

Figure S2.

SCORE=81

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BAD AVG GOOD

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Mus musculus	:	80
Rattus norvegic	:	84
Homo sapiens	:	86
Pan troglodytes	:	85
Macaca mulatta	:	86
Nomascus leucoq	:	86
Callithrix jacc	:	84
Oryctolagus cun	:	84
Bos taurus	:	81
Ovis aries	:	85
Pantholops hodq	:	76
Orcinus orca	:	85
Trichechus mana	:	85
Melopsittacus u	:	78
Gallus gallus	:	76
Anolis caroline	:	82
Alligator missi	:	72
Danio rerio	:	73
Ectocarpus sili	:	77
Zea mays	:	68
cons	:	81

Mus musculus	1	-----	0
Rattus norvegic	1	ME-----RP	4
Homo sapiens	1	ME-----RP	4
Pan troglodytes	1	ME-----RP	4
Macaca mulatta	1	ME-----RA	4
Nomascus leucog	1	ME-----RP	4
Callithrix jacc	1	ME-----RP	4
Oryctolagus cun	1	MR-----KP	4
Bos taurus	1	-----	0
Ovis aries	1	MW-----KP	4
Pantholops hodg	1	-----	0
Orcinus orca	1	ME-----RA	4
Trichechus mana	1	ME-----RP	4
Melopsittacus u	1	MEE-----	3
Gallus gallus	1	MQRV-----LRR-LLPA-----LCSAWPAALLAPRALLAPRASPMALRPAAAEA-----GGG	46
Anolis caroline	1	-----	0
Alligator missi	1	MALE-----R-----EEP	8
Danio rerio	1	MISRHFRLRAQPLVRLWRVNTDVPVVTECRKVNARVFCQSNQSKLLS-VPFN-MEDNINN	60
Ectocarpus sili	1	MI-----SA	4
Zea mays	1	ME-----GA	4
cons	1	-----	63

Mus musculus	1	-----	0
Rattus norvegic	5	AAGEIDANKCDH-----LSRGEEGTG-DLE-----TSPVG-SL	35
Homo sapiens	5	EAGGINSNECEN-----VSRKKKMSE-EFE-----ANTMD-SL	35
Pan troglodytes	5	EAGGINSNECEN-----VSRKKKMSE-EFE-----ANTMD-SL	35
Macaca mulatta	5	EAGGINSNECEN-----ESRKKKMSE-EFE-----ANTMD-SL	35
Nomascus leucog	5	EAGGVNSNECEN-----VSRKKKMSE-EFE-----ANTMD-SL	35
Callithrix jacc	5	GAGGINSNECEN-----VSRKKKI SE-EFE-----ASTMD-FL	35
Oryctolagus cun	5	KRGGI NPSECEN-----MTRN-EMSE-ELE-----MDTVD-SL	34
Bos taurus	1	-----MSE-EFE-----ANTMD-FL	13
Ovis aries	5	KHGGLNSNECES-----VSSKEKMSE-EFE-----ANTMD-FL	35
Pantholops hodg	1	-----MSE-EFE-----ANTMD-FL	13
Orcinus orca	5	GAGGINSNECEN-----VSRKREMSE-ESE-----ANTVD-SL	35
Trichechus mana	5	GAGGINSSECEN-----VSREEKMSE-EFE-----ASTVD-SL	35
Melopsittacus u	4	-----P-----YPADSVDSL M	14
Gallus gallus	47	EKPSVATDSTPK-----HDGLENMQQ-EKKT V KGNKKRTQEGKKPCPPADSVDSL M	96
Anolis caroline	1	-----	0
Alligator missi	9	PSPPPSODELENMOKIQVI EKKKKMKQ-KRK-----THAAPKSIDSL M	51
Danio rerio	61	TTVCTTADKCTK-----QOKSKTLK-EKKA KGP KKASESK-----QKQSEEN-LL	106
Ectocarpus sili	5	FVLYMA-----	10
Zea mays	5	QGSSIVTKHNKROS-----PVQRWRPVSTEAVP-----QHHQD-DIETS N	44
cons	64	-----	126

Mus musculus	102	LNEDE	-----	VNIGTDALLELKPFFVEE	123
Rattus norvegicus	141	LNEDE	-----	VNIGTDALLELKPFFVEE	162
Homo sapiens	136	LNEDE	-----	VNIGIDALLELKPFFIEE	157
Pan troglodytes	136	LNEDE	-----	VNIGIDALLELKPFFIEE	157
Macaca mulatta	136	LNEDE	-----	VNIGIDALLELKPFFIEE	157
Nomascus leucog	136	LNEDE	-----	INTGIDALLELKPFFIEE	157
Callithrix jacc	136	LNEDE	-----	VNIGTDALLELKPFFIEE	157
Oryctolagus cun	135	LNEDE	-----	INIGIDALLELKLPIEE	156
Bos taurus	114	LNEDD	-----	VNVGIDALLELKPFFVEE	135
Ovis aries	136	LNEDD	-----	VNIGVDALLELKPFFVEE	157
Pantholops hodg	114	LNEDD	-----	VNIGIDALLELKPFFVEE	135
Orcinus orca	136	LNEDE	-----	INIGIDALLELKPFFVEE	157
Trichechus mana	136	LNEDE	-----	VNTGIDALLELKPFFIEE	157
Melopsittacus u	117	SNKEE	-----	ISIAVGALSDSKDFIED	138
Gallus gallus	199	SSKEE	-----	ISIAVGALSDSKDFVED	220
Anolis caroline	103	STAAA	-----	IDNAVSAFLKSQGLIEE	124
Alligator missi	142	SSEEE	-----	VGIAVGAFLESKDSIEE	163
Danio rerio	200	STQDQ	-----	VDLAASTLSELESPLNA	221
Ectocarpus_sili	93	SEKDGSLQQARDTLEHCGDLLLEHGLSPEVDLQASASRAESVDDHMHPAALAI GDSNETAPG			155
Zea_mays	219	WNKER	-----	IDKASDVLQSVSTQVNE	240

cons 316 : : : : : 378

Mus musculus	124	I LEGKHLALPFQIGTFC	-----	GOVGFVKLADGDHVSALLEIAETAKRTFREKGILA	176
Rattus norvegicus	163	I LEGKHLTLPPHIGTFC	-----	GOVGFVKLADGDHVSALLEIAETAKRTFQEKGILA	215
Homo sapiens	158	LLQ GKHLTLPPFQIGTFC	-----	NOVGFVKLAEGDHVNSLLEIAETANRTFQEKGILV	210
Pan troglodytes	158	LLQ GKHLTLPPFQIGTFC	-----	NOVGFVKLAEGDHVNSLLEIAETANRTFQEKGILV	210
Macaca mulatta	158	LLQ GKHLTLPPFQIGTFC	-----	NOVGFVKLAEGDHINSLLEIAETANRTFQEKGILA	210
Nomascus leucog	158	LLQ GKHLTLPPFQIGTFC	-----	NOVGFVKLAEGDHVNSLLEIAETANRTFQEKGILV	210
Callithrix jacc	158	LLQ GKHLTLPPFQIGTFC	-----	NOVGFVKLAEGDHVNSLSEIAETANRTFQEKGIRA	210
Oryctolagus cun	157	ILQ GKHLTLPPFQIGSFC	-----	DRVGFVKLAEGDHINLLEIAETAKRTFQEKGMV	209
Bos taurus	136	ILQ GKPLTLPPFEGVDTFC	-----	NOVGFVKLAEGDHINSLLEIADAARTFQEKGILA	188
Ovis aries	158	ILQ GKPLTLPPFEGVDTFC	-----	NOVGFVKLAEGGHINSLLEIADAARTFQEKGILA	210
Pantholops hodg	136	ILQ GKPLTLPPFEGVDTFC	-----	NOVGFVKLAEGDHINSLLEIADAARTFQEKGILA	188
Orcinus orca	158	ILQ GKHLTLPPFQGVNFR	-----	NOVGFVKLAEGDHINPLLEIAETAERTFOAKGILA	210
Trichechus mana	158	ILQ GKHLTLPPFQGVNFR	-----	NOVGFVKLAEGDHINPLLEIAETAERTFOAKGILA	210
Melopsittacus u	139	LLKGTVDLSFQGIHFFK	-----	NEVGFVKLAENDHTAILKEIAETMTRKI FQEKGILA	191
Gallus gallus	221	LLKGTVDLSFQGIHFFK	-----	NEVAFVQLAENDHTAALSEIAETMTRKI FQEKGILA	273
Anolis caroline	125	LLQ GKPLDLSFQGTDFR	-----	NOVGFVKLSESDNTTLLKIAEIVKNLFQEKGI I I	177
Alligator missi	164	LLQ GKOLDLSFQGIHFFK	-----	NVVGFKLAEGDCTAMLMEISETMTRKI FQEKGILA	216
Danio rerio	222	LLSGRRLVLPFCGIGHFR	-----	QEVYFVRIAGEHLNLTALAEASVVRKAFEEERGITS	274
Ectocarpus_sili	156	VAAASPLMLSFRLGHFR	-----	NKILFAKLVEDEQATRLRGLASSLHRRFSEAGLVEEAAGF	213
Zea_mays	241	ALENRPISIQRLGLTCMKGFPAKARVVVVPVLEVGSEGRLAHACKVITDAFIKAGLVE	-----		298

cons 379 : : : : : * * * : 441

Mus musculus	177	-----G-----	ESRTFKE HLT FMKLSKAPMLRK	-----	KGVRKIEP	GLYEQFI	214
Rattus norvegicus	216	-----G-----	ESRTFKE HLT FMKLSKAPMLWK	-----	KGVRKIEP	GLYEQFI	253
Homo sapiens	211	-----G-----	ESRSFKE HLT FMKLSKSPWLK	-----	NGVKKIDP	DLYEKFI	248
Pan troglodytes	211	-----G-----	ESRSFKE HLT FMKLSKSLWLRK	-----	NGVKKIDP	DLYEKFI	248
Macaca mulatta	211	-----G-----	DSRSFKE HLT FMKLSKSPWLK	-----	NGVKKIDP	DLYEKFI	248
Nomascus leucog	211	-----G-----	DSRSFKE HLT FMKLSKSPWLK	-----	NGVKKIDP	DLYEKFI	248
Callithrix jacc	211	-----G-----	ESRSFKE HLT FMKLSKAPWLK	-----	NGVKKIDP	DLYEKFI	248
Oryctolagus cun	210	-----G-----	ESQS FKE HLT FMKLSKSPWLHK	-----	NGVKKIEP	ELYEKFI	247
Bos taurus	189	-----G-----	ESRTFKE HLT FMKLSRPLWLK	-----	KGVKKIDP	KLYEKFI	226
Ovis aries	211	-----G-----	ESRTFKE HLT FMKLSRSPWLK	-----	KGVKKIDP	KLYEKFI	248
Pantholops hodg	189	-----G-----	ESRTFKE HLT FMKLSKSPWLK	-----	KGVKKIDP	KLYEKFI	226
Orcinus orca	211	-----G-----	ESRTFKE HLT FMKLSKAPWLK	-----	KGVKKIDP	KEYEKFI	248
Trichechus mana	211	-----G-----	ESRSFKE HLT FMKLSKAPWLK	-----	KGVKKIDP	ELYEKFI	248
Melopsittacus u	192	-----G-----	EERDFKE HLT FMKLSKSTPLRK	-----	Q-VKKIDP	SLYEDFK	228
Gallus gallus	274	-----G-----	EERAFKE HLT FMKLSKSIQLRK	-----	Q-VKKIDS	SLYEDYK	310
Anolis caroline	178	-----G-----	DDKAFKE HLT FMKLSKSPKLRK	-----	QGVKKIDP	HLFENFK	215
Alligator missi	217	-----G-----	ENRAFKE HLT FMKLSKSPDLHK	-----	Q-VKKIDL	NLYKNFK	253
Danio rerio	275	-----A-----	DDTAFKE HLT LLKLSRAPLRR	-----	Q-----		298
Ectocarpus_sili	214	PSRKG EKRGDGDDGGGSGSGTSS	DSFEFTE HLT IMKTSKL	---RD	RG-TLIPA	DSYDRYQ	269
Zea_mays	299	-----ER-----	DVRELKI HAT VMNVRHRKSRNKRNTWTSDFDARGIFGRFG				340

cons 442 : : * * : : : 504

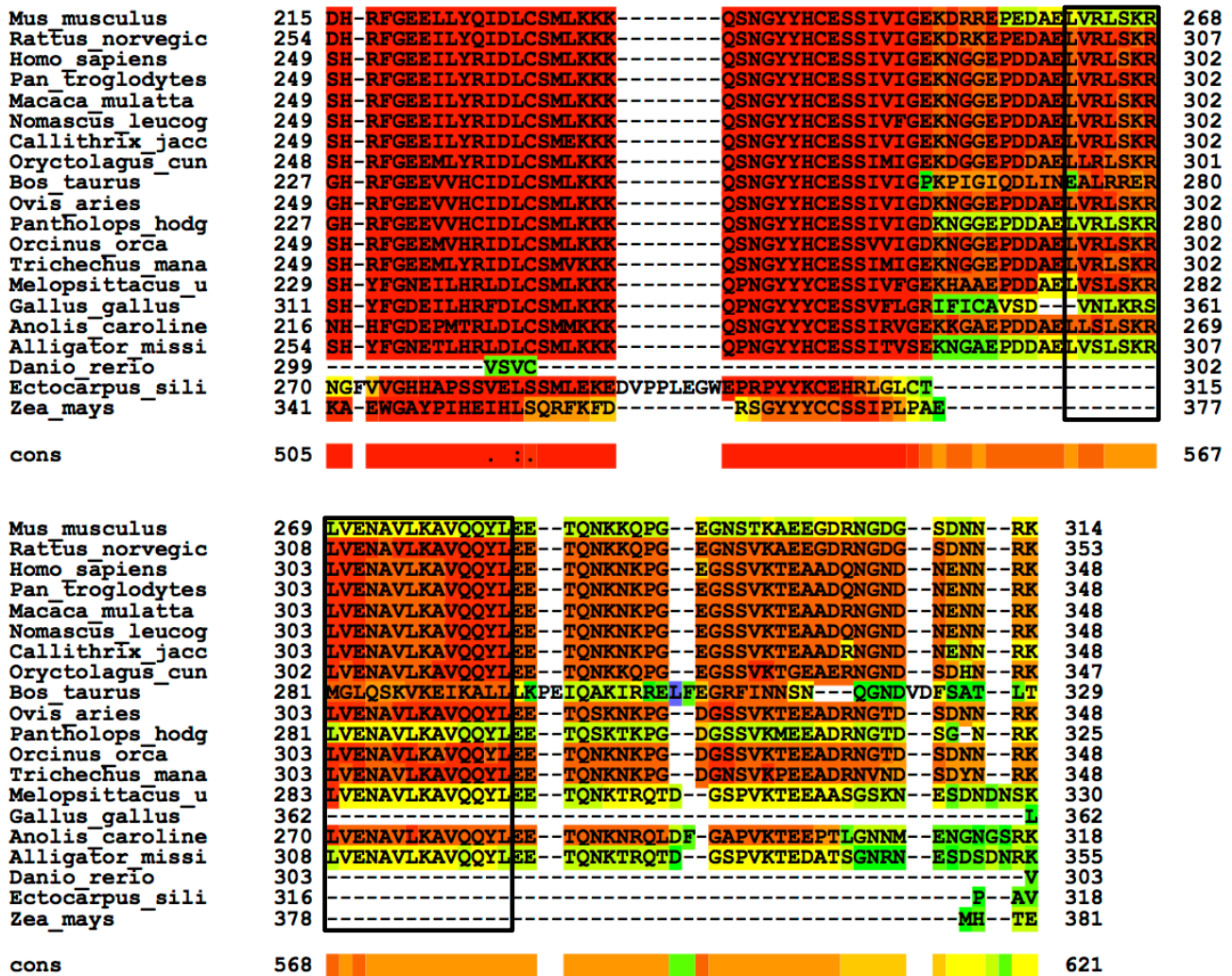


Figure S2. Protein multiple sequence alignment (MSA) of mAKAP7 γ and eukaryotic homologs. MSA of *Mus musculus* (mouse), *Rattus norvegicus* (rat), *Homo sapiens* (human), *Pan troglodytes* (chimpanzee), *Macaca mulatta* (macaque), *Nomascus leucogenys* (gibbon), *Callithrix jacchus* (marmoset), *Oryctolagus cuniculus* (rabbit), *Bos taurus* (cow), *Ovis aries* (sheep), *Pantholops hodgsonii* (antelope), *Orcinus orca* (whale), *Trichechus manatus latirostris* (manatee), *Melopsittacus undulatus* (parakeet), *Gallus gallus* (chicken), *Anolis carolinensis* (lizard), *Alligator mississippiensis* (alligator), *Danio rerio* (zebra fish), *Ectocarpus siliculosus* (brown algae), *Zea mays* (corn). NCBI reference sequences NP_061217.3, NP_001001801.1, NP_057461.2, XP_518739.2, XP_0011103953.2, XP_003255757.1, XP_002747004.1, XP_002714864.1, NP_001095736.1, XP_004011367.1, XP_005967580.1, XP_004263875.1, XP_004368981.1, XP_005154795.1, XP_004940279.1, XP_003215759.1, XP_006259840.1, XP_005173856.1, CBN75660.1 and DAA52752.1, respectively. Alignment was performed with the T-Coffee Expresso, which incorporates known protein database structures to aid alignment, with all MSA options selected (pcma_msa, mafft_msa, clustalw_msa, dialignx_msa, poa_msa, muscle_msa, probcons_msa, t_coffee_msa, amap_msa, kalign_msa, fsa_msa, mus4_msa) to ensure high confidence in the alignment (1-5). To convey confidence in the alignment, scores indicate the percent agreement between all MSA algorithms utilized in the analysis for each protein and for the consensus sequence. Additionally, color-coding indicates positional confidence of each aligned residue based on agreement between

MSA algorithms with blue indicating the least and red indicating the greatest confidence in the alignment. Conservation of sequence is indicated by Clustal MSA symbols in the consensus line (cons) with "*" indicating fully conserved, ":" strong conservation of properties and "." weak conservation of properties. Boxes indicate predicted nuclear localization signals (blue) (6-8), catalytic HxT motifs (yellow) and PKA RII-binding domain (black) (9).

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