

# Francois Spitz

## 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.

35  
papers

4,560  
citations

23  
h-index

37  
g-index

37  
ext. papers

5,611  
ext. citations

16.8  
avg, IF

5.82  
L-index

#	Paper	IF	Citations
35	Genetic dissection identifies Necdin as a driver gene in a mouse model of paternal 15q duplications. <i>Nature Communications</i> , <b>2021</b> , 12, 4056	17.4	0
34	Dissection of the Fgf8 regulatory landscape by in vivo CRISPR-editing reveals extensive intra- and inter-enhancer redundancy. <i>Nature Communications</i> , <b>2021</b> , 12, 439	17.4	8
33	Signals from the brain and olfactory epithelium control shaping of the mammalian nasal capsule cartilage. <i>ELife</i> , <b>2018</b> , 7,	8.9	16
32	Gene regulation during development in the light of topologically associating domains. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , <b>2016</b> , 5, 169-85	5.9	17
31	Gene regulation at a distance: From remote enhancers to 3D regulatory ensembles. <i>Seminars in Cell and Developmental Biology</i> , <b>2016</b> , 57, 57-67	7.5	64
30	The Shh Topological Domain Facilitates the Action of Remote Enhancers by Reducing the Effects of Genomic Distances. <i>Developmental Cell</i> , <b>2016</b> , 39, 529-543	10.2	134
29	Cis-regulatory architecture of a brain signaling center predates the origin of chordates. <i>Nature Genetics</i> , <b>2016</b> , 48, 575-80	36.3	40
28	Formation of new chromatin domains determines pathogenicity of genomic duplications. <i>Nature</i> , <b>2016</b> , 538, 265-269	50.4	396
27	Transcriptome profiling of white adipose tissue in a mouse model for 15q duplication syndrome. <i>Genomics Data</i> , <b>2015</b> , 5, 394-6		5
26	A discrete transition zone organizes the topological and regulatory autonomy of the adjacent tfap2c and bmp7 genes. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1004897	6	46
25	Model mice for 15q11-13 duplication syndrome exhibit late-onset obesity and altered lipid metabolism. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 4559-72	5.6	11
24	Hoxa2 selectively enhances Meis binding to change a branchial arch ground state. <i>Developmental Cell</i> , <b>2015</b> , 32, 265-77	10.2	51
23	Functional and topological characteristics of mammalian regulatory domains. <i>Genome Research</i> , <b>2014</b> , 24, 390-400	9.7	279
22	The architecture of gene expression: integrating dispersed cis-regulatory modules into coherent regulatory domains. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 27, 74-82	4.9	40
21	TRACER: a resource to study the regulatory architecture of the mouse genome. <i>BMC Genomics</i> , <b>2013</b> , 14, 215	4.5	13
20	A switch between topological domains underlies HoxD genes collinearity in mouse limbs. <i>Science</i> , <b>2013</b> , 340, 1234167	33.3	302
19	Phenotypic impact of genomic structural variation: insights from and for human disease. <i>Nature Reviews Genetics</i> , <b>2013</b> , 14, 125-38	30.1	340

18	An integrated holo-enhancer unit defines tissue and gene specificity of the Fgf8 regulatory landscape. <i>Developmental Cell</i> , <b>2013</b> , 24, 530-42	10.2	110
17	From remote enhancers to gene regulation: charting the genome's regulatory landscapes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20120358	5.8	26
16	Transcription factors: from enhancer binding to developmental control. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 613-26	30.1	1156
15	A regulatory archipelago controls Hox genes transcription in digits. <i>Cell</i> , <b>2011</b> , 147, 1132-45	56.2	367
14	Large-scale analysis of the regulatory architecture of the mouse genome with a transposon-associated sensor. <i>Nature Genetics</i> , <b>2011</b> , 43, 379-86	36.3	121
13	Control of vertebrate Hox clusters by remote and global cis-acting regulatory sequences. <i>Advances in Experimental Medicine and Biology</i> , <b>2010</b> , 689, 63-78	3.6	6
12	A systematic enhancer screen using lentivector transgenesis identifies conserved and non-conserved functional elements at the Olig1 and Olig2 locus. <i>PLoS ONE</i> , <b>2010</b> , 5, e15741	3.7	23
11	Uncoupling time and space in the collinear regulation of Hox genes. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000398	6	63
10	Global control regions and regulatory landscapes in vertebrate development and evolution. <i>Advances in Genetics</i> , <b>2008</b> , 61, 175-205	3.3	33
9	Characterization of mouse Dactylaplasia mutations: a model for human ectrodactyly SHFM3. <i>Mammalian Genome</i> , <b>2008</b> , 19, 272-8	3.2	17
8	Transgenic analysis of Hoxd gene regulation during digit development. <i>Developmental Biology</i> , <b>2007</b> , 306, 847-59	3.1	91
7	Inversion-induced disruption of the Hoxd cluster leads to the partition of regulatory landscapes. <i>Nature Genetics</i> , <b>2005</b> , 37, 889-93	36.3	119
6	Mouse limb deformity mutations disrupt a global control region within the large regulatory landscape required for Gremlin expression. <i>Genes and Development</i> , <b>2004</b> , 18, 1553-64	12.6	110
5	A global control region defines a chromosomal regulatory landscape containing the HoxD cluster. <i>Cell</i> , <b>2003</b> , 113, 405-17	56.2	370
4	A t(2;8) balanced translocation with breakpoints near the human HOXD complex causes mesomelic dysplasia and vertebral defects. <i>Genomics</i> , <b>2002</b> , 79, 493-8	4.3	40
3	Large scale transgenic and cluster deletion analysis of the HoxD complex separate an ancestral regulatory module from evolutionary innovations. <i>Genes and Development</i> , <b>2001</b> , 15, 2209-14	12.6	113
2	Development. The art of making a joint. <i>Science</i> , <b>2001</b> , 291, 1713-4	33.3	10
1	Two independent modes of chromosome organization are revealed by cohesin removal		20

