

**Table S1. Mascot search mass spectrum results of bands in the red frame (zone X2), blue frame (X1), and black frame (Sup35 monomer band) in Figure 3B.**

	zone X2		Sup35	X1
Database	NCBIInr	20141208 (53438708 sequences; 19231914498 residues)	NCBIInr 20141208 (53438708 sequences; 19231914498 residues)	NCBIInr 20141208 (53438708 sequences; 19231914498 residues)
Taxonomy	<i>E. coli</i>	(1254256 sequences)	<i>S. cerevisiae</i> (50241 sequences)	<i>E. coli</i> (1254256 sequences)
Protein hits	1. gi 14488508 Chain A, Omp F porin mutant Nqaaa 2. gi 545170440 outer membrane porin Omp F [ <i>E. coli</i> ] 3. gi 693025713 porin [ <i>E. coli</i> ] 4. gi 446900668 outer membrane phosphoprotein E [ <i>E. coli</i> ] 5. gi 693047316 porin [ <i>E. coli</i> ] 6. gi 486220816 chaperone protein Dna K [ <i>E. coli</i> ] 7. gi 223404 protein S1 8. gi 42837 unnamed protein product [ <i>E. coli</i> ] 9. gi 66360654 Chain A, conformation rearrangement of heat shock protein 90 upon ADP binding 10. gi 693180024 heat shock protein 90 [ <i>E. coli</i> ] 11. gi 345381202 PPIC-type PPIASE domain protein [ <i>E. coli</i> G58-1] 12. gi 33357880 Chain C, real space refined coordinates of the 30 S subunit fitted into the low resolution cryo-EM map of the Ef-G.GTP state of <i>E. coli</i> 70 S Ribosome		1. gi 618713641 Sup35[ <i>S. cerevisiae</i> ] 2. gi 3712 GST1 [ <i>S. cerevisiae</i> ] 3. gi 618713585 Sup35 [ <i>S. cerevisiae</i> ]	1. gi 333944305 Chain D, structure of The <i>E. coli</i> F1-ATP synthase inhibited by subunit epsilon gi 672830493 2. ATP synthase F0F1 subunit beta, partial [ <i>E. coli</i> ]