

Fig.S1 Sequence alignment of human TERA(VCP/p97)with Aedes TER94

A.Input Sequences

>sp|P55072|TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=4
MASGADSKGDDLSTAILKQKNRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGKKRREAVC
IVLSDDTCSDEKIRMNRVVRNLRVRLGDVVISIQPCPDVKYGKRIHVLPIDDTVEGITGNLFEVYLKPY
FLEAYRPIRKGDIFLVRGGMRAVEFKVVETDPSPYCIVAPDVIHCEGEPIKREDEEESLNEVGYYDDIG
GCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMS
KLAGESESNLRKAFFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTMDGLKQRAHVIVMA
ATNRPNSIDPALRRFGRFDREVDIGIPDATGRLEILQIHTKNMKLADDVDLEQVANETHGHVGADLAAL
CSEALQAIRKKMDLIDLEDETIDAEMNSLAVTMDDFRWALSQSNPSALRETVVEVPQVTWEDIGGLE
DVKRELQELVQYPVEHPDKFLKFGMTPSKGVLFYGPFGCGKTLAKAIANECQANFISIKGPELLTMWF
GESEANVREIFDKARQAAPCVLFFDELDSIAKARGGNIQGGGAADRVINQILTEMDGMSTKKNVFIIG
ATNRPDIIDPAILRPGRLDQLIYIPLPDEKSRVAILKANLRKSPVAKVDVLEFLAKMTNGFSGADLTEI
CQRACKLAIRESIESEIRRERERQTNPSAMEVEEDDPVEIRRDHFEEAMRFARRSVSDNDIRKYEMFA
QTLQQRGFGSFRFPSPGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG

>XP_001654680.1 transitional endoplasmic reticulum ATPase TER94 [Aedes aegypti]
MAEGKNEDLATAILKRKERNRNLIVDEAGNDDNSVISLSQAKMDELQLFRGDTVLLKGKRRKETVCIVLS
DDNCPDEKIRMNRVVRNLRVRLGDVVISIQSCPDVKYGKRVHILPIDDTVEGLTGNLFDVYLRPYFLEAY
RPIHSDDTFIVRGGMRAVEFKVVGADPSPYCIVAPETVIHCEGDPIKREEEEEALNAVGYDDIGGCRKQL
AQIKEMVELPLRHPSLFKAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESE
SNLRKAFFEEAEKKS PAIIFIDELDAIAPKREKTHGEVERRIVSQLLTMDGMKSSHVIVMAATNRPNSI
DPALRRFGRFDREIDIGIPDATGRLEVLRIHSKNMKLADDVDLEQIAAESHGHVGADLASLCSEALQQI
REKMDLIDLEDDQIDA EVLNLSLAVSMENFRYAMTKSSPSALRETVVEVPNTTWHDIGGLENVKRELQELV
QYPVEHPDKFLKFGMQPSRGVLFYGPFGCGKTLAKAIANECQANFISVKGPELLTMWFGSEANVRDIF
DKARSASPCVLFFDELDSIAKSRGGNVGDAGGAADRVINQILTEMDGMGAKKNVFIIGATNRPDIIDPAI
LRPGRLDQLIYIPLPDDKSREAILKANLRKSPVAGDVLDLYVAKVTQGFSGADLTEICQRACKLAIRQAI
EAEIRRERERTEGQSSAMDMDEDDPVPNITRAHFEEAMKFARRSVSDNDIRKYEMFAQTLQQRGFGSNF
RFPGGQSGSSSQGQSSQPTSNPADNGDDDLYS

>XP_019533679.1 transitional endoplasmic reticulum ATPase TER94 [Aedes albopictus]
MAEGKNEDLATAILKRKERNRNLIVDEAGNDDNSVISLSQAKMDELQLFRGDTVLLKGKRRKETVCIVLS
DDNCPDEKIRMNRVVRNLRVRLGDVVISIQSCPDVKYGKRVHILPIDDTVEGLTGNLFDVYLRPYFLEAY
RPIHSDDTFIVRGGMRAVEFKVVGADPSPYCIVAPETVIHCEGDPIKREEEEEALNAVGYDDIGGCRKQL
AQIKEMVELPLRHPSLFKAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESE
SNLRKAFFEEAEKNSPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTMDGMKSSHVIVMAATNRPNSI
DPALRRFGRFDREIDIGIPDATGRLEVLRIHSKNMKLADDVDLEQIAAESHGHVGADLASLCSEALQQI
REKMDLIDLEDDQIDA EVLNLSLAVSMENFRYAMTKSSPSALRETVVEVPNTTWHDIGGLENVKRELQELV
QYPVEHPDKFLKFGMQPSRGVLFYGPFGCGKTLAKAIANECQANFISVKGPELLTMWFGSEANVRDIF
DKARSASPCVLFFDELDSIAKSRGGNVGDAGGAADRVINQILTEMDGMGAKKNVFIIGATNRPDIIDPAI
LRPGRLDQLIYIPLPDDKSREAILKANLRKSPVAGDVLDLYVAKVTQGFSGADLTEICQRACKLAIRQAI
EAEIRRERERTEGQSSAMDMDEDDPVPNITRAHFEEAMKFARRSVSDNDIRKYEMFAQTLQQRGFGNMF
RFPGGQSGSSSQGQSSQPTSNPADNGDDDLYS

B. Alignment

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

- Green residues indicate active site residues (K251 and K524 in human VCP/p97)
- Yellow residues indicate allosteric inhibitor binding residues (K615 and N617 in human VCP/p97)

sp|P55072|TERA_HUMAN MASGADSKGDDLSTAILKQKNRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLK 60
XP_001654680.1 ---MAEGKNEIDLATAILKRKERPNRLIVDEAGNDDNSVISLSQAKMDELQLFRGDTVLLK
XP_019533679.1 ---MAEGKNEIDLATAILKRKERPNRLIVDEAGNDDNSVISLSQAKMDELQLFRGDTVLLK
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sp|P55072|TERA_HUMAN GKRRREAVCIVLSDDTCSDEKIRMNRVVRNLRVRLGDIVISIQPCPDVKYGKRIHVLPID 120
XP_001654680.1 GKRRKETVCIVLSDDNCPDEKIRMNRVVRNLRVRLGDIVSISQPCPDVKYGKRVHILPID
XP_019533679.1 GKRRKETVCIVLSDDNCPDEKIRMNRVVRNLRVRLGDIVSISQPCPDVKYGKRVHILPID
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sp|P55072|TERA_HUMAN DTVEGITGNLFEVYLKPYFLEAYRPIRKGDIFLVRGGMRRAVEFKVVDTPSPYCVAPDT 180
XP_001654680.1 DTVEGLTGNLFDVYLRPYFLEAYRPIHSDDTFIVRGGMRRAVEFKVVGDPSYCVAPET
XP_019533679.1 DTVEGLTGNLFDVYLRPYFLEAYRPIHSDDTFIVRGGMRRAVEFKVVGDPSYCVAPET
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sp|P55072|TERA_HUMAN VIHCEGEPIKREDEEESLNEVGYDDIGGCRKQLAQIKEMVELPLRHPLFKAIGVKPPRG 240
XP_001654680.1 VIHCEGDPIKREEEEAALNAVGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRG
XP_019533679.1 VIHCEGDPIKREEEEAALNAVGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRG
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sp|P55072|TERA_HUMAN ILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLKAFEEAEKNAPAI 300
XP_001654680.1 ILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLKAFEEAEKNSPAI
XP_019533679.1 ILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLKAFEEAEKNSPAI
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sp|P55072|TERA_HUMAN IFIDELDAIAPKREKTHGEVVERRIVSOLLTMDGLKQRAHVIVMAATNRPN SIDPALRRF 360
XP_001654680.1 IFIDELDAIAPKREKTHGEVVERRIVSOLLTMDGMKSSHVIVMAATNRPN SIDPALRRF
XP_019533679.1 IFIDELDAIAPKREKTHGEVVERRIVSOLLTMDGMKSSHVIVMAATNRPN SIDPALRRF
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sp|P55072|TERA_HUMAN GRFDREVDIGIPDATGRLEILQIHTKNM KLADDVDLEQVANETHGHV GADLAALCSEAL 420
XP_001654680.1 GRFDREIDIGIPDATGRLEVLRIHSKNM KLADDVDLEQIAAESHGHV GADLASLCSEAL
XP_019533679.1 GRFDREIDIGIPDATGRLEVLRIHSKNM KLADDVDLEQIAAESHGHV GADLASLCSEAL
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sp|P55072|TERA_HUMAN QAIRKKMDLIDLEDETIDAEVMNSLAVTMDDFRWALSQSNPSALRETVVEVPQVTWEDIG 480
XP_001654680.1 QQIREKMDLIDLEDDQIDAEVLNSLAVSMENFRYAMTKSSPSALRETVVEVPNTTWHDIG
XP_019533679.1 QQIREKMDLIDLEDDQIDAEVLNSLAVSMENFRYAMTKSSPSALRETVVEVPNTTWHDIG
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sp|P55072|TERA_HUMAN      GLEDVKRELQELVQYPVEHPDKFLKFGMTPSKGVLFYGPFGCGK TLLAKAIANECQANFI 540
XP_001654680.1          GLENVKRELQELVQYPVEHPDKFLKFGMQPSRGLVLFYGPFGCGK TLLAKAIANECQANFI
XP_019533679.1          GLENVKRELQELVQYPVEHPDKFLKFGMQPSRGLVLFYGPFGCGK TLLAKAIANECQANFI
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sp|P55072|TERA_HUMAN      SIKGPELLTMWFGSEANVREIFDKARQAAPCVLFFDELDSIAKARGGNIGDGGGAADRV 600
XP_001654680.1          SVKGPPELLTMWFGSEANVRDIFDKARSASPCVLFDELDIAKSRGGNVGDAGGAADRV
XP_019533679.1          SVKGPPELLTMWFGSEANVRDIFDKARSASPCVLFDELDIAKSRGGNVGDAGGAADRV
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sp|P55072|TERA_HUMAN      INQILTEMDGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPDEKSRVAILKAN 660
XP_001654680.1          INQILTEMDGMGAKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPDDKSREAILKAN
XP_019533679.1          INQILTEMDGMGAKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPDDKSREAILKAN
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sp|P55072|TERA_HUMAN      LRKSPVAKDVLDFLAKMTNGFSGADLTEICQRACKLAIRESEIESEIRRRERER-QTNPSA 719
XP_001654680.1          LRKSPVAGDVLDTYVAKVTQGFSGADLTEICQRACKLAIRQAIEAEIRRRERERTEGQSSA
XP_019533679.1          LRKSPVAGDVLDTYVAKVTQGFSGADLTEICQRACKLAIRQAIEAEIRRRERERTEGQSSA
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sp|P55072|TERA_HUMAN      MEVEEDDPVPEIRRDHFEEAMRFARRSVSDNDIRKYEMFAQTLQQSRGFGS-FRFPSTGNQ 778
XP_001654680.1          MDMDEDDPVPNITRAHFEEAMKFARRSVSDNDIRKYEMFAQTLQQSRGFGSNFRFPSTGNQ
XP_019533679.1          MDMDEDDPVPNITRAHFEEAMKFARRSVSDNDIRKYEMFAQTLQQSRGFGNNFRFPSTGNQ
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sp|P55072|TERA_HUMAN      GGAGPSQGSQGGGTGGSVYTEDNDDDLYG 806
XP_001654680.1          GSSSQGQGSSQPTSNP--ADNGDDDLYS
XP_019533679.1          GSSSQGQGSSQPTSNP--ADNGDDDLYS
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C. Identity Matrix

Percent Identity Matrix - created by Clustal2.1

1:	sp P55072 TERA_HUMAN	100.00	84.89	84.89
2:	XP_001654680.1	84.89	100.00	99.75
3:	XP_019533679.1	84.89	99.75	100.00