```
                    hlx A                   sB6     hlx B           hlx C
Dre ZGC:77645   MESLSAANTQFSLNLLKKISGGNASGNVFYSPVSISSALAMVSLGAKGNTADQMFKVLGFN
Dre AAQ97848    MESLSAANTQFSLNLFKKISGGNASGNVFYSPVSISSALAMVSLGAKGNTADQMFKVLGFN
Dre ZGC:64178   MEPLSAAHARFCLSLFQKISDGDSSQNVFFSPLSISAALSMLSLGAAGNTKDQMSQTLHFD

Dre CAI20745    MEGVSRANSLFALDLYRALSASSAEGNIFFSPLSISAALSMVYLGARGDTAGEMEKVLCFS
Dre ZGC:91981   MEGVSRANSLFALDLYRALSASSAEGNIFFSPLSISAALSMVYLGARGDTAGEMEKVLSFS

Hsa SERPINB1    MEQLSSANTRFALDLFLALSENNPAGNIFISPFSISSAMAMVFLGTRGNTAAQLSKTFHFN
Hsa SERPINB6    MDVLAEANGTFALNLLKTLGKDNS-KNVFFSPMSMSCALAMVYMGAKGNTAAQMAQILSFN
Hsa SERPINB2    MEDLCVANTLFALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQFN

Dre ZGC:76926   MEPVIAANTKFSLDLLKQLCQKSK-DNVLFSPLSISSALGLVLLGAKGETADQMYKVLQFF
Hsa SERPINB5    MDALQLANSAFAVDLFKQLCEKEPLGNVLFSPICLSTSLSLAQVGAKGDTANEIGQVLHFE
                         o    o   |        o|   oo oo   o     oo   o       o
                23      30      40         50      60      70          80  83

Dre ZGC:77645   NPPKPGGATPTPAQATQKPQITCGVKSQHEPQALQQPQKFELPADLKKCPAQPVPGQKAEE
Dre AAQ97848    ------------------------------------------------------SQAHQPVE
Dre ZGC:64178   ------------------------------------------------------------GAES

Dre CAI20745    ------------------------------------------------------------SVS
Dre ZGC:91981   ------------------------------------------------------------SVS

Hsa SERPINB1    ------------------------------------------------------------TVE
Hsa SERPINB6    ------------------------------------------------------KSGGGG
Hsa SERPINB2    ---------------------EVGANAVTPMTPENFTSCGFMQQIQKGSYPDAILQAQAAD

Dre ZGC:76926   ------------------------------------------------------------
Hsa SERPINB5    ------------------------------------------------------------NVK
                                                                            |
                                                                            90

                        hlx D           sA2                     hlx E   sA1
Dre ZGC:77645   QIHSSFNKFMSELNKPGAPYVLSLANRLYGEQTYQFLEKYLSDAKKYYAAGLEKVDFKNKS
Dre AAQ97848    QIHSNFNKLMRELNKPGAPYVLSLANRLYGEQTYQLIEKFLNDTKRYYDAGLEKVDFINKS
Dre ZGC:64178   QIHAGFTKLLTEMNRAGAPHTLSLASRLYGEQSCRFQETFLSDTRRLYGAELQPLDFISQP

Dre CAI20745    DFHAHFKTLISSINSPSASYILRLANRLYGEKTFSFLPMYVDSTMKLYHAEPQTVDFIRAA
Dre ZGC:91981   DVHSHFESLISSINSPSASYILRLANRLYGEKTFSFLPEYLSSSLNLYHADLQAVDFIGAS

Hsa SERPINB1    EVHSRFQSLNADINKRGASYILKLANRLYGEKTYNFLPEFLVSTQKTYGADLASVDFQHAS
Hsa SERPINB6    DIHQGFQSLLTEVNKTGTQYLLRMANRLFGEKSCDFLSSFRDSCQKFYQAEMEELDFISAV
Hsa SERPINB2    KIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFREEYIRLCQKYYSSEPQAVDFLECA

Dre ZGC:76926   KETIIYHDLYEAINQGCKNRKLKLYNRMFGDRTIDFLDGYLDKCEEWCFAGIRNVDFKTNP
Hsa SERPINB5    DIPFGFQTVTSDVNKLSSFYSLKLIKRLYVDKSLNLSTEFISSTKRPYAKELETVDFKDKL
                                  |        o         o       o|       o
                            100     110     120     130     140     150

                hlx F                                   sA3
Dre ZGC:77645   EASRVNINKWVEKNTQE--------KIKDLLPSGAIDAMTRLVLVNAIYFKGNWEKKFPKE
Dre AAQ97848    EDARVNINTWVEKNTQE--------KIKDLLPSGAIDAMTRLVLVNAIYFKGNWEEKFPKE
Dre ZGC:64178   EASRGIINRWVEQQTHE--------KIRDLLAEGSVDSLSRLVLVNAVYFKSSWERKFLEE

Dre CAI20745    DDSRQFINKWVEKQTEN--------QIKDLLQPGVVNEMTRLLLVNAIYFKGNWMHTFDAH
Dre ZGC:91981   EQSRQLINKWVEEQTEN--------KIRDLLKPGMVTGMTRLALVNAIYFKGNWLQRFNAQ

Hsa SERPINB1    EDARKTINQWVKGQTEG--------KIPELLASGMVDNMTKLVLVNAIYFKGNWKDKFMKE
Hsa SERPINB6    EKSRKHINTWVAEKTEG--------KIAELLSPGSVDPLTRLVLVNAVYFRGNWDEQFDKE
Hsa SERPINB2    EEARKKINSWVKTQTKG--------KIPNLLPEGSVDGDTRMVLVNAVYFKGKWKTPFEKK

Dre ZGC:76926   EAARAQINTWVKNKTKVDCKPDADQKCDPYKNSIENLLGKEDVSKDSVLALISVMHFEARW
Hsa SERPINB5    EETKGQINNSIKDLTDG--------HFENILADNSVNDQTKILVVNAAYFVGKWMKKFPES
                     oo  |o    o          o|                o    o  o    ooo  o    o|
                        160             170             180     190             200
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                    sC4                 sC3                 sB1                 sB2                 sB3
Dre ZGC:77645       ATKDGQFKLNKNQTKPVKMMHQKAQFPFVVIPEINSQILELPYVGKNLSMLIILPDEIEDA
Dre AAQ97848        ATRDGVFRLNKNQTKPVKMMHQKAEFPSGYIEEMKSHVLELPYAGKNLSMLIILPDEIEDA
Dre ZGC:64178       HTHEQQFRTSRNESKPVQMMFQKGRFPLAFIPDVNCQILELPYAGKELSMLVLLPNAMEDD

Dre CAI20745        ATKEMPFKINQNESRPVQMMDQVENFPYRCIPEYKLQVLELPYTQQELSMLILLPDEIKYG
Dre ZGC:91981       DTKEMPFKINQKENRPVQMMYQKKKFPFNYIYDHRVQVLELPYVKEELSMLILLPEETQDG

Hsa SERPINB1        ATTNAPFRLNKKDRKTVKMMYQKKKFAYGYIEDLKCRVLELPYQGEELSMVILLPDDIEDE
Hsa SERPINB6        NTEERLFKVSKNEEKPVQMMFKQSTFKKTYIGEIFTQILVLPYVGKELNMIIMLPDE----
Hsa SERPINB2        LNGLYPFRVNSAQRTPVQMMYLREKLNIGYIEDLKAQILELPYAG-DVSMFLLLPDEIADV

Dre ZGC:76926       AQSFEPLHTNKDKAQNGQMMQTTQIFPLGEIPDADSKMLEIPYENSDVSFLIILPNQ----
Hsa SERPINB5        ETKECPFRLNKTDTKPVQMMNMEATFCMGNIDSINCKIIELPFQNKHLSMFILLPKDVEDE
                     o    o   |     o  oo        |          |     o     |    oo  |
                               210       220       230       240       250      257

                    hlx G       hlx H           sC2         sA6             hlx I
Dre ZGC:77645       TTGLQKLEKALTYEKLMQWT---KVMRQQEVQVSLPKFKTEQTYDMKSLLVSMGMEDVFDP
Dre AAQ97848        TTGLEKLERALTYEKLMEWT-KPEVMHQREVQVSLPKFKTEQTYDMKSLLVSMGMEDVFDP
Dre ZGC:64178       GTGLEKLERALTLETLTDWT-RSDMMDVLEVEVSLPRLRVEERLELKPLLVELGMPDAFDP

Dre CAI20745        SDPLLKLESELNLQKLLDWTSRGKMDTWRKIIVRLPKFKLEIESCLSETLEKMGMSSVFQE
Dre ZGC:91981       SDPLLKLESELTIDKLHEWTNRNNMDTQTDIIVHLPRFKLEIESSLVEILMGMGMSSVFQE

Hsa SERPINB1        STGLKKIEEQLTLEKLHEWT-KPENLDFIEVNVSLPRFKLEESYTLNSDLARLGVQDLFNS
Hsa SERPINB6        TTDLRTVEKELTYEKFVEWT-RLDMMDEEEVEVSLPRFKLEESYDMESVLRNLGMTDAFEL
Hsa SERPINB2        STGLELLESEITYDKLNKWT-SKDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFNK

Dre ZGC:76926       NDGLPKLLDSMTHEKILMWT-QSHWMTPTEVTVDMPIFQLKEKYDLEEAMKALGMTDVFGD
Hsa SERPINB5        STGLEKIEKQLNSESLSQWT-NPSTMANAKVKLSIPKFKVEKMIDPKACLENLGLKHIFSE
                       o    o   |     o          |          oo        o  o|   o   o   o
                               260       270       280       290       300      310

                                                sA5         P17 15 13 11 9 7 5 3 1 1' 3'        sC1
Dre ZGC:77645       LKVNLTGMSSSNDLVLSKVVHKAFVEVNEEGTEAAAATGAVVSIRTLA---QIFNADHPFL
Dre AAQ97848        QKVNLTGMSSSNDLVLSKVIHKAFVEVNEEGTEAAAATAAIAKFLCYIPP-VSFNADHPFL
Dre ZGC:64178       QRADFSGVCAGGELLLSTVVHQSFLEVNEEGTEAAAATAAVMMTRCLMRA-ERFCADHPFL

Dre CAI20745        TKADLTGMSSNGGLFLSAVIHKAFVEVNEEGTEAAAATALLLPISACQGAFHDFIADHPFM
Dre ZGC:91981       GKADLTGMTGHGGLFLSAVAHKAFVDVNEEGTEAAAATAAIVAFCMLRE--EHFMADHPFL

Hsa SERPINB1        SKADLSGMSGARDIFISKIVHKSFVEVNEEGTEAAAATAGIATFCMLMPE-ENFTADHPFL
Hsa SERPINB6        GKADFSGMSQ-TDLSLSKVVHKSFVEVNEEGTEAAAATAAIMMMRCARFV-PRFCADHPFL
Hsa SERPINB2        GRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGG-PQFVADHPFL

Dre ZGC:76926       S-CDLSGMAS-GKLKLSKVVHGCSVNVDEKGINADTGNGGVVKSLCCKVPTNRFVADRPFL
Hsa SERPINB5        DTSDFSGMSETKGVALSNVIHKVCLEITEDGGDSIEVPGARILQHK-----DELNADHPFI
                      o  o  |        o  |  o  o        |  o  o        |          |  oo
                            316       320       330       340       350       360      370

                    sB4         sB5
Dre ZGC:77645       FFIRHNPTNTILFYGRFCSP
Dre AAQ97848        FFIRHNPTKSILFYGRFCSP
Dre ZGC:64178       MLIRHNPTGSLLFYGRVCNP

Dre CAI20745        FFIRHNPTNSILFLGRFRAPS
Dre ZGC:91981       FYIRHNPTNSILFFGRFRGPS

Hsa SERPINB1        FFIRHNSSGSILFLGRFSSP
Hsa SERPINB6        FFIQHSKTNGILFCGRFSSP
Hsa SERPINB2        FLIMHKITNCILFFGRFSSP

Dre ZGC:76926       FFIRHNPTKSILFWGRFNPQGPVN
Hsa SERPINB5        YIIRHNKTRNIIFFGKFCSP
                    |         |   oo  o   oo
                    372       380       391
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