

**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 AXXAXX sequence pattern representing predicted coiled-coil heptads is marked by a red underline.

### PvMSP3.1

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1  MKHLGSIPLFVLFNLYVLQNNVSVNENLKNPNLRNGWAGKNVTLQDEQSGLVAEEDGEEVNTKEDQNE
71  LLHKSEETDFQTQGQEVKEIGGSENEKQKQIKKANAEKKEALKEQKEAEDEVKKEIEEALDKVKKAKAEA
      abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcd
141  EEEAEIKKVVEKAKGVADKAKETAMNKAKKSKDEAEKIAGVNTNSMAYLYAGNAVTAEIEAKAEKKEAKK
      efg      abcdefgabcdef
211  AAEIAKHADVDAYELKKEAEKAOEEAEAAKTEIEKLSKVYKEGNVTEAVQSTAEAEKSASGASAKVKEAAH
      gabcdefg      abcdefgabcdefgabcdefg
281  NVAKKLMDAVQKLEKVVSTELPKDNEQAATIDNVNEVVTEAVKEKEKAMISAEVAKAEAANAEAQLAKIEA
      g      abcdefgabcdefgabcdefgabcd
351  ERAKYEANKIAEEYTDNVKGEAKKAEEKANEASSKATEASNNAKGASGEEKQTNPQAANVKAKAGEAIIKA
      efgabcdefg      abcdefgabcdefgabcdefgabcdefg
421  AKEAKKAKTEAYIALCVTKTLVAKENAKKAEQEAKNAKDKATKAAKEAEAEAKKQAEKAEKITETVKNEAK
      abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
491  TATDEEAKASTGKKDAEINAGYVDEEVYAVNIEFEIAKEAAKTAAQHKALEILDKAEKNAEIAAENATAK
      cdefg      abcdefgabcdefgabcdefg
561  AQEATKKAETAKTKATEAETAAKKAQDASEKAKAIAADVLAQKASTEAQSLKQEAEKLAEINIKKSNVTDE
      abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg      abcdefg      abcdef
631  EKAKADEAAKAKDAADQASASAKKANDAKIAATNAQVVVTLQTKKAESAKAEDAAKEAMKARDKAAFEL
      gabcdefgabcdefgabcdefgabcdefgabcdefg      abcdefgabcdefgabcdefg
701  LKIKQDVLQVDVSPSGSDNLNDVDEQVALEVGEEQQNETEDAEPQEAEEGDEEDEEDTEEEEIQDES DH
      bcdefg
771  TEESAKQAQQEKKQGEKVLNDEEAHNLLAQQHNKDNNAATEDAKLFQTI IKDFDDDDDFKNLQKQDVNA
841  LFKIK

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### PvMSP3.2

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1  MRQFFGTTILVLFNLYVLQTNVSVNENLKNPNLRNGWAGKNLALQDEQSGIDAEDGGEENTCEGQSE
71  LLQKSEAQVQTQGQEI KATGESDDPKKKKSPIEKANAEKDNALKEQEGAEAEVKKIEEAEKKVEGAEEGI
      abcdefgabcdefgabcdefgabcdefg      a
141  KNAVKKAKEAAEFAKNTATEKAKKAKEKAGEITTTASASMSAFHAI VAEMAKDVAKAANENAKKAARIIATH
      bcdefgabcdefg      abcdefg      abcdefgabcdefg
211  VAKAYEAKKEAEEAKTAEAKKEAEKAQTEVEAAKKEAEKVMAEAEKAMAEANDAAQKLVEKPEGKKTE
      abcdefgabcdefgabcdefgabcdefgabcdefg      abcdefg
281  EMEWLEEVKKKVDEAIVEIQKSLDTATQNATAAGSNATKAATEANNAIPNEAKTDKEMKDNAIIKEANVK
      abcdefgabcdefgabcdefg      abcdefgab
351  DVEDTANEAIKAAEQAKKSKAKAEILAGKAKIQVALEIAKIAAKVTGQAKNGIDELAKMATSANTLKKTS
      cdefgabcdefgabcdefgabcdefgabcdefg      abcdefgabcdefgabcd
421  TEKATEASKKAKEIEALLKKIEDIAKEEDNLVGKEEEAKKKVQEATEAKQVAIKAKAEAEIAVLVARVHL
      efgabcdefgabcdefgabcdefg      abcdefgabcdefgabcdefgabcdefg
491  AKQEVTRLVQLADEEKNKAKKAAETAENAKNAAEKVSDKVSKNVKNASEILAAVESAKTEAQTAKTEGKN
      abcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefgabcdefg
561  AEMEAADAVEEALMLEYLLSKATDAANKAKEANGDNI TSTLETAQQDALKTGLQADHIAMETFNLTQKAI
      abcdefg      ab
631  EASKKAQKAAEVAKAEAAKAEAYKAIEEVKKEEQKIKQLVAKAKESKATEEVKAAEAAEKVAKAEVDKAT
      cdefgabcdefg      abcdefgabcdefg
701  SEAEKAKTAAGEAKNASTLEAAKAKAMNAINALKEARTSIYKTEYEYLLKLIKQDVLQVLEPLKVSTEASDNV
      fgabcdefgabcdefg
771  DKNEQVAQEVEDRGSSEENDAAEEDAAPSDVEEDEDGELEDEEEEEVEQLEQPQEQQTDASSKDKGTAET
841  QKSEVDLDEGAHKLLLAGELNTANKSNNAENALFKTVFDEVRRDITQNLKQDVGQFFKQKEK

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PvMSP3.3

1 MKQLCGLAFLALLLNFLTCDNVATRGEIVNLKNPNLRNGWSMKNLSAQNEENIVHSDGSDDDVTDKEEDGE
71 VLEGQKSGSPKKSAEQKVHAQEVEVNKESLKSQAQNAKAEAEKAAKAESA KENTLDALEKVNVPTELNNEK
abcdfgabcdfgabcdfgabcdfg
141 NFAESAATEAKKQEKISTEAAEEVKEIEVDGQLEKLKNEEEKTAKKARKQEIKTEIAEQAAKAOAAKTEA
abcdfgabcd
211 ETAQKDATTA KDEAIKETGKPKSQNTTKAVTMA~~TEEEKTKDEAQ~~TASEKAGKT~~AEEA~~OKEVKGK~~T~~ADD
efgabcdfgabcdfg abcdfgabcdfgabcdfgabcdfg abcde
281 KEVSOLEEEIKELERILKI VKDLASEASSASDNAKAKLKTQIAAEVVKAEKARIEAEEAEKEAGEAKTK
fgabcdfgabcdfgabcdfgabcdfgabcdfg abcdfgabcdfgabcdfgabcdfg
351 TEATEKEV LKI SDESKAAKVKKA VEKAKEAEKQAKSEAEKAKGMADDAGGKGTNLEDVLT KLSEVLTSV
abcdfgabcdfg abcdfgabcdfgabcdfg
421 KSLASNAEVASKNAKEMTKAQIAAEVAKAEKAKIEAENAKLLADTASKA~~ENI~~AKSSKA~~AKI~~ANNVSTI
abcdfg abcdfg abcdfgabcdfgabcdfgabcdfg
491 AAESKSVATEAADEAAKALDETENPESKIAEVTEKATKAVNA~~AEEAK~~KEKAKAEVAVEVAHA EVAKEKAQ
abcdfgabcdfgabcdfgabcdfg abcde
561 EAKEAAKQVADKSKLEKAIQAADKASEKAN~~AS~~LAEALSNLESLEKETGEIV~~VEK~~VNAIEQKVQTA~~K~~NA
fg abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
631 AIEAHKEKTKAEI AVEVAKAEEAKKEADNAKVAEKAKETAEKIAKTSKST~~EKITE~~EV~~R~~KATEFAKTAGD
abcdfgabcdfgabcdfgabcdfgabcdfg abcdfg
701 ETTLAATKAESEIPSEEKNQKELLDSIKQK~~EA~~SFAQ~~S~~QEA~~I~~KAKTEAENFLEIAKEVPKAEAAK~~E~~EAAQK
abcdfgabcdfgabcdfgabcdfg abcdef
771 AATAEEAKTEVLKIAEEVNKSDASESEKKKIETANET~~AGEAEKAA~~TFAKEAADA AKDTNKAVT~~L~~AVAK
gabcdfgabcdfgabcdfg abcdfgabcdfg abcdfega
841 EKVEKALKA~~A~~EAK~~KAN~~EKASYLIRTKKQYALEPLEITSEAGYNI TEKEEQVKEEIEEQDDKASEEEEE
bcdfgabcdfgabcdfgabcdfg
911 DTQQIDQTIIDEVDISVDNEEEEGAAEQIEGEKDTPTKEAKKEEQTSGEKILDDKEAHKT LAEKFKDSN
981 TAKTGGVEFLETLISDVGEDTLKLNQQDLHQYFKGK

PvMSP3.4

1 MKHFGGIPLLVLFVNLYIHQNVVSNEIVNLKNPNLRNGWAGKDVTLQDEQONGLNAEDGDETDPNGSHNEL
71 LQKSGKAE~~L~~QMQAQDS~~SD~~KEDIKTKIDELVNK~~AE~~AANTKADTAVTEAEKLLKTATEAEKQIK~~VD~~EET
abcdfg abcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
141 AATKAKEQAEKAFAEAKIKKEEA~~KTK~~KEDAKAKAKADDAK~~KS~~ETD~~EAEL~~KAKLEEVEKLVGOAQAA~~S~~
abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
211 ~~DA~~ENEQKKA~~EWA~~A~~KI~~A~~EEL~~KKAYEAK~~K~~KARESKVAE~~EN~~AKNDATSAASGSKVQKVT~~EAI~~KIADDEM~~Q~~TAA
cdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
281 KNATEAEGAERKAEOAASEAINAIEQK~~VDA~~QSKVN~~VQ~~NEADAAS~~KA~~ATAAKNAQT~~KAE~~IAV~~FVK~~TEVS
abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
351 KEEAVK~~S~~ANAAEEAKTKAEEVATKSEEIKITNVTKSEK~~V~~KS~~AK~~SEAVNQ~~AA~~ADKA~~K~~KEA~~EAA~~ANSADKA
abcdfgabcdfgabcdfgabcdfg abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
421 QTSTK~~G~~IDNETT~~L~~STAKKEAETAASNAGKAQTDASTALAKAKAQ~~I~~ETEIAAEVVKAEKAK~~DA~~SS~~AD~~A
abcdfg abcdfgabcdfgabcdfgabcdfgabcdfgabcdfg abcdfgabcdfgabc
491 AVEARKKA~~E~~SEAEKAK~~S~~NEV~~AQE~~AAQKAQEAEALKAKGNAQTASDQAEKEAEGDGTEDKLAKVKEKEK
defgabcdfg abcdfgabcdfg abcdfgabcdfg abcdfgabcdfg
561 DASNAATAAKNARTTAEIAAEVAKAQAAKTEA~~EAA~~KVAANA~~AK~~D~~E~~AQKVADESKSAEAQKA~~AEK~~ASEAAT
cdefgabcdfg abcdfgabcdfgabcdfgabcdfgabcdfg abcdfgabcdfg
631 TAGEKAAEAAKVAD~~DAT~~SVSN~~TAT~~LS~~T~~MQEKANKAVEHAKEAKKAQTKAELAAE~~EAK~~A~~EAA~~KKEAQK~~AQE~~
cdefgabcdfg abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
701 ADAAKKEAEEIAKKEKVDAKA~~V~~AEATSALD~~TA~~KT~~K~~AKEAKDKAG~~V~~SKEVEKAEKEVEK~~V~~GD~~DA~~QKSE
gabcdfg abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
771 ITTAVSGIKGKTSEAVQAAKD~~AK~~KADLAEIALNVVKA~~E~~VANDKAKKAVPAAGVAKEDAKKAAASAEQPK
841 KEAESAE~~EG~~AEIAKEN~~E~~IEAGQK~~A~~EAEDNAAVQAKLLIAEQELKNAKA~~EN~~DEK~~F~~QS~~AK~~ANALAA~~AE~~
abcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg
911 AVKKGQA~~E~~EAANAATDKAKKA~~E~~AEKAKKAAEAESALK~~K~~LKVLEIVK~~KY~~SKRGNVVDNDEQVLNEVD
defgabcdfgabcdfgabcdfgabcdfg
981 EQASEAKEEEDEDEADDSASSDVEIEDDEEEEEEEDEEVKEEEGQAQSSAHQNSVAELLENQK~~K~~ESQEKSD
abcdfgabcdfgabcdfgabcdfgabcdfg
1051 EPPSDNNAQALLSDNYKNFTDFKKAEDLTKNIINTIDGDAGVIDTLKDFANDVNQFILNM





1 MKSNLKSTLYIIIFLYWYVHIKDEQKWVTVNAETPNLRNGWSIKNGDIHNGENNLNRKYADYLNDTVEGNS  
 71 KMDAIEEGLSGQSEDAIVKAQQEDGEVEGQQDEAALQSEDEKEAENAAEEAQKFATQAQGAEEQAQAAQ  
 abcdefgabcdefgabcdefg abcdef  
 141 AAQDEAKKITENTEKIEEAVKQATDAKEEAENESREANNAKEEADAAARKAKENKEDAVNQKIKIAQAALE  
 gabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg abcdefgabcdfgabcdfg  
 211 RAKTAATKAQTAKGAEKALETTKAEVAKELAAKEAREAEKTRAVEEAQQIAKQAEELKLTATKATQEA  
 cdefgabcdfgabcdfgabcdfg abcdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcde  
 281 QAAQAQDEAKKITENTEKIEEAVKQATDAKEEAENESREANNAKEEADAAARKAKENKEDAVNQKIKIAQ  
 fg abcdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg abcdefgabcde  
 351 SALDKATNAATNAOKAKKEAEIALERTKAEVSKELAKKEVLEAEAAQKEAKDISDKMTIANKPVNKANLA  
 fgabcdfgabcdfgabcdfgabcdfgabcdfg abcdefg abcdefg  
 421 SKRAEEALEKAKKHVATAESATEEAKGANAVEKAKEASTKAKEAEKNAKNERIKAQLAEEVAKAEAVKDE  
 abcdefgabcdfg abcdefgabcdfgabcdfg abcdefgabcdfgabcdfgabc  
 491 AEKESKAMDARRQAEAVKTANGAENAKKKAIEAGKAKGHLKKAELAKEVSSAEYEVTEDSVTKAKK  
 defgabcdfgabcdfg abcdefgabcdfgabcdfgabcdfg abcdefgabcdfg  
 561 VSEAQEEAKAKSAKELAVKAAEVATHILNAENAKKEAQQAKQAALQAKTDAKKYADQSNAEKAKEAATK  
 abcdefgabcdfgabcdfg abcdefgabcdfgabcdfgabcdfg abcdefgabc  
 631 AEAAATIATDKAKEAENEAEAAVAEAKVDPEQIPKKEEEVKKKATQAAVSEDAKKAKNEALIEAEVAKA  
 defgabcdfgabcdfgabcdfg abcdefg abcd  
 701 EAAKEEAKKAHIAAGKAKKEEAEEKAAQTAQLSEVTDAKSKAESMTTLAKEKADTAEKEANETNESAKSIQN  
 efgabcdfgabcdfgabcdfg abcdefgabcdfgabcdfgabcdfgabcdfg  
 771 EAKTEKPEDITKKIEDLKGKAEKVSNSAKEAKKAQTKAELAAVAKAAVAKDEAKKAQDAADDANKKADE  
 g abcdefgabcdfgabcdfg abcdefgabcdfgabcdfgabcdfgabc  
 841 AAKSVESKAKGEAASAAAKAKENATVAASAANEVSSKTKEAEEEEIEKNWGDEKKKEEITSKVNHVKQETS  
 defgabcdfg  
 911 KSINAAEGAKRAKEVAELALKVVSAEVENDKAKKAVTAEAAKDEAKKAVESAESKSGEAESAVEDAETA  
 abcdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg  
 981 KEEEEKEVEKKAQEAASENANAQAQLKIAEEEELKKAKEADNEEKLQSAKTKALEAVDEAVKKGQAEAAAN  
 abcdefgabcdfgabcdfgabcdfgabcdfg abcdefgabcdfgabcdfgab  
 1051 EAKNKAAKATQSAEKAKQKAAESALKKKLVLEIVKKYSKESYNTVDSDEHVLNEVEEQASEEKEEEEE  
 cdefgabcdfgabcdfgabcdfg  
 1121 EEAHESVSNVEIEDEEEEEEEEEEEETNTEGEKSEDNSPHSDTEPQEQNSVKPPEQSEKTLNDSNT  
 1191 QALLSDNYKNVANFKKMADDLTKNIISTIDGDTGVIDTLKDFaedLNQFIFSM

### PvMSP3.10

1 MKHTRSVTLYLFLLLTLCAYLTGAEVIIGSPNNEAPNSSRHHLRNGFPKNDLSLPHEEPNNLEGKNESDQ  
 71 CDTINLQGVTEKEKKTIEQASVQAQDATKPEANNAEQIQAEELQKVKTAKDESATAAKDAETAAKNAVDAG  
 abcdefgabcdfgabcdfgabcdfgabcdfgabcde  
 141 KGLDAAKGAIKKAEAAAEAKKQAGIAEKAEKDAEAAAGKKDKLEDVNSQVQIAVEASTKAKDKKTEAEIA  
 fgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg  
 211 VEIVKAVVAKEEAQKASDEAQKACEKAQKAHAKAQKASDTTKTVETFKTNAEAAAKNAKEKAGNANKAAT  
 abcdefgabcdfgabcdfgabcdfgabcdfg abcdefgabcdfgabcdfgab  
 281 EAESANELSVAKQKAKDAEEAAKEAKKEQVKAIEIAAEVAKAKVAKEEADAAQKKAEEAKKIVDKIAQDTK  
 cdefg abcdefgabcdfgabcdfg abcdefgabcdfgabcdfgabcdfg  
 351 VPEAQREAKLATQTASKATEAATEAGKKAQEAEESSKEAEEKAETSDAVKKGADAAEKAAGEAKKASJET  
 abcdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg abcdefg  
 421 EIAIEVAKAEVLNAEVKKTQOEAEKDTEAKEQAEKAKAAEEAKTHGEKAEKVGESTKAHSDEAQQENK  
 abcdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgab  
 491 NAKDASEEANRAVDALLEEAYAVEAHLARTKNAAESAHSATDMSELEKAKEEIDAANIAHQWLKATQA  
 cdefgabcdfgabcdfgabcdfgabcdfgabcdfg  
 561 ATIAKEKKEAAKVAAEKAOATAANVVKDKAAKAEAKKAETEAVKAAVEARAAEEAKQEAAKVGASKEPQE  
 abcdefgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfgabcdfg  
 631 TKNKANVEAEATGNEAKKAEDAAEEAKEAKKANEAATDANVARSEADKAIAAAKKAKKAREKAAAYGLLKT  
 abcdefgabcdfgabcdfgabcdfgabcdfg abcdefg abcdefg  
 701 KNQYVLEPLDISPESADNITSKEEQVKEEMEDQGDSDSNEAEVEEALPNGSGAQEEDVNLEMDDEEEVEE  
 771 VEENVATNQQTGGKREKRNNTNDTVDDTNADKQGFDEFDTYNDIKKVTEALVKSMTSLVSDDDPSVGDITINE  
 841 FLSDMNHFLSW

### PvMSP3.11

1 MRQFVRIAIFISLLNLYLQKDGAVRGEILNVNKTNLRNGTPEEGVPSEGELPADAQEGKGGDSIKEVIKR  
71 ASEE**TAKF**ADE**AKEA**F**KK**AQSLAEE**AKEK**AAE**AKA****VGAMNGEKDTPPTTEK**AQRASQAASAAEQK**SNEA**  
abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**  
141 QAA**V**RT**AKEQ****ETK**ALEAAQVVKGLAEKAEPTTGD**KDE****AEKKRKE****AEEAL**SAVKANLSAVEAA**KVA****AEINA**  
efgabcde**fg**abcde**fg** abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**abcde**fg**  
211 **AE****A**VEE**ANT****VM**KELAKVKATEAADA**AK**DLLGAEVAEGSN**AKAE**EAHEFLKTTNQH**IQEF**EEMPSQGGD  
bcde**fg**abcde**fg**  
281 HVKDKNEEVKEEVKEEAK**EE**AK**EE**VLES**R**GE**EE**EQ**T**LEV**ED**DDVDE**EE**DE**ED**DD**DE**DE**ED**DE**ED**DE**ED**DE**ED**  
351 D**ED**DD**GG**DD**DS**GD**ND**S**DD**DD**ND**GD**DD**H**DE**DE**DD**