Juan Valcarcel

List of Publications by Year
in descending order

121 papers	12,494 citations	31976 53 h-index	27406 106 g-index
132 all docs	132 docs citations	132 times ranked	13481 citing authors

#	Article	IF	Citations
1	Alternative pre-mRNA splicing: the logic of combinatorial control. Trends in Biochemical Sciences, 2000, 25, 381-388.	7.5	804
2	RNA-binding proteins in human genetic disease. Nature Reviews Genetics, 2021, 22, 185-198.	16.3	720
3	Distinct binding specificities and functions of higher eukaryotic polypyrimidine tract-binding proteins. Science, 1995, 268, 1173-1176.	12.6	526
4	Alternative splicing and genome complexity. Nature Genetics, 2002, 30, 29-30.	21.4	490
5	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. Cell, 2014, 156, 1324-1335.	28.9	482
6	Nucleosome positioning as a determinant of exon recognition. Nature Structural and Molecular Biology, 2009, 16, 996-1001.	8.2	406
7	Roles and mechanisms of alternative splicing in cancer â€" implications for care. Nature Reviews Clinical Oncology, 2020, 17, 457-474.	27.6	400
8	The spliceosome as a target of novel antitumour drugs. Nature Reviews Drug Discovery, 2012, 11, 847-859.	46.4	355
9	The protein Sex-lethal antagonizes the splicing factor U2AF to regulate alternative splicing of transformer pre-mRNA. Nature, 1993, 362, 171-175.	27.8	316
10	Regulation of Fas Alternative Splicing by Antagonistic Effects of TIA-1 and PTB on Exon Definition. Molecular Cell, 2005, 19, 475-484.	9.7	307
11	RBM5, 6, and 10 Differentially Regulate NUMB Alternative Splicing to Control Cancer Cell Proliferation. Molecular Cell, 2013, 52, 720-733.	9.7	292
12	Inhibition of msl-2 splicing by Sex-lethal reveals interaction between U2AF35 and the 3â€² splice site AG. Nature, 1999, 402, 838-841.	27.8	262
13	Optimization of oligonucleotide-based DNA microarrays. Nucleic Acids Research, 2002, 30, 51e-51.	14.5	256
14	Interaction of U2AF65 RS Region with Pre-mRNA Branch Point and Promotion of Base Pairing with U2 snRNA. Science, 1996, 273, 1706-1709.	12.6	253
15	The Apoptosis-Promoting Factor TIA-1 Is a Regulator of Alternative Pre-mRNA Splicing. Molecular Cell, 2000, 6, 1089-1098.	9.7	252
16	U2AF65 recruits a novel human DEAD box protein required for the U2 snRNP-branchpoint interaction.. Genes and Development, 1997, 11, 1864-1872.	5.9	237
17	Reduced fidelity of branch point recognition and alternative splicing induced by the anti-tumor drug spliceostatin A. Genes and Development, 2011, 25, 445-459.	5.9	229
18	Large-scale analysis of genome and transcriptome alterations in multiple tumors unveils novel cancer-relevant splicing networks. Genome Research, 2016, 26, 732-744.	5.5	225

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19	The Spliceosome: The Ultimate RNA Chaperone and Sculptor. Trends in Biochemical Sciences, 2016, 41, 33-45.	7.5	215
20	Multi-domain conformational selection underlies pre-mRNA splicing regulation by U2AF. Nature, 2011, 475, 408-411.	27.8	202
21	The SR protein family: pleiotropic functions in pre-mRNA splicing. Trends in Biochemical Sciences, 1996, 21, 296-301.	7.5	199
22	The splicing regulator TIA-1 interacts with U1-C to promote U1 snRNP recruitment to 5' splice sites. EMBO Journal, 2002, 21, 6882-6892.	7.8	198
23	Building specificity with nonspecific RNA-binding proteins. Nature Structural and Molecular Biology, 2005, 12, 645-653.	8.2	196
24	Post-transcriptional regulation: The dawn of PTB. Current Biology, 1997, 7, R705-R708.	3.9	178
25	CPEB1 coordinates alternative 3â€²-UTR formation with translational regulation. Nature, 2013, 495, 121-125.	27.8	156
26	RBM5/Luca-15/H37 Regulates Fas Alternative Splice Site Pairing after Exon Definition. Molecular Cell, 2008, 32, 81-95.	9.7	153
27	The Ewing Sarcoma Protein Regulates DNA Damage-Induced Alternative Splicing. Molecular Cell, 2011, 43, 353-368.	9.7	149
28	U2AF-homology motif interactions are required for alternative splicing regulation by SPF45. Nature Structural and Molecular Biology, 2007, 14, 620-629.	8.2	147
29	The hnRNP A1 protein regulates HIV-1 tat splicing via a novel intron silencer element. EMBO Journal, 2001, 20, 5748-5758.	7.8	145
30	Splicing Regulation at the Second Catalytic Step by Sex-lethal Involves 3â€² Splice Site Recognition by SPF45. Cell, 2002, 109, 285-296.	28.9	140
31	Functional Splicing Network Reveals Extensive Regulatory Potential of the Core Spliceosomal Machinery. Molecular Cell, 2015, 57, 7-22.	9.7	140
32	Genome-wide Analysis of Alternative Pre-mRNA Splicing. Journal of Biological Chemistry, 2008, 283, 1229-1233.	3.4	129
33	The pathogenicity of splicing defects: mechanistic insights into preâ€•<scp>mRNA</scp> processing inform novel therapeutic approaches. EMBO Reports, 2015, 16, 1640-1655.	4.5	127
34	Intron Removal Requires Proofreading of U2AF/3' Splice Site Recognition by DEK. Science, 2006, 312, 1961-1965.	12.6	126
35	Targeting of U2AF65 to Sites of Active Splicing in the Nucleus. Journal of Cell Biology, 1997, 137, 975-987.	5.2	115
36	Isolated pseudoâ€“RNA-recognition motifs of SR proteins can regulate splicing using a noncanonical mode of RNA recognition. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2802-11.	7.1	109

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37	Tumor suppressor properties of the splicing regulatory factor RBM10. RNA Biology, 2016, 13, 466-472.	3.1	94
38	The complete local genotypeâ€“phenotype landscape for the alternative splicing of a human exon. Nature Communications, 2016, 7, 11558.	12.8	91
39	RNA splicing contributes to the generation of mature mRNAs of Borna disease virus, a non-segmented negative strand RNA virus. Virus Research, 1994, 34, 69-79.	2.2	88
40	hnRNP A1 Proofreads 3â€² Splice Site Recognition by U2AF. Molecular Cell, 2012, 45, 314-329.	9.7	87
41	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. Cell, 2019, 176, 549-563.e23.	28.9	87
42	Argonaute-1 binds transcriptional enhancers and controls constitutive and alternative splicing in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15622-15629.	7.1	86
43	Biochemical Function of Female-Lethal (2)D/Wilms' Tumor Suppressor-1-associated Proteins in Alternative Pre-mRNA Splicing. Journal of Biological Chemistry, 2003, 278, 3040-3047.	3.4	82
44	The expanding transcriptome: the genome as the â€˜Book of Sandâ€™. EMBO Journal, 2006, 25, 923-931.	7.8	78
45	Structure, dynamics and RNA binding of the multi-domain splicing factor TIA-1. Nucleic Acids Research, 2014, 42, 5949-5966.	14.5	77
46	Alternative Splicing Microarrays Reveal Functional Expression of Neuron-specific Regulators in Hodgkin Lymphoma Cells. Journal of Biological Chemistry, 2005, 280, 4779-4784.	3.4	76
47	Genome-Wide Identification of Fas/CD95 Alternative Splicing Regulators Reveals Links with Iron Homeostasis. Molecular Cell, 2015, 57, 23-38.	9.7	76
48	Dual Function for U2AF³⁵ in AG-Dependent Pre-mRNA Splicing. Molecular and Cellular Biology, 2001, 21, 7673-7681.	2.3	73
49	Molecular mechanisms of gene expression regulation by the apoptosis-promoting protein TIA-1. , 2001, 6, 463-468.		71
50	Fas-activated Serine/Threonine Kinase (FAST K) Synergizes with TIA-1/TIAR Proteins to Regulate Fas Alternative Splicing. Journal of Biological Chemistry, 2007, 282, 1539-1543.	3.4	69
51	A novel protein domain in an ancestral splicing factor drove the evolution of neural microexons. Nature Ecology and Evolution, 2019, 3, 691-701.	7.8	63
52	Nuclear transport of influenza virus polymerase PA protein. Virus Research, 1992, 24, 65-75.	2.2	62
53	Regulation of FAS Exon Definition and Apoptosis by the Ewing Sarcoma Protein. Cell Reports, 2014, 7, 1211-1226.	6.4	62
54	Two Isoforms of the T-cell Intracellular Antigen 1 (TIA-1) Splicing Factor Display Distinct Splicing Regulation Activities. Journal of Biological Chemistry, 2007, 282, 19410-19417.	3.4	58

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55	Decrypting the genome's alternative messages. Current Opinion in Cell Biology, 2009, 21, 377-386.	5.4	55
56	Regulated M1 mRNA splicing in influenza virus-infected cells. Journal of General Virology, 1991, 72, 1301-1308.	2.9	54
57	Degradation of cellular mRNA during influenza virus infection: its possible role in protein synthesis shutoff. Journal of General Virology, 1992, 73, 575-581.	2.9	50
58	Kinetic Role for Mammalian SF1/BBP in Spliceosome Assembly and Function after Polypyrimidine Tract Recognition by U2AF. Journal of Biological Chemistry, 2000, 275, 38059-38066.	3.4	47
59	Diversity of Vertebrate Splicing Factor U2AF35. Journal of Biological Chemistry, 2004, 279, 27039-27049.	3.4	47
60	Nucleocytoplasmic Shuttling of Heterodimeric Splicing Factor U2AF. Journal of Biological Chemistry, 2001, 276, 13104-13112.	3.4	45
61	Molecular basis of differential 3â€² splice site sensitivity to anti-tumor drugs targeting U2 snRNP. Nature Communications, 2017, 8, 2100.	12.8	45
62	Estimating rates of alternative splicing in mammals and invertebrates. Nature Genetics, 2004, 36, 916-917.	21.4	44
63	The Drosophila fl(2)d Gene, Required for Female-Specific Splicing of Sxl and tra Pre-mRNAs, Encodes a Novel Nuclear Protein With a HQ-Rich Domain. Genetics, 2000, 155, 129-139.	2.9	44
64	Global analysis of alternative splicing regulation by insulin and wingless signaling in Drosophila cells. Genome Biology, 2009, 10, R11.	9.6	42
65	Chromatinâ€™s thread to alternative splicing regulation. Chromosoma, 2013, 122, 465-474.	2.2	40
66	Multiple Forms of the U2 Small Nuclear Ribonucleoprotein Auxiliary Factor U2AF Subunits Expressed in Higher Plants. Journal of Biological Chemistry, 1998, 273, 34603-34610.	3.4	39
67	Phenotypic hiding: the carryover of mutations in RNA viruses as shown by detection of mar mutants in influenza virus. Journal of Virology, 1989, 63, 4107-4109.	3.4	39
68	Haploinsufficiency, rather than the effect of an excessive production of soluble CD95 (CD95Î”TM), is the basis for ALPS Ia in a family with duplicated 3â€² splice site AG in CD95 intron 5 on one allele. Blood, 2005, 106, 1652-1659.	1.4	37
69	Differential 3â€² splice site recognition of SMN1 and SMN2 transcripts by U2AF and U2 snRNP. Rna, 2009, 15, 515-523.	3.5	36
70	A simple principle to explain the evolution of pre-mRNA splicing. Genes and Development, 2006, 20, 1679-1684.	5.9	35
71	Impaired Spermatogenesis, Muscle, and Erythrocyte Function in U12 Intron Splicing-Defective Zrsr1 Mutant Mice. Cell Reports, 2018, 23, 143-155.	6.4	33
72	Distinct mechanisms of splicing regulation in vivo by the Drosophila protein Sex-lethal. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 7343-7348.	7.1	32

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73	Distinct regulatory programs establish widespread sex-specific alternative splicing in Drosophila melanogaster. Rna, 2011, 17, 453-468.	3.5	32
74	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. Genome Biology, 2015, 16, 236.	8.8	32
75	Relationship between nucleosome positioning and progesterone-induced alternative splicing in breast cancer cells. Rna, 2015, 21, 360-374.	3.5	31
76	The conserved RNA recognition motif 3 of U2 snRNA auxiliary factor (U2AF65) is essential in vivo but dispensable for activity in vitro. Rna, 2004, 10, 240-253.	3.5	30
77	Modulation of msl-2 5â€² splice site recognition by Sex-lethal. Rna, 2001, 7, 1185-1191.	3.5	29
78	Regulation of alternative pre-mRNA splicing. Briefings in Functional Genomics & Proteomics, 2002, 1, 266-277.	3.8	28
79	Frequent somatic mutations in components of the RNA processing machinery in chronic lymphocytic leukemia. Leukemia, 2013, 27, 1600-1603.	7.2	28
80	Structural basis for the recognition of spliceosomal SmN/B/Bâ€™ proteins by the RBM5 OCRE domain in splicing regulation. ELife, 2016, 5, .	6.0	28
81	Switch in 3â€² Splice Site Recognition between Exon Definition and Splicing Catalysis Is Important for Sex-lethal Autoregulation. Molecular and Cellular Biology, 2001, 21, 1986-1996.	2.3	27
82	Smu1 and RED are required for activation of spliceosomal B complexes assembled on short introns. Nature Communications, 2019, 10, 3639.	12.8	26
83	Mutations primarily alter the inclusion of alternatively spliced exons. ELife, 2020, 9, .	6.0	24
84	Sudemycin K: A Synthetic Antitumor Splicing Inhibitor Variant with Improved Activity and Versatile Chemistry. ACS Chemical Biology, 2017, 12, 163-173.	3.4	23
85	Splicing of influenza virus matrix protein mRNA expressed from a simian virus 40 recombinant. Journal of General Virology, 1993, 74, 1317-1326.	2.9	22
86	In Vitro Correction of a Pseudoexon-Generating Deep Intronic Mutation in LGMD2A by Antisense Oligonucleotides and Modified Small Nuclear RNAs. Human Mutation, 2013, 34, 1387-1395.	2.5	22
87	Co-option of the piRNA Pathway for Germline-Specific Alternative Splicing of C.Âelegans TOR. Cell Reports, 2014, 8, 1609-1616.	6.4	22
88	Quantitative evaluation of alternatively spliced mRNA isoforms by label-free real-time plasmonic sensing. Biosensors and Bioelectronics, 2016, 78, 118-125.	10.1	22
89	Systems analysis identifies melanoma-enriched pro-oncogenic networks controlled by the RNA binding protein CELF1. Nature Communications, 2017, 8, 2249.	12.8	22
90	Breaking the second genetic code. Nature, 2010, 465, 45-46.	27.8	19

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91	U2 small nuclear ribonucleoprotein particle (snRNP) auxiliary factor of 65 kDa, U2AF65, can promote U1 snRNP recruitment to 5â€² splice sites. Biochemical Journal, 2003, 372, 235-240.	3.7	18
92	Functional Network Analysis Reveals the Relevance of SKIIP in the Regulation of Alternative Splicing by p38 SAPK. Cell Reports, 2019, 27, 847-859.e6.	6.4	15
93	Novel functions for `nuclear factors' in the cytoplasm: theSex-lethalparadigm. Seminars in Cell and Developmental Biology, 1997, 8, 561-566.	5.0	14
94	RNA Processing: Redrawing the Map of Charted Territory. Molecular Cell, 2009, 36, 918-919.	9.7	14
95	A splicing mastermind for EMT. EMBO Journal, 2010, 29, 3217-3218.	7.8	14
96	Splicing in 4D. Science, 2012, 338, 1547-1548.	12.6	14
97	Role of six single nucleotide polymorphisms, risk factors in coronary disease, inOLR1alternative splicing. Rna, 2015, 21, 1187-1202.	3.5	14
98	Alternative splicing regulation of cell-cycle genes by SPF45/SR140/CHERP complex controls cell proliferation. Rna, 2021, 27, 1557-1576.	3.5	14
99	Dynamics of alternative splicing during somatic cell reprogramming reveals functions for RNA-binding proteins CPSF3, hnRNP UL1, and TIA1. Genome Biology, 2021, 22, 171.	8.8	12
100	Mechanisms of Regulated Pre-mRNA Splicing. Molecular Biology Intelligence Unit, 1995, , 97-112.	0.2	12
101	Strict 3â€² splice site sequence requirements for U2 snRNP recruitment after U2AF binding underlie a genetic defect leading to autoimmune disease. Rna, 2011, 17, 401-411.	3.5	11
102	Site-Specific mRNA Cleavage for Selective and Quantitative Profiling of Alternative Splicing with Label-Free Optical Biosensors. Analytical Chemistry, 2019, 91, 15138-15146.	6.5	11
103	Getting to the heart of a splicing enhancer. Nature Structural Biology, 2003, 10, 6-7.	9.7	9
104	Functional Analysis of Splicing Factors and Regulators. , 1997, , 31-53.		9
105	Reconstruction of composite regulator-target splicing networks from high-throughput transcriptome data. BMC Genomics, 2015, 16, S7.	2.8	8
106	Prescribing splicing. Science, 2015, 347, 124-125.	12.6	8
107	Splicing together sister chromatids. EMBO Journal, 2014, 33, 2601-2603.	7.8	7
108	Alternative Splicing and Cancer. Journal of Nucleic Acids, 2012, 2012, 1-2.	1.2	6

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109	Unweaving the Meanings of Messenger RNA Sequences. Molecular Cell, 2006, 23, 150-151.	9.7	5
110	A splicing magic bullet. Science, 2014, 345, 624-625.	12.6	4
111	Spliceosome meets telomerase. Nature, 2008, 456, 879-880.	27.8	2
112	Viral cell biology: Influenza raids the splicing store. Nature Microbiology, 2016, 1, 16100.	13.3	2
113	Elisa Izaurralde 1959â€“2018. Nature Structural and Molecular Biology, 2018, 25, 547-547.	8.2	2
114	An optimized procedure to mutagenize long (>10 kb) plasmids by PCR. Technical Tips Online, 2000, 5, 3-6.	0.2	1
115	Powering a two-stroke RNA engine. Nature Structural and Molecular Biology, 2007, 14, 574-576.	8.2	1
116	RNAtomy of the Spliceosomeâ€™s heart. EMBO Journal, 2013, 32, 2785-2787.	7.8	1
117	Competition by the Masses. Molecular Cell, 2013, 51, 279-280.	9.7	1
118	Splicing Calls Back. Cell, 2019, 179, 1446-1447.	28.9	1
119	Cloning and expression of influenza virus segment 7. Virus Research, 1988, 11, 32.	2.2	0
120	A Guide to One of the Genome's Best-Kept Secrets. Molecular Cell, 2008, 31, 782-784.	9.7	0
121	Empowering MYC carcinogenesis via RNA loops. Molecular Cell, 2021, 81, 1365-1367.	9.7	0