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List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

870
citations

759055

12
h-index

1058333

14
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15
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docs citations

15
times ranked

838
citing authors

#	ARTICLE	IF	CITATIONS
1	eIF3a cooperates with sequences 5' of uORF1 to promote resumption of scanning by post-termination ribosomes for reinitiation on GCN4 mRNA. <i>Genes and Development</i> , 2008, 22, 2414-2425.	2.7	125
2	Embraced by eIF3: structural and functional insights into the roles of eIF3 across the translation cycle. <i>Nucleic Acids Research</i> , 2017, 45, 10948-10968.	6.5	102
3	The RNA Recognition Motif of Eukaryotic Translation Initiation Factor 3g (eIF3g) Is Required for Resumption of Scanning of Posttermination Ribosomes for Reinitiation on GCN4 and Together with eIF3i Stimulates Linear Scanning. <i>Molecular and Cellular Biology</i> , 2010, 30, 4671-4686.	1.1	99
4	Selective Translation Complex Profiling Reveals Staged Initiation and Co-translational Assembly of Initiation Factor Complexes. <i>Molecular Cell</i> , 2020, 79, 546-560.e7.	4.5	92
5	The C-Terminal Region of Eukaryotic Translation Initiation Factor 3a (eIF3a) Promotes mRNA Recruitment, Scanning, and, Together with eIF3j and the eIF3b RNA Recognition Motif, Selection of AUG Start Codons. <i>Molecular and Cellular Biology</i> , 2010, 30, 4415-4434.	1.1	86
6	The Indispensable N-Terminal Half of eIF3j/HCR1 Cooperates with its Structurally Conserved Binding Partner eIF3b/PRT1-RRM and with eIF1A in Stringent AUG Selection. <i>Journal of Molecular Biology</i> , 2010, 396, 1097-1116.	2.0	77
7	Functional and Biochemical Characterization of Human Eukaryotic Translation Initiation Factor 3 in Living Cells. <i>Molecular and Cellular Biology</i> , 2014, 34, 3041-3052.	1.1	69
8	Structural analysis of an eIF3 subcomplex reveals conserved interactions required for a stable and proper translation pre-initiation complex assembly. <i>Nucleic Acids Research</i> , 2012, 40, 2294-2311.	6.5	64
9	Human eIF3b and eIF3a serve as the nucleation core for the assembly of eIF3 into two interconnected modules: the yeast-like core and the octamer. <i>Nucleic Acids Research</i> , 2016, 44, 10772-10788.	6.5	58
10	Functional Characterization of the Role of the N-terminal Domain of the c/Nip1 Subunit of Eukaryotic Initiation Factor 3 (eIF3) in AUG Recognition. <i>Journal of Biological Chemistry</i> , 2012, 287, 28420-28434.	1.6	33
11	Adapted formaldehyde gradient cross-linking protocol implicates human eIF3d and eIF3c, k and l subunits in the 43S and 48S pre-initiation complex assembly, respectively. <i>Nucleic Acids Research</i> , 2020, 48, 1969-1984.	6.5	27
12	Dynamics of the Pollen Sequestrome Defined by Subcellular Coupled Omics. <i>Plant Physiology</i> , 2018, 178, 258-282.	2.3	23
13	A systematic computational analysis of the rRNA 3' UTR sequence complementarity suggests a regulatory mechanism influencing post-termination events in metazoan translation. <i>Rna</i> , 2016, 22, 957-967.	1.6	7
14	uS3/Rps3 controls fidelity of translation termination and programmed stop codon readthrough in co-operation with eIF3. <i>Nucleic Acids Research</i> , 2019, 47, 11326-11343.	6.5	6