Supplementary Material

Supplementary Table 1. Mass spectrometry results for the His-tagged Tf-TfR complex absorbed to a 20% Ni-NTA monolayer or to a 20% CC Affinity Grid.

Preparation Method	Component	I ^a	$\Pi_{\rm p}$
Monolayer	Human Tf	28.2	30
	Human TfR1	50.2	52
Affinity Grid	Human Tf	28.9	31
	Human TfR1	51.4	50

^a Percentage of sequence coverage for each protein identified

^b Number of unique tryptic peptides for each protein identified

Supplementary Table 2. Mass spectrometry results for the ribosomal complexes with adsorbed to a 20% CC Affinity Grid.

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Component	I ^a	IIp
Rpl1*	38.7	6
Rpl2*	23.6	7
Rpl3-human*	18.4	9
Rpl4*	24.6	4
Rpl5*	32.2	8
Rpl6*	17.6	6
Rpl7*	8.4	1
Rpl8*	12.7	2
Rpl9*	38.8	4
Rpl10*	12.7	2
Rpl11*	13.4	2
Rpl12*	6.0	1
Rpl13*	8.3	1
Rpl14*	16.2	2
Rpl15*	17.4	2
Rpl16*	10.7	1
Rpl17*	16.6	3
Rpl18*	21.6	4
Rpl19*	9.9	1
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Rpl20*	15.6	2
Rpl21*	24.3	3
Rpl22*	64.8	12
Rp123*	17.5	3
Rpl24*	58.6	6
Rpl25*	20.3	4
Rpl26*	11.2	2
Rpl27*	15.7	4
Rpl28*	17.3	3
Rpl29*	14.4	3
Rp130*	17.7	2
Rps1*	9.6	3
Rps2*	3.3	2
Rps3*	14.1	3
Rps4*	46.2	10
Rps5*	12.6	4
Rps6*	7.7	3
Rps7*	4.2	1
Rps8*	3.7	1
Rps9*	12.4	2
Rps10*	5.2	1
Rps11*	27.8	4

Rps12*	15.6	2
Rps13*	63.4	8
Rps14*	8.4	1
Rps15*	6.1	1
Rps16*	7.6	1
Rps17*	4.4	1
Rps18*	7.9	1
Rps19*	4.8	1
Rps20*	14.9	2
EfTu ¹	17.8	6

^a Percentage of sequence coverage for each protein identified

(Rpl = ribosomal protein large subunit; Rps = ribosomal protein small subunit; Eftu = elongation factor tu)

^b Number of unique tryptic peptides for each protein identified

^{*}Ribosomal proteins

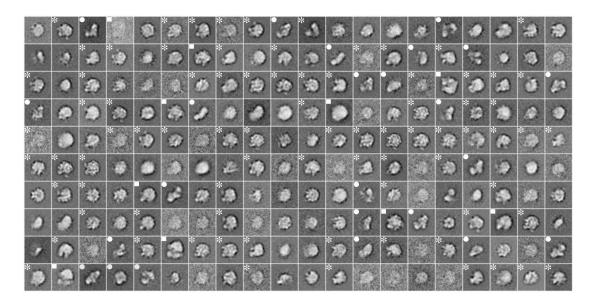
¹Ribosome associated proteins

Supplementary Table 3. Mass spectrometry results for the His-tagged AQP9 complex absorbed to a Ni-NTA agarose column or to a 20% CC Affinity Grid.

Preparation Method	Component	I ^a	Π_p
Ni-NTA column	Rat AQP9	10.3	5
Affinity Grid	Rat AQP9	25.2	8

^a Percentage of sequence coverage for each protein identified

^b Number of unique tryptic peptides for each protein identified



Supplementary Figure 1. Class averages of vitrified complexes containing Histagged rpl3 on 20% HC Affinity Grids. The 200 class averages obtained from classification of 52,507 particle images of vitrified rpl3-complexes. The side length of the individual panels is 38 nm. Class averages corresponding to projections of the 50S ribosomal subunit are marked by an asterisk, those corresponding to projections of the 70S ribosome by a square, and those corresponding to projections of the 30S ribosomal subunit by a circle.