

Kelly A Frazer

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

25,289
citations

25423

59
h-index

12940

136
g-index

161
all docs

161
docs citations

161
times ranked

42314
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultra-Sharp Nanowire Arrays Natively Permeate, Record, and Stimulate Intracellular Activity in Neuronal and Cardiac Networks. <i>Advanced Functional Materials</i> , 2022, 32, 2108378.	7.8	21
2	In heart failure reactivation of RNA-binding proteins is associated with the expression of 1,523 fetal-specific isoforms. <i>PLoS Computational Biology</i> , 2022, 18, e1009918.	1.5	19
3	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 1331-1349.	1.9	12
4	Detection and validation of novel mutations in MERTK in a simplex case of retinal degeneration using WGS and hiPSC-RPEs model. <i>Human Mutation</i> , 2021, 42, 189-199.	1.1	5
5	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. <i>Nature Genetics</i> , 2021, 53, 313-321.	9.4	42
6	Enhancer release and retargeting activates disease-susceptibility genes. <i>Nature</i> , 2021, 595, 735-740.	13.7	76
7	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	13.7	89
8	Deciphering the genetic architecture and ethnographic distribution of IRD in three ethnic populations by whole genome sequence analysis. <i>PLoS Genetics</i> , 2021, 17, e1009848.	1.5	13
9	Genomics Links Inflammation With Neurocognitive Impairment in Children Living With Human Immunodeficiency Virus Type-1. <i>Journal of Infectious Diseases</i> , 2021, 224, 870-880.	1.9	3
10	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. <i>Cell Reports</i> , 2021, 37, 110020.	2.9	25
11	Revealing Instability: Genetic Variation Underlies Variability in mESC Pluripotency. <i>Cell Stem Cell</i> , 2020, 27, 347-349.	5.2	0
12	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. <i>Nature Communications</i> , 2020, 11, 2928.	5.8	22
13	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. <i>Nature Communications</i> , 2020, 11, 2927.	5.8	67
14	Cellular deconvolution of GTEx tissues powers discovery of disease and cell-type associated regulatory variants. <i>Nature Communications</i> , 2020, 11, 955.	5.8	96
15	Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. <i>Nature Communications</i> , 2020, 11, 550.	5.8	45
16	Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen program. <i>Stem Cell Research</i> , 2020, 46, 101803.	0.3	10
17	In vitro Differentiation of Human iPSC-derived Cardiovascular Progenitor Cells (iPSC-CVPCs). <i>Bio-protocol</i> , 2020, 10, e3755.	0.2	8
18	Fibrinogen gamma gene <i>rs2066865</i> and risk of cancer-related venous thromboembolism. <i>Haematologica</i> , 2020, 105, 1963-1968.	1.7	10

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19	Mutations in topoisomerase II ^β result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019, 10, 3644.	5.8	37
20	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
21	A Network of microRNAs Acts to Promote Cell Cycle Exit and Differentiation of Human Pancreatic Endocrine Cells. <i>IScience</i> , 2019, 21, 681-694.	1.9	21
22	Association of Human iPSC Gene Signatures and X Chromosome Dosage with Two Distinct Cardiac Differentiation Trajectories. <i>Stem Cell Reports</i> , 2019, 13, 924-938.	2.3	44
23	A large-scale exome array analysis of venous thromboembolism. <i>Genetic Epidemiology</i> , 2019, 43, 449-457.	0.6	22
24	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <i>Nature Communications</i> , 2019, 10, 2078.	5.8	82
25	Human iPSC-Derived Retinal Pigment Epithelium: A Model System for Prioritizing and Functionally Characterizing Causal Variants at AMD Risk Loci. <i>Stem Cell Reports</i> , 2019, 12, 1342-1353.	2.3	32
26	Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. <i>Nature Communications</i> , 2019, 10, 1054.	5.8	100
27	Activation of hedgehog signaling associates with early disease progression in chronic lymphocytic leukemia. <i>Blood</i> , 2019, 133, 2651-2663.	0.6	15
28	Effect of prothrombotic genotypes on the risk of venous thromboembolism in patients with and without ischemic stroke. The TromsÅ Study. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 749-758.	1.9	8
29	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. <i>Nature Genetics</i> , 2019, 51, 1506-1517.	9.4	35
30	In vitro Differentiation of Human iPSC-derived Retinal Pigment Epithelium Cells (iPSC-RPE). <i>Bio-protocol</i> , 2019, 9, e3469.	0.2	6
31	Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. <i>ELife</i> , 2019, 8, .	2.8	34
32	Identification of Common and Rare Genetic Variation Associated With Plasma Protein Levels Using Whole-Exome Sequencing and Mass Spectrometry. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002170.	1.6	26
33	Insights into the Mutational Burden of Human Induced Pluripotent Stem Cells from an Integrative Multi-Omics Approach. <i>Cell Reports</i> , 2018, 24, 883-894.	2.9	85
34	IFT88 mutations identified in individuals with non-syndromic recessive retinal degeneration result in abnormal ciliogenesis. <i>Human Genetics</i> , 2018, 137, 447-458.	1.8	11
35	Cell-Surface Marker Signature for Enrichment of Ventricular Cardiomyocytes Derived from Human Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2018, 11, 828-841.	2.3	37
36	High-Throughput and Cost-Effective Characterization of Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 8, 1101-1111.	2.3	64

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37	PTEN regulates glioblastoma oncogenesis through chromatin-associated complexes of DAXX and histone H3.3. <i>Nature Communications</i> , 2017, 8, 15223.	5.8	94
38	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 533-546.e7.	5.2	157
39	iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. <i>Stem Cell Reports</i> , 2017, 8, 1086-1100.	2.3	147
40	Aberrant DNA Methylation in Human iPSCs Associates with MYC-Binding Motifs in a Clone-Specific Manner Independent of Genetics. <i>Cell Stem Cell</i> , 2017, 20, 505-517.e6.	5.2	33
41	A mutation in IFT43 causes non-syndromic recessive retinal degeneration. <i>Human Molecular Genetics</i> , 2017, 26, 4741-4751.	1.4	10
42	Identifying DNase I hypersensitive sites as driver distal regulatory elements in breast cancer. <i>Nature Communications</i> , 2017, 8, 436.	5.8	22
43	Glioblastoma cellular cross-talk converges on NF- κ B to attenuate EGFR inhibitor sensitivity. <i>Genes and Development</i> , 2017, 31, 1212-1227.	2.7	53
44	Efficient Prioritization of Multiple Causal eQTL Variants via Sparse Polygenic Modeling. <i>Genetics</i> , 2017, 207, 1301-1312.	1.2	10
45	Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. <i>BMC Bioinformatics</i> , 2017, 18, 207.	1.2	35
46	Whole Genome Sequencing Revealed Mutations in Two Independent Genes as the Underlying Cause of Retinal Degeneration in an Ashkenazi Jewish Pedigree. <i>Genes</i> , 2017, 8, 210.	1.0	14
47	Kataegis Expression Signature in Breast Cancer Is Associated with Late Onset, Better Prognosis, and Higher HER2 Levels. <i>Cell Reports</i> , 2016, 16, 672-683.	2.9	33
48	Establishing the involvement of the novel gene <i>AGBL5</i> in retinitis pigmentosa by whole genome sequencing. <i>Physiological Genomics</i> , 2016, 48, 922-927.	1.0	29
49	High-level ROR1 associates with accelerated disease progression in chronic lymphocytic leukemia. <i>Blood</i> , 2016, 128, 2931-2940.	0.6	102
50	Joint effects of cancer and variants in the factor 5 gene on the risk of venous thromboembolism. <i>Haematologica</i> , 2016, 101, 1046-1053.	1.7	28
51	PI3K δ is a molecular switch that controls immune suppression. <i>Nature</i> , 2016, 539, 437-442.	13.7	884
52	ADAR1 Activation Drives Leukemia Stem Cell Self-Renewal by Impairing Let-7 Biogenesis. <i>Cell Stem Cell</i> , 2016, 19, 177-191.	5.2	182
53	Associations Between Common and Rare Exonic Genetic Variants and Serum Levels of 20 Cardiovascular-Related Proteins. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 375-383.	5.1	18
54	Systematic transcriptome analysis reveals tumor-specific isoforms for ovarian cancer diagnosis and therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3050-7.	3.3	64

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55	Consanguinity and rare mutations outside of MCCC genes underlie nonspecific phenotypes of MCCC. <i>Genetics in Medicine</i> , 2015, 17, 660-667.	1.1	9
56	An RNA editing fingerprint of cancer stem cell reprogramming. <i>Journal of Translational Medicine</i> , 2015, 13, 52.	1.8	46
57	Transcriptome Sequencing Reveals Potential Mechanism of Cryptic 3â€™ Splice Site Selection in SF3B1-mutated Cancers. <i>PLoS Computational Biology</i> , 2015, 11, e1004105.	1.5	177
58	BAP1 mutation is a frequent somatic event in peritoneal malignant mesothelioma. <i>Journal of Translational Medicine</i> , 2015, 13, 122.	1.8	69
59	Brief Report: Oxidative Stress Mediates Cardiomyocyte Apoptosis in a Human Model of Danon Disease and Heart Failure. <i>Stem Cells</i> , 2015, 33, 2343-2350.	1.4	74
60	Reversion to an embryonic alternative splicing program enhances leukemia stem cell self-renewal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15444-15449.	3.3	36
61	Mutational Profiling Can Establish Clonal or Independent Origin in Synchronous Bilateral Breast and Other Tumors. <i>PLoS ONE</i> , 2015, 10, e0142487.	1.1	15
62	Network-based analysis identifies epigenetic biomarkers of esophageal squamous cell carcinoma progression. <i>Bioinformatics</i> , 2014, 30, 3054-3061.	1.8	15
63	Homozygous GNAS 393C-Allele Carriers with Locally Advanced Esophageal Cancer Fail to Benefit from Platinum-Based Preoperative Chemoradiotherapy. <i>Annals of Surgical Oncology</i> , 2014, 21, 4375-4382.	0.7	8
64	Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. <i>Genome Biology</i> , 2014, 15, R36.	13.9	71
65	Genetic ancestry of participants in the National Childrenâ€™s Study. <i>Genome Biology</i> , 2014, 15, R22.	13.9	11
66	miR-150 influences B-cell receptor signaling in chronic lymphocytic leukemia by regulating expression of GAB1 and FOXP1. <i>Blood</i> , 2014, 124, 84-95.	0.6	129
67	MiningABs: mining associated biomarkers across multi-connected gene expression datasets. <i>BMC Bioinformatics</i> , 2014, 15, 173.	1.2	1
68	Genome-wide mutational landscape of mucinous carcinomatosis peritonei of appendiceal origin. <i>Genome Medicine</i> , 2014, 6, 43.	3.6	94
69	Biased estimates of clonal evolution and subclonal heterogeneity can arise from PCR duplicates in deep sequencing experiments. <i>Genome Biology</i> , 2014, 15, 420.	3.8	28
70	Effective filtering strategies to improve data quality from population-based whole exome sequencing studies. <i>BMC Bioinformatics</i> , 2014, 15, 125.	1.2	101
71	Whole-Genome Sequencing Uncovers the Genetic Basis of Chronic Mountain Sickness in Andean Highlanders. <i>American Journal of Human Genetics</i> , 2013, 93, 452-462.	2.6	115
72	Identification of Liver Cancer Progenitors Whose Malignant Progression Depends on Autocrine IL-6 Signaling. <i>Cell</i> , 2013, 155, 384-396.	13.5	384

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73	Evaluation of ultra-deep targeted sequencing for personalized breast cancer care. <i>Breast Cancer Research</i> , 2013, 15, R115.	2.2	16
74	A Pan-BCL2 Inhibitor Renders Bone-Marrow-Resident Human Leukemia Stem Cells Sensitive to Tyrosine Kinase Inhibition. <i>Cell Stem Cell</i> , 2013, 12, 316-328.	5.2	167
75	Implementing genomic medicine in the clinic: the future is here. <i>Genetics in Medicine</i> , 2013, 15, 258-267.	1.1	472
76	Implementing Genomic Medicine in the Clinic. <i>Obstetrical and Gynecological Survey</i> , 2013, 68, 621-623.	0.2	1
77	Mutascope: sensitive detection of somatic mutations from deep amplicon sequencing. <i>Bioinformatics</i> , 2013, 29, 1908-1909.	1.8	22
78	ADAR1 promotes malignant progenitor reprogramming in chronic myeloid leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1041-1046.	3.3	148
79	Whole Transcriptome Sequencing Enables Discovery and Analysis of Viruses in Archived Primary Central Nervous System Lymphomas. <i>PLoS ONE</i> , 2013, 8, e73956.	1.1	9
80	High-Resolution Mutational Profiling Suggests the Genetic Validity of Glioblastoma Patient-Derived Pre-Clinical Models. <i>PLoS ONE</i> , 2013, 8, e56185.	1.1	25
81	Transcriptome Sequencing of Tumor Subpopulations Reveals a Spectrum of Therapeutic Options for Squamous Cell Lung Cancer. <i>PLoS ONE</i> , 2013, 8, e58714.	1.1	9
82	Inhibition Of Inflammation Driven Leukemia Stem Cell Self-Renewal With a Selective JAK2 Antagonist. <i>Blood</i> , 2013, 122, 1481-1481.	0.6	0
83	The Role Of CD44 Isoform Expression In Niche Resident Chronic Myeloid Leukemia Stem Cell Evolution. <i>Blood</i> , 2013, 122, 4028-4028.	0.6	0
84	Decoding the human genome. <i>Genome Research</i> , 2012, 22, 1599-1601.	2.4	37
85	Identification of high-confidence somatic mutations in whole genome sequence of formalin-fixed breast cancer specimens. <i>Nucleic Acids Research</i> , 2012, 40, e107-e107.	6.5	78
86	Detection of low prevalence somatic mutations in solid tumors with ultra-deep targeted sequencing. <i>Genome Biology</i> , 2011, 12, R124.	13.9	81
87	9p21 DNA variants associated with coronary artery disease impair interferon- γ signalling response. <i>Nature</i> , 2011, 470, 264-268.	13.7	557
88	Experimental selection of hypoxia-tolerant <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2349-2354.	3.3	105
89	Sensitive gene fusion detection using ambiguously mapping RNA-Seq read pairs. <i>Bioinformatics</i> , 2011, 27, 1068-1075.	1.8	53
90	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. <i>Genetics</i> , 2010, 185, 1081-1095.	1.2	95

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91	Accurate detection and genotyping of SNPs utilizing population sequencing data. <i>Genome Research</i> , 2010, 20, 537-545.	2.4	100
92	Population sequencing of two endocannabinoid metabolic genes identifies rare and common regulatory variants associated with extreme obesity and metabolite level. <i>Genome Biology</i> , 2010, 11, R118.	13.9	34
93	Microdroplet-based PCR enrichment for large-scale targeted sequencing. <i>Nature Biotechnology</i> , 2009, 27, 1025-1031.	9.4	425
94	Elucidating the role of 8q24 in colorectal cancer. <i>Nature Genetics</i> , 2009, 41, 868-869.	9.4	21
95	Human genetic variation and its contribution to complex traits. <i>Nature Reviews Genetics</i> , 2009, 10, 241-251.	7.7	942
96	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12273-12278.	3.3	581
97	Common vs. rare allele hypotheses for complex diseases. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 212-219.	1.5	568
98	Enrichment of sequencing targets from the human genome by solution hybridization. <i>Genome Biology</i> , 2009, 10, R116.	13.9	104
99	Evaluation of next generation sequencing platforms for population targeted sequencing studies. <i>Genome Biology</i> , 2009, 10, R32.	13.9	510
100	Method for improving sequence coverage uniformity of targeted genomic intervals amplified by LR-PCR using Illumina GA sequencing-by-synthesis technology. <i>BioTechniques</i> , 2009, 46, 229-231.	0.8	51
101	Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. <i>Nature Genetics</i> , 2008, 40, 149-151.	9.4	303
102	Genetic determinants of phenotypic diversity in humans. <i>Genome Biology</i> , 2008, 9, 215.	13.9	31
103	The Genomics Gold Rush. <i>JAMA - Journal of the American Medical Association</i> , 2007, 298, 218.	3.8	71
104	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	6.0	689
105	In Vitro Human Keratinocyte Migration Rates Are Associated with SNPs in the KRT1 Interval. <i>PLoS ONE</i> , 2007, 2, e697.	1.1	31
106	The resequencing imperative. <i>Nature Genetics</i> , 2007, 39, 439-440.	9.4	47
107	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. <i>Nature</i> , 2007, 448, 1050-1053.	13.7	406
108	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788

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109	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
110	Evaluation of the SNP tagging approach in an independent population sample—array-based SNP discovery in Sami. <i>Human Genetics</i> , 2007, 122, 141-150.	1.8	10
111	Common deletions and SNPs are in linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 82-85.	9.4	338
112	Allele-Specific KRT1 Expression Is a Complex Trait. <i>PLoS Genetics</i> , 2006, 2, e93.	1.5	64
113	Analysis of allelic differential expression in human white blood cells. <i>Genome Research</i> , 2006, 16, 331-339.	2.4	134
114	Fine-scale recombination patterns differ between chimpanzees and humans. <i>Nature Genetics</i> , 2005, 37, 429-434.	9.4	263
115	High-Resolution Whole-Genome Association Study of Parkinson Disease. <i>American Journal of Human Genetics</i> , 2005, 77, 685-693.	2.6	479
116	Variation in conserved non-coding sequences on chromosome 5q and susceptibility to asthma and atopy. <i>Respiratory Research</i> , 2005, 6, 145.	1.4	43
117	Whole-Genome Patterns of Common DNA Variation in Three Human Populations. <i>Science</i> , 2005, 307, 1072-1079.	6.0	1,074
118	Noncoding Sequences Conserved in a Limited Number of Mammals in the SIM2 Interval are Frequently Functional. <i>Genome Research</i> , 2004, 14, 367-372.	2.4	73
119	Segmental Phylogenetic Relationships of Inbred Mouse Strains Revealed by Fine-Scale Analysis of Sequence Variation Across 4.6 Mb of Mouse Genome. <i>Genome Research</i> , 2004, 14, 1493-1500.	2.4	78
120	VISTA: computational tools for comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, W273-W279.	6.5	2,033
121	Application of pooled genotyping to scan candidate regions for association with HDL cholesterol levels. <i>Human Genomics</i> , 2004, 1, 421.	1.4	83
122	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12.	2.4	210
123	Genomic DNA Insertions and Deletions Occur Frequently Between Humans and Nonhuman Primates. <i>Genome Research</i> , 2003, 13, 341-346.	2.4	81
124	Blocks of Limited Haplotype Diversity Revealed by High-Resolution Scanning of Human Chromosome 21. <i>Science</i> , 2001, 294, 1719-1723.	6.0	1,082
125	Faithful Expression of the Human 5q31 Cytokine Cluster in Transgenic Mice. <i>Journal of Immunology</i> , 2000, 164, 4569-4574.	0.4	23
126	PipMaker—A Web Server for Aligning Two Genomic DNA Sequences. <i>Genome Research</i> , 2000, 10, 577-586.	2.4	1,070

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127	Active Conservation of Noncoding Sequences Revealed by Three-Way Species Comparisons. <i>Genome Research</i> , 2000, 10, 1304-1306.	2.4	279
128	Functional screening of an asthma QTL in YAC transgenic mice. <i>Nature Genetics</i> , 1999, 23, 241-244.	9.4	64
129	Photoreceptor Localization of the KIF3A and KIF3B Subunits of the Heterotrimeric Microtubule Motor Kinesin II in Vertebrate Retina. <i>Experimental Eye Research</i> , 1999, 69, 491-503.	1.2	44
130	Computational and Biological Analysis of 680 kb of DNA Sequence from the Human 5q31 Cytokine Gene Cluster Region. <i>Genome Research</i> , 1997, 7, 495-512.	2.4	124
131	The apolipoprotein(a) gene is regulated by sex hormones and acute phase inducers in YAC transgenic mice. <i>Nature Genetics</i> , 1995, 9, 424-431.	9.4	120
132	A radiation hybrid map of the region on human chromosome 22 containing the neurofibromatosis type 2 locus. <i>Genomics</i> , 1992, 14, 574-584.	1.3	25