```
           1        10        20        30        40        50        60        70        80        90
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX                                                          MSYPATRAEQVVDTLHGVQVADPYRWLEDE
      SC                                MKNRLWLAMAAPLALATPVAFAQTPPTLAKDQAMPSLPPYPASPQVPLVEDHFGEKVSDPWRWLEAD
      FM                                        MKYNKLSVAVAAFAFAAVSAQNSNVLK----YPETKKVSHTDTYFGTQVSDPYRWLEDD
  Porcine                                                     MLSFQYPDVYRDETAIQDYHGHKVXDPYAWLEDP
    DPPIV  PWKVLLGLLGAAALVTIITVPVVLLNKGTDDATADSRKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENS
Consensus  ..........................................................yp............fg..v.#pyrwLEd.

           91       100       110       120       130       140       150       160       170       180
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   KAPEVQ--TWMTAQNAHAREALAKFPGREALAARFKELFYTDSVS----TPSRRNGRFFYVRTHKDKEKAILYWRQGESG---QEKVLLD
      SC   VRTDAKVAAVVQAQSAYTAAYLKQLPERAALEKRMKALIDYERFG----LPQRRGASVFYSWNSGLMNQSQLLVRPADAPVGTKGRVLLD
      FM   RAEDTK--AVVQQEVKFTQDYLAQIPFRDQLKKQLMDIWNYEKIS----APFKKGKYTYFSKNDGLQAQSVLYRKDAAG----KTEVFLD
  Porcine  DSEQTK--AFVEAQNKITVPFLEQXPIRGLYKERMTELYDYPKYS----CHFKKGKRYFYFYNTGLQNQRVLYYQDSLEG---EARVFLD
    DPPIV  TFDEFGHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTWSPVGHKLAYVWNNDIYVKIEPNLPSY
Consensus  ...#.k..avv.aq...t...L.q.p.r..l..r...l.dy...s.....p..rg...fy..n.gl..q..lyv.............v.ld

           181      190       200       210       220       230       240       250       260       270
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   PNGWSKDGTVSLGTWA--VSWDGKKVAFAQKPNAADEAVLHVIDVDSGEWSKVDVI----EGGKYATPKWTPDSKGFYYEWLPTD---PS
      SC   PNTWAKDGATALDAWA--ASDDGRLLAYSVQDGGSDWRTVKFVGVADGK-PLADEL----KWVKFSGLAWLGN-DALLYSRFAEP--KEG
      FM   PNKFSEKGTTSLASVS--FNKKGTLVAYSISEGGSDWNKIIILDAETKK-QLDETL----LDVKFSGISWLGD-EGFFYSSYDKP--KEG
  Porcine  PNILSDDGTVALRGYA--FSEDGEYFAYGLSASGSDWVTIKFMKVDGAK-ELPDVL----ERVKFSXMAWTHDGKGMFYNAYPQQDGKSD
    DPPIV  RITWTGKEDIIYNGITDWVYEEEVFSAYSALWWSPNGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNT
Consensus  pn.ws.dgt..l...a...s.dg...A%s....gs#w.......v...k..l.#.l....e.vk%s...w..d.kg..y........k..

           271      280       290       300       310       320       330       340       350       360
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   IKVDERPGYTTIRYHTLGTEPSKDTVVHERTGDPTTFLQSDLSRDGKYLFVYILRGWSE-NDVYWKRPGEK--------DFRLLVKGVGA
      SC   QAFQALNYNQTVWLHRLGTPQSADQPVFATPELPKRGHGASVSSDGRWVVITSSEGTDPVNTVHVARVTNGKIG-----PVTALIPDLKA
      FM   SVLSGMTDKHKVYFHKLGTKQSQDELIIGGDKFPRRYIGAYVTDDQRYLVVSAANATNG-NELYIKDLKNKT-------DFIPIITGFDS
  Porcine  GTETSTNLHQKLYYHVLGTDQSEDILCAEFPDEPKWMGGAELSDDGRYVLLSIREGXDPVNRLWYCDLQQESNGITGILKWVKLIDNFEG
    DPPIV  DSLSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWNCLVARQHIE----MSTTGWVGRFRP
Consensus  ..............h.lgt.qs.D.........p....ga..s.dgry..v....g.d..n.......................l!..f..

           361      370       380       390       400       410       420       430       440       450
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   KYE-VHAWKDRFYVLTDEGAPRQRV--FEVDPAKPARASWKEIVPEDSSASLLSVS-IVGGHLSLEYLKDATSEVRVATLKGKPVRTVQL
      SC   QWDFVDGVGDQLWFVSGDGAPLKKI--VRVDLSG-STPRFDTVVPE-SKDNLESVG-IAGNRLFASYIHDAKSQVLAFDLDGKPAGAVSL
      FM   NVNVADTDGDTLYLFTDKDAPNKRL--VKTTIQNPKAETWKDVIAE-TSEPLE-IN-TGGGYFFATYMKDAIDQVKQYDKNGKLVRAIKL
  Porcine  EYDYVTNEGTVFTFKTNRHSPNYRL--INIDFTDPEESKWKVLVPEHEKDVLEWVACVRSNFLVLCYLHDVKNTLQLHDLATGALLKIFP
    DPPIV  SEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCEL
Consensus  ....v...gd.fy..t...ap..r......d...p....wk..vpe.....le.v....gn.l...y..da...v...dl.gk......l

           451      460       470       480       490       500       510       520       530       540
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   -PGVGAASNLMGLEDLDDAYYVFTSFTTPRQIYKTSVSTGKSELWAKVDVP---MNPEQYQVEQVFYASKDGTKVPMFVVHRKDLKRDGN
      SC   -PGIGSASGLSGRPGDRHAYLSFSSFTQPATVLALDPATAKTTPWEPVHLT---FDPADFRVEQVFYPSKDGTKVPMFIVRRKDAK--GP
      FM   -PGSGNASGFGGEKTEKDLYYSFTNYITPPTIFKYNVTTGNSEVYQKPKVK---FNPENYVSEQVFYTSSDGTKIPMMISYKKGLKKDGK
  Porcine  -LEVGSVVGYSGQKKDTEIFYQFTSFLSPGIIYHCDLTKEELEPRVFREVTVKGIDASDYQTVQIFYPSKDGTKIPMFIVHKKGIKLDGS
    DPPIV  NPERCQYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNETKFWYQMILPPHFDKSKK
Consensus  .pg.g.asg.sg.k.....yy.ftsf..P..i....v.t...e......v.....#p.#y..eqvf%.sk#gTK.pmfiv..k..k.dg.

           541      550       560       570       580       590       600       610       620       630
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   APTLLYGYGG-FNVNMEANFRSSILPWLDA-GGVYAVA-NLRGGGEYGKAWHDAGRLDKKQNVFDDFHAAAEYLVQQKYTQPKRLAIYGG
      SC   LPTLLYGYGG-FNVALTPWFSAGFMTWIDS-GGAFALA-NLRGGGEYGDAWHDAGRRDKKQNVFDDFIAAGEWLIANGVTPRHGLAIEGG
      FM   NPTILYSYGG-FNISLQPAFSVVNAIWMEN-GGIYAVP-NIRGGGEYGKKWHDAGTKMQKKNVFNDFIAAGEYLQKNGYTSKEYMALSGR
  Porcine  HPAFLYGYGG-FNISITPNYSVSRLIFVRHMGGVLAVA-NIRGGGEYGETWHKGGILANKQNCFDDFQCAAEYLIKEGYTSPKRLTINGG
    DPPIV  YPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASFDGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGW
Consensus  .PtlLygYgG.fn....p.%s.....w....gg..ava.#.RGgGeyG..whdag....kqnvf#DfiaAaeyl.k.gyt..krlai.Gg

           631      640       650       660       670       680       690       700       710       720
           |--------+---------+---------+---------+---------+---------+---------+---------+---------|
      MX   SNGGLLVGAAMTQRPELYGAVVCAVPLLDMVRYHLFGSGRTWIPEYGTAEKPED-FKTLHAYSPYHHVR----PDVRYPALLMMAADHDD
      SC   SNGGLLIGAVTNQRPDLFAAASPAVGVMDMLRFDQFTAGRYWVDDYGYPEKEAD-WRVLRRYSPYHNVR----SGVDYPAILVTTADTDD
      FM   SNGGLLVGATMTMRPDLAKVAFPGVGVLDMLRYNKFTAGAGWAYDYGTAEDSKEMFEYLKSYSPYHNVK----AGTCYPSTMVITSDHDD
  Porcine  SNGGLLVATCANQRPDLFGCVIAQVGVMDMLKFHKYTIGHAWTTDYGXS-DSKQHFEWLIKYSPLHNVKLPEADDIQYPSMLLLTADHDD
    DPPIV  SYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYM--GLPTPEDNLDHYRNSTVMSRAENFK-----QVEY---LLIHGTADD
Consensus  SnGGllvga...qrpdlf......vgv.dmlr%..ft.gr.w..dygt.ed..#.f..l..ySp.hnvk......v.Yp..$..tadhDD

           721      730       740       750       760       770       780       790   796
           |--------+---------+---------+---------+---------+---------+---------+-----|
      MX   RVDPMHARKFVAAVQ----NSPGNPATALLRIEANAGHGGADQVAKAIESSVDLYSFLFQVLDVQGAQGGVAAQGR
      SC   RVVPGHSFKYTAALQ----TAAIGPKPHLIRIETRAGHGSGKPIDKQIEETADVQAFLAHFTGLTPRP
      FM   RVVPAHSFKFGSELQ----AKQSCKNPILIRIETNAGHGAGRSTEQVVAENADLLSFALYEMGIKSLK
  Porcine  RVVPLHSLKFIATLQYIVGRSRKQNNPLLIHVDTKAGHGAGKPTAKVIEEVSDMFAFIARCLNIDWIP
    DPPIV  NVHFQQSAQISKAL-------VDVGVDFQAMWYTDEDHGIASSTAHQ-HIYTHMSHFIKQCFSLP
Consensus  rVvp.hs.kf.aalq...........p.liriet.agHG.g..tak.iee..d...F....................
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