Supplementary Material

Table S1. LC-MS/MS analysis of the mitochondrial proteins identified by immunodetection with anti-Tob55/Sam50 and metaxin antibodies; Nom. Mass, nominal protein mass; stage abbreviations: **U**, unicellular; **A**, aggregation; **S**, streams

No.	Protein	Stage	AA sequence	Score	Nom. mass	pI	emPAI	Coverage [%]	Accession number/ Taxonomy
1.	Tob55/ Sam50	**U**	1 MDDDDIKIKF VNIK**SENVFL** **IETYFK**GFEK LPRRDWER**GL** **EYIVGQMEND** 51 **HVVTKGDFEI** **DPQTNEITVI** **SK**ER**GISFGV** **SANTDK**TSST R**FQLANPFGK** 101 GGLVGFEFSA GLYK**NNNGSV** **SYTDRFGNTL** **SLLKSSQDPV** **IKDR**NFK**IDE** 151 **TTLSYSFQK**N SNK**FSIFAGD** **STVSVLNK**NK **NKEHLANTGL** **AFKTGISHIY** 201 **SSNLR**SKSIN RLFK**IQNELA** **FPILSSCSFF** **KSNITYSLDF** **PLYEQLK**FR**G** 251 **DFITGGIFNF** **SK**DSMIPISE RFFNGRHYNF EGFVDSSLTE KGRSPYLGSS 301 FFFTFRTALL HKIK**DNASVM** **AYHCIGNTVL** **PLDSNETTFK** STALKLFSTN 351 SIRSSIGLGI SVDMGSADIE CSLVKPLFFN SQDELNNFAF GINIKI	603	44 719	8,51	2,10	41,00	gi|60474188 from *D. discoideum* AX4
2.	Tob55/ Sam50	**A**	1 MDDDDIKIKF VNIK**SENVFL** **IETYFK**GFEK LPRRDWER**GL** **EYIVGQMEND** 51 **HVVTKGDFEI** **DPQTNEITVI** **SK**ERGISFGV SANTDKTSST R**FQLANPFGK** 101 GGLVGFEFSA GLYK**NNNGSV** **SYTDRFGNTL** **SLLK**SSQDPV IKDRNFK**IDE** 151 **TTLSYSFQK**N SNK**FSIFAGD** **STVSVLNK**NK NK**EHLANTGL** **AFKTGISHIY** 201 **SSNLR**SKSIN RLFK**IQNELA** **FPILSSCSFF** **KSNITYSLDF** **PLYEQLK**FR**G** 251 **DFITGGIFNF** **SK**DSMIPISE RFFNGRHYNF EGFVDSSLTE KGRSPYLGSS 301 FFFTFRTALL HKIKDNASVM AYHCIGNTVL PLDSNETTFK STALKLFSTN 351 SIRSSIGLGI SVDMGSADIE CSLVKPLFFN SQDELNNFAF GINIKI	586	44 719	8,51	2,74	43	gi|60474188 from *D. discoideum* AX4
3.	Tob55/ Sam50	**S**	1 MDDDDIKIKF VNIK**SENVFL** **IETYFK**GFEK LPRRDWER**GL** **EYIVGQMEND** 51 **HVVTKGDFEI** **DPQTNEITVI** **SK**ER**GISFGV** **SANTDK**TSST R**FQLANPFGK** 101 GGLVGFEFSA GLYK**NNNGSV** **SYTDRFGNTL** **SLLKSSQDPV** **IKDR**NFK**IDE** 151 **TTLSYSFQK**N SNK**FSIFAGD** **STVSVLNK**NK **NKEHLANTGL** **AFKTGISHIY**	914	44 719	8,51	4,99	55	gi|60474188 from *D. discoideum* AX4

			201 **SSNLR**SKSIN RLFK**IQNELA** **FPILSSCSFF** **KSNITYSLDF** **PLYEQLK**FRG 251 **DFITGGIFNF** **SK**DSMIPISE RFFNGRHYNF EGFVDSSLTE KGRSPYLGSS 301 FFFTFRTALL HKIK**DNASVM** **AYHCIGNTVL** **PLDSNETTFK** STALKLFSTN 351 SIRSSIGLGI SVDMGSADIE CSLVKPLFFN SQDELNNFAF GINIKI						

No.	Protein	Stage	AA sequence	Score	Nom. mass	pI	emPAI	Coverage [%]	Accession numer/ Taxonomy
1.	Metaxin	**U**	1 MEKVIEVVKN NKLLVAATVT VSAGILYKTI SLNTNKPIFE K**DVVYVADFP** 51 **GINK**DLPSYS PFVLKVISIL EYCNIR**YEIN** **TTGDLGPNPR** KTFPYIRYND 101 EFVYDSYFIL EWISQQFKHV TPKMQQSIGS GGGSGEMDQA IDHITKR**FID** 151 **QAFTYLSAYI** **R**WVVPEYNEK IIPR**LLSSIQ** **NPIFR**SFAHK **AINQVSIQK**Y 201 K**TQVGNFSLD** **EVVSVFKSDL** **NSLSNLLGSK** TFIFGDHLSM ADISLFSTLA 251 QIYYVPVDTP IR**SILFENQN** **LLNYIQNVRS** **LIFSDAK**WEL LKQ	553	33 557	7,72	2,08	39	EAL68951.1 from *D. discoideum* AX4
2.	Metaxin	**A**	1 MEKVIEVVKN NKLLVAATVT VSAGILYKTI SLNTNKPIFE K**DVVYVADFP** 51 **GINK**DLPSYS PFVLKVISIL EYCNIR**YEIN** **TTGDLGPNPR** KTFPYIRYND 101 EFVYDSYFIL EWISQQFKHV TPK**MQQSIGS** **GGGSGEMDQA** **IDHITK**RFID 151 QAFTYLSAYI RWVVPEYNEK IIPR**LLSSIQ** **NPIFR**SFAHK AINQVSIQKY 201 K**TQVGNFSLD** **EVVSVFKSDL** **NSLSNLLGSK** TFIFGDHLSM ADISLFSTLA 251 QIYYVPVDTP IR**SILFENQN** **LLNYIQNVRS** **LIFSDAK**WEL LKQ	824	33 557	7,72	2	38	EAL68951.1 from *D. discoideum* AX4
3.	Metaxin	**S**	1 MEKVIEVVKN NKLLVAATVT VSAGILYKTI SLNTNKPIFE K**DVVYVADFP** 51 **GINK**DLPSYS PFVLKVISIL EYCNIRYEIN TTGDLGPNPR KTFPYIRYND 101 EFVYDSYFIL EWISQQFKHV TPK**MQQSIGS** **GGGSGEMDQA** **IDHITK**RFID 151 QAFTYLSAYI RWVVPEYNEK IIPR**LLSSIQ** **NPIFR**SFAHK AINQVSIQKY 201 K**TQVGNFSLD** **EVVSVFKSDL** **NSLSNLLGSK** TFIFGDHLSM ADISLFSTLA 251 QIYYVPVDTP IR**SILFENQN** **LLNYIQNVRS** **LIFSDAK**WEL LKQ	478	33 557	7,72	1,4	34	EAL68951.1 from *D. discoidem* AX4

Table S2. Examples of LC-MS/MS analysis of the TOB/SAM complex form proteins identified in this study: Tom40; mitofilin/Mic60;Mdm10; Nom. Mass, nominal protein mass; stage abbreviations: **U**, unicellular; **A**, aggregation; **S**, streams

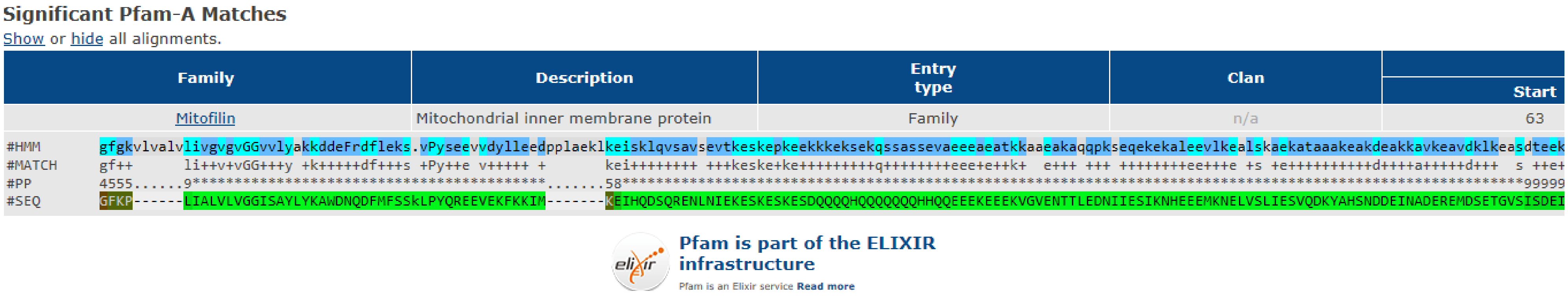
No.	Protein	Stage	AA sequence	Score	Nom. mass	pI	emPAI	Coverage [%]	Accession number/ Taxonomy
1.	Tom40	**U**	1 MEATADNNNN IDSQEQEIIG EPNFFQSFLV KNLPFYKSLP YPGK**AEDMIS** 51 **EVK**GLVNDDI YEGAKVDVTF K**ISPFFETSH** **QLNVYTPNEN** **SR**TPK**YSNQN** 101 **VYSK**DSTLLY GKIDSERRLF GRFDQGFFNN SIR**VSLTNMM** **DK**SFK**NNLAG** 151 **ELEFK**LPFMN FCLKADTENQ R**GFSFLTSIS** **KKLAIGYENS** **YLFNHSQSIK** 201 QIQFFVNNPL STWSLVVGNT AQIGSSYVYR QKNLHIGTDL VMGISQEGKF 251 MSEYSFGVRY AFQQSLVKFR **ADSHGSIFGS** **YDQMINSFTK** LNLSGSLNYF 301 AQDYKFGLGL TFQK	237	35 921	6.92	1.86	34	gi|66818277 from *D. discoideum* AX4
2.	Tom40	**A**	1 MEATADNNNN IDSQEQEIIG EPNFFQSFLV KNLPFYKSLP YPGK**AEDMIS** 51 **EVKGLVNDDI** **YEGAK**VDVTF KISPFFETSH QLNVYTPNEN SRTPK**YSNQN** 101 **VYSK**DSTLLY GKIDSERRLF GR**FDQGFFNN** **SIRVSLTNMM** **DK**SFK**NNLAG** 151 **ELEFKLPFMN** **FCLK**ADTENQ R**GFSFLTSIS** K**KLAIGYENS** **YLFNHSQSIK** 201 QIQFFVNNPL STWSLVVGNT AQIGSSYVYR QKNLHIGTDL VMGISQEGKF 251 MSEYSFGVRY AFQQSLVKFR **ADSHGSIFGS** **YDQMINSFTK** **LNLSGSLNYF** 301 **AQDYK**FGLGL TFQK	367	35 921	6.92	3.6	42	gi|66818277 from *D. discoideum* AX4
3.	Tom40	**S**	1 MEATADNNNN IDSQEQEIIG EPNFFQSFLV KNLPFYKSLP YPGKAEDMIS 51 EVK**GLVNDDI** **YEGAK**VDVTF K**ISPFFETSH** **QLNVYTPNEN** **SR**TPK**YSNQN** 101 **VYSK**DSTLLY GKIDSERRLF GR**FDQGFFNN** **SIRVSLTNMM** **DK**SFKNNLAG 151 ELEFKLPFMN FCLKADTENQ R**GFSFLTSIS** K**KLAIGYENS** **YLFNHSQSIK** 201 QIQFFVNNPL STWSLVVGNT AQIGSSYVYR QKNLHIGTDL VMGISQEGK**F** 251 **MSEYSFGVR**Y AFQQSLVKFR ADSHGSIFGS YDQMINSFTK LNLSGSLNYF 301 AQDYK**FGLGL** **TFQK**	257	35 921	6.92	1.86	34	gi|66818277 from *D. discoideum* AX4

No.	Protein	Stage	AA sequence	Score	Nom. mass	pI	emPAI	Coverage [%]	Accession number/ Taxonomy
1.	mitofilin/ Mic60	**U**	1 MSFLKINKIA LKSSTTILKS SSPLSGKTKF NHINSRSSSR SNENNYEKRY 51 YSSFSMKEDP EPSKPFGFKP LIALVLVGGI SAYLYKAWDN QDFMFSSKLP 101 YQREEVEKFK KIMKEIHQDS QRENLNIEKE SKESKESDQQ QQHQQQQQQQ 151 HHQQEEEKEE EKVGVENTTL EDNIIESIKN HEEEMKNELV SLIESVQDKY 201 AHSNDDEINA DEREMDSETG VSISDEISKL IEEHKQNEEE SLPDLLDVNY 251 GVLSIIPEAV KSAEETVENA LKKFTHSNDD DDDTTTTSII INTSDELKNH 301 NINIENGNEE SLVDSLDVNY NVLSIIPEKV KSAEEKVENV LKKFEEQYLE 351 KVEKLISENM KLKVDFDKLI NGKDDELKRV EEEIREKYRS SLDAAIEELN 401 KDLDEKLKDM DQFIKSKVFD NQAVLQETLE KQKSNLINIF KQQAESIKQS 451 ELEKRAITQL TQCIVDLQKL LHDKSAIDGA NGKGLLVRSF KNLTDLSNYD 501 QLIK**ELLSTL** **PEGFEKKPVI** **PLDTLNNQFQ** **DIAK**KLRKSQ LIDPNDNSLL 551 GKAVSELASL FIIPEKGMVQ GNDYDAILAR AEDHLRKNNL SSAIKEMESI 601 QQQSSKSSTN IDNHHLSKLT SNWIKQAKER DQLENISKLL ELKLELIHKQ	74	76013	5.00	0.12	4	gi|66826855 from *D. discoideum* AX4
2.	mitofilin/ Mic60	**U**	1 MSFLKINKIA LKSSTTILKS SSPLSGKTKF NHINSRSSSR SNENNYEKRY 51 YSSFSMKEDP EPSKPFGFKP LIALVLVGGI SAYLYKAWDN QDFMFSSKLP 101 YQREEVEKFK KIMKEIHQDS QRENLNIEKE SKESKESDQQ QQHQQQQQQQ 151 HHQQEEEKEE EKVGVENTTL EDNIIESIKN HEEEMKNELV SLIESVQDKY 201 AHSNDDEINA DEREMDSETG VSISDEISKL IEEHKQNEEE SLPDLLDVNY 251 GVLSIIPEAV K**SAEETVENA** **LKK**FTHSNDD DDDTTTTSII INTSDELKNH 301 NINIENGNEE SLVDSLDVNY NVLSIIPEKV KSAEEKVENV LKKFEEQYLE 351 KVEKLISENM KLKVDFDKLI NGKDDELKRV EEEIREKYRS SLDAAIEELN 401 KDLDEKLKDM DQFIKSKVFD NQAVLQETLE KQKSNLINIF KQQAESIKQS 451 ELEKRAITQL TQCIVDLQKL LHDKSAIDGA NGKGLLVRSF KNLTDLSNYD 501 QLIKELLSTL PEGFEKKPVI PLDTLNNQFQ DIAKKLRKSQ LIDPNDNSLL 551 GKAVSELASL FIIPEKGMVQ GNDYDAILAR AEDHLRKNNL SSAIKEMESI 601 QQQSSKSSTN IDNHHLSKLT SNWIKQAKER DQLENISKLL ELKLELIHKQ	37	76013	5.00	0.06	1	gi|66826855 from *D. discoideum* AX4

			651 QQQIKEEQQK						
3.	mitofilin/ Mic60	**S**	1 MSFLKINKIA LKSSTTILKS SSPLSGKTKF NHINSRSSSR SNENNYEKRY 51 YSSFSMKEDP EPSKPFGFKP LIALVLVGGI SAYLYKAWDN QDFMFSSKLP 101 YQREEVEKFK KIMKEIHQDS QRENLNIEKE SKESKESDQQ QQHQQQQQQQ 151 HHQQEEEKEE EKVGVENTTL EDNIIESIKN HEEEMKNELV SLIESVQDKY 201 AHSNDDEINA DEREMDSETG VSISDEISKL IEEHKQNEEE SLPDLLDVNY 251 GVLSIIPEAV KSAEETVENA LKKFTHSNDD DDDTTTTSII INTSDELKNH 301 NINIENGNEE SLVDSLDVNY NVLSIIPEKV KSAEEKVENV LKKFEEQYLE 351 KVEKLISENM KLKVDFDKLI NGKDDELKRV EEEIREKYRS SLDAAIEELN 401 KDLDEKLKDM DQFIKSKVFD NQAVLQETLE KQKSNLINIF KQQAESIKQS 451 ELEKR**AITQL** **TQCIVDLQK**L LHDKSAIDGA NGKGLLVRSF K**NLTDLSNYD** 501 **QLIK**ELLSTL PEGFEKKPVI PLDTLNNQFQ DIAKKLRKSQ LIDPNDNSLL 551 GKAVSELASL FIIPEKGMVQ GNDYDAILAR AEDHLRKNNL SSAIKEMESI 601 QQQSSKSSTN IDNHHLSKLT SNWIKQAKER DQLENISKLL ELKLELIHKQ 651 QQQIKEEQQK	68	76013	5.00	0.12	4	gi|66826855 from *D. discoideum* AX4

No.	Protein	Stage	AA sequence	Score	Nom. mass	pI	emPAI	Coverage [%]	Accession number/ Taxonomy
1.	Mdm10	**U**	1 **MKDYLQIVAE** **EIHYPSFPGP** **YHELTK**DAQI RIDFIEEVQT GISLSLDKKK 51 **GGNNFSADCG** **LMPMFYR**LEV GRDINDNQK**L** **GAIIQPEKLE** **LNYNFSPSKL** 101 **LFGGILGGK**S SR**IGGDIYVG** **VPMTPQINFE** **K**LVKK**ISTVG** **TITHETNK**TS 151 TEFKVSR**IYM** **GDIDHR**LAGL TFCYGLKPSL SLGFELYCK**F** **IQGSGASIGG** 201 **ASLGAR**HRGR AMGIQYDLAG TCNIFGDLQL TSSIGIIPNR LSFSTR**FNLN** 251 **TSNIISNIQF** **GTRINGNPII** **GNHEIPICLK** LRTDTNFENA IALDIDTPFT 301 SISIGCFGKK LDLFKNYGIN FSF	441	35 957	8.42	3.58	51	gi|66815917 from *D. discoideum* AX4
2.	Mdm10	**A**	1 **MKDYLQIVAE** **EIHYPSFPGP** **YHELTK**DAQI RIDFIEEVQT GISLSLDKKK 51 GGNNFSADCG LMPMFYRLEV GRDINDNQK**L** **GAIIQPEK**LE LNYNFSPSKL 101 LFGGILGGKS SRIGGDIYVG VPMTPQINFE KLVKK**ISTVG** **TITHETNK**TS 151 TEFKVSRIYM GDIDHRLAGL TFCYGLKPSL SLGFELYCKF IQGSGASIGG 201 ASLGARHRGR AMGIQYDLAG TCNIFGDLQL TSSIGIIPNR LSFSTRFNLN 251 TSNIISNIQF GTRINGNPII GNHEIPICLK LRTDTNFENA IALDIDTPFT 301 SISIGCFGKK LDLFKNYGIN FSF	120	35 957	8.42	0.42	14	gi|66815917 from *D. discoideum* AX4
3.	Mdm10	**S**	1 MKDYLQIVAE EIHYPSFPGP YHELTKDAQI RIDFIEEVQT GISLSLDKKK 51 GGNNFSADCG LMPMFYRLEV GRDINDNQKL GAIIQPEKLE LNYNFSPSK**L** 101 **LFGGILGGK**S SRIGGDIYVG VPMTPQINFE KLVKKISTVG TITHETNKTS 151 TEFKVSRIYM GDIDHRLAGL TFCYGLKPSL SLGFELYCKF IQGSGASIGG 201 ASLGARHRGR AMGIQYDLAG TCNIFGDLQL TSSIGIIPNR LSFSTR**FNLN** 251 **TSNIISNIQF** **GTR**INGNPII GNHEIPICLK LRTDTNFENA IALDIDTPFT 301 SISIGCFGKK LDLFKNYGIN FSF	52	35 957	8.42	0.26	8	gi|66815917 from *D. discoideum* AX4

Figure S1. Alignment of mitofilin/Mic60 identified in this study; results were generated by the Pfam model.



Significant Pfam-A Matches

Show or hide all alignments.

Family	Description	Entry type	Clan	Start
Mitofilin	Mitochondrial inner membrane protein	Family	n/a	63

```
#HMM     gfgkvlvalvlivgvgvGGvvlyakkddeFrdfleks.vPyseevvdylleedpplaeklkeisklqvsavsevtkeskepkeekkkeksekqssassevaeeeaeatkkaaeakaqqpkseqekekaleevlkealskaekataaakeakdeakkavkeavdklkeasdteek
#MATCH   gf++      li++v+vGG+++y +k+++++df+++s +Py++e v+++++ +       kei++++++++ +++keske+ke+++++++++q++++++++eee+e++k+  e+++ +++ ++++++++ee+++e +s +e++++++++++d++++a+++++d+++  s ++e+
#PP      4555......9*******************************************.......58***********************************************************************************************************99999
#SEQ     GFKP------LIALVLVGGISAYLYKAWDNQDFMFSSkLPYQREEVEKFKKIM-------KEIHQDSQRENLNIEKESKESKESDQQQQHQQQQQQHHQQEEEKEEEKVGVENTTLEDNIIESIKNHEEEMKNELVSLIESVQDKYAHSNDDEINADEREMDSETGVSISDEI
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