

Greg Elgar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11276926/publications.pdf>

Version: 2024-02-01

84
papers

8,065
citations

126907

33
h-index

58581

82
g-index

85
all docs

85
docs citations

85
times ranked

11496
citing authors

#	ARTICLE	IF	CITATIONS
1	The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution. <i>Nature Genetics</i> , 2018, 50, 270-277.	21.4	262
2	Identifying Potential Regulatory Elements by Transcription Factor Binding Site Alignment Using Partial Order Graphs. <i>International Journal of Foundations of Computer Science</i> , 2018, 29, 1345-1354.	1.1	2
3	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. <i>Nature</i> , 2017, 545, 446-451.	27.8	1,287
4	Aberrant ribonucleotide incorporation and multiple deletions in mitochondrial DNA of the murine MPV17 disease model. <i>Nucleic Acids Research</i> , 2017, 45, 12808-12815.	14.5	43
5	MPV17 Loss Causes Deoxynucleotide Insufficiency and Slow DNA Replication in Mitochondria. <i>PLoS Genetics</i> , 2016, 12, e1005779.	3.5	67
6	Complete re-sequencing of a 2Mb topological domain encompassing the FTO/IRXB genes identifies a novel obesity-associated region upstream of IRX5. <i>Genome Medicine</i> , 2015, 7, 126.	8.2	16
7	A Simple Predictive Enhancer Syntax for Hindbrain Patterning Is Conserved in Vertebrate Genomes. <i>PLoS ONE</i> , 2015, 10, e0130413.	2.5	11
8	Identification and functional characterization of novel transcriptional enhancers involved in regulating human <i>GLI3</i> expression during early development. <i>Development Growth and Differentiation</i> , 2015, 57, 570-580.	1.5	9
9	Evolution of lineage-specific functions in ancient <i>cis</i> -regulatory modules. <i>Open Biology</i> , 2015, 5, 150079.	3.6	6
10	<i>Cis</i> -regulatory control of human <i>GLI2</i> expression in the developing neural tube and limb bud. <i>Developmental Dynamics</i> , 2015, 244, 681-692.	1.8	7
11	A Reporter Assay in Lamprey Embryos Reveals Both Functional Conservation and Elaboration of Vertebrate Enhancers. <i>PLoS ONE</i> , 2014, 9, e85492.	2.5	34
12	Dissection of a <i>Ciona</i> regulatory element reveals complexity of cross-species enhancer activity. <i>Developmental Biology</i> , 2014, 390, 261-272.	2.0	8
13	Purifying Selection in Deeply Conserved Human Enhancers Is More Consistent than in Coding Sequences. <i>PLoS ONE</i> , 2014, 9, e103357.	2.5	9
14	Capturing the regulatory interactions of eukaryote genomes. <i>Briefings in Functional Genomics</i> , 2013, 12, 142-160.	2.7	5
15	Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.	21.4	588
16	Parallel Evolution of Chordate <i>Cis</i> -Regulatory Code for Development. <i>PLoS Genetics</i> , 2013, 9, e1003904.	3.5	16
17	Lens development depends on a pair of highly conserved Sox21 regulatory elements. <i>Developmental Biology</i> , 2012, 365, 310-318.	2.0	23
18	Functional Analysis of Conserved Non-Coding Regions Around the Short Stature hox Gene (<i>shox</i>) in Whole Zebrafish Embryos. <i>PLoS ONE</i> , 2011, 6, e21498.	2.5	26

#	ARTICLE	IF	CITATIONS
19	Ancient Pbx-Hox signatures define hundreds of vertebrate developmental enhancers. BMC Genomics, 2011, 12, 637.	2.8	27
20	Minor change, major difference: divergent functions of highly conserved cis-regulatory elements subsequent to whole genome duplication events. Development (Cambridge), 2011, 138, 879-884.	2.5	27
21	Early Evolution of Conserved Regulatory Sequences Associated with Development in Vertebrates. PLoS Genetics, 2009, 5, e1000762.	3.5	82
22	The <i>PAX258</i> gene subfamily: A comparative perspective. Developmental Dynamics, 2009, 238, 2951-2974.	1.8	29
23	Pan-vertebrate conserved non-coding sequences associated with developmental regulation. Briefings in Functional Genomics & Proteomics, 2009, 8, 256-265.	3.8	17
24	Tuning in to the signals: noncoding sequence conservation in vertebrate genomes. Trends in Genetics, 2008, 24, 344-352.	6.7	168
25	Chapter 12 Organization of Conserved Elements Near Key Developmental Regulators in Vertebrate Genomes. Advances in Genetics, 2008, 61, 307-338.	1.8	29
26	Divergent evolution of the myosin heavy chain gene family in fish and tetrapods: evidence from comparative genomic analysis. Physiological Genomics, 2007, 32, 1-15.	2.3	40
27	Comparative genomics using Fugu reveals insights into regulatory subfunctionalization. Genome Biology, 2007, 8, R53.	9.6	66
28	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. Genome Biology, 2007, 8, R15.	9.6	117
29	CONDOR: a database resource of developmentally associated conserved non-coding elements. BMC Developmental Biology, 2007, 7, 100.	2.1	60
30	Ultraconserved non-coding sequence element controls a subset of spatiotemporal <i>GLI3</i> expression. Development Growth and Differentiation, 2007, 49, 543-553.	1.5	35
31	Human <i>GLI3</i> Intragenic Conserved Non-Coding Sequences Are Tissue-Specific Enhancers. PLoS ONE, 2007, 2, e366.	2.5	39
32	Characterisation of conserved non-coding sequences in vertebrate genomes using bioinformatics, statistics and functional studies. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2006, 1, 46-58.	1.0	5
33	Defining a genomic radius for long-range enhancer action: duplicated conserved non-coding elements hold the key. Trends in Genetics, 2006, 22, 5-10.	6.7	69
34	Ancient duplicated conserved noncoding elements in vertebrates: A genomic and functional analysis. Genome Research, 2006, 16, 451-465.	5.5	88
35	A genomic approach to reveal novel genes associated with myotube formation in the model teleost, <i>Takifugu rubripes</i> . Physiological Genomics, 2005, 22, 327-338.	2.3	29
36	Striking nucleotide frequency pattern at the borders of highly conserved vertebrate non-coding sequences. Trends in Genetics, 2005, 21, 436-440.	6.7	27

#	ARTICLE	IF	CITATIONS
37	The Fugu and Zebrafish genomes. , 2005, , .		0
38	Prediction of cis-regulatory elements using binding site matrices – the successes, the failures and the reasons for both. Current Opinion in Genetics and Development, 2005, 15, 395-402.	3.3	57
39	Highly conserved regulatory elements around the gene may contribute to the maintenance of conserved synteny across human chromosome 7q36.3. Genomics, 2005, 86, 172-181.	2.9	61
40	Plenty more fish in the sea: Comparative and functional genomics using teleost models. Briefings in Functional Genomics & Proteomics, 2004, 3, 15-25.	3.8	5
41	A Fugu-Human Genome Synteny Viewer: web software for graphical display and annotation reports of synteny between Fugu genomic sequence and human genes. Nucleic Acids Research, 2004, 32, 2618-2622.	14.5	8
42	Highly Conserved Non-Coding Sequences Are Associated with Vertebrate Development. PLoS Biology, 2004, 3, e7.	5.6	833
43	Identification and analysis of cis-regulatory elements in development using comparative genomics with the pufferfish, Fugu rubripes. Seminars in Cell and Developmental Biology, 2004, 15, 715-719.	5.0	5
44	Identification and analysis of cis-regulatory elements in development using comparative genomics with the pufferfish, Fugu rubripes. Seminars in Cell and Developmental Biology, 2004, 15, 715-719.	5.0	9
45	Comparative analysis of vertebrate Shh genes identifies novel conserved non-coding sequence. Mammalian Genome, 2003, 14, 192-201.	2.2	23
46	AP1 genes in Fugu indicate a divergent transcriptional control to that of mammals. Mammalian Genome, 2003, 14, 514-525.	2.2	12
47	Characterisation of a gene cluster in Fugu rubripes containing the complement component C4 gene. Gene, 2003, 312, 73-83.	2.2	10
48	The nicotinic acetylcholine receptor gene family of the pufferfish, Fugu rubripes†. Genomics, 2003, 82, 441-451.	2.9	40
49	Fugu ESTs: New Resources for Transcription Analysis and Genome Annotation. Genome Research, 2003, 13, 2747-2753.	5.5	41
50	Theatre: a software tool for detailed comparative analysis and visualization of genomic sequence. Nucleic Acids Research, 2003, 31, 3510-3517.	14.5	1
51	Comparative Analysis of Vertebrate Dystrophin Loci Indicate Intron Gigantism as a Common Feature. Genome Research, 2003, 13, 764-772.	5.5	25
52	Genomic Characterisation of Putative Growth Hormone Releasing Hormone (GHRH) Receptor Genes in the Teleost Fish Fugu rubripes. DNA Sequence, 2003, 14, 129-133.	0.7	10
53	A long-range Shh enhancer regulates expression in the developing limb and fin and is associated with preaxial polydactyly. Human Molecular Genetics, 2003, 12, 1725-1735.	2.9	1,002
54	Faithful expression of a tagged Fugu WT1 protein from a genomic transgene in zebrafish: efficient splicing of pufferfish genes in zebrafish but not mice. Nucleic Acids Research, 2003, 31, 2795-2802.	14.5	11

#	ARTICLE	IF	CITATIONS
55	Molecular evolution of the vertebrate blood coagulation network. <i>Thrombosis and Haemostasis</i> , 2003, 89, 420-428.	3.4	88
56	Analyses of the Extent of Shared Synteny and Conserved Gene Orders between the Genome of <i>Fugu rubripes</i> and Human 20q. <i>Genome Research</i> , 2002, 12, 776-784.	5.5	46
57	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Fugu rubripes</i> . <i>Science</i> , 2002, 297, 1301-1310.	12.6	1,432
58	Characterization of a novel gene adjacent to PAX6, revealing synteny conservation with functional significance. <i>Mammalian Genome</i> , 2002, 13, 102-107.	2.2	42
59	Fugu orthologues of human major histocompatibility complex genes: a genome survey. <i>Immunogenetics</i> , 2002, 54, 367-380.	2.4	42
60	Characterisation of two topoisomerase 1 genes in the pufferfish (<i>Fugu rubripes</i>). <i>Gene</i> , 2001, 265, 195-204.	2.2	14
61	Characterization of the MHC class II region of the Japanese pufferfish (<i>Fugu rubripes</i>). <i>Immunogenetics</i> , 2001, 52, 174-185.	2.4	61
62	SAND, a New Protein Family: From Nucleic Acid to Protein Structure and Function Prediction. <i>Comparative and Functional Genomics</i> , 2001, 2, 226-235.	2.0	6
63	Use of the Japanese Pufferfish (<i>Fugu rubripes</i>) in Comparative Genomics. <i>Marine Biotechnology</i> , 2001, 3, S130-S140.	2.4	17
64	Gene Identification Using the Pufferfish, <i>Fugu rubripes</i> , by Sequence Scanning. , 2001, 175, 249-262.		0
65	Identification and Characterization of a β Proteasome Subunit Cluster in the Japanese Pufferfish (<i>Fugu</i>) Tj ETQq1 10,784314,rgBT /Ove	0.8	33
66	Identification and analysis of two snail genes in the pufferfish (<i>Fugu rubripes</i>) and mapping of human SNA to 20q. <i>Gene</i> , 2000, 247, 119-128.	2.2	15
67	Genomic structure and expression of parathyroid hormone-related protein gene (PTHrP) in a teleost, <i>Fugu rubripes</i> . <i>Gene</i> , 2000, 250, 67-76.	2.2	53
68	Characterization of the <i>Fugu rubripes</i> NLK and FN5 genes flanking the NF1 (Neurofibromatosis type 1) gene in the 5' direction and mapping of the human counterparts. <i>Gene</i> , 2000, 251, 63-71.	2.2	8
69	<i>Fugu Rubripes: A Fish Model Genome.</i> , 2000, , 71-96.		3
70	Three receptor genes for plasminogen related growth factors in the genome of the puffer fish <i>Fugu rubripes</i> . <i>FEBS Letters</i> , 1999, 443, 370-374.	2.8	15
71	The neural cell adhesion molecule L1: genomic organisation and differential splicing is conserved between man and the pufferfish <i>Fugu</i> . <i>Gene</i> , 1998, 208, 7-15.	2.2	35
72	Genomic characterization of the Neurofibromatosis Type 1 gene of <i>Fugu rubripes</i> . <i>Gene</i> , 1998, 222, 145-153.	2.2	17

#	ARTICLE	IF	CITATIONS
73	The Pufferfish SLP-1 Gene, a New Member of the SCL/TAL-1 Family of Transcription Factors. <i>Genomics</i> , 1998, 48, 52-62.	2.9	14
74	The identification and characterization of microsatellites in the compact genome of the Japanese pufferfish, <i>Fugu rubripes</i> : perspectives in functional and comparative genomic analyses. <i>Journal of Molecular Biology</i> , 1998, 278, 843-854.	4.2	80
75	The Pufferfish Gene Map. <i>ILAR Journal</i> , 1998, 39, 249-256.	1.8	3
76	Genomic Structure and Sequence Analysis of the Valyl-tRNA synthetase Gene of the Japanese Pufferfish, <i>Fugu rubripes</i> . <i>DNA Sequence</i> , 1997, 7, 141-151.	0.7	1
77	Regions of Human Chromosome 2 (2q32-q35) and Mouse Chromosome 1 Show Synteny with the Pufferfish Genome (<i>Fugu rubripes</i>). <i>Genomics</i> , 1997, 45, 158-167.	2.9	26
78	Cloning and sequencing of complement component C9 and its linkage to DOC-2 in the pufferfish <i>Fugu rubripes</i> . <i>Gene</i> , 1997, 200, 203-211.	2.2	44
79	Molecular cloning of major histocompatibility complex class I cDNAs from the pufferfish <i>Fugu rubripes</i> . <i>Immunogenetics</i> , 1997, 47, 170-173.	2.4	16
80	Quality not quantity: the pufferfish genome. <i>Human Molecular Genetics</i> , 1996, 5, 1437-1442.	2.9	71
81	Small is beautiful: comparative genomics with the pufferfish (<i>Fugu rubripes</i>). <i>Trends in Genetics</i> , 1996, 12, 145-150.	6.7	150
82	Comparative sequence analysis of the human and pufferfish Huntington's disease genes. <i>Nature Genetics</i> , 1995, 10, 67-76.	21.4	144
83	Genomic Structure and Nucleotide Sequence of the p53 Gene of the Puffer Fish <i>Fugu rubripes</i> . <i>Genomics</i> , 1995, 27, 442-446.	2.9	34
84	Carbamoyl phosphate synthetase (CPSase) in the PYR1-3 multigene of <i>Dictyostelium discoideum</i> . <i>DNA Sequence</i> , 1992, 2, 219-226.	0.7	5