

Table S1. Homologs of RPs in *Mus musculus*. The 37 polypeptides listed below were identified as RPs in Tang and Watson (2015).

Predicted repair protein	NCBI accession #	Conserved domains in NCBI	NCBI accession # of homolog in <i>Mus musculus</i>	E-value	Max ident.
Histone	gi 156322163	H2A H4	NP291074.1	5e-53	98%
Actin, beta	gi 156375400	Actin NBD-sugar kinase-HSP70-actin	NP_031419.1	0.0	97%
20S proteasome, alpha type 2	gi 156387508	proteasome_alpha_type_2	NP_032970.2	1e-146	84%
20S proteasome, alpha type 6	gi 156405260	proteasome_alpha_type_6	EDL36728.1	2e-158	84%
Heat shock protein 70	gi 156351241	HSPA1-2_6-8-like_NBD PTZ00009	NP_112442.2	0.0	82%
20S proteasome, alpha type 5	gi 156379569	proteasome_alpha_type_5	NP036097.1	2e-148	82%
20S proteasome, alpha type 7	gi 156401589	proteasome_alpha_type_7	NP036099.1	3e-143	82%
Stress-70 protein	gi 156402816	HSPA9-like_NBD ZIP super family dnaK	BAA04493.1	0.0	81%
20S proteasome, alpha type 1	gi 156371281	proteasome_alpha_type_1	NP036095.1	1e-139	78%
6-phosphogluconate dehydrogenase	gi 156367416	6PGD NAD_binding_2 PRK09287	NP_001074743.1	0.0	77%
Enolase	gi 156383570	enolase PLN00191	NP_001020559.1	0.0	76%
Fumarate hydratase	gi 156354249	Fumarase_classII fumC	NP_034339.2	0.0	76%
20S proteasome, beta type 5	gi 156363343	proteasome_beta_type_5	AAH12246.1	4e-121	76%
Cyclophilin	gi 156355365	cyclophilin_ABH_like	NP_598845.1	1e-87	76%

Tryparedoxin peroxidase	gi 156404129	PRX_Typ2cys PTZ00253	NP058044.1	2e-105	73%
20S proteasome, alpha type 3	gi 156371095	proteasome_alpha_type_3	EDL36567.1	4e-136	72%
Dihydrolipoamide dehydrogenase	gi 156408155	Pyr_redox_dim Pyr_redox SDR super family PRK06327	NP031887.2	0.0	72%
Dihydropyrimidine dehydrogenase	gi 156369958	DHPD_FMN Fer4_20 NAD_binding_8 HCP_like super family PRK08318 PRK11749	NP_740748.1	0.0	71%
Fructose-1,6-bisphosphate aldolase	gi 156374279	FBP_aldolase_I_a	AAH04802.1	2e-180	71%
20S proteasome, beta type 6	gi 156387836	proteasome_beta_type_6	AAH13897.1	3e-102	70%
Fumarylacetoacetase	gi 156391233	FAA_hydrolase_N FAA_hydrolase fum_ac_acetase	NP_034306.2	0.0	69%
Malate dehydrogenase	gi 156350422	MDH_glyoxysomal_mitoch ondrial PLN00106	NP_032643.2	2e-160	67%
20S proteasome, beta type 2	gi 156359803	proteasome_beta_type_2	NP_036100.3	4e-92	67%
Xaa-Pro dipeptidase	gi 156407139	Prolidase AMP_N PepP	NP032846.2	0.0	65%
Triosephosphate isomerase	gi 156385194	TIM	AAC36016.1	3e-117	65%
Alpha-aminoadipic semialdehyde dehydrogenase	gi 156356011	ALDH_F7_AASADH	NP_001120810.1	0.0	64%

Succinyl-CoA synthetase	gi 156314281	Ligase_CoA CoA_binding PRK05678	NP063932.2	8e-72	63%
Aldehyde dehydrogenase 1	gi 156369971	ALDH-SF super family	NP_033048.2	0.0	62%
Phosphoenolpyruvate carboxykinase	gi 156385552	PEPCK_GTP	Q8BH04.1	0.0	61%
Puromycin-sensitive aminopeptidase	gi 156394423	M1_APN_2 ERAP1_C Peptidase_M1	NP_032968.2	0.0	61%
20S proteasome, beta type 4	gi 156382256	proteasome_beta_type_4	NP_032971.2	2e-110	59%
Pyruvate kinase	gi 156408764	Pyruvate_Kinase	NP_001240812.1	0.0	58%
Aspartate aminotransferase	gi 156364446	AAT_like Aminotran_1_2	AAA37263.1	5e-160	54%
dipeptidylpetidase II	gi 156403949	Peptidase_S28 super family GH31_MGAM_SI_GAA	NP_114031.2	5e-153	52%
Acid alpha-glucosidase	gi 156386347	GH31_N Trefoil Glyco_hydro_31	AAH10210.1	0.0	49%
Beta-N-acetylhexosaminidases	gi 156408528	GH20_HexA_HexB-like Glycohydro_20b2	NP_034552.1	2e-166	49%
Putative aminopeptidase	gi 156372710	Peptidase_M17	XP006499506.1	4e-15	33%