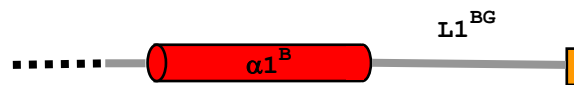


SUPPLEMENTARY INFORMATION

doi:10.1038/nature14880

Supplementary Figure 1 | Sequence alignment of the dynamin superfamily.

hsDYN3	-----	-----	-----	-----	-----	-----	1
hsDYN1	-----	-----	-----	-----	-----	-----	1
hsDYN2	-----	-----	-----	-----	-----	-----	1
xtDyn2	-----	-----	-----	-----	-----	-----	1
dmDYN	-----	-----	-----	-----	-----	-----	1
ceDyn	-----	-----	-----	-----	-----	-----	1
hsDNM1L	-----	-----	-----	-----	-----	-----	1
drDNM1L	-----	-----	-----	-----	-----	-----	1
scDnm1	-----	-----	-----	-----	-----	-----	1
hsMX1	-----	-----	-----	-----	-----MV	VSEVDIAKAD	12
hsMX2	MSKAHKPPYPY	RRRSQFSSRK	YLKEMNSFQ	QQPPPFGTVP	PQMMFPPNWQ	GAEKDAAFLA	60



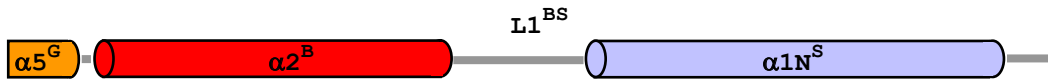
hsDYN3	-----	-----	-----MGN	REMEELIPLV	NRLQDAFSAL	QQSCLLELPQ	33
hsDYN1	-----	-----	-----MGN	RGMEDLIPLV	NRLQDAFSAL	QQNADLDLPQ	33
hsDYN2	-----	-----	-----MGN	RGMEELIPLV	NKLQDAFSSI	QQSCHLDLPQ	33
xtDyn2	-----	-----	-----MGN	RGMEELIPLV	NKLQDAFSSI	GQACNLDLPQ	33
dmDYN	-----	-----	-----	--MDSLITIV	NKLQDAFTSL	GVHMQLDLPQ	28
ceDyn	-----	-----	-----MSWQN	QGMQALIPVI	NRVQDAFSQL	GTSVSFELPQ	35
hsDNM1L	-----	-----	-----	--MEALIPVI	NKLQDVFNIV	GADI-IQLPQ	27
drDNM1L	-----	-----	-----	--MEALIPVI	NKLQDVFNIV	GADI-IQLPQ	27
scDnm1	-----	-----	-----M	ASLEDLIPTV	NKLQDVMYDS	GIDT-LDLPQ	30
hsMX1	PAAASHPLLL	NGDATVAQKN	PGSVAENNL	SQYEKVRPC	IDLIDSLRAL	GVEQDLALPA	72
hsMX2	KDFNFLTLNN	QPPPGNRSQP	RAMGPENNL	SQYEKVRPC	IDLIDSLRAL	GVEQDLALPA	120



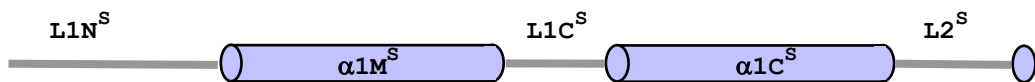
hsDYN3	I	A	V	V	G	G	S	A	G	K	S	S	V	L	E	N	F	V	G	R	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	V	L	Q	L	V	T	S	K	A	-----	78															
hsDYN1	I	A	V	V	G	G	S	A	G	K	S	S	V	L	E	N	F	V	G	R	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	V	L	Q	L	V	N	A	T	-----	78																
hsDYN2	I	A	V	V	G	G	S	A	G	K	S	S	V	L	E	N	F	V	G	R	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	I	L	Q	L	I	F	S	K	T	-----	78															
xtDyn2	I	A	V	V	G	G	S	A	G	K	S	S	V	L	E	N	F	V	G	R	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	I	L	Q	L	I	F	S	K	T	-----	78															
dmDYN	I	A	V	V	G	G	S	A	G	K	S	S	V	L	E	N	F	V	G	K	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	I	L	Q	L	I	N	G	V	T	-----	73															
ceDyn	I	A	V	V	G	G	S	A	G	K	S	S	V	L	E	N	F	V	G	K	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	I	L	Q	L	I	Q	D	R	N	-----	80															
hsDNM1L	I	V	V	G	T	O	S	S	G	K	S	S	V	L	E	S	I	V	G	R	D	L	L	P	R	G	S	G	I	V	T	R	R	P	L	I	L	Q	L	V	H	V	S	Q	E	D	K	R	K	T	T	G	E	N	G	V	E	A	87		
drDNM1L	I	A	V	V	G	T	O	S	S	G	K	S	S	V	L	E	S	I	V	G	R	D	L	L	P	R	G	S	G	I	V	T	R	R	P	L	I	L	Q	L	V	H	V	D	P	E	D	R	R	K	T	T	S	E	N	G	V	D	G	E	87
scDnm1	L	A	V	V	G	S	O	S	S	G	K	S	S	I	L	E	I	L	V	G	R	D	F	L	P	R	G	S	G	I	V	T	R	R	P	L	V	L	Q	L	N	N	I	S	P	N	S	P	L	I	E	E	D	D	N	S	V	N	P	H	90
hsMX1	I	A	V	I	G	D	O	S	S	G	K	S	S	V	L	E	A	L	S	G	-	V	A	L	P	R	G	S	G	I	V	T	R	C	P	L	V	L	K	L	K	K	L	V	N	E	D	K	W	-	120										
hsMX2	I	A	V	I	G	D	O	S	S	G	K	S	S	V	L	E	A	L	S	G	-	V	A	L	P	R	G	S	G	I	V	T	R	C	P	L	V	L	K	L	K	K	Q	P	C	E	A	W	-	-	167										



Species	Sequence	Position
hsDYN3	GYVGVNRSQ KDIDGKKDIK AAMLAERKFF LSHPAYRHIA DRMGT--PHL QKVLNQQLTN	287
hsDYN1	GYIGVVNRSQ KDIDGKKDIT AALAAERKFF LSHPSYRHIA DRMGT--PYL QKVLNQQLTN	287
hsDYN2	GYIGVVNRSQ KDIEGKKDIR AALAAERKFF LSHPAYRHMA DRMGT--PHL QKTLNQQLTN	287
xtDyn2	GYIGVVNRSQ KDIDGKKDIK AALGAERKFF LSHPGYRHIA ERMGT--PHL QKTLNQQLTN	287
dmDYN	GYIGVVNRSQ KDIEGRKDIH QALAAERKFF LSHPSYRHMA DRLGT--PYL QRVLNQQLTN	282
ceDyn	GYVGVNRSQ KDIVGRKDIR AALDAERKFF ISHPSYRHMA DRLGT--SYL QHTLNQQLTN	289
hsDNM1L	GIIGVVNRSQ LDINNKKSVT DSIRDEYAFI QKK--YPSLA NNRNGT--KYL ARTLNRLIMH	295
drDNM1L	GLIGVVNRSQ LDINNKKSVI DSIRDEHGFI QKK--YPSLA NNRNGT--KYL ARTLNRLIMH	294
scDnm1	GFVGVNRSQ QDIQLNKTVE ESLDKFEEDYF RKHPVYRTIS TKCGT--RYL AKLLNQTLIS	326
hsMX1	GYMIVKCRGQ QEIQDQLSLI EALQREKIFF ENHPYFRDLL EEGKATVPCI AEKLTSELIT	333
hsMX2	GYMIVKCRGQ QEITNRLSLA EATKKEITFF QTHPYFRVLL EEGSATVPRL AERLTTELIM	380



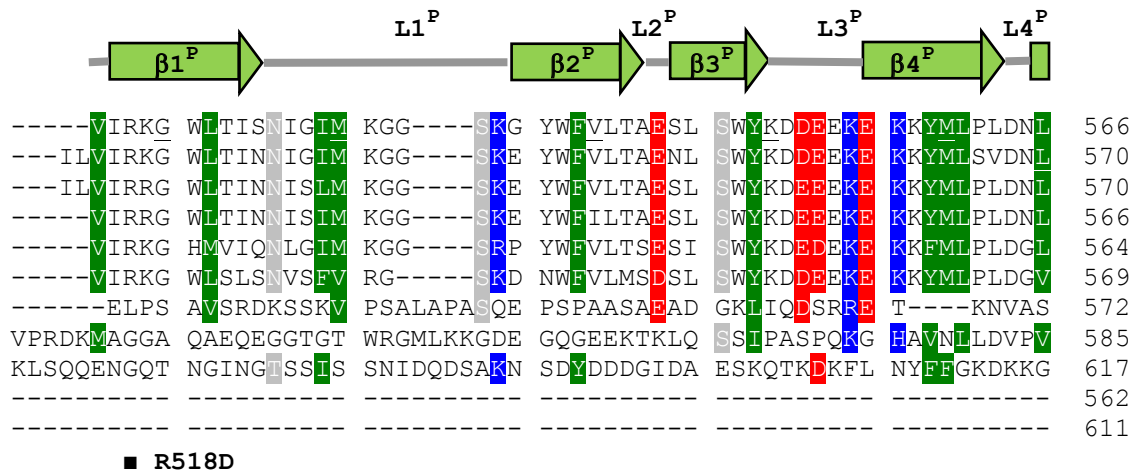
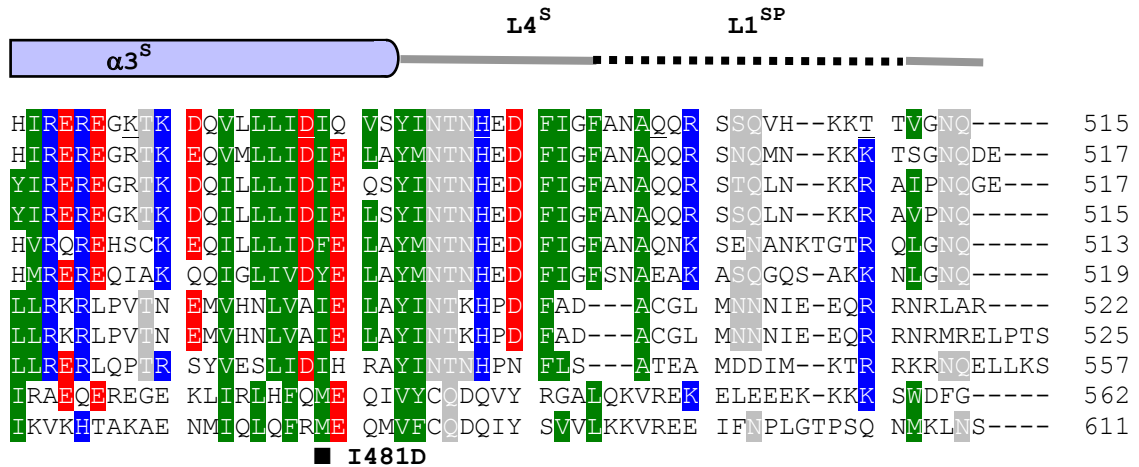
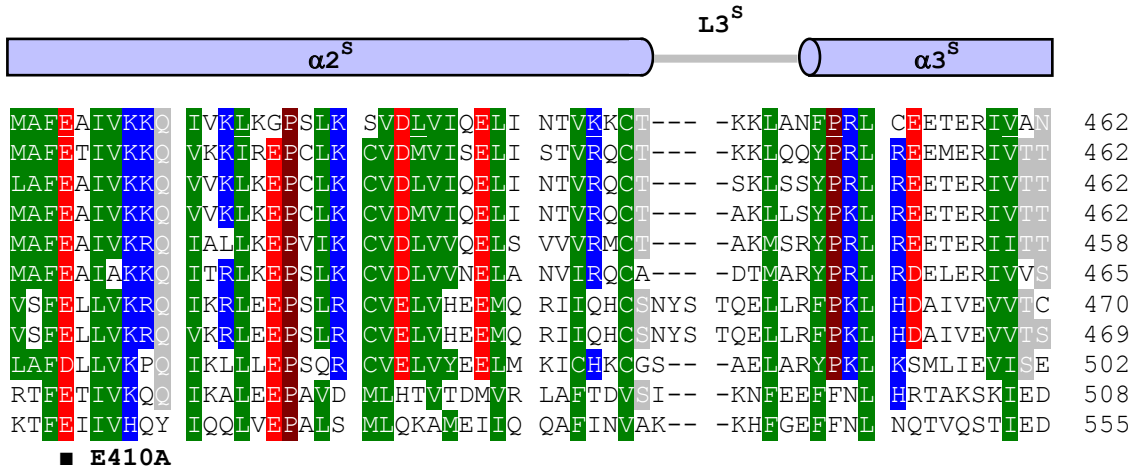
Species	Sequence	Position
hsDYN3	HIRDILPNFR NKLOGQLLSI EHEVEAYKNF KPEDPTRKTK ALLQMVOQFA VDFEKRIEES	347
hsDYN1	HIRDILPGLR NKLOSQLLSI EKEVEEYKNF RPDDPARKTK ALLQMVOQFA VDFEKRIEES	347
hsDYN2	HIRESLPALR SKLOSQLLSL EKEVEEYKNF RPDDPTRKTK ALLQMVOQFG VDFEKRIEES	347
xtDyn2	HIRETLPALR NKLOSQLLSL EKEVEEYKNF RPDDPTRKTK ALLQMVOQFG VDFEKRIEES	347
dmDYN	HIRDILPGLR DKLOKQMLIL EKEVEEYKHF QPGDASIKTK AMLQMIQQLQ SDFERTIEES	342
ceDyn	HIRDILPTLR DSLOKQMFAM EKDVAEYKNY QPNDPGRKTK ALLQMVTFQFN ADIERSTIEES	349
hsDNM1L	HIRDCLPELK TRINVLAAQY QSLLNSSYG-- --EPVDDKSA TLLQLITKFA TEYCNTIEGT	351
drDNM1L	HIRDCLPELK TRINVLAAQY QSLLNSSYG-- --EPVEDMSA TLLQLITKFA TEYCNTIEGT	350
scDnm1	HIRDKLPDIK TKLNTLISQT EQELARYGGV GATTNESRAS LVLQLMKNKFS TNFISSIDGT	386
hsMX1	HICKSLPLLE NQIKETHQRI TEELQKYGVD IPEDENEKMF FLIDKINAFN QDITALMQGE	393
hsMX2	HIQKSLPLLE GQIRESHQKA TEELRRCGAD IPSQEADKMF FLIEKIKMEN QDIEKLVEGE	440

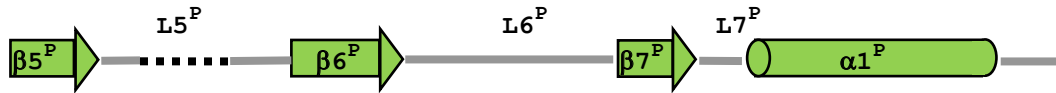


Species	Sequence	Position
hsDYN3	G-DQVDITLLEL SGGAKINRIF HERFPFEIVK MEFNEKELRR EISYAIKNIH GIRTGLFTPD	406
hsDYN1	G-DQIDITIEL SGGARINRIF HERFPFELVK MEFDEKELRR EISYAIKNIH GIRTGLFTPD	406
hsDYN2	G-DQVDITLLEL SGGARINRIF HERFPFELVK MEFDEKDLRR EISYAIKNIH GVRTGLFTPD	406
xtDyn2	G-DQVDITLLEL SGGARINRIF HERFPFELVK MEFDEKDLRR EISYAIKNIH GVRTGLFTPD	406
dmDYN	GSALVNTNEL SGGAKINRIF HERLRFEIVK MACDEKELRR EISFAIRNIH GIRVGLFTPD	402
ceDyn	SAKLVSTNEL SGGARINRLF HERFPFEIVK MEIDEKEMRK EIQYAIRNIH GIRVGLFTPD	409
hsDNM1L	A-KYIETSEL CGGARICYIF HETFGRTLES VDPLGGLNTI DILTAIRNAT GPRPALFVPE	410
drDNM1L	A-KYIETAEL CGGARICYIF HETFGRTLES VDPLGGLTTI DVLTAIRNAT GPRPALFVPE	409
scDnm1	S-SDINTKEL CGGARIIYIY NNVFGNSLKS IDPTSNLSVL DVRTAIRNST GPRPTLFVPE	445
hsMX1	E--TVGEEDI RLFTRLRHEF HKWSTIENN FQEGHKILSR KIQKFENQYR GRELPGFVNY	451
hsMX2	E--VVRENET RLYNKIREDF KNWVGILATN TQKVKNIIHE EVEKYEKQYR GKELLGFVNY	498

■ ■ ■ ■ R364S
E355A G358R K361S

■ F403D





hsDYN3	KVRDVEKSF	SSK--HIFAL	FNTEQRNVYK	DYRFLELACD	SQEDVD SWKA	SLLRAGVY PD	624
hsDYN1	KLRDVEKGF	SSK--HIFAL	FNTEQRNVYK	DYRQLELACE	TQEEVD SWKA	SFLRAGVY PE	628
hsDYN2	KIRDVEKGF	SNK--HVFAI	FNTEQRNVYK	DLRQIELACD	SQEDVD SWKA	SFLRAGVY PE	628
xtDyn2	KIRDIEKGF	STK--HIFAI	FNTEQRNVYK	DLRQIELACD	SQEDVD SWKA	SFLRAGVY PE	624
dmDYN	KLRDIEQGF	SMSRRVTFAL	FSPDGRNVYK	DYKQLELSCE	TVEDVES WKA	SFLRAGVY PE	624
ceDyn	KLKDI EGGF	SRN--HKFAL	FYPDGKNIYK	DYKQLELGCT	NLDEIDAWKA	SFLRAGVY PE	627
hsDNM1L	GGGGVGDGVQ	EPTTGNWRGM	LKTSKAEELL	AEEKSKPIPI	MPASPQK GHA	VNLLDVPV P-	631
drDNM1L	P-----	-----	-----	-----	-----	-----	586
scDnm1	QPVFDASDKK	RSIAGDGNIE	DFRNLQISDF	SLGD-----	-----	-----	651
hsMX1	-----	-----	-----	-----	-----	-----	562
hsMX2	-----	-----	-----	-----	-----	-----	611

L2^{SP}



hsDYN3	-----K SVA	ENDENGQAEN	F S M D P P O L E R O	V E T I R N L V D S	Y M S I I N K C I R	D L I P K T I M H L	678
hsDYN1	RVGDKEKASE	TEENGSDSFM	H S M D P P O L E R O	V E T I R N L V D S	Y M A I V N K T V R	D L M P K T I M H L	688
hsDYN2	-----K DQA	ENEDGAQENT	F S M D P P O L E R O	V E T I R N L V D S	Y V A I I N K S I R	D L M P K T I M H L	682
xtDyn2	-----K DQ	REEEETQENT	F S M D P P O L E R O	V E T I R N L V D S	Y I C I V N K S I R	D L M P K T I M H L	677
dmDYN	K-----Q ETQ	ENGDESASEE	S S S D P P O L E R O	V E T I R N L V D S	Y M K I V T K T T R	D M V P K A I M M L	679
ceDyn	K-----Q KAQ	EDESQQEMED	T S I D P P O L E R O	V E T I R N L V D S	Y M R I I T K T I K	D L V P K A V M H L	682
hsDNM1L	-----	-----VA	R K L S A R E Q R D	C E V I E R L I K S	Y F L I V R K N I Q	D S V P K A V M H F	673
drDNM1L	-----	-----VA	R K L S A R E Q R D	C E V I E R L I K S	Y F L I V R K N I Q	D S V P K A V M H F	628
scDnm1	-----	--IDDL ENAE	P P L T E R E F E L E	C E L I K R L I V S	Y F D I I R E M I E	D Q V P K A V M C L	699
hsMX1	-----	-----A	F O S S A T D S S	M E E I F O H I M A	Y H Q E A S K R I S	S H I P L I I Q F F	603
hsMX2	-----	-----H	F P S N E S S V S S	F T E I G I H L N A	Y F L E T S K R L A	N Q I P F I I Q Y F	652

H677D ■ L678D

L2^{BS}



hsDYN3	M I N N V K D F I N	S E L L A Q L Y S S	E D Q N T L M E E S	A E Q A Q R R D E M	L R M Y Q A L K E A	L G I I G D I S T A	738
hsDYN1	M I N N T K E F I F	S E L L A N L Y S C	G D Q N T L M E E S	A E Q A Q R R D E M	L R M Y H A L K E A	L S I I G D I N T T	748
hsDYN2	M I N N T K A F I H	H E L L A Y L Y S S	A D Q S S L M E E S	A D Q A Q R R D D M	L R M Y H A L K E A	L N I I G D I S T S	742
xtDyn2	M I N N S K D F I H	S E L L A Y L Y S S	A D Q N S L M E E S	A D Q A Q R R E D M	L R M Y H A L K E A	L K I I G D I S T S	737
dmDYN	I I N N A K D F I N	G E L L A H L Y A S	G D Q A Q M M E E S	A E S A T R R E E M	L R M Y R A C K D A	L Q I I G D V S M A	739
ceDyn	I V N O T G E F M K	D E L L A H L Y Q C	G D T D A L M E E S	Q I E A Q K R E E M	L R M Y H A C K E A	L P I I S E V N M S	742
hsDNM1L	L V N H V K D T L Q	S E L V G Q L Y K S	S L L D D L L L T E S	E D M A Q R R K E A	A D M L K A L Q G A	S Q I I A E I R E T	733
drDNM1L	L V N H V K D S L Q	S E L V G Q L Y K P	A L L D D L L L T E S	E D M A Q R R N E A	A D M L K A L Q K A	S Q V I A E I R E T	688
scDnm1	L V N Y C K D S V Q	N R L V T K L Y K E	T L F E E L L V E D	Q T L A Q D R E L C	V K S L G V Y K K A	A T L I S N I L --	757
hsMX1	M L O T Y G Q Q L Q	K A M L Q L L Q D K	D T Y S W L L K E R	S D T S D K R K F L	K E R L A R L T Q A	R R R L A Q F P G -	662
hsMX2	M L R E N G D S L Q	K A M M Q I L Q E K	N R Y S W L L Q E Q	S E T A T K R R I L	K E R T Y R L T Q A	R H A L C Q F S S K	712

hsDYN3	T V S T P A P P P V	D D S W I Q H S R R	S P P P S P T T Q R	R P T L S A P L A R	P T S G R G P A P A	I P S P G P H S G A	798
hsDYN1	T V S T P M P P P V	D D S W L Q V Q S V	P A G R R S P T S S	P T P Q R R A P A V	P P A R P G S R G P	A P G P P P A G S A	808
hsDYN2	T V S T P V P P P V	D D T W L Q S A S S	H S P T P Q R R P V	S S I H P P G R P P	A V R G P T P G P P	L I P V P V G A A	802
xtDyn2	T A T T P V P P P V	D D T W L Q N S N S	G H S P T V Q R R P	V S T V L P P S R P	P A V R G P T P G P	P L I P V P A G G S	797
dmDYN	T V S S P L P P P V	K N D W L P S G L D	N P R L S P P S P G	G V R G K P G P P A	Q S S L G G R N P P	L P P S T G R P A P	799
ceDyn	T L G D Q P P P L P	M S D Y R P H P S G	P S P V R P A P A	P P G G R Q A P M P	P R G G P G A P P P	P G M R P P P G A P	802
hsDNM1L	H I W-----	-----	-----	-----	-----	-----	736
drDNM1L	H I W-----	-----	-----	-----	-----	-----	691
scDnm1	-----	-----	-----	-----	-----	-----	757
hsMX1	-----	-----	-----	-----	-----	-----	662
hsMX2	E I H-----	-----	-----	-----	-----	-----	715

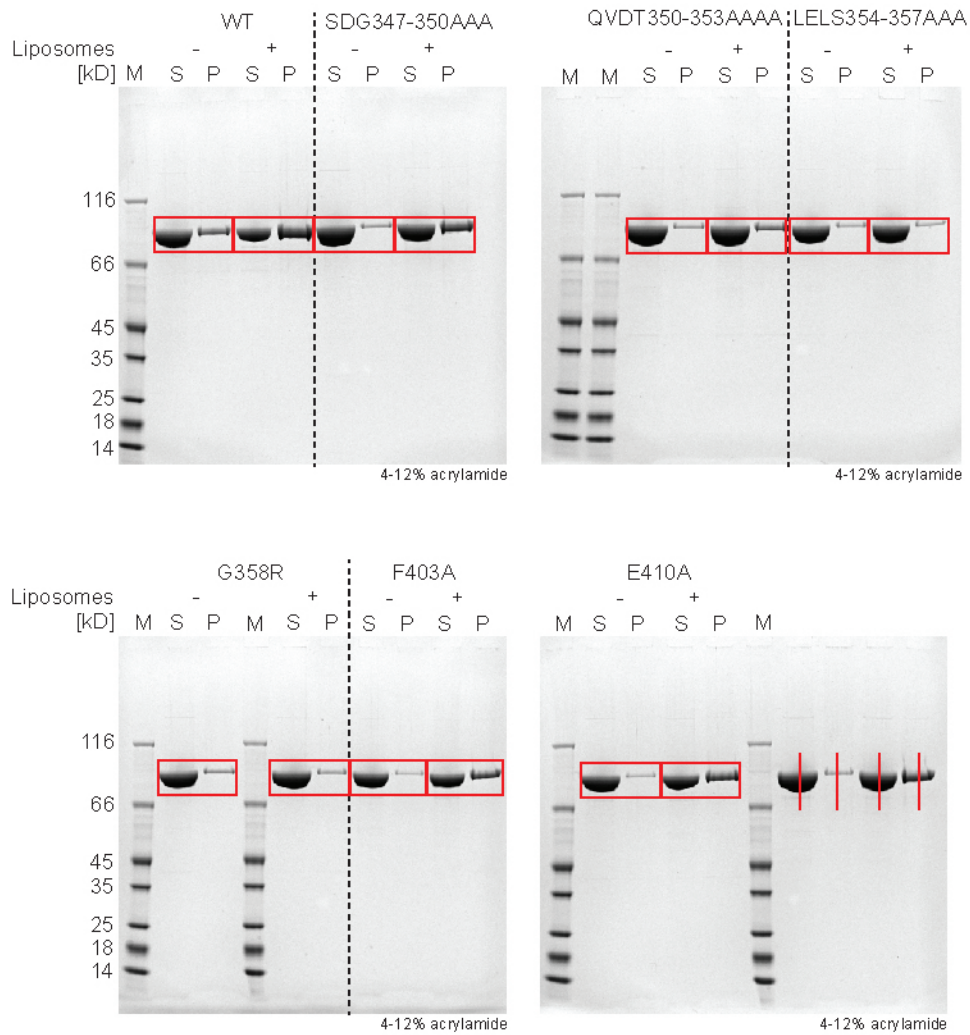
hsDYN3	PPVPFRPGPL	PPFPSSSDSF	GAPPQVPSRP	TRAPPSVPSR	RPPPSPTRPT	IIRPLESSLL	858
hsDYN1	LGGAPPVPSR	PGASPDFFGP	PPQVPSRPNR	APPGVPSRSG	QASPSRPESP	RPPFDL----	864
hsDYN2	SFSAPPIPSR	PGPQSVFANS	DLFPAPPQIP	SRPVRIPPGI	PPGVPSRRPP	AAPSRPTIIR	862
xtDyn2	AFIAPPIPSR	PGPQGPFAAA	NNDPFSAPPQ	IPSRPARIPP	GVPPGVPSRR	PPAAPTRPTI	857
dmDYN	AIPNRPGGGA	PPLPGGRPGG	SLPPPMLPSR	VSGAVGGAIV	QQSGANRYVP	ESMRGQVNQA	859
ceDyn	GGGGGMYPPL	IPTRVPTPSN	GAPEIPARPQ	VPKRPF----	-----	-----	838
hsDNM1L	-----	-----	-----	-----	-----	-----	736
drDNM1L	-----	-----	-----	-----	-----	-----	691
scDnm1	-----	-----	-----	-----	-----	-----	757
hsMX1	-----	-----	-----	-----	-----	-----	662
hsMX2	-----	-----	-----	-----	-----	-----	715

hsDYN3	D-----	-----	859
hsDYN1	-----	-----	864
hsDYN2	PAEPSLLD--	-----	870
xtDyn2	IRPAEPSLLD	-----	867
dmDYN	VGQAAINELS	NAFSSRFK	877
ceDyn	-----	-----	838
hsDNM1L	-----	-----	736
drDNM1L	-----	-----	691
scDnm1	-----	-----	757
hsMX1	-----	-----	662
hsMX2	-----	-----	715

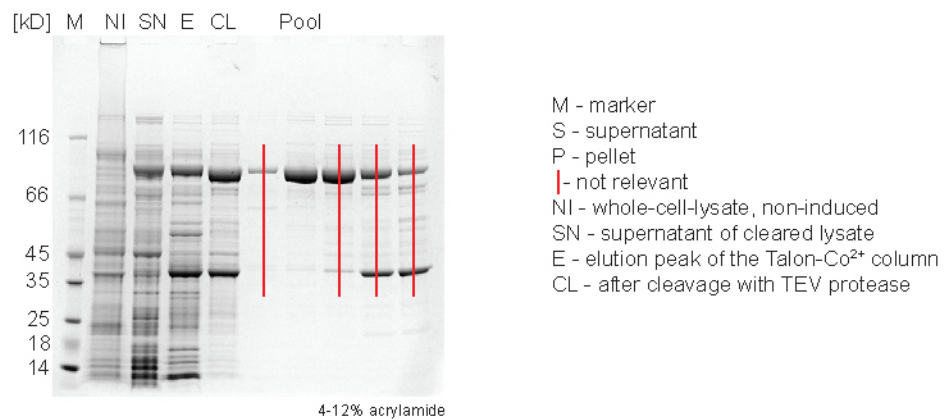
Supplementary Figure 1 | Sequence alignment of the dynamin superfamily.

Amino acid sequences of human (hs) dynamin 3 (Swiss-Prot accession number Q9UQ16), dynamin 1 (Q05193), dynamin 2 (P50570), *Xenopus tropicalis* (xt) dynamin 2 (Q5XGH8), *Drosophila melanogaster* (dm) dynamin (P27619), *Caenorhabditis elegans* (ce) dynamin (Q9U919), human dynamin 1-like protein (DNM1) (O00429), *Danio rerio* (dr) DNM1 (Q7SXN5), *Saccharomyces cerevisiae* (sc) DNM1 (P54861), human MxA (P20591) and MxB (P20592) were aligned and manually adjusted. Residues with a conservation of greater than 60% are color-coded (D,E in red; R,K,H in blue; N,Q,S,T in gray; L, I, V, F, Y, W, M, C in green, P,G in brown). Secondary structure is assigned according to the outer molecule A. Superscript letters are used to assign the domain architecture (B–BSE, G–G domain, S–stalk, P–PH domain). Residues mutated in the current study are marked (■).

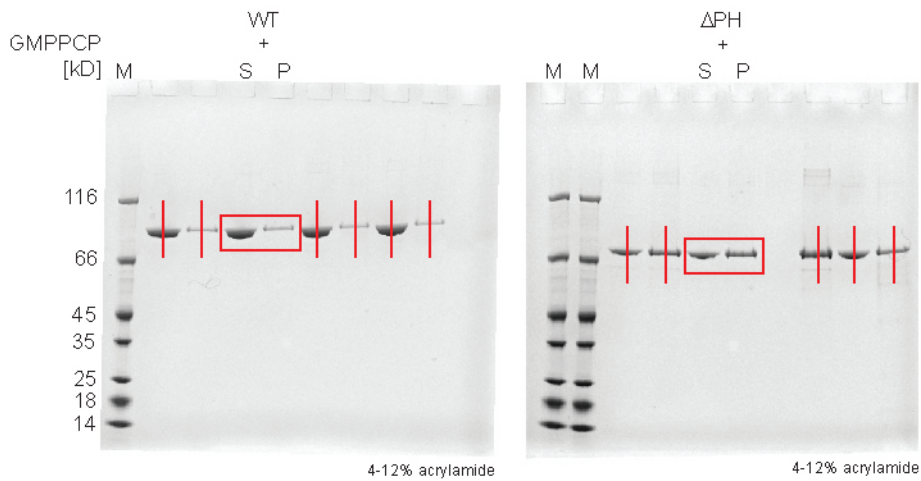
SDS-PAGE gels referring to Figure 2b



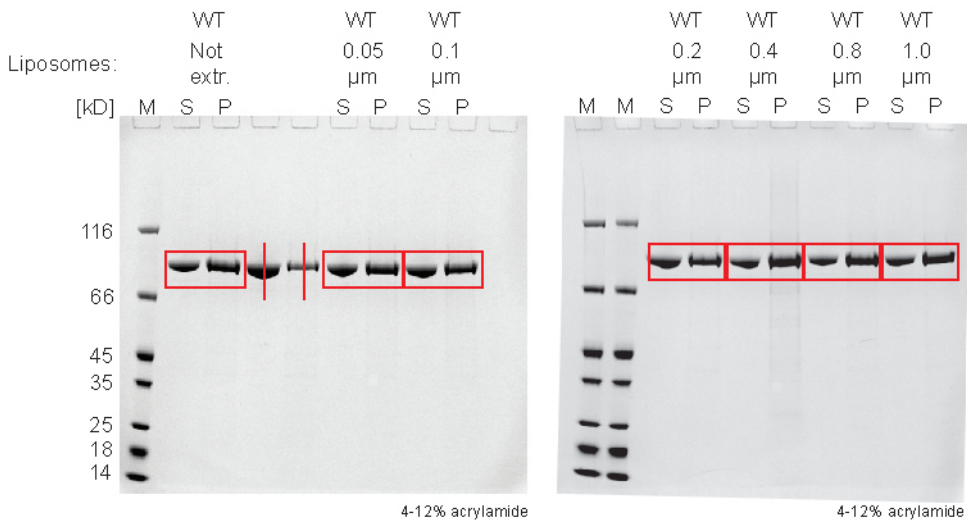
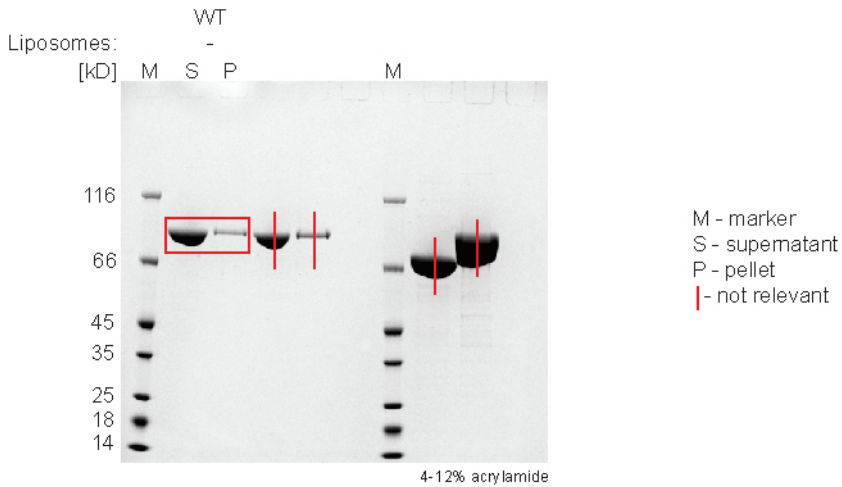
SDS-PAGE gel referring to Extended Data 1b



SDS-PAGE gels referring to Extended Data 5a



SDS-PAGE gels referring to Extended Data 5d



SDS-PAGE gels referring to Extended Data 6d

