Figure S1. Coiled-coil region of the PvMSP3 protein family members predicted by a program of Multicoil (http://groups.csail.mit.edu/cb/multicoil/cgi-bin/multicoil.cgi) with 0.5 cut-offs for scoring a coiled-coil structure. Below the amino sequence are the predicted frames of the coiled-coils represented by the 'abcdefg' convention for the heptad repeats. The repeated AXXAXXX sequence pattern representing predicted coiled-coil heptads is marked by a red underline.

PvMSP3.1

```
  1  MKHLSGIPLFVLFLNLYVLQNNVVSNENVNLKNPNLRNGWAGKNVTLQDEQSGLVAEDGEEVNTKEDQNE
 71  LLHKSEETDFQTQGQEVKEIGGSENEKKQKQIKKANEAKEKALKEQKEAEDEVKKIEEALDKVKKAKAEA
                              abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcd
141  EEEAEIKKVVEKAKGVADKAKETAMNKAKKSKDEAEKIAGVNTNSMAYLYAGNAVTAEIEAKAEKEKAKK
     efg                                                          abcdefgabcdef
211  AAEIAKHAVDAYELKKEAEKAQEEAEAAKTEIEKLSKVYKEGNVTEAVQSTAEAEKSASGASAKVKEAAH
     gabcdefg          abcdefgabcdefgabcdefg             abcdefgabcdefgabcdef
281  NVAKKLMDAVQKLEKVSTELPKDNEQAATIDNVNEVVTEAVKEKEKAMISAEVAKAEAANAEAQLAKIEA
     g                                                abcdefgabcdefgabcdefgabcd
351  ERAKYEANKIAEEYTDNVKGEAKKAEEKANEASSKATEASNNAKGASGEEKQTNPQAANVKAKAGEAIKA
     efgabcdefg            abcdefgabcdefgabcdefgabcdefg
421  AKEAKKAKTEAYIALCVTKTLVAKENAKKAEQEAKNAKDKATKAAKEAEEAKKQAEKAEKITETVKNEAK
                          abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgab
491  TATDEEAKASTGKKDAEINAGYVDEEVYAVNIEFEIAKEAAKTAAQHKALEILDKAEKNAEIAAENATAK
     cdefg                                                abcdefgabcdefgabcdefg
561  AQEATKKAETAKTKATEAETAAKKAQDASEKAKAIAADVLAQKASTEAQSLKQEAEKLAENIKKSNVTDE
     abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg     abcdefg   abcdef
631  EKAKADEAAKAAKDAADQASASAKKANDAKIAATNAQVVVTLQTKKAESAKAEDAAKEAMKARDKAAFEL
     gabcdefgabcdefgabcdefgabcdefgabcdefg             abcdefgabcdefgabcdefga
701  LKIKKQDVLEQVDVSPSGSDNLNDVDEQVALEVGEQQNETEDAEPQEAEEGDEEDEEDTEEEEIQDESDH
     bcdefg
771  TEESSAKQAAQQEKQQGEKVLNDEEAHNLLAQQHNKDNNAATEDAKLFQTIIKDFDDDDDFKNLQKDVNA
841  LFKIK
```

PvMSP3.2

```
  1  MRQFFGTTILVLFLNLYVLQTNVVSNENVNLKNPNLRNGWAGKNLALQDEQSGIDAEDGGEENTCEGQSE
 71  LLQKSEAQVQTQGQEIKATGESDDPKKKKSPIEKANEAKDNALKEQEGAEAEVKKIEEAEKKVEGAEEGI
                                  abcdefgabcdefgabcdefgabcdefg          a
141  KNAVKKAKEAAEFAKNTATEKAKKAKEKAGEITTASASMASFHAIVAEMAKDVAKAANENAKKAARIATH
     bcdefgabcdefg        abcdefg                                abcdefgabdefg
211  VAKAYEAKKEAEEAKTKAEEAKKEAEKAQTEVEAAKKEAEKVMAEAEKAMAEANDAAQKLVEKPEGKKTE
        abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg    abcdefg
281  EMEWLEEVKKKVDEAIVEIQKSLDTATQNATAAGSNATKAATEANNAIPNEAKTDKEMKDNAIIKEANVK
      abcdefgabcdefgabcdefg                                       abcdefgab
351  DVEDTANEAIKAAEQAKKSKAKAEILAGKAKIQVALEIAKIAAKVTGQAKNGIDELAKMATSANTLKKTS
     cdefgabcdefgabcdefgabcdefgabcdefg                  abcdefgabcdefgabcd
421  TEKATEASKKAKEIEALLKKIEDIAKEEDNLVGKEEEAKKKVQEATEAKQVAIKAKAEAEIAVLVARVHL
     efgabcdefgabcdefgabcdefg          abcdefgabcdefgabcdefgabcdefg
491  AKQEVTRLVQLADEEKNKAKKAAETAENAKNAAEKVSDKVSKNVKNASEILAAVESAKTEAQTAKTEGKN
      abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
561  AEMEAADAVEEALMLEYLLSKATDAANKAKEANGDNITSTLETAQQDALKTLGQADHIAMETFNLTQKAI
         abcdefg                                                        ab
631  EASKKAQKAAEVAKAEAAKAEAYKAIEEVKKEEQKIKQLVAKAKESKATEEVKAAEAAEKVAKAEVDKAT
     cdefgabcdefg  abcdefgabcdefg                        abcdefgabcdefgabcde
701  SEAEKAKTAAGEAKNASTLEAAKAKAMNAINALKEARTSIYKTEYEYLKLIKQDVLEPLKVSTEASDNVF
     fgabcdefgabcdefg
771  DKNEQVAQEVEDRGSEENDAAEEDAAPSDVEEDEGELEDEEEEEEEVEQLEQPQEQQTDASSKDKGTAET
841  QKSEDVLDDEGAHKLLAGELNTANKSNNAENALFKTVFDEVRDDTIQNLKQDVGQFFKGKEK
```

PvMSP3.3

```
   1   MKQLCGLAFLALLLNFLTCDNVATRGEIVNLKNPNLRNGWSMKNLSAQNEENIVHSDGSDDVTDKEEDGE
  71   VLEGQKGSPKKSAEQKVHAQEEVNKESLKSKAQNAKAEAEKAAKAAESAKENTLDALEKVNVPTELNNEK
                                   abcdefgabcdefgabcdefgabcdefg
 141   NFAESAATEAKKQEKISTEAAEEVKEIEVDGQLEKLKNEEEKTAKKARKQEIKTEIAEQAAKAQAAKTEA
                                                                  abcdefgabcd
 211   ETAQKDATTAKDEAIKETGKPKSQNTTKAVTMATEEEKKTKDEAQTASEKAGKTAEEAQKEVGKETADDD
       efgabcdefgabcdefg                abcdefgabcdefgabcdefgabcdefg    abcde
 281   KEVSQLEEEIKELERILKIVKDLASEASSASDNAKKAKLKTQIAAEVVKAEKARIEAEEAEKEAGEAKTK
       fgabcdefgabcdefgabcdefgabcdefgabcdefg     abcdefgabcdefgabcdefgabcdefg
 351   TEATEKEVLKISDESKAAKVKKAVEKAKEAEKQAKSEAEKAKGMADDAGGKGTTNLEDVLTKLSEVLTSV
       abcdefgabcdefg         abcdefgabcdefgabcdefg
 421   KSLASNAEVASKNAKKEMTKAQIAAEVAKAEKAKIEAENAKLLADTASKAAENIAKSSKAAKIANNVSTI
            abcdefg     abcdefg  abcdefgabcdefgabcdefgabcdefg
 491   AAEKSKVATEAADEAAKALDETENPESKIAEVTEKATKAVNAAEEAKKEKAKAEVAVEVAHAEVAKEKAQ
                                   abcdefgabcdefgabcdefgabcdefg         abcde
 561   EAKEAAKQVADKSKLEKAIQAADKASEKANEASKLAEEALSNLESLEKETGEIVEKVNAIEQKVQTAKNA
       fg            abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 631   AIEAHKEKTKAEIAVEVAKAEEAKKEADNAKVAAEKAKETAEKIAKTSKSTEKITEEVRKATEFAKTAGD
                abcdefgabcdefgabcdefgabcdefgabcdefg      abcdefg
 701   ETTLAATKAESEIPSEEKNQKELLDSIKQKAESAFQASQEAIKAKTEAENFLEIAKEVPKAEAAKEEAQK
                              abcdefgabcdefgabcdefgabcdefg                abcdef
 771   AATAAEEAKTEVLKIAEEVNKSDASESEKKKIETAANETAGEAEKAATFAKEAADAAKDTNKAVTLAVAK
       gabcdefgabcdefgabcdefg                  abcdefgabcdefg         abcdefga
 841   EKVEKALKAAKEAKKANEKASYALIRTKKQYALEPLEITSEAGYNITEKEEQVKEEIEEQDDKASEEEEE
       bcdefgabcdefgabcdefgabcdefg
 911   DTQQIDQTQIDEVDISVDNEEEEEGAAEEQIEGEKDTPTKEAKEEQTSGEKILDDKEAHKTLAEKFKDSN
 981   TAKTGGVEFLETLISDVGEDTLKNLQQDLHQYFKGK
```

PvMSP3.4

```
   1   MKHFGGIPLLVLFVNLYIHQNVVSNEIVNLKNPNLRNGWAGKDVTLQDEQNGLNAEDGDETDPNGSHNEL
  71   LQKSGKAELQMQAQDSDSKEDIKTKIDELVNKAEAANTKADTAVTEAEKLLKTATEAEKQIKVDEEKETT
                         abcdefg       abcdefgabcdefgabcdefgabcdefgabcdefg
 141   AATKAKEQAEKAFAEAKIKKEEAKTKKEDAKAKAKADDAKKSEETDEAELKAKLEEVEKLVGQAEQAAS
            abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgab
 211   DAENEQKKAEWAAKIAEELKKAYEAKKKARESKVAAENAKNDATSAASGSKVQKVTEAIKIADDEMQTAA
       cdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 281   KNATEAEGAERKAEQAASEAINAIEQKVDAQSKVNVVQNEADAASKAATAAKNAQTKAEIAVFVVKTEVS
            abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 351   KEEAVKSANAAEEAKTKAEEVATKSEEIKITNVTKSEKVKSAKSEAVNQAAAADKAKKEAEAAANSADKA
       abcdefgabcdefgabcdefgabcdefg       abcdefgabcdefgabcdefgabcdefgabcdefg
 421   QTSTKGIDNETTLSTAKKEAETAASNAGKAQTDASTALAKAKKAQIETEIAAEVVKAEKAKKDASSDADA
       abcdefg     abcdefgabcdefgabcdefgabcdefgabcdefg      abcdefgabcdefgabc
 491   AVEARKKAESEAEKAKSNEVAQEAAQKAKEQEAEALKAKGNAQTASDQAEKEAEGDGTEDKLAKVKEKEK
       defgabcdefg          abcdefgabcdefg    abcdefgabcdefg          abcdefgab
 561   DASNAATAAKNARTTAEIAAEVAKAQAAKTEAEAAKVAANAAKDEAQKVADESKSAEAQKAAEKASEAAT
       cdefgabcdefg          abcdefgabcdefgabcdefgabcdefg             abcdefgab
 631   TAGEKAAEAAKVADDATSVSNTATLSTMQEKANKAVEHAKEAKKAQTKAELAAEEAKAEAAKKEAQKAQE
       cdefgabcdefg                                abcdefgabcdefgabcdefgabcdef
 701   AADAAKKEAEEIAKKEKVDAKAVAEATSALDTAKTKAKEAKDKAGDVSKEVEKAEKEVEKVVGDDAQKSE
       gabcdefg               abcdefgabcdefgabcdefgabcdefgabcdefg
 771   ITTAVSGIKGKTSEAVQAAKDAKKAKDLAEIALNVVKAEVANDKAKKAVPAAGVAKEDAKKAAASAEQPK
 841   KEAESAEEGAEIAKENEIEAGQKAKEAEDNAAVVQAKLLIAEQELKNAKAENDTEKFQSAKANALAAAEE
         abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg  abcdefgabc
 911   AVKKGQAAEAAANAATDKAKKAAEAAEKAKKAAAESALKKKLKVLEIVKKYSKRGYNVVDNDEQVLNEVD
       defgabcdefgabcdefgabcdefgabcdefg
 981   EQASEAKEEEDEDEADDSASSDVEIEDDEEEEEEEDEEVKEEEGQAQSSAHQNSVAELENQKKESQEKSD
                                                abcdefgabcdefgabcdefgabcdefg
1051   EPPSDNNAQALLSDNYKNFTDFKKKAEDLTKNIINTIDGDAGVIDTLKDFANDVNQFILNM
```

PvMSP3.5

```
   1   MKQFCGIPLLVLFVNLYVLQNNVVSNEIVNLKNPNLRNGWVGKNLTLQDEKIVLNAEDGDEIDPNGSHIE
  71   LPQKSEKAELQMQEQGNDDNEDLKRQIGEFVDQAQLANTKADAAVAEAEKSLEKAKDAEEQVKQDEGNVT
                                abcdefg   abcdefgabcdefgabcdefgabcdefgabcdefg
 141   TATTKAKAEAQKAVDAAKTKKKDAKTNADNAKQESEKKGDQELRATLDKVKKFAEKAEQALSGAQTEQKK
             abcdefgabcdefgabcdefgabcdefg            abcdefgabcdefgabcdefgabc
 211   AEWAAKIAEELKKAYEAKRNANDSKEAAEKTKKDATSAVSDSTEQKVTASIQIIEEQKQTAVTKATEAEK
       Defgabcdefg      abcdefgabcdefgabcdefg            abcdefgabcdefgabcdef
 281   AAKETEKAAKETEQAAIEAINVIDQTTVQDKFKVVEGKADTASKAAAAAKKAQTKAQIAAYVVQTEVSKE
       gabcdefgabcdefgabcdefg                                                ab
 351   KAVKSAREANEAKTKAEDVAKESEKIKITDEDKSGNVKAAKTEAVEQANLADNAKKEAEAAAISANEAKT
       cdefgabcdefgabcdefgabcdefg       abcdefgabcdefgabcdefgabcdefgabcdefg
 421   SITVKDDDTTLNEAKTKAYDASIKAKQAEKDASNALKEAQKAQIETEIAAEVVKAEKAKKEASSDAAVAR
                 abcdefgabcdefgabcdefgabcdefgabcdefg      abcdefgabcdefgabcde
 491   EAKEKAESEANKAKSNAVAQEAAKRAQEQDVAASTAKGNAETAAKEAETAAEDNVSEETLTTVKQKVENA
       fgabcdefgabcdefgabcdefgabcdefg                                abcdefgabcd
 561   SNAATAANKARTKAEIAAEEAKAQAAKTEAEASKVAANAAKDEAQKAAEESKSAEAKKAADKASAAAKTA
       efgabcdefgabcdefg         abcdefgabcdefgabcdefg     abcdefgabcdefgabcd
 631   DEKAASAKKEADDATTESKSTTATVETMQKKADKAVEHAKEAKKAQTKAELAAEEAKAEAAKEEAKKAQE
       efgabcdefgabcdefgabcdefgabcdefgabcdefg     abcdefgabcdefgabcdefgabcdef
 701   AADAAKKEAEEIAKKEKVDAKAVAEATSALDTAKTKAKEAKDKAGDVSKEVEKAEKEVEKVVGDDAQKSE
       gabcdefg    abcdefg   abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 771   ITTAVSGIKGKTSEAVQAAKDAKKAKDLAEIALNVVKAEVANDKAKKAVTAAGVAKEDAKKAAASAEQPK
                                                abcdefgabcdefgabcdefg
 841   KEEESAEEDAEIAKENEIEAEQKAKEAEDNANAAQAQLKIAEQELKKAQEADNEEKFQSAKTNALAAAEE
         abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg          abcdefg
 911   AIKKGQAAEDAANEAKNNAVKAAEAAEKAKKAAAESALKKKLNVLEIVKKYSREGYNTVDSDEHVLNEVE
                   abcdefgabcdefgabcdefg
 981   EQASEEKEEGEREEEEEADHPILNDVEIDDDDEEEEEEEEEKEEEETEVKEEEDAKEEGHAQSSAHQSSI
                                  abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
1051   TELENPKKEYQEKSDKPPSDSNAQALLEDNYKNFTDFKKKAEDLTKNIINTIDGDAGVIETLKDFAKDMN
1121   QFILNM
```

PvMSP3.6

```
   1   MRQFFGTTILVLFLNLYVLQTNVVSNENVNLKNPNLRNGWAGKDVTLQDEQSGPNAKDGDEVNTNQDQIK
  71   LQQKSDETLLQMQGQDKEKVAESDDLKEAKEAKTKAEKEEAEAETVKQKILKAEKETEKAEQKIKDAINK
           abcdefgabcdefg           abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 141   VKEYALQKESEVKEQTKAAKFAADEATAENAKEKKETANTALGEAQKAKKEMETAAVIVAEVVKAMEAEK
       abcdefgabcdefg              abcdefgabcdefgabcdefgabcdefg          abcdef
 211   ESQKANEEAQKANQEAENAKNNIINIETEKAGADNPNSKAEQERTIVNEKAKGAIENAKQASTRATGAAQ
       gabcdefgabcdefgabcdefgabcdefg                                abcdefgabcde
 281   KATGAAQKAAEEAQKAIAAITGNVKEIPPANVEEIKKIASDAVKDAKDAKKAKGEAQINAEIVKLELAKV
       fgabcdefgabcdefgabcdefg         abcdefgabcdefgabcdefg          abcdefgab
 351   EAKKVVASANKAKKEAAAAAKTSKSAKLTAGRAVKKAEEAEAKAKILENQNEQDAISSAETAATAAVAAV
       cdefgabcdefgabcdefg   abcdefgabcdefgabcdefgabcdefg
 421   AAVATAEAAATAGNEEEKKKEAEAEGKIKTLIQKVAEAIKAANQAKKAQIEAEIAVEVAKIEEHSEVAQK
                   abcdefgabcdefgabcdefgabcdefgabcdefg          abcdefgabcdef
 491   EVEEAEKANAKAKQAASEAQEAKTQTEKAAKAAEMVKAKDLAKTEVEIATKAEKEVADAKMEADEESSEA
       gabcdefgabcdefgabcdefgabcdefgabcdefg      abcdefgabcdefgabcdefg
 561   VEKAHAIKMQLEVAINAEKKAAKEVDITKLEDAKKEAQDATKNAKELLSIVQKASTLAIAKSKNAENSLE
       abcdefgabcdefgabcdefg         abcdefgabcdefgabcdefgabcdefg    abcdefg
 631   KVKKAAEVAKAKLAKAEAKNQAEEAKAIAAKADELSKGTKASTAEKTKAEAAAKEAAAQATKAADEAGKA
               abcdefgabcdefgabcdefgabcdefgabcdefg                abcdefgabcdefg
 701   ATAADNTKKAATSAEAKVEANKAVAAAKEAIIAKIKAAHEFLKTKNQDILEPVEMFSGGTENVTDREEQV
       abcdefgabcdefg
 771   KDEVEEQGDGSNEKAEEEEEEDSESALPNGSDGLEDDVDLDVDDDVEEEENVATNHQKGGKYEKGKVTDA
 841   VDDTNADKQFGDEFDAYNDIKKVTEALVKTMTSLVSEDPSVGDTINEFLSDMNQLFLSW
```

PvMSP3.7

```
   1   MKSNLKSTLYIIFLYWYVHIKDEQKWVTVNAETPNLRNGWSIKNGDIHNGENNLNRKYADYLNDTVEGNS
  71   KMEALEEGLSGQSEEAVVKAQQEDGEVQAQQEEAVDLQLADKQAAEKAAGEAQQFAKEATQAAEQAAEDA
                                          abcdefgabcdefgabcdefg   abcdefgabcde
 141   KKAAQAEKDAKAAQDEAKEKVKNAEKINEAVEQATSAKEQAQKASGEAETAKEKAAAATKAAEQAAAAAA
       fgabcdefgabcdefg       abcdefg          abcdefgabcdefgabcdefgabcdefgab
 211   AKTTEEAKTNKQQAMDQKGLAEEALKRAKEAATNAQQAKENAEIALERTKAEVSKELAEKEVLAAKEAQK
       cdefg            abcdefgabcdefgabcdefgabcdefgabcdefg
 281   EAEAAKNKAKAASDKVTSENEAVNKATLASKRADEALGRAQEYATIAEKAAGEAQKAETVQTAQVASKKA
        abcdefgabcdefgabcdefgabcdefg          abcdefgabcdefg               ab
 351   KDAETSANYERIIAELAAEVAKAEAEKNEAEKELKEANKADEEAKAVGAAIGADKAKEKAKIEAEKAKKQ
       cdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg  abcdefgabcdefgabcdefg
 421   LDEAKKLAKEVSSAEYNVEEKSVSEAKEKVSEIQKAVTAAKTAKELAVKAAKVATHILNAEKAKTEAQQA
       abcdefgabcdefg abcdefgabcdefgabcdefgabcdefgabcdefg      abcdefgabcdefg
 491   KKDALKAKAEAEKYASDSKAEKAKEAATKAATAADTATDKATKAEKESADAVTEANVNPDEIPDKEEEVK
       abcdefgabcdefg     abcdefgabcdefgabcdefgabcdefgabcdefg                a
 561   KKATQAADFSKEAVKAKNEALIEAEVAKAEAAKEEANMAQIEAGKAKAEAEKAAQTAPLSAVTEAKKKAE
       bcdefgabcdefgabcdefg     abcdefgabcdefgabcdefg            abcdefgabcde
 631   NMATLAKEKAETAANEAKGTNESADSIRDKAKEEVTEEVTNKITEIKGKAENASKAANEAKKAQTEAELA
       fg    abcdefgabcdefgabcdefg        abcdefgabcdefgabcdefgabcdefg     ab
 701   AAVAKAAVAKHEAKKAQELADDAKKKADEEAKPVESKAKDEAASAAEKAKENAKTAEDAADEVLLKAKDA
       cdefgabcdefgabcdefgabcdefg            abcdefgabcdefgabcdefgabcdefgabcd
 771   EEEVKNNWDNQQKKADITSKVNHVKEKTSQSIDAAKAAKKAKDLAEIALNVVKAEVANDKAKKAVTTAEA
       efgabcdefg                                   abcdefgabcdefgabcdefgabcdef
 841   AKDEAKKAAASAEQPKKEAESAVEDAETAKDEEKEVEKKAQEVAENANAAQEQLKIAEQELQTAKGATSM
       gabcdefg       abcdefgabcdefg   abcdefgabcdefgabcdefgabcdefgabcdefg
 911   ETLVQAKTKALAAAEDAVKKGQAAEDAANEAKNNAAKAAEAAEKAKKAAEESALKKKLKVLEIVKKYSKE
          abcdefgabcdefg          abcdefgabcdefgabcdefg    abcdefgabcdefg
 981   GYNTVDSDEHVLNEVEEQASEAKEEEEEDDEEEAEHSLPNDVEIEDDDDEGEEEEKEEEETEVKEEEDVK
1051   EEGHAQSSAHQSSVTELENQKAQSQEKSEKPLSDSNAQALLEDNYKDVVNFKKMADGLTKNIISTIDGDT
             abcdefgabcdefgabcdefg
1121   DVLDTLKDFAEDLNQFIFSM
```

PvMSP3.8

```
   1   MKHLSGIPLLVLFLNLYVIQNNVVSNEIVNLKNPNLRNGWAGKDVTLMDEQSGLDAKDGDEVNANEDQSE
  71   LLHKSDEGSLQTQGQNNEVVEESADVKKAKKAKADAEQAEAEAQKAKQKILDAEKETEKAKKEIKDAINK
                                   abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 141   VKEYASSKESQVKKKVEEAKSAADEATKGSTKENTEQKAKAAEAALGEAQNAKVQMEKAAAIVDEVVKAM
       abcdefgabcdefg                  abcdefgabcdefgabcdefgabcdefg         ab
 211   EAEKEAQKAKEEAQKANEEAQNAKNKFVMIKPKQAGAGSPESKAEQEAKIANDKTTEAEQKAEQASAKAT
       cdefgabcdefgabcdefgabcdefg                abcdefgabcdefgabcdefgabcdefgab
 281   DAAQKATEAAQKAIEVAKKATQEKTGEEKEIEQENVTKIKEIASNAVKDAKDAKKAKREAQIKAEIVKLE
       cdefgabcdefg    abcdefgabcdefg     abcdefgabcdefgabcdefg  abcdefgabcde
 351   LAKEEAKKAVESAKKAKDEAAAAAKTSKSAKLAATRAAKKAEEAETKANLLENKNKQGPISLAATAEAAE
       fgabcdefgabcdefgabcdefg           abcdefgabcdefgabcdefg
 421   KEASTAVAAVATAEAAEKAKTEEVEKKEAEAEEKIKTLIQKVAKAIKAANQAKKAQIEAEIAVEVAKIEE
                     abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg          abcdef
 491   HSEVAQKEVEEAEKANAKAKQAASEAQEAKTQTEKAAKAAEMVKAKDLAKTEVEIATKAEKEVADAKMEA
       gabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg     abcdefgabcdefgabcdefg
 561   DEESSEAVEKAHAIKMQLEVAINAEKKAAKEVDITKLEDAKKEAQDATKNAKELLSIVQQASMLAIAKSQ
             abcdefgabcdefgabcdefg        abcdefgabcdefgabcdefgabcdefg
 631   DALNSLEKVKKAAEVAKAKLAKAEAKNQAEEAKAIAAKADELSKATKASTAEKTKAEAAAKEAAAQATKA
                       abcdefgabcdefgabcdefgabcdefg                abcdefg
 701   ADEAGKAATAADNTKKAATSAEAKVEANKAVAAAKEAIIAKIKAAHEFLKTKNQDILEPVEMFSGGTENV
       abcdefgabcdefgabcdefg
 771   TDREEQVKEEVEEQGDGNNEQAEEAEEVDESESALPNGSDGLEDDVDFDVDDGEEEEENVATNKQKGGKY
 841   EKGKVTDAVDDTNADKQFGDEFDAYNDIKKVTEALVKTMTSLVSEDPSVGDTINEFLSDMNQLFLSW
```

PvMSP3.9

```
   1   MKSNLKSTLYIIFLYWYVHIKDEQKWVTVNAETPNLRNGWSIKNGDIHNGENNLNRKYADYLNDTVEGNS
  71   KMDAIEEGLSGQSEDAIVKAQQEDGEVEGQQDEAALQSEDEKEAENAAEEAQKFATQAQGAAEQAAQAAQ
                                                abcdefgabcdefgabcdefg   abcdef
 141   AAQDEAKKITENTEKIEEAVKQATDAKEEAENESREANNAKEEADAAARKAKENKEDAVNQKKIAQAALE
       gabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg    abcdefgabcdefgab
 211   RAKTAATKAQTAKGKAEKALETTKAEVAKELAAKEAREAEKTRAVEEAQQIAKQAEEQLKTATKATQEAA
       cdefgabcdefgabcdefgabcdefg    abcdefgabcdefgabcdefgabcdefgabcdefgabcde
 281   QAAQAAQDEAKKITENTEKIEEAVKQATDAKEEAENESREANNAKEEADAAARKAKENKEDAVNQKKIAQ
       fg   abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg    abcdefgabcde
 351   SALDKATNAATNAQKAKEKAEIALERTKAEVSKELAKKEVLEAEAAQKEAKDISDKMTIANKPVNKANLA
       fgabcdefgabcdefgabcdefgabcdefgabcdefg                    abcdefg
 421   SKRAEEALEKAKKHVATAESATEEAKGANAVEKAKEASTKAKEAEKNAKNERIKAQLAAEVAKAEAVKDE
       abcdefgabcdefg     abcdefgabcdefgabcdefg      abcdefgabcdefgabcdefgabc
 491   AEKESKAAMDARRQAEAVKTANGAENAKKKAEIEAGKAKGHLKKAEELAKEVSSAEYEVTEDSVTKAKKK
       defgabcdefgabcdefg  abcdefgabcdefgabcdefgabcdefg        abcdefgabcdefg
 561   VSEAQEEAKAAKSAKELAVKAAEVATHILNAENAKKEAQQAKQAALQAKTDAKKYADQSNAEKAKEAATK
       abcdefgabcdefgabcdefg      abcdefgabcdefgabcdefgabcdefg     abcdefgabc
 631   AEAAATIATDKAKEAENEAEAAVAEAKVDPEQIPKKEEEVKKKATQAAVFSEDAKKAKNEALIEAEVAKA
       defgabcdefgabcdefgabcdefg                          abcdefg         abcd
 701   EAAKEEAKKAHIAAGKAKEEAEKAAQTAQLSEVTDAKSKAESMTTLAKEKADTAEKEANETNESAKSIQN
       efgabcdefgabcdefgabcdefg             abcdefgabcdefgabcdefgabcdefgabcdef
 771   EAKTEKPEDITKKIEDLKGKAEKVSNSAKEAKKAQTKAELAAAVAKAAVAKDEAKKAQDAADDAKNKADE
       g            abcdefgabcdefgabcdefg     abcdefgabcdefgabcdefgabcdefgabc
 841   AAKSVESKAKGEAASAAAKAKENATVAASAANEVSSKTKEAEEEIEKNWGDEKKKEEITSKVNHVKQETS
       defgabcdefg
 911   KSINAAEGAKRAKEVAELALKVVSAEVENDKAKKAVTTAEAAKDEAKKAVESAEKSKGEAESAVEDAETA
                     abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 981   KEEEKEVEKKAQEASENANEAQAQLKIAEEELKKAKEADNEEKLQSAKTKALEAVDEAVKKGQAAEAAAN
                abcdefgabcdefgabcdefgabcdefgabcdefg  abcdefgabcdefgabcdefgab
1051   EAKNKAAKATQSAEKAQKAAAESALKKKLNVLEIVKKYSKESYNTVDSDEHVLNEVEEQASEEKEEEEEE
       cdefgabcdefgabcdefgabcdefg
1121   EEAEHSVSNEVEIEDDEEEEEEEEEEGEETNTEGEKSEDNSPHSDTEPQEQNQSVKPPEQSEKTLNDSNT
1191   QALLSDNYKNVANFKKMADDLTKNIISTIDGDTGVIDTLKDFAEDLNQFIFSM
```

PvMSP3.10

```
   1   MKHTRSVTLYLFLLTLCAYLTGAEVIGGSPNNEAPNSSRHHLRNGFPGKNDSLPHEEPNNLEGKNESSDQ
  71   CDTINLGQVTEKEKKTIEQASVQAQDATKPEANNAEQIQAELQKVKTAKDESATAAKDAETAKKNAVDAG
                                     abcdefgabcdefgabcdefgabcdefgabcde
 141   KGLDAAKGAIKKAEEAAAEAKKQAGIAEKAEKDAEAAGKKDKLEDVNSQVQIAVEASTKAKDKKTEAEIA
       fgabcdefgabcdefgabcdefgabcdefgabcdefg
 211   VEIVKAVVAKEEAQKASDEAQKACEKAQKAHAKAQKASDTTKTVETFKTNAEAAAKNAKEKAGNANKAAT
         abcdefgabcdefgabcdefgabcdefgabcdefg          abcdefgabcdefgabcdefgab
 281   EAESANELSVAKQKAKDAEEAAKEAKKEQVKAEIAAEVAKAKVAKEEADAAQKKAEAAKKIVDKIAQDTK
       cdefg         abcdefgabcdefgabcdefg     abcdefgabcdefgabcdefgabcdefg
 351   VPEAQREAKLATQTASKATEAATEAGKKAQEAEESSKEAEEKAETSDAVKGKADAAEKAAGEAKKASIET
               abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg   abcdefg
 421   EIAIEVAKAEVLNAEVKKTAQEAEKDATEAKEQAEKAKAAAEEAKTHGEKAEKVGESTKAHSDEAQQENK
            abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgab
 491   NAKDASEEAENRAVDALEEAYAVEAHLARTKNAAESAKSATDMSELEKAKEEAIDAANIAHQKWLKATQA
       cdefgabcdefgabcdefgabcdefgabcdefg

 561   ATIAKEKKEAAKVAAEKAQTAANVVKDKAAKAEAKKAETEAVKAAVEARAAAEEAKQEAAKVGASKEPQE
               abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
 631   TKNKANVEAEATGNEAKKAEDAAEEAKEAAKKANEATDANVARSEADKAIAAAKKAKKAREKAAYGLLKT
        abcdefgabcdefgabcdefgabcdefgabcdefg    abcdefg     abcdefg
 701   KNQYVLEPLDISPESADNITSKEEQVKEEMEDQGDEDSNEAEVEEALPNGSGAQEEDVNLEMDDEEEVEE
 771   VEENVATNQQTGGKREKRNTNDTVDDTNADKQFGDEFDTYNDIKKVTEALVKSMTSLVSDDPSVGDTINE
 841   FLSDMNHLFLSW
```

PvMSP3.11

```
  1   MRQFVRIAIFISLLNLYLQKDGAVRGEILNVNKTNLRNGTPEEGVPSEGELPADAQEGKGGDSIKEVIKR
 71   ASEETAKFADEAKEAFKKAQSLAEEAKEKAAEAAKAVGAMNGEKDTPPTTEKAQRASQAASAAEQKSNEA
       abcdefgabcdefgabcdefgabcdefgabcdefgabcdefg         abcdefgabcdefgabcd
141   QAAVRTAKEQETKALEAAQVVKGLAEKAEPTTGDKDEAEKKRKEAEEALSAVKANLSAVEAAKVAAEINA
      efgabcdefgabcdefg                 abcdefgabcdefgabcdefgabcdefgabcdefga
211   AEAVEEANTVMKELAKVKATEAADAAKKDLLGAEVAEGSNAKAEAEAHEFLKTTNQHIQEFEEMPSQGGD
      bcdefgabcdefg
281   HVKDKNEEVKEEVKEEAKEEAKEEVLESRGEEEEQTLEVEDDVDEEEEDEEDDDDEEDEDDEEDKEDEED
351   DDEDDGGDDDSGDNDSDDDDNDGDDHDEDEDD
```