

Jussi Taipale

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

119
papers

20,821
citations

56
h-index

139
g-index

139
ext. papers

24,788
ext. citations

18.6
avg, IF

6.7
L-index

#	Paper	IF	Citations
119	Sequence determinants of human gene regulatory elements.. <i>Nature Genetics</i> , 2022 ,	36.3	2
118	Upregulation of ribosome biogenesis via canonical E-boxes is required for Myc-driven proliferation.. <i>Developmental Cell</i> , 2022 , 57, 1024-1036.e5	10.2	0
117	Rapid genome editing by CRISPR-Cas9-POLD3 fusion.. <i>ELife</i> , 2021 , 10,	8.9	2
116	A comprehensive library of human transcription factors for cell fate engineering. <i>Nature Biotechnology</i> , 2021 , 39, 510-519	44.5	40
115	Transcriptionally active enhancers in human cancer cells. <i>Molecular Systems Biology</i> , 2021 , 17, e9873	12.2	7
114	WNT2 activation through proximal germline deletion predisposes to small intestinal neuroendocrine tumors and intestinal adenocarcinomas. <i>Human Molecular Genetics</i> , 2021 , 30, 2429-2440	5.6	1
113	Human cell transformation by combined lineage conversion and oncogene expression. <i>Oncogene</i> , 2021 , 40, 5533-5547	9.2	1
112	Genetic and Epigenetic Characteristics of Inflammatory Bowel Disease-Associated Colorectal Cancer. <i>Gastroenterology</i> , 2021 , 161, 592-607	13.3	10
111	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. <i>Nature</i> , 2021 , 596, 398-403	50.4	13
110	Parity associates with chromosomal damage in uterine leiomyomas. <i>Nature Communications</i> , 2021 , 12, 5448	17.4	1
109	Structural insights into the interaction between transcription factors and the nucleosome. <i>Current Opinion in Structural Biology</i> , 2021 , 71, 171-179	8.1	0
108	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021 , 591, 147-151	50.4	23
107	CRISPR-assisted detection of RNA-protein interactions in living cells. <i>Nature Methods</i> , 2020 , 17, 685-688	21.6	36
106	MODER2: first-order Markov modeling and discovery of monomeric and dimeric binding motifs. <i>Bioinformatics</i> , 2020 , 36, 2690-2696	7.2	2
105	The transcription factor FLI1 promotes cancer progression by affecting cell cycle regulation. <i>International Journal of Cancer</i> , 2020 , 147, 189-201	7.5	7
104	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. <i>Genome Research</i> , 2020 , 30, 962-973	9.7	16
103	Nucleosome-bound SOX2 and SOX11 structures elucidate pioneer factor function. <i>Nature</i> , 2020 , 580, 669-672	50.4	63

102	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. <i>Nature Communications</i> , 2019 , 10, 1252	17.4	40
101	Gain-of-function CEBPE mutation causes noncanonical autoinflammatory inflammasomopathy. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 144, 1364-1376	11.5	20
100	Reply to "CRISPR screens are feasible in TP53 wild-type cells". <i>Molecular Systems Biology</i> , 2019 , 15, e90592.2	5	5
99	Informational limits of biological organisms. <i>EMBO Journal</i> , 2018 , 37,	13	3
98	Modular discovery of monomeric and dimeric transcription factor binding motifs for large data sets. <i>Nucleic Acids Research</i> , 2018 , 46, e44	20.1	5
97	The Human Transcription Factors. <i>Cell</i> , 2018 , 172, 650-665	56.2	840
96	Comprehensive evaluation of coding region point mutations in microsatellite-unstable colorectal cancer. <i>EMBO Molecular Medicine</i> , 2018 , 10,	12	6
95	CRISPR-Cas9 genome editing induces a p53-mediated DNA damage response. <i>Nature Medicine</i> , 2018 , 24, 927-930	50.5	555
94	The interaction landscape between transcription factors and the nucleosome. <i>Nature</i> , 2018 , 562, 76-81	50.4	127
93	The chromatin of cancer. <i>Science</i> , 2018 , 362, 401-402	33.3	4
92	Promoter capture Hi-C-based identification of recurrent noncoding mutations in colorectal cancer. <i>Nature Genetics</i> , 2018 , 50, 1375-1380	36.3	33
91	Contribution of allelic imbalance to colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 3664	17.4	11
90	A protein activity assay to measure global transcription factor activity reveals determinants of chromatin accessibility. <i>Nature Biotechnology</i> , 2018 , 36, 521-529	44.5	13
89	Two distinct DNA sequences recognized by transcription factors represent enthalpy and entropy optima. <i>ELife</i> , 2018 , 7,	8.9	17
88	Somatic MED12 Nonsense Mutation Escapes mRNA Decay and Reveals a Motif Required for Nuclear Entry. <i>Human Mutation</i> , 2017 , 38, 269-274	4.7	11
87	Damaging heterozygous mutations in NFKB1 lead to diverse immunologic phenotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 140, 782-796	11.5	69
86	Transcription factor family-specific DNA shape readout revealed by quantitative specificity models. <i>Molecular Systems Biology</i> , 2017 , 13, 910	12.2	66
85	The non-coding variant rs1800734 enhances DCLK3 expression through long-range interaction and promotes colorectal cancer progression. <i>Nature Communications</i> , 2017 , 8, 14418	17.4	34

84	Impact of cytosine methylation on DNA binding specificities of human transcription factors. <i>Science</i> , 2017 , 356,	33.3	514
83	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. <i>Cancer Research</i> , 2017 , 77, 4078-4088	10.1	16
82	Myt1l safeguards neuronal identity by actively repressing many non-neuronal fates. <i>Nature</i> , 2017 , 544, 245-249	50.4	112
81	Structural perspective of cooperative transcription factor binding. <i>Current Opinion in Structural Biology</i> , 2017 , 47, 1-8	8.1	99
80	Genome-wide screen of cell-cycle regulators in normal and tumor cells identifies a differential response to nucleosome depletion. <i>Cell Cycle</i> , 2017 , 16, 189-199	4.7	15
79	CRISPR/Cas9 screening using unique molecular identifiers. <i>Molecular Systems Biology</i> , 2017 , 13, 945	12.2	30
78	Mice deficient of super-enhancer region reveal differential control mechanism between normal and pathological growth. <i>ELife</i> , 2017 , 6,	8.9	30
77	Fast motif matching revisited: high-order PWMs, SNPs and indels. <i>Bioinformatics</i> , 2017 , 33, 514-521	7.2	7
76	DNA-dependent formation of transcription factor pairs alters their binding specificity. <i>Nature</i> , 2016 , 534, S15-S16	50.4	0
75	Multiparameter functional diversity of human C2H2 zinc finger proteins. <i>Genome Research</i> , 2016 , 26, 1742-1752	9.7	76
74	The role of enhancers in cancer. <i>Nature Reviews Cancer</i> , 2016 , 16, 483-93	31.3	201
73	Variation at 2q35 (PNKD and TMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. <i>Human Molecular Genetics</i> , 2016 , 25, 2349-2359	5.6	27
72	Oncogenic Herpesvirus Utilizes Stress-Induced Cell Cycle Checkpoints for Efficient Lytic Replication. <i>PLoS Pathogens</i> , 2016 , 12, e1005424	7.6	24
71	PeakXus: comprehensive transcription factor binding site discovery from ChIP-Nexus and ChIP-Exo experiments. <i>Bioinformatics</i> , 2016 , 32, i629-i638	7.2	8
70	Exome Sequencing of Uterine Leiomyosarcomas Identifies Frequent Mutations in TP53, ATRX, and MED12. <i>PLoS Genetics</i> , 2016 , 12, e1005850	6	71
69	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. <i>British Journal of Cancer</i> , 2016 , 115, 266-72	8.7	39
68	Somatic MED12 mutations in prostate cancer and uterine leiomyomas promote tumorigenesis through distinct mechanisms. <i>Prostate</i> , 2016 , 76, 22-31	4.2	25
67	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. <i>Nature Communications</i> , 2015 , 6, 6178	17.4	131

66	DNA-dependent formation of transcription factor pairs alters their binding specificity. <i>Nature</i> , 2015 , 527, 384-8	50.4	299
65	CTCF/cohesin-binding sites are frequently mutated in cancer. <i>Nature Genetics</i> , 2015 , 47, 818-21	36.3	286
64	Structural insights into the DNA-binding specificity of E2F family transcription factors. <i>Nature Communications</i> , 2015 , 6, 10050	17.4	27
63	Dominant NFKB1 Mutations Cause Antibody Deficiency and Autoinflammatory Episodes. <i>Blood</i> , 2015 , 126, 206-206	2.2	1
62	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. <i>ELife</i> , 2015 , 4,	8.9	140
61	Author response: Conservation of transcription factor binding specificities across 600 million years of bilateria evolution 2015 ,		2
60	A prostate cancer susceptibility allele at 6q22 increases RFX6 expression by modulating HOXB13 chromatin binding. <i>Nature Genetics</i> , 2014 , 46, 126-35	36.3	142
59	Uterine leiomyoma-linked MED12 mutations disrupt mediator-associated CDK activity. <i>Cell Reports</i> , 2014 , 7, 654-60	10.6	99
58	Exome sequencing reveals frequent inactivating mutations in ARID1A, ARID1B, ARID2 and ARID4A in microsatellite unstable colorectal cancer. <i>International Journal of Cancer</i> , 2014 , 135, 611-23	7.5	80
57	Cancer. Cancer by super-enhancer. <i>Science</i> , 2014 , 346, 1291-2	33.3	19
56	Frequent L1 retrotranspositions originating from TTC28 in colorectal cancer. <i>Oncotarget</i> , 2014 , 5, 853-9	3.3	40
55	Transcription factor binding in human cells occurs in dense clusters formed around cohesin anchor sites. <i>Cell</i> , 2013 , 154, 801-13	56.2	253
54	Identification of candidate oncogenes in human colorectal cancers with microsatellite instability. <i>Gastroenterology</i> , 2013 , 145, 540-3.e22	13.3	40
53	DNA-binding specificities of human transcription factors. <i>Cell</i> , 2013 , 152, 327-39	56.2	763
52	Lessons from functional analysis of genome-wide association studies. <i>Cancer Research</i> , 2013 , 73, 4180-4	10.1	50
51	Eleven candidate susceptibility genes for common familial colorectal cancer. <i>PLoS Genetics</i> , 2013 , 9, e1003876		57
50	Transcriptional networks controlling the cell cycle. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 75-90	3.2	18
49	Human kinome analysis reveals novel kinases contributing to virus infection and retinoic-acid inducible gene I-induced type I and type III IFN gene expression. <i>Innate Immunity</i> , 2013 , 19, 516-30	2.7	13

48	Characterization of the colorectal cancer-associated enhancer MYC-335 at 8q24: the role of rs67491583. <i>Cancer Genetics</i> , 2012 , 205, 25-33	2.3	20
47	Loss of SUFU function in familial multiple meningioma. <i>American Journal of Human Genetics</i> , 2012 , 91, 520-6	11	103
46	Mice lacking a Myc enhancer that includes human SNP rs6983267 are resistant to intestinal tumors. <i>Science</i> , 2012 , 338, 1360-3	33.3	171
45	Counting absolute numbers of molecules using unique molecular identifiers. <i>Nature Methods</i> , 2011 , 9, 72-4	21.6	637
44	MED12, the mediator complex subunit 12 gene, is mutated at high frequency in uterine leiomyomas. <i>Science</i> , 2011 , 334, 252-5	33.3	449
43	Methods for Analysis of Transcription Factor DNA-Binding Specificity In Vitro. <i>Sub-Cellular Biochemistry</i> , 2011 , 52, 155-73	5.5	16
42	Missing-in-metastasis MIM/MTSS1 promotes actin assembly at intercellular junctions and is required for integrity of kidney epithelia. <i>Journal of Cell Science</i> , 2011 , 124, 1245-55	5.3	59
41	Beyond the balance of activator and repressor. <i>Science Signaling</i> , 2011 , 4, pe29	8.8	9
40	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. <i>EMBO Journal</i> , 2010 , 29, 2147-60	13	403
39	Mutations in the circadian gene CLOCK in colorectal cancer. <i>Molecular Cancer Research</i> , 2010 , 8, 952-60	6.6	60
38	Fibroblast growth factor receptor 4 regulates tumor invasion by coupling fibroblast growth factor signaling to extracellular matrix degradation. <i>Cancer Research</i> , 2010 , 70, 7851-61	10.1	39
37	FGF receptor-4 (FGFR4) polymorphism acts as an activity switch of a membrane type 1 matrix metalloproteinase-FGFR4 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 15786-91	11.5	41
36	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. <i>Genome Research</i> , 2010 , 20, 861-73	9.7	292
35	KSHV reactivation from latency requires Pim-1 and Pim-3 kinases to inactivate the latency-associated nuclear antigen LANA. <i>PLoS Pathogens</i> , 2009 , 5, e1000324	7.6	55
34	The common colorectal cancer predisposition SNP rs6983267 at chromosome 8q24 confers potential to enhanced Wnt signaling. <i>Nature Genetics</i> , 2009 , 41, 885-90	36.3	422
33	Transcription factor PROX1 induces colon cancer progression by promoting the transition from benign to highly dysplastic phenotype. <i>Cancer Cell</i> , 2008 , 13, 407-19	24.3	140
32	Application of active and kinase-deficient kinome collection for identification of kinases regulating hedgehog signaling. <i>Cell</i> , 2008 , 133, 537-48	56.2	150
31	Hedgehog: functions and mechanisms. <i>Genes and Development</i> , 2008 , 22, 2454-72	12.6	901

30	Deletion of vascular endothelial growth factor C (VEGF-C) and VEGF-D is not equivalent to VEGF receptor 3 deletion in mouse embryos. <i>Molecular and Cellular Biology</i> , 2008 , 28, 4843-50	4.8	153
29	Hedgehog signaling. <i>Journal of Cell Science</i> , 2007 , 120, 3-6	5.3	104
28	Genome-wide prediction of mammalian enhancers based on analysis of transcription-factor binding affinity. <i>Cell</i> , 2006 , 124, 47-59	56.2	389
27	Divergence of hedgehog signal transduction mechanism between <i>Drosophila</i> and mammals. <i>Developmental Cell</i> , 2006 , 10, 177-86	10.2	190
26	Minimizing the risk of reporting false positives in large-scale RNAi screens. <i>Nature Methods</i> , 2006 , 3, 777-9	21.6	362
25	High-throughput assay for determining specificity and affinity of protein-DNA binding interactions. <i>Nature Protocols</i> , 2006 , 1, 215-22	18.8	34
24	Locating potential enhancer elements by comparative genomics using the EEL software. <i>Nature Protocols</i> , 2006 , 1, 368-74	18.8	30
23	Identification of pathways regulating cell size and cell-cycle progression by RNAi. <i>Nature</i> , 2006 , 439, 1009-13	9.1	218
22	Vascular endothelial growth factor C is required for sprouting of the first lymphatic vessels from embryonic veins. <i>Nature Immunology</i> , 2004 , 5, 74-80	19.1	1038
21	A defective response to Hedgehog signaling in disorders of cholesterol biosynthesis. <i>Nature Genetics</i> , 2003 , 33, 508-13	36.3	311
20	Hedgehog signal transduction via Smoothened association with a cytoplasmic complex scaffolded by the atypical kinesin, Costal-2. <i>Molecular Cell</i> , 2003 , 12, 1261-74	17.6	209
19	Small molecule modulation of Smoothened activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 14071-6	11.5	803
18	Inhibition of Hedgehog signaling by direct binding of cyclopamine to Smoothened. <i>Genes and Development</i> , 2002 , 16, 2743-8	12.6	1144
17	Medulloblastoma growth inhibition by hedgehog pathway blockade. <i>Science</i> , 2002 , 297, 1559-61	33.3	685
16	Hedgehog-mediated patterning of the mammalian embryo requires transporter-like function of Dispatched. <i>Cell</i> , 2002 , 111, 63-75	56.2	243
15	The Hedgehog and Wnt signalling pathways in cancer. <i>Nature</i> , 2001 , 411, 349-54	50.4	1173
14	VEGFR3 gene structure, regulatory region, and sequence polymorphisms. <i>FASEB Journal</i> , 2001 , 15, 1028-34	10.34	5
13	Effects of oncogenic mutations in Smoothened and Patched can be reversed by cyclopamine. <i>Nature</i> , 2000 , 406, 1005-9	50.4	1136

12	Latent transforming growth factor-beta binding proteins (LTBPs)--structural extracellular matrix proteins for targeting TGF-beta action. <i>Cytokine and Growth Factor Reviews</i> , 1999 , 10, 99-117	17.9	237
11	VEGFR-3 and its ligand VEGF-C are associated with angiogenesis in breast cancer. <i>American Journal of Pathology</i> , 1999 , 154, 1381-90	5.8	447
10	Hepatocyte growth factor releases mink epithelial cells from transforming growth factor beta1-induced growth arrest by restoring Cdk6 expression and cyclin E-associated Cdk2 activity. <i>Molecular and Cellular Biology</i> , 1999 , 19, 3654-63	4.8	29
9	Extracellular matrix-associated transforming growth factor-beta: role in cancer cell growth and invasion. <i>Advances in Cancer Research</i> , 1998 , 75, 87-134	5.9	160
8	Cardiovascular failure in mouse embryos deficient in VEGF receptor-3. <i>Science</i> , 1998 , 282, 946-9	33.3	646
7	Identification and characterization of a new latent transforming growth factor-beta-binding protein, LTBP-4. <i>Journal of Biological Chemistry</i> , 1998 , 273, 18459-69	5.4	101
6	Recombinant latent transforming growth factor beta-binding protein 2 assembles to fibroblast extracellular matrix and is susceptible to proteolytic processing and release. <i>Journal of Biological Chemistry</i> , 1998 , 273, 20669-76	5.4	53
5	Growth factors in the extracellular matrix. <i>FASEB Journal</i> , 1997 , 11, 51-9	0.9	721
4	Hepatocyte growth factor releases epithelial and endothelial cells from growth arrest induced by transforming growth factor-beta1. <i>Journal of Biological Chemistry</i> , 1996 , 271, 4342-8	5.4	45
3	Human mast cell chymase and leukocyte elastase release latent transforming growth factor-beta 1 from the extracellular matrix of cultured human epithelial and endothelial cells. <i>Journal of Biological Chemistry</i> , 1995 , 270, 4689-96	5.4	312
2	Association of Latent Transforming Growth Factor-.BETA. to Fibroblast Extracellular Matrix-An Insight to Proteolytic Activation.. <i>Trends in Glycoscience and Glycotechnology</i> , 1995 , 7, 277-289	0.1	3
1	Population-scale testing can suppress the spread of COVID-19		35