

Juan Valcarcel

List of Publications by Year in descending order

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121
papers

12,494
citations

36691

53
h-index

32181

105
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132
all docs

132
docs citations

132
times ranked

15009
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-binding proteins in human genetic disease. <i>Nature Reviews Genetics</i> , 2021, 22, 185-198.	7.7	720
2	Empowering MYC carcinogenesis via RNA loops. <i>Molecular Cell</i> , 2021, 81, 1365-1367.	4.5	0
3	Dynamics of alternative splicing during somatic cell reprogramming reveals functions for RNA-binding proteins CPSF3, hnRNP UL1, and TIA1. <i>Genome Biology</i> , 2021, 22, 171.	3.8	12
4	Alternative splicing regulation of cell-cycle genes by SPF45/SR140/CHERP complex controls cell proliferation. <i>Rna</i> , 2021, 27, 1557-1576.	1.6	14
5	Roles and mechanisms of alternative splicing in cancer – implications for care. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 457-474.	12.5	400
6	Mutations primarily alter the inclusion of alternatively spliced exons. <i>ELife</i> , 2020, 9, .	2.8	24
7	Smu1 and RED are required for activation of spliceosomal B complexes assembled on short introns. <i>Nature Communications</i> , 2019, 10, 3639.	5.8	26
8	Site-Specific mRNA Cleavage for Selective and Quantitative Profiling of Alternative Splicing with Label-Free Optical Biosensors. <i>Analytical Chemistry</i> , 2019, 91, 15138-15146.	3.2	11
9	Functional Network Analysis Reveals the Relevance of SKIIP in the Regulation of Alternative Splicing by p38 SAPK. <i>Cell Reports</i> , 2019, 27, 847-859.e6.	2.9	15
10	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
11	Splicing Calls Back. <i>Cell</i> , 2019, 179, 1446-1447.	13.5	1
12	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. <i>Cell</i> , 2019, 176, 549-563.e23.	13.5	87
13	Impaired Spermatogenesis, Muscle, and Erythrocyte Function in U12 Intron Splicing-Defective Zrsr1 Mutant Mice. <i>Cell Reports</i> , 2018, 23, 143-155.	2.9	33
14	Elisa Izaurralde 1959–2018. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 547-547.	3.6	2
15	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
16	Sudemycin K: A Synthetic Antitumor Splicing Inhibitor Variant with Improved Activity and Versatile Chemistry. <i>ACS Chemical Biology</i> , 2017, 12, 163-173.	1.6	23
17	Systems analysis identifies melanoma-enriched pro-oncogenic networks controlled by the RNA binding protein CELF1. <i>Nature Communications</i> , 2017, 8, 2249.	5.8	22
18	Structural basis for the recognition of spliceosomal SmN/B proteins by the RBM5 OCRE domain in splicing regulation. <i>ELife</i> , 2016, 5, .	2.8	28

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19	Large-scale analysis of genome and transcriptome alterations in multiple tumors unveils novel cancer-relevant splicing networks. <i>Genome Research</i> , 2016, 26, 732-744.	2.4	225
20	The complete local genotype-phenotype landscape for the alternative splicing of a human exon. <i>Nature Communications</i> , 2016, 7, 11558.	5.8	91
21	Viral cell biology: Influenza raids the splicing store. <i>Nature Microbiology</i> , 2016, 1, 16100.	5.9	2
22	The Spliceosome: The Ultimate RNA Chaperone and Sculptor. <i>Trends in Biochemical Sciences</i> , 2016, 41, 33-45.	3.7	215
23	Tumor suppressor properties of the splicing regulatory factor RBM10. <i>RNA Biology</i> , 2016, 13, 466-472.	1.5	94
24	Quantitative evaluation of alternatively spliced mRNA isoforms by label-free real-time plasmonic sensing. <i>Biosensors and Bioelectronics</i> , 2016, 78, 118-125.	5.3	22
25	The pathogenicity of splicing defects: mechanistic insights into pre-mRNA processing inform novel therapeutic approaches. <i>EMBO Reports</i> , 2015, 16, 1640-1655.	2.0	127
26	Reconstruction of composite regulator-target splicing networks from high-throughput transcriptome data. <i>BMC Genomics</i> , 2015, 16, S7.	1.2	8
27	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. <i>Genome Biology</i> , 2015, 16, 236.	3.8	32
28	Genome-Wide Identification of Fas/CD95 Alternative Splicing Regulators Reveals Links with Iron Homeostasis. <i>Molecular Cell</i> , 2015, 57, 23-38.	4.5	76
29	Prescribing splicing. <i>Science</i> , 2015, 347, 124-125.	6.0	8
30	Relationship between nucleosome positioning and progesterone-induced alternative splicing in breast cancer cells. <i>Rna</i> , 2015, 21, 360-374.	1.6	31
31	Role of six single nucleotide polymorphisms, risk factors in coronary disease, in OLR1 alternative splicing. <i>Rna</i> , 2015, 21, 1187-1202.	1.6	14
32	Functional Splicing Network Reveals Extensive Regulatory Potential of the Core Spliceosomal Machinery. <i>Molecular Cell</i> , 2015, 57, 7-22.	4.5	140
33	Splicing together sister chromatids. <i>EMBO Journal</i> , 2014, 33, 2601-2603.	3.5	7
34	Structure, dynamics and RNA binding of the multi-domain splicing factor TIA-1. <i>Nucleic Acids Research</i> , 2014, 42, 5949-5966.	6.5	77
35	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. <i>Cell</i> , 2014, 156, 1324-1335.	13.5	482
36	Argonaute-1 binds transcriptional enhancers and controls constitutive and alternative splicing in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15622-15629.	3.3	86

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37	A splicing magic bullet. <i>Science</i> , 2014, 345, 624-625.	6.0	4
38	Regulation of FAS Exon Definition and Apoptosis by the Ewing Sarcoma Protein. <i>Cell Reports</i> , 2014, 7, 1211-1226.	2.9	62
39	Co-option of the piRNA Pathway for Germline-Specific Alternative Splicing of <i>C.Âelegans</i> TOR. <i>Cell Reports</i> , 2014, 8, 1609-1616.	2.9	22
40	Frequent somatic mutations in components of the RNA processing machinery in chronic lymphocytic leukemia. <i>Leukemia</i> , 2013, 27, 1600-1603.	3.3	28
41	Chromatinâ€™s thread to alternative splicing regulation. <i>Chromosoma</i> , 2013, 122, 465-474.	1.0	40
42	RBM5, 6, and 10 Differentially Regulate NUMB Alternative Splicing to Control Cancer Cell Proliferation. <i>Molecular Cell</i> , 2013, 52, 720-733.	4.5	292
43	RNAatomy of the Spliceosomeâ€™s heart. <i>EMBO Journal</i> , 2013, 32, 2785-2787.	3.5	1
44	Competition by the Masses. <i>Molecular Cell</i> , 2013, 51, 279-280.	4.5	1
45	CPEB1 coordinates alternative 3â€™-UTR formation with translational regulation. <i>Nature</i> , 2013, 495, 121-125.	13.7	156
46	In Vitro Correction of a Pseudoexon-Generating Deep Intronic Mutation in LGMD2A by Antisense Oligonucleotides and Modified Small Nuclear RNAs. <i>Human Mutation</i> , 2013, 34, 1387-1395.	1.1	22
47	Isolated pseudoâ€™RNA-recognition motifs of SR proteins can regulate splicing using a noncanonical mode of RNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2802-11.	3.3	109
48	The spliceosome as a target of novel antitumour drugs. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 847-859.	21.5	355
49	Splicing in 4D. <i>Science</i> , 2012, 338, 1547-1548.	6.0	14
50	hnRNP A1 Proofreads 3â€™ Splice Site Recognition by U2AF. <i>Molecular Cell</i> , 2012, 45, 314-329.	4.5	87
51	Alternative Splicing and Cancer. <i>Journal of Nucleic Acids</i> , 2012, 2012, 1-2.	0.8	6
52	Multi-domain conformational selection underlies pre-mRNA splicing regulation by U2AF. <i>Nature</i> , 2011, 475, 408-411.	13.7	202
53	The Ewing Sarcoma Protein Regulates DNA Damage-Induced Alternative Splicing. <i>Molecular Cell</i> , 2011, 43, 353-368.	4.5	149
54	Distinct regulatory programs establish widespread sex-specific alternative splicing in <i>Drosophila melanogaster</i> . <i>Rna</i> , 2011, 17, 453-468.	1.6	32

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55	Strict 3' splice site sequence requirements for U2 snRNP recruitment after U2AF binding underlie a genetic defect leading to autoimmune disease. <i>Rna</i> , 2011, 17, 401-411.	1.6	11
56	Reduced fidelity of branch point recognition and alternative splicing induced by the anti-tumor drug spliceostatin A. <i>Genes and Development</i> , 2011, 25, 445-459.	2.7	229
57	A splicing mastermind for EMT. <i>EMBO Journal</i> , 2010, 29, 3217-3218.	3.5	14
58	Breaking the second genetic code. <i>Nature</i> , 2010, 465, 45-46.	13.7	19
59	Differential 3' splice site recognition of <i>SMN1</i> and <i>SMN2</i> transcripts by U2AF and U2 snRNP. <i>Rna</i> , 2009, 15, 515-523.	1.6	36
60	Decrypting the genome's alternative messages. <i>Current Opinion in Cell Biology</i> , 2009, 21, 377-386.	2.6	55
61	Nucleosome positioning as a determinant of exon recognition. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 996-1001.	3.6	406
62	RNA Processing: Redrawing the Map of Charted Territory. <i>Molecular Cell</i> , 2009, 36, 918-919.	4.5	14
63	Global analysis of alternative splicing regulation by insulin and wingless signaling in <i>Drosophila</i> cells. <i>Genome Biology</i> , 2009, 10, R11.	13.9	42
64	Spliceosome meets telomerase. <i>Nature</i> , 2008, 456, 879-880.	13.7	2
65	RBM5/Luca-15/H37 Regulates Fas Alternative Splice Site Pairing after Exon Definition. <i>Molecular Cell</i> , 2008, 32, 81-95.	4.5	153
66	A Guide to One of the Genome's Best-Kept Secrets. <i>Molecular Cell</i> , 2008, 31, 782-784.	4.5	0
67	Genome-wide Analysis of Alternative Pre-mRNA Splicing. <i>Journal of Biological Chemistry</i> , 2008, 283, 1229-1233.	1.6	129
68	Two Isoforms of the T-cell Intracellular Antigen 1 (TIA-1) Splicing Factor Display Distinct Splicing Regulation Activities. <i>Journal of Biological Chemistry</i> , 2007, 282, 19410-19417.	1.6	58
69	Fas-activated Serine/Threonine Kinase (FAST K) Synergizes with TIA-1/TIAR Proteins to Regulate Fas Alternative Splicing. <i>Journal of Biological Chemistry</i> , 2007, 282, 1539-1543.	1.6	69
70	Powering a two-stroke RNA engine. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 574-576.	3.6	1
71	U2AF-homology motif interactions are required for alternative splicing regulation by SPF45. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 620-629.	3.6	147
72	Unweaving the Meanings of Messenger RNA Sequences. <i>Molecular Cell</i> , 2006, 23, 150-151.	4.5	5

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73	The expanding transcriptome: the genome as the "Book of Sand". EMBO Journal, 2006, 25, 923-931.	3.5	78
74	Intron Removal Requires Proofreading of U2AF/3' Splice Site Recognition by DEK. Science, 2006, 312, 1961-1965.	6.0	126
75	A simple principle to explain the evolution of pre-mRNA splicing. Genes and Development, 2006, 20, 1679-1684.	2.7	35
76	Haploinsufficiency, rather than the effect of an excessive production of soluble CD95 (CD95 ^{sol}), is the basis for ALPS Ia in a family with duplicated 3' splice site AG in CD95 intron 5 on one allele. Blood, 2005, 106, 1652-1659.	0.6	37
77	Building specificity with nonspecific RNA-binding proteins. Nature Structural and Molecular Biology, 2005, 12, 645-653.	3.6	196
78	Alternative Splicing Microarrays Reveal Functional Expression of Neuron-specific Regulators in Hodgkin Lymphoma Cells. Journal of Biological Chemistry, 2005, 280, 4779-4784.	1.6	76
79	Regulation of Fas Alternative Splicing by Antagonistic Effects of TIA-1 and PTB on Exon Definition. Molecular Cell, 2005, 19, 475-484.	4.5	307
80	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.	1.6	30
81	Diversity of Vertebrate Splicing Factor U2AF35. Journal of Biological Chemistry, 2004, 279, 27039-27049.	1.6	47
82	Estimating rates of alternative splicing in mammals and invertebrates. Nature Genetics, 2004, 36, 916-917.	9.4	44
83	Getting to the heart of a splicing enhancer. Nature Structural Biology, 2003, 10, 6-7.	9.7	9
84	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.	1.6	82
85	U2 small nuclear ribonucleoprotein particle (snRNP) auxiliary factor of 65 kDa, U2AF65, can promote U1 snRNP recruitment to 5' splice sites. Biochemical Journal, 2003, 372, 235-240.	1.7	18
86	Optimization of oligonucleotide-based DNA microarrays. Nucleic Acids Research, 2002, 30, 51e-51.	6.5	256
87	Regulation of alternative pre-mRNA splicing. Briefings in Functional Genomics & Proteomics, 2002, 1, 266-277.	3.8	28
88	Splicing Regulation at the Second Catalytic Step by Sex-lethal Involves 3' Splice Site Recognition by SPF45. Cell, 2002, 109, 285-296.	13.5	140
89	Alternative splicing and genome complexity. Nature Genetics, 2002, 30, 29-30.	9.4	490
90	The splicing regulator TIA-1 interacts with U1-C to promote U1 snRNP recruitment to 5' splice sites. EMBO Journal, 2002, 21, 6882-6892.	3.5	198

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91	Modulation of msl-2 5' splice site recognition by Sex-lethal. <i>Rna</i> , 2001, 7, 1185-1191.	1.6	29
92	Molecular mechanisms of gene expression regulation by the apoptosis-promoting protein TIA-1. , 2001, 6, 463-468.		71
93	The hnRNP A1 protein regulates HIV-1 tat splicing via a novel intron silencer element. <i>EMBO Journal</i> , 2001, 20, 5748-5758.	3.5	145
94	Dual Function for U2AF 35 in AG-Dependent Pre-mRNA Splicing. <i>Molecular and Cellular Biology</i> , 2001, 21, 7673-7681.	1.1	73
95	Nucleocytoplasmic Shuttling of Heterodimeric Splicing Factor U2AF. <i>Journal of Biological Chemistry</i> , 2001, 276, 13104-13112.	1.6	45
96	Switch in 3' Splice Site Recognition between Exon Definition and Splicing Catalysis Is Important for Sex-lethal Autoregulation. <i>Molecular and Cellular Biology</i> , 2001, 21, 1986-1996.	1.1	27
97	An optimized procedure to mutagenize long (>10 kb) plasmids by PCR. <i>Technical Tips Online</i> , 2000, 5, 3-6.	0.2	1
98	Alternative pre-mRNA splicing: the logic of combinatorial control. <i>Trends in Biochemical Sciences</i> , 2000, 25, 381-388.	3.7	804
99	Kinetic Role for Mammalian SF1/BBP in Spliceosome Assembly and Function after Polypyrimidine Tract Recognition by U2AF. <i>Journal of Biological Chemistry</i> , 2000, 275, 38059-38066.	1.6	47
100	The Apoptosis-Promoting Factor TIA-1 Is a Regulator of Alternative Pre-mRNA Splicing. <i>Molecular Cell</i> , 2000, 6, 1089-1098.	4.5	252
101	The <i>Drosophila</i> <i>fl(2)d</i> Gene, Required for Female-Specific Splicing of <i>Sxl</i> and <i>tra</i> Pre-mRNAs, Encodes a Novel Nuclear Protein With a HQ-Rich Domain. <i>Genetics</i> , 2000, 155, 129-139.	1.2	44
102	Inhibition of msl-2 splicing by Sex-lethal reveals interaction between U2AF35 and the 3' splice site AG. <i>Nature</i> , 1999, 402, 838-841.	13.7	262
103	Multiple Forms of the U2 Small Nuclear Ribonucleoprotein Auxiliary Factor U2AF Subunits Expressed in Higher Plants. <i>Journal of Biological Chemistry</i> , 1998, 273, 34603-34610.	1.6	39
104	Targeting of U2AF65 to Sites of Active Splicing in the Nucleus. <i>Journal of Cell Biology</i> , 1997, 137, 975-987.	2.3	115
105	U2AF65 recruits a novel human DEAD box protein required for the U2 snRNP-branchpoint interaction.. <i>Genes and Development</i> , 1997, 11, 1864-1872.	2.7	237
106	Novel functions for 'nuclear factors' in the cytoplasm: the Sex-lethal paradigm. <i>Seminars in Cell and Developmental Biology</i> , 1997, 8, 561-566.	2.3	14
107	Distinct mechanisms of splicing regulation in vivo by the <i>Drosophila</i> protein Sex-lethal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 7343-7348.	3.3	32
108	Post-transcriptional regulation: The dawn of PTB. <i>Current Biology</i> , 1997, 7, R705-R708.	1.8	178

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109	Functional Analysis of Splicing Factors and Regulators. , 1997, , 31-53.		9
110	Interaction of U2AF65 RS Region with Pre-mRNA Branch Point and Promotion of Base Pairing with U2 snRNA. Science, 1996, 273, 1706-1709.	6.0	253
111	The SR protein family: pleiotropic functions in pre-mRNA splicing. Trends in Biochemical Sciences, 1996, 21, 296-301.	3.7	199
112	Distinct binding specificities and functions of higher eukaryotic polypyrimidine tract-binding proteins. Science, 1995, 268, 1173-1176.	6.0	526
113	Mechanisms of Regulated Pre-mRNA Splicing. Molecular Biology Intelligence Unit, 1995, , 97-112.	0.2	12
114	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.	1.1	88
115	The protein Sex-lethal antagonizes the splicing factor U2AF to regulate alternative splicing of transformer pre-mRNA. Nature, 1993, 362, 171-175.	13.7	316
116	Splicing of influenza virus matrix protein mRNA expressed from a simian virus 40 recombinant. Journal of General Virology, 1993, 74, 1317-1326.	1.3	22
117	Degradation of cellular mRNA during influenza virus infection: its possible role in protein synthesis shutoff. Journal of General Virology, 1992, 73, 575-581.	1.3	50
118	Nuclear transport of influenza virus polymerase PA protein. Virus Research, 1992, 24, 65-75.	1.1	62
119	Regulated M1 mRNA splicing in influenza virus-infected cells. Journal of General Virology, 1991, 72, 1301-1308.	1.3	54
120	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.	1.5	39
121	Cloning and expression of influenza virus segment 7. Virus Research, 1988, 11, 32.	1.1	0