Franck Martin

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2262349/publications.pdf

Version: 2024-02-01

50 papers	1,635 citations	331642 21 h-index	315719 38 g-index
53 all docs	53 docs citations	53 times ranked	2249 citing authors

#	Article	IF	Citations
1	Tau mRNA Metabolism in Neurodegenerative Diseases: A Tangle Journey. Biomedicines, 2022, 10, 241.	3.2	6
2	Correlated sequence signatures are present within the genomic 5â€²UTR RNA and NSP1 protein in coronaviruses. Rna, 2022, 28, 729-741.	3.5	15
3	Viral and cellular translation during SARSâ€CoVâ€2 infection. FEBS Open Bio, 2022, 12, 1584-1601.	2.3	10
4	Secondary structure of the SARS-CoV-2 5â€™-UTR. RNA Biology, 2021, 18, 447-456.	3.1	104
5	eIF3 interacts with histone H4 messenger RNA to regulate its translation. Journal of Biological Chemistry, 2021, 296, 100578.	3.4	5
6	Translation inhibitory elements from Hoxa3 and Hoxa11 mRNAs use uORFs for translation inhibition. ELife, 2021, 10, .	6.0	10
7	RNA Secondary Structure Study by Chemical Probing Methods Using DMS and CMCT. Methods in Molecular Biology, 2021, 2300, 241-250.	0.9	4
8	The viral protein NSP1 acts as a ribosome gatekeeper for shutting down host translation and fostering SARS-CoV-2 translation. Rna, 2021, 27, 253-264.	3.5	112
9	How Many Messenger RNAs Can Be Translated by the START Mechanism?. International Journal of Molecular Sciences, 2020, 21, 8373.	4.1	2
10	The nature of the purine at position 34 in tRNAs of 4-codon boxes is correlated with nucleotides at positions 32 and 38 to maintain decoding fidelity. Nucleic Acids Research, 2020, 48, 6170-6183.	14.5	17
11	A tRNA-mimic Strategy to Explore the Role of G34 of tRNAGly in Translation and Codon Frameshifting. International Journal of Molecular Sciences, 2019, 20, 3911.	4.1	2
12	A variant inMRPS14(uS14m) causes perinatal hypertrophic cardiomyopathy with neonatal lactic acidosis, growth retardation, dysmorphic features and neurological involvement. Human Molecular Genetics, 2019, 28, 639-649.	2.9	33
13	CUG initiation and frameshifting enable production of dipeptide repeat proteins from ALS/FTD C9ORF72 transcripts. Nature Communications, 2018, 9, 152.	12.8	123
14	Tracking the m 7 G-cap during translation initiation by crosslinking methods. Methods, 2018, 137, 3-10.	3.8	6
15	Viral internal ribosomal entry sites: four classes for one goal. Wiley Interdisciplinary Reviews RNA, 2018, 9, e1458.	6.4	83
16	START: STructure-Assisted RNA Translation. RNA Biology, 2018, 15, 1250-1253.	3.1	6
17	Efficient and Accurate Translation Initiation Directed by TISU Involves RPS3 and RPS10e Binding and Differential Eukaryotic Initiation Factor 1A Regulation. Molecular and Cellular Biology, 2017, 37, .	2.3	33
18	The IRES5â€²UTR of the dicistrovirus cricket paralysis virus is a type III IRES containing an essential pseudoknot structure. Nucleic Acids Research, 2017, 45, 8993-9004.	14.5	41

#	Article	IF	Citations
19	Ribosomal 18S rRNA base pairs with mRNA during eukaryotic translation initiation. Nature Communications, 2016, 7, 12622.	12.8	41
20	Synthetic Capped mRNAs for Cap-Specific Photo-Cross-Linking Experiments. Methods in Molecular Biology, 2016, 1428, 31-43.	0.9	0
21	Purification of mRNAâ€programmed translation initiation complexes suitable for mass spectrometry analysis. Proteomics, 2015, 15, 2417-2425.	2.2	25
22	Hypermethylated-capped selenoprotein mRNAs in mammals. Nucleic Acids Research, 2014, 42, 8663-8677.	14.5	45
23	RACK1 Controls IRES-Mediated Translation of Viruses. Cell, 2014, 159, 1086-1095.	28.9	149
24	Released selective pressure on a structural domain gives new insights on the functional relaxation of mitochondrial aspartyl-tRNA synthetase. Biochimie, 2014, 100, 18-26.	2.6	5
25	Cap analogs containing 6-thioguanosine â€“ reagents for the synthesis of mRNAs selectively photo-crosslinkable with cap-binding biomolecules. Organic and Biomolecular Chemistry, 2014, 12, 4841-4847.	2.8	17
26	Rapid purification of ribosomal particles assembled on histone H4 mRNA: a new method based on mRNAâ€“DNA chimaeras. Biochemical Journal, 2013, 449, 719-728.	3.7	14
27	Fifteen years of the yeast three-hybrid system: RNAâ€“protein interactions under investigation. Methods, 2012, 58, 367-375.	3.8	18
28	Cap-Assisted Internal Initiation of Translation of Histone H4. Molecular Cell, 2011, 41, 197-209.	9.7	93
29	Binding of human SLBP on the 3â€²-UTR of histone precursor H4-12 mRNA induces structural rearrangements that enable U7 snRNA anchoring. Nucleic Acids Research, 2006, 34, 4987-4995.	14.5	11
30	Expression of metazoan replication-dependent histone genes. Biochimie, 2005, 87, 827-834.	2.6	52
31	Two distinct domains of the Â subunit of Aquifex aeolicus leucyl-tRNA synthetase are involved in tRNA binding as revealed by a three-hybrid selection. Nucleic Acids Research, 2004, 32, 3294-3303.	14.5	13
32	Single amino acid changes in AspRS reveal alternative routes for expanding its tRNA repertoire in vivo. Nucleic Acids Research, 2004, 32, 4081-4089.	14.5	8
33	Mutation and Evolution of the Magnesium-Binding Site of a Class II Aminoacyl-tRNA Synthetaseâ€. Biochemistry, 2004, 43, 7028-7037.	2.5	12
34	Critical residues for RNA discrimination of the histone hairpin binding protein (HBP) investigated by the yeast three-hybrid system. FEBS Letters, 2004, 556, 265-270.	2.8	11
35	Results and prospects of the yeast three-hybrid system. FEBS Letters, 2004, 556, 7-12.	2.8	28
36	Enzymes Assembled fromAquifex aeolicusandEscherichia coliLeucyl-tRNA Synthetasesâ€. Biochemistry, 2003, 42, 7694-7700.	2.5	7

#	Article	IF	Citations
37	A yeast knockout strain to discriminate between active and inactive tRNA molecules. Nucleic Acids Research, 2003, 31, 4729-4737.	14.5	14
38	Leucyl-tRNA Synthetase Consisting of Two Subunits from Hyperthermophilic Bacteria Aquifex aeolicus. Journal of Biological Chemistry, 2002, 277, 41590-41596.	3.4	28
39	In vivo selection of lethal mutations reveals two functional domains in arginylâ€“tRNA synthetase. Rna, 2000, 6, 434-448.	3.5	15
40	Positive and negative mutant selection in the human histone hairpin-binding protein using the yeast three-hybrid system. Nucleic Acids Research, 2000, 28, 1594-1603.	14.5	29
41	Kinetic Analysis of the Effect on Fab Binding of Identical Substitutions in a Peptide and Its Parent Protein. Biochemistry, 1999, 38, 3530-3537.	2.5	29
42	Characterization of the Calf Thymus Hairpin-binding Factor Involved in Histone Pre-mRNA 3â€² End Processing. Journal of Biological Chemistry, 1997, 272, 10435-10441.	3.4	8
43	Mirror image alternative interaction patterns of the same tRNA with either class I arginyl-tRNA synthetase or class II aspartyl-tRNA synthetase. Nucleic Acids Research, 1997, 25, 4899-4906.	14.5	23
44	Characterization of a thermosensitive Escherichia coli aspartyl-tRNA synthetase mutant. Journal of Bacteriology, 1997, 179, 3691-3696.	2.2	11
45	The gene for histone RNA hairpin binding protein is located on human chromosome 4and encodes a novel type of RNA binding protein. EMBO Journal, 1997, 16, 769-778.	7.8	142
46	The class II aminoacyl-tRNA synthetases and their active site: Evolutionary conservation of an ATP binding site. Journal of Molecular Evolution, 1995, 40, 499-508.	1.8	44
47	Genetic selection for activeE.coliamber tRNAAsnexclusively led to glutamine inserting suppressors. Nucleic Acids Research, 1995, 23, 779-784.	14.5	6
48	Overproduction and Purification of Native and Queuine-lacking Escherichia coli tRNAAsp Role of the Wobble Base in tRNAAsp Acylation. Journal of Molecular Biology, 1993, 234, 965-974.	4.2	27
49	Role of dimerization in yeast aspartyl-tRNA synthetase and importance of the class II invariant proline.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 10816-10820.	7.1	63
50	Crystallization of aspartyl-tRNA synthetase-tRNAAsp complex from Escherichia coli and first crystallographic results. Journal of Molecular Biology, 1992, 224, 1171-1173.	4.2	19