Rudolf S N Fehrmann

List of Publications by Year
in descending order

97	16,433	81839 39	46771 89
papers	citations	h-index	g-index

104	104	104	30598
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
3	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
4	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
5	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	9.4	871
6	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
7	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
8	Evidence Based Selection of Housekeeping Genes. PLoS ONE, 2007, 2, e898.	1.1	617
9	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	1.5	324
10	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	9.4	313
11	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
12	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	1.5	307
13	Relevance of Tumor-Infiltrating Immune Cell Composition and Functionality for Disease Outcome in Breast Cancer. Journal of the National Cancer Institute, 2017, 109, djw192.	3.0	296
14	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	1.5	247
15	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
16	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	1.5	194
17	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	15.2	158
18	Survival-Related Profile, Pathways, and Transcription Factors in Ovarian Cancer. PLoS Medicine, 2009, 6, e1000024.	3.9	156

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19	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	4.1	134
20	Immune microenvironment composition in nonâ€small cell lung cancer and its association with survival. Clinical and Translational Immunology, 2020, 9, e1142.	1.7	119
21	mRNA-1273 COVID-19 vaccination in patients receiving chemotherapy, immunotherapy, or chemoimmunotherapy for solid tumours: a prospective, multicentre, non-inferiority trial. Lancet Oncology, The, 2021, 22, 1681-1691.	5.1	118
22	MAPK pathway activity plays a key role in PDâ€L1 expression of lung adenocarcinoma cells. Journal of Pathology, 2019, 249, 52-64.	2.1	117
23	Involvement of the TGF-Î² and Î²-Catenin Pathways in Pelvic Lymph Node Metastasis in Early-Stage Cervical Cancer. Clinical Cancer Research, 2011, 17, 1317-1330.	3.2	113
24	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL , and CARD9. Hepatology, 2011, 53, 1977-1985.	3.6	110
25	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	9.4	96
26	BRCA2 deficiency instigates cGAS-mediated inflammatory signaling and confers sensitivity to tumor necrosis factor-alpha-mediated cytotoxicity. Nature Communications, 2019, 10, 100.	5.8	91
27	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. Thorax, 2015, 70, 21-32.	2.7	89
28	Theranostics Using Antibodies and Antibody-Related Therapeutics. Journal of Nuclear Medicine, 2017, 58, 83S-90S.	2.8	85
29	Perioperative systemic therapy and cytoreductive surgery with HIPEC versus upfront cytoreductive surgery with HIPEC alone for isolated resectable colorectal peritoneal metastases: protocol of a multicentre, open-label, parallel-group, phase II-III, randomised, superiority study (CAIRO6). BMC Cancer, 2019, 19, 390.	1.1	83
30	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. Bioinformatics, 2011, 27, 2104-2111.	1.8	81
31	ATR inhibition preferentially targets homologous recombination-deficient tumor cells. Oncogene, 2015, 34, 3474-3481.	2.6	80
32	Molecular imaging biomarkers for immune checkpoint inhibitor therapy. Theranostics, 2020, 10, 1708-1718.	4.6	68
33	Consideration of breast cancer subtype in targeting the androgen receptor. , 2019, 200, 135-147.		65
34	Profiling Studies in Ovarian Cancer: A Review. Oncologist, 2007, 12, 960-966.	1.9	63
35	Current smokingâ€specific gene expression signature in normal bronchial epithelium is enhanced in squamous cell lung cancer. Journal of Pathology, 2009, 218, 182-191.	2.1	63
36	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59

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37	Regulators of homologous recombination repair as novel targets for cancer treatment. Frontiers in Genetics, 2015, 6, 96.	1.1	58
38	COVID-19 vaccination: the VOICE for patients with cancer. Nature Medicine, 2021, 27, 568-569.	15.2	53
39	Transcriptional effects of copy number alterations in a large set of human cancers. Nature Communications, 2020, 11, 715.	5.8	53
40	Identification of genes and pathways associated with cytotoxic T lymphocyte infiltration of serous ovarian cancer. British Journal of Cancer, 2010, 103, 685-692.	2.9	43
41	TPX2/Aurora kinase A signaling as a potential therapeutic target in genomically unstable cancer cells. Oncogene, 2019, 38, 852-867.	2.6	43
42	Polygenic scores associated with educational attainment in adults predict educational achievement and ADHD symptoms in children. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 510-520.	1.1	40
43	The antibodyâ€“drug conjugate target landscape across a broad range of tumour types. Annals of Oncology, 2017, 28, 3083-3091.	0.6	40
44	Clinical utility of circulating tumor DNA as a response and follow-up marker in cancer therapy. Cancer and Metastasis Reviews, 2020, 39, 999-1013.	2.7	38
45	Overexpression of Cyclin E1 or Cdc25A leads to replication stress, mitotic aberrancies, and increased sensitivity to replication checkpoint inhibitors. Oncogenesis, 2020, 9, 88.	2.1	37
46	Growth Differentiation Factor 15 (GDF-15) Plasma Levels Increase during Bleomycin- and Cisplatin-Based Treatment of Testicular Cancer Patients and Relate to Endothelial Damage. PLoS ONE, 2015, 10, e0115372.	1.1	37
47	Integrative Kinome Profiling Identifies mTORC1/2 Inhibition as Treatment Strategy in Ovarian Clear Cell Carcinoma. Clinical Cancer Research, 2018, 24, 3928-3940.	3.2	35
48	Serotonin and Dopamine Receptor Expression in Solid Tumours Including Rare Cancers. Pathology and Oncology Research, 2020, 26, 1539-1547.	0.9	35
49	89Zr-labeled Bispecific T-cell Engager AMG 211 PET Shows AMG 211 Accumulation in CD3-rich Tissues and Clear, Heterogeneous Tumor Uptake. Clinical Cancer Research, 2019, 25, 3517-3527.	3.2	34
50	Perioperative Systemic Therapy vs Cytoreductive Surgery and Hyperthermic Intraperitoneal Chemotherapy Alone for Resectable Colorectal Peritoneal Metastases. JAMA Surgery, 2021, 156, 710-720.	2.2	34
51	Extraintestinal Manifestations and Complications in Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2014, 20, 1.	0.9	31
52	Glypican 3 Overexpression across a Broad Spectrum of Tumor Types Discovered with Functional Genomic mRNA Profiling of a Large CancerÂDatabase. American Journal of Pathology, 2018, 188, 1973-1981.	1.9	30
53	Application of a comprehensive subtelomere array in clinical diagnosis of mental retardation. European Journal of Medical Genetics, 2005, 48, 250-262.	0.7	29
54	CD47 Expression Defines Efficacy of Rituximab with CHOP in Nonâ€“Germinal Center B-cell (Non-GCB) Diffuse Large B-cell Lymphoma Patients (DLBCL), but Not in GCB DLBCL. Cancer Immunology Research, 2019, 7, 1663-1671.	1.6	28

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55	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	1.4	27
56	Cyclin E expression is associated with high levels of replication stress in triple-negative breast cancer. Npj Breast Cancer, 2020, 6, 40.	2.3	27
57	Defining the risk of toxicity in phase I oncology trials of novel molecularly targeted agents: a single centre experience. Annals of Oncology, 2012, 23, 1968-1973.	0.6	26
58	Cancer cell-expressed SLAMF7 is not required for CD47-mediated phagocytosis. Nature Communications, 2019, 10, 533.	5.8	26
59	A bioinformatical and functional approach to identify novel strategies for chemoprevention of colorectal cancer. Oncogene, 2011, 30, 2026-2036.	2.6	22
60	Functional Genomic mRNA Profiling of a large cancer data base demonstrates mesothelin overexpression in a broad range of tumor types. Oncotarget, 2015, 6, 28164-28172.	0.8	22
61	Gallbladder Cancer: Current Insights in Genetic Alterations and Their Possible Therapeutic Implications. Cancers, 2021, 13, 5257.	1.7	22
62	Improving gene function predictions using independent transcriptional components. Nature Communications, 2021, 12, 1464.	5.8	20
63	Identification of relevant drugable targets in diffuse large B-cell lymphoma using a genome-wide unbiased CD20 guilt-by association approach. PLoS ONE, 2018, 13, e0193098.	1.1	20
64	Immunogenicity after second and third mRNA-1273 vaccination doses in patients receiving chemotherapy, immunotherapy, or both for solid tumours. Lancet Oncology, The, 2022, 23, 833-835.	5.1	18
65	An mRNA expression-based signature for oncogene-induced replication-stress. Oncogene, 2022, 41, 1216-1224.	2.6	17
66	Identification of novel therapeutic targets in anaplastic thyroid carcinoma using functional genomic mRNA-profiling: Paving the way for new avenues?. Surgery, 2017, 161, 202-211.	1.0	16
67	Treatment with high-dose simvastatin inhibits geranylgeranylation in AML blast cells in a subset of AML patients. Experimental Hematology, 2012, 40, 177-186.e6.	0.2	15
68	Comparison of Carboplatin With 5-Fluorouracil vs. Cisplatin as Concomitant Chemoradiotherapy for Locally Advanced Head and Neck Squamous Cell Carcinoma. Frontiers in Oncology, 2020, 10, 761.	1.3	14
69	Considering the biology of late recurrences in selecting patients for extended endocrine therapy in breast cancer. Cancer Treatment Reviews, 2018, 70, 118-126.	3.4	13
70	Transcriptional Activity and Stability of CD39+CD103+CD8+ T Cells in Human High-Grade Endometrial Cancer. International Journal of Molecular Sciences, 2020, 21, 3770.	1.8	13
71	A New Perspective on Transcriptional System Regulation (TSR): Towards TSR Profiling. PLoS ONE, 2008, 3, e1656.	1.1	11
72	A retrospective analysis of clinical outcome of patients with chemo-refractory metastatic breast cancer treated in a single institution phase I unit. British Journal of Cancer, 2010, 103, 607-612.	2.9	11

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73	Quantitative proteomics analysis identifies MUC1 as an effect sensor of EGFR inhibition. Oncogene, 2019, 38, 1477-1488.	2.6	11
74	Functional Genomic mRNA Profiling of Colorectal Adenomas: Identification and in vivo Validation of CD44 and Splice Variant CD44v6 as Molecular Imaging Targets. Theranostics, 2017, 7, 482-492.	4.6	10
75	Data-Driven Prioritization and Review of Targets for Molecular-Based Theranostic Approaches in Pancreatic Cancer. Journal of Nuclear Medicine, 2017, 58, 1899-1903.	2.8	9
76	Intraoperative MET-receptor targeted fluorescent imaging and spectroscopy for lymph node detection in papillary thyroid cancer: novel diagnostic tools for more selective central lymph node compartment dissection. European Journal of Nuclear Medicine and Molecular Imaging, 2022, 49, 3557-3570.	3.3	7
77	Liver glycogen phosphorylase is upregulated in glioblastoma and provides a metabolic vulnerability to high dose radiation. Cell Death and Disease, 2022, 13, .	2.7	6
78	Data-Driven prioritisation of antibody-drug conjugate targets in head and neck squamous cell carcinoma. Oral Oncology, 2018, 80, 33-39.	0.8	5
79	Transcriptional regulators CITED2 and PU.1 cooperate in maintaining hematopoietic stem cells. Experimental Hematology, 2019, 73, 38-49.e7.	0.2	4
80	Genome-wide association study of cardiovascular disease in testicular cancer patients treated with platinum-based chemotherapy. Pharmacogenomics Journal, 2021, 21, 152-164.	0.9	4
81	Robust metabolic transcriptional components in 34,494 patient-derived cancer-related samples and cell lines. Cancer & Metabolism, 2021, 9, 35.	2.4	4
82	Validation of Novel Molecular Imaging Targets Identified by Functional Genomic mRNA Profiling to Detect Dysplasia in Barrettâ€™s Esophagus. Cancers, 2022, 14, 2462.	1.7	4
83	Identification and Validation of Esophageal Squamous Cell Carcinoma Targets for Fluorescence Molecular Endoscopy. International Journal of Molecular Sciences, 2021, 22, 9270.	1.8	3
84	Indispensable benefit of independent investigator-driven research in a changing clinical trial landscape. ESMO Open, 2017, 2, e000272.	2.0	2
85	Driving innovation for rare skin cancers: utilizing common tumours and machine learning to predict immune checkpoint inhibitor response. Immuno-Oncology Technology, 2019, 4, 1-7.	0.2	2
86	The gut wallâ€™s potential as a partner for precision oncology in immune checkpoint treatment. Cancer Treatment Reviews, 2022, 107, 102406.	3.4	2
87	Data-driven prioritization and preclinical evaluation of therapeutic targets in glioblastoma. Neuro-Oncology Advances, 2020, 2, vdaa151.	0.4	1
88	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. Annals of the Rheumatic Diseases, 2011, 70, A21-A21.	0.5	0
89	P04.22 Data-driven prioritization and evaluation of novel therapeutic targets in glioblastoma. Neuro-Oncology, 2018, 20, iii283-iii283.	0.6	0
90	A large pooled analysis refines gene expression-based molecular subclasses in cutaneous melanoma. OncoImmunology, 2019, 8, 1558664.	2.1	0

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91	Abstract 161: Discovery of novel methylation-based biomarkers for epithelial ovarian cancer using oligonucleotide microarrays. , 2010, , .		0
92	In Vivo Treatment of AML Patients with High-Dose Simvastatin Inhibits Geranylgeranylation In AML Cells. Blood, 2010, 116, 3280-3280.	0.6	0
93	Abstract 2960: A combined bioinformatics and proteomics approach identifies DNA repair factors regulated by the APC/C. , 2011, , .		0
94	Macrophage inhibitory cytokine 1 plasma levels in testicular cancer patients during cisplatin combination treatment and their relation to endothelial damage.. Journal of Clinical Oncology, 2012, 30, e15035-e15035.	0.8	0
95	Abstract 1315: CtIP is regulated by the APC/C-Cdh1 to mediate cell cycle-dependent control of DNA repair. , 2014, , .		0
96	Abstract 1406: Towards an RNA expression-based signature for oncogene-induced replication stress. , 2017, , .		0
97	CD47 Expression Defines the Efficacy of Rituximab in Non-Germinal Center B-Cell (non-GCB) Diffuse Large B-Cell Lymphoma (DLBCL). Blood, 2018, 132, 2852-2852.	0.6	0