

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

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Tscl-PA      1 NVIEKIIIGDLESSMTLENEEAKKLVLLSQNKQKQVYVHLDYFFVDSQRILEVLVKA 60
Submitted_Sequence 1 NVIEKIIIGDLESSMTLENEEAKKLVLLSQNKQKQVYVHLDYFFVDSQRILEVLVKA 60

Tscl-PA      61 QAPHDGYIFDKLDOCLKQSGQRVQSLQVFCFIVRSHPTWLYKIEKHRLIKSVFKH HEK 120
Submitted_Sequence 61 QAPHDGYIFDKLDOCLKQSGQRVQSLQVFCFIVRSHPTWLYKIEKHRLIKSVFKH HEK 120

Tscl-PA      121 EIVPLMSALLCIITLLPIIPNSVPHFLNDLFEVFGHLASWKLQSNKLPDEKLVMQLGL 180
Submitted_Sequence 121 EIVPLMSALLCIITLLPIIPNSVPHFLNDLFEVFGHLASWKLQSNKLPDEKLVMQLGL 180

Tscl-PA      181 QMLFHLRYGNYPCSFIAVLVEFIKRGMGQGFQRTIKPLMTVKVHPMLVTATPETEVNH 240
Submitted_Sequence 181 QMLFHLRYGNYPCSFIAVLVEFIKRGMGQGFQRTIKPLMTVKVHPMLVTATPETEVNH 240

Tscl-PA      241 TNWKEKPSGVVTCANLSLPVLLPETSNEGGSTAYPHTPGYSRNTSNTSNTDYSTQLRE 300
Submitted_Sequence 241 TNWKEKPSGVVTCANLSLPVLLPETSNEGGSTAYPHTPGYSRNTSNTSNTDYSTQLRE 300

Tscl-PA      301 FQQRSHVITRFDSFASGDVSPINSPHNKIATTSGGIPLTPPTSFILPLQSNHNSQLMVG 360
Submitted_Sequence 301 FQQRSHVITRFDSFASGDVSPINSPHNKIATTSGGIPLTPPTSFILPLQSNHNSQLMVG 360

Tscl-PA      361 NTGSSPPEAAVEATPETTPLEDMRDIEQPCRAVNSHAVRAIFAVSQPSPPHNSQSQFS 420
Submitted_Sequence 361 NTGSSPPEAAVEATPETTPLEDMRDIEQPCRAVNSHAVRAIFAVSQPSPPHNSQSQFS 420

Tscl-PA      421 FFOVSRKAESSSHSYLEVNRGTAYDRKLSQVIQGRHNVERSVKPCSSLPEINSESLV 480
Submitted_Sequence 421 FFOVSRKAESSSHSYLEVNRGTAYDRKLSQVIQGRHNVERSVKPCSSLPEINSESLV 480

Tscl-PA      481 GGSVTSVTGEVAAVGECNETDRNLCSVOGLHKPTSRSMHQIAKKRNRNMASYSNGGSC 540
Submitted_Sequence 481 GGSVTSVTGEVAAVGECNETDRNLCSVOGLHKPTSRSMHQIAKKRNRNMASYSNGGSC 540

Tscl-PA      541 ADSRSSAAKASWSTEAPMOKTKSCSAISGMHQHLEENDCADSSQVQICMGNTQ 600
Submitted_Sequence 541 ADSRSSAAKASWSTEAPMOKTKSCSAISGMHQHLEENDCADSSQVQICMGNTQ 600

Tscl-PA      601 KTGSRQRSGRNLAIAPKETAASCTHASTQTVEGLDSAPAQYENMLIELLECKEQRID 660
Submitted_Sequence 601 KTGSRQRSGRNLAIAPKETAASCTHASTQTVEGLDSAPAQYENMLIELLECKEQRID 660

Tscl-PA      661 YERNLLYPQDILASTIKHAIKANSTDAQQQLMCLQLEYESYKRSIHAERKRLMGRSR 720
Submitted_Sequence 661 YERNLLYPQDILASTIKHAIKANSTDAQQQLMCLQLEYESYKRSIHAERKRLMGRSR 720

Tscl-PA      721 DKRSLEMERDRLREQLKNFDKXKDLINMDQAIRLANERQNIHQEELGEMRAKQHELE 780
Submitted_Sequence 721 DKRSLEMERDRLREQLKNFDKXKDLINMDQAIRLANERQNIHQEELGEMRAKQHELE 780

Tscl-PA      781 EKKCLRQANDLQTRLTSELARHEHMYELESRGQVFSLGTQLQHTQQQADIGLQCKQE 840
Submitted_Sequence 781 EKKCLRQANDLQTRLTSELARHEHMYELESRGQVFSLGTQLQHTQQQADIGLQCKQE 840

Tscl-PA      841 LARLEAEFIIMGEVQVRCRDLAEIDNFRANDEELQMLQESSNLELAEPRSLDEKTSQ 900
Submitted_Sequence 841 LARLEAEFIIMGEVQVRCRDLAEIDNFRANDEELQMLQESSNLELAEPRSLDEKTSQ 900

Tscl-PA      901 ESHNKKISQLQAQLANSEKANTEQKRLSTVXDEYEKFFSVNKKYDVQKKIIMQMEK 960
Submitted_Sequence 901 ESHNKKISQLQAQLANSEKANTEQKRLSTVXDEYEKFFSVNKKYDVQKKIIMQMEK 960

Tscl-PA      961 KHMNQPFQQTGHTNCSPTDRTDIASSIERNSPLSTSLASSELSASLSTELKLNHL 1020
Submitted_Sequence 961 KHMNQPFQQTGHTNCSPTDRTDIASSIERNSPLSTSLASSELSASLSTELKLNHL 1020

Tscl-PA      1021 VDTTIFPDVLMKNGGAQFEIAPKPAVDLASSASTASAINIVHALCLPSTSGQHTL 1080
Submitted_Sequence 1021 VDTTIFPDVLMKNGGAQFEIAPKPAVDLASSASTASAINIVHALCLPSTSGQHTL 1080

Tscl-PA      1081 TNPHPHPHLHQQQQQDGLQ 1100
Submitted_Sequence 1081 TNPHPHPHLHQQQQQDGLQ 1100
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