S3 | **MIT domains of VSP4 ATPase**

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257372942|Halob|Halomicrobium_mukohataei_DSM_12286  -------MDLGQYKEDILQEQYEEYLKKGKSHLDQENHEKAAKAFSQSLDRLEELETI-------RETTYPDRKEQLESSISKLKSGEALSE
PHpred (confidence>=3)                                  hhhhhhhhhhhhhhhhhh.h    hhhhhhhhhhhhhhhhhhhhhhh       hh     hhhhhhhhhhhh.......
241905101|Metha|Methanocaldococcus_infernus_ME      --MEIDLSGVLFSQFKKTKREYEKAKEQ----NNTILAKKKALECAKLLRLLAKYDKY-------NEKSYLEKAEKWEMVAKNINNILLSSS
261403117|Metha|Methanocaldococcus_vulcanius_M7     --MEIDLSGALMNQFKKAKLDYEKAKKN----GNMSLAKKKALECSKLLKELAKYDTY-------NAKSYVEKAEKWQIVAENINEVFESKT
254170018|Therm|Thermococcus_barophilus_MP          --MPVDLSGPLLSEFERAKKEFERAVAA----GDMETARRSALRCASILRQLARHVPY-------NGELYLKKAKKWEDVAGQIERGEYGRK
254171848|Therm|Thermococcus_sp-_AM4                --MPVDLSGPLLSAFRKAKREFEDAIKK----GDKETARKKALECARILKQLSKYDEF-------NCESYLKKAKKWEVIAKEVEEGRYGAK
254172320|Therm|Thermococcus _sp-_AM4               ------MQSLYLSLFEECKREYERALGR----GHFEAAREYALKCARILRVLAEKVPG-------KREFYLEKAESWERAAKEIKSKPPSTA
240103023|Therm|Thermococcus_gammatolerans_EJ3      ------MQSLHLSLFEEFKRKYERALGR----GDPEAARDYALKCARILKALAEKVPG-------KREFYLEKAESWEKAARELEARPPSPV
240103029|Therm|Thermococcus_gammatolerans_EJ3      --MPVDLSGPLMSAFRKAKKEFEEAIKK----GDKETAKKKALECARILKQLSKYDEF-------NRESYLKKAKKWEAIAKEVEEGHYGVK
219851941|Metha|Methanosphaerula palustris E1-9c    -RELGSVVIPTSEPLEEAVAAYTRAREH----GDLVQARKSALECAQLLVILAEAEPQ-------YSSAYLEKADDWKAIARSLTQHLEDEP
57641074|Therm|Thermococcus_kodakarensis_KOD1       ------MQRSHEILISKYERAYWDAVER----GEFSRARVLAIKCAGLFRELASLNLE-------FSDYYLEMAKQWEKRAGELENGHRYSQ
14521065|Therm|Pyrococcus_abyssi_GE5                ------MYRLQLLQVQKCQEEFERALSL----GHYDKARLIALRCAELLRKIASENLS-------LSHILLEEAKKWEEKAKNVRKRREGKN
14591092|Therm|Pyrococcus_horikoshii_OT3            ------MHRLQILQVQKCHEEFEKAMAL----GQYDKARLIALRCSELLRNLASENLD-------LSHILLEEAKKWEDKARNIRKKKEARN
Consensus_aa:                  ..                  ......      ..hpch...@.cA...    Gp...A+..AlcCt.lh..Ltp....       ..c.hlcbAcpWp..A.plpp......
Consensus_ss:                                             hhhhhhhhhhhhhhhhhhh      hhhhhhhhhhhhhhhhhhh          hhhhhhhhhhhhhhhhhh

257076944|Therm|Ferroplasma_acidarmanus_fer1        ------MTETKIDHVSLLIRKAIEEESS----GNKNEAARTYKAAYKEVLEIASRSTGK------IKQKRLEQAANLKKIYESIGGEAVEED
16082186|Therm|Thermoplasma_acidophilum_DSM_1728    -MRVLDDIDEKIDKATKLLQGGIKEESL----GHKDKAKEYYFAAYRLMLEAANASPPD------LKKKRLDQCNIILSAYQRVNENRTAPA
13541213|Therm|Thermoplasma_volcanium_GSS1          ---MSDDVQNKIEKATKLLHAGIKEEEN----GHKDKAKEYYLVAYRVMLEAANDSPSD------LKKKRLDQCALILNAYKRVSGERTDFT

218883494|Therm|Desulfurococcus_kamchatkensis_1221n --MIAVSMQYLVDKGIEYAHKAVSADKA----GDYETAIKYYNSAIDLLSKYLKLYPDS-----PLAETYRDLVQKYKNRVALLEKYLSNSV
126466168|Therm|Staphylothermus_marinus_F1          -----MSLQYLIEKGTEYAHKAVAADKK----GDYETAIKYYKAAIDLFLKYLRLYPDS-----SMSDFYRGLIIKYKSRVKVLEKHIEKIG
118576017|Cenar|Cenarchaeum_symbiosum_A             ---MSMAPQELENSASRYAGEAIKCDSQ----GARGMAIANYQKAIDSLVRLMHLYPRS-----KLNQLYKERTTSYQKRIKALRESGSVEP
161528596|marin|Nitrosopumilus_maritimus_SCM1       ---MSMAPQELENTASKYASEAIKFDSQ----GARGQAITYYQQAIDALVKLLQLYPNS-----KLNPIYKERCNSYHNRINALQQAHGVEP
156937784|Therm|Ignicoccus_hospitalis_KIN4-I        -------MSRLDRLAQFYIRKAKEAEAV----GRRDEALANYKNAAEVIQKLLDLYPDH-----PLKKAYLESLKNIKLKLNALQEEIMSEP
146304435|Therm|Metallosphaera_sedula_DSM_5348      ----MSAQVMLEEMARKYAIAAVRADKE----GRREDAINNYKKAIEVLTQIVTLYPDM-----VARNAYEQMINEYKKRLETLNQMVPEGG
227827584|Therm|Sulfolobus_islandicus_M-14-25       ----MSAQVMLEDMARKYAILAVKADKE----GKVEDAITYYKKAIEVLSQIIVLYPES-----VARTAYEQMINEYKKRISYLEKVLPASS
70607129|Therm|Sulfolobus_acidocaldarius_DSM_639    ----MSAQVMLEEMARKYAINAVKADKE----GNAEEAITNYKKAIEVLAQLVSLYRDG-----STAAIYEQMINEYKRRIEVLKELIPADG
2V6Y|Therm|Sulfolobus solfataricus                  ----MSAQVMLEDMARKYAILAVKADKE----GKVEDAITYYKKAIEVLSQIIVLYPES-----VARTAYEQMINEYKKRISYLEKVLPASS
2V6Y                                                ------hhhhhhhhhhhhhhhhhhh-------hhhhhhhhhhhhhhhhhhh----------hhhhhhhhhhhhhhhhh--------
15921478|Therm|Sulfolobus_tokodaii_str-_7           ----MSAQSMLEEMARKYAINAVKADKE----GKAEDAINNYKKAIEILSQLIALYPDS-----PSIKVYEQMINEYKKRIEVLKEAVPASG
14601103|Therm|Aeropyrum_pernix_K1                  ----MRAVPYLEGSAKKYALAAVDAEKR----GDYEAAIVNLNKAIEYLTEIVRNYPDY-----PLAHIYRRLIAQYRRKVKDLEKKARMIP
124027677|Therm|Hyperthermus_butylicus_DSM_5456     ---MSAGLHRLEAIARSYALAAVKADRE----GRIQEAIANYKKAIEVLAKIVSLYPDN-----PLAHVYRGIIQQYQRRVEQLEKLGVPAT
Consensus_aa:                                          M..h...L...tp.Yh..A.pt-......G....Al..hppAh-.l.phh..YPc.......h..hY...h.php.+lp.Lpp......
Consensus_ss:                                              h hhhhhhhhhhhhhhhhhhh      hhhhhhhhhhhhhhhhhhhhh         hhhhhhhhhhhhhhhhhhhhhh h
MIT domain consensus (PMC1236530)                   ...........h..Ah.hl.+Al..D.... ....-.Al..hY.Al-hLl.ul.h.....................YL.RAE..........
                                                                                c            i   i ii  i  i              i   i   i  iicii  i
7019569|Metaz|Homo_sapiens VPS4A                    ------MTTSTLQKAIDLVTKATEEDKA----KNYEEALRLYQHAVEYFLHAIKYEAHSD----KAKESIRAKCVQYLDRAEKLKDYLRSKE
17865802|Metaz|Homo_sapiens VPS4B                   ----MSSTSPNLQKAIDLASKAAQEDKA----GNYEEALQLYQHAVQYFLHVVKYEAQGD----KAKQSIRAKCTEYLDRAEKLKEYLKNKE
11875211|Metaz|Homo_sapiens spastin                 ----AERVRVFHKQAFEYISIALRIDEDEKA-GQKEQAVEWYKKGIEELEKGIAVIVTGQGEQCERARRLQAKMMTNLVMAKDRLQLLEKMQ
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