

# Manuel Irimia

## List of Publications by Year in descending order

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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	A compendium of RNA-binding motifs for decoding gene regulation. <i>Nature</i> , 2013, 499, 172-177.	13.7	1,281
2	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593.	6.0	905
3	Elephant shark genome provides unique insights into gnathostome evolution. <i>Nature</i> , 2014, 505, 174-179.	13.7	689
4	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. <i>Nature</i> , 2016, 540, 423-427.	13.7	603
5	Widespread intron retention in mammals functionally tunes transcriptomes. <i>Genome Research</i> , 2014, 24, 1774-1786.	2.4	554
6	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. <i>Cell</i> , 2014, 159, 1511-1523.	13.5	546
7	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	13.7	377
8	Tissue-Specific Alternative Splicing Remodels Protein-Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 884-892.	4.5	366
9	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. <i>Nature</i> , 2013, 498, 241-245.	13.7	326
10	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
11	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
12	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	13.7	224
13	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
14	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
15	Alternative splicing: decoding an expansive regulatory layer. <i>Current Opinion in Cell Biology</i> , 2012, 24, 323-332.	2.6	151
16	Regulated aggregative multicellularity in a close unicellular relative of metazoa. <i>ELife</i> , 2013, 2, e01287.	2.8	139
17	A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis. <i>Molecular Cell</i> , 2014, 56, 90-103.	4.5	131
18	An alternative splicing event amplifies evolutionary differences between vertebrates. <i>Science</i> , 2015, 349, 868-873.	6.0	128

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19	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
20	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
21	MBNL1 and RBFOX2 cooperate to establish a splicing programme involved in pluripotent stem cell differentiation. <i>Nature Communications</i> , 2013, 4, 2480.	5.8	120
22	Essential roles for the splicing regulator nSR100/SRRM4 during nervous system development. <i>Genes and Development</i> , 2015, 29, 746-759.	2.7	115
23	Autism-like phenotype and risk gene mRNA deadenylation by CPEB4 mis-splicing. <i>Nature</i> , 2018, 560, 441-446.	13.7	113
24	Origin of Spliceosomal Introns and Alternative Splicing. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016071-a016071.	2.3	112
25	Retention of paternal DNA methylome in the developing zebrafish germline. <i>Nature Communications</i> , 2019, 10, 3054.	5.8	99
26	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
27	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
28	Coevolution of genomic intron number and splice sites. <i>Trends in Genetics</i> , 2007, 23, 321-325.	2.9	93
29	Alternative splicing landscapes in <i>Arabidopsis thaliana</i> across tissues and stress conditions highlight major functional differences with animals. <i>Genome Biology</i> , 2021, 22, 35.	3.8	93
30	Spliceosomal introns as tools for genomic and evolutionary analysis. <i>Nucleic Acids Research</i> , 2008, 36, 1703-1712.	6.5	91
31	Impact of gene gains, losses and duplication modes on the origin and diversification of vertebrates. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 83-94.	2.3	87
32	Gene Expansion and Retention Leads to a Diverse Tyrosine Kinase Superfamily in Amphioxus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1841-1854.	3.5	79
33	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
34	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. <i>Molecular Cell</i> , 2018, 72, 496-509.e9.	4.5	75
35	Origin of introns by "intronization" of exonic sequences. <i>Trends in Genetics</i> , 2008, 24, 378-381.	2.9	74
36	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , 2020, 77, 1176-1192.e16.	4.5	69

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37	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
38	When good transcripts go bad: artifactual RT-PCR splicing and genome analysis. <i>BioEssays</i> , 2008, 30, 601-605.	1.2	64
39	Mystery of intron gain: new data and new models. <i>Trends in Genetics</i> , 2009, 25, 67-73.	2.9	64
40	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
41	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. <i>PLoS Computational Biology</i> , 2013, 9, e1003030.	1.5	62
42	Origin of exon skipping-rich transcriptomes in animals driven by evolution of gene architecture. <i>Genome Biology</i> , 2018, 19, 135.	3.8	61
43	Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. <i>ELife</i> , 2015, 4, e08904.	2.8	59
44	Rare Coding Sequence Changes are Consistent with Ecdysozoa, not Coelomata. <i>Molecular Biology and Evolution</i> , 2007, 24, 1604-1607.	3.5	58
45	Best practice standards for circular RNA research. <i>Nature Methods</i> , 2022, 19, 1208-1220.	9.0	58
46	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. <i>Nature Communications</i> , 2020, 11, 2631.	5.8	57
47	<i>Splice</i> : Unix tools for alternative splicing analysis. <i>Bioinformatics</i> , 2019, 35, 130-132.	1.8	56
48	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
49	Conserved developmental expression of <i>Fezf</i> 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
50	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242.	3.4	51
51	The alternative splicing factor <i>Nova2</i> regulates vascular development and lumen formation. <i>Nature Communications</i> , 2015, 6, 8479.	5.8	50
52	Quantitative regulation of alternative splicing in evolution and development. <i>BioEssays</i> , 2009, 31, 40-50.	1.2	49
53	Widespread Evolutionary Conservation of Alternatively Spliced Exons in <i>Caenorhabditis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 375-382.	3.5	48
54	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016, 5, .	2.8	48

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55	Splicing in the eukaryotic ancestor: form, function and dysfunction. <i>Trends in Ecology and Evolution</i> , 2009, 24, 447-455.	4.2	47
56	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
57	Postnatal isoform switch and protein localization of LEF1 and TCF7L2 transcription factors in cortical, thalamic, and mesencephalic regions of the adult mouse brain. <i>Brain Structure and Function</i> , 2013, 218, 1531-1549.	1.2	44
58	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
59	Rare Genomic Characters Do Not Support Coelomata: Intron Loss/Gain. <i>Molecular Biology and Evolution</i> , 2008, 25, 620-623.	3.5	40
60	Evolutionarily conserved A-to-I editing increases protein stability of the alternative splicing factor <i>Novo1</i> . <i>RNA Biology</i> , 2012, 9, 12-21.	1.5	40
61	Evolutionary recruitment of flexible <i>Esrp</i> -dependent splicing programs into diverse embryonic morphogenetic processes. <i>Nature Communications</i> , 2017, 8, 1799.	5.8	40
62	Absence of Tangentially Migrating Glutamatergic Neurons in the Developing Avian Brain. <i>Cell Reports</i> , 2018, 22, 96-109.	2.9	40
63	Stepwise assembly of the <i>Nova</i> -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
64	A novel LICAM isoform with angiogenic activity generated by NOVA2-mediated alternative splicing. <i>ELife</i> , 2019, 8, .	2.8	38
65	Evolutionary origin and functional divergence of totipotent cell homeobox genes in eutherian mammals. <i>BMC Biology</i> , 2016, 14, 45.	1.7	37
66	An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement. <i>Genome Research</i> , 2012, 22, 642-655.	2.4	35
67	Widespread Recurrent Evolution of Genomic Features. <i>Genome Biology and Evolution</i> , 2012, 4, 486-500.	1.1	34
68	Intron mis-splicing: no alternative?. <i>Genome Biology</i> , 2008, 9, 208.	13.9	33
69	Convergent Evolution of Clustering of Iroquois Homeobox Genes across Metazoans. <i>Molecular Biology and Evolution</i> , 2008, 25, 1521-1525.	3.5	33
70	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
71	Huntington's disease-specific mis-splicing unveils key effector genes and altered splicing factors. <i>Brain</i> , 2021, 144, 2009-2023.	3.7	32
72	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

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73	Rare Genomic Characters Do Not Support Coelomata: RGC_CAMs. <i>Journal of Molecular Evolution</i> , 2008, 66, 308-315.	0.8	30
74	Ancient cis-regulatory constraints and the evolution of genome architecture. <i>Trends in Genetics</i> , 2013, 29, 521-528.	2.9	30
75	Comparative genomics of the Hedgehog loci in chordates and the origins of Shh regulatory novelties. <i>Scientific Reports</i> , 2012, 2, 433.	1.6	29
76	Cooperative epithelial phagocytosis enables error correction in the early embryo. <i>Nature</i> , 2021, 590, 618-623.	13.7	28
77	Deep conservation of cis-regulatory elements in metazoans. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130020.	1.8	26
78	Gene architecture directs splicing outcome in separate nuclear spatial regions. <i>Molecular Cell</i> , 2022, 82, 1021-1034.e8.	4.5	26
79	Complex selection on 5' splice sites in intron-rich organisms. <i>Genome Research</i> , 2009, 19, 2021-2027.	2.4	25
80	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
81	Stability Depends on Positive Autoregulation in Boolean Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003916.	1.5	23
82	RES complex is associated with intron definition and required for zebrafish early embryogenesis. <i>PLoS Genetics</i> , 2018, 14, e1007473.	1.5	23
83	Nodal/Activin pathway is a conserved neural induction signal in chordates. <i>Nature Ecology and Evolution</i> , 2017, 1, 1192-1200.	3.4	22
84	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
85	Functional Genomics Evidence Unearths New Moonlighting Roles of Outer Ring Coat Nucleoporins. <i>Scientific Reports</i> , 2014, 4, 4655.	1.6	20
86	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
87	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
88	Preferential binding of a stable G3BP ribonucleoprotein complex to intron-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
89	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
90	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

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91	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
92	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
93	Silencing of SRRM4 suppresses microexon inclusion and promotes tumor growth across cancers. <i>PLoS Biology</i> , 2021, 19, e3001138.	2.6	15
94	Parallel evolution of a splicing program controlling neuronal excitability in flies and mammals. <i>Science Advances</i> , 2022, 8, eabk0445.	4.7	15
95	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
96	A developmentally programmed splicing failure contributes to DNA damage response attenuation during mammalian zygotic genome activation. <i>Science Advances</i> , 2022, 8, eabn4935.	4.7	14
97	Genome Evolution: Where Do New Introns Come From?. <i>Current Biology</i> , 2012, 22, R529-R531.	1.8	13
98	Ancient Genomic Regulatory Blocks Are a Source for Regulatory Gene Deserts in Vertebrates after Whole-Genome Duplications. <i>Molecular Biology and Evolution</i> , 2020, 37, 2857-2864.	3.5	13
99	Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 664912.	1.4	12
100	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
101	Neuronal-specific microexon splicing of <i>TAF1</i> mRNA is directly regulated by SRRM4/nSR100. <i>RNA Biology</i> , 2020, 17, 62-74.	1.5	11
102	ExOrthist: a tool to infer exon orthologies at any evolutionary distance. <i>Genome Biology</i> , 2021, 22, 239.	3.8	11
103	Diversity and Evolution of Spliceosomal Systems. <i>Methods in Molecular Biology</i> , 2014, 1126, 13-33.	0.4	11
104	Specialization of the photoreceptor transcriptome by <i>Srrm3</i> -dependent microexons is required for outer segment maintenance and vision. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
105	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
106	Is There a Prechordal Region and an Acroterminal Domain in Amphioxus?. <i>Brain, Behavior and Evolution</i> , 2022, 96, 334-352.	0.9	6
107	Gene Regulatory Networks of Epidermal and Neural Fate Choice in a Chordate. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
108	The X-linked splicing regulator MBNL3 has been co-opted to restrict placental growth in eutherians. <i>PLoS Biology</i> , 2022, 20, e3001615.	2.6	4

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109	In response to letter from Benoit Chabot. <i>BioEssays</i> , 2008, 30, 1257-1258.	1.2	1
110	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
111	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
112	Boosting Macroevolution: Genomic Changes Triggering Qualitative Expansions of Regulatory Potential. <i>Fascinating Life Sciences</i> , 2019, , 175-207.	0.5	0