

MARF <i>D. melanogaster</i>	TLQARIEEAKGNPPHMGAI AEGFQIRYFEFQDFERKFEE	CI	SQSAVTKTKFQQHSSRGK	SV	408
FZ01 <i>C. elegans</i>	VLESRLKAR-GLVQ-KAYQAEHGTRALEFQNFERHFEH	CI	SRSAIHTKFEAHNRAH	EM	378
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MFN1 <i>H. sapiens</i>	LATVKNIMDSVNLAAEDKRHYSVEEREDQIDRLDFIRNQMNL	LL	LDVKKKIK	VEE	407
MFN1 <i>M. musculus</i>	LDTVKNILDSVNVAAAEKRVYSMEEREDQIDRLDFIRNQMNL	LL	LDVKKKIK	VEE	407
MFN1 <i>G. gallus</i>	IDTVKNIMDAINVAAAEKRVLSMEEREDQKDRLDFVRNQLN	IL	EDTKEKIK	RV	408
MFN1 <i>D. rerio</i>	TETVKDIMDQINITAAEKRVVLSLEEREYLIDRLDFVRNQLN	LI	QDIKKIK	KA	403
MARF <i>D. melanogaster</i>	SGDMKSMLDNIYERITIFRNKQDQKNLLTERIQGTETQMMQV	TRE	MKMIHNM	VEE	468
FZ01 <i>C. elegans</i>	IGKMRNLNLSVLTSAAEQRSKLNQNNLNESRTRFNECRVNF	TQ	FEKAYRE	TEQ	438
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MFN1 <i>H. sapiens</i>	KVSCAMTDEICRLSVLVDFEFCSEFHPNPVVKIYKSELNKH	IED	GMGRNLADR	CTDE	467
MFN1 <i>M. musculus</i>	KVSCAMTDEICRLSVLVDFEFCSEFHPTPSVLKVKYKSELNKH	IED	GMGRNLADR	CTNE	467
MFN1 <i>G. gallus</i>	KVSSAMTDEICRLSVLVDFEYSDFHSPQVLKLYKTELNKH	IED	GLGKNLADR	CSSE	468
MFN1 <i>D. rerio</i>	KVSNAMAEIICRLSVIIDEFRSDFHSPQMLKMYKSDLLSH	IE	QGMGKNLAF	RCSDA	463
MARF <i>D. melanogaster</i>	KVSKALNEEIWRGLVLIDEFNMPFPERVLVNIYKKELN	NAH	VESGLG	SNLRARL	528
FZ01 <i>C. elegans</i>	KVSADFFEEIARLDAIIDRFQDFGSSSGMTKYKEDLAI	FV	DKLSSD	LEARCT	498
	*** : ** *	..:.*	..:.*	..:.*	..:.*
MFN1 <i>H. sapiens</i>	LVLQTQQEIIENLKPLLPAGI--QDKLHTLI-PCKKFDLS	YNL	NHKLCS	DFQED	524
MFN1 <i>M. musculus</i>	SILQSQQEIIENLKPLLPAGI--QNKLHTLI-PCKKFDLS	YDL	NCHKLCS	DFQED	524
MFN1 <i>G. gallus</i>	SMHQSQQEIIENLKPLLPAGI--QNQLHLI-PCRKFDLS	YDL	NCHSLC	ADFD	525
MFN1 <i>D. rerio</i>	SVQCSQQDMIECLKPLPSAA--QTQLHMLI-PSRKFE	LS	YDLN	CATLCS	520
MARF <i>D. melanogaster</i>	NVESAQTEMTDRMHALVNEQLLATSTKMVV-RTQPFEM	LY	SLNC	QNLCA	587
FZ01 <i>C. elegans</i>	RIWNLENDMFQYVTKILAEPY--QNKLEEVWRYRAPFK	FS	CVDV	PALVND	556
	: : : : : :	. . :	*.:	:: *	***:**. **
MFN1 <i>H. sapiens</i>	SLGWSSLVHRFLGPRNAQRVLLGL--SEPIFQLPRSLAS	TPTAPT	-----	ATPD	573
MFN1 <i>M. musculus</i>	SLGWSSLVHRFLGSTNAQRVLLGL--SEPIFQVPRSLAS	TPTAP	SNP-----	AAPD	573
MFN1 <i>G. gallus</i>	SLGWTSLVNRFLGPKHAQRVLLGL--ADPNLQIPRPLAT	TPSA	ALP-----	AATPE	575
MFN1 <i>D. rerio</i>	SLGWSALVHRFLGFPVNAKRALMLV---DQNLQLTAPT	--TP	APAVVQ	SQNSRAL	575
MARF <i>D. melanogaster</i>	SWGIAAMIRQFTGKVRERSKKQOPALVNRQSSIGHSV	-STPT	TPV	EATPV	646
FZ01 <i>C. elegans</i>	TFGLHAIIRRIIAYRSQGPVTAI---NTNLLTPLSLKQ	Q-----	SEKNS	VRD	605
	: * :::**. :	:	:	:	:
MFN1 <i>H. sapiens</i>	NASQEELMITLVTGLASVTSRT	SMGI	IIVGGV	IWKTIG	633
MFN1 <i>M. musculus</i>	NAAQEELMITLITGLASLTSRT	SMGI	IIVGGV	IWKTIG	633
MFN1 <i>G. gallus</i>	NTSPDDFMVPLVMSLASLTSRT	SMSI	IIVGGV	IWKTIG	635
MFN1 <i>D. rerio</i>	SVTQEELMLTMVNNLASVTSRT	SMSV	IIVGGV	VWRTIG	635
MARF <i>D. melanogaster</i>	GITPEQLSLISRFVSSIGSQG	TVGG	LVVAG	VMLKTI	706
FZ01 <i>C. elegans</i>	ASEEQAMMTQMVLTSAAFLANG	SLG	LVVGGI	VYKAVG	765
	: :	:: . . :::	:::**.***:	:::**.***:	: * . * **:
MFN1 <i>H. sapiens</i>	TTHAKERAFKQQFVNYATEKLRMIVSSTSANC	SHQV	QQ	IATTF	693
MFN1 <i>M. musculus</i>	TTRAKERAFKQQFVNYATEKLMIVSFTSANC	SHQV	QQEM	MATTF	693
MFN1 <i>G. gallus</i>	TTKAKERAFKQQFVNYATEKLMIVSLSANC	SHQV	QQEM	MATTF	695
MFN1 <i>D. rerio</i>	TTKAKERALKKQFVDYATEKLMIVSFTSANC	SHQV	QQEM	IATTF	695
MARF <i>D. melanogaster</i>	TNSAKERTFKSQYVRHATKKLKMIVDLTSANC	SHQV	QQLS	STF	766
FZ01 <i>C. elegans</i>	NSGAKEQHLKEQFRSHLAARMQQVSTAHTHCH	ETQA	IRE	MDQV	725
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MFN1 <i>H. sapiens</i>	EIARLPKEIDQLEKIQNNSKLLRNKAVQLENELE	N	FTKQ	FLPSS	741
MFN1 <i>M. musculus</i>	EIARLSKEIDQLEKIQNNSKLLRNKAVQLESELE	N	FSKQ	FLPSS	741
MFN1 <i>G. gallus</i>	EIARLSKEIDQLENIQSHSKQLRNKAIHLENE	L	DHFT	KHFLQ	740
MFN1 <i>D. rerio</i>	DIQRLTDKIQKLETVQNRSKVLRHKATALEM	Q	LEDF	SSQY	740
MARF <i>D. melanogaster</i>	ELKTLDSQLNILEANQKQLKLLRNKANYIQNE	L	DI	FEHNY	810
FZ01 <i>C. elegans</i>	DLDVQKTQIDAVDSTIRTLGTIKGKAVFLLRN	LEQ	FASSY	LRSDS	774
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Alignment MFN2

█ Conserved cysteine residues
█ GTPase domain
█ HR1
█ HR2
█ TMD

MFN2 <i>H. sapiens</i>	-----MS-----LLFSRCNSIVTVKK	16
MFN2 <i>M. musculus</i>	-----MS-----LLFSRCNSIVTVKK	16
MFN2 <i>G. gallus</i>	-----VGDEAQPSPRQSS-----LL---ILGFFTLKK	23
MFN2 <i>D. rerio</i>	-----MS-----LVFPRPNTSVIGKK	16
MARF <i>D. melanogaster</i>	MAAYLNRTISMVGTQGTGFADDDRHASSTDTVDKSGPGSPLSRFNSSLQSQSGSTMAANLLP	60
FZ01 <i>C. elegans</i>	-----MSGTAS-----LVHTLPASGDSNHRGLHS	24

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Fisl M. musculus      KSTQFEYAWCLVRSKYNE DIRRGIVLLEELL PKGS-KEEQRDYVFYLAVGNRYRLKEYEKA 90
Fisl G. gallus       RRCRFYAWGLLRSRYNSDVRKGVAMFRELMDAGA-PEEQRDVYVYLAVGNRYRLKEYEQA 118
Fisl D. rerio        RDTTFEYAWCLIRSKYTNDIVKGIQLLEELVHTSK-KDDQDRDFLYLAVANYRLKEYERA 90
Fisl D. melanogaster TDTKFEYAFCLVRSRYTNDVVRKGMILEELART-H-PDGRRDYIYLAFGNARIKEYTSG 90
Fisl C. elegans      AASTFAFAHAMIGSKNKLVDKEGIVCLEKLLRDEDEDRTSKRNYVYLAVAHARIKQYDLA 93

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Fisl H. sapiens      LKYVRGLLQTEPQNNQAKELERLIDKAMKKDGLVGM AIVGGMALGVAGLAGLI GLAVSKS 150
Fisl M. musculus     LKYVRGLLQTEPQNNQAKELERLIDKAMKKDGLVGM AIVGGMALGVAGLAGLI GLAVSKS 150
Fisl G. gallus       LKYV GALLQAEFGNTQGLRLQQLVRCMHRGEPHCAP----- 155
Fisl D. rerio        LKYIRTL LKNEPDKNQALELEKLIKDALKKDGLVGM AIVGGIGLVAGLAGLI GLAVSKG 150
Fisl D. melanogaster LKYCRAFLDIES-NDQVRSLEEYIKKEIDKEVAKGMV VAGGAALVGGILGL-GIAMARN 148
Fisl C. elegans      LGYIDVLLDAEGDNQQAATLKSISKSAMTHDGLIGAAIVGGGALALAGLV AIFSMSRK-- 151

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Fisl H. sapiens      KS---- 152
Fisl M. musculus     KS---- 152
Fisl G. gallus       -----
Fisl D. rerio        AKS--- 153
Fisl D. melanogaster KQKREK 154
Fisl C. elegans      -----

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Alignment MFF

■ Repeated domains
■ Coiled coil domain
■ TMD

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MFF H. sapiens      MSKGTSSDSTSLGRVSRAAFPSPTAAEMAEISRIQYEM EYTEGISQRMRVPEKLVKVAEPNA 60
MFF M. musculus     -----MAEISRIQYEM EYTEGISQRMRVPEKLVKVAEPNA 34
MFF G. gallus       -----MSGAAFPSP-AAEMAEINRLQYEM EYTEGISQRMRVPEKLVKVAEPNA 46
MFF D. rerio        -----MAEIVNRHIEYLEYTEGISQRMRIPE RLKIASGSS 34

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MFF H. sapiens      DLEQGFQEGVFNASVIMQVPERIVVAGNEDV SFSRPADLDLIQSTPFKPLALKTPPRVL 120
MFF M. musculus     DLEQEFQDGVFNASVIMQVPERIVVTGNEDIS FSRPADLDLIQSTPFKPLALKTPPRVL 94
MFF G. gallus       DLEKNIPEGFPNASVTM QVPERIVVAGN SEDIPLSRPDLDDLQSTPFKPLALKTPPRVI 106
MFF D. rerio        EEPPLGLNA--SHSTMMLVPERIV IAGDNDARFGRPRDLDIQSTPLETVELKTPPRVL 92

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MFF H. sapiens      TLSERPLDFDLERLPP-TPQN-EEIRAVGRLKRERSMSEN-AVRQNGQLVRNDSLWHR 177
MFF M. musculus     TLSERPLDFDLERPLP-TPQS-EESRAVGRLKRERSMSEN-AVRQNGQLVRNDSI---- 147
MFF G. gallus       SLSDRPLDFLDLEKPPQTPQN-EEVRSVGR LKRERSMSEN-ATRQNGQLARNDMSM---- 160
MFF D. rerio        TLNDQPLDFLEPEPAANSTAQP REEMKSHFRSRREQC RSENSTMRRNGQINKHDF---- 147

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MFF H. sapiens      DSAPRNKISRFAQAPISAPEYTVTPSPQARVCP PHMLPEDGANLSSARGILSLIQSSSTR 237
MFF M. musculus     -----VTPSPQARVCP PHMLPEDGANLSSARGILSLIQSSSTR 186
MFF G. gallus       -----
MFF D. rerio        -----ASPSPSRAPVRVCPPLISPEDSQNLNSASGV LNYIKSTTR 188

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MFF H. sapiens      AYQQILDVLDENRRPVLRGSSA-AATSNPHHDNVR YGISNIDTTIEGTSDDLTVVDAASL 296
MFF M. musculus     AYQQILDVLDENRRPVLRGSSA-AATSNPHHDNVR YGISNLDAAIEGASDDMTVVDAASL 245
MFF G. gallus       -----PVLRGSSAATTSNPHHDNTRYGLSNMDTTLEGT PDDMTVVDAASL 206
MFF D. rerio        AYQQVLEVLDDSQRG-----RASLVTFDASVENT PDDAGLTVDAASL 229

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MFF H. sapiens      RRQIIKLNRRRLQLLEENKERAKREVMYSITVAFW LLNSWLWFR 342
MFF M. musculus     RRQIIKLNRRRLQLLEENKERAKREVMYSITVAFW LLNSWLWFR 291
MFF G. gallus       RRQIIKLNRRRLQLLEENKERAKREIMYSITVAFW LLNSWLWFR 252
MFF D. rerio        RRQIIKLNRRRLQLLEHENKERAKREVMYSLTVAFW LVNSWIWLR 275

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Alignment GDAP1

■ GST domains
■ HD
■ TMD

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GDAP1 H. sapiens      -----MA--ERQEEQ-----RGS PPLRAEGKADAEVKLILYHWTSHSFSSQKVR LVI AE 46
GDAP1 M. musculus     -----MA--RRQDEA-----RAGVPLRVEGPPDKEVHLILYHWTSHSFSSQKVR LVI AE 46
GDAP1 G. gallus       -----MAGPGGAAPLVLVYHWTQSFSSQKVR LAI AE 31
GDAP1 D. rerio        MAVENIGEGESQDEKEILIKKDAQDSGEIVESTKTKA SKLILYHWTQSFSSQKVR LAI AE 60

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GDAP1L1 G. gallus          MVLDDQIEAELEKRRKLEYQGQKCELWLCGCVFTLADILLGATLHRLKFLGLSKKYWEDGSE 295
GDAP1L1 D. rerio          MVLDDQVEAELEKRRKLEYQGQKCELWLCGPTFTLADICLGATLHRLKFLGLSRKYWEDGSR 295
*****:*****:***:*****:*****:*****:*****:*****

GDAP1L1 H. sapiens        PNLQSF FERVQRRFAFRKVLGDIHTTLLSAVINAFRLVKKRPPSEFGASFLMGSLGGMG 355
GDAP1L1 M. musculus       PNLQSF FERVQRRFAFRKVLGDIHTTLLSAVINAFRLVKKRPPSEFGASFLMGSLGGMG 358
GDAP1L1 G. gallus        PNLQSF FDRIQRRFAFRKVLGDIHTTLLSAVINAFRLVKKRPPSEFGASFLMGSLGGMG 355
GDAP1L1 D. rerio          PNLQSF FERVQKRYAFRKLVDIHTTLLSAVINAFRMVKKKPPSEFGASFLMGSLGGMG 355
*****:***:***:*****:*****:*****:*****:*****

GDAP1L1 H. sapiens        YFAYWYLKKKYI 367
GDAP1L1 M. musculus       YFAYWYLKKKYI 370
GDAP1L1 G. gallus        YFAYWYLKKKYI 367
GDAP1L1 D. rerio          YFAYWFLKKKYM 367
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Alignment Mid49

■ Transmembrane region
■ Disordered region
■ Drp1 recruitment domain

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Mid49 H. sapiens          MAEFSQKRGKRRSDEGLGSMVDFLLANARLVLGVGGAAVLGIATLAVKRFIDRATSPRDE 60
Mid49 M. musculus        MAEFSQKQRKQSGSEGLGSVDFLLANARLVLGVGGAAVLGIATLAVKRLIDRATSPPDE 60
Mid49 D. rerio           ----MYSGKRRGEDGIAAVIDFLLSNAARLVLGVGGAAVLGIATLAVKRLIERAGRPDE 56
                          *:..*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

Mid49 H. sapiens          DD--TKGDSWKELSLLRATSPQKQPQPPA-----ALSQPVLPAPSSSAPEG 105
Mid49 M. musculus        DD--TKGDSWKELSLLRATSPQKQPQPPA-----AFSQPLATGSPSPSPVPE 105
Mid49 D. rerio           EPDKRMTDSWEELSLVSASPRLHKGIEGVMMKQIAAATKKAELSQPIE----MPSSEPO 112
                          : . ***:***: * : : : : : : : : : : : : : : : : : : : : *

Mid49 H. sapiens N       PAETDPEVTPQLSSPAPLCLTLQERLLAFERDRVTIPAAQVALAKQLAGDIALELQAYFR 165
Mid49 M. musculus        PTPIHSPTTPKFSTIAPLCLTFQERLLAFERKHVITPEAHVTLAKQLAGDIALELQAYLR 165
Mid49 D. rerio           RCDADFPFPQRKRMDLCLVTFADRLQYYRTRVCLSAEEVCVAQQRALDIATEIQAFILH 172
                          . : . *:*:*:* : * * * * * * * * * * * * * * * * * * * * * *

Mid49 H. sapiens          SKFPPELPGAFVPGGPLYDGLQAGAADHVRLVPLVLEPGLWSLVPGVDTVARDPRCWAV 225
Mid49 M. musculus        SKFPPELPGALVPGGPLYDGLQAGTAEHVRLAPLELEPGLWSLVPGVDTVAREPRCWAV 225
Mid49 D. rerio           SKHPDMLPGDMTLAGSLDDDLQVVTADHACLIVPLQLESSLWTPTAGEDTFLGHPOYCMV 232
                          **:*:*:*:* : . * * * * * * * * * * * * * * * * * * * * * * *

Mid49 H. sapiens          RRTQLEFCPRGSSPWRFLVGGYLSRVLLELLRKALASVNWPAIGSLGCLIRPSMAS 285
Mid49 M. musculus        RRTQLEFHPRGCSPPWRFLVGGYLSRVLLELLRKALSASVNWPAIGSLGCLIWPDVAS 285
Mid49 D. rerio           RRENLEYFPRGRSYWDRHLLGAYLSSRLVCEQLSKAVMESMNWPSLTGTLECEVRPVLGS 292
                          **:*:*:* * * * * * * * * * * * * * * * * * * * * * * * * * * *

Mid49 H. sapiens          EELLLLEVQHERLELT---VAVLVAVPGVDA-DDRLLLAWPLEGLAGNLWLQDLYPVEAA 340
Mid49 M. musculus        EELLLKVQHECLEFT---LAVLMVVPGAST-DDRLLLAWPLEGLASNLWLQDLYPVETA 340
Mid49 D. rerio           PELKLEIQGLTQSSHDSGERFYITVLPTRVRLGQMTLMAQREITGSFDYVWYQSLYSSETA 352
                          **:*:*:* . : : * . : * : : * . : * * * * * * * *

Mid49 H. sapiens          RLRALDDHDAGTRRRRLLLLCAVCRGCSALGQLGRGHLTQVVLRLGEDNVDTWEALGER 400
Mid49 M. musculus        RLRALDDQDAGTRRRRLLLCGICRGHPALVRLGWSHLTQVVLHLGEEVAVWTEEALGER 400
Mid49 D. rerio           RLAALDQADSGARRKCKLTKLAVCRNCPALRKLNGSHISNVVLHMSEKETDWSESAFAFSNR 412
                          ** * * * * : * * * * * * * * * * * * * * * * * * * * * * *

Mid49 H. sapiens          FLQALELLIGSLEQASLPCHFNPVSNLFLSSLRREEIDDIGYALYSGLQPEPEGLL- 454
Mid49 M. musculus        FLQALEFLVGSLEQASLPCHFNPVSNLLGNFREEEIDDIGYVLYSGLQVPESLF- 454
Mid49 D. rerio           FLQAITELIGYLETGVLPYFKANVNLFGQFTEDDIDEMGFMLYCAVTEPEIILLI 467
                          *****: * * * * * * * * * * * * * * * * * * * * * * * *

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Alignment Mid51

■ Transmembrane region
■ Disordered region
■ NT domain (N-terminus)
■ Drp1 recruitment domain
■ NT domain (C-terminus)

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Mid51 H. sapiens          -MAGAGERKGGKDDNGIGTAIDFVLSNARLVLGVGGAAVLGIATLAVKRMYDRAISAPTS 59
Mid51 M. musculus        -MAGAGERKGGKDDNGIGTAIDFVLSNARLVLGVGGAAVLGIATLAVKRMYDRAISAPTS 59
Mid51 D. rerio           MAGVNGDRKGGKDDNGLGTAIDFVLSNARLVLGVGGAAVLGIATLAVKRMYDRALSAPTS 60
                          . *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

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