

# Alignment of Tsc1-PA vs. Submitted\_Sequence

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**Identity:** 1067/1100 (97.0%), **Similarity:** 1090/1100 (99.1%), **Gaps:** 0/1100 ( 0.0%)

Tsc1-PA	1	MVIEKIIGDLESNMTLENEEAKRKLVELLSQNKEQWVVKFMDLYFFTGSQRILEVLVKA	60
Submitted_Sequence	1	MVIEKIIGDLESNMTLENEEAKRKLVELLSQNKEQWL VQFMDLYFFKTGSQRILEVLVKA	60
Tsc1-PA	61	QAPHDGYIFDKLDDCLKQSQHRVQSLQVFCFIVRHHPTWLYKIEKHRLIKSVFKLMTHEK	120
Submitted_Sequence	61	QAPHDGYIFDKLDDCLKQSQHRVQSLQVFCFIVRHHPTWLYKIEKHRLIKSVFKLLTHEK	120
Tsc1-PA	121	EIVPLMSALLCIITLLPIIPNSVPNFLNDLFEVFGHLASWKLQNSNKL PDEKLVHLQLGL	180
Submitted_Sequence	121	EIVPLMSALLCIITLLPIIPNSVPNFLNDLFEVFGHLASWKLQNSNKL PDEKLVHLQLGL	180
Tsc1-PA	181	QMLFHRLYGMYPSCFIAYLVEFIKRGNGGGIFQHTIKPLLNTVRVHPMLVTATPETEVNN	240
Submitted_Sequence	181	QMLFHRLYGMYPSCFIAYLVEFIKRGNGGGIFQHTIKPLLNTVRVHPMLVTATPETEVNN	240
Tsc1-PA	241	TRWKEMEPHDVVMECANLSLPVLLPETSNEEDGSYAYPMTPGYSRMTSNTSNTDYSYQLRE	300
Submitted_Sequence	241	TRWKEMEPHDVVVECANLSLPVLLPETSNEEDGSYAYPMTPGYSRMTSNTSNTDYSYQLRE	300
Tsc1-PA	301	FQQSRNVYTRFDSFASGDDVGPIWSPHNEIATTSSGIPLTPTTSFILPLQ PAMNSQLMVG	360
Submitted_Sequence	301	FQQSRNIYTRFDSFASGGELGPIWSPHNEIATTSSGIPLTPTTSFILPLQ PSMNSQLMVG	360
Tsc1-PA	361	MTGSSPPEAAVEATPETTPCLKDMRDIKQPGRAVNSHAVRAIFAVSQPSSPMR KDQQSQFS	420
Submitted_Sequence	361	MTGSSPPEAAVEATPETTPCLKDMRDIKQPGRAVNSHAVRAIFAVSQPSSPMR KEQQSQFS	420
Tsc1-PA	421	FPDVSREAEESHSYLEVNRTAYDRRLSQVIQDRHNVERSVNTPCSSLPEINSDLSLV	480
Submitted_Sequence	421	FPDVSREAEESHSYLEVNRTAYDRRLSQVIQDRHNVERSVNAPCSSLPEINSEL SLV	480
Tsc1-PA	481	GGSVYPSVTQEVAAVCGECNETDRNLCSVGGLHMPTSRSMHQLAKKRRNRMASYS GNGSC	540
Submitted_Sequence	481	GGSVYPPVNQEVAAVCGECNETDRNLCSVGGLHMPTSRSMHQLAKKRRNRMASYS GNGSC	540
Tsc1-PA	541	ADSRSSAAKKASWSTEAEENPMRRTKSCSALS GMRQQHLEENDDEADCSSQRQRGENGNTQ	600
Submitted_Sequence	541	ADSRSSAAKKASWSTEAEENPMRRTKSCSALAGLRQQHLEENDDEADCAHRQRAENGNTQ	600
Tsc1-PA	601	KTGSR LQRSGRNLAISAPKDTARSC THASTQTVEGLDSAPAQYENWLI ELLLECKEQRID	660
Submitted_Sequence	601	KTGSR LQRSGRNMAISAPKDPARSC THAATQTVEGLDSAPAQYENWLI ELLLECKEQRID	660
Tsc1-PA	661	YERNLLYPQDILDEYIKHAIKANESFDAEQGLMCLQLEYESYRRS IHAERNRRLMGRSR	720
Submitted_Sequence	661	YERNLLYPQDILDDYIKHAIKANETFDAEQGLMCLQLEYESYRRS IHAERNRRLMGRSR	720

Tsc1-PA	721	DKRSLEMERDRLREQLKNFDAKNKDLANKMDQAIRLANERQNIHQEELGEMRAKYQHELE	780
		*****.*****	
Submitted_Sequence	721	DKRSLEMERDRLREQLKNFDAKNKDLASKMDQAIRLANERQNIHQEELGEMRAKYQHELE	780
Tsc1-PA	781	EKKCLRQANDDLQTRLTSELARHKEMNYELESRLGQVFSLGTELQHTQQQADIGLQCKQE	840
		*****	
Submitted_Sequence	781	EKKCLRQANDDLQTRLTSELARHKEMNYELESRLGQVFSLGTELQHTQQQADIGLQCKQE	840
Tsc1-PA	841	LARLEAEFIIMGEVQVRCRDRLAEIDNFRARDEELQMLQESSNLELKDRLRHSLDEKTSQL	900
		*****:*****	
Submitted_Sequence	841	LARLEAEFIIMGEVQVRCRDRLAEIDNFRARDEELQMLQESSNLELKELRHSLDEKTSQL	900
Tsc1-PA	901	ESMKHKISDLQAQLANSEKAMTEQKRLSTVKDEYEEKFKSVNKKYDVQKKIIMQMEEKL	960
		*****	
Submitted_Sequence	901	ESMKHKISDLQAQLANSEKAMTEQKRLSTVKDEYEEKFKSVNKKYDVQKKIIMQMEEKL	960
Tsc1-PA	961	MMMMQQPQGTTGHNTCSPDTRTDIASSIERNSPSTSLASSESLSASLRSTELKNLHQL	1020
		*****	
Submitted_Sequence	961	MMMMQQPQGTTGHNTCSPDTRTDIASSIERNSPSTSLASSESLSASLRSTELKNLHQL	1020
Tsc1-PA	1021	VDTPTIPDVLNSMAGGAQFEDEVPPAVDLASSASTASAINIVPHALDLPSTSGGIGHTL	1080
		****:*****:***** ** *****:*****	
Submitted_Sequence	1021	VDTPSIPDVLNSLAGGAQFEDGVRLPAVDLASSASTASAINIVPHALDLPSTSGGVGHTL	1080
Tsc1-PA	1081	THPHPHPHLHLQQQQQDQLQ	1100
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Submitted_Sequence	1081	THPHPHPHLHLQQQQQDQLQ	1100