Spt16N_N Lobe

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P.t._SPT16-1    1  --------------------MDKVQIALQNKEKKNNKLAITTLRK--------ANQFDCLAVLIGTSHTSNIGIQ-KGFQ
T.t._SPT16      1  --------------------MSKVKADI-FYQHHKQLLSVWNK-----QPQYANIDAFLIKNGK-DQGGNKIKTSAIS
P.t._SPT16-2c   1  --------------------MDKKIIADV-FQRHLDQLTSRLND----------DIPAICIISGK-EDGSIKPKTKALF
P.t._SPT16-2a   1  --------------------MDKKIIADV-FQRHLEQLVSRLNE----------DVPAICIISGK-EDGSIKPKTKALF
P.t._SPT16-2b   1  --------------------MDKKIIADV-FQRHLEQLVSRLND----------DIPAICIISGK-EDGSIKPKTKALF
A.t._SPT16      1  MADSRNGNARAPPSGVPPKAGNTYSIDVKN-EISRARALYEHWKK--HS-ADLWGSADALATPPASDDLRYLKSSAIN
S.p._Spt16      1  --------------------MAEYEIDEIT-FHKRLGILLTSWKNEEDG-KTLFQDCDSILVTVGAHDTNPYQKSTALH
S.c._Spt16      1  --------------------MEELNIDFDV-FKKRIELLYSKYNE-------FEGSPNSLLFVLGSSNAENPYQKTTILH
C.e._SPT16      1  --------------------MSGKRAVLNKDL-FFQRAERLYEHWEK---G-ADGLDSIKSLAFVYG--ETDNPYTKTSALF
D.m._Dre4       1  --------------------MSSFVLDKEA-FVRRVKRLYTEWRAPSIGHDDALRNLDCIMSIVGV-EEDVYYSKSMALQ
H.s._SPT16H     1  --------------------MAVTLDKDA-YYRRVKRLYSNWRK---G-EDEYANVDAIVVSVGV-DEEIYAKSTALQ
M.m._Supt16     1  --------------------MAVTLDKDA-YYRRVKRLYSNWRK---G-EDEYASIDAIVVSVGV-DEEIYAKSTALQ
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Spt16N_N Lobe

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P.t._SPT16-1   52  QWYLGCELMDCILIMSTKMLCILADEVMFQKLKHL-----SDIKMKTFTIFFLIKNIKKNNH---QQFQFALERLRKEYP
T.t._SPT16     52  VWYFGFLFIDTILLIKKTFAIIGGNKKINMLKSVQ----EHAEAKEYNLVFLEKDQANNSNQLQQLFEILDKDINKSS-
P.t._SPT16-2c  48  VWLFGYDMIETVFIATRKQIFYLASDKKLQMMEET-----KQRLGGRYEVHFYKKVADNRDS-----FFKIRQKLGN---
P.t._SPT16-2a  48  VWLFGYDMIETVFIATKKQIFYLASDKKLQMMEET-----KQKLSGKFEVHFYKKGNDNRES-----FDKIRQKLGN---
P.t._SPT16-2b  48  VWLFGYDMIETVFIATKKQIFYLASDKKLQMMEET-----KHKLSGKFEVHFYKKMNDNKDA-----FDKIRQKIGN---
A.t._SPT16     77  IWLLGYEFPDTIMVFTKKQIHFLCSRNKASLLEVV-----KKPAHDELKLDVIMHVKPKGDD-GTGLMDAIFRAIRDLSR
S.p._Spt16     59  TWLLGYEFPSTLILLEKHRITILTSVNKANMLTKL-----AETKGAAADVNILKRTKDAEEN--KKLFEKLIEYIRATN-
S.c._Spt16     53  NWLLSYEFPATLIALVPGKVIIITSSAKAKHLQKAIDL--FKDPESKITIELWQRNNKEPEL-NKKLFDDVIALINSAG-
C.e._SPT16     56  TWLFGHEIADTVLLLLKDHIYILGSNRKVEFFGSVTGD--NQSSGKVPTVSTLLRDKTDKDA---GNFEKLIDHIKSAG-
D.m._Dre4      59  IWLLGYELTDTISVFCSDAVYFLTSKKKIEFLKQTQ----NITEEGFPEINLLVRDRTDKDQ---GNFEKLIKALQNSKK
H.s._SPT16H    54  TWLFGYELTDTIMVFCDDKIIFMASKKKVEFLKQIANTKGNENANGAPAITLLREKNESNK---SSFDKMIEAIKESKN
M.m._Supt16    54  TWLFGYELTDTIMVFCDDKIIFMASKKKVEFLKQIANTKGNENANGAPAITLLREKNESNK---SSFDKMIDAIKESKS
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Spt16_N Lobe   Spt16N_Peptidase M24

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P.t._SPT16-1  124  G---NNYRLAINLSDGQKSPLITEFNQFID----QNHLIKVDCTSFLKELINNDNKDIFEYYNTCGKINSYYMKF-VSQR
T.t._SPT16    127  ------FNIGTLAKRQQVGPFMTEYDSFIKD---KNQYKFADCSVFVQPCLSVKDQNEISYIGKAAKVSVYLESK-LIKE
P.t._SPT16-2c 115  ------GKIGMPTTEQQAGSLATEWYDY------KGWSQIVDASQLISDVLAVKDDQEQABINQSSQLTTRLEKK-LIKQ
P.t._SPT16-2a 115  ------VKLGMPTTEKQAGSLAAEWYEY------KGWQQIVDANQLISDVLAVKDDQEQGEIQQSSQLTTRLEKK-LIKQ
P.t._SPT16-2b 115  ------VKLGMPTTEKQAGSLAAEWYEY------KGWQQIVDATQLIGDVLAVKDDQEQGEIQQSSQLTTRLEKK-LIKQ
A.t._SPT16    151  GDGNDSQVVGHIAREAPECKLLETWTERLK----NANEQFVDITGGLSDLFAVKDDTEVMSVKKAAYLAYSVMKNVVVPN
S.p._Spt16    131  ------KKVGVFPKDKTQCKFINEWDSIFEPV--KSBFNLVDASLGLAKCIAIKDEQELANTKGASRVSVAVMSKYFVDE
S.c._Spt16    129  ------KTVGIPEKDSYQGKFMTEWNPVWEAAVKENEFNVIDISLGLSKVWEVKDVNEQAFISVSSKGSDKFMDL-LSNE
C.e._SPT16    130  ------GDVGNFVKEKFSSEFVSSANKALE----EGGVNKNDVILAFTHLFAVKDDKEMDLIRKSAQATTASATA-ARAR
D.m._Dre4     132  G-----KRLGVFAKDAYPCEESEAWKKSLT----ASKEEHVDISTIIAYLMCPKDESEINNIRKASLVSMDIFNKYLKDE
H.s._SPT16H   131  G-----KKIGVFSKDKFPGEFVKSWNDCLN----KEGFDKIDISAVVAYTIAVKEDGEINLMKKAASITSEVFNKFFKER
M.m._Supt16   131  G-----KKIGVFSKDKFPGEFVKSWSDCLN----KEGFDKVDISAVVAYTIAVKEDGEINLMKKAASITSEVFNKFFKER
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Spt16N_Peptidase M24

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P.t._SPT16-1  196  TELAIKFNENTTNYSITQAVKREKSSDLNQMAIRRKEGL--------Q-GNYDIILS-STVQSGGQYNVSASE-STQSRLV
T.t._SPT16    197  TETITEDEGKKTHSQIATMIEGLISNEKELKKISEEICG--------ESDNIDIAYVPIVQSGGKYDLKPNAQSNEDILS
P.t._SPT16-2c 182  IEDSIDVGTRITHQDLAKKVEQSLDNDKQ--KVIKDLGL--------QDGLYDFAYTPIIQSGGNY--QQVDGPNKDYLS
P.t._SPT16-2a 182  IEDSIDVGTRITHQDLAKKVEQSLENDKQ--KVMKEIGL--------QDGLYDFAYTPIIQSGGNY--QQVDGPNKDYLS
P.t._SPT16-2b 182  IEDSIDVGTRITHQDLAKKVEQSLENDKQ--KVMKEIGL--------QDGLYDFAYTPIIQSGGNY--QQVEGPNKDYLS
A.t._SPT16    227  LESAIDEPKDVTHSALMDLTEKAILEPTK-----ASVKL--------KPENVDICYPPIFQSGGKEDLKPSAASNDELLT
S.p._Spt16    203  LSTYIDQGKKITHSKFSDQMESLIDNEAFFQTKSLKLGDI--------DLDQLEWCYTPIIQSGGSYDLKPSAITDDRNLH
S.c._Spt16    202  MVRAVDEELKITNAKLSDKIENKIDDVKFLKQLSPDLSALCCPPNYKFNFDLLDWTYSPIIQSGKKEDLRVSARSTNDQLY
C.e._SPT16    199  YVEIIDQEKRVRHSVLSNEFAAFVKDSKV----QQAIT--------AKYEADTCYDPIVMSGGNYSFKWNHESSESHLH
D.m._Dre4     203  TMDIIDSDRKVKHNKLSDLGCEAATGEKKY------TSGL--------DPRLLDMAYPPIIQSGGAYSLKFSAVADKNPLH
H.s._SPT16H   202  VMEIVDADEKVRHSKLADSVEKAIEEKKY------LACA--------DPSTVEMCYPPIIQSGGGNYNLKFSVVSDKNHVH
M.m._Supt16   202  VMEIVDADEKVRHSKLADSVEKAIEEKKY------LACA--------DPSTVEMCYPPIIQSGGGNYNLKFSVVSDKNHVH
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Spt16N_Peptidase M24

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P.t._SPT16-1    265 GD---VVIYSFCCQYMQSQSYCTRTLLFQPNQELEQIYRVILNVHAFALG-LVKEDIQFKQIYRETQNIWETIFKDDPEM
T.t._SPT16      269 YD---TIIVSVGTKYMEYHANIVRTLFIDPTNDQKKIYQRVYELQNQIAV-QLKPGIKLKTVYENAVNFIN---EKVPQL
P.t._SPT16-2c   250 SD---VIIISLGTQVNEYNTNCIRTLFINPTEVQKKLYNTLIEVQSKTIG-LITVGTPLNQVYKEAVPTIQ---QKIQEI
P.t._SPT16-2a   250 SD---VIIQLGTQVNEYNTNCIRTLFINPTEIQKKLYNALIEVQSKIIT-LMTIGVSLNVVEKESLQLIQ---YKLQEL
P.t._SPT16-2b   250 SD---VIIQLGTQVNEYNTNCIRTLFINPTEIQKKLYNALIEVQNKIIT-LMTIGTTLNSVEKEALQLIQ---QKLQEL
A.t._SPT16      294 YDPASIITCAVGARYNSYCSNVARTYLIDATSLQSKAYEVLIKAHEAALD-ALRSGRKTNTYQAALSVVE---KNAPEF
S.p._Spt16      276 GD---VVLCSIGFRYKSYCSNVGRTYLFDPDSEQQKNYSFLVALQKKLFE-YCRDGAVTGDIYTKILGLIR---AKRPDL
S.c._Spt16      282 GN--GCILASCGIRYNNYCSNITRTFLIDPSEEMANNYDFLLTIQKEIVTNILKPGRTPKEVYESVIEYIE---KTKPEL
C.e._SPT16      265 SQ-FGTIITSFGARLSEYCTNLTRTMLIFPSSELETAYEAILAAELAVIA-ALKPGAKISDVYKIGIDTLT---EKSPKL
D.m._Dre4       269 FG---VIVCSIGARYKSYCSNISRTFLVNPTEAMQENYTFLVSVQEEILK-LLVPGTKLCDVYEKTIDFVK---KEKPSM
H.s._SPT16H     268 FG---AITCAVGIREKSYCSNLVRTLMVDPSQEVQONYNFLLQIQEELIK-ELRHGVKICDVYNAVIDVVK---KQKPEL
M.m._Supt16     268 FG---AITCAMGIREKSYCSNLVRTLMVDPTQEVQENYNFLLQIQEELIK-ELRHGVKICDVYNSVIDVVK---KQKPEL
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Spt16N_Peptidase M24

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P.t._SPT16-1    341 ---KMKFE-TDIGYLIG-----SQMLIDNHNIE-THQDRMAVVIRMFVDNILVQLPFYPERTNIAICLADTIFV---VSG
T.t._SPT16      342 ---KDKLP-ANFGFGIGLEFRESNLYINAKNEK-EVEEGMVENVVVGFDNLQSE-----KEKAYAIQISDTVAI-RKQNT
P.t._SPT16-2c   323 NITNVQLP-SSFGYGIGLELKEPFLAISEKSTH-LVAKNEVYFVQVTLENLSNGQ----KGISYTISVGDVIVV---TNG
P.t._SPT16-2a   323 NLQNLQLP-TSFGYGIGLELKESCITINEKSTH-VVTKGEVYFVNVSLENVQNGQ----KNITYTYQVGDVIVI---TNG
P.t._SPT16-2b   323 NLLNLQLP-NSLGYGIGLELKESNLVINEKSTH-VVAKGEVYFVNVVMENVPNGQ----KNIVYTIQVGDVIVI---TNG
A.t._SPT16      370 ---VDKLT-KSAGTGIGLEFRESGININAKNDK-VIRPKMAENVSLIGFONLECESESRSKNKKESLLADTVLV---TDQ
S.p._Spt16      349 ---EPNFV-RNIGAGIGIEFRESSLLVNAKNPR-VLQAGMTLNISIGFGNLINPHPKNSQSKEYALLIDTIQI---TRS
S.c._Spt16      357 ---VPNFT-KNIGSLIGLEFRDSNFTILNVKNDYRKIQRGDCFNISFGFNNLKDSQ----SANNYALQLADTVQIPLDETE
C.e._SPT16      340 ---AETLNKKELGPATGIEFRESRLAISAKCDE-VVKAGMVEIVYIGVDSIPNKN-KGEKGKPAAIAISDTIILV--KEEG
D.m._Dre4       342 ---VDNLP-KSFGPAMGLEFRENSVIGPKCQA-LLKKNMVENLHVGISNLTNPEATDKEGKNYALFTGDTVLV--GEQS
H.s._SPT16H     341 ---LNKLT-KNLGFGMGIEFREGSLVINSKNQY-KLKKGMVESINLGFSDLTNKEGKKPEEKTYALFTGDTVLV--DEDG
M.m._Supt16     341 ---LNKLT-KNLGFGMGIEFREGSLVINSKNQY-KLKKGMVESINLGFSDLTNKEGKKPEEKTYALFTGDTVLV--DEDG
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Spt16N_Peptidase M24

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P.t._SPT16-1    408 IEDCVITKAEKEFTFVSYQPTEEGE----------RFFK--STFQKNENSD-VLHQSEKITR----EQFEQAELNKIKND
T.t._SPT16      411 PNAVMTFKVSKKYEDISYSIQDEGQDEEQEEEEDDLEKE-NLIQDGRRTRNAYHKNTTIVS--------EKERQKH--
P.t._SPT16-2c   394 AANVTTNSIPKAYKQISYQIQEEDEQPAQKQ----QEKQ--TDAPKEGRTRAPRNQQIQIQR-------ENEKQRQIH--
P.t._SPT16-2a   394 ATTITTQQIPKAYKQISYQIQEEDEPERKP-----AEVQ--TDKDKPIRAR-PRNQQIQIQR-------ENEKQRQIH--
P.t._SPT16-2b   394 AATITTQQIPKAYKQISYQIQEEDEPERKP-----AEVQ--TDKDKPIRAR-PRNQQIQIQR-------ENEKQRQIH--
A.t._SPT16      442 KPELLTK-CSKSVKDVAYSFKEDEEE--------KERK--KARTSGSENY-ITKTALRSLD----HVVSKEELRKQH--
S.p._Spt16      421 DPIVFTD-SPKAQGDISYFFGEDDSSLEDGV----KERK---PPTRGTATISSHKGKTRSET--RDLDDSAEKRRVEH--
S.c._Spt16      429 PPRFLTN-YTKAKSQISFYFNNETEDNNKKKS---SEAT--KVPSKPDRNSKILRTKLRGEARGGAEDAQKEQIRKEN--
C.e._SPT16      413 DNEIITEKAKSRLKSNVIKFKEEQENREAEKD---NDQK--KVLGRGQRSV-VLTDQTRNKT-------TNEELRKER--
D.m._Dre4       415 PASVMTP-SKKKIKNVGIFIKDDSDEEDVDDKKTAKEDQGTELLGRSKRNA-VLESKLRNEI-------NTEERKKEH--
H.s._SPT16H     414 PATVLTS-VKKKVKNVGIFLKNEDBEEEEEK---DEAE--DLLGRGSRAA-LLTERTRNDM-------TAEEKRRAH--
M.m._Supt16     414 PATILTS-VKKKVKNVGIFLKNEDEEEEEEK---DEAE--DLLGRGSRAA-LLTERTRNDM-------TAEEKRRAH--
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Spt16D

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P.t._SPT16-1    471 QEKLKEIKQYELEVRLNDCQ--TRQEPKLLVKVDQLQAFQKEDQFDQ---YPKGETAVDQDKSAILIPIICTHYPFHALT
T.t._SPT16      478 QLELREVKLKELQERYNNNGFLSNKINSRALELDKVQCYGGPQDTPKE--YKKNQTHIDAAHNAILLPVNGELVPFHISL
P.t._SPT16-2c   459 QEKLAKDKQNELEQRLEQDQFVQNSQETKALELDKLQCYQKSEQYPKD--LQKGQIYIDNQKCAVLVPILGTHVPFHVSC
P.t._SPT16-2a   457 QEKLAKDKQTELEQRLEQDQFVQNQQEVKALELDKLICYQRPEQYPKE--LQKGQIYIDNQKCALLVPMGTHIPFHVSC
P.t._SPT16-2b   457 QEKLAKDKQTELEQRLEQDQFVQNQQEVKALELDKLICYQRPEQYPKE--LQKGQIYIDNQKCALLVPMGTHIPFHVSC
A.t._SPT16      504 QAELARQKNEETARRLAGDSSGAGDSRSTAKTSADVVAYKNVNDMPHK----ELMIQVDTRNEAVLLPIYGSLVPFHVAT
S.p._Spt16      489 QKQLASRKQAEGLQRFAQGSVPSSGIEKP--TVKRFESYKRDSQLPQA--IGELRILVDYRAQSIILPIFGRPVPFHIST
S.c._Spt16      501 QKKLHEKLEKNGLLRFSAADA-NGPDSEPRQYFKKYESYVRDSQLPTN--IRDLRIHVDWKSQTIILPIYGRPVPFHINS
C.e._SPT16      478 QKELGVQLNELAKARLSKQGGGTDEKKSK----KSNVSYKTEERFPQDADVQKMLIFVDRKYDSVVPIFGIPVPFHISM
D.m._Dre4       484 QKELAAQQLNERAKDRLARQGNSKEVEKVR----KNTVSYKSISQMPREPEVKELKLYVDKKYETVIMPVFGIQVPFHIST
H.s._SPT16H     478 QKELAAQLNEEAKRRLTEQKGEQCIQKAR----KSNVSYKNPSLMPKEPHIREMKIYIDKKYETVIMPVFGIATPFHIAT
M.m._Supt16     478 QKELAAQLNEEAKRRLTEQKGEQCIQKAR----KSNVSYKNPSLMPKEPHIREMKIYIDKKYETVIMPVFGIATPFHIAT
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Spt16D

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P.t._SPT16-1   546 IQNVSVKELPNGAGEITIRFWTNEFHID---TR-EFESM-LQDQMFLKEITLRNQEFIK--------LQDIENEINVCRD
T.t._SPT16     556 IKNYSKNDEGKT-HTLRLNFHNPGSGSN-LANI-TFEKI-DGQIVFIKEITFRSKN----------AKNVLETIKKIKD
P.t._SPT16-2c  537 IKNMG--------SSIRINFFTSEITAG---QI-QFEQI-DGETIFIKELQYRSKK-----------SDRPQNLILQIKQ
P.t._SPT16-2a  535 IKNVSKIDEGKMGSSIRINFFTSEITAG---QI-QFEKV-DGETIFIKELQYRSKK-----------SDRPQNLILQIKS
P.t._SPT16-2b  535 IKNVSKIDEGKMGSSIRINFFTSEITAG---QI-QFEKV-DGETIFIKELQYRSKK-----------SDRPQNLILQIKS
A.t._SPT16     580 IRTVSGNQDTNRNCYIRLIFNVPGTPFNPHESN-SLKNQ-GAI--YLKEVSFRIKD-----------SRHSSEVTQQIKT
S.p._Spt16     565 LKNASKNDEGNF-VYLRLNFVSPGQIGGKKDEL-PFEDP-NAQ--FIRSFTFRSSN-----------NSRMSQVFKDIQD
S.c._Spt16     578 YKNGSKNEEGEY-TYLRLNFNSPGSSGGISKKVEELEYEESADNQFVRSITLRSKD-----------GDRVSETFKQIAD
C.e._SPT16     554 IKNCSQSVEGDF-TYLRINFAIPGSQVG-KFSG-QFFHP-LAH--YMKEITTRASNIKDHHSDSTAPSHNLSTAFRLIKE
D.m._Dre4      560 IKNISQSVEGEY-TYLRINFFHPGATMGRNEGG-LYFQP-EAT--FVKEVTYRSSNVKE-HGEVGAPSANLNNAFRLIKE
H.s._SPT16H    554 IKNISMSVEGDY-TYLRINFYCPGSALGRNEGN-IFENP-EAT--FVKEITYRASNIKA-PGEQTVPALNLQNAFRIIKE
M.m._Supt16    554 IKNISMSVEGDY-TYLRINFYCPGSALGRNEGN-IFENP-EAT--FVKEITYRASNMKA-PGEQTVPALNLQNAFRIIKE
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P.t._SPT16-1   613 DARRKQIEKQLEVDKFDFVIEKLTVLPKN--TE-CLSKVYMRFTQSQKTRSPEGFVECHENGFRYKS-ARGE-VIDFTFT
T.t._SPT16     621 LQAKVKQTDQEAANKDELVEQDKLQL-RNTKRF-ALFNLKVREAISK-QKVN-GMLELHLNGFRYMT-TKNE-KVDVIEK
P.t._SPT16-2c  593 LQKKVKAEQQVEREKQHVGELEPLIVSKSGRKP-IFKDLKVRFTFGS-GKAA-GILEVNSNGFRYVH-SNKE-QLDIVFK
P.t._SPT16-2a  599 LQKKVKTEQQVEREKQNVGEMEPLILNKGGRKP-IFKDLKVRFTFGS-GKAA-GILEVHTNGFRYIH-SNKE-QLDIVFK
P.t._SPT16-2b  599 LQKKVKTEQQVEREKQNVGETEPLIINKGGRKP-IFKDLKVRFTFGS-GKAA-GILEVHTNGFRYIH-SNKE-QLDIVFK
A.t._SPT16     645 LRRQVMARESERAERATLVTQEKLQLAGN-FKFLRLSELWIREPFSGRKIP-GILEAHANGFRYSL-TRPDERVDVLEA
S.p._Spt16     629 MKKAATKRETERKEFADVIEQDKLIEIKNKRPA-HINDVYVRFAIDG-KRLP-GFTEIHQNGIRYQSPLRSDSHIDLFS
S.c._Spt16     646 LKKEATKREQERKALADVVQQDKLIENKTGRTK-RLDQIFVRENPDT-KRVP-STVFIHENGIRFQSPLRTDSRIDILFS
C.e._SPT16     628 VQKRFKTEEAEEREKEGAVKQDKLILSQNKLNF-KLKDLLIRFNTIQ-KRIT-GSLEAHTNGFRYTS-LRGD-RIDVLYN
D.m._Dre4      634 VQKRFKTREAEEREKEDLVKQDTLIISQNKGNP-KLKDLYIRFNIVT-KRMT-GSLEAHSNGFRYIS-VRGD-KVDILYN
H.s._SPT16H    628 VQKRYKTREAEEKEKEGIVKQDSLVINLNRSNP-KLKDLYIRFNIAQ-KRMQ-GSLEAHVNGFRFTS-VRGD-KVDILYN
M.m._Supt16    628 VQKRYKTREAEEKEKEGIVKQDSLVINLNRSNP-KLKDLYIRFNIAQ-KRMQ-GSLEAHVNGFRFTS-VRGD-KVDILYN
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P.t._SPT16-1   688 SIKHCFFVSPEDEVIACIHFIFKMPIKCGKIMFSQIQFYRDIEGASEQEAAR------RKVRLFDIDHVF-EKKVQDRRL
T.t._SPT16     695 NIKHAIFQPCDNEMIVAIHFNLKNPIMIGKKKVWDVQFYTEAGLPPEDIN--------NRRFGHDYDEIEEEQMEKARRK
P.t._SPT16-2c  668 NIKHYIYQSPEQDIIAALHFHLHSPIVLGKRKTHDVQFYCEVGGAVEHLEGR------RKNNKNDDDEIEEEERLRVFRK
P.t._SPT16-2a  674 NIKHYIYQSPEQDIIAALHFHLHSPIVLGKRKTHDVQFYCEVGGAVEHLEGR------KKTNRNDEIEEEERLRMHRR
P.t._SPT16-2b  674 NIKHYIYQSPEQDIIAALHFHLHSPIVLGKRKTHDVQFYCEVGGAVEHLEGR------KKTNRNDEIEEEERLRMHRR
A.t._SPT16     723 NIKHAFQPAEKEMITLLHFHLHNHIMVGTKKTKDVQFYVEVMDVVQSLGG-------GRRSAYDPDEIDEEQRERDRKN
S.p._Spt16     706 NMKHLFFQPCEGELIVLIHVHLKAPIMVGKRKTQDVQFYREVSDIQFDETGNKK----RKYMYGDEDELEQEQEERRKRA
S.c._Spt16     723 NIKNLIFQSCKGELIVVIFIHLKNPILMGKKKIQDVQFYREASDMSVDETGGGRRGQSRFRRYGDEDELEQEQEERRKRA
C.e._SPT16     703 NIKHAFFQPCDNEMIIILHFHLKNPVLWGKKKYKDVQFYTEVGEITTDLG-------KYHFMQDRDDMQSEQQEREMRR
D.m._Dre4      709 NIKSAFFQPCDGEMIILLHFHLKYAIMFGKKKHVDVQFYTEVGEITTDLG--------KHQFMHDRDDLAAEQAERELRH
H.s._SPT16H    703 NIKHALFQPCDGEMIIVLHFHLKNAIMFGKKRHTDVQFYTEVGEITTDLG--------KHQFMHDRDDLYAEQMEREMRH
M.m._Supt16    703 NIKHALFQPCDGEMIIVLHFHLKNAVMFGKKRHTDVQFYTEVGEITTDLG--------KHQFMHDRDDLYAEQMEREMRH
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Spt16M_Rtt106

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P.t._SPT16-1   761 EELKNFESFIQQSEQY-----YKRFNIKFERLEKQYSEEGNYAKERVVFQPTQSCLVNIVDQPFFTLTLENVIIMCCERV
T.t._SPT16     767 KLNKDFEAFYKEVENQ------LGDKIKFEVPYANLGFYGSFSRSTCLLQPTQNTLMNIIERPFFIMSLEEVELACFERM
P.t._SPT16-2c  742 KVAREFEVFIKTIEEM-----GADYKIQFEKPFRDLGFEGNWNRARLFLQPTHNTLMNVVESPFFIITISEVEICCFERI
P.t._SPT16-2a  748 KVAKEFEVFIKTIEEI-----GADYKISFEKPFRDLGFEGNWNRARLFLQPTRDTLMNVVESPFFIITINEVEICCFERI
P.t._SPT16-2b  748 KVAKEFEVFIKTIEEI-----GADYKISFEKPFRDLGFEGNWNRARLFLQPTRDTLMNVVESPFFIITINEVEICCFERI
A.t._SPT16     796 KINMDFNHFANKVNDMWQLPQFASLDLEFTQELRELGFHGVFHKTSAFLIPTSSCLVELIEYPFLVVSLSEIEIVNLERV
S.p._Spt16     782 QLDREFKSFAEKIAEA------SEGRIELDIPFRELAENGVEFRSNVLLQPTTDCLVQITDTPFTVITLNEIEIAHLERV
S.c._Spt16     803 ALDKEFKYFADALAEA------SNGLLTVENTFRDLGFQGVFNRSAVFCMPTTDCLVQLIEPPFLVINLEEVEICILERV
C.e._SPT16     775 RLNAAFNSFCEKVSRL------TNDQFEFDSPFAGLGFFGVFYRSATTLKPTASCLVNLTEWPFFIVTLSEVELVHFERV
D.m._Dre4      781 KLKTAFKSFCEKVETM------TKSVVFEFDTFRELGFPGAEFRSTVTLQPTSGSLVNLTEWPPFVTLDDVELVHFERV
H.s._SPT16H    775 KLKTAFKNFIEKVEAL------TKEELEFEVPFRDLGFNGAEYRSTCLLQPTSSALVNATEWPPFVVTLDEVELIHFERV
M.m._Supt16    775 KLKTAFKNFIEKVEAL------TKEELEFEVPFRDLGFNGAEYRSTCLLQPTSSALVNATEWPPFVVTLDEVELIHFERV
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Spt16M_Rtt106

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P.t._SPT16-1   836 QEETISFDLVAVLKDLEAQVIRIEAIDREDLKKIQQWLNKKKILFFQTTSGLMWRNMQFSIQKDFPLFVYDGGWATVMKD
T.t._SPT16     841 IGRLKNFDIVFIFKDYEKQVTRIASIPIDKAEIVKNWLNSQNILYFESTKSFSWANIIKTIRQDIGGFIEDGGWNIILG-
P.t._SPT16-2c  817 IPGIKSFDLVFVFKNYDRQVLRIESIDIKDLEGVKNWLDRMNLLFFEVAQNLVWKNVLAQIQKDIPGFVQDGGWTNILAE
P.t._SPT16-2a  823 IPGIKSFDLVFVFKNYDKQVLRIESIDIKDLEGVKNWLDRMNLLFFEVGQNLVWKNVLGQIQKDIPGFVQDGGWTNILAE
P.t._SPT16-2b  823 IPGIKSFDLVFVFKNYDKQVLRIESIDIKDLEGVKNWLDRMNLLFFEVGQNLVWKNVLGQIQKDIPGFVQDGGWTNILAE
A.t._SPT16     876 GFGQKNFDMAIIFKDFKKDVLRVDSVPTSSLEGIKEWLDTTDIKYYESKLNLNWRQILKTITDDPQSFIDDGGWEFLNLD
S.p._Spt16     856 QFGLKNFDIVFLFQDFRRPPTHINLIPMEQLDNVKEWLDSCDICFYEGPLNLNWTTIMKTVNEDPIAFFEGGWGFIGAP
S.c._Spt16     877 QFGLKNFDMVFVYKDFNKPVTHINTVPIESLDFLKQWLTDMDIPYTVSTINLNWATIMKSLQDDPYQFFLDGGWNFLATG
C.e._SPT16     849 SLQLKNFDMVFIFKDYKIKPQMVAQIPMSSIDKIKEWLHTCDIWYSEGIQSLNWAKVMKTITDDLEAFFEEGGWSFINVE
D.m._Dre4      855 QFHLRNFDMIFVFKEYNKKVAMVNAIPMNMLDHVKEWLNSCDIRYSEGVQSLNWQKIMKTITDDPEGFFEQGGWTFLDPE
H.s._SPT16H    849 QFHLKNFDMVIIVKDYSKKVTMINAIPVASLDPIKEWLNSCDIKYTEGVQSLNWTKIMKTIVDDPEGFFEQGGWSFLEPE
M.m._Supt16    849 QFHLKNFDMVIVVKDYSKKVTMINAIPVASLDPIKEWLNSCDIKYTEGVQSLNWTKIMKTIVDDPEGFFEQGGWSFLEPE
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                         **     *   Spt16C_MBD
P.t._SPT16-1   916 HM--EHAPIQQFNDEP--LFEEDSSNGPTSVSEFEFEQDKKNNKYLHLQKDDESLFSDLVESE--LIMSELDIQERRKRK
T.t._SPT16     920 ----EDEGEDEDPDEGDEDFSVEQDE-------EEEESEEISESDEDFDDEESASDFEGDEDLSEEGQSWSDLEENARK
P.t._SPT16-2c  897 SE--EEEGDEDDPEAGDSEFSPEQSEE-------DGDDDSDFTEDDDDGDDEDDDGGSDDDDL-SEVLDLNNISEQDDD
P.t._SPT16-2a  903 SE--EEGDEEDDPEAGDSEFSPGESGD-------DGDDDSDFTEDDEDGDDDGDDDD-DDEDL--STVLDLNKISDQDED
P.t._SPT16-2b  903 SE--EEGDEEDDPEAGDSEFSPGESGD-------DGDDDSDFTEDDEDGDDDDGDDDDDDEDL--STVLDLNKISDQDED
A.t._SPT16     956 GS--DSESGGSEESDK--GYEPSDVEVES-----ESEDEASEESLVESDDDEEDSEQESEE--EKGKTWDELEREATN
S.p._Spt16     936 S---DDEGDDSVEEVS--EYEASDADP-------SDEEEEESEEYSEDASEEDGYSESEVDE--ESGEDWDELERKARQ
S.c._Spt16     957 SD--DEASDESEEEVS--EYEASEDDVSD---ESAFSEDEEGSEVDDDISGDESEDYT-GDES--EEGEDWDELEKKAAR
C.e._SPT16     929 SD--NEEAMDDSDDDSD--AYDEEELASAGSGS-ESPDEDSEGE---ETESDDDDEGSLDSDE--SECKDWSDLEPEAAN
D.m._Dre4      935 SG--SEGENETAESEEDEAYNPTDAE--------SDEESDEDSEYSEASEDSEESDEDLGSDE--ESGKDWSDLEREAAE
H.s._SPT16H    929 GEGSDAEEGDSESEIEDETFNPSEDDY-------EEEEDSDEDYSSEAEESDYSKESLGSSE--ESGKDWDELEEEARK
M.m._Supt16    929 GEGSDAEDGDSESEIEDETFNPSEDDY-------EEEEDSDEDYSSEAEESDYSKESLGSSE--ESGKDWDELEEEARK
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P.t._SPT16-1    990 K--VKYNE------------ID------------------------------------------------------------
T.t._SPT16      988 EEERR-------------------------KQQQVKPTKPV--------------PQKRR---------------
P.t._SPT16-2c   967 DD-DESDS-------------DKPRHKNKSKPQSKPQPKPQQKETSVKPTQ----QQKRPPPRK---------------
P.t._SPT16-2a   971 DEDEDSDS-------------DKNRRKANSRPQQKPQHKPQNKPQGKPQQS-VQPHRSNQPQKRQPP-------------
P.t._SPT16-2b   972 DEDEDSDS-------------DKHKRKANSRPQQKPQHKPQNKPQQHKPQQSGPPPRSNQPQKRQPPRK-----------
A.t._SPT16     1025 AD-REHGV-------------ESDSEEERKRR--KMKAFGKSPEGTSGGGG-SSSMKNMPESKRKHR-------------
S.p._Spt16     1002 EDAKHDAE-------------EE------------------------------------------RPSKKRHP-------------
S.c._Spt16     1027 AD-RGANE-------------RD----------------------------------------------
C.e._SPT16      999 AD-KRREV-------------EE-----------PSRDRDRKRPHSSKSG----------PSHKRRK-------------
D.m._Dre4      1003 ED-RNHDYAADDKPRNGKFDSKKHGKSSKHSPSKSSKDKYNSPDKHHSSSSSGNKSSSKDKDRKRSPDDSRDNGHKSKKS
H.s._SPT16H    1000 AD-RESRY------------EEEEEQSR-----SMSRKRKASVHSSGRGSNRGSRHSSAPKKKRK-------------
M.m._Supt16    1000 AD-RESRY------------EEEEEQSR-----SMSRKRKASVHSSGRGSNRGSRHSSAPKKKRK-------------
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P.t._SPT16-1        --
T.t._SPT16          --
P.t._SPT16-2c       --
P.t._SPT16-2a       --
P.t._SPT16-2b       --
A.t._SPT16          --
S.p._Spt16          --
S.c._Spt16          --
C.e._SPT16          --
D.m._Dre4      1082 RH
H.s._SPT16H         --
M.m._Supt16         --
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