

Matti Kankainen

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

3,659
citations

172207

29
h-index

149479

56
g-index

91
all docs

91
docs citations

91
times ranked

5830
citing authors

#	ARTICLE	IF	CITATIONS
1	Somatic <math>STAT3</math> mutations in CD8 ⁺ T cells of healthy blood donors carrying human T-cell leukemia virus type 2. <i>Haematologica</i> , 2022, 107, 550-554.	1.7	11
2	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 388-401.	7.7	73
3	T and NK cell abundance defines two distinct subgroups of renal cell carcinoma. <i>OncImmunology</i> , 2022, 11, 1993042.	2.1	16
4	Oncolytic adenovirus decreases the proportion of TIM-3 ⁺ subset of tumor-infiltrating CD8 ⁺ T cells with correlation to improved survival in patients with cancer. , 2022, 10, e003490.		10
5	Targeting Apoptosis Pathways With BCL2 and MDM2 Inhibitors in Adult B-cell Acute Lymphoblastic Leukemia. <i>HemaSphere</i> , 2022, 6, e701.	1.2	4
6	Single-cell characterization of leukemic and non-leukemic immune repertoires in CD8+ T-cell large granular lymphocytic leukemia. <i>Nature Communications</i> , 2022, 13, 1981.	5.8	23
7	Epigenetic modifier gene mutations in chronic myeloid leukemia (CML) at diagnosis are associated with risk of relapse upon treatment discontinuation. <i>Blood Cancer Journal</i> , 2022, 12, 69.	2.8	10
8	Copy number alterations define outcome in Philadelphia chromosomepositive acute lymphoblastic leukemia. <i>Haematologica</i> , 2022, , .	1.7	1
9	Metatranscriptomic assessment of burn wound infection clearance. <i>Clinical Microbiology and Infection</i> , 2021, 27, 144-146.	2.8	4
10	RUNX1 mutations in blast-phase chronic myeloid leukemia associate with distinct phenotypes, transcriptional profiles, and drug responses. <i>Leukemia</i> , 2021, 35, 1087-1099.	3.3	32
11	CD73 contributes to anti-inflammatory properties of afferent lymphatic endothelial cells in humans and mice. <i>European Journal of Immunology</i> , 2021, 51, 231-246.	1.6	12
12	Comparison of Structural and Short Variants Detected by Linked-Read and Whole-Exome Sequencing in Multiple Myeloma. <i>Cancers</i> , 2021, 13, 1212.	1.7	5
13	Somatic mutations in lymphocytes in patients with immune-mediated aplastic anemia. <i>Leukemia</i> , 2021, 35, 1365-1379.	3.3	41
14	Mutational landscape of chronic myeloid leukemia: more than a single oncogene leukemia. <i>Leukemia and Lymphoma</i> , 2021, 62, 2064-2078.	0.6	15
15	STAT3 activation in large granular lymphocyte leukemia is associated with cytokine signaling and DNA hypermethylation. <i>Leukemia</i> , 2021, 35, 3430-3443.	3.3	20
16	Cancer-Associated Fibroblasts Modulate Transcriptional Signatures Involved in Proliferation, Differentiation and Metastasis in Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2021, 13, 3361.	1.7	16
17	Vascular adhesion protein-1 defines a unique subpopulation of human hematopoietic stem cells and regulates their proliferation. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 7851-7872.	2.4	1
18	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , 2020, 11, 5070.	5.8	44

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19	KIT pathway upregulation predicts dasatinib efficacy in acute myeloid leukemia. <i>Leukemia</i> , 2020, 34, 2780-2784.	3.3	6
20	Characterization of p190-Bcr-Abl chronic myeloid leukemia reveals specific signaling pathways and therapeutic targets. <i>Leukemia</i> , 2020, 35, 1964-1975.	3.3	35
21	Genomics of asthma, allergy and chronic rhinosinusitis: novel concepts and relevance in airway mucosa. <i>Clinical and Translational Allergy</i> , 2020, 10, 45.	1.4	26
22	Adult-Onset Anti-Citrullinated Peptide Antibody-Negative Destructive Rheumatoid Arthritis Is Characterized by a Disease-Specific CD8+ T Lymphocyte Signature. <i>Frontiers in Immunology</i> , 2020, 11, 578848.	2.2	11
23	Somatic mTOR mutation in clonally expanded T lymphocytes associated with chronic graft versus host disease. <i>Nature Communications</i> , 2020, 11, 2246.	5.8	20
24	Neutralizing natural anti-IL-17F autoantibodies protect Autoimmune Polyendocrine Syndrome Type 1 (APS-1) patients from asthma. <i>Clinical Immunology</i> , 2020, 219, 108512.	1.4	3
25	Immunogenomic Landscape of Hematological Malignancies. <i>Cancer Cell</i> , 2020, 38, 380-399.e13.	7.7	109
26	Somatic mutations and T-cell clonality in patients with immunodeficiency. <i>Haematologica</i> , 2020, 105, 2757-2768.	1.7	18
27	Integrated drug profiling and CRISPR screening identify essential pathways for CAR T-cell cytotoxicity. <i>Blood</i> , 2020, 135, 597-609.	0.6	134
28	Mutation accumulation in cancer genes relates to nonoptimal outcome in chronic myeloid leukemia. <i>Blood Advances</i> , 2020, 4, 546-559.	2.5	36
29	Hierarchical clustering in evaluating inflammatory upper airway phenotypes; increased symptoms in adults with allergic multimorbidity. <i>Asian Pacific Journal of Allergy and Immunology</i> , 2020, 38, 239-250.	0.2	3
30	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. <i>Npj Systems Biology and Applications</i> , 2019, 5, 20.	1.4	32
31	Donor Simvastatin Treatment in Heart Transplantation. <i>Circulation</i> , 2019, 140, 627-640.	1.6	24
32	Birch pollen allergen immunotherapy reprograms nasal epithelial transcriptome and recovers microbial diversity. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2293-2296.e11.	1.5	11
33	Exome Sequencing Identifies Susceptibility Loci for Sarcoidosis Prognosis. <i>Frontiers in Immunology</i> , 2019, 10, 2964.	2.2	13
34	CRISPR Screens Identify Mechanisms of Natural Killer Cell Evasion across Blood Cancers. <i>Blood</i> , 2019, 134, 3597-3597.	0.6	3
35	Aggressive natural killer-cell leukemia—mutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. <i>Nature Communications</i> , 2018, 9, 1567.	5.8	107
36	P1606 Blood transcriptome profiling in suspected cardiac sarcoidosis. <i>European Heart Journal</i> , 2018, 39, .	1.0	0

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37	Characterizing the Key Metabolic Pathways of the Neonatal Mouse Heart Using a Quantitative Combinatorial Omics Approach. <i>Frontiers in Physiology</i> , 2018, 9, 365.	1.3	34
38	Association of tamoxifen resistance and lipid reprogramming in breast cancer. <i>BMC Cancer</i> , 2018, 18, 850.	1.1	113
39	Somatic Mutations in T Cells As Possible Regulators of Immunodeficiency. <i>Blood</i> , 2018, 132, 515-515.	0.6	1
40	RUNX1 Mutations Identify an Entity of Blast Phase Chronic Myeloid Leukemia (BP-CML) Patients with Distinct Phenotype, Transcriptional Profile and Drug Vulnerabilities. <i>Blood</i> , 2018, 132, 4257-4257.	0.6	6
41	Interleukin 8 activity influences the efficacy of adenoviral oncolytic immunotherapy in cancer patients. <i>Oncotarget</i> , 2018, 9, 6320-6335.	0.8	10
42	Genome-Scale CRISPR Screens Identify Essential Genes for Sensitivity to Natural Killer Cells in Hematological Malignancies. <i>Blood</i> , 2018, 132, 732-732.	0.6	0
43	Systematic drug sensitivity testing reveals synergistic growth inhibition by dasatinib or mTOR inhibitors with paclitaxel in ovarian granulosa cell tumor cells. <i>Gynecologic Oncology</i> , 2017, 144, 621-630.	0.6	26
44	Functional genomics provides insights into the role of <i>Propionibacterium freudenreichii</i> ssp. <i>shermanii</i> JS in cheese ripening. <i>International Journal of Food Microbiology</i> , 2017, 241, 39-48.	2.1	19
45	The impact of RNA sequence library construction protocols on transcriptomic profiling of leukemia. <i>BMC Genomics</i> , 2017, 18, 629.	1.2	42
46	<i>Fusarium</i> mycotoxin enniatin B: Cytotoxic effects and changes in gene expression profile. <i>Toxicology in Vitro</i> , 2016, 34, 309-320.	1.1	20
47	Phase I study with ONCOS-102 for the treatment of solid tumors – an evaluation of clinical response and exploratory analyses of immune markers. , 2016, 4, 17.		155
48	Chronic Activation of Innate Immunity Correlates With Poor Prognosis in Cancer Patients Treated With Oncolytic Adenovirus. <i>Molecular Therapy</i> , 2016, 24, 175-183.	3.7	26
49	Pseudoexons provide a mechanism for allele-specific expression of <i>APC</i> in familial adenomatous polyposis. <i>Oncotarget</i> , 2016, 7, 70685-70698.	0.8	17
50	Mutational Landscape of Aggressive Natural Killer Cell Leukemia and Drug Sensitivity Profiling Reveal Therapeutic Options in Natural Killer Cell Malignancies. <i>Blood</i> , 2016, 128, 2921-2921.	0.6	0
51	Novel Mutations in Patients with Blast Crisis or Accelerated Phase Chronic Myeloid Leukemia. <i>Blood</i> , 2016, 128, 1924-1924.	0.6	0
52	Loss of <i>Rad51c</i> accelerates tumorigenesis in sebaceous glands of <i>Trp53</i> mutant mice. <i>Journal of Pathology</i> , 2015, 235, 136-146.	2.1	9
53	Comparative Analysis of Whole-Genome Sequences of Influenza A(H1N1)pdm09 Viruses Isolated from Hospitalized and Nonhospitalized Patients Identifies Missense Mutations That Might Be Associated with Patient Hospital Admissions in Finland during 2009 to 2014. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
54	Genome-Wide Analysis of Evolutionary Markers of Human Influenza A(H1N1)pdm09 and A(H3N2) Viruses May Guide Selection of Vaccine Strain Candidates. <i>Genome Biology and Evolution</i> , 2015, 7, 3472-3483.	1.1	23

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55	Repeated intratumoral administration of ONCOS-102 leads to systemic antitumor CD8 ⁺ T-cell response and robust cellular and transcriptional immune activation at tumor site in a patient with ovarian cancer. <i>Oncolmmunology</i> , 2015, 4, e1017702.	2.1	46
56	Immunological data from cancer patients treated with Ad5/3-E2F- β 24-GMCSF suggests utility for tumor immunotherapy. <i>Oncotarget</i> , 2015, 6, 4467-4481.	0.8	63
57	Local treatment of a pleural mesothelioma tumor with ONCOS-102 induces a systemic antitumor CD8 ⁺ T-cell response, prominent infiltration of CD8 ⁺ lymphocytes and Th1 type polarization. <i>Oncolmmunology</i> , 2014, 3, e958937.	2.1	39
58	Comparative genomics of <i>Lactobacillus crispatus</i> suggests novel mechanisms for the competitive exclusion of <i>Gardnerella vaginalis</i> . <i>BMC Genomics</i> , 2014, 15, 1070.	1.2	101
59	Comparative proteome profiling of bovine and human <i>Staphylococcus epidermidis</i> strains for screening specifically expressed virulence and adaptation proteins. <i>Proteomics</i> , 2014, 14, 1890-1894.	1.3	7
60	Genomics and Proteomics Provide New Insight into the Commensal and Pathogenic Lifestyles of Bovine- and Human-Associated <i>Staphylococcus epidermidis</i> Strains. <i>Journal of Proteome Research</i> , 2014, 13, 3748-3762.	1.8	16
61	Comparative Exoprotein Profiling of Different <i>Staphylococcus epidermidis</i> Strains Reveals Potential Link between Nonclassical Protein Export and Virulence. <i>Journal of Proteome Research</i> , 2014, 13, 3249-3261.	1.8	17
62	Gene expression analysis of tumors demonstrates an induction of Th1 type immune response following intratumoral administration of ONCOS-102 in refractory solid tumor patients. , 2014, 2, P230.		1
63	Effects of ellagitannin-rich berries on blood lipids, gut microbiota, and urolithin production in human subjects with symptoms of metabolic syndrome. <i>Molecular Nutrition and Food Research</i> , 2013, 57, 2258-2263.	1.5	93
64	Nonpathogenic <i>Lactobacillus rhamnosus</i> activates the inflammasome and antiviral responses in human macrophages. <i>Gut Microbes</i> , 2012, 3, 510-522.	4.3	49
65	Systems-level analysis of clinically different phenotypes of juvenile nasopharyngeal angiofibromas. <i>Laryngoscope</i> , 2012, 122, 2728-2735.	1.1	7
66	BLANNOTATOR: enhanced homology-based function prediction of bacterial proteins. <i>BMC Bioinformatics</i> , 2012, 13, 33.	1.2	12
67	Effect of acid stress on protein expression and phosphorylation in <i>Lactobacillus rhamnosus</i> GG. <i>Journal of Proteomics</i> , 2012, 75, 1357-1374.	1.2	130
68	Comparative Proteome Cataloging of <i>Lactobacillus rhamnosus</i> Strains GG and Lc705. <i>Journal of Proteome Research</i> , 2011, 10, 3460-3473.	1.8	53
69	Growth phase-associated changes in the proteome and transcriptome of <i>Lactobacillus rhamnosus</i> GG in industrial-type whey medium. <i>Microbial Biotechnology</i> , 2011, 4, 746-766.	2.0	77
70	Adhesive polypeptides of <i>Staphylococcus aureus</i> identified using a novel secretion library technique in <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2011, 11, 117.	1.3	6
71	Identification of regulatory elements in the <i>AGT1</i> promoter of ale and lager strains of brewer's yeast. <i>Yeast</i> , 2011, 28, 579-594.	0.8	24
72	Proteomics and Transcriptomics Characterization of Bile Stress Response in Probiotic <i>Lactobacillus rhamnosus</i> GG. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S18.	2.5	167

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73	MPEAâ€™ metabolite pathway enrichment analysis. <i>Bioinformatics</i> , 2011, 27, 1878-1879.	1.8	85
74	Probiotic <i>Lactobacillus rhamnosus</i> downregulates FCER1 and HRH4 expression in human mast cells. <i>World Journal of Gastroenterology</i> , 2011, 17, 750.	1.4	63
75	Mucosal Adhesion Properties of the Probiotic <i>Lactobacillus rhamnosus</i> GG SpaCBA and SpaFED Pilin Subunits. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2049-2057.	1.4	189
76	Genome Sequence of <i>Lactobacillus crispatus</i> ST1. <i>Journal of Bacteriology</i> , 2010, 192, 3547-3548.	1.0	38
77	LOCPâ€™ locating pilus operons in Gram-positive bacteria. <i>Bioinformatics</i> , 2009, 25, 1187-1188.	1.8	8
78	Proteome Analysis of <i>Lactobacillus rhamnosus</i> GG Using 2-D DIGE and Mass Spectrometry Shows Differential Protein Production in Laboratory and Industrial-Type Growth Media. <i>Journal of Proteome Research</i> , 2009, 8, 4993-5007.	1.8	56
79	Comparative genomic analysis of <i>Lactobacillus rhamnosus</i> GG reveals pili containing a human-mucus binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17193-17198.	3.3	654
80	Regulation of xylose metabolism in recombinant <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2008, 7, 18.	1.9	86
81	MATLIGN: a motif clustering, comparison and matching tool. <i>BMC Bioinformatics</i> , 2007, 8, 189.	1.2	21
82	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2006, 34, e124-e124.	6.5	13
83	POXO: a web-enabled tool series to discover transcription factor binding sites. <i>Nucleic Acids Research</i> , 2006, 34, W534-W540.	6.5	10
84	POCO: discovery of regulatory patterns from promoters of oppositely expressed gene sets. <i>Nucleic Acids Research</i> , 2005, 33, W427-W431.	6.5	17
85	POBO, transcription factor binding site verification with bootstrapping. <i>Nucleic Acids Research</i> , 2004, 32, W222-W229.	6.5	49
86	DANCER: a program for digital anatomical reconstruction of gene expression data. <i>Nucleic Acids Research</i> , 2003, 31, 132e-132.	6.5	0