

# Anna Herrmannová

## 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  
g-index

15  
all docs

15  
docs citations

15  
times ranked

838  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Dynamics of the Pollen Sequestrome Defined by Subcellular Coupled Omics. <i>Plant Physiology</i> , 2018, 178, 258-282.	2.3	23
5	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
6	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
7	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
8	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
9	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
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	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
12	The RNA Recognition Motif of Eukaryotic Translation Initiation Factor 3g (eIF3g) Is Required for Resumption of Scanning of Posttermination Ribosomes for Reinitiation on <i>GCN4</i> and Together with eIF3i Stimulates Linear Scanning. <i>Molecular and Cellular Biology</i> , 2010, 30, 4671-4686.	1.1	99
13	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
14	eIF3a cooperates with sequences 5' of uORF1 to promote resumption of scanning by post-termination ribosomes for reinitiation on <i>GCN4</i> mRNA. <i>Genes and Development</i> , 2008, 22, 2414-2425.	2.7	125