

# Virginie Marchand

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

63

papers

1,759

citations

23

h-index

41

g-index

71

ext. papers

2,340

ext. citations

9.6

avg, IF

5.13

L-index

#	Paper	IF	Citations
63	Systematic mapping of rRNA 2FO methylation during frog development and involvement of the methyltransferase Fibrillarin in eye and craniofacial development in <i>Xenopus laevis</i> . <i>PLoS Genetics</i> , <b>2022</b> , 18, e1010012	6	0
62	Ribosomal RNA 2F-methylations regulate translation by impacting ribosome dynamics.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119, e2117334119	11.5	1
61	Balancing of mitochondrial translation through METTL8-mediated mC modification of mitochondrial tRNAs. <i>Molecular Cell</i> , <b>2021</b> , 81, 4810-4825.e12	17.6	4
60	FTO-mediated cytoplasmic mA demethylation adjusts stem-like properties in colorectal cancer cell. <i>Nature Communications</i> , <b>2021</b> , 12, 1716	17.4	23
59	Implication of repeat insertion domains in the trans-activity of the long non-coding RNA ANRIL. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 4954-4970	20.1	3
58	NOseq: amplicon sequencing evaluation method for RNA m6A sites after chemical deamination. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e23	20.1	12
57	Isolation, Extraction and Deep-Sequencing Analysis of Extracellular RNAs (exRNAs) from Human Plasma. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2300, 165-182	1.4	0
56	AlkAniline-Seq: A Highly Sensitive and Specific Method for Simultaneous Mapping of 7-Methyl-guanosine (mG) and 3-Methyl-cytosine (mC) in RNAs by High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2298, 77-95	1.4	1
55	Mapping of 7-methylguanosine (mG), 3-methylcytidine (mC), dihydrouridine (D) and 5-hydroxycytidine (hoC) RNA modifications by AlkAniline-Seq. <i>Methods in Enzymology</i> , <b>2021</b> , 658, 25-47	1.7	1
54	Quantitative and Qualitative Assessment of Small RNA Preparations. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2300, 17-29	1.4	
53	Non-Redundant tRNA Reference Sequences for Deep Sequencing Analysis of tRNA Abundance and Epitranscriptomic RNA Modifications. <i>Genes</i> , <b>2021</b> , 12,	4.2	2
52	Instrumental analysis of RNA modifications. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , <b>2021</b> , 56, 178-204	8.7	7
51	Analysis of RNA Modifications by Second- and Third-Generation Deep Sequencing: 2020 Update. <i>Genes</i> , <b>2021</b> , 12,	4.2	15
50	Mapping rRNA 2FO-methylations and identification of C/D snoRNAs in <i>Arabidopsis thaliana</i> plants. <i>RNA Biology</i> , <b>2021</b> , 18, 1760-1777	4.8	6
49	Analysis of pseudouridines and other RNA modifications using HydraPsiSeq protocol. <i>Methods</i> , <b>2021</b> ,	4.6	3
48	Constitutive and variable 2FO-methylation (Nm) in human ribosomal RNA. <i>RNA Biology</i> , <b>2021</b> , 1-10	4.8	3
47	Cell culture NAIL-MS allows insight into human tRNA and rRNA modification dynamics in vivo. <i>Nature Communications</i> , <b>2021</b> , 12, 389	17.4	10

46	2,6-Diaminopurine as a highly potent corrector of UGA nonsense mutations. <i>Nature Communications</i> , <b>2020</b> , 11, 1509	17.4	16
45	Survey and Validation of tRNA Modifications and Their Corresponding Genes in sp Subtilis Strain 168. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	10
44	Machine learning of reverse transcription signatures of variegated polymerases allows mapping and discrimination of methylated purines in limited transcriptomes. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 3734-3746	20.1	20
43	Holistic Optimization of Bioinformatic Analysis Pipeline for Detection and Quantification of 2FO-Methylations in RNA by RiboMethSeq. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 38	4.5	12
42	tRNA 2FO-methylation by a duo of TRM7/FTSJ1 proteins modulates small RNA silencing in Drosophila. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 2050-2072	20.1	17
41	Ribosomal RNA 2FO-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. <i>NAR Cancer</i> , <b>2020</b> , 2, zcaa036	5.2	12
40	HydraPsiSeq: a method for systematic and quantitative mapping of pseudouridines in RNA. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, e110	20.1	27
39	Bacterial tRNA 2FO-methylation is dynamically regulated under stress conditions and modulates innate immune response. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 12833-12844	20.1	8
38	Manganese Ions Individually Alter the Reverse Transcription Signature of Modified Ribonucleosides. <i>Genes</i> , <b>2020</b> , 11,	4.2	5
37	Ribosomal Proteins Regulate MHC Class I Peptide Generation for Immunosurveillance. <i>Molecular Cell</i> , <b>2019</b> , 73, 1162-1173.e5	17.6	42
36	Diversity and heterogeneity of extracellular RNA in human plasma. <i>Biochimie</i> , <b>2019</b> , 164, 22-36	4.6	16
35	2F-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> , <b>2019</b> , 25, 869-880 <sup>58</sup>		12
34	Absolute Quantification of Noncoding RNA by Microscale Thermophoresis. <i>Angewandte Chemie - International Edition</i> , <b>2019</b> , 58, 9565-9569	16.4	15
33	Graphical Workflow System for Modification Calling by Machine Learning of Reverse Transcription Signatures. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 876	4.5	6
32	Mapping and Quantification of tRNA 2FO-Methylation by RiboMethSeq. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1870, 273-295	1.4	8
31	RNA ribose methylation (2FO-methylation): Occurrence, biosynthesis and biological functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2019</b> , 1862, 253-269	6	66
30	FTSJ3 is an RNA 2FO-methyltransferase recruited by HIV to avoid innate immune sensing. <i>Nature</i> , <b>2019</b> , 565, 500-504	50.4	91
29	A Vastly Increased Chemical Variety of RNA Modifications Containing a Thioacetal Structure. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 7893-7897	16.4	31

28	APRDX1 mutant allele causes a MMACHC secondary epimutation in cblC patients. <i>Nature Communications</i> , <b>2018</b> , 9, 67	17.4	45
27	Double methylation of tRNA-U54 to 2FO-methylthymidine (Tm) synergistically decreases immune response by Toll-like receptor 7. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 9764-9775	20.1	10
26	Engineering of a DNA Polymerase for Direct m A Sequencing. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 417-421	16.4	50
25	Quantification of 2FO-Me Residues in RNA Using Next-Generation Sequencing (Illumina RiboMethSeq Protocol). <i>Methods in Molecular Biology</i> , <b>2018</b> , 1649, 29-48	1.4	9
24	Entwicklung einer DNA-Polymerase für die direkte m6A-Sequenzierung. <i>Angewandte Chemie</i> , <b>2018</b> , 130, 424-428	3.6	14
23	Detection and Analysis of RNA Ribose 2FO-Methylations: Challenges and Solutions. <i>Genes</i> , <b>2018</b> , 9,	4.2	26
22	AlkAniline-Seq: Profiling of m7G and m3C RNA Modifications at Single Nucleotide Resolution. <i>Angewandte Chemie</i> , <b>2018</b> , 130, 17027-17032	3.6	
21	AlkAniline-Seq: Profiling of m G and m C RNA Modifications at Single Nucleotide Resolution. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 16785-16790	16.4	66
20	High-Throughput Mapping of 2FO-Me Residues in RNA Using Next-Generation Sequencing (Illumina RiboMethSeq Protocol). <i>Methods in Molecular Biology</i> , <b>2017</b> , 1562, 171-187	1.4	7
19	Identification of sites of 2FO-methylation vulnerability in human ribosomal RNAs by systematic mapping. <i>Scientific Reports</i> , <b>2017</b> , 7, 11490	4.9	67
18	Evidence for rRNA 2FO-methylation plasticity: Control of intrinsic translational capabilities of human ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 12934-12939	11.5	128
17	Next-Generation Sequencing-Based RiboMethSeq Protocol for Analysis of RNA 2FO-Methylation. <i>Biomolecules</i> , <b>2017</b> , 7,	5.9	30
16	Illumina-based RiboMethSeq approach for mapping of 2FO-Me residues in RNA. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e135	20.1	116
15	High-throughput sequencing for 1-methyladenosine (m(1)A) mapping in RNA. <i>Methods</i> , <b>2016</b> , 107, 110-21.6	4.6	35
14	Quantification and quality control of a small non-coding RNA preparation. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1296, 17-28	1.4	1
13	Study of RNA-Protein Interactions and RNA Structure in Ribonucleoprotein Particles (RNPs) <b>2014</b> , 975-1016		
12	The EJC binding and dissociating activity of PYM is regulated in Drosophila. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004455	17	
11	An intracellular transmission control protocol: assembly and transport of ribonucleoprotein complexes. <i>Current Opinion in Cell Biology</i> , <b>2012</b> , 24, 202-10	9	37

10	Control of RNP motility and localization by a splicing-dependent structure in oskar mRNA. <i>Nature Structural and Molecular Biology</i> , <b>2012</b> , 19, 441-9	17.6	85
9	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. <i>RNA Biology</i> , <b>2011</b> , 8, 325-42	4.8	32
8	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> , <b>2011</b> , 39, 3388-403	20.1	4
7	Drosophila Ge-1 promotes P body formation and oskar mRNA localization. <i>PLoS ONE</i> , <b>2011</b> , 6, e20612	3.7	20
6	Alternative splicing: regulation of HIV-1 multiplication as a target for therapeutic action. <i>FEBS Journal</i> , <b>2010</b> , 277, 867-76	5.7	63
5	2-D structure of the A region of Xist RNA and its implication for PRC2 association. <i>PLoS Biology</i> , <b>2010</b> , 8, e1000276	9.7	192
4	Role of RNA structure and protein factors in the control of HIV-1 splicing. <i>Frontiers in Bioscience - Landmark</i> , <b>2009</b> , 14, 2714-29	2.8	23
3	Drosophila PTB promotes formation of high-order RNP particles and represses oskar translation. <i>Genes and Development</i> , <b>2009</b> , 23, 195-207	12.6	93
2	A Janus splicing regulatory element modulates HIV-1 tat and rev mRNA production by coordination of hnRNP A1 cooperative binding. <i>Journal of Molecular Biology</i> , <b>2002</b> , 323, 629-52	6.5	81
1	Study of RNA-Protein Interactions and RNA Structure in Ribonucleoprotein Particles 172-204		2