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List of Publications by Year
in descending order

43 papers	798 citations	430843 18 h-index	580810 25 g-index
43 all docs	43 docs citations	43 times ranked	781 citing authors

#	Article	IF	Citations
1	Elucidating the molecular mechanisms associated with TARS2-related mitochondrial disease. Human Molecular Genetics, 2022, 31, 523-534.	2.9	12
2	Commonality and diversity in tRNA substrate recognition in t6A biogenesis by eukaryotic KEOPSs. Nucleic Acids Research, 2022, 50, 2223-2239.	14.5	14
3	Human lysyl-tRNA synthetase evolves a dynamic structure that can be stabilized by forming complex. Cellular and Molecular Life Sciences, 2022, 79, 128.	5.4	2
4	Molecular basis for human mitochondrial tRNA m3C modification by alternatively spliced METTL8. Nucleic Acids Research, 2022, 50, 4012-4028.	14.5	18
5	Distinct pathogenic mechanisms of various RARS1 mutations in Pelizaeus-Merzbacher-like disease. Science China Life Sciences, 2021, 64, 1645-1660.	4.9	7
6	The human tRNA taurine modification enzyme GTPBP3 is an active GTPase linked to mitochondrial diseases. Nucleic Acids Research, 2021, 49, 2816-2834.	14.5	18
7	Mutually exclusive substrate selection strategy by human m3C RNA transferases METTL2A and METTL6. Nucleic Acids Research, 2021, 49, 8309-8323.	14.5	21
8	Modifications of the human tRNA anticodon loop and their associations with genetic diseases. Cellular and Molecular Life Sciences, 2021, 78, 7087-7105.	5.4	15
9	Selective and competitive functions of the AAR and UPR pathways in stress-induced angiogenesis. Cell Discovery, 2021, 7, 98.	6.7	6
10	Nitrosative stress inhibits aminoacylation and editing activities of mitochondrial threonyl-tRNA synthetase by S-nitrosation. Nucleic Acids Research, 2020, 48, 6799-6810.	14.5	11
11	Hearing impairment-associated KARS mutations lead to defects in aminoacylation of both cytoplasmic and mitochondrial tRNALys. Science China Life Sciences, 2020, 63, 1227-1239.	4.9	18
12	Molecular basis for t6A modification in human mitochondria. Nucleic Acids Research, 2020, 48, 3181-3194.	14.5	24
13	Instability of the mitochondrial alanyl-tRNA synthetase underlies fatal infantile-onset cardiomyopathy. Human Molecular Genetics, 2019, 28, 258-268.	2.9	19
14	Newly acquired N-terminal extension targets threonyl-tRNA synthetase-like protein into the multiple tRNA synthetase complex. Nucleic Acids Research, 2019, 47, 8662-8674.	14.5	16
15	The G3-U70-independent tRNA recognition by human mitochondrial alanyl-tRNA synthetase. Nucleic Acids Research, 2019, 47, 3072-3085.	14.5	25
16	Editing activity for eliminating mischarged tRNAs is essential in mammalian mitochondria. Nucleic Acids Research, 2018, 46, 849-860.	14.5	30
17	A threonyl-tRNA synthetase-like protein has tRNA aminoacylation and editing activities. Nucleic Acids Research, 2018, 46, 3643-3656.	14.5	27
18	A natural non-Watsonâ€“Crick base pair in human mitochondrial tRNAThr causes structural and functional susceptibility to local mutations. Nucleic Acids Research, 2018, 46, 4662-4676.	14.5	19

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19	Mutations inKARScause early-onset hearing loss and leukoencephalopathy: Potential pathogenic mechanism. Human Mutation, 2017, 38, 1740-1750.	2.5	25
20	Translational Quality Control by Bacterial Threonyl-tRNA Synthetases. Journal of Biological Chemistry, 2016, 291, 21208-21221.	3.4	16
21	Sequence-specific and Shape-selective RNA Recognition by the Human RNA 5-Methylcytosine Methyltransferase NSun6. Journal of Biological Chemistry, 2016, 291, 24293-24303.	3.4	30
22	A Human Disease-causing Point Mutation in Mitochondrial Threonyl-tRNA Synthetase Induces Both Structural and Functional Defects. Journal of Biological Chemistry, 2016, 291, 6507-6520.	3.4	40
23	C-terminal Domain of Leucyl-tRNA Synthetase from Pathogenic Candida albicans Recognizes both tRNASer and tRNALeu. Journal of Biological Chemistry, 2016, 291, 3613-3625.	3.4	6
24	Degenerate Connective Polypeptide 1 (CP1) Domain from Human Mitochondrial Leucyl-tRNA Synthetase. Journal of Biological Chemistry, 2015, 290, 24391-24402.	3.4	13
25	Identification of Lethal Mutations in Yeast Threonyl-tRNA Synthetase Revealing Critical Residues in Its Human Homolog. Journal of Biological Chemistry, 2015, 290, 1664-1678.	3.4	10
26	tRNA recognition by a bacterial tRNA Xm32 modification enzyme from the SPOUT methyltransferase superfamily. Nucleic Acids Research, 2015, 43, 7489-7503.	14.5	20
27	Calpain Cleaves Most Components in the Multiple Aminoacyl-tRNA Synthetase Complex and Affects Their Functions. Journal of Biological Chemistry, 2015, 290, 26314-26327.	3.4	10
28	A bridge between the aminoacylation and editing domains of leucyl-tRNA synthetase is crucial for its synthetic activity. Rna, 2014, 20, 1440-1450.	3.5	12
29	A minimalist mitochondrial threonyl-tRNA synthetase exhibits tRNA-isoacceptor specificity during proofreading. Nucleic Acids Research, 2014, 42, 13873-13886.	14.5	21
30	Coexistence of bacterial leucyl-tRNA synthetases with archaeal tRNA binding domains that distinguish tRNALeu in the archaeal mode. Nucleic Acids Research, 2014, 42, 5109-5124.	14.5	16
31	Interdomain communication modulates the tRNA-dependent pre-transfer editing of leucyl-tRNA synthetase. Biochemical Journal, 2013, 449, 123-131.	3.7	9
32	Aminoacylation and translational quality control strategy employed by leucyl-tRNA synthetase from a human pathogen with genetic code ambiguity. Nucleic Acids Research, 2013, 41, 9825-9838.	14.5	21
33	Human cytoplasmic ProX edits mischarged tRNAPro with amino acid but not tRNA specificity. Biochemical Journal, 2013, 450, 243-252.	3.7	17
34	Translational fidelity maintenance preventing Ser mis-incorporation at Thr codon in protein from eukaryote. Nucleic Acids Research, 2013, 41, 302-314.	14.5	31
35	A naturally occurring nonapeptide functionally compensates for the CP1 domain of leucyl-tRNA synthetase to modulate aminoacylation activity. Biochemical Journal, 2012, 443, 477-484.	3.7	13
36	Role of tRNA amino acid-accepting end in aminoacylation and its quality control. Nucleic Acids Research, 2011, 39, 8857-8868.	14.5	38

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37	Functional characterization of leucine-specific domain 1 from eukaryal and archaeal leucyl-tRNA synthetases. Biochemical Journal, 2010, 429, 505-513.	3.7	8
38	Post-transfer editing by a eukaryotic leucyl-tRNA synthetase resistant to the broad-spectrum drug AN2690. Biochemical Journal, 2010, 430, 325-333.	3.7	14
39	tRNA-dependent Pre-transfer Editing by Prokaryotic Leucyl-tRNA Synthetase. Journal of Biological Chemistry, 2010, 285, 3235-3244.	3.4	47
40	A Unique Insertion in the CP1 Domain of Giardia lamblia Leucyl-tRNA Synthetase. Biochemistry, 2009, 48, 1340-1347.	2.5	8
41	Two tyrosine residues outside the editing active site in Giardia lamblia leucyl-tRNA synthetase are essential for the post-transfer editing. Biochemical and Biophysical Research Communications, 2009, 386, 510-515.	2.1	4
42	Unique Residues Crucial for Optimal Editing in Yeast Cytoplasmic Leucyl-tRNA Synthetase Are Revealed by Using a Novel Knockout Yeast Strain. Journal of Biological Chemistry, 2008, 283, 22591-22600.	3.4	27
43	The CP2 Domain of Leucyl-tRNA Synthetase Is Crucial for Amino Acid Activation and Post-transfer Editing. Journal of Biological Chemistry, 2008, 283, 36608-36616.	3.4	40