

# Matthew T Weirauch

## List of Publications by Year in descending order

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Version: 2024-02-01

131  
papers

21,934  
citations

47006

47  
h-index

12272

133  
g-index

165  
all docs

165  
docs citations

165  
times ranked

34377  
citing authors

#	ARTICLE	IF	CITATIONS
1	TSLP disease-associated genetic variants combined with airway TSLP expression influence asthma risk. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 79-88.	2.9	11
2	CASCADE: high-throughput characterization of regulatory complex binding altered by non-coding variants. <i>Cell Genomics</i> , 2022, 2, 100098.	6.5	3
3	Blocking UBE2N abrogates oncogenic immune signaling in acute myeloid leukemia. <i>Science Translational Medicine</i> , 2022, 14, eabb7695.	12.4	13
4	Lupus enhancer risk variant causes dysregulation of IRF8 through cooperative lncRNA and DNA methylation machinery. <i>Nature Communications</i> , 2022, 13, 1855.	12.8	16
5	Definition of germ layer cell lineage alternative splicing programs reveals a critical role for Quaking in specifying cardiac cell fate. <i>Nucleic Acids Research</i> , 2022, 50, 5313-5334.	14.5	5
6	Epigenetic and transcriptional dysregulation in CD4+ T cells in patients with atopic dermatitis. <i>PLoS Genetics</i> , 2022, 18, e1009973.	3.5	5
7	Nasal DNA methylation differentiates severe from non-severe asthma in African-American children. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1836-1845.	5.7	19
8	Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 632-640.	0.9	103
9	Comprehensive Review of Steroid-Sensitive Nephrotic Syndrome Genetic Risk Loci and Transcriptional Regulation as a Possible Mechanistic Link to Disease Risk. <i>Kidney International Reports</i> , 2021, 6, 187-195.	0.8	4
10	Replication and meta-analyses nominate numerous eosinophilic esophagitis risk genes. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 255-266.	2.9	25
11	Conserved regulatory logic at accessible and inaccessible chromatin during the acute inflammatory response in mammals. <i>Nature Communications</i> , 2021, 12, 567.	12.8	15
12	SLE non-coding genetic risk variant determines the epigenetic dysfunction of an immune cell specific enhancer that controls disease-critical microRNA expression. <i>Nature Communications</i> , 2021, 12, 135.	12.8	48
13	Second-hand smoke and NFE2L2 genotype interaction increases paediatric asthma risk and severity. <i>Clinical and Experimental Allergy</i> , 2021, 51, 801-810.	2.9	11
14	U2AF2 binds <i>IL7R</i> exon 6 ectopically and represses its inclusion. <i>Rna</i> , 2021, 27, 571-583.	3.5	7
15	Mechanisms of stearyl CoA desaturase inhibitor sensitivity and acquired resistance in cancer. <i>Science Advances</i> , 2021, 7, .	10.3	38
16	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	3.8	19
17	Deciphering cis-regulatory grammar with deep learning. <i>Nature Genetics</i> , 2021, 53, 266-268.	21.4	6
18	Global discovery of lupus genetic risk variant allelic enhancer activity. <i>Nature Communications</i> , 2021, 12, 1611.	12.8	39

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19	IRF1 governs the differential interferon-stimulated gene responses in human monocytes and macrophages by regulating chromatin accessibility. <i>Cell Reports</i> , 2021, 34, 108891.	6.4	46
20	<i>Drosophila</i> Fezf functions as a transcriptional repressor to direct layer-specific synaptic connectivity in the fly visual system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	14
21	Methylation quantitative trait locus analysis of chronic postsurgical pain uncovers epigenetic mediators of genetic risk. <i>Epigenomics</i> , 2021, 13, 613-630.	2.1	5
22	TOP1 inhibition therapy protects against SARS-CoV-2-induced lethal inflammation. <i>Cell</i> , 2021, 184, 2618-2632.e17.	28.9	80
23	PKM2-dependent metabolic skewing of hepatic Th17 cells regulates pathogenesis of non-alcoholic fatty liver disease. <i>Cell Metabolism</i> , 2021, 33, 1187-1204.e9.	16.2	60
24	Lupus Susceptibility Region Containing <i>CDKN1B</i> rs34330 Mechanistically Influences Expression and Function of Multiple Target Genes, Also Linked to Proliferation and Apoptosis. <i>Arthritis and Rheumatology</i> , 2021, 73, 2303-2313.	5.6	11
25	Runx1 shapes the chromatin landscape via a cascade of direct and indirect targets. <i>PLoS Genetics</i> , 2021, 17, e1009574.	3.5	19
26	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	3.8	18
27	Epigenetic Analysis of the Chromatin Landscape Identifies a Repertoire of Murine Eosinophil-Specific PU.1-Bound Enhancers. <i>Journal of Immunology</i> , 2021, 207, 1044-1054.	0.8	4
28	Runx Transcription Factors in T Cells—What Is Beyond Thymic Development?. <i>Frontiers in Immunology</i> , 2021, 12, 701924.	4.8	21
29	Aiolos regulates eosinophil migration into tissues. <i>Mucosal Immunology</i> , 2021, 14, 1271-1281.	6.0	10
30	Olaparib Inhibits Tumor Growth of Hepatoblastoma in Patient-Derived Xenograft Models. <i>Hepatology</i> , 2021, 74, 2201-2215.	7.3	12
31	Enhancers with cooperative Notch binding sites are more resistant to regulation by the Hairless co-repressor. <i>PLoS Genetics</i> , 2021, 17, e1009039.	3.5	4
32	Epstein-Barr virus nuclear antigen 2 extensively rewires the human chromatin landscape at autoimmune risk loci. <i>Genome Research</i> , 2021, 31, 2185-2198.	5.5	24
33	AP-1 activity induced by co-stimulation is required for chromatin opening during T cell activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	80
34	The genetic etiology of eosinophilic esophagitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 9-15.	2.9	48
35	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , 2020, 3, 424.	4.4	26
36	Disease-associated KIF3A variants alter gene methylation and expression impacting skin barrier and atopic dermatitis risk. <i>Nature Communications</i> , 2020, 11, 4092.	12.8	24

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37	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	3.8	54
38	Super-enhancer switching drives a burst in gene expression at the mitosis-to-meiosis transition. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 978-988.	8.2	38
39	Multi-level analysis of reproduction in an Antarctic midge identifies female and male accessory gland products that are altered by larval stress and impact progeny viability. <i>Scientific Reports</i> , 2020, 10, 19791.	3.3	18
40	Single-nucleus RNA-seq identifies transcriptional heterogeneity in multinucleated skeletal myofibers. <i>Nature Communications</i> , 2020, 11, 6374.	12.8	187
41	Type I interferon sensing unlocks dormant adipocyte inflammatory potential. <i>Nature Communications</i> , 2020, 11, 2745.	12.8	41
42	The Promise and Peril of Natural Killer Cell Therapies in Pulmonary Infection. <i>Immunity</i> , 2020, 52, 887-889.	14.3	18
43	Brown marmorated stink bug, <i>Halyomorpha halys</i> (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. <i>BMC Genomics</i> , 2020, 21, 227.	2.8	60
44	Molecular mechanisms underlying milk production and viviparity in the cockroach, <i>Diploptera punctata</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 120, 103333.	2.7	7
45	Human Virus Transcriptional Regulators. <i>Cell</i> , 2020, 182, 24-37.	28.9	52
46	Genomic programming of IRF4-expressing human Langerhans cells. <i>Nature Communications</i> , 2020, 11, 313.	12.8	22
47	Gli3 utilizes Hand2 to synergistically regulate tissue-specific transcriptional networks. <i>ELife</i> , 2020, 9, .	6.0	15
48	Sox17 and $\beta$ -catenin co-occupy Wnt-responsive enhancers to govern the endoderm gene regulatory network. <i>ELife</i> , 2020, 9, .	6.0	35
49	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	8.8	71
50	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. <i>Nature Communications</i> , 2019, 10, 3927.	12.8	49
51	Genetic, Inflammatory, and Epithelial Cell Differentiation Factors Control Expression of Human Calpain-14. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 729-736.	1.8	16
52	Similarity regression predicts evolution of transcription factor sequence specificity. <i>Nature Genetics</i> , 2019, 51, 981-989.	21.4	105
53	TET1 contributes to allergic airway inflammation and regulates interferon and aryl hydrocarbon receptor signaling pathways in bronchial epithelial cells. <i>Scientific Reports</i> , 2019, 9, 7361.	3.3	28
54	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	8.8	114

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55	Sex- and developmental-specific transcriptomic analyses of the Antarctic mite, <i>Alaskozetes antarcticus</i> , reveal transcriptional shifts underlying oribatid mite reproduction. <i>Polar Biology</i> , 2019, 42, 357-370.	1.2	8
56	Enrichment of Genomic Pathways Based on Differential DNA Methylation Associated With Chronic Postsurgical Pain and Anxiety in Children: A Prospective, Pilot Study. <i>Journal of Pain</i> , 2019, 20, 771-785.	1.4	28
57	Hand2 Functions to Synergistically Activate Gli Target Genes in Mandibular Neural Crest Cells. <i>FASEB Journal</i> , 2019, 33, 73.1.	0.5	0
58	<i>Neurospora crassa</i> developmental control mediated by the FLB-3 transcription factor. <i>Fungal Biology</i> , 2018, 122, 570-582.	2.5	14
59	A plausibly causal functional lupus-associated risk variant in the STAT1-STAT4 locus. <i>Human Molecular Genetics</i> , 2018, 27, 2392-2404.	2.9	34
60	Transcription factors operate across disease loci, with EBNA2 implicated in autoimmunity. <i>Nature Genetics</i> , 2018, 50, 699-707.	21.4	286
61	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	3.3	215
62	The Human Transcription Factors. <i>Cell</i> , 2018, 172, 650-665.	28.9	2,048
63	Nasal DNA methylation is associated with childhood asthma. <i>Epigenomics</i> , 2018, 10, 629-641.	2.1	38
64	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	27.8	224
65	SKI controls MDS-associated chronic TGF- $\beta$ 2 signaling, aberrant splicing, and stem cell fitness. <i>Blood</i> , 2018, 132, e24-e34.	1.4	21
66	Defective transcription elongation in a subset of cancers confers immunotherapy resistance. <i>Nature Communications</i> , 2018, 9, 4410.	12.8	17
67	Hepatic Ago2-mediated RNA silencing controls energy metabolism linked to AMPK activation and obesity-associated pathophysiology. <i>Nature Communications</i> , 2018, 9, 3658.	12.8	29
68	Degenerate Pax2 and Senseless binding motifs improve detection of low-affinity sites required for enhancer specificity. <i>PLoS Genetics</i> , 2018, 14, e1007289.	3.5	14
69	PARP1 activation increases expression of modified tumor suppressors and pathways underlying development of aggressive hepatoblastoma. <i>Communications Biology</i> , 2018, 1, 67.	4.4	35
70	Genetic variants with gene regulatory effects are associated with diisocyanate-induced asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 959-969.	2.9	14
71	Diesel exhaust and house dust mite allergen lead to common changes in the airway methylome and hydroxymethylome. <i>Environmental Epigenetics</i> , 2018, 4, dvy020.	1.8	37
72	AMP kinase promotes glioblastoma bioenergetics and tumour growth. <i>Nature Cell Biology</i> , 2018, 20, 823-835.	10.3	106

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73	Therapeutic Targeting of the Ubiquitin Conjugating Enzyme UBE2N in Myeloid Malignancies. <i>Blood</i> , 2018, 132, 4050-4050.	1.4	0
74	Transcriptional determinants of tolerogenic and immunogenic states during dendritic cell maturation. <i>Journal of Cell Biology</i> , 2017, 216, 779-792.	5.2	82
75	KIF3A genetic variation is associated with pediatric asthma in the presence of eczema independent of allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 595-598.e5.	2.9	18
76	Paternally Inherited DLK1 Deletion Associated With Familial Central Precocious Puberty. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 1557-1567.	3.6	145
77	Temporal, spatial, and phenotypical changes of PDGFR $\pm$ expressing fibroblasts during late lung development. <i>Developmental Biology</i> , 2017, 425, 161-175.	2.0	78
78	Ubiquitination of hnRNPA1 by TRAF6 links chronic innate immune signaling with myelodysplasia. <i>Nature Immunology</i> , 2017, 18, 236-245.	14.5	85
79	Identification of Functional and Expression Polymorphisms Associated With Risk for Antineutrophil Cytoplasmic Autoantibody-Associated Vasculitis. <i>Arthritis and Rheumatology</i> , 2017, 69, 1054-1066.	5.6	130
80	The Epstein-Barr Virus B-ZIP Protein Zta Recognizes Specific DNA Sequences Containing 5-Methylcytosine and 5-Hydroxymethylcytosine. <i>Biochemistry</i> , 2017, 56, 6200-6210.	2.5	17
81	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. <i>New England Journal of Medicine</i> , 2017, 377, 1156-1167.	27.0	309
82	A FOXO1-induced oncogenic network defines the AML1-ETO preleukemic program. <i>Blood</i> , 2017, 130, 1213-1222.	1.4	36
83	Control of species-dependent cortico-motoneuronal connections underlying manual dexterity. <i>Science</i> , 2017, 357, 400-404.	12.6	92
84	Non-base-contacting residues enable kaleidoscopic evolution of metazoan C2H2 zinc finger DNA binding. <i>Genome Biology</i> , 2017, 18, 167.	8.8	33
85	DNA methylation at the mu-1 opioid receptor gene ( <i>OPRM1</i> ) promoter predicts preoperative, acute, and chronic postsurgical pain after spine fusion. <i>Pharmacogenomics and Personalized Medicine</i> , 2017, Volume 10, 157-168.	0.7	40
86	Nasal DNA methylation differentiates corticosteroid treatment response in pediatric asthma: A pilot study. <i>PLoS ONE</i> , 2017, 12, e0186150.	2.5	35
87	Analysis of chromatin accessibility in human epidermis identifies putative barrier dysfunction-sensing enhancers. <i>PLoS ONE</i> , 2017, 12, e0184500.	2.5	8
88	Requirement for Dicer in Maintenance of Monosynaptic Sensory-Motor Circuits in the Spinal Cord. <i>Cell Reports</i> , 2016, 17, 2163-2172.	6.4	8
89	Topoisomerase 1 inhibition suppresses inflammatory genes and protects from death by inflammation. <i>Science</i> , 2016, 352, aad7993.	12.6	132
90	Screening for Functional Non-coding Genetic Variants Using Electrophoretic Mobility Shift Assay (EMSA) and DNA-affinity Precipitation Assay (DAPA). <i>Journal of Visualized Experiments</i> , 2016, , .	0.3	11

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91	Multiple layers of transcriptional regulation by PLZF in NKT-cell development. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7602-7607.	7.1	82
92	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165.	12.8	184
93	GABP± Binding to Overlapping ETS and CRE DNA Motifs Is Enhanced by CREB1: Custom DNA Microarrays. G3: Genes, Genomes, Genetics, 2015, 5, 1909-1918.	1.8	4
94	Divergence of transcriptional landscape occurs early in B cell activation. Epigenetics and Chromatin, 2015, 8, 20.	3.9	28
95	CressInt : A user-friendly web resource for genome-scale exploration of gene regulation in Arabidopsis thaliana. Current Plant Biology, 2015, 3-4, 48-55.	4.7	3
96	Making it big in allergy. Journal of Allergy and Clinical Immunology, 2015, 135, 43-45.	2.9	8
97	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. Nature Biotechnology, 2015, 33, 555-562.	17.5	271
98	SpDamID: Marking DNA Bound by Protein Complexes Identifies Notch-Dimer Responsive Enhancers. Molecular Cell, 2015, 59, 685-697.	9.7	50
99	Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. Nature Biotechnology, 2015, 33, 831-838.	17.5	2,206
100	Genome-Wide Association Study Identifies Novel Loci Associated With Diisocyanate-Induced Occupational Asthma. Toxicological Sciences, 2015, 146, 192-201.	3.1	48
101	Lupus Risk Variant Increases pSTAT1 Binding and Decreases ETS1 Expression. American Journal of Human Genetics, 2015, 96, 731-739.	6.2	36
102	MiR-125a targets effector programs to stabilize Treg-mediated immune homeostasis. Nature Communications, 2015, 6, 7096.	12.8	133
103	Transcription Factor Repertoire of Homeostatic Eosinophiloipoiesis. Journal of Immunology, 2015, 195, 2683-2695.	0.8	43
104	Affinity regression predicts the recognition code of nucleic acid±binding proteins. Nature Biotechnology, 2015, 33, 1242-1249.	17.5	55
105	The IRF5±TNPO3 association with systemic lupus erythematosus has two components that other autoimmune disorders variably share. Human Molecular Genetics, 2015, 24, 582-596.	2.9	74
106	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	14
107	Mapping and analysis of Caenorhabditis elegans transcription factor sequence specificities. ELife, 2015, 4, .	6.0	85
108	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. ELife, 2014, 3, e02626.	6.0	84

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109	Whole Exome Sequencing for Familial Bicuspid Aortic Valve Identifies Putative Variants. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 677-683.	5.1	41
110	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in <i>A. thaliana</i> . <i>Cell Reports</i> , 2014, 8, 2015-2030.	6.4	249
111	Myeloid Malignancies with Chromosome 5q Deletions Acquire a Dependency on an Intrachromosomal NF- $\kappa$ B Gene Network. <i>Cell Reports</i> , 2014, 8, 1328-1338.	6.4	64
112	The 253â€b inversion and deep intronic mutations in <i>UNC13D</i> are present in North American patients with familial hemophagocytic lymphohistiocytosis 3. <i>Pediatric Blood and Cancer</i> , 2014, 61, 1034-1040.	1.5	33
113	Transcription factor binding to <i>Caenorhabditis elegans</i> first introns reveals lack of redundancy with gene promoters. <i>Nucleic Acids Research</i> , 2014, 42, 153-162.	14.5	27
114	DNA methylation dynamics during <i>ex vivo</i> differentiation and maturation of human dendritic cells. <i>Epigenetics and Chromatin</i> , 2014, 7, 21.	3.9	85
115	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	28.9	1,515
116	Genome-wide association analysis of eosinophilic esophagitis provides insight into the tissue specificity of this allergic disease. <i>Nature Genetics</i> , 2014, 46, 895-900.	21.4	243
117	Quantifying Inter-Laboratory Variability in Stable Isotope Analysis of Ancient Skeletal Remains. <i>PLoS ONE</i> , 2014, 9, e102844.	2.5	116
118	A versatile, highly efficient, and potentially safer <i>piggyBac</i> transposon system for mammalian genome manipulations. <i>FASEB Journal</i> , 2013, 27, 4429-4443.	0.5	21
119	A compendium of RNA-binding motifs for decoding gene regulation. <i>Nature</i> , 2013, 499, 172-177.	27.8	1,281
120	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	17.5	341
121	Extensive Rewiring and Complex Evolutionary Dynamics in a <i>C. elegans</i> Multiparameter Transcription Factor Network. <i>Molecular Cell</i> , 2013, 51, 116-127.	9.7	83
122	Early evolution of the T-box transcription factor family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16050-16055.	7.1	80
123	CG methylated microarrays identify a novel methylated sequence bound by the CEBPB   ATF4 heterodimer that is active <i>in vivo</i> . <i>Genome Research</i> , 2013, 23, 988-997.	5.5	111
124	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , 2013, 2, e00675.	6.0	379
125	A Catalogue of Eukaryotic Transcription Factor Types, Their Evolutionary Origin, and Species Distribution. <i>Sub-Cellular Biochemistry</i> , 2011, 52, 25-73.	2.4	107
126	Structural basis for recognition of AT-rich DNA by unrelated xenogeneic silencing proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10690-10695.	7.1	204



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127	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	12.6	1,937
128	Conserved expression without conserved regulatory sequence: the more things change, the more they stay the same. <i>Trends in Genetics</i> , 2010, 26, 66-74.	6.7	139
129	Dramatic changes in transcription factor binding over evolutionary time. <i>Genome Biology</i> , 2010, 11, 122.	9.6	11
130	Transcriptional Map of Respiratory Versatility in the Hyperthermophilic Crenarchaeon <i>Pyrobaculum aerophilum</i> . <i>Journal of Bacteriology</i> , 2009, 191, 782-794.	2.2	46
131	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709