

Supplementary data for Friedman *et al.*, N-terminal Domain of Yeast Telomerase Reverse Transcriptase: Recruitment of Est3p to the Telomerase Complex.

Shown is an alignment of nine TERT sequences obtained from database sources. Sequences were aligned by Clustal wPPC and adjusted manually. ScEst2p, *Saccharomyces cerevisiae*; CaTERT, *Candida albicans*; SpTRT1p, *Schizosaccharomyces pombe*; OtTERT, *Oxytricha trifallax*; Eap123, *Euplotes aediculatus*; TtTERT, *Tetrahymena thermophila*; hTERT, human; mTERT, mouse; aTERT, *Arabidopsis thaliana*. Identical positions are indicated in black; positions showing amino acid similarity are highlighted in gray. *S. cerevisiae* Est2p residues that comprise Regions I, II, and III are shown in red. Residues in Est2p that were mutated in this study are indicated (*). Alignment of the reverse transcriptase motifs is indicated in color. Note that the Motif E alignment for *S. cerevisiae* is altered from that published by Nakamura *et al.* (1997)* based on the additional sequence information.

*Nakamura, T.M., Morin, G.B., Chapman, K.B., Weinrich, S.L., Andrews, W.H., Lingner, J., Harley, C.B., and Cech, T.R. (1997). Telomerase catalytic subunit homologs from fission yeast and human. *Science* 277, 955-959.

ScEst2p 1 -----
CaTERT 1 -----
SpTrt1p 1 -----
OtTERT 1 MSAKKPVQSKLNIGNPTIPVTSNRSTAPKVPVGPQPFVFNQEKKQQSQNTTTGAFRSNQNN
Eap123 1 -----
TtTERT 1 -----MQKINN
hTERT 1 -----
mTERT 1 -----
aTERT 1 -----

ScEst2p 1 -----MKILFEFIQDKLDIDLQTNSTYK-----ENLKCGHFNGLDE--
CaTERT 1 -----MTVKVNEKKTLLQYVLDNT-----SN-DVPLLP SLKE--
SpTrt1p 1 --MTEHHTPKSRI LRFLENQYVYLCTLN DYVQLVIRGSPA--SSYSN-ICERLRS DVQTS
OtTERT 61 ANSGGNGNFELDDLHLALKSCNEIGSAKTLFCFEMELQKINDKIPSKKNTELIKNDPQFQ
Eap123 1 MEVDVDNQADNHGIEHSALKTCEEIKEAKTLYSNLQKVI R----CRNQSQSHYKDLEDIK
TtTERT 7 INNKNQMLTRKEDLTVLQISALKYVSNLYEFLATEK-----IVQTS ELDTQFQ
hTERT 1 ---MPRAPRCRAVRSILLR--SHYREVLPLATFVRRIGP-----QGWRLVQFGDPA--
mTERT 1 ---MTRAPRCPAVRSILLR--SRYREVWPLATFVRRIGP-----EGRRLVQFGDPK--
aTERT 1 ---MPRKPRHRVPEILWR--LFGNRARNLNDALVDLIPN-----RNIQPEQCRGQ--

Region I

ScEst2p 37 -----ILTTCFALPNSRKIALPCL--PGDLSHK-----AVIDHCLIIYLLTG---ELYNNV
CaTERT 32 -----YMETVLVYK-SIKRPLPAI--RPQESFD-----EFMKELVTRLVM---EKSNNV
SpTrt1p 56 FSIF--LHSTVVGFD SKPDEGVQFS--SPKCSQS---ELIANVVKQMFDES-FERRRNL
OtTERT 121 YFCHNTILCTEQSYDEKTIEKLA KL--EYKLEYKNSYIDMISKVIKELLIE---NKLNKL
Eap123 56 IFAQTNIVATPRDYNEEDFKVIAR--KEVFSTG-LMIELIDKCLVELLSSSDVS DRQKL
TtTERT 58 EFLTTTIIASEQNLVENYKQYNQPN-FSOLTIK---QVIDDSIILGN---KQNYV
hTERT 46 --AFRALVAQCLVCMHWGSPPPADLSFHQVSSLK---ELVARVQLRICE---RGAKNV
mTERT 46 --IYRTLVAQCLVCMHWGSPPPADLSFHQVSSLK---ELVARVQLRICE---RNERNV
aTERT 48 --GCLGCS SDKPAFLRSDDP IHYRKL LHRCFVVLH--EQTPPLLD FSPTS--WWSQREI

ScEst2p 82 ITFGYKIA-----RNEDVN-----NSLFC HS-----ANVNVTLIKGAANKMFHSLVIG
CaTERT 75 IAYGYKTS-----AMESRS---IFTTFHSS-----GNFILHTITSHNWTIFLLIG
SpTrt1p 107 LMKGF SMNHEDF-RAMHVNGV--QNDLVSIF-----PNYLISILESKNWQLLEITIG
OtTERT 176 QTFGYKLVNNEFGNQHLGMMQONQDSSHNSNFMVKCDYINLNKQCMITKNWEKVYFYLIG
Eap123 112 QCFGEQLK-----GNQLA-----KTHLLTA-----LSTQKQYFFQDEFWQVRAMIG
TtTERT 108 QQIGTTTI-----G-----FYVEYEN-----INLSRQTYSSNERNLINIFG
hTERT 97 IAFGFALLD-----GARGPPEAFTTSVRSYLP-----NTVTDALRGSGAWGLLRRVG
mTERT 97 IAFGFELLN-----EARGP PMAFTSSVRSYLP-----NTVIETLRVSGAWMLLRSRVG
aTERT 102 VERIIE MMQS---GCDCQNVICARYDKYDQ-----SSPILELITSSWEFLLRVIG

ScEst2p 124 TYAFVDLLIN--YTVIQFNGQFFTQIVGNRCNEP-----HLPPK-----
CaTERT 118 PKKFELELLVNNKGFVSKVNGES-VQIFGD-VNS-----H-----
SpTrt1p 156 SDAMHYLLSKGSI FEALPNDNY-LQISGIPLFKNN-----VFEETVSK-----
OtTERT 236 DHLFMHIYKEYMIFL KTRDESL-VQISGTNIEFCYLNEKLGRLQAAFYE-----
Eap123 153 NEIFRHLYTKYLIFQRTSEGTL-VQFCGNNVFDH-----LKVND-----
TtTERT 145 EEDFKYFLIDFLVFTKVEQNGY-LQVAGVCLNQYFS--VQVKQKKWY-----
hTERT 146 DDVLVHLLARCALEVLVAPSCA-YQVCGPPLYQLGAATQARPPPHASG-PRRRLG-----
mTERT 146 DDLLVYLLAHCALYLLVPPSCA-YQVCGSPLYQICATTDIWPVSASYPTRPVGRNFTN
aTERT 150 HDVMVYLLQQTSEIFLPLLGKKH-QQVSGPPLCIKHKRTLSVHENKRKR-----

ScEst2p 161 -----WVQRSSSSSATAA---QIKQLTEP-----
CaTERT 150 -----R-KAVVVS-----KYITK-----
SpTrt1p 198 -----KRKRTIETSI TQNK S--ARKEVSWNS-----
OtTERT 283 -----GPNKNAANSAAQGSNPEANDLISAEQRKIN-----
Eap123 191 -----KFDKQKGGAAD-----MNEPR-----
TtTERT 189 -----KNFNMNGKATSNNNQNNANLSNEKKQENQ-----
hTERT 199 ---CERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGS
mTERT 205 LRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTSVPSAKKARCYPVPRVEEGPHRQVL
aTERT 197 -----DDN-VQPPTKRQWLS SAVDDCPKDDSATITPIVGEDVDQHREK

ScEst2p 182 -----VT--NQFLHKLINSSSFFP-----YSKILPSSSSIKK**TDL**
 CaTERT 162 -----FNVLYNSYSRDFSR-----FEMIRPSIQITILQDILS
 SpTrt1p 222 -----IS--ISRFSIFYRSSYKFKQD-----LYFNLHSICDRNT**VH**MW
 OtTERT 313 -----TAI--VMKKTKYNIKAADESYLTNQEKGFWDQIKRNRFLFYCAH
 Eap123 208 -----CCSTCKYNVKNEKDHFLNNINVPNWNMKSRTIRFYCTH
 TtTERT 219 -----YIYPEIQRSQIF**YC**NHMGREPGVFKSSFFNYSEIKKGFQ**FKVIQ**E
 hTERT 256 WAHPGRTRGSPDRGFC**W**VSPARP-AEEATSLLEGALSGTRHSHSPVGRQHAGPPSTSRPP
 mTERT 265 PTPSGKSWVPSP----ARSPEVPTAE**KD**LSSKGVSDLSLSG-SVCCKHKP**S**STLS**S**PP
 aTERT 239 KTTK-RS-----R**YL**KRRR**KQR**K**VN**FKK**V**DCNAPCITPSTNGK**V**STGN**DE**ML**H**IG

* Region II * *

ScEst2p 218 **REAIFP**-----**TNLVKIPQRLKVR**-----
 CaTERT 193 FSGLNP-----GRSSKRYR**GF**KS**L**-----
 SpTrt1p 259 **L**OWIFPRQ-----**FGL**INAFQVKQL**HKV**PLV**SQ**-----
 OtTERT 356 **Q**NRFFQKH-----ILNSK**TLS**QQQ**IRDN**IYKE**V**F-----
 Eap123 247 **F**NRNNQFFK-----KHEFVSNKNNISAM**DRAQT**FTN**I**F-----
 TtTERT 264 KLQGRQFIN-----S---DK**I**KPDHPQ**TII**K**KL**LLKEY**Q**-----
 hTERT 315 RPWDTPCPPVYA**ETK**----HFLYSSGD-KEQLRPS**FL**SSLRPSLT**GARR**VE**T**IF-----
 mTERT 320 **R**ONAFQLRP-FI**ETR**----HFLYSRGDQ**ER**L**NPS**FLSNLQPNLT**GARR**VE**I**IF-----
 aTERT 290 **I**NGSLTDFVKQAKQ**V**KRNK**NFK**FL**S**ETYS**VI**PPNH**L**KL**T**LR**PNC**SD**S**KL**LM**NH**I**F**GE**VN

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ScEst2p 237 -----**T**N**L**T**L**Q**K**L**L**K**R**H**K**R**N**I**V**S-----**I**L**N**S**I**C**P**P-----
 CaTERT 212 -----LSRI**T**I**AND**KK**CR**Y**D**I**L**Y**AK**F---IG**T**S**K**C**N**-----
 SpTrt1p 288 -----ST**V**V**P**K**R**L**L**K**V**Y**P**L**IE**Q**T**A**K**R**L**H**R**L**S**L**S**K---V**Y**N**H**Y**C**P-----
 OtTERT 385 -----G**F**N**R**V**R**A**E**L**K**G**V**M**S**I**IE**Q**V**I**V**N**Q**K**F**D**E**K**Y**---Y**L**S**K**N**C**P**L**P**E**N**W**K---N
 Eap123 281 -----R**F**N**R**I**R**K**L**K**D**K**V**I**E**K**I**A**Y**M**L**E**K**V**K**D**F**N**E**N**Y**---Y**L**T**K**S**C**P**L**P**E**N**W**R---S
 TtTERT 295 -----S**K**N**F**S**C**Q**E**E**R**D**L**F**L**E**F**T**E**K**I**V**Q**N**F**N**I**N**E**N**Y**---L**L**K**K**F**C**K**L**P**E**N**Y**Q**S**L**S**K**E**
 hTERT 366 -----L**G**S**R**P**W**M**P**G**T**P**R**R**L**P**R**L**P**Q**R**Y**W**Q**M**R**P**L**F**L**L**---G**N**H**A**Q**C**P**Y**G**V**L**L**K**T**H**C**P**L**
 mTERT 371 -----L**G**S**R**P**R**T**S**G**P**L**C**R**T**H**R**L**S**R**R**Y**W**Q**M**R**P**L**F**Q**Q**L---V**N**H**A**E**C**Q**Y**V**R**L**L**R**S**H**C**R**F**
 aTERT 350 **V**W**S**T**T**P**S**H**G**K**N**C**P**S**G**S**I**C**L**Y**H**S**L**L**K**S**L**K**N**L**I**G**K**T**K**S**S**H**L**K**M**L**D**K**H**C**P**V**L**L**L**Q**E**D---A**L**

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ScEst2p 264 **LEG**TVL**D**LS**H**L**S**R**Q**-----S**P**-----K**ER**V**L**K**F**I**V**I**L**Q**K**L**L**P**Q**
 CaTERT 239 F**AN**V**V**S**N**K**T**E**I**S-----Q**VI**Q**F**V**L**L**V**L**G**K**L**L**P**L
 SpTrt1p 324 Y**ID**TH**D**D**E**K**I**L**S****Y**S-----L**K**-----P**N**Q**V**F**A**F**R**S**I**L**V**R**V**F**P**K
 OtTERT 430 L**K**K**S**F**L**E**D**A**A**V**S**G**E**-----L**R**G**Q**V**R**Q**L**F**E**Y**Q**D**Q**R**Q**I**S**N**F**L**T**E**F**V**AN**V**F**P
 Eap123 326 R**K**Q**K**I**E**N**L**I**N**K**T**R**E**-----E**K**S**K**Y**E**E**L**F**S**Y**T**D**N**K**C**V**T**Q**F**I**N**E**F**F**Y**N**I**L**P**
 TtTERT 344 V**K**Q**I**V**Q**S**E**N**K**A**N**Q**Q**-----S**C**E**N**L**F**N**S**L**Y**D**T**E**I**S**K**Q**I**T**N**F**R**Q**L**I**Q**N**C**V**P**
 hTERT 416 R**AA**V**T**P**AA**G**V**C**A**R**E**K**P**Q**G**S**V**A**A**P**E**E**E**D**T**D**P**R**R**L**V**Q**L**L**R**Q**H**S**S**P**W**Q**V**Y**G**F**R**A**C**L**R**R**L**V**P**P
 mTERT 421 R**T**A**N**Q**Q**V**T**D**A**L**N**-----T**S**P**P**H**L**M**D**L**R**L**H**S**S**P**W**Q**V**Y**G**F**R**A**C**L**C**K**V**V**S**A
 aTERT 408 **K**S**G**T**T**S**Q**S**S**R**R**Q**K**A**D**K**L**P**H**G**S**S**S**S**Q**T**G**K**P**K**C**P**S**V**E**E**R**K**L**Y**C**T**N**D**Q**V**S**F**I**W**A**L**C**R**Y**I**V**P**E**

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ScEst2p 298 **EM**E**G**S**K**K**N**K**G**K**I**K**N**-**I**N**L**L**L**S**L**P**L**N**G**Y**L**P**F**D**S**L**L**K**L**R**L**K**D**F**R**W**L**F**I**S**D**I**W**F**T**K**H**-----
 CaTERT 267 D**AW**G**G**V**S**N**K**-**K**I**I**K**D**R**V**D**F**L**L**G**AN**E**K**I**H**M**D**D**L**F**R**G**T**R**L**K**D**F**K**W**L**G**R**A**H**Q**I**S**S**K**Q**-----
 SpTrt1p 358 L**I**W**G**N**Q**R**I**F**E**I**L**K**D**-L**E**T**F**L**K**L**S**R**Y**E**S**F**S**L**H**Y**L**M**S**N**I**K**I**S**E**I**E**W**L**V**L**G**R**S**N**A**K**M**C**-----
 OtTERT 476 **K**N**E**L**E**G**K**N**K**-**K**I**F**N**K**K**L**Q**V**K**F**N**R**F**E**S**F**T**K**I**S**L**N**K**F**R**V**N**E**V**S**W**L**S**F**K**C**D**D**E**N**K**K**-----
 Eap123 372 **K**D**E**L**T**G**R**N**R**-**K**N**F**Q**K**V**K**Y**V**E**L**N**K**H**E**L**I**H**K**N**L**L**E**K**I**N**T**R**E**I**S**W**Q**V**E**T**S**A**K**H**F**Y-----
 TtTERT 390 N**Q**L**L**G**K**K**N**F-**K**V**F**L**E**K**I**Y**E**F**V**Q**M**K**R**F**E**N**Q**V**L**D**Y**I**C**F**M**D**V**F**D**V**E**W**F**V**D**L**K**N**Q**K**F**T**Q**-----
 hTERT 476 G**L**W**G**S**R**H**N**E**R**R**F**L**R**N-**T**K**K**F**I**S**L**G**K**H**A**K**L**S**I**Q**E**L**T**W**K**M**S**V**R**D**C**A**W**L**R**R**S**P**G**V**G**C**V**P-----
 mTERT 466 S**L**W**G**T**R**H**N**E**R**R**F**F**K**N-**L**K**K**F**I**S**L**G**K**Y**G**K**L**S**I**Q**E**L**M**W**K**M**K**V**E**D**C**H**W**L**R**S**S**P**G**K**D**R**V**P-----
 aTERT 468 S**L**L**G**T**H**Q**M**R**V**L**R**K**N**-**L**A**W**F**V**S**R**R**R**N**E**K**T**V**N**Q**F**I**H**K**V**K**P**S**D**F**P**F**A**R**K**E**L**C**C**M**V**N**G**H**E**L

Motif T

ScEst2p 353 --N**F**E**N**L**N**Q--**L**A**I**C**F**I**S****S**L**F**R**Q**L**I**P**K**I**I**Q**T**F**F**C**P**I**S**S**T**V**T**--I**V**E**R**H**D**T**R**N**K**I**T**P
 CaTERT 322 --D**F**E**L**R**T**A--**F**L**K**G**Y**L**W**L**F**E**H**L**L**K**N**I**L**R**S**F**W**T**E**T**S**S**I**V**S**S**E**L**N**Y**F**Q**Y**L**K**E**L**Y**E**S
 SpTrt1p 414 L**S**D**F**E**K**R**K**Q--**I**F**A**E**T**Y**W**L**Y**N**S**F**I**P**L**Q**S**F**Y**I**T**E**S**S**D**L**R**N-**R**T**V**E**R**H**D**I**W**K**L**L**C**R**P**
 OtTERT 531 --F**F**M**N**E**N**E**H**-**V**F**F**K**V**L**K**V**F**E**D**L**A**I**T**L**M**C**Y**F**Y**S**E**K**A**K**E**Y**Q**-**R**I**F**Y**R**E**N**I**W**N**M**I**M**R**L**
 Eap123 427 --Y**F**D**H**E**N**I**Y**-**V**L**W**K**L**R**R**I**E**D**L**V**S**L**I**R**C**F**F**V**T**E**Q**Q**S**Y**S**-**K**T**Y**Y**R**E**N**I**W**D**V**I**M**K**M**
 TtTERT 445 **K**R**K**Y**I**S**D**K**R**K-**I**L**G**D**L**I**V**E**I**N**K**I**V**I**P**V**L**R**Y**N**F**Y**T**E**K**H**K**E**G**S-**Q**I**F**Y**R**E**P**I**W**K**L**V**S**K**L**
 hTERT 531 --A**A**E**H**R**L**R**E**E**I**L**A**K**F**L**H**N**I**M**S**V**Y**V**V**E**L**L**R**S**F**F**V**T**E**T**T**F**Q**K**N**-**R**L**F**F**Y**R**R**S**V**W**S**K**L**Q**S**I
 mTERT 521 --A**A**E**H**R**L**R**E**R**I**L**A**T**E**L**F**W**I**M**D**T**Y**V**V**Q**L**L**R**S**F**F**Y**T**E**S**T**F**Q**K**N**-**R**L**F**F**Y**R**R**S**V**W**S**K**L**Q**S**I
 aTERT 527 **Q**S**E**S**I**R**S**T**Q**O**M**L**C**T**K**W**I**S**S**L**F**L**E**I**V**K**L**V**H**F**N**F**A**E**S**Q**G**G**R**L-**N**I**Y**Y**R**R**S****H**E**R**L**I**S**K**

ScEst2p 407 FIVE-YFKTYLVEN--NVGQFN--HNSYTLNFNHSMRRII--PKKSNNEFRITAI PCRGA
 CaTERT 378 WWSK-YAKNNLVKMP SKIQEQLPCGKIKLI PKRSSFFVICVEIFRSLKILNKKLELDTL
 SpTrt1p 471 FETS-MKMEAFEKINENNVM----DTQKTTLP PAVIRLL--PKNIFRITN-LRKRFL
 OtTERT 587 SADD-LLKQNLKQVEKKEMFI----FCESQNFAPGKRLI--PKGDTFRPIMT--FNRKI
 Eap123 483 SADD-LLKQNLKQVEKKEMFI----WKKSLGFAPGKRLI--PKATTFRPIMT--FNKKI
 TtTERT 503 TVVK-LEENLEKVEKLIPE-----DSFQKYPQGLRII--PKKGSFRPIMT--FLRKD
 hTERT 588 GTRQHILKRVQLRELSAEVFRQ---HREARPALTSRLRFTI--PKPDGLRPIVNM DYVVGGA
 mTERT 578 GVRQHILERVRLRELSQEEVFRH---HQDTWLAMPICRLRFTI--PKPNGLRPIVNM SYSMGT
 aTERT 586 ELSKALDGYVLVDATAEASSR-----KKL--SDFRFL--PKANGVRMVL D--FSSSS

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ScEst2p 460 DEE--EFTIY-KENHKNAIQPTQKILEYLR-NKRPTSFTKIYSPTQIADRIKEFKQRLLK
 CaTERT 437 EKEKREFERYRKEVLLPVGQILRLKLSKLR-DTYESYRASHVSSSDVAEKILDYRDSLIT
 SpTrt1p 523 IKQ----MGSNKKMLVSTNQTLRPVASILK-HLINEESSGIPFNLEVYMKLLTFKKDLLK
 OtTERT 638 PNQVGKQFSR--MTTNNKIQTAHMMMLKNLKSKMFKHSFGFAVFNYDDIMRVENFVQKWK
 Eap123 534 VNSD---RKTIKLTTNTKLLNSHLMLKTLK NRMFKDPFGFAVFNYDDVMKVEEFVCKWK
 TtTERT 553 KQK----NI-KLNLNQILMDSQLVFRNLK-DMLGQKIGYSVFDNKQISEKFAQFIEKWK
 hTERT 643 RTFR---REKRAERLTSRVKALFSVLNYER-ARRPGLLGASVLGLDDIHRARTFVLRVR
 mTERT 633 RALG---RRKQAQHTQRLKTLFSLMNYER-TKHPHLMGSSVLGMNDIYRTWRAVFLRVR
 aTERT 632 RSQ-----SIRDTTHAVLKDTIQ-LKEPDVILGSSVFDHDDFYRNLCPYLIHLR

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ScEst2p 516 KFNNVLP ELYFVNFDMKSCYDSIPRMECHRLI-KDALKNE-NG----FVVR-----
 CaTERT 496 RLG-EIPKLFILNSOMKBCYDRISQPVLMKKI-EELFENQDNKTI--YYVRY-----
 SpTrt1p 578 HRM-FGRKRYFVRIDAKSCYDRIKQDLFRIV-KKKIKDPEFVIR--KYATIH-----
 OtTERT 696 QIN--SPRLYFVAMDTEKCYDNVDCERVNFFQKSDLMDEKEYFILNTEVILKPK-----
 Eap123 591 QVG--QPRLYFATMDTEKCYDSVNRKLSLTFKTKLLSSDFWIMTAQIILKPK-----
 TtTERT 606 NKG--RPQLYFVTLDAKKCYDSIDQMKLNFNFNQSLLIQDTYFINKYLLFQRNKRPLLQI
 hTERT 699 AQD-PPPELYFVKMDTGAYDNIPODELTEVIAI IKP-QNTYCVRRYAVVQKA---AH-
 mTERT 689 ALD-QTPTMYFVMDTGAYDAIPOGKLEVVANMIRHSESTYCIROAVVRED---SQ-
 aTERT 677 SQSGELPPLYFVMDVFKAFDSVDQGLLHVT-QSFLKDEYILNRCRLVCCGK-----

ScEst2p 561 ---SQY-----EFNTNTGV---LKLFNVVNA-SRVPKPYELIYIDNVRTVH
 CaTERT 545 ---AQLDASHK-----LKKVKTTIDTQYHNLNLISS-SRHLSNCKSLVDKTKTIA
 SpTrt1p 627 ---ATSDRATKN-----FVSEAFSYFDMVPEKVVQL-LSMKTSDTIFVDFVDYWT
 OtTERT 747 ---NNIIVERSN-----FRKLPKQYFRYKFOKIGIDGSSYPTLFEILEDEFNDLN
 Eap123 642 ---NNIVIDSKN-----FRKKEMKDYFRQKFOKIALEGGQYPTLFSVLENEQNDLN
 TtTERT 664 QQTNNINSAMEIEEEKINKKPEKMDNINFPYFNLKERQIAYS LYDDDDQIILQKGFKEIQ
 hTERT 753 ---GHVRKAFKS-----HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVEIQSSSLN
 mTERT 744 ---GOVHKSFR-----QVTTLSDLQPYMGQFLKHLQSDASALRNSVVIHQSISMN
 aTERT 729 ---RSN-----WVNKILVSSDKNSNFSRFTSTVPYNALQSIVVDKGENHR

B'

ScEst2p 599 L--SNQDVIN-----VEMEIFKTALWVEDK-----CYIREGDFQGSLSAPVVD
 CaTERT 591 L--QKGNILE-----VCRSQIYDVVGSVKDARGNLH---LYKRKRGFQGFSLLSIFCD
 SpTrt1p 674 K--SSSEIFK-----MLKEHLSGHIVKIGNS-----QYLQKVGIPQGSILSSFLCH
 OtTERT 795 M--KRTIIVEQEQRKFKNDLLQPVLKICQNNYVTFNKKQYKQMKGIPQGLCSYILSS
 Eap123 690 A--KKT LIVEAKQRNYFKNDLLQPVINICQYNYINFNGKFKYKQTKGIPQGLCSYILSS
 TtTERT 724 SDDRPFIVINQDKPRCTITKDIHNNHLKHSIQYNVISFNKVKFRQKRGIPQGLNSGVLCS
 hTERT 800 E--ASSGLFD-----VFLRFMCHHAVRIRGK-----SYVQCQGIPOGSILSLLCS
 mTERT 793 E--SSSSLFD-----FFLHFLRHSVVKIGDR-----CYTQCQGIPOGSILSLLCS
 aTERT 771 V--RKKDLMV-----WIGNMLKNNMLQLDKS-----FVYQIAGIPQGHRLSSLLCC

C

ScEst2p 643 LVYDDLL-IFYSEFKASPSQD-----TILKLAADDFLISTDQ---QQ
 CaTERT 640 ILYSAMV-HDCFQFLWWSKQD-----FLFVRLVDDFLVLPDSNIYDQ
 SpTrt1p 718 FYMEDLI-DEYLSFTKKKG-----SVLLRVVDDFLFITVNNKDAKK
 OtTERT 853 FYYNLE-ENALQFLRKESMDPEK-----PEINLLMRLTDDYLLMTTEKNNAML
 Eap123 748 FYYATLE-ESSLGFLRDESMNPEN-----PNVNLMLRLTDDYLLMTTQENNAVL
 TtTERT 784 FYCKLE-HEYTFLNNAEQVN-----GSINLLMRLTDDYLLMTSDSQNALN
 hTERT 844 LCFQDME-NKLFAGLRRDG-----LLLRLVDDFLVLPHTLHAKT
 mTERT 837 LCFQDME-NKLFAGLRQDQ-----LLLRFVDDFLVLPHTLDQAKT
 aTERT 815 FYYHLERTLIYPFLLEASKDVSSKECSREEELIIPTSYKLLRFIDYLLFVSTSRDQASS

D E

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ScEst2p 682 VNIKK-----LAMGGFQKYNKA-NRDKILAVSS-QSDDDTVIQ----FCAMHIFVK
CaTERT 682 VHNI-----LSGKILESYGAFV-NKDKTVVN--QTTTKTSID----FVGLVNTT
SpTrt1p 758 FNLNLSLRGFEKHNFSSTLEKTVINFE-NSNGLINNTF-FNESKRRMP----FFGFSVNM
OtTERT 901 FTEKLYQLSLGNFFKFMKLLKTNFALNLQKIGC-TNT-TQDIDSINDDLFFWTGTSIDIK
Eap123 796 FTEKLVNSRENGFKFNMKKLLQTSFPLSPSKFAKYGMDSVVEEQNIVQDYCDWTGTSIDMK
TtTERT 830 LTVQLQNCANNNGFMFNDDQKITTNFQ-FPQEDYNLEHFKISVQNECQ----WTGKSIDMN
hTERT 883 FRTLVRGVPEYGCVVNLRRTVVNFVPEDEALGGTAFVQMPAHGLFP----WGCLLLDTR
mTERT 876 FHLSTLVHGVPEYGCMINLQKTVVNFVPEPGTLGGAAPYQLPAHCLFP----WGCLLLDTR
aTERT 875 FYHRLKHGFKDYNCFMNETKFCINFE-DKEEHRCSSNRMFVGDNGVP-FVFWTGLLINSR

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ScEst2p 729 -----ELEVWKHSSTMNNFHIRSKSSKGIFRS--LIALFNTRISYKTIIDTNLNS
CaTERT 726 -----DLSIKRNSGLISLVTTNFRFTKTLVKY--LKTFFYQINLEGVLLDCSFGV
SpTrt1p 812 SLDTLLACPKIDEALFNSTSVELTKHMGSFFYKILRS--SLASFAQVFIDITHNSKFN
OtTERT 960 TLN-----IIQNINIKKEGILCTLNLVNMQTNESILWLKKKLKSFLMNNISFYFKSTINT
Eap123 856 TLA-----LMPNINLRIEGILCTLNLVNMQTKKASMWLKKLKSFLMNNITHYFRKTIT
TtTERT 885 TLE-----IKSIQKQTQQEINQTNVAISIKNLKSQKLNKLRSLFLNQLIDYFNPIN
hTERT 939 TLEV-----QSDYSSVARTSIRASLTFNRGFKAGRNMRRKLFGLVRLKCHSLFLDLQVNS
mTERT 932 TLEV-----FCDYSGVAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLELDLQVNS
aTERT 933 TLEV-----QVDYTRMLSGHISSTFSVAWQNKPVNRLRQKLCYFLVPKCHPILFEDSNINS

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ScEst2p 776 TNTVL-----MQIDHVVKNISEC--YKSAFKDLS-----
CaTERT 773 LENVL-----ENMGSLRLRLVLR--FKTKFTSIVK-----
SpTrt1p 870 CCNIYRLGYSM-CMRAQAYLKRMDI--FIPQRMFITD-----
OtTERT 1014 KQFANITLSKL-YIAAAEKYVACCQE--FKRFHENTSL-----
Eap123 910 EDFANKTLNKL-FISCGYKYMOCAKE--YKDHFKKNLA-----
TtTERT 939 FEGLCRQLYHHSKATVMKHYPFMTKL--FQIDLKSKQYSVQYGKENTNENFLKDILYTT
hTERT 994 LQTVCTNIYKILLQAYREHACVLQLP-FHQVQVWKNPTFFLR-----
mTERT 987 LQTVCTNIYKIFLLQAYREHACVIQLP-FDQVRKNTLFFFLG-----
aTERT 988 GEIVRLNIYQIFLLAAMKFHCYVYEVSRFWKLHPQTLFK-----

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ScEst2p 803 ----INVTQNMQFHSFQRIIEMTVS----GCPITKCDPIIEYE-----
CaTERT 801 ----YDTFHICYKFKFTFYDISNYTIV---KYVETNSLDWDGAP-----
SpTrt1p 905 ----LLNVIGRKIWKKLAELIGYTSRR---FLSSAEVKWLFCLG-----
OtTERT 1049 ----GGQNDIKIIEIYVVISRFFK----YLCVNVKSPVFERDDY-----
Eap123 945 ----MSSMIDLEVSKIYYSVTRAFFK----YLCVNIKDTIFGEEHY-----
TtTERT 997 VEDVCKILCYLQFEDEINSNIKEIFKN---LYSWIMWDIIVSYLKKKKQFKGYLNKLLQK
hTERT 1035 -VISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLK-----
mTERT 1028 -IISQASCCYAILKVKNPGMTLKAS---GSFPPEAAHWLCYQAFLLK-----
aTERT 1027 ---FITISVRYMFRLINRRVRRINTGSSFRPLKLYKEEVIWLGLD-----

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ScEst2p 839 --VRFTILN----GILESLSNNTSKFKDNIILIRKEIQHLQAYIYIYIHIVN-----
CaTERT 837 ---LLNCIKQ----IIVKEFSS---FES-YLEIIEWVQTLNI-----
SpTrt1p 942 ---MRDGLKPS--FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFHRRHAD-----
OtTERT 1087 ---QOFFIYSL--KFEITRFKQKNEFAG-VYKILKAKEKKLEVAKIEFOIQ-----
Eap123 983 ---PDFFLSTL--KHEIEIFS TKKYIFNR-VCMILKAKEAKLKSQDQCSLIQYDA----
TtTERT 1054 IRKSRFFYLKEGCKSLQLILSQQKYQLNKKELEAEFIDLNNLIQDIKILPKISAKSNQ
hTERT 1082 -LTRHRVTYVPLLGLSLRTAQTQLSRKLPGTTTALAEAAANPALPSDFKTI-----
mTERT 1072 -LAAHSVYKCLLGLPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTI-----
aTERT 1070 ---AYIQVLKKNRSRVRMLLIYLKSALSKHSLSQQLSSELKYATDRSNSSSLWKLNY---

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ScEst2p -----
CaTERT -----
SpTrt1p -----
OtTERT -----
Eap123 -----
TtTERT 1114 QNTN
hTERT -----
mTERT -----
aTERT -----

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