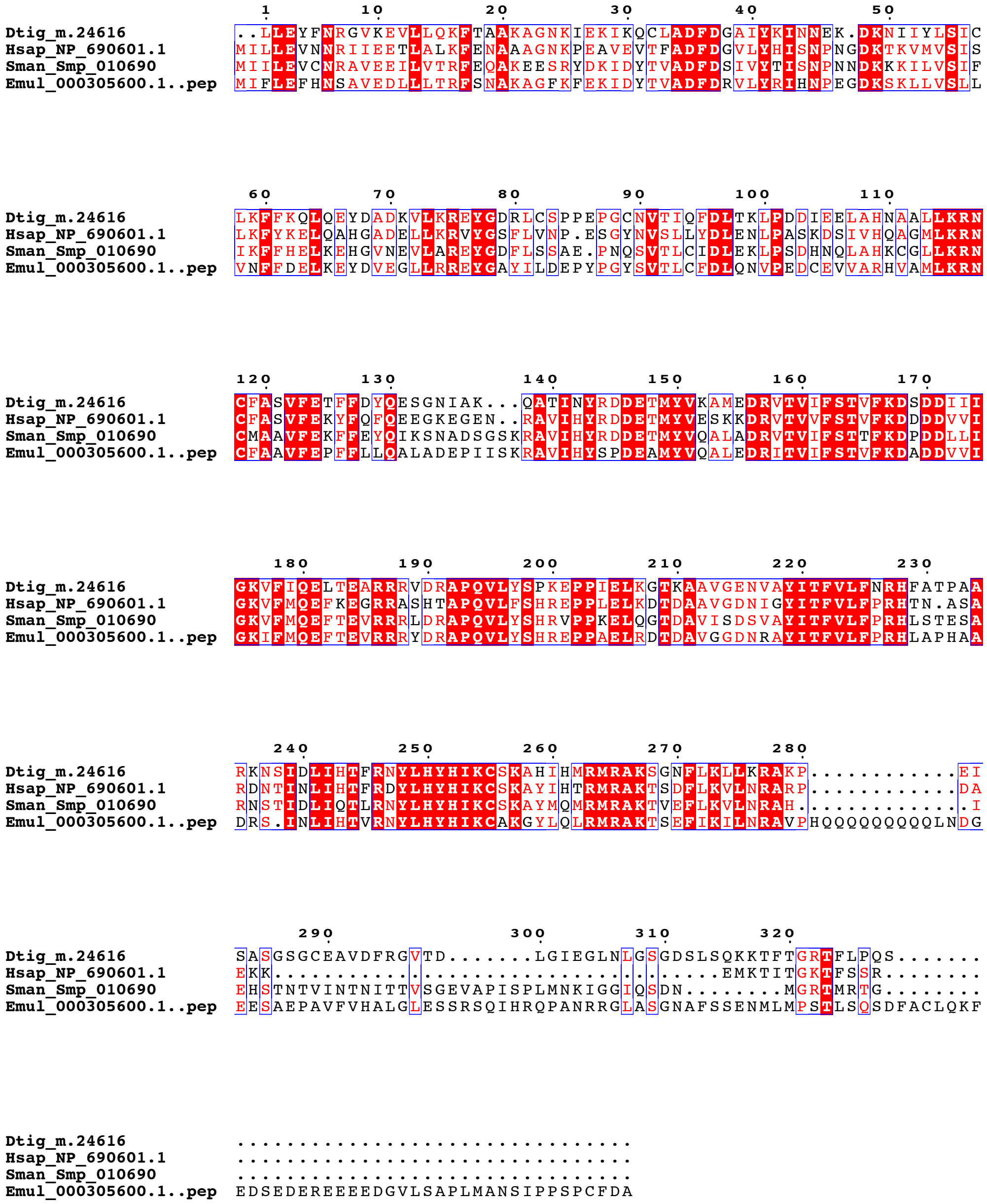

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                        .        .         .         .         .          .
Dtig_m.24616          ..LLEYFNRGVKEVLLQKFTAAKAGNKIEKIKQCLADFDGAIYKINNEK.DKNIIYLSIC
Hsap_NP_690601.1      MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSIS
Sman_Smp_010690       MIILEVCNRAVEEILVTRFEQAKEESRYDKIDYTVADFDSIVYTISNPNNDKKKILVSIF
Emul_000305600.1..pep MIFLEFHNSAVEDLLLTRFSNAKAGFKFEKIDYTVADFDRVLYRIHNPEGDKSKLLVSLL

                       60        70        80        90        100       110
                        .         .         .         .         .         .
Dtig_m.24616          LKFFKQLQEYDADKVLKREYGDRLCSPPEPGCNVTIQFDLTKLPDDIEELAHNAALLKRN
Hsap_NP_690601.1      LKFYKELQAHGADELLKRVYGSFLVNP.ESGYNVSLLYDLENLPASKDSIVHQAGMLKRN
Sman_Smp_010690       IKFFHELKEHGVNEVLAREYGDFLSSAE.PNQSVTLCIDLEKLPSDHNQLAHKCGLLKRN
Emul_000305600.1..pep VNFFDELKEYDVEGLLRREYGAYILDEPYPGYSVTLCFDLQNVPEDCEVVARHVAMLKRN

                       120       130          140       150       160       170
                        .         .            .         .         .         .
Dtig_m.24616          CFASVFETFFDYQESGNIAK...QATINYRDDETMYVKAMEDRVTVIFSTVFKDSDDIII
Hsap_NP_690601.1      CFASVFEKYFQFQEEGKEGEN..RAVIHYRDDETMYVESKKDRVTVVFSTVFKDDDDVVI
Sman_Smp_010690       CMAAVFEKFFEYQIKSNADSGSKRAVIHYRDDETMYVQALADRVTVIFSTTFKDPDDLLI
Emul_000305600.1..pep CFAAVFEPFFLLQALADEPIISKRAVIHYSPDEAMYVQALEDRITVIFSTVFKDADDVVI

                          180       190       200       210       220       230
                           .         .         .         .         .         .
Dtig_m.24616          GKVFIQELTEARRRVDRAPQVLYSPKEPPIELKGTKAAVGENVAYITFVLFNRHFATPAA
Hsap_NP_690601.1      GKVFMQEFKEGRRASHTAPQVLFSHREPPLELKDTDAAVGDNIGYITFVLFPRHTN.ASA
Sman_Smp_010690       GKVFMQEFTEVRRRLDRAPQVLYSHRVPPKELQGTDAVISDSVAYITFVLFPRHLSTESA
Emul_000305600.1..pep GKIFMQEFTEVRRRYDRAPQVLYSHREPPAELRDTDAVGGDNRAYITFVLFPRHLAPHAA

                          240       250       260       270       280
                           .         .         .         .         .
Dtig_m.24616          RKNSIDLIHTFRNYLHYHIKCSKAHIHMRMRAKSGNFLKLLKRAKP............EI
Hsap_NP_690601.1      RDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVLNRARP............DA
Sman_Smp_010690       RNSTIDLIQTLRNYLHYHIKCSKAYMQMRMRAKTVEFLKVLNRAH..............I
Emul_000305600.1..pep DRS.INLIHTVRNYLHYHIKCAKGYLQLRMRAKTSEFIKILNRAVPHQQQQQQQQQLNDG

                            290              300       310       320
                             .                .         .         .
Dtig_m.24616          SASGSGCEAVDFRGVTD.......LGIEGLNLGSGDSLSQKKTFTGRTFLPQS.......
Hsap_NP_690601.1      EKK....................................EMKTITGKTFSSR........
Sman_Smp_010690       EHSTNTVINTNITTVSGEVAPISPLMNKIGGIQSDN........MGRTMRTG........
Emul_000305600.1..pep EESAEPAVFVHALGLESSRSQIHRQPANRRGLASGNAFSSENMLMPSTLSQSDFACLQKF

Dtig_m.24616          ................................
Hsap_NP_690601.1      ................................
Sman_Smp_010690       ................................
Emul_000305600.1..pep EDSEDEREEEEDGVLSAPLMANSIPPSPCFDA
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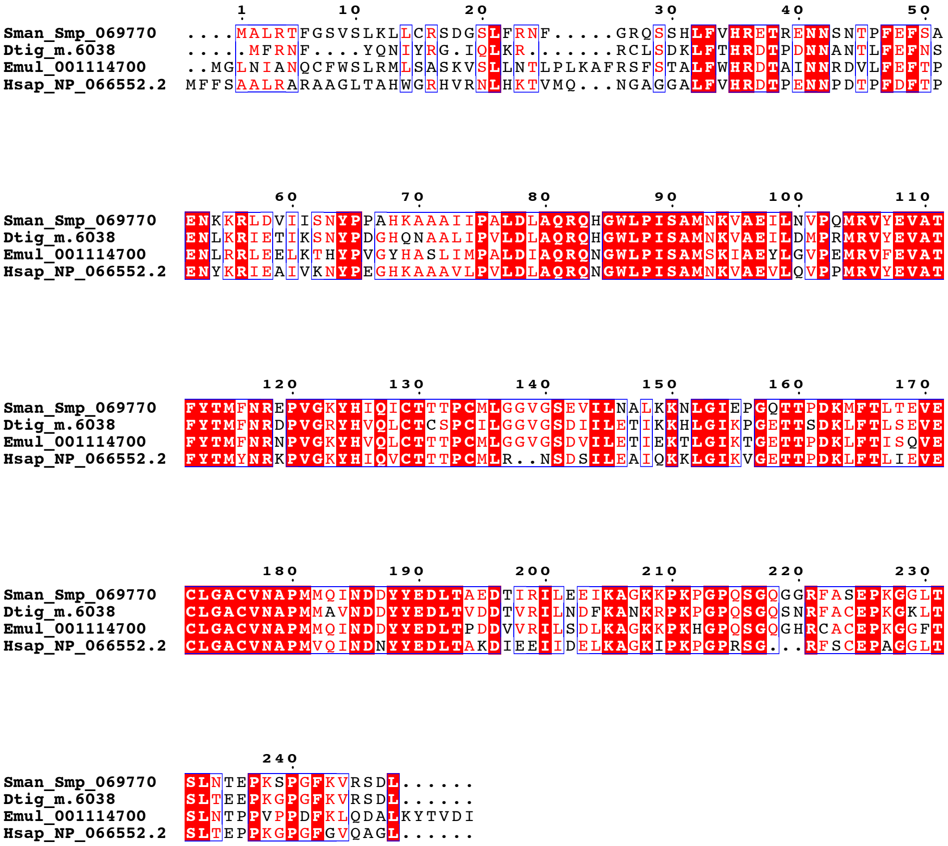

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                      1        10        20             30        40        50
Sman_Smp_069770   ....MALRTFGSVSLKLLCRSDGSLFRNF.....GRQSSHLFVHRETRENNSNTPFEFSA
Dtig_m.6038       .....MFRNF....YQNIYRG.IQLKR.......RCLSDKLFTHRDTPDNNANTLFEFNS
Emul_001114700    ..MGLNIANQCFWSLRMLSASKVSLLNTLPLKAFRSFSTALFWHRDTAINNRDVLFEFTP
Hsap_NP_066552.2  MFFSAALRARAAGLTAHWGRHVRNLHKTVMQ...NGAGGALFVHRDTPENNPDTPFDFTP

                          60        70        80        90       100       110
Sman_Smp_069770   ENKKRLDVIISNYPPAHKAAAIIPALDLAQRQHGWLPISAMNKVAEILNVPQMRVYEVAT
Dtig_m.6038       ENLKRIETIKSNYPDGHQNAALIPVLDLAQRQHGWLPISAMNKVAEILDMPRMRVYEVAT
Emul_001114700    ENLRRLEELKTHYPVGYHASLIMPALDIAQRQNGWLPISAMSKIAEYLGVPEMRVFEVAT
Hsap_NP_066552.2  ENYKRIEAIVKNYPEGHKAAAVLPVLDLAQRQNGWLPISAMNKVAEVLQVPPMRVYEVAT

                         120       130       140       150       160       170
Sman_Smp_069770   FYTMFNREPVGKYHIQICTTTPCMLGGVGSEVILNALKKNLGIEPGQTTPDKMFTLTEVE
Dtig_m.6038       FYTMFNRDPVGRYHVQLCTCSPCILGGVGSDIILETIKKHLGIKPGETTSDKLFTLSEVE
Emul_001114700    FYTMFNRNPVGKYHVQLCTTTPCMLGGVGSDVILETIEKTLGIKTGETTPDKLFTISQVE
Hsap_NP_066552.2  FYTMYNRKPVGKYHIQVCTTTPCMLR..NSDSILEAIQKKLGIKVGETTPDKLFTLIEVE

                         180       190       200       210       220       230
Sman_Smp_069770   CLGACVNAPMMQINDDYYEDLTAEDTIRILEEIKAGKKPKPGPQSGQGGRFASEPKGGLT
Dtig_m.6038       CLGACVNAPMMAVNDDYYEDLTVDDTVRILNDFKANKRPKPGPQSGQSNRFACEPKGKLT
Emul_001114700    CLGACVNAPMMQINDDYYEDLTPDDVVRILSDLKAGKKPKHGPQSGQGHRCACEPKGGFT
Hsap_NP_066552.2  CLGACVNAPMVQINDNYYEDLTAKDIEEIIDELKAGKIPKPGPRSG...RFSCEPAGGLT

                         240
Sman_Smp_069770   SLNTEPKSPGFKVRSDL......
Dtig_m.6038       SLTEEPKGPGFKVRSDL......
Emul_001114700    SLNTPPVPPDFKLQDALKYTVDI
Hsap_NP_066552.2  SLTEPPKGPGFGVQAGL......
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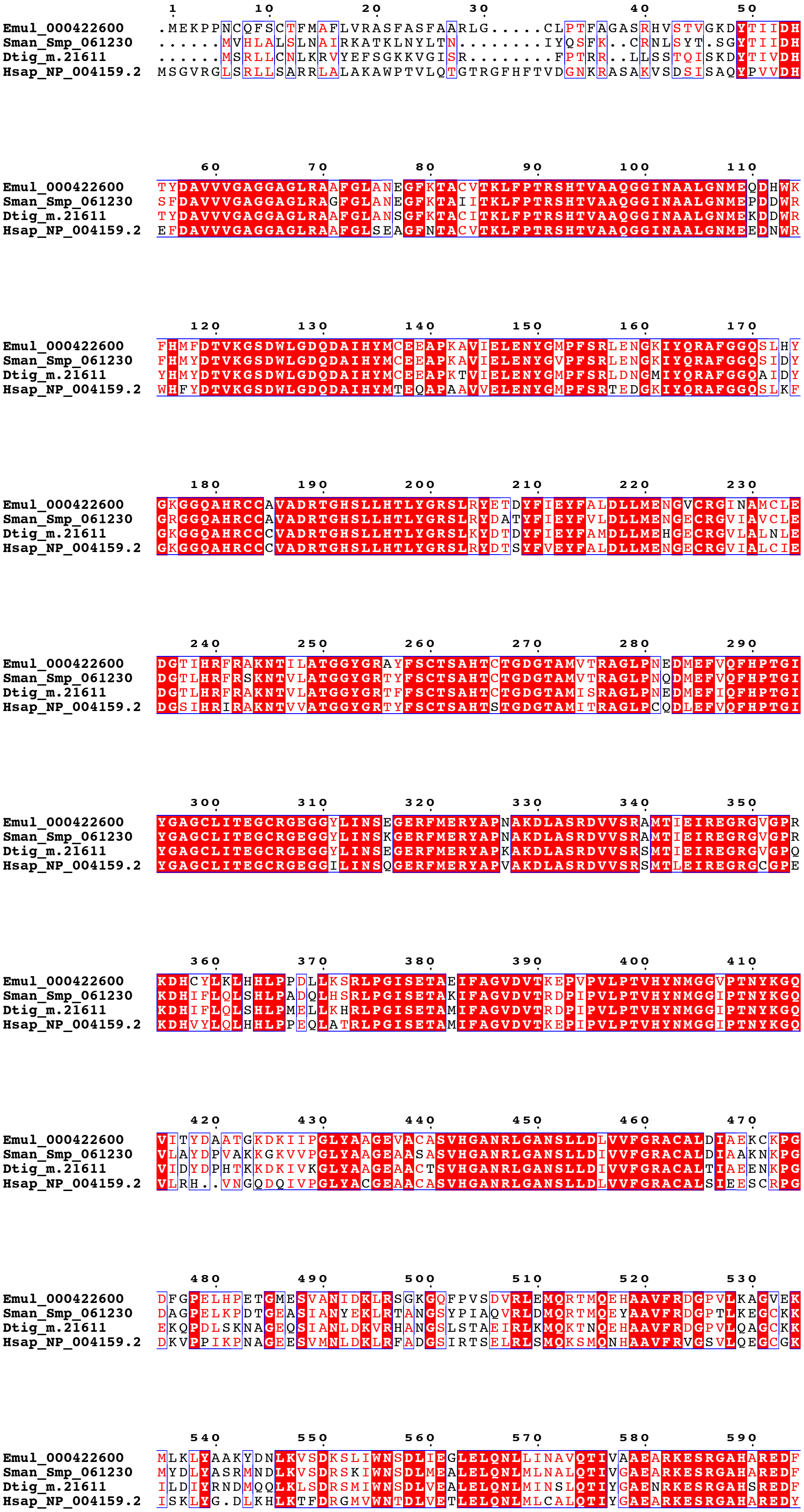

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                     1       10        20        30             40        50
Emul_000422600     .MEKPPNCQFSCTFMAFLVRASFASFAARLG.....CLPTFAGASRHVSTVGKDYTIIDH
Sman_Smp_061230    ......MVHLALSLNAIRKATKLNYLTN........IYQSFK..CRNLSYT.SGYTIIDH
Dtig_m.21611       ......MSRLLCNLKRVYEFSGKKVGISR........FPTRR..LLSSTQISKDYTIVDH
Hsap_NP_004159.2   MSGVRGLSRLLSARRLALAKAWPTVLQTGTRGFHFTVDGNKRASAKVSDSISAQYPVVDH

                       60        70        80        90       100       110
Emul_000422600     TYDAVVVGAGGAGLRAAFGLANEGFKTACVTKLFPTRSHTVAAQGGINAALGNMEQDHWK
Sman_Smp_061230    SFDAVVVGAGGAGLRAGFGLANEGFKTAIITKLFPTRSHTVAAQGGINAALGNMEPDDWR
Dtig_m.21611       TYDAVVVGAGGAGLRAAFGLANSGFKTACITKLFPTRSHTVAAQGGINAALGNMEKDDWR
Hsap_NP_004159.2   EFDAVVVGAGGAGLRAAFGLSEAGFNTACVTKLFPTRSHTVAAQGGINAALGNMEEDNWR

                      120       130       140       150       160       170
Emul_000422600     FHMFDTVKGSDWLGDQDAIHYMCEEAPKAVIELENYGMPFSRLENGKIYQRAFGGQSLHY
Sman_Smp_061230    FHMYDTVKGSDWLGDQDAIHYMCEEAPKAVIELENYGVPFSRLENGKIYQRAFGGQSIDY
Dtig_m.21611       YHMYDTVKGSDWLGDQDAIHYMCEEAPKTVIELENYGMPFSRLDNGMIYQRAFGGQAIDY
Hsap_NP_004159.2   WHFYDTVKGSDWLGDQDAIHYMTEQAPAAVVELENYGMPFSRTEDGKIYQRAFGGQSLKF

                      180       190       200       210       220       230
Emul_000422600     GKGGQAHRCCAVADRTGHSLLHTLYGRSLRYETDYFIEYFALDLLMENGVCRGINAMCLE
Sman_Smp_061230    GRGGQAHRCCAVADRTGHSLLHTLYGRSLRYDATYFIEYFVLDLLMENGECRGVIAVCLE
Dtig_m.21611       GKGGQAHRCCCVADRTGHSLLHTLYGRSLKYDTDYFIEYFAMDLLMEHGECRGVLALNLE
Hsap_NP_004159.2   GKGGQAHRCCCVADRTGHSLLHTLYGRSLRYDTSYFVEYFALDLLMENGECRGVIALCIE

                      240       250       260       270       280       290
Emul_000422600     DGTIHRFRAKNTILATGGYGRAYFSCTSAHTCTGDGTAMVTRAGLPNEDMEFVQFHPTGI
Sman_Smp_061230    DGTLHRFRSKNTVLATGGYGRTYFSCTSAHTCTGDGTAMVTRAGLPNQDMEFVQFHPTGI
Dtig_m.21611       DGTLHRFRAKNTVLATGGYGRTFFSCTSAHTCTGDGTAMISRAGLPNEDMEFIQFHPTGI
Hsap_NP_004159.2   DGSIHRIRAKNTVVATGGYGRTYFSCTSAHTSTGDGTAMITRAGLPCQDLEFVQFHPTGI

                      300       310       320       330       340       350
Emul_000422600     YGAGCLITEGCRGEGGYLINSEGERFMERYAPNAKDLASRDVVSRAMTIEIREGRGVGPR
Sman_Smp_061230    YGAGCLITEGCRGEGGYLINSKGERFMERYAPNAKDLASRDVVSRAMTIEIREGRGVGPR
Dtig_m.21611       YGAGCLITEGCRGEGGYLINSEGERFMERYAPKAKDLASRDVVSRSMTIEIREGRGVGPQ
Hsap_NP_004159.2   YGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPE

                      360       370       380       390       400       410
Emul_000422600     KDHCYLKLHHLPPDLLKSRLPGISETAEIFAGVDVTKEPVPVLPTVHYNMGGVPTNYKGQ
Sman_Smp_061230    KDHIFLQLSHLPADQLHSRLPGISETAKIFAGVDVTRDPIPVLPTVHYNMGGIPTNYKGQ
Dtig_m.21611       KDHIFLQLSHLPMELLKHRLPGISETAMIFAGVDVTRDPIPVLPTVHYNMGGIPTNYKGQ
Hsap_NP_004159.2   KDHVYLQLHHLPPEQLATRLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKGQ

                      420       430       440       450       460       470
Emul_000422600     VITYDAATGKDKIIPGLYAAGEVACASVHGANRLGANSLLDLVVFGRACALDIAEKCKPG
Sman_Smp_061230    VLAYDPVAKKGKVVPGLYAAGEAASASVHGANRLGANSLLDIVVFGRACALDIAAKNKPG
Dtig_m.21611       VIDYDPHTKKDKIVKGLYAAGEAACTSVHGANRLGANSLLDIVVFGRACALTIAEENKPG
Hsap_NP_004159.2   VLRH..VNGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIEESCRPG

                      480       490       500       510       520       530
Emul_000422600     DFGPELHPETGMESVANIDKLRSGKGQFPVSDVRLEMQRTMQEHAAVFRDGPVLKAGVEK
Sman_Smp_061230    DAGPELKPDTGEASIANYEKLRTANGSYPIAQVRLDMQRTMQEYAAVFRDGPTLKEGCKK
Dtig_m.21611       EKQPDLSKNAGEQSIANLDKVRHANGSLSTAEIRLKMQKTNQEHAAVFRDGPVLQAGCKK
Hsap_NP_004159.2   DKVPPIKPNAGEESVMNLDKLRFADGSIRTSELRLSMQKSMQNHAAVFRVGSVLQEGCGK

                      540       550       560       570       580       590
Emul_000422600     MLKLYAAKYDNLKVSDKSLIWNSDLIEGLELQNLLINAVQTIVAAEARKESRGAHAREDF
Sman_Smp_061230    MYDLYASRMNDLKVSDRSKIWNSDLMEALELQNLMLNALQTIVGAEARKESRGAHAREDF
Dtig_m.21611       ILDIYRNDMQQLKLSDRSMIWNSDLVEALELQNLMINSLQTIYGAENRKESRGAHSREDF
Hsap_NP_004159.2   ISKLYG.DLKHLKTFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDY
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                      600       610       620       630       640       650
Emul_000422600       RQRIDEYDYSKPIEGQTKKPMSEHWRKHTMSYQNLKTGAVKLEYRPVIDKTLDQNVCPTV
Sman_Smp_061230      PNRVDELDYSKPIDGQKPKPFEEHWRKHTLSYQDVKTGAVKLEYRPVIDATLDAKSCPSV
Dtig_m.21611         KTRIDEYDYSKTIEGQVQKPMEQHWRKHTLAYQNISTGEVKLVYRPVIDKTLDDSKCHTV
Hsap_NP_004159.2     KVRIDEYDYSKPIQGQQKKPFEEHWRKHTLSYVDVGTGKVTLEYRPVIDKTLNEADCATV
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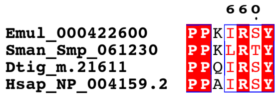

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                      660
Emul_000422600       PPKIRSY
Sman_Smp_061230      PPKLRTY
Dtig_m.21611         PPQIRSY
Hsap_NP_004159.2     PPAIRSY
```