

Virginie Marchand

List of Publications by Year in descending order

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64
papers

2,858
citations

201674

27
h-index

189892

50
g-index

71
all docs

71
docs citations

71
times ranked

3083
citing authors

#	ARTICLE	IF	CITATIONS
1	2-D Structure of the A Region of Xist RNA and Its Implication for PRC2 Association. PLoS Biology, 2010, 8, e1000276.	5.6	212
2	Evidence for rRNA 2â€²-O-methylation plasticity: Control of intrinsic translational capabilities of human ribosomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12934-12939.	7.1	197
3	Illumina-based RiboMethSeq approach for mapping of 2â€²-O-Me residues in RNA. Nucleic Acids Research, 2016, 44, e135-e135.	14.5	178
4	FTSJ3 is an RNA 2â€²-O-methyltransferase recruited by HIV to avoid innate immune sensing. Nature, 2019, 565, 500-504.	27.8	151
5	RNA ribose methylation (2â€²-O-methylation): Occurrence, biosynthesis and biological functions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 253-269.	1.9	120
6	AlkAnilineâ€³Seq: Profiling of m ⁷ G and m ³ C RNA Modifications at Single Nucleotide Resolution. Angewandte Chemie - International Edition, 2018, 57, 16785-16790.	13.8	119
7	Control of RNP motility and localization by a splicing-dependent structure in oskar mRNA. Nature Structural and Molecular Biology, 2012, 19, 441-449.	8.2	109
8	<i>Drosophila</i> PTB promotes formation of high-order RNP particles and represses <i>oskar</i> translation. Genes and Development, 2009, 23, 195-207.	5.9	108
9	Identification of sites of 2â€²-O-methylation vulnerability in human ribosomal RNAs by systematic mapping. Scientific Reports, 2017, 7, 11490.	3.3	91
10	A Janus Splicing Regulatory Element Modulates HIV-1 tat and rev mRNA Production by Coordination of hnRNP A1 Cooperative Binding. Journal of Molecular Biology, 2002, 323, 629-652.	4.2	87
11	FTO-mediated cytoplasmic m6Am demethylation adjusts stem-like properties in colorectal cancer cell. Nature Communications, 2021, 12, 1716.	12.8	83
12	Ribosomal Proteins Regulate MHC Class I Peptide Generation for Immunosurveillance. Molecular Cell, 2019, 73, 1162-1173.e5.	9.7	81
13	Alternative splicing: regulation of HIVâ€¹ multiplication as a target for therapeutic action. FEBS Journal, 2010, 277, 867-876.	4.7	74
14	HydraPsiSeq: a method for systematic and quantitative mapping of pseudouridines in RNA. Nucleic Acids Research, 2020, 48, e110-e110.	14.5	72
15	Engineering of a DNA Polymerase for Direct m ⁶ A Sequencing. Angewandte Chemie - International Edition, 2018, 57, 417-421.	13.8	66
16	A PRDX1 mutant allele causes a MMACHC secondary epimutation in cblC patients. Nature Communications, 2018, 9, 67.	12.8	64
17	Nextâ€³Generation Sequencingâ€³Based RiboMethSeq Protocol for Analysis of tRNA 2â€²â€³Methylation. Biomolecules, 2017, 7, 13.	4.0	49
18	High-throughput sequencing for 1-methyladenosine (m1A) mapping in RNA. Methods, 2016, 107, 110-121.	3.8	47

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19	2,6-Diaminopurine as a highly potent corrector of UGA nonsense mutations. Nature Communications, 2020, 11, 1509.	12.8	46
20	Machine learning of reverse transcription signatures of variegated polymerases allows mapping and discrimination of methylated purines in limited transcriptomes. Nucleic Acids Research, 2020, 48, 3734-3746.	14.5	45
21	A Vastly Increased Chemical Variety of RNA Modifications Containing a Thioacetal Structure. Angewandte Chemie - International Edition, 2018, 57, 7893-7897.	13.8	44
22	Balancing of mitochondrial translation through METTL8-mediated m3C modification of mitochondrial tRNAs. Molecular Cell, 2021, 81, 4810-4825.e12.	9.7	44
23	An Intracellular Transmission Control Protocol: assembly and transport of ribonucleoprotein complexes. Current Opinion in Cell Biology, 2012, 24, 202-210.	5.4	43
24	Detection and Analysis of RNA Ribose 2'-O-Methylations: Challenges and Solutions. Genes, 2018, 9, 642.	2.4	42
25	Ribosomal RNA 2'-O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. NAR Cancer, 2020, 2, zcaa036.	3.1	40
26	Identification of protein partners of the human immunodeficiency virus 1 tat ^{rev} exon 3 leads to the discovery of a new HIV-1 splicing regulator, protein hnRNP K. RNA Biology, 2011, 8, 325-342.	3.1	39
27	Analysis of RNA Modifications by Second- and Third-Generation Deep Sequencing: 2020 Update. Genes, 2021, 12, 278.	2.4	38
28	tRNA 2'-O-methylation by a duo of TRM7/FTSJ1 proteins modulates small RNA silencing in Drosophila. Nucleic Acids Research, 2020, 48, 2050-2072.	14.5	30
29	Absolute Quantification of Noncoding RNA by Microscale Thermophoresis. Angewandte Chemie - International Edition, 2019, 58, 9565-9569.	13.8	29
30	Role of RNA structure and protein factors in the control of HIV-1 splicing. Frontiers in Bioscience - Landmark, 2009, Volume, 2714.	3.0	28
31	Bacterial tRNA 2'-O-methylation is dynamically regulated under stress conditions and modulates innate immune response. Nucleic Acids Research, 2020, 48, 12833-12844.	14.5	27
32	Mapping rRNA 2'-O-methylations and identification of C/D snoRNAs in Arabidopsis thaliana plants. RNA Biology, 2021, 18, 1760-1777.	3.1	27
33	Drosophila Ge-1 Promotes P Body Formation and oskar mRNA Localization. PLoS ONE, 2011, 6, e20612.	2.5	27
34	Diversity and heterogeneity of extracellular RNA in human plasma. Biochimie, 2019, 164, 22-36.	2.6	26
35	Instrumental analysis of RNA modifications. Critical Reviews in Biochemistry and Molecular Biology, 2021, 56, 178-204.	5.2	26
36	NOseq: amplicon sequencing evaluation method for RNA m6A sites after chemical deamination. Nucleic Acids Research, 2021, 49, e23-e23.	14.5	25

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37	Cell culture NAIL-MS allows insight into human tRNA and rRNA modification dynamics in vivo. Nature Communications, 2021, 12, 389.	12.8	24
38	Ribosomal RNA 2â€²-O-methylations regulate translation by impacting ribosome dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2117334119.	7.1	24
39	The EJC Binding and Dissociating Activity of PYM Is Regulated in Drosophila. PLoS Genetics, 2014, 10, e1004455.	3.5	23
40	2â€²-O-methylation within prokaryotic and eukaryotic tRNA inhibits innate immune activation by endosomal Toll-like receptors but does not affect recognition of whole organisms. Rna, 2019, 25, 869-880.	3.5	22
41	Survey and Validation of tRNA Modifications and Their Corresponding Genes in Bacillus subtilis sp Subtilis Strain 168. Biomolecules, 2020, 10, 977.	4.0	21
42	Holistic Optimization of Bioinformatic Analysis Pipeline for Detection and Quantification of 2â€²-O-Methylations in RNA by RiboMethSeq. Frontiers in Genetics, 2020, 11, 38.	2.3	21
43	Constitutive and variable 2â€²-O-methylation (Nm) in human ribosomal RNA. RNA Biology, 2021, 18, 88-97.	3.1	20
44	Entwicklung einer DNA-Polymerase fÃ¼r die direkte m ⁶ -Sequenzierung. Angewandte Chemie, 2018, 130, 424-428.	2.0	15
45	Double methylation of tRNA-U54 to 2â€²-O-methylthymidine (Tm) synergistically decreases immune response by Toll-like receptor 7. Nucleic Acids Research, 2018, 46, 9764-9775.	14.5	15
46	Manganese Ions Individually Alter the Reverse Transcription Signature of Modified Ribonucleosides. Genes, 2020, 11, 950.	2.4	15
47	Quantification of 2â€²-O-Me Residues in RNA Using Next-Generation Sequencing (Illumina RiboMethSeq) Tj ETQq1 1 0.784314 rgBT /OV	0.9	14
48	Mapping of 7-methylguanosine (m7G), 3-methylcytidine (m3C), dihydrouridine (D) and 5-hydroxycytidine (ho5C) RNA modifications by AlkAniline-Seq. Methods in Enzymology, 2021, 658, 25-47.	1.0	14
49	Mapping and Quantification of tRNA 2â€²-O-Methylation by RiboMethSeq. Methods in Molecular Biology, 2019, 1870, 273-295.	0.9	13
50	High-Throughput Mapping of 2â€²-O-Me Residues in RNA Using Next-Generation Sequencing (Illumina) Tj ETQq0 0 0 rgBT /Overlock 10	0.9	12
51	Graphical Workflow System for Modification Calling by Machine Learning of Reverse Transcription Signatures. Frontiers in Genetics, 2019, 10, 876.	2.3	10
52	Non-Redundant tRNA Reference Sequences for Deep Sequencing Analysis of tRNA Abundance and Epitranscriptomic RNA Modifications. Genes, 2021, 12, 81.	2.4	10
53	Analysis of pseudouridines and other RNA modifications using HydraPsiSeq protocol. Methods, 2022, 203, 383-391.	3.8	9
54	Systematic mapping of rRNA 2â€²-O methylation during frog development and involvement of the methyltransferase Fibrillarlin in eye and craniofacial development in Xenopus laevis. PLoS Genetics, 2022, 18, e1010012.	3.5	9

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55	AlkAniline-Seq: A Highly Sensitive and Specific Method for Simultaneous Mapping of 7-Methyl-guanosine (m7G) and 3-Methyl-cytosine (m3C) in RNAs by High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2298, 77-95.	0.9	8
56	Structural and functional analysis of the Rous Sarcoma virus negative regulator of splicing and demonstration of its activation by the 9G8 SR protein. <i>Nucleic Acids Research</i> , 2011, 39, 3388-3403.	14.5	6
57	Implication of repeat insertion domains in the <i>trans</i> -activity of the long non-coding RNA ANRIL. <i>Nucleic Acids Research</i> , 2021, 49, 4954-4970.	14.5	6
58	Machine learning algorithm for precise prediction of 2'-O-methylation (Nm) sites from experimental RiboMethSeq datasets. <i>Methods</i> , 2022, 203, 311-321.	3.8	4
59	Studies of mutations of assembly factor Hit1 in budding yeast suggest translation defects as the molecular basis for PEHO syndrome. <i>Journal of Biological Chemistry</i> , 2022, 298, 102261.	3.4	3
60	Study of RNA-Protein Interactions and RNA Structure in Ribonucleoprotein Particles. , 0, , 172-204.		2
61	Quantification and Quality Control of a Small Non-Coding RNA Preparation. <i>Methods in Molecular Biology</i> , 2015, 1296, 17-28.	0.9	1
62	Isolation, Extraction and Deep-Sequencing Analysis of Extracellular RNAs (exRNAs) from Human Plasma. <i>Methods in Molecular Biology</i> , 2021, 2300, 165-182.	0.9	1
63	AlkAniline-Seq: Profiling of m7G and m3C RNA Modifications at Single Nucleotide Resolution. <i>Angewandte Chemie</i> , 2018, 130, 17027-17032.	2.0	0
64	Quantitative and Qualitative Assessment of Small RNA Preparations. <i>Methods in Molecular Biology</i> , 2021, 2300, 17-29.	0.9	0