

TGGT1_229180+26_1	1968.036234	2792.63733	-0.50487	0.0010237	0.026224	sp O00410 IP05 HUMAN Importin-5 OS=Homo sapiens GN=IP05 PE=1 SV=4//3.46538e-06
TGGT1_206610+26_1	1614.841282	2286.272864	-0.50161	0.0015576	0.03523	sp O95018 ODP24 ARATH Dihydrolysoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic OS=Arabidopsis thaliana GN=LT2A PE=2 SV=1//1.48784e-13
TGGT1_310750+26_1	2357.76408	3331.157714	-0.49806	0.0012396	0.030112	sp O91383 TME07 HUMAN Transmembrane emp-24 domain-containing protein 7 OS=Homo sapiens GN=TME07 PE=1 SV=2//8.22477e-11
TGGT1_288920+26_1	2134.925994	3016.120344	-0.49851	0.0012460	0.030112	sp O87681 AKC0C DICDI ABC transporter G family member 12 OS=Dictyostelium discoideum GN=abcG12 PE=3 SV=1//1.01377e-49
TGGT1_262380+26_1	1127.139348	1589.204414	-0.49564	0.0018677	0.039854	sp O748X8 EFTU_GEOSI Elongation factor Tu OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=efu1 PE=3 SV=1//1.08697e-172
TGGT1_257550+26_1	1752.865091	2460.813643	-0.48942	0.0017938	0.039352	-//
TGGT1_203600+26_1	1464.754779	2048.902856	-0.48419	0.0022981	0.045325	-//
TGGT1_254820+26_1	1124.718803	1850.652211	-0.48235	0.0023918	0.046518	-//
TGGT1_243920+26_1	2316.187883	3226.772342	-0.47834	0.0012121	0.029778	sp P55862 MCM5A XENLA DNA replication licensing factor mcm5-A OS=Xenopus laevis GN=mcm5-a PE=1 SV=2//1.10936e-149
TGGT1_214970+26_1	4346.055993	6049.141373	-0.47702	0.0011121	0.027975	sp P97310 MCM2 MOUSE DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3//3.39335e-159
TGGT1_270510+26_1	6619.576552	9195.966194	-0.47426	0.00077432	0.021401	sp O6MEC9 SYN PARUW Asparagine-tRNA ligase OS=Protochlamydia amoebophila (strain UWE25) GN=asn5 PE=3 SV=1//3.35879e-172
TGGT1_203630+26_1	13661.94874	18530.50723	-0.47177	0.00066371	0.019363	sp O5Y908 ROP4 TOKGO Rhostry protein 4 OS=Toxoplasma gondii GN=ROP4 PE=1 SV=1//1.96699e-81
TGGT1_273460+26_1	3643.800895	5049.942245	-0.47082	0.0008917	0.022074	sp O6P878 EIF3L_XENTR Eukaryotic translation initiation factor 3 subunit 1 OS=Xenopus tropicalis GN=EIF3L PE=2 SV=1//1.61084e-96
TGGT1_243200+26_1	6124.62741	8480.15355	-0.46947	0.0023144	0.045433	-//
TGGT1_218240+26_1	3878.562833	5349.939708	-0.464	0.0025364	0.048543	-//
TGGT1_213570+26_1	2179.030654	2996.12985	-0.45941	0.0010934	0.027746	-//
TGGT1_411430+26_1	3125.001252	4290.479996	-0.45728	0.0022568	0.045146	sp O5Y808 ROP4_TOXGO Rhostry protein 4 OS=Toxoplasma gondii GN=ROP4 PE=1 SV=1//2.47048e-13
TGGT1_255690+26_1	3025.948661	4148.675075	-0.45526	0.0014172	0.033076	sp O81983 SYS HELAN Serine-tRNA ligase OS=Heliolanthus annuus PE=2 SV=1//1.37664e-163
TGGT1_314400+26_1	2123.387669	2886.432828	-0.44292	0.0021828	0.044087	sp P21839 ODDB_BOVIN 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Bos taurus GN=BCKDHB PE=1 SV=2//1.15377e-160
TGGT1_226960+26_1	9838.558483	13352.70477	-0.44061	0.0018425	0.039787	sp F41GR5 PFP82 ARATH Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta 2 OS=Arabidopsis thaliana GN=PFP-BETA2 PE=3 SV=1//6.68423e-28
TGGT1_318310+26_1	1879.042679	2549.545125	-0.44024	0.0019844	0.041475	sp P23254 TKT1_YEAST Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TKL1 PE=1 SV=4//0
TGGT1_311240+26_1	3819.110786	5143.509539	-0.42952	0.002413	0.046821	sp P42825 DNA2 ARATH Chaperone protein dna2 2 OS=Arabidopsis thaliana GN=AT2 PE=1 SV=2//3.27851e-127
TGGT1_225050+26_1	4222.05482	5661.093664	-0.42314	0.0021116	0.043217	sp O23255 SAHH1_ARATH Adenosylhomocysteinease 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1//0
TGGT1_261950+26_1	5913.201426	7794.848041	-0.39858	0.0022382	0.045097	sp P56480 ATP8 MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2//0
TGGT1_290200+26_1	5634.519024	7396.337087	-0.39252	0.0022736	0.045267	sp O8T882 TADH ARAIR Tauroopine dehydrogenase OS=Arabidopsis thaliana GN=tadh PE=1 SV=1//1.61004e-56
TGGT1_240210+26_1	0	0	#NAME?	3.27e-45	3.05E-42	sp O81609 S20A1 MOUSE Sodium-dependent phosphate transporter 1 OS=Mus musculus GN=Slc20a1 PE=1 SV=1//8.52597e-36

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