Thomas LaFramboise

List of Publications by Year
in descending order

89	6,296	159585 30	79698 73
papers	citations	h-index	g-index

92	92	92	13156
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Eltrombopag inhibits TET dioxygenase to contribute to hematopoietic stem cell expansion in aplastic anemia. Journal of Clinical Investigation, 2022, 132, .	8.2	15
2	Circulating microbial content in myeloid malignancy patients is associated with disease subtypes and patient outcomes. Nature Communications, 2022, 13, 1038.	12.8	13
3	Genome-wide proteinâ€“DNA interaction site mapping in bacteria using a double-stranded DNA-specific cytosine deaminase. Nature Microbiology, 2022, 7, 844-855.	13.3	12
4	Rare germline alterations of myeloperoxidase predispose to myeloid neoplasms. Leukemia, 2022, 36, 2086-2096.	7.2	2
5	Novel DNA Methylation Biomarker Panel for Detection of Esophageal Adenocarcinoma and High-Grade Dysplasia. Clinical Cancer Research, 2022, 28, 3761-3769.	7.0	2
6	Metagenomic markings of myeloid malignancies. Genes and Diseases, 2022, , .	3.4	0
7	Cisplatin-Mediated Upregulation of APE2 Binding to MYH9 Provokes Mitochondrial Fragmentation and Acute Kidney Injury. Cancer Research, 2021, 81, 713-723.	0.9	24
8	Mitochondrial DNA Content Is Linked to Cardiovascular Disease Patient Phenotypes. Journal of the American Heart Association, 2021, 10, e018776.	3.7	11
9	Exonic variants undergoing allele-specific selection in cancers. BMC Medical Genomics, 2021, 14, 142.	1.5	0
10	Single cell RNA sequencing of AML initiating cells reveals RNA-based evolution during disease progression. Leukemia, 2021, 35, 2799-2812.	7.2	41
11	Clinical and basic implications of dynamic T cell receptor clonotyping in hematopoietic cell transplantation. JCI Insight, 2021, 6, .	5.0	12
12	Evaluating the Bioenergetics Health Index Ratio in Leigh Syndrome Fibroblasts to Understand Disease Severity. International Journal of Molecular Sciences, 2021, 22, 10344.	4.1	4
13	The similarity of class II HLA genotypes defines patterns of autoreactivity in idiopathic bone marrow failure disorders. Blood, 2021, 138, 2781-2798.	1.4	27
14	Mutant TP53 prevents Telomere Shortening in Acute Myeloid Leukemia. Blood, 2021, 138, 375-375.	1.4	2
15	Rare germline variant contributions to myeloid malignancy susceptibility. Leukemia, 2020, 34, 1675-1678.	7.2	8
16	Myeloid neoplasms with germline predisposition: Practical considerations and complications in the search for new susceptibility loci. Best Practice and Research in Clinical Haematology, 2020, 33, 101191.	1.7	6
17	Complexities and pitfalls in analyzing and interpreting mitochondrial DNA content in human cancer. Journal of Genetics and Genomics, 2020, 47, 349-359.	3.9	1
18	Type of TP53 Mutations Affects Subclonal Configuration and Selection Pressure for Acquisition of Additional Hits in Contralateral Alleles. Blood, 2020, 136, 25-25.	1.4	0

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19	Impact of HLA Evolutionary Divergence on Clinical Features of Patients with Aplastic Anemia and Paroxysmal Nocturnal Hemoglobinuria. Blood, 2020, 136, 2-3.	1.4	0
20	Immunogenomics of Aplastic Anemia: The Role of HLA Somatic Mutations and the HLA Evolutionary Divergence. Blood, 2020, 136, 20-21.	1.4	0
21	Characterization of the Blood and Bone Marrow Microbiome of MDS Patients and Associations with Clinical Features. Blood, 2020, 136, 34-35.	1.4	1
22	Mitochondrial genomics in the cancer cell line encyclopedia and a scoring method to effectively pair cell lines for cytoplasmic hybridization. Mitochondrion, 2019, 46, 256-261.	3.4	1
23	CytoConverter: a web-based tool to convert karyotypes to genomic coordinates. BMC Bioinformatics, 2019, 20, 467.	2.6	5
24	Impact of germline CTC 1 alterations on telomere length in acquired bone marrow failure. British Journal of Haematology, 2019, 185, 935-939.	2.5	9
25	FA Gene Carrier Status Predisposes to Myeloid Neoplasms and Bone Marrow Failure in Adults. Blood, 2019, 134, 452-452.	1.4	2
26	Molecular Dissection of Del(5q): Distinction between Primary and Secondary Del(5q) and Pathogenetic Implications. Blood, 2019, 134, 4221-4221.	1.4	0
27	Mutational Type and Configuration of an Individual Gene May Differentially Impact the Clinical and Phenotypic Features. Blood, 2019, 134, 2992-2992.	1.4	0
28	TET2 Loss Accelerates Leukemogenesis By Disrupting Mismatch Repair Proteins. Blood, 2019, 134, 1200-1200.	1.4	0
29	MPO as a Novel Susceptibility Gene in Myeloid Malignancies. Blood, 2019, 134, 5402-5402.	1.4	1
30	ANKRD26 Coding Variants Presenting with Giant Platelets and a Predisposition to Myeloid Neoplasia. Blood, 2019, 134, 4233-4233.	1.4	0
31	Genetics of Monosomy 7 and Del(7q) in MDS Informs Potential Therapeutic Targets. Blood, 2019, 134, 1703-1703.	1.4	2
32	The DNMT1-associated lincRNA DACOR1 reprograms genome-wide DNA methylation in colon cancer. Clinical Epigenetics, 2018, 10, 127.	4.1	34
33	Germline loss-of-function SAMD9 and SAMD9L alterations in adult myelodysplastic syndromes. Blood, 2018, 132, 2309-2313.	1.4	38
34	Consequences of mutant TET2 on clonality and subclonal hierarchy. Leukemia, 2018, 32, 1751-1761.	7.2	54
35	Unexpected cancer-predisposition gene variants in Cowden syndrome and Bannayan-Riley-Ruvalcaba syndrome patients without underlying germline PTEN mutations. PLoS Genetics, 2018, 14, e1007352.	3.5	27
36	Invariant Patterns of Clonal Succession Determines Specific Phenotypic and Clinical Features of Myelodysplastic Syndromes (MDS). Blood, 2018, 132, 104-104.	1.4	0

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37	Distinct Features of Chip-Derived and De Novo MDS. Blood, 2018, 132, 2572-2572.	1.4	0
38	Opposing Pathogenesis of Germline SAMD9/SAMD9L Variants in Adult Myelodysplastic Syndrome (MDS). Blood, 2018, 132, 4351-4351.	1.4	0
39	Molecular Spectrum of CSF3R variants Correlate with Specific Myeloid Malignancies and Secondary Mutations. Blood, 2018, 132, 4389-4389.	1.4	1
40	Molecular features of early onset adult myelodysplastic syndrome. Haematologica, 2017, 102, 1028-1034.	3.5	20
41	Heteroplasmic shifts in tumor mitochondrial genomes reveal tissue-specific signals of relaxed and positive selection. Human Molecular Genetics, 2017, 26, 2912-2922.	2.9	56
42	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	21.4	348
43	Detection and quantification of mitochondrial DNA deletions from next-generation sequence data. BMC Bioinformatics, 2017, 18, 407.	2.6	29
44	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	1.8	34
45	Phase I/II study of azacitidine and capecitabine/oxaliplatin (CAPOX) in refractory CIMP-high metastatic colorectal cancer: evaluation of circulating methylated vimentin. Oncotarget, 2016, 7, 67495-67506.	1.8	42
46	Germline compound heterozygous poly-glutamine deletion inUSF3may be involved in predisposition to heritable and sporadic epithelial thyroid carcinoma. Human Molecular Genetics, 2016, 26, ddw382.	2.9	14
47	Oncogenic PIK3CA mutations reprogram glutamine metabolism in colorectal cancer. Nature Communications, 2016, 7, 11971.	12.8	203
48	Pathogenic Relevance of Germ Line TET2 Alterations. Blood, 2016, 128, 3160-3160.	1.4	2
49	the Impact of Clonal Dynamics on Prognosis and Outcome in Myelodysplastic Syndromes. Blood, 2016, 128, 4287-4287.	1.4	0
50	Landscape of Subclonal Mutations in Myelodysplastic Syndromes (MDS) Allows for a Novel Hierarchy of Clonal Advantage By Combining Germline and Somatic Mutations. Blood, 2016, 128, 957-957.	1.4	0
51	Germline and somatic SDHx alterations in apparently sporadic differentiated thyroid cancer. Endocrine-Related Cancer, 2015, 22, 121-130.	3.1	30
52	Whole-exome sequencing enhances prognostic classification of myeloid malignancies. Journal of Biomedical Informatics, 2015, 58, 104-113.	4.3	9
53	Serial Sequencing in Myelodysplastic Syndromes Reveals Dynamic Changes in Clonal Architecture and Allows for a New Prognostic Assessment of Mutations Detected in Cross-Sectional Testing. Blood, 2015, 126, 709-709.	1.4	2
54	PCR-Free Enrichment of Mitochondrial DNA from Human Blood and Cell Lines for High Quality Next-Generation DNA Sequencing. PLoS ONE, 2015, 10, e0139253.	2.5	28

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55	Determinants of Phenotypic Commitment and Clonal Progression--Conclusions from the Study of Clonal Architecture in CMML. Blood, 2015, 126, 2848-2848.	1.4	0
56	The Complete Mutatome and Clonal Architecture of Del(5q). Blood, 2015, 126, 608-608.	1.4	1
57	DB2: a probabilistic approach for accurate detection of tandem duplication breakpoints using paired-end reads. BMC Genomics, 2014, 15, 175.	2.8	7
58	Mutational patterns in the breast cancer mitochondrial genome, with clinical correlates. Carcinogenesis, 2014, 35, 1046-1054.	2.8	65
59	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. Blood, 2014, 124, 823-823.	1.4	4
60	Analysis of Clonal Hierarchy Shows That Other Ancestral Events May Precede Evolution of Del(5q) in Myeloid Neoplasms. Blood, 2014, 124, 4605-4605.	1.4	1
61	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641.	28.9	300
62	Clinical â€œMUTATOMEâ€•Of Myelodysplastic Syndrome; Comparison To Primary Acute Myelogenous Leukemia. Blood, 2013, 122, 518-518.	1.4	2
63	Comprehensive Identification Of Germline Alterations In Telomerase Complex Genes By Whole Exome Sequencing Of MDS and Related Myeloid Neoplasms. Blood, 2013, 122, 522-522.	1.4	0
64	Calling amplified haplotypes in next generation tumor sequence data. Genome Research, 2012, 22, 362-374.	5.5	10
65	Epigenomic Enhancer Profiling Defines a Signature of Colon Cancer. Science, 2012, 336, 736-739.	12.6	304
66	Activation of the AXL kinase causes resistance to EGFR-targeted therapy in lung cancer. Nature Genetics, 2012, 44, 852-860.	21.4	1,049
67	Characterizing Mutational Heterogeneity in a Glioblastoma Patient with Double Recurrence. PLoS ONE, 2012, 7, e35262.	2.5	58
68	A 32 kb Critical Region Excluding Y402H in CFH Mediates Risk for Age-Related Macular Degeneration. PLoS ONE, 2011, 6, e25598.	2.5	46
69	Losing balance: Hardyâ€“Weinberg disequilibrium as a marker for recurrent loss-of-heterozygosity in cancer. Human Molecular Genetics, 2011, 20, 4831-4839.	2.9	6
70	Allelic Selection of Amplicons in Glioblastoma Revealed by Combining Somatic and Germline Analysis. PLoS Genetics, 2010, 6, e1001086.	3.5	27
71	Dual specificity phosphatase 6 (DUSP6) is an ETS-regulated negative feedback mediator of oncogenic ERK signaling in lung cancer cells. Carcinogenesis, 2010, 31, 577-586.	2.8	158
72	CHD7 Targets Active Gene Enhancer Elements to Modulate ES Cell-Specific Gene Expression. PLoS Genetics, 2010, 6, e1001023.	3.5	213

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73	The tumor suppressor Cdc73 functionally associates with CPSF and CstF 3â€² mRNA processing factors. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 755-760.	7.1	116
74	Single nucleotide polymorphism arrays: a decade of biological, computational and technological advances. Nucleic Acids Research, 2009, 37, 4181-4193.	14.5	340
75	A flexible rank-based framework for detecting copy number aberrations from array data. Bioinformatics, 2009, 25, 722-728.	4.1	8
76	Genomic distribution of CHD7 on chromatin tracks H3K4 methylation patterns. Genome Research, 2009, 19, 590-601.	5.5	210
77	An optimization framework for unsupervised identification of rare copy number variation from SNP array data. Genome Biology, 2009, 10, R119.	9.6	22
78	Predicting drug susceptibility of nonâ€“small cell lung cancers based on genetic lesions. Journal of Clinical Investigation, 2009, 119, 1727-1740.	8.2	230
79	Epitope tagging of endogenous proteins for genome-wide ChIP-chip studies. Nature Methods, 2008, 5, 163-165.	19.0	92
80	SNP Arrays in Heterogeneous Tissue: Highly Accurate Collection of Both Germline and Somatic Genetic Information from Unpaired Single Tumor Samples. American Journal of Human Genetics, 2008, 82, 903-915.	6.2	47
81	Frequency of Germline Genomic Homozygosity Associated With Cancer Cases. JAMA - Journal of the American Medical Association, 2008, 299, 1437.	7.4	46
82	PLASQ: a generalized linear model-based procedure to determine allelic dosage in cancer cells from SNP array data. Biostatistics, 2007, 8, 323-336.	1.5	47
83	High-throughput oncogene mutation profiling in human cancer. Nature Genetics, 2007, 39, 347-351.	21.4	927
84	Toward accurate high-throughput SNP genotyping in the presence of inherited copy number variation. BMC Genomics, 2007, 8, 211.	2.8	9
85	A transforming MET mutation discovered in non-small cell lung cancer using microarray-based resequencing. Cancer Letters, 2006, 239, 227-233.	7.2	35
86	Sensitive mutation detection in heterogeneous cancer specimens by massively parallel picoliter reactor sequencing. Nature Medicine, 2006, 12, 852-855.	30.7	313
87	Homozygous Deletions and Chromosome Amplifications in Human Lung Carcinomas Revealed by Single Nucleotide Polymorphism Array Analysis. Cancer Research, 2005, 65, 5561-5570.	0.9	309
88	Allele-Specific Amplification in Cancer Revealed by SNP Array Analysis. PLoS Computational Biology, 2005, 1, e65.	3.2	100
89	Genomic representations using concatenates of Type IIB restriction endonuclease digestion fragments. Nucleic Acids Research, 2004, 32, e121-e121.	14.5	20