

Q9H992 MARH7_HUMAN MESKPSRIPRRISVQPSSS--LSARMMSGG-----RGSLLNDTYHSRDSFFRLDSEYQS-----TSASASASPFQSAWYSESEITQGARSRSONQQRDHD 88
H2QIV6 H2QIV6_PANTR MESKPSRIPRRISVQPSSS--LSARMMSGG-----RGSLLNDTYHSRDSFFRLDSEYQS-----TSASASASPFQSAWYSESEITQGARSRSONQQRDHD 88
F7E884 F7E884_CALJA MESKPSRIPRRISVQPSSS--LSARMMSGG-----RGSLLNDTYHSRDSFFRLDSEYQS-----TSASASASPFQSTWYSESEITQGARSRSONQQRDHD 88
G1SEZ6 G1SEZ6_RABIT MESKPSRIPRRISVQPSSS--LSARMMSGG-----RGSFFNDAYHSRDSFFRLDSEYQV-----TSASASASPFQSTWYSESEITQGARSRSONQQRDHD 88
Q9WV66 MARH7_MOUSE MESKPSRIPRRISVQPSGS--LSTRMVSNGN-----RGTSLNDYHSRDSFFRLDSEYQS-----ASASACASPCQAWYSESEITQGARARACTQQRDHD 88
F7EQU7 F7EQU7_MONDO MESKPSRIPRRITVEPSSSLARTVSGG-----RGSGMNDAYHPRESPPFLNLSHESNLLHTSGRDWGFGEREHAETPWKFTSSSPAHFSGTIFERFPWGSFLGSRSLAHSLSLTPFQSAWYSESEITQGARPRLONQQRDHD 141
E1C485 E1C485_CHICK MESKPSRIPRRISVQAPSSITLGSRTLTG-----NSLAGAYGARDSSRLDSEYQESDVLSSDRDWGIGEREHENPWKLTSSSTHYSGLLDHPRSGRFLG--TRNRLSTSSSHPTFCYDDESERTOGAYSRLLHSQQDSD 136
F1RAT0 F1RAT0_DANRE MDSKRRRPFPAVSSSSLSLSPSLSSSSSSALSASRLYGRGCVLGRDRFSDASVKLDSDYQGSRLSSPRVYSSITSRHEN-----WKLSTPVTSSSSSSSCDRSWLSSSGDRARLIDSRRLGTYCGLLTSQDSE 134
H3CVR1 H3CVR1_TETNG -----



Q9H992 MARH7_HUMAN SKRPKLSCTNCT--TSAGRNVGNGLNLTLS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENSMSTLQLNTSSTN--HQLPSEHOTILSSRD--SRNSLR--SN 225
H2QIV6 H2QIV6_PANTR SKRPKLSCTNCT--TSAGRNVGNGLNLTLS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENSMSTLQLNTSSTN--HQLPSEHOTILSSRD--SRNSLR--SN 225
F7E884 F7E884_CALJA SKRPKLSCTNCT--TSAGRNVGNGLNLTLS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENSMSTLQLNTSSTN--HQLPSEHOTILSSRD--SRNSLR--SN 225
G1SEZ6 G1SEZ6_RABIT SKRPKLSCTNCT--TSAGRNVGNGLNLTLS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENSMSTLQLNTSSTN--HQLPSEHOTILSSRD--SRNSLR--SN 229
Q9WV66 MARH7_MOUSE SKRPKLSCTNCASTSAGRNNGSGLNLTIS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENAVSTLQLNTSSTN--HQLPSEHOTVPSYRDSRSTR--SH 228
F7EQU7 F7EQU7_MONDO SKRPKLSCTNCT--TSAGRNNGSGLNLTIS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENAVSTLQLNTSSTN--HQLPSEHOTVPSYRDSRSTR--SH 280
E1C485 E1C485_CHICK SKRPKLSCTNCT--TSAGRNNGSGLNLTIS--DSSWRH-----SQVPRSSSMVLGSGFGTDLMRERRDLERRTDSISINLMDYSHRSGDFTTSSYVQDRVPS--YSQGARPKENAVSTLQLNTSSTN--HQLPSEHOTVPSYRDSRSTR--SH 269
F1RAT0 F1RAT0_DANRE SKRAKLSYTNREVVRSRSTSKPATSYSTLGSWKSISIPLSR-----SRIPRSMVMFGLGTLVREERLEL--IDQSFNNLVDSHYRNSDFSSAYFDPRPASTYAEAGARPKENLSALRLN--ASMN--HQLPSEHOTVPSYRDSRSTR--TS 282
H3CVR1 H3CVR1_TETNG SKRAKLSYTNREVVRSRSTSKPATSYSTLGSWKSISIPLSR-----SRIPRSMVMFGLGTLVREERLEL--IDQSFNNLVDSHYRNSDFSSAYFDPRPASTYAEAGARPKENLSALRLN--ASMN--HQLPSEHOTVPSYRDSRSTR--TS 86



Q9H992 MARH7_HUMAN FSSR-----ESESRS-----NTQPGFSYSSSRDEAPIISNSERVVSSQRPFOE--SSDNEGRRTTRRLLSRIASSMSSTFFSRRSSQDSLNTSRSLNSNSYVSPRILLTASQSRSNVPSASEVDPNRAEASQGFRLRRRWGLSSLSH 362
H2QIV6 H2QIV6_PANTR FSSR-----ESESRS-----NTQPGFSYSSSRDEAPIISNSERVVSSQRPFOE--SSDNEGRRTTRRLLSRIASSMSSTFFSRRSSQDSLNTSRSLNSNSYVSPRILLTASQSRSNVPSASEVDPNRAEASQGFRLRRRWGLSSLSH 362
F7E884 F7E884_CALJA FSSR-----ESESRS-----NTQPGFSYSSSRDEAPIISNSERVVSSQRPFOE--SSDNEGRRTTRRLLSRIASSMSSTFFSRRSSQDSLNTSRSLNSNSYVSPRILLTASQSRSNVPSASEVDPNRAEASQGFRLRRRWGLSSLSH 362
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F7EQU7 F7EQU7_MONDO FSSR-----ESESRS-----NTQPGFSYSSSRDEAPIISNSERVVSSQRPFOE--SSDNEGRRTTRRLLSRIASSMSSTFFSRRSSQDSLNTSRSLNSNSYVSPRILLTASQSRSNVPSASEVDPNRAEASQGFRLRRRWGLSSLSH 418
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H2QIV6 H2QIV6_PANTR NHSSSESDSENFQOESRGRNTGWLSSSLRNRCPLFRRRRREGRDESSRIPTSDTSSRS--HIFRRRESNEVVHLEAQNPLGAAANRPOASAAASSATGGSTSDSAQGGRRNTGIAGILPGSLFRFAVPPALGSLNLDNVMITVDIIPSGW 511
F7E884 F7E884_CALJA NHSSSESDSENFQOESRGRNTGWLSSSLRNRCPLFRRRRREGRDESSRIPTSDTSSRS--HIFRRRESNEVVHLEAQNPLGAAANRPOASAAASSATGGSTSDSAQGGRRNTGIAGILPGSLFRFAVPPALGSLNLDNVMITVDIIPSGW 511
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F7EQU7 F7EQU7_MONDO NPNETGSENFQOESRGRNTGWLSSSLRNRCPLFRRRRREGRDESSRIPTSDTSSRS--HIFRRRESNEVVHLEAQNPLGAAANRPOASAAASSATGGSTSDSAQGGRRNTGIAGILPGSLFRFAVPPALGSLNLDNVMITVDIIPSGW 568
E1C485 E1C485_CHICK SLNLDSDGESVYRDESSRNTGWLSSSLRNRCPLFRRRRREGRDESSRIPTSDTSSRS--HIFRRRESNEVVHLEAQNPLGAAANRPOASAAASSATGGSTSDSAQGGRRNTGIAGILPGSLFRFAVPPALGSLNLDNVMITVDIIPSGW 502
F1RAT0 F1RAT0_DANRE VQES--TDVPEQESLPPAGLSWLN--WNRCPLFRRRRREGRDESSRIPTSDTSSRS--HIFRRRESNEVVHLEAQNPLGAAANRPOASAAASSATGGSTSDSAQGGRRNTGIAGILPGSLFRFAVPPALGSLNLDNVMITVDIIPSGW 560
H3CVR1 H3CVR1_TETNG YRSGSTQAGPASRRPEPGATSSWLSLRLRERCPLLRRLRHRARDEQRSSGSSPDDE-----EEEEKEEGAVGLGAFNGGSPR-----LGDEVRPDVAEESPRRRRVGVCNTEAFPRFLV 325



Q9H992 MARH7_HUMAN N---SADGK--SDKTKSAPSRDPERLQKIKESLLEDSE--EEEGDLCRICMAAASSNLLIEPCKCTGSLQVYHQDCMKKWLQAKINSGSSLEAVTTCELCKEKLELNLDFDIHELHRAHANEQ--AEYEFISSGLYLVLVLLHLCEQSF 654
H2QIV6 H2QIV6_PANTR N---SADGK--SDKTKSAPSRDPERLQKIKESLLEDSE--EEEGDLCRICMAAASSNLLIEPCKCTGSLQVYHQDCMKKWLQAKINSGSSLEAVTTCELCKEKLELNLDFDIHELHRAHANEQ--AEYEFISSGLYLVLVLLHLCEQSF 654
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F7EQU7 F7EQU7_MONDO N---SDGQ--NDKTKLPLSRDPERLQKIKESLLEDSE--DEEGDLCRICMAAASSNLLIEPCKCTGSLQVYHQDCMKKWLQAKINSGSSLEAVTTCELCKEKLELNLDFDIHELHRAHANEQ--AEYEFISSGLYLVLVLLHLCEQSF 776
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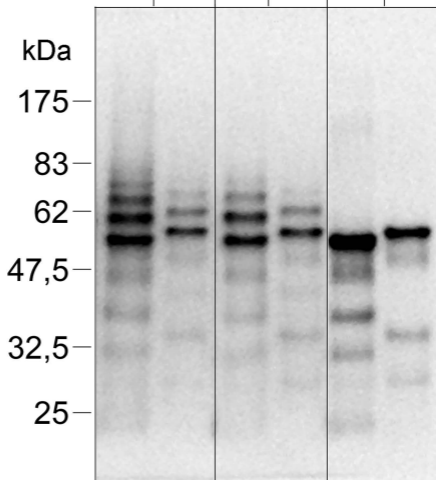
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F7E884 F7E884_CALJA SDMMGNTNEPSTRVFINLARLQAHMEDLETSEDDSEEDGDHNRTFDIA----- 704
G1SEZ6 G1SEZ6_RABIT SDMMGNTNEPSTRVFINLARLQAHMEDLETSEDESEEDGDHNRTFDIA----- 708
Q9WV66 MARH7_MOUSE SDMMGNTIEPSTRVFINLARLQAHMEDLETSEDEF----- 693
F7EQU7 F7EQU7_MONDO SDMLGTASEASTRVFINLARLQAHMEDLETSEDESEEDGDHNRDFDMA----- 776
E1C485 E1C485_CHICK SDMLGTASEASTRVFINLARLQAHMEDLETSEDDSE----- 685
F1RAT0 F1RAT0_DANRE SDVLGAVNDAG----FFNLARLQAHMEDNLESSYAESEDEVEDSRPSIDFCDELEDDDEEEEEEEV 768
H3CVR1 H3CVR1_TETNG SDVLGAVDAG----LNVLRILQAHMEDNLESMFLF----- 505



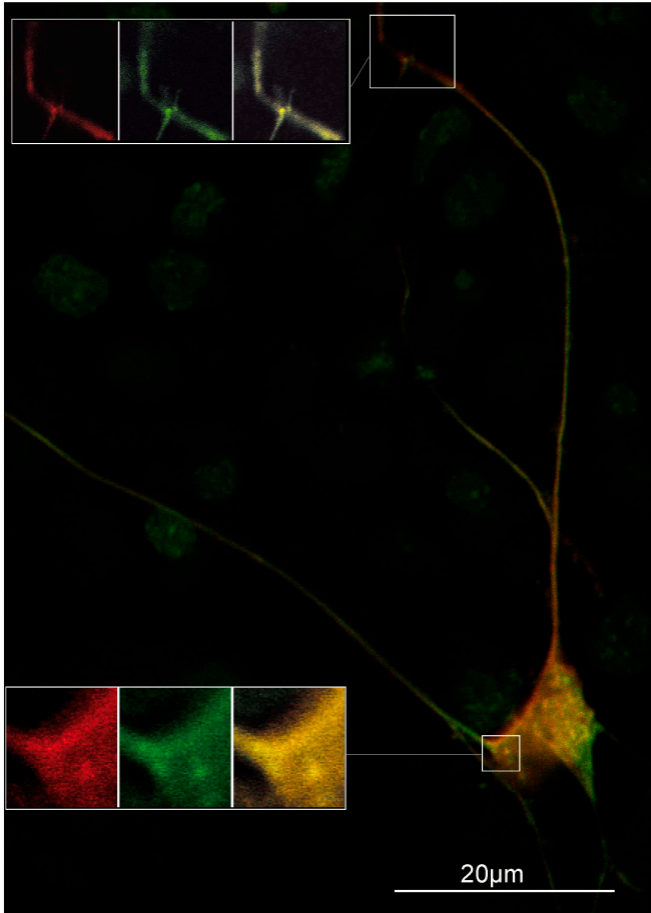
suppl. Figure 1

Mg-ATP	+	+	+	+	+	+
E1	+	+	+	+	+	+
E2 UbcH5c	+	+	+	+	-	-
E3 AxoRing	+	+	+	+	+	+
Ub	+	+	m	m	+	+

Substrate Tau	0N	2N	0N	2N	0N	2N
	4R	3R	4R	3R	4R	3R



blot: a-tau



suppl. Figure 3