Matti Kankainen

List of Publications by Year
in descending order

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	Comparative genomic analysis of *Lactobacillus rhamnosus* GG reveals pili containing a human-mucus binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17193-17198.	3.3	654
2	Mucosal Adhesion Properties of the Probiotic *Lactobacillus rhamnosus* GG SpaCBA and SpaFED Pilin Subunits. Applied and Environmental Microbiology, 2010, 76, 2049-2057.	1.4	189
3	Proteomics and Transcriptomics Characterization of Bile Stress Response in Probiotic Lactobacillus rhamnosus GG. Molecular and Cellular Proteomics, 2011, 10, S1-S18.	2.5	167
4	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
5	Integrated drug profiling and CRISPR screening identify essential pathways for CAR T-cell cytotoxicity. Blood, 2020, 135, 597-609.	0.6	134
6	Effect of acid stress on protein expression and phosphorylation in Lactobacillus rhamnosus GG. Journal of Proteomics, 2012, 75, 1357-1374.	1.2	130
7	Association of tamoxifen resistance and lipid reprogramming in breast cancer. BMC Cancer, 2018, 18, 850.	1.1	113
8	Immunogenomic Landscape of Hematological Malignancies. Cancer Cell, 2020, 38, 380-399.e13.	7.7	109
9	Aggressive natural killer-cell leukemiaÂmutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. Nature Communications, 2018, 9, 1567.	5.8	107
10	Comparative genomics of Lactobacillus crispatus suggests novel mechanisms for the competitive exclusion of Gardnerella vaginalis. BMC Genomics, 2014, 15, 1070.	1.2	101
11	Effects of ellagitannin–rich berries on blood lipids, gut microbiota, and urolithin production in human subjects with symptoms of metabolic syndrome. Molecular Nutrition and Food Research, 2013, 57, 2258-2263.	1.5	93
12	Regulation of xylose metabolism in recombinant Saccharomyces cerevisiae. Microbial Cell Factories, 2008, 7, 18.	1.9	86
13	MPEA–metabolite pathway enrichment analysis. Bioinformatics, 2011, 27, 1878-1879.	1.8	85
14	Growth phase–associated changes in the proteome and transcriptome of *Lactobacillus rhamnosus* GG in industrial–type whey medium. Microbial Biotechnology, 2011, 4, 746-766.	2.0	77
15	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 388-401.	7.7	73
16	Immunological data from cancer patients treated with Ad5/3-E2F-Î"24-GMCSF suggests utility for tumor immunotherapy. Oncotarget, 2015, 6, 4467-4481.	0.8	63
17	ProbioticLactobacillus rhamnosusdownregulatesFCER1andHRH4expression in human mast cells. World Journal of Gastroenterology, 2011, 17, 750.	1.4	63
18	Proteome Analysis of *Lactobacillus rhamnosus* GG Using 2-D DIGE and Mass Spectrometry Shows Differential Protein Production in Laboratory and Industrial-Type Growth Media. Journal of Proteome Research, 2009, 8, 4993-5007.	1.8	56

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19	Comparative Proteome Cataloging of Lactobacillus rhamnosus Strains GG and Lc705. Journal of Proteome Research, 2011, 10, 3460-3473.	1.8	53
20	POBO, transcription factor binding site verification with bootstrapping. Nucleic Acids Research, 2004, 32, W222-W229.	6.5	49
21	Nonpathogenic Lactobacillus rhamnosus activates the inflammasome and antiviral responses in human macrophages. Gut Microbes, 2012, 3, 510-522.	4.3	49
22	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. OncoImmunology, 2015, 4, e1017702.	2.1	46
23	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. Nature Communications, 2020, 11, 5070.	5.8	44
24	The impact of RNA sequence library construction protocols on transcriptomic profiling of leukemia. BMC Genomics, 2017, 18, 629.	1.2	42
25	Somatic mutations in lymphocytes in patients with immune-mediated aplastic anemia. Leukemia, 2021, 35, 1365-1379.	3.3	41
26	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. OncoImmunology, 2014, 3, e958937.	2.1	39
27	Genome Sequence of Lactobacillus crispatus ST1. Journal of Bacteriology, 2010, 192, 3547-3548.	1.0	38
28	Mutation accumulation in cancer genes relates to nonoptimal outcome in chronic myeloid leukemia. Blood Advances, 2020, 4, 546-559.	2.5	36
29	Characterization of p190-Bcr-Abl chronic myeloid leukemia reveals specific signaling pathways and therapeutic targets. Leukemia, 2020, 35, 1964-1975.	3.3	35
30	Characterizing the Key Metabolic Pathways of the Neonatal Mouse Heart Using a Quantitative Combinatorial Omics Approach. Frontiers in Physiology, 2018, 9, 365.	1.3	34
31	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	1.4	32
32	RUNX1 mutations in blast-phase chronic myeloid leukemia associate with distinct phenotypes, transcriptional profiles, and drug responses. Leukemia, 2021, 35, 1087-1099.	3.3	32
33	Chronic Activation of Innate Immunity Correlates With Poor Prognosis in Cancer Patients Treated With Oncolytic Adenovirus. Molecular Therapy, 2016, 24, 175-183.	3.7	26
34	Systematic drug sensitivity testing reveals synergistic growth inhibition by dasatinib or mTOR inhibitors with paclitaxel in ovarian granulosa cell tumor cells. Gynecologic Oncology, 2017, 144, 621-630.	0.6	26
35	Genomics of asthma, allergy and chronic rhinosinusitis: novel concepts and relevance in airway mucosa. Clinical and Translational Allergy, 2020, 10, 45.	1.4	26
36	Identification of regulatory elements in the *AGT1* promoter of ale and lager strains of brewer's yeast. Yeast, 2011, 28, 579-594.	0.8	24

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37	Donor Simvastatin Treatment in Heart Transplantation. Circulation, 2019, 140, 627-640.	1.6	24
38	Genome-Wide Analysis of Evolutionary Markers of Human Influenza A(H1N1)pdm09 and A(H3N2) Viruses May Guide Selection of Vaccine Strain Candidates. Genome Biology and Evolution, 2015, 7, 3472-3483.	1.1	23
39	Single-cell characterization of leukemic and non-leukemic immune repertoires in CD8+ T-cell large granular lymphocytic leukemia. Nature Communications, 2022, 13, 1981.	5.8	23
40	MATLIGN: a motif clustering, comparison and matching tool. BMC Bioinformatics, 2007, 8, 189.	1.2	21
41	Fusarium mycotoxin enniatin B: Cytotoxic effects and changes in gene expression profile. Toxicology in Vitro, 2016, 34, 309-320.	1.1	20
42	Somatic mTOR mutation in clonally expanded T lymphocytes associated with chronic graft versus host disease. Nature Communications, 2020, 11, 2246.	5.8	20
43	STAT3 activation in large granular lymphocyte leukemia is associated with cytokine signaling and DNA hypermethylation. Leukemia, 2021, 35, 3430-3443.	3.3	20
44	Functional genomics provides insights into the role of Propionibacterium freudenreichii ssp. shermanii JS in cheese ripening. International Journal of Food Microbiology, 2017, 241, 39-48.	2.1	19
45	Somatic mutations and T-cell clonality in patients with immunodeficiency. Haematologica, 2020, 105, 2757-2768.	1.7	18
46	POCO: discovery of regulatory patterns from promoters of oppositely expressed gene sets. Nucleic Acids Research, 2005, 33, W427-W431.	6.5	17
47	Comparative Exoprotein Profiling of DifferentStaphylococcus epidermidisStrains Reveals Potential Link between Nonclassical Protein Export and Virulence. Journal of Proteome Research, 2014, 13, 3249-3261.	1.8	17
48	Pseudoexons provide a mechanism for allele-specific expression of <i>APC</i> in familial adenomatous polyposis. Oncotarget, 2016, 7, 70685-70698.	0.8	17
49	Genomics and Proteomics Provide New Insight into the Commensal and Pathogenic Lifestyles of Bovine- and Human-Associated <i>Staphylococcus epidermidis</i> Strains. Journal of Proteome Research, 2014, 13, 3748-3762.	1.8	16
50	Cancer-Associated Fibroblasts Modulate Transcriptional Signatures Involved in Proliferation, Differentiation and Metastasis in Head and Neck Squamous Cell Carcinoma. Cancers, 2021, 13, 3361.	1.7	16
51	T and NK cell abundance defines two distinct subgroups of renal cell carcinoma. OncoImmunology, 2022, 11, 1993042.	2.1	16
52	Mutational landscape of chronic myeloid leukemia: more than a single oncogene leukemia. Leukemia and Lymphoma, 2021, 62, 2064-2078.	0.6	15
53	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in Arabidopsis thaliana. Nucleic Acids Research, 2006, 34, e124-e124.	6.5	13
54	Exome Sequencing Identifies Susceptibility Loci for Sarcoidosis Prognosis. Frontiers in Immunology, 2019, 10, 2964.	2.2	13

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55	BLANNOTATOR: enhanced homology-based function prediction of bacterial proteins. BMC Bioinformatics, 2012, 13, 33.	1.2	12
56	CD73 contributes to anti‑inflammatory properties of afferent lymphatic endothelial cells in humans and mice. European Journal of Immunology, 2021, 51, 231-246.	1.6	12
57	Birch pollen allergen immunotherapy reprograms nasal epithelial transcriptome and recovers microbial diversity. Journal of Allergy and Clinical Immunology, 2019, 143, 2293-2296.e11.	1.5	11
58	Adult-Onset Anti-Citrullinated Peptide Antibody-Negative Destructive Rheumatoid Arthritis Is Characterized by a Disease-Specific CD8+ T Lymphocyte Signature. Frontiers in Immunology, 2020, 11, 578848.	2.2	11
59	Somatic <I>STAT3</I> mutations in CD8<sup>+</sup> T cells of healthy blood donors carrying human T-cell leukemia virus type 2. Haematologica, 2022, 107, 550-554.	1.7	11
60	POXO: a web-enabled tool series to discover transcription factor binding sites. Nucleic Acids Research, 2006, 34, W534-W540.	6.5	10
61	Interleukin 8 activity influences the efficacy of adenoviral oncolytic immunotherapy in cancer patients. Oncotarget, 2018, 9, 6320-6335.	0.8	10
62	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
63	Epigenetic modifier gene mutations in chronic myeloid leukemia (CML) at diagnosis are associated with risk of relapse upon treatment discontinuation. Blood Cancer Journal, 2022, 12, 69.	2.8	10
64	Loss of <i>Rad51c</i> accelerates tumourigenesis in sebaceous glands of <i>Trp53</i>‑mutant mice. Journal of Pathology, 2015, 235, 136-146.	2.1	9
65	LOCP—locating pilus operons in Gram-positive bacteria. Bioinformatics, 2009, 25, 1187-1188.	1.8	8
66	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. Genome Announcements, 2015, 3, .	0.8	8
67	Systems‑level analysis of clinically different phenotypes of juvenile nasopharyngeal angiofibromas. Laryngoscope, 2012, 122, 2728-2735.	1.1	7
68	Comparative proteome profiling of bovine and human <i>Staphylococcus epidermidis</i> strains for screening specifically expressed virulence and adaptation proteins. Proteomics, 2014, 14, 1890-1894.	1.3	7
69	Adhesive polypeptides of Staphylococcus aureus identified using a novel secretion library technique in Escherichia coli. BMC Microbiology, 2011, 11, 117.	1.3	6
70	KIT pathway upregulation predicts dasatinib efficacy in acute myeloid leukemia. Leukemia, 2020, 34, 2780-2784.	3.3	6
71	RUNX1 Mutations Identify an Entity of Blast Phase Chronic Myeloid Leukemia (BP-CML) Patients with Distinct Phenotype, Transcriptional Profile and Drug Vulnerabilities. Blood, 2018, 132, 4257-4257.	0.6	6
72	Comparison of Structural and Short Variants Detected by Linked-Read and Whole-Exome Sequencing in Multiple Myeloma. Cancers, 2021, 13, 1212.	1.7	5

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73	Metatranscriptomic assessment of burn wound infection clearance. Clinical Microbiology and Infection, 2021, 27, 144-146.	2.8	4
74	Targeting Apoptosis Pathways With BCL2 and MDM2 Inhibitors in Adult B-cell Acute Lymphoblastic Leukemia. HemaSphere, 2022, 6, e701.	1.2	4
75	Neutralizing natural anti-IL-17F autoantibodies protect Autoimmune Polyendocrine Syndrome Type 1 (APS-1) patients from asthma. Clinical Immunology, 2020, 219, 108512.	1.4	3
76	Hierarchical clustering in evaluating inflammatory upper airway phenotypes; increased symptoms in adults with allergic multimorbidity. Asian Pacific Journal of Allergy and Immunology, 2020, 38, 239-250.	0.2	3
77	CRISPR Screens Identify Mechanisms of Natural Killer Cell Evasion across Blood Cancers. Blood, 2019, 134, 3597-3597.	0.6	3
78	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
79	Somatic Mutations in T Cells As Possible Regulators of Immunodeficiency. Blood, 2018, 132, 515-515.	0.6	1
80	Vascular adhesion protein-1 defines a unique subpopulation of human hematopoietic stem cells and regulates their proliferation. Cellular and Molecular Life Sciences, 2021, 78, 7851-7872.	2.4	1
81	Copy number alterations define outcome in Philadelphia chromosomepositive acute lymphoblastic leukemia. Haematologica, 2022, , .	1.7	1
82	DANCER: a program for digital anatomical reconstruction of gene expression data. Nucleic Acids Research, 2003, 31, 132e-132.	6.5	0
83	P1606Blood transcriptome profiling in suspected cardiac sarcoidosis. European Heart Journal, 2018, 39, .	1.0	0
84	Mutational Landscape of Aggressive Natural Killer Cell Leukemia and Drug Sensitivity Profiling Reveal Therapeutic Options in Natural Killer Cell Malignancies. Blood, 2016, 128, 2921-2921.	0.6	0
85	Novel Mutations in Patients with Blast Crisis or Accelerated Phase Chronic Myeloid Leukemia. Blood, 2016, 128, 1924-1924.	0.6	0
86	Genome-Scale CRISPR Screens Identify Essential Genes for Sensitivity to Natural Killer Cells in Hematological Malignancies. Blood, 2018, 132, 732-732.	0.6	0