

<i>Pf</i>	<i>MnmA</i>	MLIF F F F F F F F F F F K Y I Y N I F I L T C F Y I T L S S Y Y F I I S F I F S T L M F F Y F C T F Y V I S L F F L Y I S	60
<i>Sy</i>	<i>MnmA</i>	-----	0
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	0
<i>Pf</i>	<i>MnmA</i>	S F C K S I K V T Q L Y D K K I K I K S F I N N Y L V S C R K K K Y I Y N N V D D K S N I G T F N L Y H N I R D N N N N	120
<i>Sy</i>	<i>MnmA</i>	-----	0
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	0
<i>Pf</i>	<i>MnmA</i>	N N N N D N N N N L K K R D D V L F P L C N K N I I N D V Q K I Y D E V N N I K D K E Q K I N Y L M E Q C S S L C K E N	180
<i>Sy</i>	<i>MnmA</i>	-----	0
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	0
<i>Pf</i>	<i>MnmA</i>	Y F P P I L N L N K A Y R N K R I D E F N K G N K N F Y I N E V G K N I W Y K Y V N R C D E I L F M A I D I Q I D E D E	240
<i>Sy</i>	<i>MnmA</i>	-----	0
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	0
<i>Pf</i>	<i>MnmA</i>	Q R N N S I K D V H D V H D D N I K T C T L I K D D K H F E K Y K D I H N D N I L K N I L P L D K K I D S I K N M L N H	300
<i>Sy</i>	<i>MnmA</i>	-----	0
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	0
<i>Pf</i>	<i>MnmA</i>	K Y M K K K K C I I T I D A Y S N N L I L Y C F L Y L I L K H I N K M Y L Y S F M N I Q I K E I T A K L K E L F D L H F	360
<i>Sy</i>	<i>MnmA</i>	-----	0
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	0
<i>Pf</i>	<i>MnmA</i>	N V H H I I D Y I H E Y I Y N F L M S Y H I K R K K N K S K N M K E K D I K N V F A N N I I I S D E E N K H I S K E S S	420
<i>Sy</i>	<i>MnmA</i>	-----	3
<i>Bs</i>	<i>MnmA</i>	-----	0
<i>Ec</i>	<i>MnmA</i>	-----	0
<i>At</i>	<i>MnmA</i>	-----	0
<i>Sc</i>	<i>Mtu1</i>	-----	14
<i>Pf</i>	<i>MnmA</i>	D M Y K K K T T I T T T T T T K K K K N T M K L F T Y P R I A H M L S G G V D S L M A L H L L E R K K F Y V D N Y F F N	480
<i>Sy</i>	<i>MnmA</i>	S P Y P L ----- V A P E I A G S P R P R I V A A L S G G V D S S T V A A I L H E Q Q Y A V E G V T L -	51
<i>Bs</i>	<i>MnmA</i>	----- M E K R P E D T R V V V G M S G G V D S S V A A L L L K E Q Q Y D V I G I F M K	40
<i>Ec</i>	<i>MnmA</i>	----- M - S E T A K K V I V G M S G G V D S S V S A W L L Q Q Q Y Q V E G L F M K	38
<i>At</i>	<i>MnmA</i>	----- M - P E K P L R V A V L L S G G V D S S V A L R L L H A A G H S C T A F Y L K	38
<i>Sc</i>	<i>Mtu1</i>	- M L A R Y L N L I G R R S A S P Y R P Q R L P A K F D N V I V A M S S G V D S S V A A A L F A G E F P N T R G V Y M Q	59

Pf MnmA -FTN-----A----DC-SKNDIKYVKDICKNNKRNLFIIININDEYFDEVLPVPM LFF 525
Sy MnmA -WLMRG-----KGQC---CT--DGLVDAAAICEQLGIPHHIVDSRELFQANIVDYLVAG 99
Bs MnmA NWDDTD-----ENGF---CTATEDYEDVIRVCNQIGIPYYAVNFEKQYYEKVFQYFLDE 91
Ec MnmA NWEEDD-----GEEY---CTAAADLADAQAVCDKLGIELHTVNFAAEYWDNVFELFLAE 89
At MnmA IWFQEG-----FENFWNQCPWEDDLKYAKHVCEQVDVPLEVVHLTDEYWERVVSYIEE 92
Sc Mtu1 NWSESQSLDDPGKE----PC-YERDWRDVNRVAKHLNIRVDKVNFEQDYWIDVFEPMLRG 114

Pf MnmA YADGKVPNPDIMCNQKIKYNFFLKVIKSIYKQKWNRYRTKSKLCNYDFISTGHYAMIRTND 585
Sy MnmA YADGITPLPCSQCNKLVKFGPLLTARETL-----GISQIATGHYARVRFNS 146
Bs MnmA YKAGRTPNPVDVLCNKEIKFKAFLEHA-LSL-----GADYLATGHYARVD--R 135
Ec MnmA YKAGRTPNPDILCNKEIKFKAFLEFAAEDL-----GADYIATGHYVRR--D 134
At MnmA YRCGRTPNPVDVLCNTRIKFGAFMDAI-SDM-----EYDYVGS GHYAKVVHPP 138
Sc Mtu1 YSEGSTPNPDIGCNKFKVFGKLRWLDEKYG-----TGNYWLVTGHYARVM--Q 161

Pf MnmA KNNPNNIFNNNLFIKKKKKKIKNIKNKKNIKNKNNIKNKNNNNNIYTYNIYNLHNDNIKT 645
Sy MnmA E----- 147
Bs MnmA S----- 136
Ec MnmA V----- 135
At MnmA AD----- 140
Sc Mtu1 EM----- 163

Pf MnmA NYKKNKYFYKLLVSNDDKKDQTFLLSSFNHIQLSKFIFPLSLYTKKDVKKYMENNINN 705
Sy MnmA -----LGRYQLLRAVDRQKDQSYFLYDLSQEHLAHSLFPLGNYTKAQTRQIAARYGLVT 201
Bs MnmA -----GGKVRMLRGIDENKDQTYFLNQLTEDTSLKVMFPIGELQKSRVREIAKEAELAT 190
Ec MnmA -----DGKSRLRLGLSDNKDQSYFLYTLSEHQIAQSLFPVGELEKPOVRKIAEDLGLVT 189
At MnmA ----QNDASSVLELSQDMVKDQTYFLSHLSQTQLKRLLFPLGCVKKDEVKRLATQFDLPN 196
Sc Mtu1 ----NGKGLFHLLRSIYRPKDQSYYSLSQINSTVLSLLLPIGHLTKPEVRDLAKYAGLPT 219

Pf MnmA YNHKETKGLCLFGN---IDMQTL LHKYFVNTEKDDIKNKQONEDNIFKENNILNLNNNFNQ 762
Sy MnmA ANKPESQDLCLIET--YGSMRNF LDQHLGQRPGEIVDT-Q----- 238
Bs MnmA ATKKDS TGICFIGE---RNFKTFLSQYLPAPGDMMTM-D----- 226
Ec MnmA AKKDS TGICFIGE---RKFREFLGRYLPAPGKIITV-D----- 225
At MnmA KDRKDSQGICFLGK---IKFSDFVCRHIGEMEGII LEAES----- 233
Sc Mtu1 AEKPDSQGICFVNNSQH GKFKNFLKHYLPSSPGDIITVDPQS----- 261

Pf MnmA NEKKKKKEKLLVDITTTSSHLKKFRETFFPKMNLHYKNYLINLDDQTI LDINSDIHL YA 822
Sy MnmA -----GRVLGSHQGIHHT 252
Bs MnmA -----GEVKGRHDGLMYYT 240
Ec MnmA -----GDEIGE HQGLMYHT 239
At MnmA -----GDFLGNHRGFWFYT 247
Sc Mtu1 -----GAKTTWGRHDGLWSYT 277

Pf MnmA IGQHKNVTNYLHNLYNKKMININGYKKKHVKNVISSFQWIVVYKIKRDMSTNLIHNFYIY 882
Sy MnmA VGQRKGLGI-----ASS-----RPLYVVRIDAA-----MNRVV 280
Bs MnmA IGQRHGLGI-----GGS-----GEPWFAVGKDL-----KNILY 269
Ec MnmA LGQRKGLGI-----GGTKE-----GTEEPWYVVDKDVE-----NNILV 272
At MnmA IGQRQGLRL-----PG-----GPWYVVEKDTK-----NNVVF 274
Sc Mtu1 IGQKVGISM-----PQADP-----NYQGTWV FVSEKLRD-----TNEIL 310

Pf MnmA LTKNYDQDLFTHIRTKCKLHN IKWIEGKLPACIKKQFKKYNKINKKKKKINNNNNKYKTN 942
Sy MnmA VGEREEAT-----QAEAWVRQVNWVST-PAPD----- 306
Bs MnmA VDQGFHNPLI--YSDKITATN ISWVRS DIMKG----- 299
Ec MnmA VAQGHEHPRL--MSVGLIAQQLHWVDRE PFTG----- 302
At MnmA VSRNYYSIDK--RRRIFRVGSLRWNSGKPSGK----- 304
Sc Mtu1 IVRGRDNPAL--YSDTMRIENFSSLG PREDTINA----- 342

Pf MnmA	ETFHVYNNIQESGKKKKKKKVKNI PHDEKTI FVKIRNS---EQIKKAKIKFSLSNNTAYL	999
Sy MnmA	-----E-----PLAVEVQVRYS---TPAVPATLIPESPERVK-L	336
Bs MnmA	-----E-----EISCTAKFRYS---QEDHKVTVRMTGEGEAE-V	329
Ec MnmA	-----TMRCTVKTRYR---QTDIPCTVKALDDRIE-V	331
At MnmA	-----VR-----ELRC--KVRHG---PGFYS CSFEMEGDGDVAVV	334
Sc Mtu1	-----FQN-----TGALITLQFRSLQVPVQIKSCKLNRSADNLDITI	378
Pf MnmA	KVKQKDTGFS PGQIITLYFPFI IKKNNKVTYITNLNKYNNLINTNKNTIYYHCLGSATIS	1059
Sy MnmA	QFAEPQFGVTPGQA AVWYHGD-----LLLGGGILE	366
Bs MnmA	IFDEQVRAVTPGQAVVFYDGE-----ECLGGGTID	359
Ec MnmA	IFDEPVA AVTPGQSAVFYNGE-----VCLGGGIIE	361
At MnmA	HLDEDDQGLAAGQFAAFYEGT-----TCIGSGVIL	364
Sc Mtu1	HLASKQRAITPGQSCCLYIDD-----RVLGSGPIS	408
Pf MnmA	NQFLDYNLYQH IKNI--HQIND-----LNMSK-----	1084
Sy MnmA	RPSP-----	370
Bs MnmA	DVYKDGTKLWYV-----	371
Ec MnmA	QRLPLPV-----	368
At MnmA	ESWDDQCFPVCAKALQLAALEDKTKLGKPVKIMTMPTMSSVEADTGEASAEQKLVNA	421
Sc Mtu1	HVNNNDTHA-----	417

Figure 3- figure supplement 1- source data 1. Multiple sequence alignment used for **Figure 3(A)** and **Figure 3- figure supplement 1**.