Jose Luis Gomez-Skarmeta

List of Publications by Year
in descending order

122 papers	8,416 citations	44042 48 h-index	54882 84 g-index
138 all docs	138 docs citations	138 times ranked	13040 citing authors

#	Article	IF	Citations
1	Obesity-associated variants within FTO form long-range functional connections with IRX3. Nature, 2014, 507, 371-375.	13.7	1,079
2	araucan and caupolican, Two Members of the Novel Iroquois Complex, Encode Homeoproteins That Control Proneural and Vein-Forming Genes. Cell, 1996, 85, 95-105.	13.5	310
3	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	13.7	224
4	Dynamics of enhancer chromatin signatures mark the transition from pluripotency to cell specification during embryogenesis. Genome Research, 2012, 22, 2043-2053.	2.4	219
5	Active DNA demethylation at enhancers during the vertebrate phylotypic period. Nature Genetics, 2016, 48, 417-426.	9.4	210
6	Silencing of *Smed*-β*catenin1* generates radial-like hypercephalized planarians. Development (Cambridge), 2008, 135, 1215-1221.	1.2	192
7	Long-range gene regulation links genomic type 2 diabetes and obesity risk regions to *HHEX*, *SOX4*, and *IRX3*. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 775-780.	3.3	189
8	TEAD and YAP regulate the enhancer network of human embryonic pancreatic progenitors. Nature Cell Biology, 2015, 17, 615-626.	4.6	188
9	A functional survey of the enhancer activity of conserved non-coding sequences from vertebrate Iroquois cluster gene deserts. Genome Research, 2005, 15, 1061-1072.	2.4	174
10	Cis-regulation of achaete and scute: shared enhancer-like elements drive their coexpression in proneural clusters of the imaginal discs.. Genes and Development, 1995, 9, 1869-1882.	2.7	171
11	Genome-Wide Profiling of p63 DNA–Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. PLoS Genetics, 2010, 6, e1001065.	1.5	169
12	Zebrafish enhancer detection (ZED) vector: A new tool to facilitate transgenesis and the functional analysis of *cis*-€regulatory regions in zebrafish. Developmental Dynamics, 2009, 238, 2409-2417.	0.8	153
13	Iroquois genes: genomic organization and function in vertebrate neural development. Current Opinion in Genetics and Development, 2002, 12, 403-408.	1.5	149
14	Evolutionary comparison reveals that diverging CTCF sites are signatures of ancestral topological associating domains borders. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7542-7547.	3.3	147
15	Identification of the vertebrate Iroquois homeobox gene family with overlapping expression during early development of the nervous system. Mechanisms of Development, 1997, 69, 169-181.	1.7	146
16	The Dynamic Regulatory Genome of Capsaspora and the Origin of Animal Multicellularity. Cell, 2016, 165, 1224-1237.	13.5	139
17	Xiro, a Xenopus homolog of the Drosophila Iroquois complex genes, controls development at the neural plate. EMBO Journal, 1998, 17, 181-190.	3.5	133
18	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. Science, 2021, 372, 984-989.	6.0	132

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19	Extensive conservation of ancient microsynteny across metazoans due to *cis*-regulatory constraints. Genome Research, 2012, 22, 2356-2367.	2.4	126
20	Odd-skipped genes encode repressors that control kidney development. Developmental Biology, 2007, 301, 518-531.	0.9	124
21	Deep conservation of wrist and digit enhancers in fish. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 803-808.	3.3	121
22	A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation. Nature Genetics, 2016, 48, 336-341.	9.4	113
23	Half a century of neural prepatterning: the story of a few bristles and many genes. Nature Reviews Neuroscience, 2003, 4, 587-598.	4.9	112
24	The Iroquois homeodomain proteins are required to specify body wall identity in Drosophila. Genes and Development, 1999, 13, 1754-1761.	2.7	110
25	araucan and caupolican provide a link between compartment subdivisions and patterning of sensory organs and veins in the Drosophila wing.. Genes and Development, 1996, 10, 2935-2945.	2.7	106
26	MIR retrotransposon sequences provide insulators to the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4428-37.	3.3	104
27	Restless Legs Syndrome-associated intronic common variant in *Meis1* alters enhancer function in the developing telencephalon. Genome Research, 2014, 24, 592-603.	2.4	102
28	Genome-wide CTCF distribution in vertebrates defines equivalent sites that aid the identification of disease-associated genes. Nature Structural and Molecular Biology, 2011, 18, 708-714.	3.6	95
29	iroquois: a prepattern gene that controls the formation of bristles on the thorax ofDrosophila. Mechanisms of Development, 1996, 59, 63-72.	1.7	94
30	Transphyletic conservation of developmental regulatory state in animal evolution. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14186-14191.	3.3	94
31	Noggin and Noggin-Like Genes Control Dorsoventral Axis Regeneration in Planarians. Current Biology, 2011, 21, 300-305.	1.8	93
32	Temporal uncoupling of the DNA methylome and transcriptional repression during embryogenesis. Genome Research, 2011, 21, 1313-1327.	2.4	92
33	The colorectal cancer risk at 18q21 is caused by a novel variant altering *SMAD7* expression. Genome Research, 2009, 19, 987-993.	2.4	85
34	*meis1* regulates *cyclin D1* and *c-myc* expression, and controls the proliferation of the multipotent cells in the early developing zebrafish eye. Development (Cambridge), 2008, 135, 799-803.	1.2	83
35	Hoxd13 Contribution to the Evolution of Vertebrate Appendages. Developmental Cell, 2012, 23, 1219-1229.	3.1	83
36	Early evolution of the T-box transcription factor family. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16050-16055.	3.3	80

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37	Dioxin receptor and SLUG transcription factors regulate the insulator activity of B1 SINE retrotransposons via an RNA polymerase switch. Genome Research, 2011, 21, 422-432.	2.4	76
38	Topologically associated domains: a successful scaffold for the evolution of gene regulation in animals. Wiley Interdisciplinary Reviews: Developmental Biology, 2017, 6, e265.	5.9	75
39	Allelic Variation at the 8q23.3 Colorectal Cancer Risk Locus Functions as a Cis-Acting Regulator of EIF3H. PLoS Genetics, 2010, 6, e1001126.	1.5	74
40	An evolutionarily conserved three-dimensional structure in the vertebrate Irx clusters facilitates enhancer sharing and coregulation. Nature Communications, 2011, 2, 310.	5.8	73
41	A conserved Shh cis-regulatory module highlights a common developmental origin of unpaired and paired fins. Nature Genetics, 2018, 50, 504-509.	9.4	72
42	The Xenopus Irx genes are essential for neural patterning and define the border between prethalamus and thalamus through mutual antagonism with the anterior repressors Fezf and Arx. Developmental Biology, 2009, 329, 258-268.	0.9	68
43	Heartbeat-Driven Pericardiac Fluid Forces Contribute to Epicardium Morphogenesis. Current Biology, 2013, 23, 1726-1735.	1.8	68
44	Identification of the first recurrent PAR1 deletion in LÃ©ri-Weill dyschondrosteosis and idiopathic short stature reveals the presence of a novel *SHOX* enhancer. Journal of Medical Genetics, 2012, 49, 442-450.	1.5	63
45	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	3.4	63
46	Xiro homeoproteins coordinate cell cycle exit and primary neuron formation by upregulating neuronal-fate repressors and downregulating the cell-cycle inhibitor XGadd45-γ. Mechanisms of Development, 2002, 119, 69-80.	1.7	56
47	A dual requirement for Iroquois genes during *Xenopus* kidney development. Development (Cambridge), 2008, 135, 3197-3207.	1.2	55
48	Conserved developmental expression of Fezf in chordates and Drosophila and the origin of the Zona Limitans Intrathalamica (ZLI) brain organizer. EvoDevo, 2010, 1, 7.	1.3	55
49	CTCF counter-regulates cardiomyocyte development and maturation programs in the embryonic heart. PLoS Genetics, 2017, 13, e1006985.	1.5	54
50	Long-range regulatory interactions at the 4q25 atrial fibrillation risk locus involve PITX2c and ENPEP. BMC Biology, 2015, 13, 26.	1.7	53
51	Conservative route to genome compaction in a miniature annelid. Nature Ecology and Evolution, 2021, 5, 231-242.	3.4	51
52	Characterization of the accessible genome in the human malaria parasite Plasmodium falciparum. Nucleic Acids Research, 2018, 46, 9414-9431.	6.5	50
53	Conserved cross-interactions in Drosophila and Xenopus between Ras/MAPK signaling and the dual-specificity phosphatase MKP3. Developmental Dynamics, 2005, 232, 695-708.	0.8	49
54	Suppression of Bmp4 signaling by the zinc-finger repressors Osr1 and Osr2 is required for Wnt/β-catenin-mediated lung specification in *Xenopus*. Development (Cambridge), 2012, 139, 3010-3020.	1.2	49

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55	A novel function for the Xslug gene: control of dorsal mesendoderm development by repressing BMP-4. Mechanisms of Development, 2000, 97, 47-56.	1.7	48
56	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
57	The developmental epigenomics toolbox: ChIP-seq and MethylCap-seq profiling of early zebrafish embryos. Methods, 2013, 62, 207-215.	1.9	47
58	Comparative epigenomics in distantly related teleost species identifies conserved *cis*-regulatory nodes active during the vertebrate phylotypic period. Genome Research, 2014, 24, 1075-1085.	2.4	47
59	A Polymorphic Enhancer near GREM1 Influences Bowel Cancer Risk through Differential CDX2 and TCF7L2 Binding. Cell Reports, 2014, 8, 983-990.	2.9	45
60	New technologies, new findings, and new concepts in the study of vertebratecis-regulatory sequences. Developmental Dynamics, 2006, 235, 870-885.	0.8	40
61	The 14q22.2 colorectal cancer variant rs4444235 shows cis-acting regulation of BMP4. Oncogene, 2012, 31, 3777-3784.	2.6	39
62	Xenopus brain factor-2 controls mesoderm, forebrain and neural crest development. Mechanisms of Development, 1999, 80, 15-27.	1.7	38
63	Gene regulatory network architecture in different developmental contexts influences the genetic basis of morphological evolution. PLoS Genetics, 2018, 14, e1007375.	1.5	38
64	Multiple enhancers located in a 1-Mb region upstream of POU3F4 promote expression during inner ear development and may be required for hearing. Human Genetics, 2010, 128, 411-419.	1.8	35
65	An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement. Genome Research, 2012, 22, 642-655.	2.4	35
66	Coenzyme Q10 and alpha-tocopherol protect against amitriptyline toxicity. Toxicology and Applied Pharmacology, 2009, 235, 329-337.	1.3	34
67	Cracking the genome's second code: Enhancer detection by combined phylogenetic footprinting and transgenic fish and frog embryos. Methods, 2006, 39, 212-219.	1.9	33
68	New frontiers in the evolution of fin development. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 540-552.	0.6	32
69	Meis1 coordinates a network of genes implicated in eye development and microphthalmia. Development (Cambridge), 2015, 142, 3009-20.	1.2	32
70	Xiro-1controls mesoderm patterning by repressingbmp-4expression in the spemann organizer. Developmental Dynamics, 2001, 222, 368-376.	0.8	31
71	The *osr1* and *osr2* genes act in the pronephric anlage downstream of retinoic acid signaling and upstream of *wnt2b* to maintain pectoral fin development. Development (Cambridge), 2012, 139, 301-311.	1.2	31
72	Evolution of embryonic cis-regulatory landscapes between divergent Phallusia and Ciona ascidians. Developmental Biology, 2019, 448, 71-87.	0.9	29

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73	Assay for transposase-accessible chromatin and circularized chromosome conformation capture, two methods to explore the regulatory landscapes of genes in zebrafish. Methods in Cell Biology, 2016, 135, 413-430.	0.5	28
74	Asthma-associated genetic variants induce IL33 differential expression through an enhancer-blocking regulatory region. Nature Communications, 2021, 12, 6115.	5.8	28
75	The Irx gene family in zebrafish: genomic structure, evolution and initial characterization of irx5b. Development Genes and Evolution, 2004, 214, 277-284.	0.4	27
76	Profiling of conserved non-coding elements upstream of SHOX and functional characterisation of the SHOX cis-regulatory landscape. Scientific Reports, 2016, 5, 17667.	1.6	27
77	RE-1 Silencer of Transcription/Neural Restrictive Silencer Factor Modulates Ectodermal Patterning during Xenopus Development. Journal of Neuroscience, 2006, 26, 2820-2829.	1.7	26
78	Deep conservation of *cis*-regulatory elements in metazoans. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130020.	1.8	26
79	Evolutionary emergence of the *rac3b* / *rfng* / *sgca* regulatory cluster refined mechanisms for hindbrain boundaries formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3731-E3740.	3.3	26
80	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	9.4	26
81	Identification and Analysis of Conserved cis-Regulatory Regions of the MEIS1 Gene. PLoS ONE, 2012, 7, e33617.	1.1	20
82	Understanding the regulatory genome. International Journal of Developmental Biology, 2009, 53, 1367-1378.	0.3	19
83	Genetic regulation of amphioxus somitogenesis informs the evolution of the vertebrate head mesoderm. Nature Ecology and Evolution, 2019, 3, 1233-1240.	3.4	19
84	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. Nature Communications, 2021, 12, 3116.	5.8	19
85	Several Cis-regulatory Elements Control mRNA Stability, Translation Efficiency, and Expression Pattern of Prrxl1 (Paired Related Homeobox Protein-like 1). Journal of Biological Chemistry, 2013, 288, 36285-36301.	1.6	17
86	*SIRPB1* copy‑number polymorphism as candidate quantitative trait locus for impulsive‑disinhibited personality. Genes, Brain and Behavior, 2014, 13, 653-662.	1.1	17
87	Dynamic changes in the epigenomic landscape regulate human organogenesis and link to developmental disorders. Nature Communications, 2020, 11, 3920.	5.8	17
88	Formation of posterior cranial placode derivatives requires the Iroquois transcription factor irx4a. Molecular and Cellular Neurosciences, 2009, 40, 328-337.	1.0	16
89	A conserved function of the chromatin ATPase Kismet in the regulation of hedgehog expression. Developmental Biology, 2011, 350, 382-392.	0.9	16
90	Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. BMC Genomics, 2012, 13, 713.	1.2	16

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91	Embryonic DNA methylation: insights from the genomics era. Briefings in Functional Genomics, 2014, 13, 121-130.	1.3	16
92	Genome-wide epigenetic cross-talk between DNA methylation and H3K27me3 in zebrafish embryos. Genomics Data, 2015, 6, 7-9.	1.3	16
93	The conserved barH-like homeobox-2 gene barhl2 acts downstream of orthodentricle-2 and together with iroquois-3 in establishment of the caudal forebrain signaling center induced by Sonic Hedgehog. Developmental Biology, 2014, 396, 107-120.	0.9	15
94	Cis-regulatory landscapes in development and evolution. Current Opinion in Genetics and Development, 2017, 43, 17-22.	1.5	15
95	Dissecting the Transcriptional Regulatory Properties of Human Chromosome 16 Highly Conserved Non-Coding Regions. PLoS ONE, 2011, 6, e24824.	1.1	13
96	An evolutionary perspective of regulatory landscape dynamics in development and disease. Current Opinion in Cell Biology, 2018, 55, 24-29.	2.6	13
97	Ancient Genomic Regulatory Blocks Are a Source for Regulatory Gene Deserts in Vertebrates after Whole-Genome Duplications. Molecular Biology and Evolution, 2020, 37, 2857-2864.	3.5	13
98	The Xiro-repressed gene CoREST is expressed in Xenopus neural territories. Mechanisms of Development, 2002, 110, 209-211.	1.7	12
99	A mobile insulator system to detect and disrupt *cis*-regulatory landscapes in vertebrates. Genome Research, 2014, 24, 487-495.	2.4	12
100	Assaying Chromatin Accessibility Using ATAC-Seq in Invertebrate Chordate Embryos. Frontiers in Cell and Developmental Biology, 2020, 7, 372.	1.8	12
101	Characterization of New Otic Enhancers of the Pou3f4 Gene Reveal Distinct Signaling Pathway Regulation and Spatio-Temporal Patterns. PLoS ONE, 2010, 5, e15907.	1.1	12
102	Xenopus Xlmo4 is a GATA cofactor during ventral mesoderm formation and regulates Ldb1 availability at the dorsal mesoderm and the neural plate. Developmental Biology, 2003, 264, 564-581.	0.9	11
103	A role for insulator elements in the regulation of gene expression response to hypoxia. Nucleic Acids Research, 2012, 40, 1916-1927.	6.5	11
104	Yap1b, a divergent Yap/Taz family member, cooperates with yap1 in survival and morphogenesis via common transcriptional targets. Development (Cambridge), 2019, 146, .	1.2	10
105	4Cin: A computational pipeline for 3D genome modeling and virtual Hi-C analyses from 4C data. PLoS Computational Biology, 2018, 14, e1006030.	1.5	9
106	The *Shh* / *Gli3* gene regulatory network precedes the origin of paired fins and reveals the deep homology between distal fins and digits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	9
107	Gain of gene regulatory network interconnectivity at the origin of vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114802119.	3.3	9
108	XTIF2, a Xenopus homologue of the human transcription intermediary factor, is required for a nuclear receptor pathway that also interacts with CBP to suppress Brachyury and XMyoD. Mechanisms of Development, 2000, 91, 119-129.	1.7	6

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109	Matricellular protein SPARC/osteonectin expression is regulated by DNA methylation in its core promoter region. Developmental Dynamics, 2015, 244, 693-702.	0.8	6
110	A common copy-number variant within SIRPB1 correlates with human Out-of-Africa migration after genetic drift correction. PLoS ONE, 2018, 13, e0193614.	1.1	6
111	Engineered Salmonella allows real-time heterologous gene expression monitoring within infected zebrafish embryos. Journal of Biotechnology, 2012, 157, 413-416.	1.9	5
112	Deletion 1q43â€44 in a patient with clinical diagnosis of Warburgâ€"Micro syndrome. American Journal of Medical Genetics, Part A, 2015, 167, 1243-1251.	0.7	5
113	Boundary sequences flanking the mouse tyrosinase locus ensure faithful pattern of gene expression. Scientific Reports, 2020, 10, 15494.	1.6	5
114	Making Reporter Gene Constructs to Analyze Cis-regulatory Elements. Methods in Molecular Biology, 2012, 772, 397-408.	0.4	5
115	ATAC-Seq for Assaying Chromatin Accessibility Protocol Using Echinoderm Embryos. Methods in Molecular Biology, 2021, 2219, 253-265.	0.4	5
116	Multidimensional chromatin profiling of zebrafish pancreas to uncover and investigate disease-relevant enhancers. Nature Communications, 2022, 13, 1945.	5.8	5
117	Gene Regulatory Networks of Epidermal and Neural Fate Choice in a Chordate. Molecular Biology and Evolution, 2022, 39, .	3.5	4
118	Regulatory Architecture of the RCA Gene Cluster Captures an Intragenic TAD Boundary, CTCF-Mediated Chromatin Looping and a Long-Range Intergenic Enhancer. Frontiers in Immunology, 0, 13, .	2.2	4
119	*sox21a* directs lateral line patterning by modulating FGF signaling. Developmental Neurobiology, 2015, 75, 80-92.	1.5	3
120	A novel chromatin insulator regulates the chicken folate receptor gene from the influence of nearby constitutive heterochromatin and the Î²-globin locus. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 955-965.	0.9	3
121	Reprogramming Nuclear Architecture: Just a TAD. Cell Stem Cell, 2019, 24, 679-681.	5.2	2
122	Editorial. Seminars in Cell and Developmental Biology, 2016, 57, 1.	2.3	0