

**Additional file #1 for:**

Research Article

**Functional evolution of ADAMTS genes: Evidence from analyses of phylogeny and gene organization**

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***Additional File 1 – (NMLVadamtsalign1.pdf) Alignment used for phylogenetic analyses of human ADAMTS proteins and invertebrate homologs .*** Unambiguously aligned amino acid sites, indicated by the “mask” line in the alignment, were used for phylogenetic analyses (figure 1). Intron positions in the corresponding genomic sequence are indicated, with color-coding for intron phases (table 1 and figure 3).

#NEXUS  
 [AC Nicholson, SB Malik, JM Logsdon Jr, E van Meir, 2004. Functional evolution of ADAMTS genes:]  
 [evidence from analyses of phylogeny and gene organization. Contact: john-logsdon@uiowa.edu]  
 [Intron phases marked 0, 1, 2]  
 BEGIN DATA;

DIMENSIONS NTAX=23 NCHAR=2611;  
 FORMAT DATATYPE=PROTEIN SYMBOLS = " 1 2 3 4" MISSING=? GAP=- INTERLEAVE ;

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MATRIX
[
  10      20      30      40      50      60]
[
  .       .       .       .       .       .]
ADAMTS6  -----MEILWKT-LTWILSLIMAS-----S [19]
ADAMTS10 -----MAPACQIL-RWALALGLG-----L [18]
ADAMTS18 -----MECALLLACAFPAAGSGPPRGLAGLGRVAKA-----LQLCCLCCASVAAAL [46]
ADAMTS16 -----MKPRARGWRGLAALW-MLLAQVAEQAPACAM-GPAAAAPGSPSPVPRP [45]
ADAMTS7   -----MPGGPSPR-SPAPLLRPLLLLLLCA-LAPG----- [27]
ADAMTS12 -----MPCAQRSW-LANLSVVAQLLNFGA-LCYG----- [27]
ADAMTS17 -----MCDGALLPPLVLP----- [13]
ADAMTS19 MRLTHICCCCLLYQLGFLSNGIVSEIFQFAPDREWEVVPALWRREPVPDPAGGSGGSADP [60]
ADAMTS2   -----MDPPAGAARRLLCPAL-LLLLLLLPPPLPPP-PP-----PAN [36]
ADAMTS3   -----MVLLS-LWLIAAALVEVRTSA-DG----- [22]
ADAMTS14 -----MAP-LRALLSYLLPLHICAL-CA----- [20]
ADAMTS13 ----- [0]
dCG4096  -----MWIR-SRWLGLLLHYWLWVVV-TQGGGVRPLYGLHSD [34]
ADAMTS4   -----MSQTGSHPG-RGLAGRWLWGAQPCL-LLP-----I [28]
ADAMTS5   -----MLLGWASLLLCA-FRLPLAAVGPAATPA-QDK-----A [31]
ADAMTS8   -----MFPAPAAP----- [8]
ADAMTS1   -----MQRAVPEGFG-RRKLGSDMGNAERAP-GS----- [27]
ADAMTS15 ----- [0]
dCG6107  -----MPDGAANLHAVAHNLRSKRCANRIPHFSLSIFQ [33]
ADAMTS9   -----MQFVSWATLLTLL-VRDLAEMGSPDAAA-VRKDR----- [33]
ADAMTS20 -----MRNAWELTGPVAVVA-EA----- [17]
mask     ----- [0]
gon-1    -----MRS-IGGSFHLLQPVVAAL [18]
[Intron          1          2          ]

[
  70      80      90      100     110     120]
[
  .       .       .       .       .       .]
ADAMTS6  EFHSDHRLSYSSQEEFLTYLEHYQLTIPIRVDQNGAFLSFTVKN---DKHSRRRRRSMDDPI [76]
ADAMTS10 MFEVTH--AFRSQDEFLSSLESYEIAFPTRVDHNGALLAFSPPP---PRRQRRG----- [67]
ADAMTS18 ASDSSGASGLNDDYFVTPVEVDSDAGSYISHDILH-----NGRKKRS----- [89]
ADAMTS16 PPPAERPFGWMEKGEYDLVSAYEVDRHGDYVSHIMH-----HQRRRRAV----- [89]
ADAMTS7   -----APGPAPGRATEGRAALDIVHPVRVDAGGSFLSYELWP---RALRKR----- [71]
ADAMTS12 -----RQPQPGPVRFPDRRQEHFIKGLPEYHVVGPRVDASGHFLSYGLHYPTSSRR [80]
ADAMTS17 VLLLLVWGLDPGTAVGDAAADVEVVLVWRVPRDDVHLPLPAAPGPRRRRRPRTPPAAPR [73]
ADAMTS19 GWVRGVGGGGSARAQAAGSSREVRVAPVPLEEPVEGRSESRRLRPPPPPEGEDEELES [120]
ADAMTS2   ARLAAAADPPG---GPLGHGAERILAVPVRTDAQRLVSHVVSAATS RAGVRARRAAP-- [91]
ADAMTS3   QAGNEEMVQID---LPIKRYREYELVTPVSTNLEGRYLSHTLSASHKKRSARDVSNP-- [77]
ADAMTS14 ---AAGSRTPE---HLSGKLSDYGVTVPCSTDFRGRFLSHVVSGPAAASAGSMVDTTP [74]
ADAMTS13 ----- [0]
dCG4096  ELVAGEGQLVPPRRVHPDGAFMTHQLEYAHE-----LDHRRHRQRRSLNSEHDTQA [85]
ADAMTS4  VPLSWLVWLLLLLLASLLPSARLASPLPREEEIVFPEKNGSV-----LPG----- [74]
ADAMTS5  GQPPTAAAAAQPRRRQGEVQERAEPGPHPLAQRRRRSKGLVQN-----IDQL----- [80]
ADAMTS8  RWLPFLLLLLLLLLPLARGAPARPAAGGQASELVVPTRLP----- [48]
ADAMTS1  RSFGPVPTLLLLAAALLAVSDALGRPSEDEELVPELER-----APG----- [70]
ADAMTS15 -----MLLLGILTFLAFAGRTAGGSEPEREVVVVIRLDPDINGRRYYWRGPE----- [46]
dCG6107  LEVKKRCEWCHKYIQKMSTHWRQNAclyACCIaFLLGMLIMFHLGLRSAHKGQEELPQS [93]
ADAMTS9  -----LHPRQVFLLETLGEYEIVSPIRVNALGEPFPNTNVHFKRTRRSINSATDPWPA [85]
ADAMTS20 ----LVRTLTSYEVVIPERVNEFGEVFPQSHHFSRQKRSS-EALEPMP----- [60]
mask     ----- [0]
Ce gon-1  ILLVVCLVYALQSGGTISEFSSDVLFSRAKYSG---VPVHHSRWRQDAGIHVIDSHHIV [75]
[Intron          3          4          ]

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[           130           140           150           160           170           180]
[           .           .           .           .           .           .]
[Modal, ≥80%, full maj.                                     L]
ADAMTS6      -----DPQQAVSKLFFKLSAYGKHFHLNL [100]
ADAMTS10     -----TGATAESRLFYKVASPSTHFLNL [91]
ADAMTS18     -----AQNARSSLHYRFSAFGQELHLEL [112]
ADAMTS16     -----AVSEVESLHLRLKGRHDFHMDL [112]
ADAMTS7      -----VSVRRDAPAFYELQYRGRELRFNL [95]
ADAMTS12     KR-----LDGS-EDWVYYRISHEEKDLFFNL [106]
ADAMTS17     A-RPG-----ERALLLHLPAGFRDLYLQL [96]
ADAMTS19     QELPRGSSGAAALSPGAPASWQPPPPQPPSPPPAQHAEPDGEVLLRIPAFGRDLYLLL [180]
ADAMTS2      -----VRTPSFPGGN--E-EEPGSHLFYNVTVFGRDLHLRL [124]
ADAMTS3      -----EQLFFNITAFGKDFHLRL [95]
ADAMTS14     T-LPRHS-----SHLRVARSPHGGTLWPGRVGRHSLYFNVTVFGEKELHLRL [121]
ADAMTS13     -----MHQRHPRA [8]
dCG4096     A-DLHLL-----LPLANETLHLEL [103]
ADAMTS4      -----SGAPAR-LLCRLQAFGETLLEL [96]
ADAMTS5      -----YSGGK-VGYLVYAGRRFLDL [102]
ADAMTS8      -----GSAGE-LALHLSAFGKGFVLR [69]
ADAMTS1      -----HGTTR----LRLHAFDQQLDLEL [89]
ADAMTS15     -----DSGDQG-LIFQITAFQEDFYLHL [68]
dCG6107     THPLANSPPATPATLHPRRLDNDTSTDHEPPDGLDDLDEEHSFAFVMPKTVYNYSLEAD [153]
ADAMTS9     F-ASS-----SSSTSSQAHYRLSAFGQQLFNL [113]
ADAMTS20     -----FR--THYRFTAYGQLFQLNL [78]
mask      ----- [0]
Ce gon-1     RRDSYGR-----RGKRDVTSTDRRRRLQGVARDCGHACHLRL [112]

[           190           200           210           220           230           240]
[           .           .           .           .           .           .]
[Modal, ≥80%, full maj.                                     ]
ADAMTS6     TLNTDFVSKHFTVEYW----- [116]
ADAMTS10     TRSSRLLAGHVSVEYW----- [107]
ADAMTS18     KP-SAILSSHFIQVL----- [127]
ADAMTS16     RTSSSLVAPGFIVQTL----- [128]
ADAMTS7      TANQHLLAPGFVSETR----- [111]
ADAMTS12     TVNQGFLSNSYIMEKR----- [122]
ADAMTS17     RRDLRFLSRGFEVEE----- [111]
ADAMTS19     RRDGRFLAPRFAVEQRPNPGPGPT----- [204]
ADAMTS2      RPNARLVAPGATMEWQG--E----- [142]
ADAMTS3      KPNTQLVAPGAVVEWHETSLVPGNITDPINNHQ----- [128]
ADAMTS14     RPNRRLVVPGSSVEWQE-----D----- [139]
ADAMTS13     RCPPLCVAGILACGFLGCV----- [28]
dCG4096     MAHSYFLAPNLVVERHRRDLRTRSPLTTRHL----- [134]
ADAMTS4     EQDSGVQVEGLTVQYLG----- [113]
ADAMTS5     ERDGSVGIAGFVPAGGG----- [119]
ADAMTS8     APDDSFLLAPEFKIERLG----- [86]
ADAMTS1     RPDSSFLAPGFTLQNVGRK----- [108]
ADAMTS15     TPDQFLAPAFSTEHLG-V----- [86]
dCG6107     LIYESKRNSDINSFLKE[SASAFAMTGYRNSNEIWDPHQYNLNVFGRQLHLVLRQDAS [213]
ADAMTS9     TANAGFIAPLFTVTLGTPGV----- [134]
ADAMTS20     TADASFLAAGYTEVHLGTP----- [97]
mask      ----- [0]
gon-1     RSDDAVYIVHLHRWNQIPDSHNK[SVPHFSNSNFAPMVLYLDSE----- [155]
Intron           5           6           ]

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[                250          260          270          280          290          300]
[                .                .                .                .                .                .]
[Modal, ≥80%, full maj.                C G                G ]
ADAMTS6      -----GKDGPPQWKH--DFLDNCHYTGYYLDQQRSTT-KVALSNCCVG- [153]
ADAMTS10     -----TREGLAWQR--AARPHCLYAGHLQGGQASSS-HVAISTCCGG- [144]
ADAMTS18     -----GKDGASETQ-KPEVQQCFYQGFIRNDSSSSS--VAVSTCAG- [164]
ADAMTS16     -----GKTGTTKSVQTLPPEDFCFYQGSLRSHRNSS--VALSTCQG- [166]
ADAMTS7      -----RRGGLGRAHIRAHTPACHLLGEVQDPELEGGLAAISACDG- [151]
ADAMTS12     -----YGNLSHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHG- [162]
ADAMTS17     -----AGAARRRGRPAELCFYSGRVLGHPGSL--VSLSSACGAA [147]
ADAMTS19     -----GAASAPQPPAPPDAGCFYTGAVLRHPGSL--ASFSTCCGG- [241]
ADAMTS2      -----KGTTRVEPLLGSCLYVGDVAGLAEASS--VALSNCCDG- [177]
ADAMTS3      -----PGSATYRIRKTEPLQTNCAYVGDIVDIPGTS--VAISNCDG- [167]
ADAMTS14     -----FRELFRQPLRQECVYTGGVTGMPGAA--VAISNCDG- [173]
ADAMTS13     -----GPSHFQQ5CLQALEPQ-----AVSS----- [48]
dCG4096      -----NCHFHGKVRGQPATNVAISTCAGLVSCPNFC-VLPELITLCQ- [175]
ADAMTS4      -----QAPELLGGAEPGTYLTGTINGDPESV--ASLHWDGGA [148]
ADAMTS5      -----TSAPWRHRSHCFYRGTVDASPRSL--AVFDLCGGL [152]
ADAMTS8      -----GSGRATGGERLRGCFFSGTVNGEPESL--AAVSLCRG- [122]
ADAMTS1      -----SGSETPLPETDLAHCFYSGTVNGDPSSA--AALSLCEG- [144]
ADAMTS15     -----PLQGLTGGSSDLRRCFYSGDVNAEPDSF--AAVSLCGG- [122]
dCG6107     F-VHNHSMTHRIRILKEGEEHPGPETEAEAERHLGCFYSGYVEDDPHSM--VSVSLCGG- [269]
ADAMTS9      -----NQTKFYSEE-EAELKHCFYKYVNTNSEHT--AVISLCSG- [171]
ADAMTS20     -----ERGAWESDAGSDLRHCFYRGQVNSQEDYK--AVVSLCGG- [135]
mask        -----11111111-----1111----- [13]
Ce gon-1     -----EEVRGMSRTDPDCIYRAHVKGVHQHSIVNLCDSEDG- [192]
[Intron      7                ]
[                Prodomain                ]
[                310          320          330          340          350          360]
[                .                .                .                .                .                .]
[≥80%, full maj.G                P                H                ]
ADAMTS6      --LHGVIATEDEEYFIEPLKN-TTEDSKHFSYENG-HPHVIYKSALQRHLYDHSHCGV [209]
ADAMTS10     --LHGLIVADEEEYLIEPLHG--GPKGSR-SPEE-SGPHVVYKRSLRHPHLDTACGVR [198]
ADAMTS18     --LSGLIRTRKNEFLISPLQL-LAQEHNYSSPAGHHPHVLYKRTAEEKIQRYRGYPGSG [221]
ADAMTS16     --LSGMIRTEADYFLRPLSH-LSWKLGRAAQGSSPSHVLYKRSTEPHAPGASEVLVTS [223]
ADAMTS7      --LKGVFQLSNEDYFIEPLDS--APARPG-----HAQPHVVYKRQAPERLAQRGDSSAPS [202]
ADAMTS12     --LTGFFQLPHGDFFIEPVKK--HPLVEG-----GYHPHIVYRRQKVPETKEPTCGLKD- [212]
ADAMTS17     GGLVGLIQLGQEQVLIQPLNN--SQGPFS-----G-REHLIRRKWSLTPSPSAEAQRPEQ [199]
ADAMTS19     --GLMGFIQLNEDFIFIEPLND-----TMAITG-HPHRVYRQRSMEEKVTEKSALHS [291]
ADAMTS2      --LAGLIRMEEEEFFIEPLEK--GLAAQEAEQ--G-RVHVYRRPPTSPLGGPQALDTG [230]
ADAMTS3      --LAGMIKSDNEEYFIEPLER--GKQMEEE-K--G-RIHVYKRSAVEQAPI----- [211]
ADAMTS14     --LAGLIRTDSTDFFIEPLER--GQQEKEA-S--G-RTHVVYRREAVQEWAEPDGLHN [225]
ADAMTS13     -----YLSPGAPLK-----G1PPSPGFQRQRQ----- [70]
dCG4096      --VGHIRTAGNEYFIEPSKEHEPHP-----VNG-HPHVVFQRSSVKPK1SLRKRNKRK [225]
ADAMTS4      --LLGVLQYRGAELHLQPLEGGTPNSAGGP-----GAHILRRKSP----- [186]
ADAMTS5      DGFFAVKHARYTLKPLLRGPWAEEEKRVYGDGSARILHVYTREGFSFEALPPRASCE-- [210]
ADAMTS8      --LSGSFLLDGEEFTIQPQGA--GGSLA-----QPHRLQRWGPAGARPLPR----- [164]
ADAMTS1      --VRGAFYLLGEAYFIQPLPAASERLATAAPEKPPAPLQFHLLRRNRQGDVGG--TCGV [200]
ADAMTS15     --LRGAFGYRGAEYVISPLPN--ASA--PAAQRNSQGAHLLQRRGVPG----- [164]
dCG6107     --MTGYIKTSFGALLIQPVNR--TSSDE-----VLHRVFRKSQRNARHAVSKFEL-- [315]
ADAMTS9      --MLGTFRSHDGDYFIEPLQS--MDEQEDEEEQN--KPHIIYRRSAPQREPSTGR----- [220]
ADAMTS20     --LTGTFKGQNGEYFLEPIMK--ADGNEYED--GHNKPHLIYRQDLNNSFLQT----- [182]
mask        -----11111111-----11111111----- [30]
Ce gon-1     --LYGMLALPSGIHTVEPIIS--GNTGE1D-----GASRHRQHLVRKFDPMHFKSF----- [239]
[Intron      8                9                10                11                ]

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[                               370       380       390       400       410       420]
[                               .           .           .           .           .           .]
[Modal, ≥80%, full maj. ]
ADAMTS6      SD-----TRSGKPWWLNDTSTVSYSLP [232]
ADAMTS10     -----KPKWGRPWLLRRLKPPFARP [219]
ADAMTS18     RNYPGYSPSHIPHASQSRETEYHHRRLQKQHFCEGRKKYAPKPTEDTYLRFDEYGS--- [278]
ADAMTS16     R-----TWELAHQPLHSSDLRLGLPQKQHFCEGRKKYAPQPPKEDLFLPDEYKS--- [273]
ADAMTS7      TCGVQV-----YPELESRR---ERWEQRQQW [225]
ADAMTS12     -----SVNISQKQELWREKWERHNL [233]
ADAMTS17     LCKVLT----E-----KPKPTW-----GRPSRDW [219]
ADAMTS19     HYCGIISD-----KGRPRSRIA----- [309]
ADAMTS2      -----ASLDSLDSLALGVLEEHN [251]
ADAMTS3      --DMSKDFHYRE-----DLEGLDDLGTVYGNIHQQLN [242]
ADAMTS14     EA-----EGLGDLPNLLGLVGDQLG--- [245]
ADAMTS13     ----- [70]
dCG4096     RGGKSGSGAEVSNCGTREP RRMRLEWQARGKVKVQGGRQIRRRHHHHHHHHHHKHKYR [285]
ADAMTS4      -----ASGQGPNCN-----VKAP----LGSPS--P [205]
ADAMTS5     -TPAS-TPEAHEHAPAHNP-----SGRAALASQL-----LDQSALSPAGGSGP-QTW [255]
ADAMTS8     -----GPEWEVETGEGQRQER-----GDHQEDSEEE---SQEEEAEGASEPPPLG [207]
ADAMTS1     VDDEPRP-TGKAETEDDEGTE-----GEDEGPQWS-----PQDPALQGVGQPTG- [245]
ADAMTS15     -----GPGSDPTSRCGVASGW-----NPAILRALD-----PYKPRRAGFGESRSRR [205]
dCG6107     -----GLDDFMKLEQVQEEQKSKSRKLN----- [340]
ADAMTS9     -----HACDTSEKKNRHSKDKKKTRARKWGERI [248]
ADAMTS20     -----LKYCSVSESIKETSLPFHTYSNMNEDLN [211]
mask [30]
Ce gon-1    -----DHLNSTSVNETETTVATWQDQWEDVIEKAKA----- [269]
[Intron 12 13]

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[                               430       440       450       460       470       480]
[                               .           .           .           .           .           .]
[Modal, ≥80%, full maj. ]
ADAMTS6     INNTHI--HH-----RQKR-----SVSIERFVETLVVAD [259]
ADAMTS10    LGNETE--RGQP-----GLKR-----SVSRERYVETLVVAD [248]
ADAMTS18    -SG-----RPRRSAG---KSQKGLNVETLVVAD [302]
ADAMTS16    -CL-----RHKRSLRS--HRNEELNVETLVVVD [299]
ADAMTS7     RRP-----RLRRLHQR--SVSKEKWVETLVVAD [251]
ADAMTS12    SRS-----LSRR-----SISKERWVETLVVAD [255]
ADAMTS17    -----RERRNAI---RLTSEHTVETLVVAD [241]
ADAMTS19    -----ESGRGKRYSY---KLPQYNIETVVVAD [334]
ADAMTS2     SS-----RRRARH---AADDYNIETLVVAD [275]
ADAMTS3     ETM-----RRRRH---AGENDYNIETLVVAD [265]
ADAMTS14    DTE-----RKRRH---AKPGSYSIEVLLVVD [268]
ADAMTS13    -----RQRR-----AAGGILHLELLVAVG [89]
dCG4096     HHQOKISRPVHTKFKYETQFQTE----PDHAEIPRRR-----SISSPRHVETLVVAD [334]
ADAMTS4     RPR-----RAKR-----FASLSRFVETLVVAD [227]
ADAMTS5     WR-----RRRR-----SISRARQVELLVAD [276]
ADAMTS8     ATS-----RTKR-----FVSEARFVETLLVAD [229]
ADAMTS1     GSI-----RKKR-----FVSSHRYVETMLVAD [267]
ADAMTS15    RSG-----RAKR-----FVSIPIRYVETLVVAD [227]
dCG6107     -----RKKR---HYADVNDQVYTVLEVLIAVD [363]
ADAMTS9     NLAGDVAALNSGLATEAFSAYGNKTDNTREKRTHRRTKR-----FLSYPRFVEVLVAD [302]
ADAMTS20    VMKERVLGHTSKNV-----PLKDERRHSRKKR-----LISYPRYIEIMVTAD [253]
mask [49]
Ce gon-1    -----R1111-----11111111111111 [49]
Ce gon-1    -----RSRR-----AANSWDHYVEVLVAD [289]
[Intron 14]
[ furin prodomain cleavage motif ]

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[                                490      500      510      520      530      540]
[                                .          .          .          .          .          .]
[>80%, full maj. HG           Y LT                      S                      ]
ADAMTS6      KMMVG YHGRKDIEHYILSV MNIVAKLYR DSSLGNVVNIIVARLIVLTEDQPENLE-INH-H [317]
ADAMTS10     KMMVAYHGRRDVEQYVLAIMNIVAKLFQDSSLGSTVNILVTRLILLTETDQPTLE-ITH-H [306]
ADAMTS18     KKMVEKHGKGNVTYYILTVMNMVSGLFKDGITIGSDINVVVSLILLEQEPGGLL-INH-H [360]
ADAMTS16     KKMMQNHGHENITTYVLTILNMVSA LFKDGITGGNINIAIVGLILLEDEQPGLV-ISH-H [357]
ADAMTS7      AKMVEYHGQPQVESVLTIMNMVAGLFHDP SIGNP I HITIVRVLVLEDEEEDLK-ITH-H [309]
ADAMTS12     TKMIEYHGSENVESYILT IMNMVTGLFHNPSIGNA IHIVVRLILLEEEEOGLK-IVH-H [313]
ADAMTS17     ADMVQYHGAEAAQRFILTVMNMVYNM FQHQS LGIKINIQT KLVLRRQRAKLS-IGH-H [299]
ADAMTS19     PAMVSYHGADAARRFIL TLNMVFNL FQHKSLGVQVNL RVIKLILLHETPELY-IGH-H [392]
ADAMTS2      DSVVQFHGKEHVQKYLLTL MNIVNEIYHDESLGAHINVL VRIILLSY GKSMSL-IEIGN [334]
ADAMTS3      DSVVRFHGKEHVQNYLLT LMNIVNEIYHDESLGVHIN VVLRMIMLYAKSISL-IERGN [324]
ADAMTS14     DSVVRFHGKEHVQNYLLT LMNIVDEIYHDESLGVHIN IALVRLISLVYRQSLSL-IERGN [327]
ADAMTS13     PDVFQAHQE-DTERYVLTNLNIGAELLRDP SLAGQFRVH LVKMVILTEPECAPN-ITA-N [146]
dCG4096     ATMSAFHR--DLNGYLLT IMNMVSALYKDP SIGNSI EIVVRI IQLDEEESQLQLNL TQN [392]
ADAMTS4      DKMAAFHGA-GLKRYLLT VMAAA AKAFKHP SIRNPVSLV VTRLVILGSGEGPQ-VGP-S [284]
ADAMTS5      ADMARLYGR-GLQHYLLT LASI ANRLYSHAS IENHIRLAVVKVVL GDKDKSLE-VSK-N [333]
ADAMTS8      ASMAAFYGA-DLQNHIL TLM SVAARIYKHP SIKNS INLMVVKV LIVED EKWGPE-VSD-N [286]
ADAMTS15     QSMAEFHGS-GLKH YLLTLFSVAARLYKHP SIRNSVSLV VVKILVIHDEQK GPE-VTS-N [324]
ADAMTS1      ESMVKFHGA-DLEHYLLT LLA TAARLYRHPSILN P INIVVVKV LLLRDRD SGPK-VTG-N [284]
dCG6107     NSMKQFHGE-DLQHYLL LIMSIVSSIFADAS I GNSIRILLVRL ISLPNIN-----DQTHS [417]
ADAMTS9      NRMVSYHGE-NLQHYIL TMSI VAS IYKDP SIGNLIN I VIVNLV IHNEQDGPS-ISF-N [359]
ADAMTS20     AKVVS AHGS-NLQNYIL TMSI VATIYKDP SIGNL I HVVVKLVMIHREEGPV-INF-D [310]
mask        11111111--1111111111111111111111111111111111111111111-----1 [96]
Ce gon-1    TKMYEYHGR-SLEDYVLT LFTVASIYRHQSLRASIN VVVVKLIVLKTENAGPR-ITQ-N [346]
[Intron          15           16           17 ]

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[                                550      560      570      580      590      600]
[                                .          .          .          .          .          .]
[>80%, full maj. L C W                          D A      TR D ]
ADAMTS6      ADKSLDSFCKWQKSILSHQSDGNTIPENG---IAHHDNAV LITR YDICTYKNKP-CGTL [372]
ADAMTS10     AGKSLDSFCKWQKSIVNHS HGNAI P ENG---VANHDTAVLITR YDICIYKNKP-CGTL [361]
ADAMTS18     ADQSLNSFCQWQSALIGKNG-----KRHDHAILL TGDFDICSWKNEP-CDTL [405]
ADAMTS16     ADHTLSSFCQWQSGLMGKDG-----TRHDHAILL TGLDICSWKNEP-CDTL [402]
ADAMTS7      ADNTLKSFCWQKSINMKGDAH P-----LHHDTAILL TRKDLCAAMNRP-CETL [357]
ADAMTS12     AEKTLSSFCKWQKSINPKSDLN P-----VHHDVAVLL TRKDICAGFNRP-CETL [361]
ADAMTS17     GERSLESFCHWQNEEYGGARYLGN NQVPGGKDDP PLVDAAVFVTR YDFCVHKDEP-CDTV [358]
ADAMTS19     GEKMLSFCKWQHEEF GKNDI HLEMSTNWGEDM TSVDAA ILITR YDFCVHKDEP-CDTV [451]
ADAMTS2      PSQSL ENVCRWAYLQK PDTGHD-----EYHDHAI FLTRQDFGP-----SGMQ [377]
ADAMTS3      PSRSL ENVCRWASQQQRSDLNHS-----EHDHAI FLTRQDFGP-----AGMQ [367]
ADAMTS14     PSRSL ENVCRWAHSQQQRDP SHA-----EHDHVVFLTRQDFGP-----SGMQ [370]
ADAMTS13     LTSLLSVCWSQ T INPEDD TDP-----GHADLVLYI TR YDLELPDGN--RQVR [193]
dCG4096     AQKNLDRFCSYQHKLNK GSEKDP-----HHHDVAILITR KNICANN---CMTL [437]
ADAMTS4      AAQT LRSFCAWQRGLNTPEDSDP-----DHFDTAILFTRQYDL C-GVST--CDTL [330]
ADAMTS5      AATTLKNFCWKQH QHNQLGDDHE-----EHYDAILFTR EDLC-GHHS--CDTL [379]
ADAMTS8      GGLTLRNFNCNWRFRNQPSDRHP-----EHYDTAILL TRQYFC-GQEGL-CDTL [333]
ADAMTS1      AALTLRNFNCNQKHNP P SDRDA-----EHYDAILFTRQYDL C-GSQT--CDTL [370]
ADAMTS15     AALTLRNFCAWQKKNKVSDKHP-----EYWDTAILFTRQYDL C-GATT--CDTL [330]
dCG6107     SNEMLKHFCQFINQ-----SGYERDTAMLITR YPICGSVPGKICHML [459]
ADAMTS9      AQTTLKNLCQWQHSKNSP GGI-----HHDTAVLLTRQYD IC-RAHDK-CDTL [403]
ADAMTS20     GATTLKNFCSWQQTQNDLDDVHP-----SHHDTAVLITR YD IC-SSKEK-CNML [357]
mask        111111111111111-----111111111111111-----1111 [128]
Ce gon-1    AQQTLQDFCWRQYYNDPDDSSV-----QHHDVAILL TRKD IC-RSQGK-CDTL [393]
[Intron          18           19,20         21 ]

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[           730           740           750           760           770           780]
[           .           .           .           .           .           . ]
[Modal, >=80%, full maj.  PG   Y   QC   G   C   C   LWC   ]
ADAMTS6    ---PKRDFLYPAVAPG--QVYDADEQCRFQYGATSRQCKYG-----EVCRELWCLSK--S [516]
ADAMTS10   ---PRQDFVYPTVAPG--QAYDADEQCRFQHGVKSRQCKYG-----EVCSELWCLSK--S [505]
ADAMTS18   ---KQAGQYKYDPKLPG--QIYDADTQCKWQFQGAKAKLCSLG--FVKDICKSLWCHRV--G [550]
ADAMTS16   --KPVKEYKYPEKLPG--ELYDANTQCKWQFGEKAKLCMLD-FKKADICKALWCHRI--G [548]
ADAMTS7    ---AKDIIDFPSVPPG--VLYDVSHQCRQLQYGAYSAFCEM----DNVCHTLWCSV--G [500]
ADAMTS12   ---KKKGLKSKVIAPG--VIYDVHHQCCQLQYGNATFQCQEVE----NVCQTLWCSV--K [504]
ADAMTS17   ---RSQHTVRLPHKLPG--MHYSANEQCQLIFGMNATFCRNME----ILMCAGLWCLVE--G [504]
ADAMTS19   --QSVNSVMVPSKLPG--MTYTADEQCQILFGLPLASFQEMQ---HVICTGLWCKVE--G [597]
ADAMTS2    --FAHDWPALP-QLPG--LHYSMNEQCRFDFGLGYMMCTA--FRTFDPCKQLWCSHPD-N [522]
ADAMTS3    --FDHDWPKLP-ELPG--INYSMDEQCRFDFGVGYKMCTA--FRTFDPCKQLWCSHPD-N [512]
ADAMTS14   --FDPAWQPP-ELPG--INYSMDEQCRFDFGSGYQCLTA--FRTFEPCKQLWCSHPD-N [514]
ADAMTS13   RPQPGSAGHPDAPQPG--LYYSANEQCRVAFGPKAVACTFA-REHLDMCQALSCHTDPLD [343]
dCG4096    T--PLDEYNYPGELPG--MRYNARGQCRQLQYFNLTDSIEVGACSAPEHFCSTLWCKVNGE- [588]
ADAMTS4    ----EAPLHLPTVTPFG--KDYDADRQCQLTFQPDPSRHCPQL----PPPCAALWCSGHLNG [478]
ADAMTS5    ----RQKQILGPEELPG--QTYDATQCQLTFGMNATFCRNME----DVCARLWCAVVRQG [525]
ADAMTS8    ----GAALPLPTGLPGRMALYQLDQCQRQIFGPDFRHCPNT--SAQDVCAQLWCHTDGAE [484]
ADAMTS1    ----HNPIQLPGDLPG--TSYDANRCQCFTFGEDSKHCPDA----ASTCSTLWCTGTSGG [517]
ADAMTS15   ----SKPISLPELPG--ASYTLSQCCELAFQVGSKPCPYM----QYCTKLWCTGKAKG [476]
dCG6107    ----GAHWPYQTPERLPG--EYSLDAQCQLSFGNDFGYCPTD----EECKRLWLNRTSGN [608]
ADAMTS9    ---ESRPYPLPVQLPG--ILYVNVKQCCELIFGPGSQCPCPY----MMQCRLWLNNTVNGV [549]
ADAMTS20   ---DEEINYLNPSLPG--SRYDGNKQCCELAFGPGSQMCPHI----ENICMHLWCTSTEKL [503]
mask       ----111111-1111-1111111111111111111111111111----1111111111---- [246]
Ce gon-1   VERRYEDVVFVRDEPG--KKYDAHQCCKFVFGPASELCPYM----ETCRLWLCATFYGS [561]
[Intron                                         29, 30, 31 ]

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[           790           800           810           820           830           840]
[           .           .           .           .           .           . ]
[>=80%, full maj.C   P   GT C   C   G C   G   W   W   ]
ADAMTS6    NR--CVTNS--IPAAEGTLCQTGNIKGCYCQGDVFPFGTW-PQSI--DGCWGPWSLWGE [569]
ADAMTS10   NR--CITNS--IPAAEGTLCQTHITIDKGCYKRVCFPGSR-PEGV--DGAWGPWTFWGD [558]
ADAMTS18   HR--CETKF--MPAAEGTVCGL----SMWCRRGQCQVKFGEGLGPRPI--HGQWSAWSKWSE [600]
ADAMTS16   RK--CETKF--MPAAEGTICGH----DMWCRGGQCVKYGDEGPKPT--HGHWSDWSSWS [598]
ADAMTS7    TT--CHSKL--DAAVDGTRCGE----NKWCLSGECPVVGFR-PEAV--DGCWGSWSAWSI [549]
ADAMTS12   GF--CRSKL--DAAADGTQCGE----KWC MAGKCI TVGKK-PESI--PGWGRWSPW [553]
ADAMTS17   DTS--CKTKL--DPPLDGTECGA----DKWCRAGECVSKTPI-PEHV--DGDWSPWGAWS [554]
ADAMTS19   EKE--CRTKL--DPPMDGTDCDL----GKWC KAGECTSR TSA-----PEHLAGEWSLW [644]
ADAMTS2    PYF--CKTKK--GPPLDGTMCAP----GKHC FKGHC IWLT---PDILKRDGSGAWSP [572]
ADAMTS3    PYF--CKTKK--GPPLDGTECAA----GKWCYKGC MWK---NANQQKDGNWGSWTKFGS [562]
ADAMTS14   PYF--CKTKK--GPPLDGTECAP----GKWC FKGHC IWKS---PEQTYGDGGSWSTKFGS [565]
ADAMTS13   QSS--CSRLL--VPLLDGTECGV----EKWCSKGRCSRSLVELTP-IAAVHGRWSSWGFRSP [395]
dCG4096    ---CVTHM--RPTAGTLCGR----NKWQNGKCVRREELA--V-----NGCWGDWSEWSE [634]
ADAMTS4    HAM--CQTKH--SPWADGTPCGP----AQACMGGRC LHMDQLD FNIPQAGCWGPWP [531]
ADAMTS5    QMV--CLTKK--LPAVEGTPCGK----GRICLQKCVDKTKKYYSTSSHGNWGSWGW [578]
ADAMTS8    PL--CHTKNGSLPWADGTPCGP----GHLCEGSGCLPEEVEVERPKPVVDGCVAPWGPW [538]
ADAMTS1    VLV--CQTKH--FPWADGTSCGE----GKWCINGKCVNKTDRKHFDTPFHGNWGMWGP [570]
ADAMTS15   QMV--CQTRH--FPWADGTSCGE----GKCLKLGACVERHNLNKHRV--DGSWAKWD [527]
dCG6107    SNEQCASSN--LPWADGTPCGSS----GHWCRGKCVSNKHGY--GRQVNGCWGPWP [661]
ADAMTS9    HKG--CRTQH--TPWADGTECEP----GKHCYGFVCKEMDVPV-T--DGSWGSWS [599]
ADAMTS20   HKG--CFTQH--VPPADGTDCGP----GMVHCRHGCLVNKETE---TRPVNGEWGPWP [554]
mask       ----11111-1111111111----1111111111111111111111111111----1111111111 [285]
Ce gon-1   QMG--CRTQH--MPWADGTPCDESR--SMFCHHGACVRLAPESL--TKIDGQWGD [614]
[Intron                                         32       33       ▲ ]
[                                           Thrombospondin → ]

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[ 850 860 870 880 890 900 ]  
[ . . . . . ]  
[ ≥80%, maj. CSR CG G R C P P G G C G C C FR QC ]  
ADAMTS6 CSRTC~~GGG~~VSSSLRHCDS~~P~~A~~ESGGG~~KYCLGERKRYRSCNTD~~E~~CP~~L~~---GSRDFREKQCAD [626]  
ADAMTS10 CSRTC~~GGG~~VSSSSRHCDSP~~R~~TIGGGKYCLGERRRHRSNTD~~E~~CPP---GSQDFREVQCSE [615]  
ADAMTS18 CSRTC~~GGG~~VK~~Q~~RHCNNK~~P~~QY~~G~~GLFCPGSSRIYQLCNINFCNE---NSLDFRAQQCAE [657]  
ADAMTS16 CSRTC~~GGG~~VSHRSRLCTN~~P~~K~~PSHGG~~KFC~~E~~GS~~T~~R~~T~~L~~K~~L~~C~~NSQKCP~~R~~---DSVDFRAQQCAE [655]  
ADAMTS7 CSR~~SCGMG~~VQSAERQCTQPT~~P~~KY~~K~~GRYCVGERKRFRLCNLQACPA---GRPSFRHVQCSE [606]  
ADAMTS12 CSRTC~~GAG~~VQSAERLCNN~~P~~E~~P~~K~~F~~GGKYCTGERKRYR~~C~~LN~~V~~H~~P~~CRS---EAP~~T~~FR~~Q~~MCSE [610]  
ADAMTS17 CSRTC~~G~~TGARFRQRKCDN~~P~~PG~~P~~GG~~T~~HC~~P~~GASVEHAVCENL~~P~~CPK---GLPSFRDQCQA [611]  
ADAMTS19 CSRTC~~S~~AGISSRERK~~C~~--PGLDSEARD~~C~~NG~~P~~PRKQYRICEN~~P~~PCPA---GLPGFRDWQCQA [699]  
ADAMTS2 CSRTC~~G~~TGVKFRTRQCDN~~P~~H~~P~~ANGG~~R~~TC~~S~~GLAYDFQLCSRD~~C~~PD---SLADFREEQCQR [629]  
ADAMTS3 CSRTC~~G~~TGVFRTRQCDN~~P~~M~~P~~INGGQ~~C~~PGVNF~~E~~YQLCNT~~E~~EC~~Q~~K---HFEDFRAQQCQ [619]  
ADAMTS14 CSR~~SCGGG~~VRSRSRRCN~~P~~SPAYGGRL~~C~~LG~~P~~MF~~E~~YQVCN~~S~~EE~~C~~PG---TYEDFRAQQCAK [622]  
ADAMTS13 CSR~~SCGGG~~VVTRRRQCDN~~P~~RF~~A~~FGGRACV~~G~~ADLQAEMCNTQACEK---TQLEFMSQQCAR [452]  
dCG4096 CSR~~SCGGG~~VSTQORECDN~~P~~V~~P~~ANGG~~V~~FCIGERKRYKICRKR~~P~~CPA---E~~E~~PSFRAQQCAR [691]  
ADAMTS4 CSRTC~~GGG~~VQFSSRDCT~~R~~PVPRNGGKYCEGRTRFRSCNTED~~C~~PT--GSA~~T~~TFREEQCAA [589]  
ADAMTS5 CSR~~SCGGG~~VQFAIRRCN~~P~~PARNNGRYCTGKRAIYRSCSLM~~P~~CP~~P~~---NGS~~S~~FRHQCEA [635]  
ADAMTS8 CSRTC~~GGG~~VQF~~S~~HRECKD~~P~~E~~P~~QNGGRYCLGRRAKYQSCHTEEC~~P~~PP---DGSFR~~Q~~CEK [595]  
ADAMTS1 CSRTC~~GGG~~VQYTMRECDN~~P~~V~~P~~KNGGKYCEGKRVRYS~~C~~NLEDC~~P~~D--NNG~~S~~TFREEQCEA [628]  
ADAMTS15 CSRTC~~GGG~~VQLARRQCTN~~P~~T~~P~~ANGGKYCEGVRVKYRSCNLE~~F~~CPSS-A~~S~~GKSFREEQCEA [586]  
dCG6107 CS~~L~~T~~CGGG~~VQESRRCN~~Q~~PV~~P~~ENG~~G~~YK~~C~~TGSRK~~K~~YRSCN~~T~~HQCP~~P~~---GSM~~D~~PREQCYA [718]  
ADAMTS9 CSRTC~~GGG~~IKTAIRECN~~R~~PE~~P~~KNGGKYCVGR~~R~~MKFKSCNTE~~P~~CLK---QKRD~~F~~RDEQCAH [656]  
ADAMTS20 CSRTC~~GGG~~IESATRRCN~~R~~PE~~P~~PRNGG~~N~~YCVGRRMKFRSCNTD~~S~~CPK---GTQDFREKQCSD [611]  
mask 111 [341]  
Ce gon-1 CSRTC~~GGG~~VQKGLRDCDS~~P~~K~~P~~RN~~G~~GYCVGQ~~R~~EYRYS~~C~~NTQ~~C~~CPW---DTQ~~P~~YREVQCSE [671]  
[Intron 34 35 36, 37, 38 ]

[ 910 920 930 940 950 960 ]  
[ . . . . . ]  
[ Modal, ≥80%, full maj. W C L C V DGT C ]  
ADAMTS6 FDNM--PFRGKYY---NW~~K~~PYTGG---~~G~~-VK~~P~~CA~~L~~NC~~L~~AE~~G~~YNFYTERAPAV~~I~~DGTQCNA [677]  
ADAMTS10 FDSI--PFRGKFY---KW~~K~~TYRGG---~~G~~-V~~K~~A~~C~~SL~~T~~S~~L~~AE~~G~~FN~~F~~YTERAAAV~~V~~DGT~~P~~CRP [666]  
ADAMTS18 YNSK--PFRGWFY---QW~~K~~PYTKVEE--~~E~~--DR~~C~~KLYC~~K~~AEN~~F~~EFF~~F~~AMSG~~K~~V~~K~~DGT~~P~~CSP [709]  
ADAMTS16 HNSR--RFRGRHY---KW~~K~~PYTQVED--~~Q~~--D~~L~~C~~K~~L~~Y~~C~~I~~AE~~G~~F~~D~~FFF~~S~~L~~S~~N~~K~~V~~K~~DGT~~P~~CSE [707]  
ADAMTS7 FDAM--LYKGQLH---TW~~V~~PVVDN----V~~N~~P~~C~~EL~~H~~CR~~P~~ANE~~Y~~FA~~K~~KLRDAV~~V~~DGT~~P~~CYQ [656]  
ADAMTS12 FDTV--PYKNELY---H~~W~~PFIFNP----A~~H~~P~~C~~EL~~Y~~CR~~P~~IDGQF~~S~~E~~K~~MLD~~A~~V~~I~~DGT~~P~~CFE [660]  
ADAMTS17 HDR---LSPK~~K~~G---LL~~T~~AV~~V~~VD--~~K~~---P~~C~~E~~L~~Y~~C~~S~~P~~L~~G~~K~~E~~S~~P~~LL~~V~~ADR~~V~~L~~D~~G~~T~~P~~C~~GP [660]  
ADAMTS19 YSVR--TSSPKHIL---Q~~W~~QAVLDEE--~~K~~---P~~C~~A~~L~~F~~C~~S~~P~~V~~G~~K~~E~~Q~~P~~ILL~~S~~E~~K~~V~~M~~DGT~~S~~CGY [750]  
ADAMTS2 WDLY--FEHGDAQH---H~~W~~L~~P~~HEHRDA--~~K~~--ER~~C~~H~~L~~Y~~C~~E~~S~~RET~~G~~EV~~V~~SM~~K~~RM~~V~~HDGT~~R~~C~~S~~Y [682]  
ADAMTS3 RNSH--FEYQNTKH---H~~W~~LPYEH~~P~~D~~P~~--~~K~~--KR~~C~~H~~L~~Y~~C~~Q~~S~~KET~~G~~D~~V~~A~~Y~~M~~K~~QL~~V~~HDGT~~H~~C~~S~~Y [672]  
ADAMTS14 RNSY--YVHQNAKH---SW~~V~~PYEPDDD-A--Q~~K~~C~~E~~L~~I~~C~~Q~~SAD~~T~~G~~D~~V~~F~~FM~~N~~Q~~V~~VHDGT~~R~~C~~S~~Y [675]  
ADAMTS13 TDGQ~~P~~LRSS~~P~~GGAS~~F~~Y~~H~~WGAA~~V~~PHS~~Q~~G~~D~~--A~~L~~C~~R~~H~~M~~C~~R~~A~~I~~G~~E~~S~~F~~I~~M~~K~~R~~G~~D~~S~~F~~L~~D~~G~~T~~R~~C~~M~~P~~ [510]  
dCG4096 FDNV--SYQ~~G~~ATYK---W~~L~~PF~~F~~DKN--~~N~~---P~~C~~K~~L~~F~~C~~S~~D~~V~~D~~T~~T~~I~~I~~A~~N~~W~~G~~A~~T~~V~~L~~DGT~~P~~CTL [741]  
ADAMTS4 YNHR--TDL~~F~~K~~S~~F~~P~~GP~~M~~D~~W~~V~~P~~RYT~~G~~V~~A~~--P--Q~~D~~Q~~C~~K~~L~~T~~C~~Q~~A~~R~~A~~L~~G~~Y~~V~~V~~L~~E~~P~~R~~V~~V~~D~~G~~T~~P~~C~~SP [646]  
ADAMTS5 KNGY--QSDAK~~G~~V~~K~~T~~F~~EV~~W~~V~~P~~KYAG~~V~~L--P--A~~D~~V~~C~~K~~L~~T~~C~~R~~A~~K~~G~~T~~G~~Y~~V~~V~~F~~S~~P~~K~~V~~T~~D~~G~~T~~E~~C~~R~~P~~ [692]  
ADAMTS8 YNAY--NYTD~~M~~D~~G~~N--LL~~Q~~W~~V~~PKYAG~~V~~S--P--R~~D~~R~~C~~K~~L~~F~~C~~R~~A~~R~~G~~R~~S~~E~~F~~K~~V~~F~~E~~A~~R~~V~~I~~D~~G~~T~~L~~C~~G~~P [651]  
ADAMTS1 HNEF--SKAS~~F~~SG~~P~~AV~~E~~W~~I~~PKYAG~~V~~S--P--K~~D~~R~~C~~K~~L~~I~~C~~Q~~A~~K~~G~~I~~G~~Y~~F~~V~~L~~Q~~P~~K~~V~~V~~D~~G~~T~~P~~C~~SP [685]  
ADAMTS15 FNGY--NH~~S~~T~~N~~RL~~T~~LA~~V~~AV~~W~~PKYSG~~V~~S--P--R~~D~~K~~C~~K~~L~~I~~C~~R~~A~~N~~G~~T~~G~~Y~~F~~V~~L~~AP~~K~~V~~V~~D~~G~~T~~L~~C~~S~~P [643]  
dCG6107 MNGRN--MN~~I~~P~~G~~V~~N~~PD~~T~~K~~W~~V~~P~~KY~~E~~K---~~D~~---A~~C~~K~~L~~F~~C~~R~~M~~D~~M~~K~~V~~T~~Y~~F~~M~~L~~K~~S~~M~~V~~T~~D~~G~~T~~S~~CAV [771]  
ADAMTS9 FDGK--HF~~N~~I~~N~~GL~~L~~PN~~V~~R~~W~~V~~P~~KYSGI--~~L~~M~~K~~D~~R~~C~~K~~L~~F~~C~~R~~V~~A~~G~~N~~T~~A~~Y~~Q~~L~~R~~D~~R~~V~~I~~D~~G~~T~~P~~C~~G~~Q [713]  
ADAMTS20 FNGK--H~~L~~D~~I~~S~~G~~I~~P~~SN~~V~~R~~W~~L~~P~~RYSGI--~~C~~T~~K~~D~~R~~C~~K~~L~~Y~~C~~Q~~V~~A~~G~~T~~N~~Y~~F~~Y~~L~~L~~K~~D~~M~~V~~E~~D~~G~~T~~P~~C~~GT [668]  
mask 11-----1111111-----11111111111111111111111111111111 [380]  
Ce gon-1 FNNK~~D~~I~~G~~I~~Q~~G~~V~~A~~S~~T~~N~~H~~W~~V~~P~~KYAN~~V~~PN--ER~~C~~K~~L~~Y~~C~~R~~L~~S~~G~~S~~A~~A~~F~~Y~~L~~L~~R~~D~~K~~V~~V~~D~~G~~T~~P~~C~~D~~R [729]  
[Intron 39 40 ]



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[          1090      1100      1110      1120      1130      1140]
[          .          .          .          .          .          .]
[≥80%, full maj.      G      Y      E          ]
ADAMTS6      WPRK---FDVAG--TAFHYKRPTEDEESLE-----ALGPTSENLIVMVLLQ----- [816]
ADAMTS10     QPHR---LPLAG--TTFQLRQGPDOVQSLE-----ALGPINASLIVMVLAR----- [805]
ADAMTS18     WPGE---FPFAG--TTFEYQRSFNREERLY-----APGPTNETLVFEILMQ----- [848]
ADAMTS16     WPGR---YKFSG--TTFDYRRSYNEENLI-----ATGPTNETLIVELLFQ----- [846]
ADAMTS7      WNGD---YQVAG--TFTTYARR-GNWENLT-----SPGPTKEPVWIQLLFQ----- [796]
ADAMTS12     WNGN---YKLAG--TVFQYDRK-GDLEKLM-----ATGPTNESVWIQLLFQ----- [800]
ADAMTS17     LPGE---FQIAG--TTVRYVRR-GLWEKIS-----AKGPTKLPPLHMLVLLFH----- [797]
ADAMTS19     HSGA---FNLAG--TTVHYVRR-GLWEKIS-----AKGPTTAPLHLLVLLFQ----- [887]
ADAMTS2      ASSK---TFIAG--VEWEYRDE-DGRETLQ-----TMGPLHGTITVLVIVPG----- [824]
ADAMTS3      AKSR---TFIDLG--VEWDYNIE-DDIESLH-----TDGPLHDPVIVLIIPQEN----- [814]
ADAMTS14     ATSR---TFTAMG--LEWEDAVE-DAKESLK-----TSGPLPEAIALALPTEG----- [818]
ADAMTS13     PNTTYPSLLEDG---RVEYRVALTEDRLPRLEEIRIWGPLQEDADIQVYRRYGEEYGN-- [667]
dCG4096     MPGE---FEIAG--AESLYDRV-DEQETIT-----IPQPIQHSISLYAIVRGN----- [885]
ADAMTS4      PSPT---DVVLPGA-VSLRYSGATAAESTLS-----GHGPLAQPLTLQVLVAGN----- [790]
ADAMTS5      TSET---IIDING--TVMNYSGWSHRDFLHGM---GSATKEILILVQILATDP----- [839]
ADAMTS8      AIEQ---DILVKG--TILKYSGSIATLERLQ-----SFRPLPEPLTVQLLTVPGE----- [797]
ADAMTS1      TLEQ---DIMYKG--VVLRYSGSSAALERIR-----SFSPLKEPLTIQVLTVGN----- [830]
ADAMTS15     AVER---DLVVKG--SLLRYSGTGTAVESLQ-----ASRPILEPLTVEVLSVGK----- [788]
dCG6107     YPLK---FVYAG--VTMQYTGSSVVEQVN---TTYSWKLSRDLIVQIISLDV----- [931]
ADAMTS9      MAKR---E-IRIG-NAVVEYSGSETAVERIN---STDRIEQELLLQVLSVGK----- [858]
ADAMTS20     TSKK---EINVQGTRVIEYSGSNNAVERIN---STNRQEKELLQVLCVGN----- [814]
mask        1111----111----111111-1111111-----11111111111111----- [505]
Ce gon-1    LARQ---QIAFQD-TVLEYSGSDAIIERIN---GTGPIRSDIYVHVLSVG----- [874]
[Intron
48
]

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[          1150      1160      1170      1180      1190      1200]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj.      Y          ]
ADAMTS6      -----EQNLGIRYKFNVPITRTGSDNEVGFT----- [843]
ADAMTS10     -----TELPALRYRFNAPIARDSLPPYS----- [828]
ADAMTS18     -----GKNPGIAWKYALPKVMNGTPPATKRPAT----- [877]
ADAMTS16     -----GRNPGVAWEYSMPRLGTEKQPPAQPSYT----- [874]
ADAMTS7      -----ESNPGVHYETIHREAGHDEVPPPVFS----- [824]
ADAMTS12     -----VTNPGIKYETIQKDLDNDVEQMYF----- [826]
ADAMTS17     -----DQDYGIHYETVPVNRTAENQSEPEKPQDSLFI----- [830]
ADAMTS19     -----DQNYGLHYETIPSDLPENQSSKAPELFM----- [918]
ADAMTS2      -----DTRVSLTYKYMIHEDSLN-VDDNNVLEEDSVVYE----- [857]
ADAMTS3      -----DTRSSLTYKYIIHEDSVPTINSNNVIQELDTFE----- [848]
ADAMTS14     -----GPRSSLAYKYVIHEDLLPLIGSNNVLEEMDTYE----- [852]
ADAMTS13     -----LTRPDITFTYFQPKPRQAWV----- [687]
dCG4096     -----ESNAGIFYEFTLPALNVTAGRQFQ----- [909]
ADAMTS4      -----PQDTRLRYSFFVPRPTPSTPRPTFQDWLHRRAQILEILRRRP----- [832]
ADAMTS5      -----TKPLDVRYSFFVPKKSTPKVNS-VTSHGSNKVGSHTSQFQ-- [878]
ADAMTS8      -----VFPPKVKYTFFVPNDVDFSMQS-SKERATTNIIQPLLH-AQ- [836]
ADAMTS1      -----ALRPKIKYTYFVKKKESFNAIPTFSA----- [857]
ADAMTS15     -----MTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSN----- [830]
dCG6107     -----SPSKRQDTVLLSYSTIDKPPDYEAEVEIYR----- [975]
ADAMTS9      -----LYNPDVRYSFNIPIEDKPQQFY----- [880]
ADAMTS20     -----LYNPDVHYSFNIPLEERSDMFT----- [836]
mask        11111111111111111111----- [523]
Ce gon-1    -----SHPPDISYEYMTAAVPNAVIRPISSALYL----- [903]

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AC Nicholson, SB Malik, JM Logsdon Jr, E van Meir, 2004. Functional evolution of ADAMTS genes: evidence [from analyses of phylogeny and gene organization. Contact: [john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu)]

[Intron phases marked 0, 1, 2]

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[                1210      1220      1230      1240      1250      1260]
[                .        .        .        .        .        .]
[≥80%, full maj.  W          C   C   G          C          C          P]

ADAMTS6      -----WNHQF-WSECSATCAGGQRQEVVCKRLDDNSIVQNNY--CDPDSK-P [887]
ADAMTS10     -----WHYAP-WTKCSAQCAGGSVQAVECRNQLDSSAVAPHY--CSAHSK-L [872]
ADAMTS18     -----WSIVQ--SECSVSCGGGINVKAICLRQNTQVNSSF---CSAKTK-P [919]
ADAMTS16     -----WAIVR--SECSVSCGGGIMTVREGCYRDLKFQVNMSF---CNPKTR-P [916]
ADAMTS7      -----WHYGP-WTKCTVTCGRGVQRQNVYCLERQAGPVDEEH---CDPLGR-P [867]
ADAMTS12     -----WQYGH-WTECSVTCGTGTRRQTAHCIIKGRGMVKATF---CDPETQ-P [869]
ADAMTS17     -----WTHSG-WEGCSVQCGGGRRRTIVSCTRIVNKTTLVNDSDCPQASR-P [876]
ADAMTS19     -----WTHTS-WEDCDATCGGGRKRTTVSCTKIMSKNISIVDNECKYLTK-P [964]
ADAMTS2      -----WALKK-WSPCSKPCGGGQFTKYGCRRRLDHKMVHRGF--CAALSK-P [901]
ADAMTS3      -----WALKS-WSQVSKPCGGGQYTKYGCRRKSDNKMVHRSF--CEANKK-P [892]
ADAMTS14     -----WALKS-WAPCSKACGGGQFTKYGCRRRRDHMMVQRHL--CDHKKR-P [896]
ADAMTS13     -----WAIVR--GPCSVSCGAGIRWVNYCLDQARKELVETVQ--CQGSQQ-P [730]
dCG4096     -----WRLSN-WTACSASCGGGVQHREPICQENGKGESNEPFQ--RIVSIK-R [953]
ADAMTS4      -----WAGRK----- [837]
ADAMTS5      -----WVTGP-WLACSRTCDTGWHTRTVQCQDGNRKLAKG----CPLSQR-P [919]
ADAMTS8      -----WVLGD-WSECSSTCGAGWQRRTVECRDPSGQASAT----CNKALK-P [877]
ADAMTS1      -----WVIEE-WGECSKSCELGWQRRLVECRDINGQPASE----CAKEVK-P [898]
ADAMTS15     QVEQPDDRPPARWVAGS-WGPCSASCGSGLKRAVDCRGSAGQRTVPA----CDAHR-P [884]
dCG6107     -----WEMQA-PSNCDSLCE-GRSHRLPACISTQGVKVAPQF--CDKSAM-P [1018]
ADAMTS9      -----WNSHGPWQACSKPCQ-GERRKKLVCTRESDQLTVSDQR--CDRLPQ-P [924]
ADAMTS20     -----WDPYGPWEGCTKMCQ-GLQRRNITCIHKSDHSVVSDKE--CDHLPL-P [880]
mask        -----11111----- [528]
Ce gon-1     -----WRVDTWTECDRACR--GQQSQKLMCLDMSTHRQSHDRN--CQNVLK-P [947]
[Intron          49 ]

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[                1270      1280      1290      1300      1310      1320]
[                .        .        .        .        .        .]
[≥80%, full maj.  C   C          ]
ADAMTS6      PENQRACNTEPCPPE-WFIGDWLECSKTCDGGMRTRAVL-CIRKIGPSEEETLDYSG-CL [944]
ADAMTS10     PKRQRACNTEPCPPD-WVGNWLSLCSRSCDAGVRSRSVV-CQRRVSAAEEKALDDSA-CP [929]
ADAMTS18     VTEPKICNAFSCPAY-WMPGEWSTCSKACAGQSRKIQ-CVQKKPFQKEAVLHSL-CP [976]
ADAMTS16     VTGLVPCKVSACPPS-WSVGNWSACSRTCGGGAQSRFVQ-C-TRRVHYDSEFVPASL-CP [972]
ADAMTS7      DDQQRKCEQPCPAR-WWAGEWQLCSSCGPGLSRRAVLCIRSVGLDEQSALEPPA-CE [925]
ADAMTS12     NGRQKCHEKACPPR-WWAGEWEACSATCGPHEKRTVLCIQTMVSDEQ-ALPPTD-CQ [926]
ADAMTS17     EPQVRRCNLHPCQSR-WVAGPWSPCSATCEKGFQHREVT-CVYQLQNGTHVATRPLY-CP [933]
ADAMTS19     EPQIRKCNEQPCQTR-WMMTEWTPCSRTCGKGMSRQVA-CTQQLSNGTLIRARERD-CI [1021]
ADAMTS2      KAIRRACNPECSQPVVTGEWEPCSQTCGRTGMQVRSVRCIQPLHDNTTRSVHAKH-CN [960]
ADAMTS3      KPIRRCNIQECTHPLWVAEEWEHCTKTCGSSGYQLRTVRCLQPLDGTNRSVHSKY-CM [951]
ADAMTS14     KPIRRRCNQHPCSQPVVTEEWGACSRSCGLGVQTRGIQCLLPLSNGTHKVMPAKA-CA [955]
ADAMTS13     PAWPEACVLEPCPPY-WAVGDFGPCSASCGGLRERFV-RCVEAQSLLKTLPPAR--CR [786]
dCG4096     NLLIALGDTLPC----WTHAKN-KR-PARQSRG----- [980]
ADAMTS4      ----- [837]
ADAMTS5      SAFKQ-CLLKKC----- [930]
ADAMTS8      EDAKP-CESQLCPL----- [890]
ADAMTS1      ASTRP-CADHPCPQ--WQLGEWSSCSKTCGKYKRSLK-CLSHDGGVLSHES----CD [949]
ADAMTS15     VETQA-CGEP-CPT--WELSAWSPCSKSCGRGFRRSLK-CVGHGGRLLARDQ----CN [934]
dCG6107     KIDDRACNTD-CRLN-ITVTSISESAACGELGTREKTYACVQTFTNMQRSNIVDMSYCK [1076]
ADAMTS9      GHITEPCGTD-CDLR-WHVASRSESAQCGLGYRTLDIY-CAKYSRLDGKTEKVDDGFCS [981]
ADAMTS20     SFVTQSCNTD-CELR-WHVIGKSECSSQCGYRTLDIH-CMKYSIHEGQTVQVDDHYCG [937]
mask        ----- [528]
Ce gon-1     KQATRMCNID-CSTR-WITEDVSSSAKCGSGQKRQRVS-CVKMEGDRQTPASEHL--CD [1002]
[Intron          50 ]

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[                1330      1340      1350      1360      1370      1380]
[                .                .                .                .                .                .]
[≥80%, full maj.      C      C                                ]
ADAMTS6      THRPVEKEP---CNNQS-CP PQ-WVALDWSECTPKCGP-GFKHRIVLCKSSDLSKTFPAA [998]
ADAMTS10     QFRPPVLEA---CHGPT-CPPE-WAALDWSECTPSCGP-GLRHRVVLCKSADHRATLPPA [983]
ADAMTS18     VSTPTQVQA---CN SHA-CP PQ-WSLGPWSQCSKTCGR-GVRKRELLCKGSAEATLPESQ [1030]
ADAMTS16     QFAPSSRQA---CNSQS-CP PA-WSAGPWABCSHTCGK-GWRKRAVACKSTNPSARAQLL [1026]
ADAMTS7      HLP RPPTETP--CNRHVPCPAT-WAVGNWSQCSVTCEG-GTQRRNVLCTNDTGVP----- [976]
ADAMTS12     HLLKPKTLLS--CNRDILCPSD-WTVGNWSECSVSCGG-GVIRSVTCAKNHDEP----- [977]
ADAMTS17     GPRPAVQS---CEGQD-CLSI-WEASEWSQCSASC GK-GVWKRTVACTNSQ GK----- [981]
ADAMTS19     GPKPASAQR---CEGQD-CMTV-WEAGVWSECSVKCGK-GIRHRTVRCTNPRKK----- [1069]
ADAMTS2      DARPESRRA---CSREL-CPGR-WRAGPWSQCSVTCEG-GTQERPVP CRTADDSFGI--- [1011]
ADAMTS3      GDRPESRRP---CNRVP-CPAQ-WKTGPWSECSVTCEG-GTEVRQVLCRAGDH----- [1005]
ADAMTS14     GDRPEARRP---CLRVP-CPAQ-WRLGAWSQCSATCGE-GIQQRQVVCRTNANSLGH--- [1006]
ADAMTS13     AGAQQPAVALET CNPQP-CPAR-WEVSEPSCTSAGGA-GLALENETCVPGADGLEAPVT [843]
dCG4096     -----CGDQP-CPAH-WWPGPWQFCPVTCRPVGFVAPPQRRRSVVCLDEHDVV [1026]
ADAMTS4     ----- [837]
ADAMTS5     ----- [930]
ADAMTS8     ----- [890]
ADAMTS1     PLKKPKHFIDF-CTMAE-CS----- [967]
ADAMTS15     LHRKPQELDF--CVLRP-C----- [950]
dCG6107     LKFDVAYHEE--CREG--C---WVLSWSTCSKSCGT-GSQQREAHCYLHNSRVSDDL- [1126]
ADAMTS9     SHPKPSNREK--CSGE--CNTGGWRYSAWTECSKSCDG-GTQRRRAICVNTRNDVLDDSK [1036]
ADAMTS20    DQLKPPPTQEL--CHGN--CVFTRWHYSEWSQCSRSCGG-GERSRESYCMNNFGHRLADNE [992]
mask                                               [528]
Ce gon-1    RNSKPSDIAS--CYID--CSGRKWN YGEWTS CSETCGSNGMKHRKSYCVDDSNRRVDESL [1058]
[Intron                51      52                                ]

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[                1390      1400      1410      1420      1430      1440]
[                .                .                .                .                .                .]
[Modal, ≥80%, full maj.                                ]
ADAMTS6      Q---CPEESKPPVRIR---CSLGR--CPPPR-----WVTGD [1026]
ADAMTS10     H---CSPA AKPPATMR---CNLRR--CPPAR-----WVAGE [1011]
ADAMTS18     ---CTSLRPPELQEG---CVLGR--CPKNSRLQ-----WVASS [1060]
ADAMTS16     PDAV-CTSEPKPRMHEA---CLLQR--CHKPKKLQ-----WL VSA [1060]
ADAMTS7      ---CDEAQQPASEVT---CSLPL--CR-----WPLGT [1000]
ADAMTS12     ---CDVTRKPN SRAL---CGLQQ--CP-----SS [998]
ADAMTS17     ---CDASTRPRAE EA---CEDYSG-CYE-----WKTGD [1007]
ADAMTS19     ---CVLSTRPREAED---CEDYSK-CYV-----WRMGD [1095]
ADAMTS2      ---CQEERP ETART-CRLGPCPRN- ISDPSKKS YVV-----QWLSRP [1048]
ADAMTS3      ---CDGEKPESVRA-CQLPPCND-EP----- [1027]
ADAMTS14     ---CEGDRPD TVQV---CSLPACGGNHQNSTVRADVWELVTPEG-----QWVPQS [1041]
ADAMTS13     EGGP-SVDEKLPAPEP---CVGMS--CPPGWGH- DATSAGEKAPSPWGSIRTGAQAAHV [896]
dCG4096     VADAE CGHLQKPAEME---PCESSLPICR TK----- [1054]
ADAMTS4     ----- [837]
ADAMTS5     ----- [930]
ADAMTS8     ----- [890]
ADAMTS1     ----- [967]
ADAMTS15     ----- [950]
dCG6107     ---CNPRTKPHLNTLIGICNTES--CPTYTKSP-ALAVSN-----WVIGE [1166]
ADAMTS9     ---CTHQEKVTIQR---CSEFP--CPQ-----WKSGD [1060]
ADAMTS20    ---CQELSRVTREN---CNEFS--CPS-----WAASE [1016]
mask                                               [528]
Ce gon-1    ---CGREQKEATERE---CNRIP--CPR-----WVYGH [1083]
[Intron                53      54, 55                                ]

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[                               1450      1460      1470      1480      1490      1500]
[                               .           .           .           .           .           .]
[Modal, ≥80%, full maj. ]
ADAMTS6   WGQ----CSAQCGLGQQMRTVQCLS YTGQASSD-----CLETVRPPSMQQ--CESK-C [1072]
ADAMTS10  WGE----CSAQCGVGQRQRSVRCTSH TQASHE-----CTEALRPPTTQQ--CEAK-C [1057]
ADAMTS18  WSE----CSATCGLGVRKREMKCSEKGFQ GK LITFPERR-CRNIKKPNLDLEETCNRAC [1115]
ADAMTS16  WSQ----SVTCERG TQKRFLKCAEKYVSG KYRELASKK-CSHLPKPSLELERACAPLPC [1115]
ADAMTS7   LGPEGS GSGSSSHEL FNEADFI PHHLAPRPS PASSPKPG-TMGNAIEEEAPELDLPGPVF [1059]
ADAMTS12  RRVLKP NKGTISNGKNPPTLKPVP PPTS RPRMLTTP TGP-----ESMSTSTPAISSP [1050]
ADAMTS17  WST----SSSTCGKGLQSRV VQCMHKVTGRHGSE-----CPALSKPAPYRQ--CYQEV C [1055]
ADAMTS19  WSK----SITCGKGMQSRVI QCMHKITGRHGNE-----CFSSEKPAAYRP--CHLQPC [1143]
ADAMTS2   -----DPDSPIRKISSKHCQGD KSI FCRMEVLSRYCSIPGYNKLS----CKS--C [1093]
ADAMTS3   -----CLGDKSIFCQMEVLARYCSIPGYNKLC----CES--C [1027]
ADAMTS14  -----PLHPIYKISST E PCTGDRS VFCQMEVLD RYCSIPGYHRL----CCVS-C [1095]
ADAMTS13  WTPAAGSCSVSCGRGIMELRFLC MDSALRVPVQEEL----CGLASKPGSRREV-CQAVPC [951]
dCG4096   ----- [1054]
ADAMTS4   ----- [837]
ADAMTS5   ----- [930]
ADAMTS8   ----- [890]
ADAMTS1   ----- [967]
ADAMTS15  ----- [950]
dCG6107  WGE----CNEWCEKTRSVS---C SHPYGIG-----CGSRKPKDVRK---CCHIKY [1206]
ADAMTS9   WSE----CLVTCGKGHKHRQVWCQFGEDRLNDRM-----CDPETKPTSMQT--CQQPEC [1108]
ADAMTS20  WSE----CLVTCGKGTKQRQVWCQLNVDHLS DGF-----CNSSTKPESLSP--CELHTC [1064]
mask     ----- [528]
Ce gon-1  WSE----CSRSCDGGVKMRHAQCLD AADREHTHSR-----CGPAQTQEH----CNEHAC [1129]
[Intron   56      57      58 ]

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[                               1510      1520      1530      1540      1550      1560]
[                               .           .           .           .           .           .]
[Modal, ≥80%, full maj. ]
ADAMTS6   D-----S-TPI SNTEEKDVNKVAYCPLVLKFKFCSRAYFRQMCCCKTCQGH----- [1117]
ADAMTS10  D-----SPTPGDGP EEEKDVNKVAYCPLVLKFKFQCSRAYFRQMCCCKTCQGH----- [1103]
ADAMTS18  PAHPVYNM VAG---WYSLPWQQCTVTCGGGVQTRSVHCVQQGRPSS-----CLLH [1163]
ADAMTS16  PRHPPFAAAGPSRGSWFAS PWSQCTASC GGGVQTRSVQCLAGGRPASG-----CLLH [1167]
ADAMTS7   VDDFYDYNFINFHEDLSYGPSEEPDL DLAGTGDRTPPPHSRPAAPSTGSPVPATEPPAA [1119]
ADAMTS12  SPTTASKEGDLGGKQWQDSSTQPELSSRYL ISTGSTSQPIILTSQSLSIQSPSEENVSSSDT [1110]
ADAMTS17  NDRINANTITSPRLA LTYKCTRDQWTVYCRVIREKNLCQDMRWYQRCCQTCRDFYANKM [1115]
ADAMTS19  NEKINVNTITSPRLA LTFKCLGDQWPVYCRVIREKNLCQDMRWYQRCCETCRDFYAQKL [1150]
ADAMTS2   NLYNNLTNVEGRIEPPPGKHNDIDVF----- [1119]
ADAMTS3   SKRSSTLPPPYLLEAAETHDDVISNP----- [1076]
ADAMTS14  IKKASGFNPGPDGPPTS LPP----- [1115]
ADAMTS13  PA-----RWQYKLAACSVSCGRGVVRRILYCARAHGEDDGEIILLDTQCQGL [998]
dCG4096   ----- [1054]
ADAMTS4   ----- [837]
ADAMTS5   ----- [930]
ADAMTS8   ----- [890]
ADAMTS1   ----- [967]
ADAMTS15  ----- [950]
dCG6107  TSD-----WTD SVQCGEGVKKRKKQ SCTRVIKPDVPGTR---KRRVY [1246]
ADAMTS9   AS-----WQAGPWQCSVTCGQYQLRAVKCIIGTYMSVVDND---CNAA [1151]
ADAMTS20  AS-----WQVGPWGPCTTTCG HGYQMRDVKCVNELASAVLEDE---CHEA [1107]
mask     ----- [528]
Ce gon-1  TW-----WQFGVWSDCSAKCGDGVQYRDANCTDRHRSVLPEHR----CLKM [1171]
[Intron   59, 60, 61, 62 ]

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[           1570      1580      1590      1600      1610      1620]
[           .         .         .         .         .         .]
[Modal, >=80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 QKPPVLRACNTNFCP----- [1178]
ADAMTS16 QKPSASLACNTHFCP----- [1182]
ADAMTS7  KEEGVLGPWSPSPWPSQAGRSPPPPSEQTPGNPLINFLPEEDTPIGAPDLGLPSLSWPRV [1179]
ADAMTS12 GPTSEGGLVATTTSGSGLSSSRNPITWVPVTPFYNTLTKGPEMEIHSGSGEEREQPEDKDE [1170]
ADAMTS17 RQPPSS----- [1122]
ADAMTS19 QQKS----- [1150]
ADAMTS2 ----- [1119]
ADAMTS3  SDLPRSLVMP TSLVPYHSETPAKKMSLSSISSVGGPNAYAAFRPNSKPDGANLRQSAQQ [1136]
ADAMTS14 ----- [1115]
ADAMTS13 PRPEQEACSL EPCPPR[K]VMSLGPCSASCGLTARRSVACVQLDQGQDVEVDEAACAAL [1058]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 QLQVECLGLEALSC----- [1260]
ADAMTS9  TRPTDTQ-----[C]SATCGKGRMRYVSCRDENGSVADESAC-ATLPR [1192]
ADAMTS20 SRPSDRQ-----[C]SVSCGRGTQARYVSCRDALDRIADESYC-AHLPR [1148]
mask ----- [528]
Ce gon-1  EKIIT-KPCHRESCPKYKLGESQ-CSVSCEDGWSSRRVSCVSGNGTEVDMSLC-GTASD [1228]
[Intron           64       65           ]

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[           1630      1640      1650      1660      1670      1680]
[           .         .         .         .         .         .]
[Modal, >=80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7  STDGLQTPATPESQNDFPVGKDSQSQLPPPWRDRTNVFKDDEEPKGRGAPHLPPRPSST [1239]
ADAMTS12 SNPVIWTKIRVFGNDAPVESTEMPLAPLTPDLSRESWWPPFSTVMEGLLPSQRPTTSET [1230]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1150]
ADAMTS2  -MPTLPVPTVAMEVRPSPSTPLEVPLNASSTNATEDHPETNAVDEPYKIHGLEDEVQPPN [1178]
ADAMTS3  AGSKTVRLVTVPSSPPTKRVHLSSASQMAAASFFAASDSIGASSQARTSKKDGIIDNRR [1196]
ADAMTS14 ----- [1115]
ADAMTS13 VRPEASVPCLIADCTYRWHVGTWME[SV]SCGDGIQRRRDTCLGPPQAQAPVPADFCQHLPK [1118]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  PVAKEE-CSVTPCGQ--WKALDWSS[SV]TCGGRATRQVMCVNYS DHVIDRSECDQDYIP [1249]
ADAMTS20 PAEIWD-CFTP-CGE--WQAGDWSP[SV]ASC GHGKTRQVLCMNYHQPIDENY-CDPEVRP [1203]
mask ----- [528]
Ce gon-1  RPASHQTCNLGTCPF--WRNTDWSA[SV]SCGIGHRERTTECIYREQSV DASF-CGDTKMP [1285]
[Intron           66           ]

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[           1690       1700       1710       1720       1730       1740]
[           .           .           .           .           .           .]
[Modal, >=80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7  LPPLSPVGSTHSSPSDVAELWTGGTVAWEPALEGGLGPVDSELWPTVGVASLLPPIAP [1299]
ADAMTS12  GTPRVEGMVTEKPANTLLPLGGDHQPEPSGKTANRNHLKLPNNMNQTKSSEFVLTEEDAT [1290]
ADAMTS17  ----- [1122]
ADAMTS19  ----- [1150]
ADAMTS2   LI PRRPSPYEKTRNQRIQELIDEMRKKEMLGKF----- [1211]
ADAMTS3   PTRSSTLER----- [1205]
ADAMTS14  ----- [1115]
ADAMTS13  PVTVRGCWAGPCVGGQTPSLVPHEEAAAPGRTTATPAGASLEWSQARGLLFSPAPQPRRL [1178]
dCG4096   ----- [1054]
ADAMTS4   ----- [837]
ADAMTS5   ----- [930]
ADAMTS8   ----- [890]
ADAMTS1   ----- [967]
ADAMTS15  ----- [950]
dCG6107   ----- [1260]
ADAMTS9   ETDQDCSMSPCPQRTPD SGLAQHPFQNE DYRPRSAS-----PSRTHVLGGNQWRTGP [1301]
ADAMTS20  LMEQECSLAACPPAHSHFPSSPVQPSYYLSTNLPLTQKLEDNENQVVHPSVRGNQWRTGP [1263]
mask ----- [528]
Ce gon-1  ETSQTCHLLPCTS-----WKPSH [1303]
[Intron ]

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[           1750       1760       1770       1780       1790       1800]
[           .           .           .           .           .           .]
[Modal, >=80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7  LPPEMVKVRDSSLEPGTSPFPAPGPGSWDLQTVAVWGTFLPTTLTGLGHMPEPALNPGPKGQ [1359]
ADAMTS12  SLITEGFLNASNYQLTNGHGSAAHWIVGNWSECSTTCGLGAYWKRVECTTQMDSDCAAI [1350]
ADAMTS17  ----- [1122]
ADAMTS19  ----- [1150]
ADAMTS2   ----- [1211]
ADAMTS3   ----- [1205]
ADAMTS14  ----- [1115]
ADAMTS13  LPGPQENS VQSS CGRQHLEPTGTIDMRGPGQADCAVAIGRPLGEVVTLRVLESSLNC SA [1238]
dCG4096   ----- [1054]
ADAMTS4   ----- [837]
ADAMTS5   ----- [930]
ADAMTS8   ----- [890]
ADAMTS1   ----- [967]
ADAMTS15  ----- [950]
dCG6107   ----- [1260]
ADAMTS9   WGACSSSTCAGGSQRRVVVCQDENG YTAND---CVERIKPDEQRACESGPCPQ----- [1350]
ADAMTS20  WGSQSSSCSGLQHRAVVCQDENGQSASY---CDAASKPPELQCCGPGPCPQ----- [1312]
mask ----- [528]
Ce gon-1  WSPCSVTCGSGIQTRSVSCTRGSEGTIVDEYFCDRTRPRLKKTCEKDTCDGPRVLQKLQ [1363]
[Intron ]
           67       68       69

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[          1810      1820      1830      1840      1850      1860]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7  PESLSPEVPLSSRLLSTPAWDSPANSHRVPETQPLAPSLAEAGPPADPLVVRNASWQAGN [1419]
ADAMTS12 QRPDPAKRCHLRPCAGWKVGNWSKCSRNCSSGGFKIREIQCVDSRDRHNLRFHCFQFLAGI [1410]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1150]
ADAMTS2  ----- [1211]
ADAMTS3  ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 GMLLLWGRLTWRKMCRKLLDMTFSSKTNLTVVRQRCGRPGGGVLLRYGSQLAPETFYRE [1298]
dCG4096 ----- [1054]
ADAMTS4  ----- [837]
ADAMTS5  ----- [930]
ADAMTS8  ----- [890]
ADAMTS1  ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  -----WAYGNWGEITKLCGGGIRTRLVVCQRSNGERFPDLSCEILDKPPDREQCNTHA [1403]
ADAMTS20 -----WNYGNWGEISQTCGGGIKSRVLVICQFPNGQILEDHNCEIVNKPPSVIQCHMHA [1365]
mask ----- [528]
Ce gon-1 ADVVPIRWATGPWTACSATCGNGTQRLLKCRDHVRDLPDEY-CNHLDKEVSTRNCRLRD [1422]
[Intron 70 71 ]

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[          1870      1880      1890      1900      1910      1920]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7  WSECSTTCGLGAVWRPVRCSGRDEDCAPAGRPPARRCHLRPCAT----- [1465]
ADAMTS12 PPPLSMSCNPEFCEAWQVEPWSQCSRSCGGGVQERGVFCPGGLCDWTKRPTSTMSCNEHL [1470]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1150]
ADAMTS2  ----- [1211]
ADAMTS3  ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 DMQLFGPWGEIVSPSLSPATSNAGGCRFLINVAPHARIAIHALATNMGAGTEGANASYI [1358]
dCG4096 ----- [1054]
ADAMTS4  ----- [837]
ADAMTS5  ----- [930]
ADAMTS8  ----- [890]
ADAMTS1  ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  CPHDAAWSTGPWSSCSVSCGRGHKQRNVY-CMAKDGSHPLESY---CKHLAKPHGHRKCR [1459]
ADAMTS20 CPADVSWHQEPWTSCSASCGRKRYREVF-CIDQFQRKLEDTN---CSQVQKPPTHKACR [1421]
mask ----- [528]
Ce gon-1 CSY---WKMAEWEPCATCGTHVQQSRNVTCVSAEDGGRTILKDVDCDVQKRPTSARNCR [1479]
[Intron 72 ]

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[          1930      1940      1950      1960      1970      1980]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7 -----WHSGNWSKCSRSCGGGSSVRDVQCVDTDRDLRPLRPFHCQPGPAKPPA [1512]
ADAMTS12 CCH-----WATGNWDLCTSCGGGFQKRIVQCVPEGNKTEDQDQCLCDHKPRPP [1520]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1150]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 LIRDTHSLRRTAFHGGQVLYWESESSQAEMEFSEGFLKAQASLRGQYWTLQSWVPEMQDP [1418]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 GGRCPK-----WKAGAWSQSVSCGRGVQQRHVGCQIGTHKIARETECNPYTRPESER [1512]
ADAMTS20 SVRCPS-----WKANSWNEQSVTCGSGVQQRDVYCRKLGVGQVVEEMCDQSTRPCSQR [1474]
mask ----- [528]
Ce gon-1 LEPCPKGEEHIGSWIIGDWSKCSASC GGWRRRSVSCTSSSCDETRKPKMFDKCN EELCP [1539]
[Intron 73 74 ]
[          1990      2000      2010      2020      2030      2040]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7 HRPCGAQPCLSWYTSSWRECSEACGGGEQQRLVTCPEPGL-----CEEALRPNTTRPC [1565]
ADAMTS12 EFKKCNQQACKKSADLLCTKDKLSASFQTLKAMKCSVPTVRAECCFSCPQTHITHTQR [1580]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1150]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 QSWKGREGT----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 DCQGPRCPLYTWRAEEWQEITKTCGEGSRYRKVVCVDDNKNEVHGARCDVSKRPVDRESC [1572]
ADAMTS20 RC-----WSQDCVQHKGMERGLNLCANNCGFSYRQRITYCTEIPSTKHKHLHRLRP [1525]
mask ----- [528]
Ce gon-1 PLTNNS-----WQISPWTHQSVSCGGGVQRRKIWCEDVLSGRKQDDIECSEIKPREQRDC [1594]
[Intron 75 ]

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[          2050      2060      2070      2080      2090      2100]
[          .          .          .          .          .          .]
[Modal, >80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1178]
ADAMTS16 ----- [1182]
ADAMTS7  NTHPCTQ-WVVGFWGQCSAPCGGGVQRRLVKCVNTQTGLPEEDSDQCGHEAWPESSRPCG [1624]
ADAMTS12  QRRQRLLQKSKEL----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1150]
ADAMTS2  ----- [1211]
ADAMTS3  ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1  ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  SLHPCEYVWITGEWSECSVTGCGKGYQRLVSCSEIYTGKENYEYSSQTTINCPGTQPPSV [1632]
ADAMTS20  IVYQECFVVPSSQVYQCINSCLHLATWVKVGSKSVTCGIGIMKRQVKCITKHGLSSDL [1585]
mask ----- [528]
Ce gon-1  EMPPCRSHYHNKTSSASMTSLSSSNSNTTSSASASSLPILPPVVSQTSAWSACSAKCGR [1654]
[Intron                               76                               ]

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[          2110      2120      2130      2140      2150      2160]
[          .          .          .          .          .          .]
[Modal, >80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 -----APEKREDPS [1187]
ADAMTS16 -----IAEKKDAF----- [1190]
ADAMTS7  TEDCEPVEPPRCERDRLSFGFCETLRLLLGRCQLPTIRTQCCRSCSPPSHGAPSRGHQ RVA [1684]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1162]
ADAMTS2  ----- [1211]
ADAMTS3  ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1  ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  HPCYL RDCPV SATWRVGNWGS SVSCGVGMQRVSVQCLNNAVQPSHLCRSDLKPEERKTC [1692]
ADAMTS20  CLNHLKPGAQKKCYANDCKS-----FTTCKEIQV [1614]
mask ----- [528]
Ce gon-1  GTKRRVVECVNPSLNVTVASTECDQTKKPVEEVRCRTKHCPRWKTTTSSCSVTGCRGIR [1714]
[Intron                               77 78                               79                               ]

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[          2170      2180      2190      2200      2210      2220]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 CVDDFFNWCHLVPQHGVCNHHKFGYKQCKSCTRKI----- [1221]
ADAMTS16 CKDYFHWCYLVPQHGMCCHKFYKQCKTCSKSNL----- [1225]
ADAMTS7  RR----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2  ----- [1211]
ADAMTS3  ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4  ----- [837]
ADAMTS5  ----- [930]
ADAMTS8  ----- [890]
ADAMTS1  ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  RNVYN----- [1697]
ADAMTS20 KN-HIRKDG DY YLN IKGRI I KVL----- [1636]
mask ----- [528]
Ce gon-1 RREVQCYRGRKNLVS DSECNPKTKLNSVANCFPVACPAYRWNVTPWSKCKDECARGQQT [1774]

[          2230      2240      2250      2260      2270      2280]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7  ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2  ----- [1211]
ADAMTS3  ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4  ----- [837]
ADAMTS5  ----- [930]
ADAMTS8  ----- [890]
ADAMTS1  ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9  ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 RRVHCISTSGKRAAPRMCELARAPTSIRECDTSNCPYEWVPGDWQTCSKSCGEGVQTREV [1834]

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[           2290      2300      2310      2320      2330      2340]
[           .         .         .         .         .         .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7 ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 RCRRKINFNSTIPIIIFMLEDEPAVPKEKCELFPKPNESQTCELNPCDSEFKWSFGPWGEC [1894]

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[           2350      2360      2370      2380      2390      2400]
[           .         .         .         .         .         .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7 ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 SKNCGQGI RRRRVKCVANDGRRVERVKCTTKKPRRTQYCFERNCLPSTCQELKSQNVKAK [1954]

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```

[           2410      2420      2430      2440      2450      2460]
[           .         .         .         .         .         .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7 ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 DGNVTILLDGFTEIEYCHRMNSTIPKAYLNVNPRTNFAEVYGKKLIYPHTCPFNGDRNDS [2014]

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[           2470      2480      2490      2500      2510      2520]
[           .         .         .         .         .         .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7 ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 CHCEDGDASAGLTRFNKVRIDLNRKFHLADYTFAKREYGVHVPYGTAGDCYSMKDCPQ [2074]

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[          2530      2540      2550      2560      2570      2580]
[          .          .          .          .          .          .]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7 ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 GIFSIDLKSAGLKLVDLWEDQGHRSSRIDRFYNNAKVIGHCGGFCGKCSPERYKGLI [2134]

[          2590      2600      2610]
[          .          .          . ]
[Modal, ≥80%, full maj. ]
ADAMTS6 ----- [1117]
ADAMTS10 ----- [1103]
ADAMTS18 ----- [1221]
ADAMTS16 ----- [1225]
ADAMTS7 ----- [1686]
ADAMTS12 ----- [1593]
ADAMTS17 ----- [1122]
ADAMTS19 ----- [1207]
ADAMTS2 ----- [1211]
ADAMTS3 ----- [1205]
ADAMTS14 ----- [1115]
ADAMTS13 ----- [1427]
dCG4096 ----- [1054]
ADAMTS4 ----- [837]
ADAMTS5 ----- [930]
ADAMTS8 ----- [890]
ADAMTS1 ----- [967]
ADAMTS15 ----- [950]
dCG6107 ----- [1260]
ADAMTS9 ----- [1697]
ADAMTS20 ----- [1636]
mask ----- [528]
Ce gon-1 FEVNTKLLNHVKNGGHIDDELDDDFSGDMD [2165]
;
END;

```