

**Supplementary Table 12.** Reactome pathway results for protein-protein interaction module 3

Reactome pathway	p-value	Genes
Translation	1.00E-11	<i>RPL32, EIF3L, RPS5, SEC61G, RPS27L, RPL15, EIF3A, SRP9, RPS12</i>
Formation of a pool of free 40S subunits	1.15E-10	<i>RPL32, EIF3L, RPS5, RPS27L, RPL15, EIF3A, RPS12</i>
L13a-mediated translational silencing of ceruloplasmin expression	2.04E-10	<i>RPL32, EIF3L, RPS5, RPS27L, RPL15, EIF3A, RPS12</i>
SRP-dependent cotranslational protein targeting to membrane	2.15E-10	<i>RPL32, RPS5, SEC61G, RPS27L, RPL15, SRP9, RPS12</i>
GTP hydrolysis and joining of the 60S ribosomal subunit	2.15E-10	<i>RPL32, EIF3L, RPS5, RPS27L, RPL15, EIF3A, RPS12</i>
Cap-dependent translation Initiation	3.10E-10	<i>RPL32, EIF3L, RPS5, RPS27L, RPL15, EIF3A, RPS12</i>
Eukaryotic translation initiation	3.10E-10	<i>RPL32, EIF3L, RPS5, RPS27L, RPL15, EIF3A, RPS12</i>
Major pathway of rRNA processing in the nucleolus and cytosol	4.27E-09	<i>TBL3, RPL32, IMP3, RPS5, RPS27L, RPL15, RPS12</i>
rRNA processing in the nucleus and cytosol	5.86E-09	<i>TBL3, RPL32, IMP3, RPS5, RPS27L, RPL15, RPS12</i>
rRNA processing	7.92E-09	<i>TBL3, RPL32, IMP3, RPS5, RPS27L, RPL15, RPS12</i>
Formation of the ternary complex and subsequently the 43S complex	9.31E-08	<i>EIF3L, RPS5, RPS27L, EIF3A, RPS12</i>
Translation initiation complex formation	1.56E-07	<i>EIF3L, RPS5, RPS27L, EIF3A, RPS12</i>
Ribosomal scanning and start codon recognition	1.56E-07	<i>EIF3L, RPS5, RPS27L, EIF3A, RPS12</i>
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	1.67E-07	<i>EIF3L, RPS5, RPS27L, EIF3A, RPS12</i>
Viral mRNA translation	8.64E-07	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Peptide chain elongation	8.64E-07	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Eukaryotic translation Termination	1.03E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Eukaryotic translation Elongation	1.03E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Selenocysteine synthesis	1.03E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
NMD independent of the EJC	1.12E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Response of EIF2AK4 (GCN2) to amino acid deficiency	1.43E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
NMD enhanced by the EJC	2.39E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
NMD	2.39E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Selenoamino acid metabolism	2.65E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Influenza viral RNA transcription and replication	4.52E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>

Cellular response to starvation	8.00E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Influenza infection	8.00E-06	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Regulation of expression of Slits and Robos	1.15E-05	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Metabolism of RNA	1.28E-05	<i>TBL3, RPL32, IMP3, RPS5, RPS27L, RPL15, RPS12</i>
Signaling by Robo receptors	2.98E-05	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Metabolism of proteins	3.46E-05	<i>RPL32, EIF3L, RPS5, SEC61G, RPS27L, RPL15, EIF3A, SRP9, RPS12</i>
Metabolism of amino acids and derivatives	2.44E-04	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
SARS-CoV-1 modulates host translation machinery	4.92E-04	<i>RPS5, RPS27L, RPS12</i>
SARS-CoV-2 modulates host translation machinery	9.35E-04	<i>RPS5, RPS27L, RPS12</i>
Axon guidance	0.00106	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Nervous system development	0.001251	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
SARS-CoV-1-host interactions	0.003272	<i>RPS5, RPS27L, RPS12</i>
Cellular responses to stress	0.003957	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
Cellular responses to stimuli	0.004219	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>
SARS-CoV-1 infection	0.007024	<i>RPS5, RPS27L, RPS12</i>
Infectious disease	0.008026	<i>RPL32, RPS5, RPS27L, RPL15, RPS12</i>

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NMD, nonsense-mediated decay; EJC, exon junction complex; SARS-CoV-1, severe acute respiratory syndrome coronavirus 1; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.