylation and integrative omics of age in human skeletal muscle. Journal of Cachexia, Sarcopenia and Muscle, 2021, 12, 1064-1078.	7.3	37
14	Techniques for RNA extraction from cells cultured in starPEGâ€“heparin hydrogels. Open Biology, 2021, 11, 200388.	3.6	2
15	Using Monozygotic Twins to Dissect Common Genes in Posttraumatic Stress Disorder and Migraine. Frontiers in Neuroscience, 2021, 15, 678350.	2.8	10
16	Novel compound heterozygous missense mutations in GDAP1 cause Charcotâ€“Marieâ€“Tooth type 4A. Journal of Genetics, 2021, 100, 1.	0.7	0
17	Mechanical Pressure Driving Proteoglycan Expression in Mammographic Density: a Self-perpetuating Cycle?. Journal of Mammary Gland Biology and Neoplasia, 2021, 26, 277-296.	2.7	2
18	A combinatorial in silico approach for microRNA-target identification: Order out of chaos. Biochimie, 2021, 187, 121-130.	2.6	3

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19	Multi-phenotype genome-wide association studies of the Norfolk Island isolate implicate pleiotropic loci involved in chronic kidney disease. Scientific Reports, 2021, 11, 19425.	3.3	1
20	Long-Term Consumption of Anthocyanin-Rich Fruit Juice: Impact on Gut Microbiota and Antioxidant Markers in Lymphocytes of Healthy Males. Antioxidants, 2021, 10, 27.	5.1	11
21	Skeletal muscle methylome and transcriptome integration reveals profound sex differences related to muscle function and substrate metabolism. Clinical Epigenetics, 2021, 13, 202.	4.1	20
22	Label-free isolation and cultivation of patient-matched human mammary epithelial and stromal cells from normal breast tissue. European Journal of Cell Biology, 2021, 100, 151187.	3.6	2
23	Epigenetic Regulation of miR-92a and TET2 and Their Association in Non-Hodgkin Lymphoma. Frontiers in Genetics, 2021, 12, 768913.	2.3	8
24	Discriminating head trauma outcomes using machine learning and genomics. Journal of Molecular Medicine, 2021, , 1.	3.9	0
25	Investigating diagnostic sequencing techniques for CADASIL diagnosis. Human Genomics, 2020, 14, 2.	2.9	12
26	Saliva as a comparable-quality source of DNA for Whole Exome Sequencing on Ion platforms. Genomics, 2020, 112, 1437-1443.	2.9	4
27	Genetic variants associated with exercise performance in both moderately trained and highly trained individuals. Molecular Genetics and Genomics, 2020, 295, 515-523.	2.1	14
28	Regulatory Mechanisms of Epigenetic miRNA Relationships in Human Cancer and Potential as Therapeutic Targets. Cancers, 2020, 12, 2922.	3.7	84
29	Stromal fibroblasts regulate microvascular-like network architecture in a bioengineered breast tumour angiogenesis model. Acta Biomaterialia, 2020, 114, 256-269.	8.3	17
30	Heparanase Promotes Syndecan-1 Expression to Mediate Fibrillar Collagen and Mammographic Density in Human Breast Tissue Cultured ex vivo. Frontiers in Cell and Developmental Biology, 2020, 8, 599.	3.7	14
31	Comprehensive Exonic Sequencing of Hemiplegic Migraine-Related Genes in a Cohort of Suspected Probands Identifies Known and Potential Pathogenic Variants. Cells, 2020, 9, 2368.	4.1	17
32	Three-Dimensional Models as a New Frontier for Studying the Role of Proteoglycans in the Normal and Malignant Breast Microenvironment. Frontiers in Cell and Developmental Biology, 2020, 8, 569454.	3.7	10
33	An investigation of genetic polymorphisms in heparan sulfate proteoglycan core proteins and key modification enzymes in an Australian Caucasian multiple sclerosis population. Human Genomics, 2020, 14, 18.	2.9	4
34	Comprehensive Exonic Sequencing of Known Ataxia Genes in Episodic Ataxia. Biomedicines, 2020, 8, 134.	3.2	8
35	Syndecan-1 Facilitates the Human Mesenchymal Stem Cell Osteo-Adipogenic Balance. International Journal of Molecular Sciences, 2020, 21, 3884.	4.1	12
36	HSPGs glypicanâ€1 and glypicanâ€4 are human neuronal proteins characteristic of different neural phenotypes. Journal of Neuroscience Research, 2020, 98, 1619-1645.	2.9	8

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37	Tiered analysis of whole-exome sequencing for epilepsy diagnosis. Molecular Genetics and Genomics, 2020, 295, 751-763.	2.1	13
38	Investigating the influence of mtDNA and nuclear encoded mitochondrial variants on high intensity interval training outcomes. Scientific Reports, 2020, 10, 11089.	3.3	7
39	Exploring Neuronal Vulnerability to Head Trauma Using a Whole Exome Approach. Journal of Neurotrauma, 2020, 37, 1870-1879.	3.4	6
40	An epigenetic clock for human skeletal muscle. Journal of Cachexia, Sarcopenia and Muscle, 2020, 11, 887-898.	7.3	70
41	Variant Call Formatâ€"Diagnostic Annotation and Reporting Tool. Journal of Molecular Diagnostics, 2019, 21, 951-960.	2.8	5
42	Genome-wide allele-specific methylation is enriched at gene regulatory regions in a multi-generation pedigree from the Norfolk Island isolate. Epigenetics and Chromatin, 2019, 12, 60.	3.9	12
43	Ion torrent high throughput mitochondrial genome sequencing (HTMGS). PLoS ONE, 2019, 14, e0224847.	2.5	11
44	Single Nucleotide Polymorphisms in MIR143 Contribute to Protection Against Non-Hodgkin Lymphoma (NHL) in Caucasian Populations. Genes, 2019, 10, 185.	2.4	9
45	A causal role for TRESK loss of function in migraine mechanisms. Brain, 2019, 142, 3852-3867.	7.6	49
46	An emerging role for epigenetic factors in relation to executive function. Briefings in Functional Genomics, 2018, 17, 170-180.	2.7	8
47	The NRP1 migraine risk variant shows evidence of association with menstrual migraine. Journal of Headache and Pain, 2018, 19, 31.	6.0	19
48	Next Generation Sequencing Methods for Diagnosis of Epilepsy Syndromes. Frontiers in Genetics, 2018, 9, 20.	2.3	102
49	Heparan Sulfate Proteoglycans as Drivers of Neural Progenitors Derived From Human Mesenchymal Stem Cells. Frontiers in Molecular Neuroscience, 2018, 11, 134.	2.9	10
50	Exome Sequencing Diagnoses X-Linked Moesin-Associated Immunodeficiency in a Primary Immunodeficiency Case. Frontiers in Immunology, 2018, 9, 420.	4.8	24
51	Expression QTL analysis of glaucoma endophenotypes in the Norfolk Island isolate provides evidence that immune-related genes are associated with optic disc size. Journal of Human Genetics, 2018, 63, 83-87.	2.3	1
52	Investigation of the CADM2 polymorphism rs17518584 in memory and executive functions measures in a cohort of young healthy individuals. Neurobiology of Learning and Memory, 2018, 155, 330-336.	1.9	1
53	Current Understanding of DNA Methylation and Age-related Disease. , 2018, 2, 1-1.		6
54	Investigation of polymorphisms in genes involved in estrogen metabolism in menstrual migraine. Gene, 2017, 607, 36-40.	2.2	15

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55	Ion channelopathies and migraine pathogenesis. Molecular Genetics and Genomics, 2017, 292, 729-739.	2.1	21
56	Geneâ€centric analysis implicates nuclear encoded mitochondrial protein gene variants in migraine susceptibility. Molecular Genetics & Genomic Medicine, 2017, 5, 157-163.	1.2	6
57	BDNF Variants May Modulate Long-Term Visual Memory Performance in a Healthy Cohort. International Journal of Molecular Sciences, 2017, 18, 655.	4.1	19
58	A CREB1 Gene Polymorphism (rs2253206) Is Associated with Prospective Memory in a Healthy Cohort. Frontiers in Behavioral Neuroscience, 2017, 11, 86.	2.0	7
59	Exploiting Heparan Sulfate Proteoglycans in Human Neurogenesisâ€"Controlling Lineage Specification and Fate. Frontiers in Integrative Neuroscience, 2017, 11, 28.	2.1	46
60	Methylome-wide association study of whole blood DNA in the Norfolk Island isolate identifies robust loci associated with age. Aging, 2017, 9, 753-768.	3.1	27
61	Dysregulated MicroRNA Expression Profiles and Potential Cellular, Circulating and Polymorphic Biomarkers in Non-Hodgkin Lymphoma. Genes, 2016, 7, 130.	2.4	17
62	Data defining markers of human neural stem cell lineage potential. Data in Brief, 2016, 7, 206-215.	1.0	20
63	Targeted next generation sequencing identifies novel NOTCH3 gene mutations in CADASIL diagnostics patients. Human Genomics, 2016, 10, 38.	2.9	21
64	Methylenetetrahydrofolate Reductase CpG Islands: Epigenotyping. Journal of Clinical Laboratory Analysis, 2016, 30, 335-344.	2.1	5
65	Cell surface heparan sulfate proteoglycans as novel markers of human neural stem cell fate determination. Stem Cell Research, 2016, 16, 92-104.	0.7	62
66	Association of the microRNA-Single Nucleotide Polymorphism rs2910164 in miR146a with sporadic breast cancer susceptibility: A case control study. Gene, 2016, 576, 256-260.	2.2	20
67	Genetic and epigenetic variants in the MTHFR gene are not associated with non-Hodgkin lymphoma. Meta Gene, 2015, 6, 91-95.	0.6	8
68	Genetic association analysis of miRNA SNPs implicates MIR145 in breast cancer susceptibility. BMC Medical Genetics, 2015, 16, 107.	2.1	28
69	A Potential Epigenetic Marker Mediating Serum Folate and Vitamin B₁₂Levels Contributes to the Risk of Ischemic Stroke. BioMed Research International, 2015, 2015, 1-4.	1.9	43
70	Human Mesenchymal Stem Cells Retain Multilineage Differentiation Capacity Including Neural Marker Expression after Extended In Vitro Expansion. PLoS ONE, 2015, 10, e0137255.	2.5	68
71	Mitochondrial Genome Acquisition Restores Respiratory Function and Tumorigenic Potential of Cancer Cells without Mitochondrial DNA. Cell Metabolism, 2015, 21, 81-94.	16.2	582
72	Effects of Dietary Folate Intake on Migraine Disability and Frequency. Headache, 2015, 55, 301-309.	3.9	28

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73	Case-control study of ADARB1 and ADARB2 gene variants in migraine. Journal of Headache and Pain, 2015, 16, 511.	6.0	6
74	Association of heparan sulfate proteoglycans SDC1 and SDC4 polymorphisms with breast cancer in an Australian Caucasian population. Tumor Biology, 2015, 36, 1731-1738.	1.8	17
75	Computational epigenetic profiling of CpG islets in MTHFR. Molecular Biology Reports, 2014, 41, 8285-8292.	2.3	13
76	Genetic Analysis of <scp>GRIA2</scp> and <scp>GRIA4</scp> Genes in Migraine. Headache, 2014, 54, 303-312.	3.9	8
77	Association Study of <scp>MTHFD</scp>1 Coding Polymorphisms <scp>R</scp>134<scp>K</scp> and <scp>R</scp>653<scp>Q</scp> With Migraine Susceptibility. Headache, 2014, 54, 1506-1514.	3.9	12
78	Heparan Sulfate Proteoglycans and Human Breast Cancer Epithelial Cell Tumorigenicity. Journal of Cellular Biochemistry, 2014, 115, 967-976.	2.6	42
79	Genetic polymorphisms in miRNAs targeting the estrogen receptor and their effect on breast cancer risk. Meta Gene, 2014, 2, 226-236.	0.6	14
80	Mesenchymal stem cells, neural lineage potential, heparan sulfate proteoglycans and the matrix. Developmental Biology, 2014, 388, 1-10.	2.0	49
81	Potential antioxidant response to coffee â€" A matter of genotype?. Meta Gene, 2014, 2, 525-539.	0.6	5
82	Investigation of Brainâ€Derived Neurotrophic Factor (<scp>BDNF</scp>) Gene Variants in Migraine. Headache, 2014, 54, 1184-1193.	3.9	26
83	In silico analyses reveal common cellular pathways affected by loss of heterozygosity (LOH) events in the lymphomagenesis of Non-Hodgkinâ€™s lymphoma (NHL). BMC Genomics, 2014, 15, 390.	2.8	8
84	Epigenetics and migraine; complex mitochondrial interactions contributing to disease susceptibility. Gene, 2014, 543, 1-7.	2.2	19
85	Association of the SNP rs2623047 in the HSPG modification enzyme SULF1 with an Australian Caucasian Breast Cancer Cohort. Gene, 2014, 547, 50-54.	2.2	6
86	Association of a <scp>GRIA3</scp> Gene Polymorphism With Migraine in an <scp>A</scp>ustralian Caseâ€Control Cohort. Headache, 2013, 53, 1245-1249.	3.9	22
87	Analysis of 3 common polymorphisms in the KCNK18 gene in an Australian Migraine Case-control cohort. Gene, 2013, 528, 343-346.	2.2	14
88	Association study of the calcitonin gene-related polypeptide-alpha (CALCA) and the receptor activity modifying 1 (RAMP1) genes with migraine. Gene, 2013, 515, 187-192.	2.2	24
89	Investigation of lymphotoxin Î± genetic variants in migraine. Gene, 2013, 512, 527-531.	2.2	8
90	BDNF and TNF-Î± polymorphisms in memory. Molecular Biology Reports, 2013, 40, 5483-5490.	2.3	27

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91	Genetic Variation in Cytokine-Related Genes and Migraine Susceptibility. Twin Research and Human Genetics, 2013, 16, 1079-1086.	0.6	8
92	Investigation of APOE isoforms and the association between APOE E3 and E4 with migraine in the Australian Caucasian population. NeuroReport, 2013, 24, 499-503.	1.2	4
93	Review: Alternative Splicing (AS) of Genes As An Approach for Generating Protein Complexity. Current Genomics, 2013, 14, 182-194.	1.6	80
94	Genotypes of the MTHFR C677T and MTRR A66G genes act independently to reduce migraine disability in response to vitamin supplementation. Pharmacogenetics and Genomics, 2012, 22, 741-749.	1.5	65
95	The human Î¼-opioid receptor gene polymorphism (A118G) is associated with head pain severity in a clinical cohort of female migraine with aura patients. Journal of Headache and Pain, 2012, 13, 513-519.	6.0	24
96	Heritability and genome-wide linkage analysis of migraine in the genetic isolate of Norfolk Island. Gene, 2012, 494, 119-123.	2.2	18
97	Role of the apolipoprotein E and catechol-O-methyltransferase genes in prospective and retrospective memory traits. Gene, 2012, 506, 135-140.	2.2	13
98	Effect of Coffee Combining Green Coffee Bean Constituents with Typical Roasting Products on the Nrf2/ARE Pathway in Vitro and in Vivo. Journal of Agricultural and Food Chemistry, 2012, 60, 9631-9641.	5.2	51
99	Comparison of genomic DNA extraction techniques from whole blood samples: a time, cost and quality evaluation study. Molecular Biology Reports, 2012, 39, 5961-5966.	2.3	63
100	Induction of antioxidative Nrf2 gene transcription by coffee in humans: depending on genotype?. Molecular Biology Reports, 2012, 39, 7155-7162.	2.3	41
101	Confirmation that Xq27 and Xq28 are susceptibility loci for migraine in independent pedigrees and a case-control cohort. Neurogenetics, 2012, 13, 97-101.	1.4	8
102	Development of an eight gene expression profile implicating human breast tumours of all grade. Molecular Biology Reports, 2012, 39, 3879-3892.	2.3	19
103	Association of a Notch 3 gene polymorphism with migraine susceptibility. Cephalalgia, 2011, 31, 264-270.	3.9	25
104	Investigation of the 1758G>C and 2880A>G variants within the NCOA3 gene in a breast cancer affected Australian population. Gene, 2011, 482, 68-72.	2.2	8
105	Semaphorinâ€“plexin signalling genes associated with human breast tumourigenesis. Gene, 2011, 489, 63-69.	2.2	28
106	Significant differences in gene expression of GABA receptors in peripheral blood leukocytes of migraineurs. Gene, 2011, 490, 32-36.	2.2	27
107	Association study of calcitonin gene-related polypeptide-alpha (CALCA) gene polymorphism with migraine. Brain Research, 2011, 1378, 119-124.	2.2	24
108	Investigation of Two Wnt Signalling Pathway Single Nucleotide Polymorphisms in a Breast Cancer-Affected Australian Population. Twin Research and Human Genetics, 2011, 14, 562-567.	0.6	10

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109	Analysis of the MTHFR C677T variant with migraine phenotypes. BMC Research Notes, 2010, 3, 213.	1.4	40
110	Synergism between Wnt3a and Heparin Enhances Osteogenesis via a Phosphoinositide 3-Kinase/Akt/RUNX2 Pathway. Journal of Biological Chemistry, 2010, 285, 26233-26244.	3.4	86
111	Gene Expression Profiling in Human Breast Cancer - Toward Personalised Therapeutics?~!2009-04-21~!2010-02-19~!2010-07-06~!. Open Breast Cancer Journal, 2010, 2, 46-59.	0.2	6
112	The osteogenic transcription factor Runx2 regulates components of the fibroblast growth factor/proteoglycan signaling axis in osteoblasts. Journal of Cellular Biochemistry, 2009, 107, 144-154.	2.6	87
113	Purification and characterization of heparan sulfate from human primary osteoblasts. Journal of Cellular Biochemistry, 2009, 108, 1132-1142.	2.6	10
114	The heparan sulfate proteoglycan (HSPG) glypicanâ€3 mediates commitment of MC3T3â€E1 cells toward osteogenesis. Journal of Cellular Physiology, 2009, 220, 780-791.	4.1	68
115	Heparan Sulfate Proteoglycans, Tumour Progression and the Cancer Stem Cell Niche. Current Cancer Therapy Reviews, 2009, 5, 256-260.	0.3	5
116	Matrix metalloproteinase localisation by in situ-RT-PCR in archival human breast biopsy material. Molecular and Cellular Probes, 2008, 22, 83-89.	2.1	7
117	Osteogenic Differentiation of Murine Embryonic Stem Cells is Mediated by Fibroblast Growth Factor Receptors. Stem Cells and Development, 2007, 16, 305-318.	2.1	42
118	Glycosaminoglycan and growth factor mediated murine calvarial cell proliferation. Journal of Molecular Histology, 2007, 38, 415-424.	2.2	17
119	Temporal and functional changes in glycosaminoglycan expression during osteogenesis. Journal of Molecular Histology, 2007, 38, 469-481.	2.2	13
120	Sustained release and osteogenic potential of heparan sulfate-doped fibrin glue scaffolds within a rat cranial model. Journal of Molecular Histology, 2007, 38, 425-433.	2.2	40
121	Genetic investigation of methylenetetrahydrofolate reductase (MTHFR) and catechol-O-methyl transferase (COMT) in multiple sclerosis. Brain Research Bulletin, 2006, 69, 327-331.	3.0	23
122	In vitro and in vivo MMP gene expression localisation by In Situ-RT-PCR in cell culture and paraffin embedded human breast cancer cell line xenografts. BMC Cancer, 2006, 6, 18.	2.6	14
123	Sulfated glycosaminoglycans mediate the effects of FGF2 on the osteogenic potential of rat calvarial osteoprogenitor cells. Journal of Cellular Physiology, 2006, 209, 811-825.	4.1	57
124	TNF and TNF receptor expression and insulin sensitivity in human omental and subcutaneous adipose tissue â€" influence of BMI and adipose distribution. Diabetes and Vascular Disease Research, 2006, 3, 26-33.	2.0	48
125	Analysis of chromosome 1 microsatellite markers and the FHM2-ATP1A2gene mutations in migraine pedigrees. Neurological Research, 2005, 27, 647-652.	1.3	14
126	Locked nucleic acid (LNA) single nucleotide polymorphism (SNP) genotype analysis and validation using real-time PCR. Nucleic Acids Research, 2004, 32, e55-e55.	14.5	143

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127	Stimulation of MMP-11 (stromelysin-3) expression in mouse fibroblasts by cytokines, collagen and co-culture with human breast cancer cell lines. BMC Cancer, 2004, 4, 40.	2.6	26
128	Loss of chromosomal integrity in human mammary epithelial cells subsequent to escape from senescence. Journal of Mammary Gland Biology and Neoplasia, 2001, 6, 235-243.	2.7	39
129	Normal human mammary epithelial cells spontaneously escape senescence and acquire genomic changes. Nature, 2001, 409, 633-637.	27.8	604
130	ISâ€RTâ€PCR assay detection of MTâ€MMP in a human breast cancer cell line. IUBMB Life, 1996, 39, 553-561.	3.4	2
131	Evaluation of an ancestry prediction strategy for historical military remains using a World War II-era sample and pedigrees with family-level admixture. Australian Journal of Forensic Sciences, 0, , 1-18.	1.2	0