

Hmd	E Mm(S2)	-----MKVAIILGAGCYRTHAAAGITNFSRASQVAKEAGIPEIAMTHSTITMGAE	49
Hmd	E Mj(DSM_2661)	-----MKIAIILGAGCYRTHAAAGITNFSRACEVAKEVVGKPEIALTHSSITYGAE	49
Hmd	E Mth(dH)	-----MIDMKLAILGAGCYRTHAAAGITNFSRACEVAEMVVGKPEIAMTHSTITMGAE	52
Hmd	E Mtm	-----MKLAILGAGCYRTHAAAGITNFSRACEVAEMVVGKPEIAMTHSTITMGAE	49
Hmd	E Mk(AV19)	-----MVEINKVAIILGAGCWRTHAATGITTFKRACEVADEGTIKEAALTHSSVTVYAVE	53
Hmd	P Mm(S2)	-----MKVTVYGAGNQNLYVNLNLPPTYGGVPPYGGSRMAIEFAKAG-----	43
Hmd	P1 Mj(DSM_2661)	MRNIRKIKVDNMKVSIVYGAGNQNLYINKLNLPEKFGGEPYGGSRMAIEFAEAG-----	54
Hmd	P2 Mj(DSM_2661)	-----MKISIVYGAGNQRLYLEQLKVPEKFGGEPYGGAGMAIEFAKAG-----	43
Hmd	P1 Mt(dH)	-----MKRVIAMKVTVYGAGNQLYTDLNLPERYGGEAPYGGSRMAMEFAMAG-----	49
Hmd	P1 Mtm	-----MITMKVTVYGAGNQLYTELNLPEKYGGEAPYGGSRMAMEFAQAG-----	46
Hmd	P2 Mt(dH)	-----MSTMKVAVYGAGNQLYVDQLNLPEKYGGEAPYGGSRMAIEFAEAG-----	46
Hmd	P2 Mtm	-----MSTMKVAVYGAGNQLYVDQLNLPEKYGGEAPYGGSRMAIEFAEAG-----	46
Hmd	P1 Mk(AV19)	-----MATVAVLGFGNQRLYERIG--AAEKLGGEPFFGGAAMAIEFAEAG-----	43
Hmd	P2 Mk(AV19)	-----MEVHYELPLGGAHLAYRAAEAG-----	22
Hmd	E Mm(S2)	LLHLIPEITEVVVSDPCFAEPPGMVVLID-----QFDYKAVMEAHLAGDAEKVMPEIREAV	104
Hmd	E Mj(DSM_2661)	LLHLVPDVKEVIVSDPCFAEPPGLVVID-----EFDPKVEVMEAHLSGNPESIMPKIREVV	104
Hmd	E Mth(dH)	LKELAG-VDEVVADVPVFDN--QFTVID-----DFAYEDVIEAHKE-DPEKIMPQIREKV	103
Hmd	E Mtm	LKELAG-VDEVVADVPVFDN--QFTVID-----DFAYEDVIEAHKE-DPENIMPQIREKV	100
Hmd	E Mk(AV19)	LKHLAG-VDEVVSDPVFDAD-GFTVVVDIEEDCDVDLDEFIKAHLEGNPEDVMPKLRDyv	111
Hmd	P Mm(S2)	-----HDVILAEP-----	51
Hmd	P1 Mj(DSM_2661)	-----HDVVLAEP-----	62
Hmd	P2 Mj(DSM_2661)	-----HDVVLSEP-----	51
Hmd	P1 Mt(dH)	-----HDVILAEP-----	57
Hmd	P1 Mtm	-----HEVTLAEP-----	54
Hmd	P2 Mt(dH)	-----HDVVLAEP-----	54
Hmd	P2 Mtm	-----HDVVLAEP-----	54
Hmd	P1 Mk(AV19)	-----HDVVLAEP-----	51
Hmd	P2 Mk(AV19)	-----HDVVLCDP-----	30
Hmd	E Mm(S2)	KAKAKETPKPPKGCIFVHPETVG----LKVTDASDVEAVKDADIVITWLPKGGSQPAIIE	160
Hmd	E Mj(DSM_2661)	KAKAKELPKPPKACIHLVHPEDVG----LKVTSDDREAVEGADIVITWLPKGNKQPDIIK	160
Hmd	E Mth(dH)	NEVAKELPKPPEGAIHPTHPEDLG----FEITDDREAVADADFIMTWFPKGDMPQPIID	159
Hmd	E Mtm	NEVAKELPKPPEGAIHPTHPEDLG----FEITDDREAVADADFIMTWFPKGDMPQPIIN	156
Hmd	E Mk(AV19)	NDIADDVPPKPPKGAIFLSPEEMEDKLDIVVTTDDAEAVEDADMIISWLPKGGVQPDIFK	171
Hmd	P Mm(S2)	-----NKSNTLDEQWKIVVEEAG----VKVLTDDAEAAKEAEIAIFFTPPFGKKTVEIAK	00
Hmd	P1 Mj(DSM_2661)	-----NKNIMSDDLWKKVEDAG----VKVVSDDVEAAKHGEIHVLFPPFGKATFRIAK	111
Hmd	P2 Mj(DSM_2661)	-----NRDVMSSDDLWKKVEDAG----VKVVSDDIEAAKHGEIHVLFPPFRITLNIAN	100
Hmd	P1 Mt(dH)	-----SREFLDDEQWSMVEEAG----VTVTDNDKEAASEAEVAVLFTPPFGKGTFSIAR	106
Hmd	P1 Mtm	-----VRDVLDDGHWNLVEEAG----VTVTDNDKEASAEADVAVLFTPPFGKGTVRIAR	103
Hmd	P2 Mt(dH)	-----ARDMLDDAHWKVVEDAG----VTVTDNDAEAAASEAEIAVLFPPFGKKTPEIAK	103
Hmd	P2 Mtm	-----AREMLDDAHWKVVEDAG----VTVTDSDAEAAASEAEMAVLFTPPFGKKTFDIAK	103
Hmd	P1 Mk(AV19)	-----NLSEQDPEHVDRVADAG----VELTEDDAQAVEGAEMVVLFTPPFG-ATGGIIR	99
Hmd	P2 Mk(AV19)	-----SFDISE-ESMERLESAG----VELVTDTAGVEHGEIQILFTPPFG-HTVKIAR	77
Hmd	E Mm(S2)	KFASEIKKGAIVTHACTIPTPKFAKIFKDLG-----RDDLNIIAYHPGAVPEMKGQAFI	214
Hmd	E Mj(DSM_2661)	KFADAIPEGAIVTHACTIPTTKFAKIFKDLG-----REDLNITSYHPGCVPEMKGQVYI	214
Hmd	E Mth(dH)	KFIDDIKPGAIVTHACTIPTTKFYKIFEKKGDLVTKPETLNVTSYHPGAVPEMKGQVYI	219
Hmd	E Mtm	KFIDDIKPGAIVTHACTIPTTKFYKIFEQKHGDLVTKPETLNVTSYHPGAVPEMKGQVYI	216
Hmd	E Mk(AV19)	KIIDDIPGECIVANTCTIPTRQFKEMFEDMG-----RDDLQVTSYHPATVPEHKGQVYV	225
Hmd	P Mm(S2)	TILPHLPQNAIIANTCTVSPVILYTMLEVELR---TKRKDIGITSMHPAAVPGTPOHGHI	157
Hmd	P1 Mj(DSM_2661)	TIIEHPVENAIIANTCTVSPVLYYSLEPILR---TKRKDVGISSMHPAAVPGTPOHGHI	168
Hmd	P2 Mj(DSM_2661)	TIIEHPVENAIIANTCTIPTVLYRSLEGILR---LKRKDVGISSMHPAAVPGTPOHGHI	157
Hmd	P1 Mt(dH)	EILPELPEGSVIANCTVSPVLYYVLEKELK---LERTDVGVSMMHPAAVPGTPOHGHI	163
Hmd	P1 Mtm	EILPELPEGAVIANCTVSPVLYYVLEKELK---MDRTDIGVSSMHPAAVPGTPOHGHI	160
Hmd	P2 Mt(dH)	NITNHLPEGAVIANCTVSPVLYYVLERELR---RDRKDLGIASMMHPAAVPGTPOHGHI	160
Hmd	P2 Mtm	DITKHLPEGAVIANCTVSPVLYYVLERELR---RDRQDLGIASMMHPAAVPGTPOHGHI	160
Hmd	P1 Mk(AV19)	EIASHLEEGAVVCTCTSSAFEIHESLYEAGL---EVPEAVGVMPAHPAGIPGTENHRAI	156
Hmd	P2 Mk(AV19)	ELLDDVREGAVLCTCTCPPIALYHGLEGELR---TKREDVGVSSFPAGIPGAETQDLI	134
Hmd	E Mm(S2)	SEG-----LADAEKVEEFCMAKTARGEAFKMPANLISPVCMDGSAVTAPVYAAI	264
Hmd	E Mj(DSM_2661)	AEG-----YASEEAVNKLYEIGKIARGKAFKMPANLIGPVCMDCSAVTATVYAGL	264
Hmd	E Mth(dH)	AEG-----YASEEAINTLFELGQKARGNAYRLPAELLGVPVCMDCSALTATYAGI	269
Hmd	E Mtm	AEG-----YASEDAIETLFELGQKARGNAYRLPAELLGVPVCMDCSALTAMTYACI	266
Hmd	E Mk(AV19)	AEG-----YADEEVVEAVYELGEKARGLAFKVPGYLLGVPVCMDASAVTAIVYAGL	275
Hmd	P Mm(S2)	VISSKAT--NGTEYASDEQIEKCVKLTESIETKPYLVPADVSATVSDMGSLTAVTLAGV	215
Hmd	P1 Mj(DSM_2661)	VIGGKTT--DGKELATEEQIKKAVELAKSAGKEAYVVPADVSSVVDMDGSLVTAVALSGV	226
Hmd	P2 Mj(DSM_2661)	TIAGKAL--EGKEYATEDQINKLVELVKSVMGKIPYVTPADVVPVAVADMALVTAVALGV	215
Hmd	P1 Mt(dH)	VIGGRPT--AELDMATDEQVSRCAELAESTGKKAYIVPADVTSAVADMGSLVTAVALAGV	221
Hmd	P1 Mtm	VIGGRPT--AELDIATDEQIARCAELAESTGKTAYVVPADVTSAVADMGSLVTAVALAGV	218
Hmd	P2 Mt(dH)	VIGGHSS--SELDIATDEQISRCVELAESCGKVAYVVPADVSSAVADMGSLVTAVALSGV	218
Hmd	P2 Mtm	VIGGHSS--SELDIATDEQISRCVELAESCGKTAYVVPADVSSAVADMGSLVTAVALSGV	218
Hmd	P1 Mk(AV19)	ITARGETG--NGTVLATEEQAEVVEVLSSTGKEVFPVLPVPELVSVVGDLSVLLKRVIEA	214
Hmd	P2 Mk(AV19)	LVADARSEESGIELASEEQVERCVNLAEDMGYDVYVL--DPELISSIGDMSVVLTVRIVQA	193
N-terminal domain ← → C-terminal domain			
Hmd	E Mm(S2)	LAYRDAVTQILGAPADFAQMMADEAISQILDLMRNEGKIKNMEKLNPKALTGTADSMCFG	324
Hmd	E Mj(DSM_2661)	LAYRDAVTKILGAPADFAQMMADEALTOIHNLMKEKGIANMEEALDPAALLGTADSMCFG	324
Hmd	E Mth(dH)	LSYRDSVTQVLGAPAGFAQMMAKESLEQITALEKVGIDKMEEHLDPGALLGTADSMNFG	329
Hmd	E Mtm	LSYRDSVTQVLGAPASFAQMMAKESLEQITALEKVGIDKMEENLDPGALLGTADSMNFG	326
Hmd	E Mk(AV19)	LTPRDACTDILGAPVDFTQNMAVEALQMAKFMEEEGLDKLEALDPAALTNTADSMNFG	335
Hmd	P Mm(S2)	LDYYSVGTQVIKAPKMKVEQQILMTLQTMASLVESGVDGLVKALNPELLSKAASSMHLL	275
Hmd	P1 Mj(DSM_2661)	LDYITVGRKIINAPKMKIEQQVIMTLQTMASLVETSIGIEGMVKALNPELLIRSASSMKLL	286
Hmd	P2 Mj(DSM_2661)	LDYIRVGTQIINAPKDMIEKQILISLQTIASIIETSGMEGLMKVFNKDALSSAKNMLID	275
Hmd	P1 Mt(dH)	LDYIYVGTQIIKAPKEMVEKQILMTLQTMASLVETSIGVDGMAAAINPELLVKSARSMHLL	281
Hmd	P1 Mtm	LDYIYVGTQIIKAPKEMVEKQILMTLQTMASLVETSIGVDGMARAMNPELLVKSARSMHLL	278
Hmd	P2 Mt(dH)	LDYIYVGTQIIKAPKEMVEKQILMTLQTIASLVETSIGVNGMLKAMNPELLVRSARSMHLL	278
Hmd	P2 Mtm	LDYIYVGTQIIKAPVEMVEKQILMTLQTIASLVETSIGVNGMLKAMNPELLVRSARSMHLL	278
Hmd	P1 Mk(AV19)	LKEFCVAVKALG-APQEMIDRQAMMTLATLAALIEAGGIGG-----LLETLDDEEAIE	264
Hmd	P2 Mk(AV19)	ICNYFSVARICGAPIEMIEEQVEEVLSTMAYLVGRYGLDAPDRMD-GKLLRLSLRNMLT	252
Hmd	E Mm(S2)	-----PLAD--ILPASLVLEKH-ANENKCECGCSIKP	354
Hmd	E Mj(DSM_2661)	-----PLAE--ILPTALKVLEKHKVVEEKGKTKCEIMS	355
Hmd	E Mth(dH)	-----ASAD--ILPTVFEILEKRKK-----	347
Hmd	E Mtm	-----ASAE--ILPTVFEILEKRKK-----	344
Hmd	E Mk(AV19)	-----PLADTEILPKALEVLEKYSKKA-----	358
Hmd	P Mm(S2)	DQKDLDAALEILTHLDGELEKASTVAEIKPTTLVAAQSLVKELETIGGAAANGAIKRS	335
Hmd	P1 Mj(DSM_2661)	DRQKDLDAALEILQNLDETLEKAEVEKAEIKPTTLVAAQSLVKEIKTLIGGAAANGAIKRS	346
Hmd	P2 Mj(DSM_2661)	ERQEDLNALAKIIEEFDKST---IGEKDISQTYLVAPQALIKEAVSLIGKSAVEGMIRRS	332
Hmd	P1 Mt(dH)	DEQEELDAALKKISDLNDDVMKWIEGAEVNHTDLVAAQALTGELKTVIGDRAAEGTIRRC	341
Hmd	P1 Mtm	DEQEELDAALRKISQLNDDVMKWIEGAEVKHTDLVAAQALTGELKTVMGDRAAEGTIRRC	338
Hmd	P2 Mt(dH)	EEQEELDAALNTLSDLNDDVMKWIEKGEIRHTDLVAAQALAKEIKNLMGGKAAEGTIRRC	338
Hmd	P2 Mtm	EEQEELDAALNTLADLDDEVTQWINKGEIRHTDLVAAQALAKELKNLMGGKAAEGTIRRC	338
Hmd	P1 Mk(AV19)	ASYSNMEPFVVDG-----VEEPEGEPVERFVVLPGREATREAVIELVGERGWRTVMRA	316
Hmd	P2 Mk(AV19)	EDVERVVDFFERC--YVDLLSGDRESMRELSMMVPPDKLVDRVREIVGEAPVQYARRRF	310
Hmd	E Mm(S2)	-----	= top 10 MFS scoring residue in best RAPDF model
Hmd	E Mj(DSM_2661)	QKE----- 358	= top 10 MFS scoring residue in best C-score model
Hmd	E Mth(dH)	-----	= top 10 MFS scoring residue in both models
Hmd	E Mtm	-----	
Hmd	E Mk(AV19)	-----	
Hmd	P Mm(S2)	TKKLFQ-- 341	
Hmd	P1 Mj(DSM_2661)	ARKLFEH-- 353	
Hmd	P2 Mj(DSM_2661)	SNKLFK-- 338	
Hmd	P1 Mt(dH)	MRKMFEE-- 347	
Hmd	P1 Mtm	MRKMFEE-- 344	
Hmd	P2 Mt(dH)	MRKMFEE-- 344	
Hmd	P2 Mtm	MRKMFEE-- 344	
Hmd	P1 Mk(AV19)	WVDLYKHH 324	
Hmd	P2 Mk(AV19)	FEERRWGS 318	