

A**DAVID Gene Ontology – Functional Annotation**

<i>Biological Process</i>	<i>Count</i>	<i>P-value</i>
Translation	76	7.3x10 ⁻⁶⁷
mRNA metabolic process	20	7.5x10 ⁻⁷
Protein folding	13	1.4x10 ⁻⁶
RNA splicing	15	7.1x10 ⁻⁶
mRNA processing	16	3.5x10 ⁻⁵
Translation initiation	7	3.6x10 ⁻⁵
RNA processing	21	4.5x10 ⁻⁵
Microtubule-based process	14	5.5x10 ⁻⁵
Protein localization	29	5.9x10 ⁻⁵
Regulation of protein complex disassembly	7	7.4x10 ⁻⁵
<i>Cellular Components</i>		
Cytosolic part	14	5.2x10 ⁻¹¹
Large ribosomal subunit	10	1.8x10 ⁻⁸
Melanosome	12	2.7x10 ⁻⁷
Pigment granule	12	2.7x 10 ⁻⁷
Cytosol	29	3.9 x 10 ⁻⁷
Cytosolic large ribosomal subunit	5	3.1x10 ⁻⁶
Eukaryotic translation initiation factor 3 complex	5	4.1x10 ⁻⁵
Microtubule	15	8.9x10 ⁻⁵
Cytoskeletal part	30	9.2x10 ⁻⁵
Cytosolic small ribosomal subunit	4	1.0x10 ⁻⁴
<i>Molecular Function</i>		
Structural constituent of ribosome	57	6.0x10 ⁻⁶⁰
Structural molecular activity	70	1.6x10 ⁻⁴⁵
RNA binding	57	8.4x10 ⁻²³
Nucleotide binding	87	1.2x10 ⁻¹³
Translation factor activity, nucleic acid binding	16	2.1x10 ⁻¹⁰
Ribonucleotide binding	66	1.3x10 ⁻⁸
ATPase activity	22	3.6x10 ⁻⁸
rRNA binding	8	1.5x10 ⁻⁷
Unfolded protein binding	11	4.5x10 ⁻⁷
Translation initiation factor activity	10	1.5x10 ⁻⁶

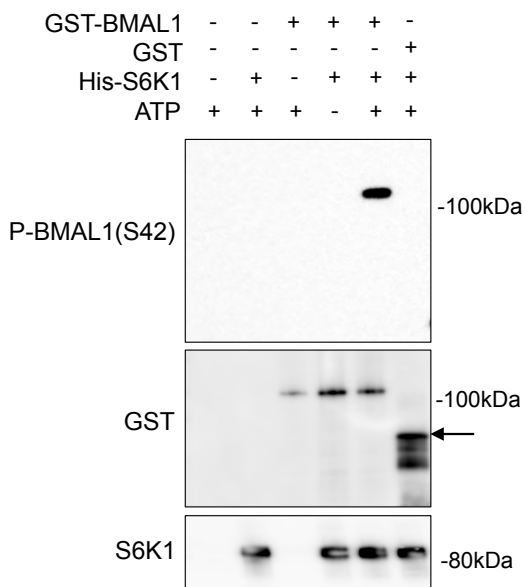
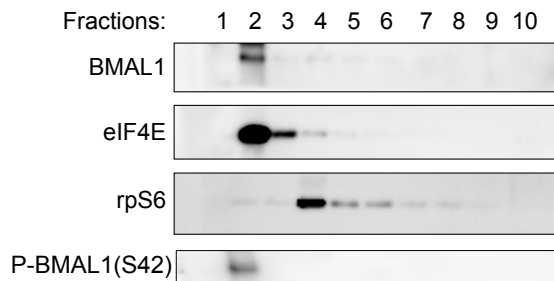
B**C**

Figure S1