

Sy MnmA -----MATSPY---PLVA----PEIAGSPSRPRIVAALSGGVDSSVVAAILHEQ 42
Bs MnmA -----MEKRPEDTRVVVGMSSGGVDSSVAALLLKEQ 30
Ec MnmA -----MSETAKKVIIVGMSSGGVDSSVSAWLLQQQ 28
At MnmA -----MPEKPLRVAVLLSGGVDSSVALRLLHAA 28
Sc Mtul MLARYLNLIGRRSASPY---RP-----QRLPAKFDNVIIVAMSSGGVDSSVAAALFAGE 49
Pf MnmA -----MYKKKTTITTTTTTCKKKKNTMKLFYPRIAHMLSGGVDLSMALHLLERK 470
Bm MnmA -----SLYRRSY---GFEVHDLYRLRSKSSSPNKVAMLISSGGVDSSVALWMLKSQ 281
Ta MnmA -----ELKKQDN---PTKGPKRTSMFQSPRSKKRVAVLVSSGGVDSSLALWIMKSR 319
Tg MnmA -----DLFASTT---ETCEEKRELRRSAASSPPQVAVLLSSGGVDSSVSLCLLQQR 853
Et MnmA -----AAKSRVSLPLSDGAGAEVHVLVSSGGVDSAVSLLLMREW 482

Sy MnmA GYAVEGVTL--WLMRG-----KGQCC--DGLVDAAAICE 73
Bs MnmA GYDVIGIFMKNWDDTD-----ENGFC--TATEDYEDVIRVCN 65
Ec MnmA GYQVEGLEFMKNWEEDD-----GEEYCTAAADLADAQAVCD 63
At MnmA GHSCTAFYFKIWFQEGFE-----NFWNQ--CPWEDDLKYAKHVCE 66
Sc Mtul FPNTRGVYMQNWSESQSL-----DDPGKEPCY--ERDWRDVNRVAK 88
Pf MnmA KFYVDNYE--FNF-----TNADC--SKNDIKYVKDICK 499
Bm MnmA GYNVHAFYFKAFG-----SDSPG--CTVAEDIRYATDCCN 314
Ta MnmA GFDVQAFHLKVNDL-----SNGPGLC--SSNDISYAMEVCN 353
Tg MnmA GFAPQAFFIKVWLPPELLLVSRHLNRLLD-----SGLAPAAAGG--CGWERDLLFADQVCR 906
Et MnmA GFRPKPIFLKVWAPAAQMKEQLQGRYQQEKLDIAAASATAAAA--CPWREDAKAAA--VAA 541

Sy MnmA QLGIPHHIVDSRELFQANIVDYLVAAGYADGITPLPCSQC*
Bs MnmA QIGIPYYAVNFEKQYYEKVFQYFLDEYKAGRTPNPDVLCNKEIKFKAFLEHA--LSLG--A 122
Ec MnmA KLGIELHTVNFAAEYWDNVFELFLAEYKAGRTPNPDIILCNKEIKFKAFLEFAAEDLG--A 121
At MnmA QVDVPLEVVHLTDEYWERVVSYIEEYRCGRTPNPDVLCNTRIKFGAFMDAI--SDME--Y 123
Sc Mtul HLNIRVDKVNFEQDYWIDVFEPMRLRGYSEGSTPNPDIGCNKFVKFGKLEWLDEKYGTGN 148
Pf MnmA NNKRNLFIININDEYFDEVLPMLFFYADGKVPNPDIMCNQKIKYNFFLKVIKSIYKQKW 559
Bm MnmA VLGVPPLHILPVEDVYNRAVMQYMVEGYRAGNTPNPDVICNREVKFGYFLNLTSEFG--F 372
Ta MnmA ILRVTLHVLPLFSQVYDKHILSDVLDYRKGEVNPDIILCNSRIKFGFLKMA--TDWG--F 410
Tg MnmA QARVPLEVLPQEAYWEGVVQQLDEARQGLTPNPDWWCNQRVKFGAFLDLL--DGRE--T 963
Et MnmA AAGLSLEVVPMQQYVWDRVISGFLEGARAGLTLNPDWSCN*SSVKFGAFAETL--DAVD--Y 598

Sy MnmA SQ-----IATGHYARVRFN----- 145
Bs MnmA DY-----LATGHYARVD----- 134
Ec MnmA DY-----IATGHYVRR----- 133
At MnmA DY-----VGS GHYAKVVHPPADQN----- 142
Sc Mtul YW-----LVTGHYARVMQEM----- 163
Pf MnmA NYRTKS-----KLCNYDFISTGHYAMIRTNDKNNPNNIFNNNLF 598
Bm MnmA DM-----VASGHYARINPOYFIPPOQSNG---- 396
Ta MnmA DY-----VATGHYATLCDDFFTKEQIKSPS--- 435
Tg MnmA RFSARRIAGESEGENEKEEADMPFLRNSSRWTVASGHYARVVPAAETSRRSEEGE--- 1020
Et MnmA R-----IASGHYARILID----- 611

Sy MnmA -----SELGRYQLL 154
Bs MnmA -----RSGGKVRML 143
Ec MnmA -----DVDGKSRLI 142
At MnmA -----DASSVLE 149
Sc Mtul -----NGKGLFHLL 172
Pf MnmA IKKKKKKIKNIKKNKNIKKNKNNIKKNKNNNNIYTYNIYNLHNDNIKTNYKNNKYFYKLL 658
Bm MnmA -----TQSSFVRFNELE 408
Ta MnmA -----YLDGC-----TSINGYYRIKRLC 453
Tg MnmA -----DTEDRDED-----GEEDRGDKERGSEEERTRLF 1049
Et MnmA -----EGCPRLI 618

*

Sy MnmA RAVDRQKDQSYFLYDLSQEHLAHS LFPLGNYTKAQTRQIAARYGLVTANKPESQDLCLIE 214
Bs MnmA RGIDENKDQTYFLNQLTEDITLSKVMFPIGELQKSRVREIAKEAELATATKKDSTGICFIG 203
Ec MnmA RGLDSNKDQSYFLYTL SHEQIAQSLFFVGELEKPVVRKIAEDLGLVTAKKDSTGICFIG 202
At MnmA LSQDMVKDQTYFLSHLSQTQLKRLLFPLGCVKKDEVRKLATQFDLPNKDRKDSQGICFLG 209
Sc Mtul RSIYRPKDQSYYSLSQINSTVLSLLLP IGH LTKPEVRDLAKYAGLPTAEK PDSQGICFVN 232
Pf MnmA VSNDKKKDQTF FLS SFNHIQLSKFI FPLSLYTKKDVKKYMNENNINNYNHKETKGLCLFG 718
Bm MnmA TSYYVNKDQTYFLSRLSSAQLGKMICPLGVHKKMVRALAYINGLGTQARDDSMGVCFLG 468
Ta MnmA LSTDTVKDQTYFLSRLNQNQMSRLIFPIGNILKTQVRDFAKTVGLPTYNKKDSFGLCFLE 513
Tg MnmA RGKDRRKDQSYFLSGLSQRQLRRLVTPVGDMEKVEVRRLAAALDLPTARRQDSQGLCFLG 1109
Et MnmA RGVDLTKDQSYFLSGLSSLQLSRLLFVVGALLKTQVRKIAVSWGLPSSQRPDSQGLCFLG 678

Sy MnmA T--YGSMRNF LDQHLGQRPGEIVDTQGR----- 240
Bs MnmA E---RNFKTFLSQYLPAQPGDMMTMDGE----- 228
Ec MnmA E---RKFREFLGRYLPAQPGKIITVDGD----- 227
At MnmA K---IKFSDFVCRHIGEMEGII LEAESG----- 234
Sc Mtul NSQHGFKNFLKH YLPSSPGDIITVDPQSG----- 262
Pf MnmA N---IDMQTLLHKYFVNTEKDDIKNKQNE DNI FKENNILN LNNNFNQNEKKKKKEKKLLV 775
Bm MnmA R---LDLRQFLKAHLGETPGQIIDYKSK----- 493
Ta MnmA D---LDLSEYLT KTLGESRGPIVEYETN----- 538
Tg MnmA N---LSLSFFFRHFLGSSTGPVLHFPS C----- 1134
Et MnmA P---LPVSQFLMHL LGE EEPV IHFPTG----- 703

Sy MnmA -----VLGSHQGIHHYTVGQRKGLGIASS-- 264
Bs MnmA -----VKGRHDGLMYYTIGQRHGLGIGGS-- 252
Ec MnmA -----EIGE HQGLMYHTLGQRKGLGIGGTK 252
At MnmA -----DFLGNHRGFWFYTI GQRQGLRLPGG-- 259
Sc Mtul -----AKTTWGRHDGLWSYTI GQKVGISMPQAD 290
Pf MnmA DITTTSSHLKKFRET FIPKMNLHYKNYLINLDDQTILDINS DIHLYAIGQHKNVTNYLHN 835
Bm MnmA -----QVIGQHTGLYNYTI GQRQGLGVSIDH 519
Ta MnmA -----KVI GEHNGLYNFTIGQKKTINNYLNP 564
Tg MnmA -----LALGSHDGLWNFTV GQRKGVTPCID-- 1159
Et MnmA -----VSI GRHKGLWGFTV GQQKGVVPLLD-- 728

Sy MnmA -----RPLYVVRID-----AAMNRVVVGEREEAT----- 288
Bs MnmA -----GEPWFVAVGKD-----LEKNILYVDQGFHNPLL--- 279
Ec MnmA EG-----TEEPWYVVDKD-----VENNILVVAQGHEHPRL--- 282
At MnmA -----PWYVVEKD-----TKNNVVFVSRNYYSID---K 284
Sc Mtul PN-----YQGTWV FVSEKL-----RDTNEILIVRGRDNPAL--- 320
Pf MnmA LYNKKMININGYKKKHVKNVISS FQWIVVYK KIKRDMSTNLIHNF IYLTKNYDQDLFT-- 893
Bm MnmA GG-----EEGGWFV VSKD-----AASNTLYVTKEYNSRHFTGR 552
Ta MnmA KH-----VGNTPKYVVKKD-----IYKNTLYV SASYNEDFFFTNP 598
Tg MnmA -----VARVRRLS-----SLPDSSL-TPHAASVDSEGS 1186
Et MnmA -----PRLCRRCH-----GASGG----- 741

Sy MnmA -----QAEAWVRQVNWVST-PAPDEP--LAVEVQVRY-----RTPAVPATL----- 326
Bs MnmA -----YSDKITATNISWVRS DIMK GEE--ISCTAKFRY-----RQEDHKVTV----- 319
Ec MnmA -----MSVGLIAQQLHWVDRE PFTG-T--MRCTVKTRY-----RQTDI PCTV----- 321
At MnmA RRRIRFRVGS L-----RWNSGKPSG-----KVREL RCKVRHGPGF 318
Sc Mtul -----YSDTMRIENFSS LGPREDTINAFQNTGALTLQF-----RSLQVPVQI----- 362
Pf MnmA ----- 893
Bm MnmA SC-IR--RAFSLAHVRWNNPILLNSHG-----IN-----EAD--YI----- 583
Ta MnmA RG-IR--SSFKVRDFFWNTPDYKDLIN-----KV-----QSEVSDNFKFKV KLRHTPNY 644
Tg MnmA EEQTARAGDSRRRQARAPP GKPTKASA-----TGQGRQAADDEERRLLEAKCHR---DGD 1238
Et MnmA ----- 741

Sy MnmA	IP-----ESPERVKLQFAEPQFGVTPGQAAVWYHGDL-----LLGGGILE	366
Bs MnmA	RM-----TGEGEAEVIFDEQVRAVTPGQAVVFYDGE-----CLGGGTID	359
Ec MnmA	KA-----LDDDRIEVIFDEPVAAVTPGQSAVFYNGEV-----CLGGGIIE	361
At MnmA	YSCSFEMEG--DGDVAVVHLDDEDDQGLAAGQFAAFYEGTT-----CIGSGV--	362
Sc Mtul	KSCKLN--RSADNLDITIHLSKQRAITPGQSCCLYIDDR-----VLGSGPIS	408
Pf MnmA	-----	893
Bm MnmA	-----K-----AEWEPPITRRDIKTMQDLTLDRNVASTE----	612
Ta MnmA	NYCNINFKGDEATDL-----QKWLPTTYELAAATIASV--DNSKCSIKMI--	687
Tg MnmA	DSCLRSANHTVRGRLECT----DNADRPDGRVVPVLSEGNEAPS-----SSSCSSSAEAD	1288
Et MnmA	-----	741
Sy MnmA	RPSP-----	370
Bs MnmA	DVYKDGTK-----LWYV-----	371
Ec MnmA	QRLPLPV-----	368
At MnmA	-----ILESWDDQCFPVCAKALQLAALED-----KTKLG-----KPVKIMTMPTMS	403
Sc Mtul	HVNNNDTH-----A-----	417
Pf MnmA	-----	893
Bm MnmA	-----KLFL---KV-----RNGTVL-----YEAECLKL----	631
Ta MnmA	-----QLILTFCTI-----EDVGF-----HTADSKATTIA	713
Tg MnmA	EGQEEGGDRQSRLSSSSFAACLSGSPQNLFEFANPFRTGLGAASLAGRWVVAAKHPPSN	1348
Et MnmA	-----PPKLSGPWSVVGKLEPAN	759
Sy MnmA	-----	370
Bs MnmA	-----	371
Ec MnmA	-----	368
At MnmA	-----SVEADTGE--ASAE-----QKLVNA-----	421
Sc Mtul	-----	417
Pf MnmA	-----HIR	896
Bm MnmA	-----SPPIRKGQGVTOHGWAFL-----DRSDPGLAT----GQYAA--LYRGNIC	670
Ta MnmA	LFFIFGSKNDEKDGTSIELEDIV-----HEPAPSEHG----SKKSP--SELHIYE	757
Tg MnmA	ALFVVSEKEMKAAA--AVAES-----VGYSLDVLAAGPGVRT-LGDSQTYLLALLLTLLQ	1398
Et MnmA	ALFVVSKEEEAAAE--DRLRALATEPGNYSEPLGA--PLLRAAANGDKAAALALKLRQLR	815
Sy MnmA	-----	370
Bs MnmA	-----	371
Ec MnmA	-----	368
At MnmA	-----	421
Sc Mtul	-----	417
Pf MnmA	TKCKLHNIKWIEGKLPACIKKQFKKYN-----KINKKKKKINNNNNKY	939
Bm MnmA	IGSGIIYQSF-----	680
Ta MnmA	IGKPIDYLDWKQHKRTNSSQSGRNGTHGKTHTEKRRNSDPTKRKSVHKPQRITSELEQKT	817
Tg MnmA	KFLRVDNIQWISHPPCAACNAEEQ-----PVS---RDPSFLGTLGSRDPRARLRGDE	1450
Et MnmA	TCLRVDNIRWFHGKAPAGFDASATL-----QPGCLREEGPTL-AAVAASAVAAKT-NTA	868
Sy MnmA	-----	370
Bs MnmA	-----	371
Ec MnmA	-----	368
At MnmA	-----	421
Sc Mtul	-----	417
Pf MnmA	KTN-----ETFHVYNNIQESGKKKKKKKVK--N-----IPH-----	968
Bm MnmA	-----	680
Ta MnmA	KPNS-PQQTTHKQQTNTKEQNTNKQSSVEQKTKADQSGPITRPF-----SPSV	866
Tg MnmA	KSLETADEFAFLRWALEGSRDKRPRLYDVQVRHAAGTACAAIHRVRVRLCLFPPERRSPSF	1510
Et MnmA	LPMERPA-ESFL----TG-SSKGGAGFVVQVRHSAGFHGVAKHNFKVLVSRGH-----	916

<i>Sy</i> MnmA	-----	370
<i>Bs</i> MnmA	-----	371
<i>Ec</i> MnmA	-----	368
<i>At</i> MnmA	-----	421
<i>Sc</i> Mtul	-----	417
<i>Pf</i> MnmA	-----DEKTI FVKIRNS-----	980
<i>Bm</i> MnmA	-----	680
<i>Ta</i> MnmA	LKPSEKAERVFSSNEKPAVQQRLFKPRENKYQKRTERYD TDMDFEKIFNPVHENAKDDEP	926
<i>Tg</i> MnmA	LSPSAVSEESG-----GRRK-----ESRAPFGPSRVETSAGSS	1543
<i>Et</i> MnmA	-----SGNSS	921
<i>Sy</i> MnmA	-----	370
<i>Bs</i> MnmA	-----	371
<i>Ec</i> MnmA	-----	368
<i>At</i> MnmA	-----	421
<i>Sc</i> Mtul	-----	417
<i>Pf</i> MnmA	EQIKKAKIKFSLSNNTAYLKVKQKDTGFSPGQIITLYFPFI IKKNNKVTYITNLNKYNNL	1040
<i>Bm</i> MnmA	-----	680
<i>Ta</i> MnmA	GSYMPFESIYDLSLDKCRLNKAFPPKGPAG-----HKFE-----	961
<i>Tg</i> MnmA	GAWTAW-----IELAEPDEGLAPGQIAAIYE GEE-----	1572
<i>Et</i> MnmA	PIEEAE-----LLEEPDVGLAPGQVAAFYRDDE-----	950
<i>Sy</i> MnmA	-----	370
<i>Bs</i> MnmA	-----	371
<i>Ec</i> MnmA	-----	368
<i>At</i> MnmA	-----	421
<i>Sc</i> Mtul	-----	417
<i>Pf</i> MnmA	INTNKNTIYYHCLGSATISNQFLD-----YNLYQH IKNIHQINDLNMS-K-----	1084
<i>Bm</i> MnmA	-----	680
<i>Ta</i> MnmA	-----CIDLDVIRVSKDFKNISLVNANVIHPKSNTHKICKISFDNKVLVDKVDD	1010
<i>Tg</i> MnmA	-----CLGAGRISARQQG-----	1585
<i>Et</i> MnmA	-----CIGSGRISALQGS-----	963
<i>Sy</i> MnmA	-----	370
<i>Bs</i> MnmA	-----	371
<i>Ec</i> MnmA	-----	368
<i>At</i> MnmA	-----	421
<i>Sc</i> Mtul	-----	417
<i>Pf</i> MnmA	-----	1084
<i>Bm</i> MnmA	-----	680
<i>Ta</i> MnmA	SMEFTAVVLEHVRSISILSVISTNPNMERSAIQFVITGKDKINVMNDYVSV MSTILKSEL	1070
<i>Tg</i> MnmA	-----MAVEAALRSAGL	1597
<i>Et</i> MnmA	-----FALKSIIDRLG-	974
<i>Sy</i> MnmA	- 370	
<i>Bs</i> Mnm	- 371	
<i>Ec</i> MnmA	- 368	
<i>At</i> MnmA	- 421	
<i>Sc</i> Mtul	- 417	
<i>Pf</i> MnmA	- 1084	
<i>Bm</i> MnmA	- 680	
<i>Ta</i> MnmA	- 1070	
<i>Tg</i> MnmA	N 1598	
<i>Et</i> MnmA	- 974	

Figure 3- figure supplement 3- source data 2. Multiple sequence alignment used for **Figure 3- figure supplement 3(E)**.