

# Manuel Irimia

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3438859/publications.pdf>

Version: 2024-02-01

112  
papers

11,528  
citations

50170

46  
h-index

34900

98  
g-index

142  
all docs

142  
docs citations

142  
times ranked

18147  
citing authors

#	ARTICLE	IF	CITATIONS
1	Is There a Prechordal Region and an Acroterminal Domain in Amphioxus?. Brain, Behavior and Evolution, 2022, 96, 334-352.	0.9	6
2	Parallel evolution of a splicing program controlling neuronal excitability in flies and mammals. Science Advances, 2022, 8, eabk0445.	4.7	15
3	Gene architecture directs splicing outcome in separate nuclear spatial regions. Molecular Cell, 2022, 82, 1021-1034.e8.	4.5	26
4	Gene Regulatory Networks of Epidermal and Neural Fate Choice in a Chordate. Molecular Biology and Evolution, 2022, 39, .	3.5	4
5	A developmentally programmed splicing failure contributes to DNA damage response attenuation during mammalian zygotic genome activation. Science Advances, 2022, 8, eabn4935.	4.7	14
6	The X-linked splicing regulator MBNL3 has been co-opted to restrict placental growth in eutherians. PLoS Biology, 2022, 20, e3001615.	2.6	4
7	Best practice standards for circular RNA research. Nature Methods, 2022, 19, 1208-1220.	9.0	58
8	Specialization of the photoreceptor transcriptome by <i>Srrm3</i> -dependent microexons is required for outer segment maintenance and vision. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
9	Conservative route to genome compaction in a miniature annelid. Nature Ecology and Evolution, 2021, 5, 231-242.	3.4	51
10	Alternative splicing landscapes in Arabidopsis thaliana across tissues and stress conditions highlight major functional differences with animals. Genome Biology, 2021, 22, 35.	3.8	93
11	Cooperative epithelial phagocytosis enables error correction in the early embryo. Nature, 2021, 590, 618-623.	13.7	28
12	Silencing of SRRM4 suppresses microexon inclusion and promotes tumor growth across cancers. PLoS Biology, 2021, 19, e3001138.	2.6	15
13	Huntington's disease-specific mis-splicing unveils key effector genes and altered splicing factors. Brain, 2021, 144, 2009-2023.	3.7	32
14	Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. Frontiers in Molecular Neuroscience, 2021, 14, 664912.	1.4	12
15	ExOrthist: a tool to infer exon orthologies at any evolutionary distance. Genome Biology, 2021, 22, 239.	3.8	11
16	Neuronal-specific microexon splicing of <i>TAF1</i> mRNA is directly regulated by SRRM4/nSR100. RNA Biology, 2020, 17, 62-74.	1.5	11
17	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
18	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. Nature Communications, 2020, 11, 2631.	5.8	57

#	ARTICLE	IF	CITATIONS
19	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , 2020, 77, 1176-1192.e16.	4.5	69
20	<i>sluc</i> : Unix tools for alternative splicing analysis. <i>Bioinformatics</i> , 2019, 35, 130-132.	1.8	56
21	Retention of paternal DNA methylome in the developing zebrafish germline. <i>Nature Communications</i> , 2019, 10, 3054.	5.8	99
22	Boosting Macroevolution: Genomic Changes Triggering Qualitative Expansions of Regulatory Potential. <i>Fascinating Life Sciences</i> , 2019, , 175-207.	0.5	0
23	Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of <i>Dscam</i> exon 9 variable exons. <i>Rna</i> , 2019, 25, 1353-1365.	1.6	16
24	ARGLU1 is a transcriptional coactivator and splicing regulator important for stress hormone signaling and development. <i>Nucleic Acids Research</i> , 2019, 47, 2856-2870.	6.5	20
25	A novel protein domain in an ancestral splicing factor drove the evolution of neural microexons. <i>Nature Ecology and Evolution</i> , 2019, 3, 691-701.	3.4	63
26	A novel LICAM isoform with angiogenic activity generated by NOVA2-mediated alternative splicing. <i>ELife</i> , 2019, 8, .	2.8	38
27	Absence of Tangentially Migrating Glutamatergic Neurons in the Developing Avian Brain. <i>Cell Reports</i> , 2018, 22, 96-109.	2.9	40
28	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	13.7	224
29	The Integrator complex regulates differential snRNA processing and fate of adult stem cells in the highly regenerative planarian <i>Schmidtea mediterranea</i> . <i>PLoS Genetics</i> , 2018, 14, e1007828.	1.5	14
30	Origin of exon skipping-rich transcriptomes in animals driven by evolution of gene architecture. <i>Genome Biology</i> , 2018, 19, 135.	3.8	61
31	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. <i>Molecular Cell</i> , 2018, 72, 496-509.e9.	4.5	75
32	RES complex is associated with intron definition and required for zebrafish early embryogenesis. <i>PLoS Genetics</i> , 2018, 14, e1007473.	1.5	23
33	Autism-like phenotype and risk gene mRNA deadenylation by CPEB4 mis-splicing. <i>Nature</i> , 2018, 560, 441-446.	13.7	113
34	Major Roles for Pyrimidine Dimers, Nucleotide Excision Repair, and ATR in the Alternative Splicing Response to UV Irradiation. <i>Cell Reports</i> , 2017, 18, 2868-2879.	2.9	41
35	An atlas of alternative splicing profiles and functional associations reveals new regulatory programs and genes that simultaneously express multiple major isoforms. <i>Genome Research</i> , 2017, 27, 1759-1768.	2.4	316
36	Molecular basis of differential 3' splice site sensitivity to anti-tumor drugs targeting U2 snRNP. <i>Nature Communications</i> , 2017, 8, 2100.	5.8	45

#	ARTICLE	IF	CITATIONS
37	Evolutionary recruitment of flexible Esrp-dependent splicing programs into diverse embryonic morphogenetic processes. <i>Nature Communications</i> , 2017, 8, 1799.	5.8	40
38	Nodalâ€“Activin pathway is a conserved neural induction signal in chordates. <i>Nature Ecology and Evolution</i> , 2017, 1, 1192-1200.	3.4	22
39	Origin and evolution of the chordate central nervous system: insights from amphioxus genoarchitecture. <i>International Journal of Developmental Biology</i> , 2017, 61, 655-664.	0.3	8
40	Molecular regionalization of the developing amphioxus neural tube challenges major partitions of the vertebrate brain. <i>PLoS Biology</i> , 2017, 15, e2001573.	2.6	96
41	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. <i>Nature</i> , 2016, 540, 423-427.	13.7	603
42	Misregulation of an Activity-Dependent Splicing Network as a Common Mechanism Underlying Autism Spectrum Disorders. <i>Molecular Cell</i> , 2016, 64, 1023-1034.	4.5	121
43	Preferential binding of a stable G3<sc>BP</sc> ribonucleoprotein complex to intronâ€“retaining transcripts in mouse brain and modulation of their expression in the cerebellum. <i>Journal of Neurochemistry</i> , 2016, 139, 349-368.	2.1	17
44	Evolutionary origin and functional divergence of totipotent cell homeobox genes in eutherian mammals. <i>BMC Biology</i> , 2016, 14, 45.	1.7	37
45	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016, 5, .	2.8	48
46	The alternative splicing factor Nova2 regulates vascular development and lumen formation. <i>Nature Communications</i> , 2015, 6, 8479.	5.8	50
47	Essential roles for the splicing regulator nSR100/SRRM4 during nervous system development. <i>Genes and Development</i> , 2015, 29, 746-759.	2.7	115
48	An alternative splicing event amplifies evolutionary differences between vertebrates. <i>Science</i> , 2015, 349, 868-873.	6.0	128
49	Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. <i>ELife</i> , 2015, 4, e08904.	2.8	59
50	Stability Depends on Positive Autoregulation in Boolean Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003916.	1.5	23
51	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. <i>Cell</i> , 2014, 159, 1511-1523.	13.5	546
52	Elephant shark genome provides unique insights into gnathostome evolution. <i>Nature</i> , 2014, 505, 174-179.	13.7	689
53	A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis. <i>Molecular Cell</i> , 2014, 56, 90-103.	4.5	131
54	Widespread intron retention in mammals functionally tunes transcriptomes. <i>Genome Research</i> , 2014, 24, 1774-1786.	2.4	554

#	ARTICLE	IF	CITATIONS
55	Origin of Spliceosomal Introns and Alternative Splicing. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016071-a016071.	2.3	112
56	Functional Genomics Evidence Unearths New Moonlighting Roles of Outer Ring Coat Nucleoporins. Scientific Reports, 2014, 4, 4655.	1.6	20
57	Diversity and Evolution of Spliceosomal Systems. Methods in Molecular Biology, 2014, 1126, 13-33.	0.4	11
58	A compendium of RNA-binding motifs for decoding gene regulation. Nature, 2013, 499, 172-177.	13.7	1,281
59	Impact of gene gains, losses and duplication modes on the origin and diversification of vertebrates. Seminars in Cell and Developmental Biology, 2013, 24, 83-94.	2.3	87
60	Postnatal isoform switch and protein localization of LEF1 and TCF7L2 transcription factors in cortical, thalamic, and mesencephalic regions of the adult mouse brain. Brain Structure and Function, 2013, 218, 1531-1549.	1.2	44
61	Deep conservation of cis-regulatory elements in metazoans. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130020.	1.8	26
62	MBNL1 and RBFOX2 cooperate to establish a splicing programme involved in pluripotent stem cell differentiation. Nature Communications, 2013, 4, 2480.	5.8	120
63	Ancient cis-regulatory constraints and the evolution of genome architecture. Trends in Genetics, 2013, 29, 521-528.	2.9	30
64	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. Nature, 2013, 498, 241-245.	13.7	326
65	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. PLoS Computational Biology, 2013, 9, e1003030.	1.5	62
66	Genome of Acanthamoeba castellanii highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 2013, 14, R11.	13.9	296
67	Regulated aggregative multicellularity in a close unicellular relative of metazoa. ELife, 2013, 2, e01287.	2.8	139
68	Evolutionarily conserved A-to-I editing increases protein stability of the alternative splicing factor Nova1. RNA Biology, 2012, 9, 12-21.	1.5	40
69	Widespread Recurrent Evolution of Genomic Features. Genome Biology and Evolution, 2012, 4, 486-500.	1.1	34
70	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
71	Comparative genomics of the Hedgehog loci in chordates and the origins of Shh regulatory novelties. Scientific Reports, 2012, 2, 433.	1.6	29
72	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Nature, 2012, 492, 59-65.	13.7	377

#	ARTICLE	IF	CITATIONS
73	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593.	6.0	905
74	5-hmC in the brain is abundant in synaptic genes and shows differences at the exon-intron boundary. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1037-1043.	3.6	221
75	Tissue-Specific Alternative Splicing Remodels Protein-Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 884-892.	4.5	366
76	Genome Evolution: Where Do New Introns Come From?. <i>Current Biology</i> , 2012, 22, R529-R531.	1.8	13
77	Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. <i>BMC Genomics</i> , 2012, 13, 713.	1.2	16
78	Extensive conservation of ancient microsynteny across metazoans due to cis-regulatory constraints. <i>Genome Research</i> , 2012, 22, 2356-2367.	2.4	126
79	A Comparative Transcriptomic Analysis Reveals Conserved Features of Stem Cell Pluripotency in Planarians and Mammals. <i>Stem Cells</i> , 2012, 30, 1734-1745.	1.4	181
80	Alternative splicing: decoding an expansive regulatory layer. <i>Current Opinion in Cell Biology</i> , 2012, 24, 323-332.	2.6	151
81	Contrasting 5' and 3' Evolutionary Histories and Frequent Evolutionary Convergence in Meis/hth Gene Structures. <i>Genome Biology and Evolution</i> , 2011, 3, 551-564.	1.1	16
82	Transphyletic conservation of developmental regulatory state in animal evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14186-14191.	3.3	94
83	Distinct and redundant expression and transcriptional diversity of MEIS gene paralogs during chicken development. <i>Developmental Dynamics</i> , 2011, 240, 1475-1492.	0.8	21
84	Stepwise assembly of the Nova-regulated alternative splicing network in the vertebrate brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5319-5324.	3.3	38
85	Internal and External Paralogy in the Evolution of Tropomyosin Genes in Metazoans. <i>Molecular Biology and Evolution</i> , 2010, 27, 1504-1517.	3.5	23
86	Conserved developmental expression of Fezf in chordates and <i>Drosophila</i> and the origin of the Zona Limitans Intrathalamica (ZLI) brain organizer. <i>EvoDevo</i> , 2010, 1, 7.	1.3	55
87	From the American to the European amphioxus: towards experimental Evo-Devo at the origin of chordates. <i>International Journal of Developmental Biology</i> , 2009, 53, 1359-1366.	0.3	11
88	Evolution of Alternative Splicing Regulation: Changes in Predicted Exonic Splicing Regulators Are Not Associated with Changes in Alternative Splicing Levels in Primates. <i>PLoS ONE</i> , 2009, 4, e5800.	1.1	16
89	Complex selection on splice sites in intron-rich organisms. <i>Genome Research</i> , 2009, 19, 2021-2027.	2.4	25
90	Mystery of intron gain: new data and new models. <i>Trends in Genetics</i> , 2009, 25, 67-73.	2.9	64

#	ARTICLE	IF	CITATIONS
91	Quantitative regulation of alternative splicing in evolution and development. <i>BioEssays</i> , 2009, 31, 40-50.	1.2	49
92	22-P008 Comparison of Sowah and Iroquois expression patterns in metazoans: Together but not scrambled. <i>Mechanisms of Development</i> , 2009, 126, S331.	1.7	0
93	Splicing in the eukaryotic ancestor: form, function and dysfunction. <i>Trends in Ecology and Evolution</i> , 2009, 24, 447-455.	4.2	47
94	Rare Genomic Characters Do Not Support Coelomata: RGC_CAMs. <i>Journal of Molecular Evolution</i> , 2008, 66, 308-315.	0.8	30
95	When good transcripts go bad: artifactual RT-PCR "splicing" and genome analysis. <i>BioEssays</i> , 2008, 30, 601-605.	1.2	64
96	In response to letter from Benoit Chabot. <i>BioEssays</i> , 2008, 30, 1257-1258.	1.2	1
97	Origin of introns by "intronization" of exonic sequences. <i>Trends in Genetics</i> , 2008, 24, 378-381.	2.9	74
98	Intron mis-splicing: no alternative?. <i>Genome Biology</i> , 2008, 9, 208.	13.9	33
99	Convergent Evolution of Clustering of Iroquois Homeobox Genes across Metazoans. <i>Molecular Biology and Evolution</i> , 2008, 25, 1521-1525.	3.5	33
100	Spliceosomal introns as tools for genomic and evolutionary analysis. <i>Nucleic Acids Research</i> , 2008, 36, 1703-1712.	6.5	91
101	Origins of Human Malaria: Rare Genomic Changes and Full Mitochondrial Genomes Confirm the Relationship of <i>Plasmodium falciparum</i> to Other Mammalian Parasites but Complicate the Origins of <i>Plasmodium vivax</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1192-1198.	3.5	18
102	Gene Expansion and Retention Leads to a Diverse Tyrosine Kinase Superfamily in <i>Amphioxus</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1841-1854.	3.5	79
103	Rare Genomic Characters Do Not Support Coelomata: Intron Loss/Gain. <i>Molecular Biology and Evolution</i> , 2008, 25, 620-623.	3.5	40
104	Evolutionary Convergence on Highly-Conserved 3' Intron Structures in Intron-Poor Eukaryotes and Insights into the Ancestral Eukaryotic Genome. <i>PLoS Genetics</i> , 2008, 4, e1000148.	1.5	65
105	Widespread Evolutionary Conservation of Alternatively Spliced Exons in <i>Caenorhabditis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 375-382.	3.5	48
106	Origins of Human Malaria: Rare Genomic Changes and Full Mitochondrial Genomes Confirm the Relationship of <i>Plasmodium falciparum</i> to Other Mammalian Parasites but Complicate the Origins of <i>Plasmodium vivax</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 2511-2511.	3.5	1
107	High Qualitative and Quantitative Conservation of Alternative Splicing in <i>Caenorhabditis elegans</i> and <i>Caenorhabditis briggsae</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 909-917.	3.5	32
108	Rare Coding Sequence Changes are Consistent with Ecdysozoa, not Coelomata. <i>Molecular Biology and Evolution</i> , 2007, 24, 1604-1607.	3.5	58

#	ARTICLE	IF	CITATIONS
109	Functional and evolutionary analysis of alternatively spliced genes is consistent with an early eukaryotic origin of alternative splicing. <i>BMC Evolutionary Biology</i> , 2007, 7, 188.	3.2	75
110	Coevolution of genomic intron number and splice sites. <i>Trends in Genetics</i> , 2007, 23, 321-325.	2.9	93
111	Very Little Intron Gain in <i>Entamoeba histolytica</i> Genes Laterally Transferred from Prokaryotes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1824-1827.	3.5	30
112	CpG island promoter hypermethylation of the Ras-effector gene <i>NORE1A</i> occurs in the context of a wild-type K-ras in lung cancer. <i>Oncogene</i> , 2004, 23, 8695-8699.	2.6	55