```
Dmel13425_43-152   ---------FRERSQSDWENVWHQETHSRCRDKLVRQLYWACEKDIYRL-TR---------RNKKRTGNDEAWIKKTTTE  61
Dmel5116_1-107     -MMFRSVIPVLLFLIPLLLSAQAANSLRACGPALMDMLRVACPNGFNSMFAK---------RGT--LGLFDYEDHLADLD  68
Dmel11016_2-133    SKPLSFISMVAVILLASSTVKLAQGT--LCSEKLNEVLSMVCEEYNPVIPHK---------RAM--PGADSDLDALNPLQ  67
Dmel11015_20-152   IAAMLTAAMAMVTPTGSGHQLLPPGNHKLCGPALSDAMDVVCPHGFNTLPRK---------RESLLGNSDDDEDTEQEVQ  71
Dmel11017_30-116   ----------------------------TMKLCGRKLPETLSKLCVYGFNAM-TK---------RTL-------------DPVN  33
Dmel13472_79-106   ----------------------------------------------------------------RK---------RDL-----------------  5
Dmel11018_9-134    -------ALLLLLATVSQLLQPVQGRRKMCGEALIQALDVICVNGFTRRVRRSSASKDARVRDLIRKLQQPDEDIEQETE  73
                                   10        20        30        40        50        60        70        80

Consensus
XXXXXXXAMVLXXLTXSXLXXLAQGTHKLCGXXLXXALXVXCXNGFNRXPRKSSASKDARVRDLXRXGXDDDEDXXQXXX
```

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Dmel13425_43-152   PDGSTWLH----------------------------VNYANMFLRSRRSDGNTPSISNECCTKAGCTWEEYAEYCPS  110
Dmel5116_1-107     SSES--------------------------------HHMNSLSSIRRDFR----GVVDSCCRK-SCSFSTLRAYCD-  107
Dmel11016_2-133    FVQEFEEE---DNSISEPLRSALFPGSYLGGVLNSLAEVRRRTRQRQ----GIVERCCKK-SCDMKALREYCS-  132
Dmel11015_20-152   DDSSMWQTLDGAGYSFSPLLTNL----------YGSEVLIKMRRHRRHLTGGVYDECCVK-TCSYLELAIYCL-  133
Dmel11017_30-116   FNQI-------DGFEDRSLLERLLS--------DSSVQMLKTRRLRD----GVFDECCLK-SCTMDEVLRYCAA  87
Dmel13472_79-106   ----------------------------------------------------------Q----NVTDLCCKSGGCTYRELLQYCK-  28
Dmel11018_9-134    TGRLKQKHTDADTEKGVP----------------PAVGSGRKLRRHRR----RIAHECCKE-GCTYDDILDYCA-  126
                                  90        100       110       120       130       140       150

Consensus
FDQSXWXHXDXDGXXXXPLLXXLXXGSYLGGVLXSSASXRKRRRHRRXXTXGVVDECCKKXXCTYDELLEYCAX
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