

Lanatina.XP_013417278.1_proteasome_subunit_alpha_t -----MSRGSSAGFDRHITIFSPGRLYQVEYAFKAINQGGLTSVSVRGKDSAVVVTKQKVPDKLLDASTVTHLY
Dmelanogaster.Prosalapha7_proteasome_alpha7_subunit -----MSTIGTGYDLASQFSPDGRVFDIDYASKAVEKSG-TVIGIRGKDAVVLAWEKIITSKLYEPDAGGRIF
Egranulosus.XP_024352159.1_Proteasome_subunit_alph -----MSSIGTGYDLASQFSPGEGVFQIEYAYKAVENSQ-TAVALKGKDGVVFAVENIVLSKLYEPGCVKRIF
Avaga.UJR15799.1_hypothetical_protein_I4U23_002731 -----MSSIGSGYDLASQFSPDGRVFQVEYANKAVEASG-TIVALRCKDGVAFVIEKIVTSRLYESGSSKKRIH
Avaga.UJR30804.1_hypothetical_protein_I4U23_018322 -----MSSIGSGYDLASQFSPDGRVFQVEYANKAVEASG-TVVALRCKDGVAFVIEKIVTSRLYESGSSKKRIH
Cintestinalis.LOC100177476_proteasome_subunit_alph -----MSSIGTGYDLASQAQFSPDGRVFQVEYAKAVENSQ-TAIGIRCRDGVVLAWEKLIITSKLHEDLSNQIRIF
Aplanci.LOC110982874_proteasome_subunit_alpha_type -----MSSIGTGYDLASQFSPDGRVFQVEYAKAVENSQ-TVIGLRCKDGVVFGVEKLVITSKLYETGNSKRIF
Bbelcheri.LOC109471095_proteasome_subunit_alpha_ty -----MSSIGTGYDLASQFSPDGRVFQVEYANKAVENSQ-TAVGIRGKDGVVFAVEKLVQSKLYEAGANKRIF
Hsapies.NP_002779.1_proteasome_subunit_alpha_type -----MSSIGTGYDLASSTFSPDGRVFQVEYAMKAVENSQ-TAIGIRCKDGVVFGVEKLVLSKLYEEGNSKRIF
Lanatina.XP_013384393.1_proteasome_subunit_alpha_t -----MSSIGTGYDLASQFSPDGRVFQVEYAKAVENSQ-TAVAIRGKDGVVFAVEKIVASKLYEKGRANKRIV
Myessoensis.XP_021370576.1_proteasome_subunit_alph -----MSSIGTGYDLASQAQFSPDGRVFQVEYALKAVENSQ-TAVGVRGRDGVVFGVEKLVITSKLYEAGANKRIF
Cintestinalis.LOC100176195_proteasome_subunit_alph MISQPFVIIITYLPILYLTQNSFFLLSYINVMFMTRESEYDRGVNTFSPEGRLFQVEYAEIAIKLGS-TAIGIQTAGDGVVLAWEKRTISPLIEASSIEKVF
Bbelcheri.LOC109486945_proteasome_subunit_alpha_ty -----MFLTRSEYDRGVNTFSPEGRLFQVEYAEIAIKLGS-TAIGIQTAGDGVVLAWEKRTISPLMVSTSVEKIV
Aplanci.LOC110982065_proteasome_subunit_alpha_type -----MFQTRSEYDRGVNTFSPEGRLFQVEYAEIAIKLGS-TALGIQTSSEGVCLAVEKRVTSPLMESTSIEKIV
Hsapies.NP_002781.2_proteasome_subunit_alpha_type -----MFLTRSEYDRGVNTFSPEGRLFQVEYAEIAIKLGS-TAIGIQTSSEGVCLAVEKRTISPLMEPSSIEKIV
Lanatina.XP_013415237.1_proteasome_subunit_alpha_t -----MFLTRSEYDRGVNTFSPEGRIFQVEYAEIAIKLGS-TAIGIQTSSEGVVLAWEKRVTSPLIEPSSIEKIV
Myessoensis.XP_021360390.1_Proteasome_subunit_alph -----MFLTRSEYDRGVNTFSPEGRLFQVEYAEIAIKLGS-TAIGIQTSSEGVVLAWEKRVTSPLIEATASIEKVM
Egranulosus.XP_024351634.1_Proteasome_subunit_alph -----MTARVDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVKADCVVLCVEKKAHTKLQNDRTVHKIS
Dmelanogaster.Prosalapha4_proteasome_alpha4_subunit -----MSSRYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGKNDIVVLGVEKKAIVAKLQDERTVRKIC
Avaga.UJR13309.1_hypothetical_protein_I4U23_000327 -----MAGEYDITAITVFSPDGRLFQVEYAEIAIKLGS-TAVGVRGKNDIVVLGVEKKAIVAKLQDERTVRKIC
Avaga.UJR34060.1_hypothetical_protein_I4U23_021471 -----MAGEYDITAITVFSPDGRLFQVEYAEIAIKLGS-TAVGVRGKNDIVVLGVEKKAIVAKLQDERTVRKIC
Cintestinalis.LOC100176760_proteasome_subunit_alph -----MSSRYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGKNDIVVLGVEKKAIVAKLQDERTVRKIC
Bbelcheri.LOC109473572_proteasome_subunit_alpha_ty -----MSSRYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGKNDIVVLGVEKKAIVAKLQDERTVRKIC
Lanatina.XP_013389043.1_proteasome_subunit_alpha_t -----MSSYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGNDIVVLGVEKKAIVAKLQDERTVRKIA
Myessoensis.XP_021354253.1_proteasome_subunit_alph -----MSSRYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGNDIVVLGVEKKAIVAKLQDERTVRKIA
Aplanci.LOC110989014_proteasome_subunit_alpha_type -----MSSRYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGNDIVVLGVEKKAIVAKLQDERTVRKIC
Hsapies.NP_002783.1_proteasome_subunit_alpha_type -----MSYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGVRGNDIVVLGVEKKAIVAKLQDERTVRKIC
Hsapies.NP_001020267.1_proteasome_subunit_alpha-t -----MASRYDRAITVFSPDGHLFQVEYAEIAIKLGS-TAVGIRGTINIVVLGVEKKAIVAKLQDERTVRKIC
0â 20â 40â 60â 80â
Lanatina.XP_013417278.1_proteasome_subunit_alpha_t QLTENIGCVMTGMVADSRSQVQRARYEAAWNRKYGYEIPVDMCLKRIADINQVYTSQAGV-----RPLGCTMILGYDDENGPIQYKTPDAGYCYGYKA
Dmelanogaster.Prosalapha7_proteasome_alpha7_subunit TIEKNIGMAVAGLVADGNFVADIAEQEAAHYRQFQEQAIPLKHLCHRVAGVYHAYTLYSAV-----RPFGLSIIILASWDEVEGPQLYKIEPSGGSFGYFA
Egranulosus.XP_024352159.1_Proteasome_subunit_alph SIDEHIGMVVAGLHSDTKALVEIARNECTSYRENFSGSPIPVKSLCERISIMMHAYTLYSAI-----RPFGLSIIILGSYE-KDGPHLVIEPSGMYAYEG
Avaga.UJR15799.1_hypothetical_protein_I4U23_002731 NVDKHIGMAVAGLLADARQLLSVARDEAKKYKYDGVSPVKYLAADRLAMYHAYTLYGFV-----RPFQCGIILAAEY-SDGAGLYGVESPGVYTNFYG
Avaga.UJR30804.1_hypothetical_protein_I4U23_018322 NVDKHIGMAVAGLLADARQLLSVARDEAKKYKYDGVSPVKYLAADRLAMYHAYTLYGFV-----RPFQCGIILAAEY-SDGAGLYGVESPGVYTNFYG
Cintestinalis.LOC100177476_proteasome_subunit_alph NIDKHVGMVAGLLADAREIVDIARNEASNYRQYQCGPIPLKHLTERVAMYHAYTLYSSV-----RPFGLSIIILASYL-SDGAGMYMIDPSGVLGYNG
Aplanci.LOC110982874_proteasome_subunit_alpha_type NADRHVGMVAGLLADARQLVETARDEASEYRSAGYGPILPKYLAERVAMYHAYTLYSAV-----RPFQCGSIVLGSYE-EKTPQLVIMIDPSGVTGYHG
Bbelcheri.LOC109471095_proteasome_subunit_alpha_ty NIDRHIGMAVAGLLADARQISEIARDEASNFYRNGGAIPCKNLSDRVAMYHAYTLYSHV-----RPFQCGSIVLGSYEDKDDGPOLYMMIDPSGVHMGYHG
Hsapies.NP_002779.1_proteasome_subunit_alpha_type NVDRHVGMVAGLLADARSLADIAREEASNFYSRNGGNIPLKHLADRVAMYHAYTLYSAV-----RPFQCGSIVLGSYEDKDDGPOLYMMIDPSGVSYGYWG
Lanatina.XP_013384393.1_proteasome_subunit_alpha_t NIDSHVGMVAGLLADARNIVEEGREEASYSRNFSGPIPLKMLADRVAGVYHAHTLTSSV-----RPFQCGSIVLGSYE-EGGQPLVILIDPSGVTGYHG
Myessoensis.XP_021370576.1_proteasome_subunit_alph NVDPQHIGMAVAGLLADARQVVFETAREECSNRYRNYGSGPIPKHMTDRVSLYVHAHTLTSSV-----RPFQGSALIVGSYEDGDPQMYMIDPSGVSYGYHG
Cintestinalis.LOC100176195_proteasome_subunit_alph EIDTHVGCAMSGLIADSKMTIDRARVEAQNHWFITFEKMRVQSITKAVSNLALQFGEEDSEPGAMSRPFGVALLFAGID-EKGPQLFHMDSPTGTVQYDA
Bbelcheri.LOC109486945_proteasome_subunit_alpha_ty EIDSHIGCAMSGLIADSRMTIDRARVEAQNHWFITFEKMSIEATVQAVCNLAMOFGDEEDDASGAMSRPFGVALLFAGMD-EKGPQLFHMDSPTGTVQYDA
Aplanci.LOC110982065_proteasome_subunit_alpha_type EIDAHIGCAMSGLIADAKTLIDKARVEITQNHWFITFEKMSIEATVQAVCNLAMOFGDEEDDASGAMSRPFGVALLFAGMD-EKGPQLFHMDSPTGTVQYDA
Hsapies.NP_002781.2_proteasome_subunit_alpha_type EIDHHIGCAMSGLIADSKMTIDRARVEAQNHWFITFEKMSIEATVQAVCNLALAFGEEDDASGAMSRPFGVALLFAGID-DKGPQLFHMDSPTGTVQYDA
Lanatina.XP_013415237.1_proteasome_subunit_alpha_t EVDHIGCAMSGLIADSRITIDKARVEAQNHWFITFEKMSIEATVQAVCNLALQFGEEDDASGAMSRPFGVALLFAGID-HKGPQLFHMDSPTGTVQYDA
Myessoensis.XP_021360390.1_proteasome_subunit_alph LLDHEIAVAFAGLTADARILIDMRICECKSYRLTVEDEPVSEYIARHMAQLKQKYTSQNGR-----RPFQGSIIILCGVNDQGSSTHLYQTDPSGTTHYHWA
Dmelanogaster.Prosalapha4_proteasome_alpha4_subunit MLDNHVMAFAGLTADARIMNRAQVEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Avaga.UJR13309.1_hypothetical_protein_I4U23_000327 VLDHVMAMFAGLTADARILMHRARIEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Cintestinalis.LOC100176760_proteasome_subunit_alph VLDHVMAMFAGLTADARILMHRARIEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Bbelcheri.LOC109473572_proteasome_subunit_alpha_ty LDDHVMAMFAGLTADARILINRARVEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Lanatina.XP_013389043.1_proteasome_subunit_alpha_t LDDHVMAMFAGLTADARILINRARVEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Myessoensis.XP_021354253.1_proteasome_subunit_alph LIDDHVALFAGLTADARILINRARTEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Aplanci.LOC110989014_proteasome_subunit_alpha_type LIDDHVMAMFAGLTADARILINRARTEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Hsapies.NP_002783.1_proteasome_subunit_alpha_type ALDNDVCMAMFAGLTADARIVINRARVEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
Hsapies.NP_001020267.1_proteasome_subunit_alpha-t ALDDHVMAMFAGLTADARIVINRARVEQCQSHRLNVDEPVTLEYITRFIAQLKQKYTSQNGR-----RPFGLSIIILGFGDADGSAHLEFQTEPSGIFYEYKA
100â 120â 140â 160â 180â
Lanatina.XP_013417278.1_proteasome_subunit_alpha_t TAAGAKQLEANSFLEKIKKK-----QDFDFNETVEMAITCLSTILSIDFKPSEIEVGVDV-----EHPK-----FRVLTEEIEDRHLVRIAEK-----
Dmelanogaster.Prosalapha7_proteasome_alpha7_subunit CASGKAKQLAKTMEKKLKM-D-----RTDELVESAGEIIVKVHDE-LKDKDFRFEMGLV-----GRVTGGLHLINPSELTEKARKAGDAANKDEDSDN
Egranulosus.XP_024352159.1_Proteasome_subunit_alph CAIGKARQAKTEIEKLIKGD-----M-NIQOLIKEAAKVIYTVHDE-IDKNFELDLSWV-----GAKTDSRHQVPPPEVHQEADYAKASLSEESGDL
Avaga.UJR15799.1_hypothetical_protein_I4U23_002731 IAVGKAQQTAKTEIEKLIKLT-----L-KLEDGIEKAAKIIYQVHDE-VKDRMFELELSWV-----GQVNDGKHQVPTDVFEDAEDYAKASLSEESGDL
Avaga.UJR30804.1_hypothetical_protein_I4U23_018322 IAVGKAQQTAKTEIEKLIKLT-----L-SLEDGIEKAAKIIYQVHDE-VKDRMFELELSWV-----GQINDGKHQVPTDVFETAESYAKASLSEESGDL
Cintestinalis.LOC100177476_proteasome_subunit_alph CAMGKARQAKTEIEKLIKLE-----L-SCREALNEAAKIIYVHDE-VKDKAFQQLLSWV-----CAESGGVHQRVPTDVFETAESYAKASLSEESGDL
Aplanci.LOC110982874_proteasome_subunit_alpha_type CAIGKARQAKTEIEKLIKLT-----L-SCREALNEAAKIIYVHDE-VKDKAFQQLLSWV-----CAESGGVHQRVPTDVFETAESYAKASLSEESGDL
Bbelcheri.LOC109471095_proteasome_subunit_alpha_ty CAIGKARQAKTEIEKLIKMT-----Q-SCRDILVEKAAKIIYVHDE-VKDKAFQQLLSWV-----GQVNDGKHQVPTDVFETAESYAKASLSEESGDL
Hsapies.NP_002779.1_proteasome_subunit_alpha_type CAIGKARQAKTEIEKLIKMT-----M-TCRDILVEKAAKIIYVHDE-VKDKAFQQLLSWV-----GQVNDGKHQVPTDVFETAESYAKASLSEESGDL
Lanatina.XP_013384393.1_proteasome_subunit_alpha_t CAIGKARQAKTEIEKLIKMT-----M-TCREILKEAAKIIYVHDE-VKDKAFQQLLSWV-----GQVNDGKHQVPTDVFETAESYAKASLSEESGDL
Myessoensis.XP_021370576.1_proteasome_subunit_alph CAIGKARQAKTEIEKLIKMT-----M-PCRDILVEKAAKIIYVHDE-VKDKAFQQLLSWV-----GQVNDGKHQVPTDVFETAESYAKASLSEESGDL
Cintestinalis.LOC100176195_proteasome_subunit_alph KAIGSASEGAQTSLEQPHKS-----M-TIEEAQKSLITILKQVMEKLTSTNVAVATVTK-----EQKE-----HMFSSKEEIEAIAKDL-----
Bbelcheri.LOC109486945_proteasome_subunit_alpha_ty KAIGSGSEGAQSSLQEVYHKS-----M-TLKEALKSALTILKQVMEKLTSTNVAVATVTK-----EKRF-----HMFSSKEEIEVVKDL-----
Aplanci.LOC110982065_proteasome_subunit_alpha_type KAIGSGSEGAQSSLQETVHKS-----M-TLKEACKALVILKQVMEKLTSTNVAVATVTK-----EKRF-----HMFSSKEEIEAIAEM-----
Hsapies.NP_002781.2_proteasome_subunit_alpha_type RAIGSASEGAQSSLQEVYHKS-----M-TLKEAIIKSSLIILKQVMEKLTSTNVAVATVTK-----GQNL-----HMFSSKEEIEVVKDL-----
Lanatina.XP_013415237.1_proteasome_subunit_alpha_t KAIGSASEGAQSSLQEVYHKS-----M-TLKEACKNALTILKQVMEKLTSTNVAVATVTK-----AAGT-----KLFSSKEEIEVVKDL-----
Myessoensis.XP_021360390.1_proteasome_subunit_alph KAIGSGSEGAQSSLQEVYHKS-----M-TLKEACKNALTILKQVMEKLTSTNVAVATVTK-----AAGT-----KLFSSKEEIEVVKDL-----
Dmelanogaster.Prosalapha4_proteasome_alpha4_subunit NAIGKNSKAAREFLEKNIYSE-----AVTTQEAITKLAVKALFVQVQ-----GAKHMEIGVMRRSDYKPEP-IAEWKMLTIEIEEYVKAIEREREETEKKK
Avaga.UJR13309.1_hypothetical_protein_I4U23_000327 NATGRSAKVREFLEKNIYSE-----EVANEHGAVKLAIRALLEVAQS-----GQNNLEVAIMEN-----GKPL-----KMLDDTVDITVYKIEKEKEELEKKK
Cintestinalis.LOC100176760_proteasome_subunit_alph NAIGRQAKTVREYLEKAYTET-----IYESTHESIKLCIRALLEVQVS-----GSKNVEIAYMIR-----HKPL-----KTLASAEVEKYIAEIDKNEIEAEKKK
Bbelcheri.LOC109473572_proteasome_subunit_alpha_ty NAIGRSKTVREYLEKAYTET-----LADSDAEICIKLAKALLEVQVS-----GSKNVEIAYMIR-----DEPL-----KMLSVEEIEKIMAEVEKEKEEAEKKK
Lanatina.XP_013389043.1_proteasome_subunit_alpha_t NAIGRSKTVREYLEKAYTET-----LADSDAEICIKLAKALLEVQVS-----GSKNVEIAYMIR-----DEPL-----KMLSVEEIEKIMAEVEKEKEEAEKKK
Myessoensis.XP_021354253.1_proteasome_subunit_alph NAIGRSKTVREYLEKAYTET-----LADSDAEICIKLAKALLEVQVS-----GSKNVEIAYMIR-----DEPL-----KMLSVEEIEKIMAEVEKEKEEAEKKK
Aplanci.LOC110989014_proteasome_subunit_alpha_type NAIGRSKTVREYLEKAYTET-----LADSDAEICIKLAKALLEVQVS-----GSKNVEIAYMIR-----DEPL-----KMLSVEEIEKIMAEVEKEKEEAEKKK
Hsapies.NP_002783.1_proteasome_subunit_alpha_type NAIGRSKTVREYLEKAYTET-----LADSDAEICIKLAKALLEVQVS-----GSKNVEIAYMIR-----DEPL-----KMLSVEEIEKIMAEVEKEKEEAEKKK
Hsapies.NP_001020267.1_proteasome_subunit_alpha-t NAIGRSKTVREYLEKAYTET-----LADSDAEICIKLAKALLEVQVS-----GSKNVEIAYMIR-----DEPL-----KMLSVEEIEKIMAEVEKEKEEAEKKK
200â 220â 240â 260â 280â
Lanatina.XP_013417278.1_proteasome_subunit_alpha_t -----ETH-----
Dmelanogaster.Prosalapha7_proteasome_alpha7_subunit -----ETH-----
Egranulosus.XP_024352159.1_Proteasome_subunit_alph -----EIGML-----
Avaga.UJR15799.1_hypothetical_protein_I4U23_002731 -----DEM-----
Avaga.UJR30804.1_hypothetical_protein_I4U23_018322 -----DEM-----
Cintestinalis.LOC100177476_proteasome_subunit_alph -----E-----
Aplanci.LOC110982874_proteasome_subunit_alpha_type -----DEDI-----
Bbelcheri.LOC109471095_proteasome_subunit_alpha_ty -----EDDL-----
Hsapies.NP_002779.1_proteasome_subunit_alpha_type -----DNM-----
Lanatina.XP_013384393.1_proteasome_subunit_alpha_t -----DEDM-----
Myessoensis.XP_021370576.1_proteasome_subunit_alph -----EDL-----
Cintestinalis.LOC100176195_proteasome_subunit_alph -----EDL-----

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Bbelcheri.LOC109486945_proteasome_subunit_alpha_ty -----
Aplanci.LOC110982065_proteasome_subunit_alpha_type -----
Hsapiens.NP_002781.2_proteasome_subunit_alpha_type -----
Lanatina.XP_013415237.1_proteasome_subunit_alpha_t -----
Myessoensis.XP_021360390.1_proteasome_subunit_alph -----
Egranulosus.XP_024351634.1_Proteasome_subunit_alph QKKEASAGSSF-----
Dmelanogaster.Prosalpha4_proteasome_alpha4_subunit QKK-----
Avaga.UJR13309.1_hypothetical_protein_I4U23_000327 QAKQIGGGSTTTTALTQTSRKD
Avaga.UJR34060.1_hypothetical_protein_I4U23_021471 QAKQIGGATTAPSLTTQTSKKE
Cintestinalis.LOC100176760_proteasome_subunit_alph KMKKSS-----
Bbelcheri.LOC109473572_proteasome_subunit_alpha_ty KSKTSS-----
Lanatina.XP_013389043.1_proteasome_subunit_alpha_t QKSGK-----
Myessoensis.XP_021354253.1_proteasome_subunit_alph QKK-----
Aplanci.LOC110989014_proteasome_subunit_alpha_type QKKTGQTS-----
Hsapiens.NP_002783.1_proteasome_subunit_alpha_type QKKAS-----
Hsapiens.NP_001020267.1_proteasome_subunit_alpha-t SKKSV-----
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Number of sequences: 28
Alignment width: 323
Sequence type: aa

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