

## SUPPLEMENTARY DATA

Figure S1. Secondary structure prediction done with Network Protein Sequence Analysis Server (43);

A: secondary structure prediction for GluRS: residues 181-205; For the amino acids 181-200 there is a random coil region predicted and for 201-205 an extended strand; B: secondary structure prediction for MetRS: residues 141-210; Amino acids 160-172 are a random coil region, 173-175 an extended strand and 176-195 are again a random coil region.

A

	150	160	170	180	190	200	210
UNK_208330	KVDVNVSRWYTLLEMDPIFG	EAHDFLSKSLLELKKSANV	GKKKETHKANFEIDLPDA	KMG	EVVTRFPPEP		
DSC	ccccccchh	cccccccc	hhhhhhhhhhhhhhhhhh	cccccccccccccccccccc	cccccccccccccccccccc	eeeecccccc	
MLRC	ccccchhhhhhhhh	ccccchhhhhhhhhhhhh	hhhhhhhhhhhhhhhhhh	cccccccccccccccccccc	eeeecccccccccccccccc	eeeecccccc	
PHD	ccchhhhhhhheeee	cccccccccccccccccccc	cccccccccccccccccccc	cccccccccccccccccccc	cccccccccccccccccccc	eeeecccccc	
Predator	hcccccccccccccccc	cccccccccccccccccccc	hhhhhhhhhhhhhhhh	ccccchhhhhhh	cccccccccccccccccccc	eeeecccccc	
Sec.Cons.	cccc??hhheeecccc	??h??hhhhhhhhhhhh	??cccccccccccccccccccc	cccccccccccccccccccc	eeeecccccc		

B

	150	160	170	180	190	200	210
UNK_228150	KFPELPSKVVHNAVALAKK	HVPERDSSSFKNIGAVKI	QADLTVKPKDSEILEPKP	NERNILIT	SALFYVNNVP		
DSC	ccccchhhhhhhhhhh	cccccccccccccccccccc	hhhhhhheeehhhh	cccccccccccccccccccc	eeeecccccccccccccccc	eeeecccccc	
MLRC	chhhhhhhhhhhhhhh	cccccccccccccccccccc	eeeecccccccccccccccc	cccccccccccccccccccc	eeeecccccccccccccccc	eeeecccccc	
PHD	hcchhhhhhhhh	cccccccccccccccccccc	eeeecccccccccccccccc	cccccccccccccccccccc	eeeecccccccccccccccc	eeeecccccc	
Predator	ccccccccchhhhhhhhh	cccccccccccccccccccc	hhhhhhhh	cccccccccccccccccccc	eeeecccccccccccccccc	eeeecccccc	
Sec.Cons.	ccc??hhhhhhhhhhhh	??cccccccccccccccccccc	eeee????cccccccccccccccc	eeeecccccc			

Figure S2. Guinier plots of experimental scattering data;  
1: Pentameric complex MetRS:GluRS:Arc1p:tRNAs (grey); 2: Trimeric complex of MetRS:GluRS:Arc1p (turquoise); 3: GluRS:Arc1p (lilac); 4: MetRS:Arc1p complex (yellow); 5: GluRS (red); 6: MetRS (blue); 7: Arc1p (green).

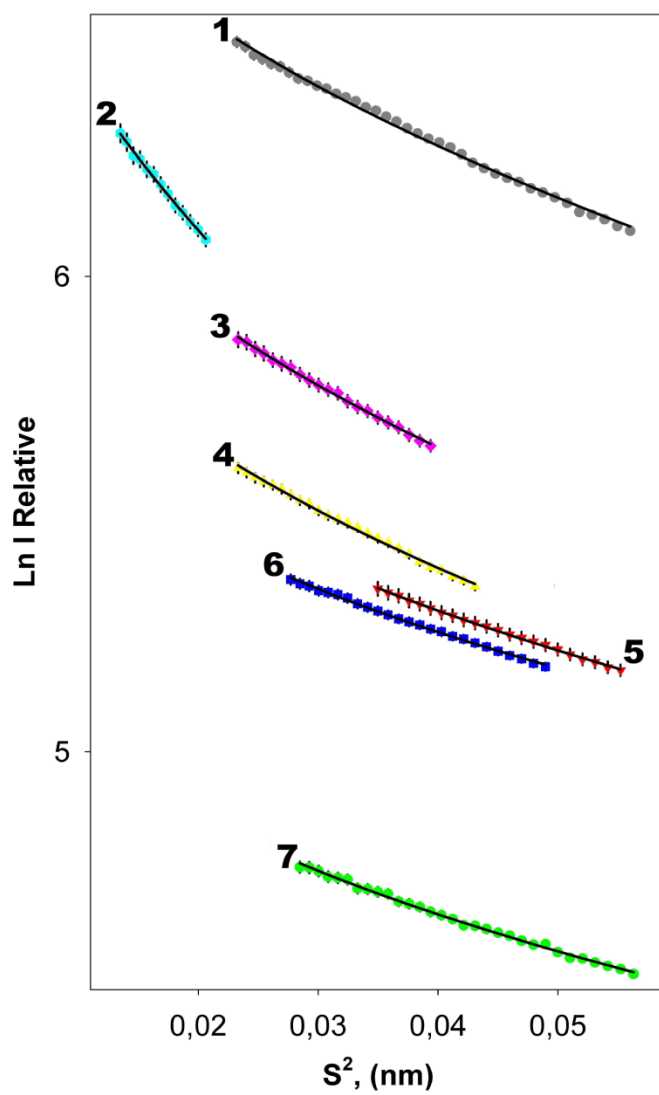
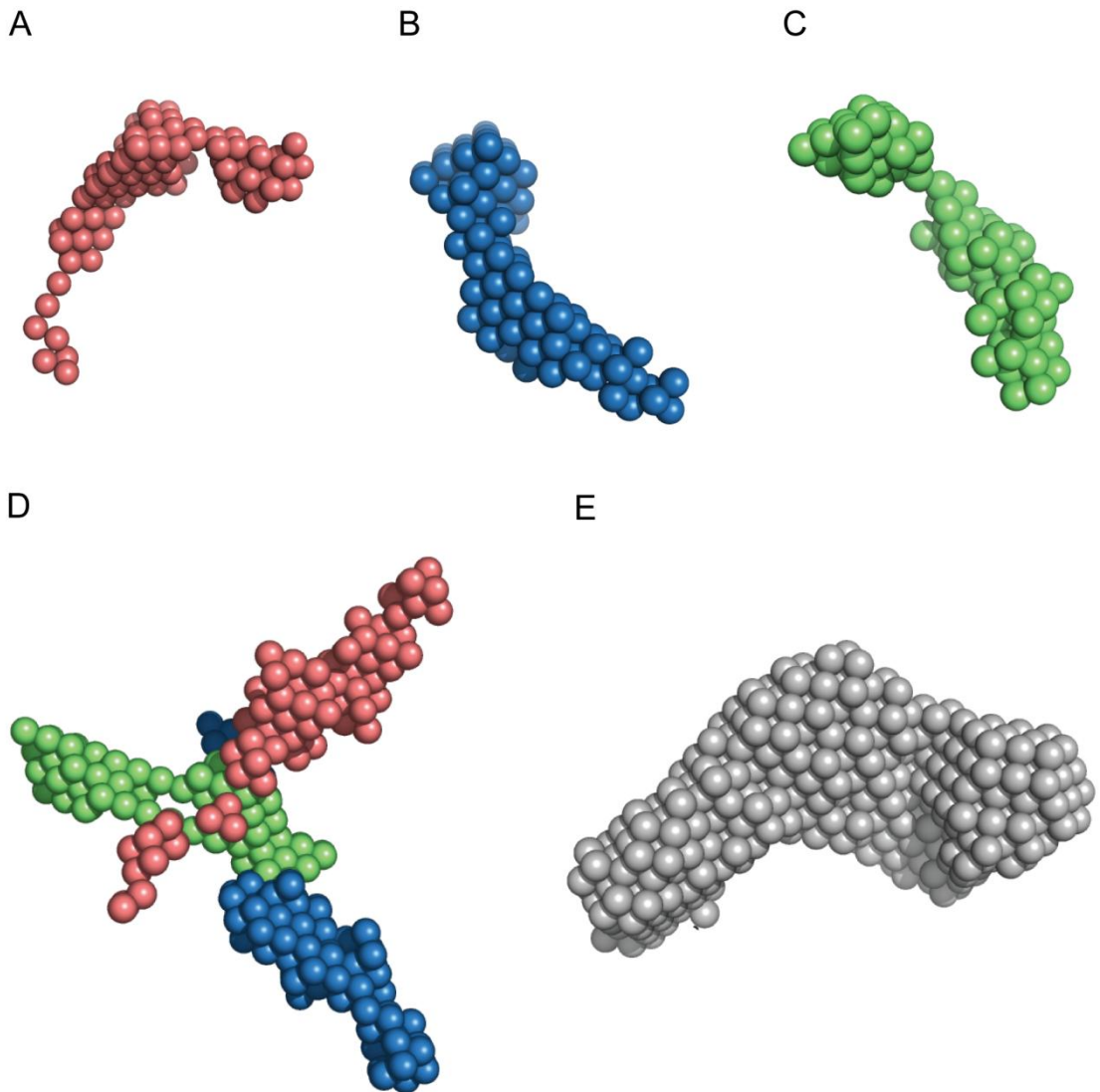


Figure S3. *Ab initio* Models;

A: GluRS (red), B: MetRS (blue), C: Arc1p (green), D: trimeric complex and E: pentameric complex

The models were obtained by analyzing the SAXS data with the Program DAMMIN. Proteins are shown with densely packed beads.



## SUPPLEMENTARY METHODS

### EMSA assay

To analyze the binding of the tRNAs to the trimeric complex, the trimeric complex (MAG) was used in a 10  $\mu$ M concentration (1  $\mu$ l) in a total reaction volume of 20  $\mu$ l. Each unlabeled tRNA was applied in a 1:1 molar ratio to the complex as the highest concentration (1.5  $\mu$ l). The  $^{32}$ P labeled tRNAs were added in the same concentration steps (0.5-1.5  $\mu$ l) as the unlabeled ones (Figure 3). The reactions were incubated on ice for 30 minutes and then loaded on a 6% native gel.

### SUPPLEMENTARY REFERENCES

43. Combet,C., Blanchet,C., Geourjon,C. and Deléage,G. (2000) NPS@: network protein sequence analysis. *Trends Biochem Sci.*, **25**, 147-50.
44. Simader,H. and Suck,D. (2006) Expression, purification, crystallization and preliminary phasing of the heteromerization domain of the tRNA-export and aminoacylation cofactor Arc1p from yeast. *Acta. Crystallograph Sect. F: Struct. Biol. Cryst. Commun.*, **62**, 346-349.