

Hunter B Fraser

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

6,780
citations

117453

34
h-index

123241

61
g-index

109
all docs

109
docs citations

109
times ranked

9773
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary Rate in the Protein Interaction Network. <i>Science</i> , 2002, 296, 750-752.	6.0	798
2	Factors underlying variable DNA methylation in a human community cohort. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17253-17260.	3.3	414
3	Protein dispensability and rate of evolution. <i>Nature</i> , 2001, 411, 1046-1049.	13.7	373
4	Noise Minimization in Eukaryotic Gene Expression. <i>PLoS Biology</i> , 2004, 2, e137.	2.6	370
5	N-WASP deficiency reveals distinct pathways for cell surface projections and microbial actin-based motility. <i>Nature Cell Biology</i> , 2001, 3, 897-904.	4.6	308
6	Functional genomic analysis of the rates of protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5483-5488.	3.3	255
7	Population-specificity of human DNA methylation. <i>Genome Biology</i> , 2012, 13, R8.	13.9	247
8	Coevolution of gene expression among interacting proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9033-9038.	3.3	221
9	Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse. <i>Nature Genetics</i> , 2015, 47, 544-549.	9.4	221
10	Gene expression drives local adaptation in humans. <i>Genome Research</i> , 2013, 23, 1089-1096.	2.4	217
11	Conservation and Evolution of Cis-Regulatory Systems in Ascomycete Fungi. <i>PLoS Biology</i> , 2004, 2, e398.	2.6	207
12	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3264-3269.	3.3	201
13	Modularity and evolutionary constraint on proteins. <i>Nature Genetics</i> , 2005, 37, 351-352.	9.4	174
14	Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing. <i>Cell</i> , 2018, 175, 544-557.e16.	13.5	166
15	Evidence for widespread adaptive evolution of gene expression in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2977-2982.	3.3	161
16	Ageing and Gene Expression in the Primate Brain. <i>PLoS Biology</i> , 2005, 3, e274.	2.6	160
17	A simple dependence between protein evolution rate and the number of protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2003, 3, 11.	3.2	152
18	Genetic variation in MHC proteins is associated with T cell receptor expression biases. <i>Nature Genetics</i> , 2016, 48, 995-1002.	9.4	151

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19	Accounting for biases in riboprofiling data indicates a major role for proline in stalling translation. <i>Genome Research</i> , 2014, 24, 2011-2021.	2.4	142
20	Extensive conservation of ancient microsynteny across metazoans due to <i>cis</i> -regulatory constraints. <i>Genome Research</i> , 2012, 22, 2356-2367.	2.4	126
21	Evolution at two levels of gene expression in yeast. <i>Genome Research</i> , 2014, 24, 411-421.	2.4	124
22	Pooled ChIP-Seq Links Variation in Transcription Factor Binding to Complex Disease Risk. <i>Cell</i> , 2016, 165, 730-741.	13.5	107
23	Common variants spanning <i>PLK4</i> are associated with mitotic-origin aneuploidy in human embryos. <i>Science</i> , 2015, 348, 235-238.	6.0	106
24	Genome-wide approaches to the study of adaptive gene expression evolution. <i>BioEssays</i> , 2011, 33, 469-477.	1.2	89
25	The somatic mutation landscape of the human body. <i>Genome Biology</i> , 2019, 20, 298.	3.8	84
26	Common polymorphic transcript variation in human disease. <i>Genome Research</i> , 2009, 19, 567-575.	2.4	70
27	Evolutionary rate depends on number of protein-protein interactions independently of gene expression level. <i>BMC Evolutionary Biology</i> , 2004, 4, 13.	3.2	68
28	Systematic Detection of Polygenic <i>cis</i> -Regulatory Evolution. <i>PLoS Genetics</i> , 2011, 7, e1002023.	1.5	61
29	Discordance of DNA Methylation Variance Between two Accessible Human Tissues. <i>Scientific Reports</i> , 2015, 5, 8257.	1.6	56
30	The Quantitative Genetics of Phenotypic Robustness. <i>PLoS ONE</i> , 2010, 5, e8635.	1.1	55
31	Primate cell fusion disentangles gene regulatory divergence in neurodevelopment. <i>Nature</i> , 2021, 592, 421-427.	13.7	52
32	Fine-mapping <i>cis</i> -regulatory variants in diverse human populations. <i>ELife</i> , 2019, 8, .	2.8	51
33	High-resolution mapping of <i>cis</i> -regulatory variation in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10736-E10744.	3.3	50
34	Transcript Length Mediates Developmental Timing of Gene Expression Across <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 2879-2889.	3.5	49
35	Rate of evolution and gene dispensability. <i>Nature</i> , 2003, 421, 497-498.	13.7	46
36	Polygenic <i>cis</i> -regulatory adaptation in the evolution of yeast pathogenicity. <i>Genome Research</i> , 2012, 22, 1930-1939.	2.4	46

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37	Humanâ€“chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution. <i>Nature Genetics</i> , 2021, 53, 467-476.	9.4	46
38	Behavior-dependent <i>cis</i> regulation reveals genes and pathways associated with bower building in cichlid fishes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11081-E11090.	3.3	42
39	Codon Usage and Selection on Proteins. <i>Journal of Molecular Evolution</i> , 2006, 63, 635-653.	0.8	40
40	Worldwide patterns of human epigenetic variation. <i>Nature Ecology and Evolution</i> , 2017, 1, 1577-1583.	3.4	40
41	Tissue-Specific cis-Regulatory Divergence Implicates <i>eloF</i> in Inhibiting Interspecies Mating in <i>Drosophila</i> . <i>Current Biology</i> , 2018, 28, 3969-3975.e3.	1.8	37
42	The cis-regulatory effects of modern human-specific variants. <i>ELife</i> , 2021, 10, .	2.8	36
43	The Molecular Mechanism of a Cis-Regulatory Adaptation in Yeast. <i>PLoS Genetics</i> , 2013, 9, e1003813.	1.5	35
44	Improving Estimates of Compensatory cisâ€“trans Regulatory Divergence. <i>Trends in Genetics</i> , 2019, 35, 3-5.	2.9	33
45	Dissecting the Genetic Basis of a Complex cis-Regulatory Adaptation. <i>PLoS Genetics</i> , 2015, 11, e1005751.	1.5	30
46	A pooling-based approach to mapping genetic variants associated with DNA methylation. <i>Genome Research</i> , 2015, 25, 907-917.	2.4	30
47	A Novel Test for Selection on cis-Regulatory Elements Reveals Positive and Negative Selection Acting on Mammalian Transcriptional Enhancers. <i>Molecular Biology and Evolution</i> , 2013, 30, 2509-2518.	3.5	25
48	Bacterial Retrons Enable Precise Gene Editing in Human Cells. <i>CRISPR Journal</i> , 2022, 5, 31-39.	1.4	22
49	Coevolution, modularity and human disease. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 637-644.	1.5	21
50	cis-Regulatory changes in locomotor genes are associated with the evolution of burrowing behavior. <i>Cell Reports</i> , 2022, 38, 110360.	2.9	19
51	Detecting selection with a genetic cross. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22323-22330.	3.3	18
52	Local Adaptation of Sun-Exposure-Dependent Gene Expression Regulation in Human Skin. <i>PLoS Genetics</i> , 2016, 12, e1006382.	1.5	18
53	Spatially varying cis-regulatory divergence in <i>Drosophila</i> embryos elucidates cis-regulatory logic. <i>PLoS Genetics</i> , 2018, 14, e1007631.	1.5	16
54	Molecular mechanisms of coronary disease revealed using quantitative trait loci for TCF21 binding, chromatin accessibility, and chromosomal looping. <i>Genome Biology</i> , 2020, 21, 135.	3.8	16

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55	Comparative expression profiling reveals widespread coordinated evolution of gene expression across eukaryotes. <i>Nature Communications</i> , 2018, 9, 4963.	5.8	13
56	GRINS: Genetic elements that recode assembly-line polyketide synthases and accelerate their diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
57	Disentangling Sources of Selection on Exonic Transcriptional Enhancers. <i>Molecular Biology and Evolution</i> , 2016, 33, 585-590.	3.5	9
58	Lineage-specific selection and the evolution of virulence in the <i>Candida</i> clade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
59	Cis-regulatory evolution in prokaryotes revealed by interspecific archaeal hybrids. <i>Scientific Reports</i> , 2017, 7, 3986.	1.6	8
60	Transcriptome diversity is a systematic source of variation in RNA-sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009939.	1.5	7
61	Divergent patterns of selection on metabolite levels and gene expression. <i>Bmc Ecology and Evolution</i> , 2021, 21, 185.	0.7	4
62	Reply to Zhang and Xu: Environment is indeed important in any phenotypic study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2022917118.	3.3	0