

# Virginie Marchand

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

2,858  
citations

201575

27  
h-index

189801

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.	2.6	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.	3.3	197
3	Illumina-based RiboMethSeq approach for mapping of 2â€²-O-Me residues in RNA. Nucleic Acids Research, 2016, 44, e135-e135.	6.5	178
4	FTSJ3 is an RNA 2â€²-O-methyltransferase recruited by HIV to avoid innate immune sensing. Nature, 2019, 565, 500-504.	13.7	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.	0.9	120
6	AlkAnilineâ€²Seq: Profiling of m<sup>7</sup>G and m<sup>3</sup>C RNA Modifications at Single Nucleotide Resolution. Angewandte Chemie - International Edition, 2018, 57, 16785-16790.	7.2	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.	3.6	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.	2.7	108
9	Identification of sites of 2â€²-O-methylation vulnerability in human ribosomal RNAs by systematic mapping. Scientific Reports, 2017, 7, 11490.	1.6	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.	2.0	87
11	FTO-mediated cytoplasmic m6Am demethylation adjusts stem-like properties in colorectal cancer cell. Nature Communications, 2021, 12, 1716.	5.8	83
12	Ribosomal Proteins Regulate MHC Class I Peptide Generation for Immunosurveillance. Molecular Cell, 2019, 73, 1162-1173.e5.	4.5	81
13	Alternative splicing: regulation of HIVâ€²1 multiplication as a target for therapeutic action. FEBS Journal, 2010, 277, 867-876.	2.2	74
14	HydraPsiSeq: a method for systematic and quantitative mapping of pseudouridines in RNA. Nucleic Acids Research, 2020, 48, e110-e110.	6.5	72
15	Engineering of a DNA Polymerase for Direct m<sup>6</sup>A Sequencing. Angewandte Chemie - International Edition, 2018, 57, 417-421.	7.2	66
16	A PRDX1 mutant allele causes a MMACHC secondary epimutation in cblC patients. Nature Communications, 2018, 9, 67.	5.8	64
17	Nextâ€²Generation Sequencingâ€²Based RiboMethSeq Protocol for Analysis of tRNA 2â€²-O-Methylation. Biomolecules, 2017, 7, 13.	1.8	49
18	High-throughput sequencing for 1-methyladenosine (m1A) mapping in RNA. Methods, 2016, 107, 110-121.	1.9	47

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19	2,6-Diaminopurine as a highly potent corrector of UGA nonsense mutations. <i>Nature Communications</i> , 2020, 11, 1509.	5.8	46
20	Machine learning of reverse transcription signatures of variegated polymerases allows mapping and discrimination of methylated purines in limited transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 3734-3746.	6.5	45
21	A Vastly Increased Chemical Variety of RNA Modifications Containing a Thioacetal Structure. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7893-7897.	7.2	44
22	Balancing of mitochondrial translation through METTL8-mediated m3C modification of mitochondrial tRNAs. <i>Molecular Cell</i> , 2021, 81, 4810-4825.e12.	4.5	44
23	An Intracellular Transmission Control Protocol: assembly and transport of ribonucleoprotein complexes. <i>Current Opinion in Cell Biology</i> , 2012, 24, 202-210.	2.6	43
24	Detection and Analysis of RNA Ribose 2'-O-Methylations: Challenges and Solutions. <i>Genes</i> , 2018, 9, 642.	1.0	42
25	Ribosomal RNA 2'-O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. <i>NAR Cancer</i> , 2020, 2, zcaa036.	1.6	40
26	Identification of protein partners of the human immunodeficiency virus 1 <i>tat</i> / <i>rev</i> exon 3 leads to the discovery of a new HIV-1 splicing regulator, protein hnRNP K. <i>RNA Biology</i> , 2011, 8, 325-342.	1.5	39
27	Analysis of RNA Modifications by Second- and Third-Generation Deep Sequencing: 2020 Update. <i>Genes</i> , 2021, 12, 278.	1.0	38
28	tRNA 2'-O-methylation by a duo of TRM7/FTSJ1 proteins modulates small RNA silencing in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2020, 48, 2050-2072.	6.5	30
29	Absolute Quantification of Noncoding RNA by Microscale Thermophoresis. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9565-9569.	7.2	29
30	Role of RNA structure and protein factors in the control of HIV-1 splicing. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 2714.	3.0	28
31	Bacterial tRNA 2'-O-methylation is dynamically regulated under stress conditions and modulates innate immune response. <i>Nucleic Acids Research</i> , 2020, 48, 12833-12844.	6.5	27
32	Mapping rRNA 2'-O-methylations and identification of C/D snoRNAs in <i>Arabidopsis thaliana</i> plants. <i>RNA Biology</i> , 2021, 18, 1760-1777.	1.5	27
33	<i>Drosophila</i> Ge-1 Promotes P Body Formation and oskar mRNA Localization. <i>PLoS ONE</i> , 2011, 6, e20612.	1.1	27
34	Diversity and heterogeneity of extracellular RNA in human plasma. <i>Biochimie</i> , 2019, 164, 22-36.	1.3	26
35	Instrumental analysis of RNA modifications. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021, 56, 178-204.	2.3	26
36	NOseq: amplicon sequencing evaluation method for RNA m6A sites after chemical deamination. <i>Nucleic Acids Research</i> , 2021, 49, e23-e23.	6.5	25

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37	Cell culture NAIL-MS allows insight into human tRNA and rRNA modification dynamics in vivo. <i>Nature Communications</i> , 2021, 12, 389.	5.8	24
38	Ribosomal RNA 2â€²-O-methylations regulate translation by impacting ribosome dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2117334119.	3.3	24
39	The EJC Binding and Dissociating Activity of PYM Is Regulated in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2014, 10, e1004455.	1.5	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. <i>Rna</i> , 2019, 25, 869-880.	1.6	22
41	Survey and Validation of tRNA Modifications and Their Corresponding Genes in <i>Bacillus subtilis</i> sp Subtilis Strain 168. <i>Biomolecules</i> , 2020, 10, 977.	1.8	21
42	Holistic Optimization of Bioinformatic Analysis Pipeline for Detection and Quantification of 2â€²-O-Methylations in RNA by RiboMethSeq. <i>Frontiers in Genetics</i> , 2020, 11, 38.	1.1	21
43	Constitutive and variable 2â€²-O-methylation (Nm) in human ribosomal RNA. <i>RNA Biology</i> , 2021, 18, 88-97.	1.5	20
44	Entwicklung einer DNA-Polymerase fÃ¼r die direkte m <sup>6</sup> -Sequenzierung. <i>Angewandte Chemie</i> , 2018, 130, 424-428.	1.6	15
45	Double methylation of tRNA-U54 to 2â€²-O-methylthymidine (Tm) synergistically decreases immune response by Toll-like receptor 7. <i>Nucleic Acids Research</i> , 2018, 46, 9764-9775.	6.5	15
46	Manganese Ions Individually Alter the Reverse Transcription Signature of Modified Ribonucleosides. <i>Genes</i> , 2020, 11, 950.	1.0	15
47	Quantification of 2â€²-O-Me Residues in RNA Using Next-Generation Sequencing (Illumina RiboMethSeq) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.4	14
48	Mapping of 7-methylguanosine (m7G), 3-methylcytidine (m3C), dihydrouridine (D) and 5-hydroxycytidine (ho5C) RNA modifications by AlkAniline-Seq. <i>Methods in Enzymology</i> , 2021, 658, 25-47.	0.4	14
49	Mapping and Quantification of tRNA 2â€²-O-Methylation by RiboMethSeq. <i>Methods in Molecular Biology</i> , 2019, 1870, 273-295.	0.4	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	0.4	12
51	Graphical Workflow System for Modification Calling by Machine Learning of Reverse Transcription Signatures. <i>Frontiers in Genetics</i> , 2019, 10, 876.	1.1	10
52	Non-Redundant tRNA Reference Sequences for Deep Sequencing Analysis of tRNA Abundance and Epitranscriptomic RNA Modifications. <i>Genes</i> , 2021, 12, 81.	1.0	10
53	Analysis of pseudouridines and other RNA modifications using HydraPsiSeq protocol. <i>Methods</i> , 2022, 203, 383-391.	1.9	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 <i>Xenopus laevis</i> . <i>PLoS Genetics</i> , 2022, 18, e1010012.	1.5	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.	0.4	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.	6.5	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.	6.5	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.	1.9	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.	1.6	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.	0.4	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.	0.4	1
63	AlkAniline-Seq: Profiling of m7G and m3C RNA Modifications at Single Nucleotide Resolution. <i>Angewandte Chemie</i> , 2018, 130, 17027-17032.	1.6	0
64	Quantitative and Qualitative Assessment of Small RNA Preparations. <i>Methods in Molecular Biology</i> , 2021, 2300, 17-29.	0.4	0