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Supporting information for article:

Crystal structure of the RNA-recognition motif of *Drosophila melanogaster* tRNA (uracil-5-)-methyltransferase homolog A (TRMT2A)

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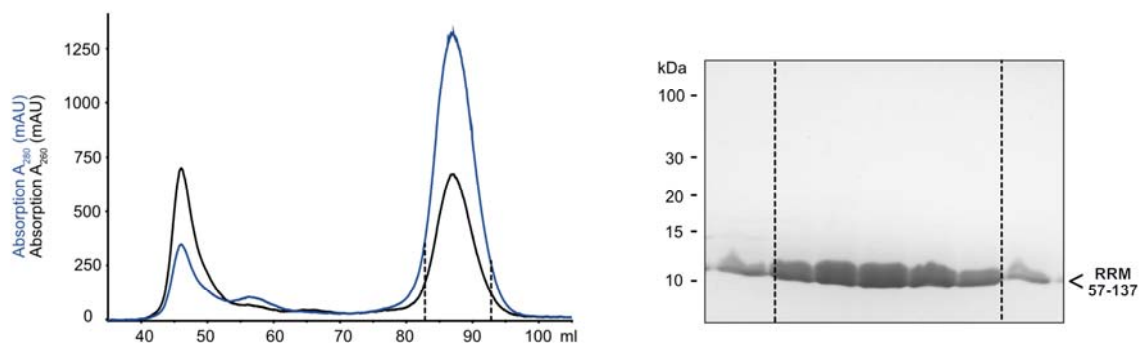


Figure S1 Elution profile of size-exclusion chromatography using a Superdex 75, (S75, 10/300 GL) column shows the last step of *dm*TRMT2A RRM (57-137) purification. A corresponding SDS PAGE (right) from fractions between both dotted lines in the elution profile (left) shows the expected size of the RRM at around 10-11 kDa (calculated molecular weight: 9.8 kDa). Dashed lines on the gel image (right) show fractions used for concentration and subsequent crystallization.

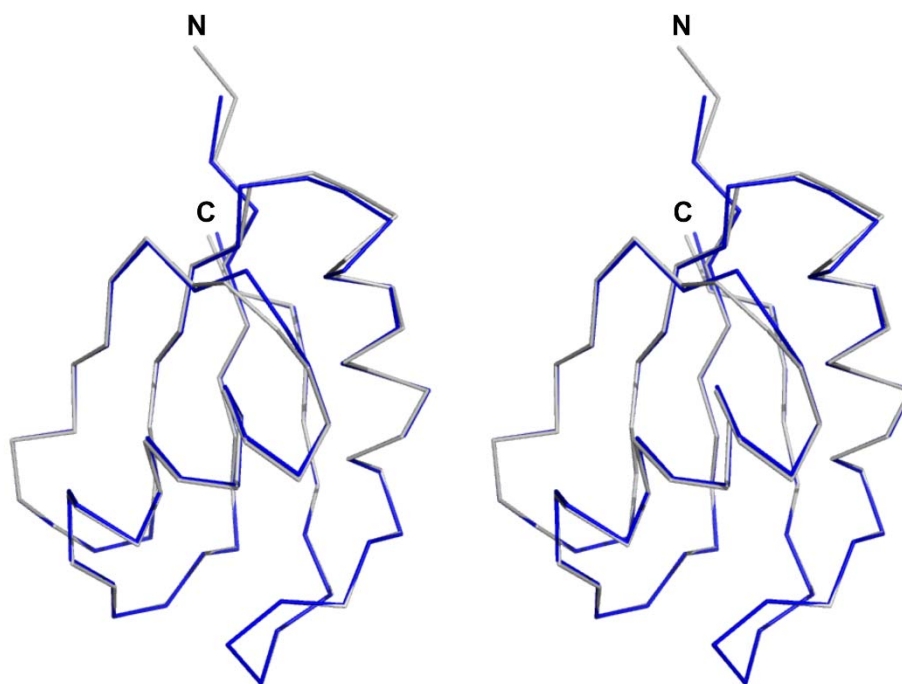


Figure S2 The crystals of *dmTRMT2A* RRM contain two molecules in the asymmetric unit with r.m.s.d value of 0.39 Å for 74 superimposed $C\alpha$ atoms. The figure shows a stereo view of the overlap of both independent chains: A – navy blue and B – grey. The figure was prepared with *PyMOL* (Schrödinger and DeLano, 2020).

Table S1 Conservation of the amino acid residues in position 2 of the RNP2 and in position 3 and 5 of the RNP1 in the analysed RRM structures.

The values in the table include r.m.s.d. in Å and sequence identity in % (%seq).

PDB ID	Organism	RNP2 Position 2	RNP1 Position 3	RNP1 Position 5	r.m.s.d.	%seq	Reference
7PV5	<i>D. melanogaster</i>	E64	F99	F101	-	-	This study
7NTO	<i>H. sapiens</i>	E76	C111	F113	1.65	32	Margreiter <i>et al.</i> , 2022
1B7F	<i>D. melanogaster</i>	I128	Y168	F170	1.27	29	Handa <i>et al.</i> , 1999
3L3C	<i>H. sapiens</i>	Y13	Q54	F56	1.33	18	Cochrane <i>et al.</i> , 2009
3D2W	<i>M. musculus</i>	F194	F229	F231	1.79	22	Kuo <i>et al.</i> , 2009
4IUF	<i>H. sapiens</i>	L107	F147	F149	1.51	17	Kuo <i>et al.</i> , 2014
6DG0	<i>C. elegans</i>	F24	V60	F62	1.43	16	unpublished