

Additional file 1

Multiple sequence alignment of selected actinin protein sequences

An alignment prepared using ClustalX of human actinin-1, -2, -3 and -4, as well as actinin sequences from select model organisms. Sequence conservation is plotted beneath the alignment and conserved residues marked and color-coded according to the default ClustalX settings. Locations of PFAM protein domains as identified in the Protein Data Bank for human actinin-2 (PDB ID: 4D1E) are indicated in red below the alignment. Known disease/phenotype associated mutations for the human actinins are identified in red text above the alignment. Accession numbers for sequences are as follows: *HsACTN1* = NP_001093.1; *HsACTN2* = NP_001094.1; *HsACTN3* = NP_001095.2; *HsACTN4* = NP_004915.2; *DdACTN* = XP_646979; *DmACTN* = NP_477484; *CeACTN* = NP_506127; *SpACTN* = NP_594295. Hs = *Homo sapiens*; Dm = *Drosophila melanogaster*; Ce = *Caenorhabditis elegans*; Dd = *Dictyostelium discoideum*; Sp = *Schizosaccharomyces pombe*

ACTN2 Q9R ↘ ACTN1 D22N ↘ ACTN1 Q32K ↘ ACTN4 W59R ↘ ACTN1 R46Q/W ↘

HsACTN1 -MDHYDSQQ-----TNDYMQPEEDWDRDLLLDPAAWEKQQRKFTTAWCNSHLR-KAGTQIENIEEDFR 60
HsACTN4 MVDYHAANQSYOYGPSSAGNGAGGGGSMGDYMAQEDDWRDLLLDPAAWEKQQRKFTTAWCNSHLR-KAGTQIENIDEDFR 79
HsACTN2 -MNQIEPG-----VQYNYVYDEDEYMQEEEDWRDLLLDPAAWEKQQRKFTTAWCNSHLR-KAGTQIENIEEDFR 67
HsACTN3 MMMVMQPEG-----LGAGEGRFAGGGGGGEYMQEEDWDRDLLLDPAAWEKQQRKFTTAWCNSHLR-KAGTQIENIEEDFR 74
DmACTN MMMENGLSMEY-----GDGYMEQEEEWEREGLLDPAAWEKQQRKFTTAWCNSHLR-KAGTADNIEEDFR 63
CeACTN MVDYYQOPP-----SYHQPGYDYTOEEEDWREGLLDPAAWEKQQRKFTTAWCNSHLR-KAGTSIDTIEEDFR 66
DdACTN -----MSEETPVSGNDKQ--LLNKAWETQKFTTAWCNSHLR-KLGSSTIEQIDTDF 51
SpACTN -----MQANQWQSVGNRTFTKWFNTKLSRRDLPSVFDLRKDL 38

1.....10.....20.....30.....40.....50.....60.....70.....80



ACTN2 G111V ↘ ACTN1 V105I ↘ ACTN2 A119T ↘ ACTN4 I149A ↘

HsACTN1 DGLKMLLLEVISGERLAKPERG-KMRVHKISNVNKALDFIASKGVKLVSIGAEEIVDGNVKMTLGMIIWIIILRFAIQDI 139
HsACTN4 DGLKMLLLEVISGERLPKPERG-KMRVHKINNVNKALDFIASKGVKLVSIGAEEIVDGNAKMTLGMIIWIIILRFAIQDI 158
HsACTN2 NGLKMLLLEVISGERLPKDRG-KMRFHKIANVNKALDYIASKGVKLVSIGAEEIVDGNVKMTLGMIIWIIILRFAIQDI 146
HsACTN3 NGLKMLLLEVISGERLPRDKG-KMRFHKIANVNKALDFIASKGVKLVSIGAEEIVDGNLKMIIWIIILRFAIQDI 153
DmACTN NGLKMLLLEVISGETLPKDRG-KMRFHKIANVNKALDFIASKGVHLSVIGAEEIVDGNLKMIIWIIILRFAIQDI 142
CeACTN NGLKMLLLEVISGEPLPKDRG-KMRFHKIANVNKALEVIESKGVKLVSIGAEEIVDGNVKMTLGLIWIILRFAIQDI 145
DdACTN DGIKLAQLLEISNDPVPKVNKTPKLRHNIQNVLCKLIESHGKLVIGAEELVDKMLKMTLGMIIWIIILRFAIQDI 131
SpACTN DGILLIQLEIIGDENLGRYNRNPRMRVHRLNENKALEVIKSKGMPLTNI GPADIVDGNLKLILGLIWIILRFIADI 118

.....90.....100.....110.....120.....130.....140.....150.....160



HsACTN1 SVEETSAAKEGILLWCORRTAPYK-NVNIQNFHISWKDGLGFCALIHRRRPELIDYGKLRKDDPLTNLNTAFDVAEKYLDI 218
HsACTN4 SVEETSAAKEGILLWCORRTAPYK-NVNVQNFHISWKDGLAFNALIHRRRPELIEYDKLRKDDPVTNLNNAFVEAEKYLDI 237
HsACTN2 SVEETSAAKEGILLWCORRTAPYR-NVNIQNFHTSWKDGGLCALIHRRRDLIDYSKLNKDDPIGNINLAMEIAEKHLDI 225
HsACTN3 SVEETSAAKEGILLWCORRTAPYR-NVNVQNFHTSWKDGGLCALIHRRRDLIDYAKLRKDDPIGNLNTAFVEAEKYLDI 232
DmACTN SVEEMTAKEGILLWCORRTAPYK-NVNVQNFHLSFKDGLAFCALIHRRRDLIDYAKLSKDNPLENLNTAFDVAEKYLDI 221
CeACTN NVEELSARDGILLWCORRTAPYN-NVNVQNFHNSWKDGLAFCALIHRRRDLIDYSOLHKGDP IHNLNLAFDIAEKHLDI 224
DdACTN SIEELTAKEGILLWCORRTAPYD-RVKVGNFHTSFQDGLAFCALIHRRRDLINFDLSLNKDDKAGNLQAFDIAEKELDI 210
SpACTN NEEGLTAKEGILLWCORRTANYHPEVDVQDFTRSWTNGLAFCALIHRRRDLIDYKLDKKNHRANMQLAFDIAQKSGIGI 198

.....170.....180.....190.....200.....210.....220.....230.....240



ACTN2 M228T ↘ ACTN4 K255E ↘ ACTN4 T259I ↘ ACTN4 S262P ↘ ACTN1 E225K ↘ ACTN1 G251R ↘

HsACTN1 PKMLDAEDIVGTARPDEKAIMTYVSSFYHAFSGAOK-----AETAANRICKVLAVNQE 271
HsACTN4 PKMLDAEDIVNTARPDEKAIMTYVSSFYHAFSGAOK-----AETAANRICKVLAVNQE 290
HsACTN2 PKMLDAEDIVNTPKPDERAIMTYVSCFYHAFAGAEQ-----AETAANRICKVLAVNQE 278
HsACTN3 PKMLDAEDIVNTPKPDEKAIMTYVSCFYHAFAGAEQ-----AETAANRICKVLAVNQE 285
DmACTN PRMLDPPDLQNTALPDERAVMTYVSSFYHAFSGAOK-----AETAANRICKVLAVNQE 274
CeACTN PKMLDAEDVSS--RHPDEKAIMTYVSCFYHAFNRMRDPPPPVIRPPPPORVVVAPPPERDWRKDAETAANRICKVLAVNQE 302
DdACTN PKMLDVSMDLQNTALPDERAVMTYVVAQYHAFSGAOK-----AETAANRICKVLAVNQE 263
SpACTN PRLIEVEDVCDVDRPDERAIMTYVAEYHAFSTLTK-----VETAARRVERFTEVLMS 251

.....250.....260.....270.....280.....290.....300.....310.....320



HsACTN1 NEQLMEDYEKLASDLEWIRRTIPWLENRVPEENTMHAMQOKLEDFRDYRRLHKPPKVOEKCOLEINFNTLOTKLRLSNRP 351
HsACTN4 NEHLMEDYEKLASDLEWIRRTIPWLEDVPOKTIQEMQOKLEDFRDYRVRVHKPPKVOEKCOLEINFNTLOTKLRLSNRP 370
HsACTN2 NERLMEEYERLASELLEWIRRTIPWLENRTPEKTMQAMOKLEDFRDYRRLHKPPKVOEKCOLEINFNTLOTKLRLSNRP 358
HsACTN3 NEKLMEEYERLASELLEWIRRTIPWLENRVGEPMSAMOKLEDFRDYRRLHKPPRIQEKCOLEINFNTLOTKLRLSNRP 365
DmACTN NERLMEEYERLASELLEWIRRTIPWLNRSQADNSLAGVOKKLEEYRTYRRLHKPPRVEQAKLETNFNTLOTKLRLSNRP 354
CeACTN NEKMEDYENLASDLLAWINRWMPWANRSTDDTLQQAOKLEDFRNYRREKPPRIEDKGRLETNFNTLOTKLRLSNRP 382
DdACTN LEQTKSDYLKRANELVQWINDKQASLESRDFGDSIESVQSFMANHKEYKTEKPPKGOEVSLEAIYNSLOTKLRLIKRE 343
SpACTN THDMKIDYSRMKRLLGSIARMQEYWHYVQFENNYTQVQSHSNNAKFKATEKREWVKEKIDLESLLGTIQNLKTYQLR 331

.....330.....340.....350.....360.....370.....380.....390.....400



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HsACTN1	AFMPSEGRMVS ^D INNAWG ^C LE ^Q VEKGYE ^E WLLNE ^I RRLE ^R LDHLAEK ^F ROKAS ^I HEAW ^T DGKEAM ^L RQKDY ^E TATLSE ^I K	431
HsACTN4	AFMPSEGRMVS ^D INNGW ^H LE ^Q AEKGYE ^E WLLNE ^I RRLE ^R LDHLAEK ^F ROKAS ^I HEAW ^T DGKEAM ^L KHRDY ^E TATLSD ^I K	450
HsACTN2	AFMPSEGRMVS ^D IAGAW ^Q RLE ^Q AEKGYE ^E WLLNE ^I RRLE ^R LEHLAEK ^F ROKAS ^T HETWAY ^G KE ^Q ILLQKDY ^E SASL ^T EV ^R	438
HsACTN3	AFMPSEGLVSDIANAW ^R GLE ^Q VEKGYE ^D WLLSE ^I RRLE ^R LQHLAEK ^F ROKAS ^L HEAW ^T RGKEEM ^L SQRDY ^S ALLQ ^E EV ^R	445
DmACTN	A ^Y L ^P T ^E G ^K T ^V S ^D I ^S N ^S W ^K G ^L E ^L A ^E K ^A F ^E E ^W L ^L A ^E T ^M R ^L E ^R L ^E H ^L A ^O K ^F K ^H K ^A D ^A H ^E D ^W T ^R G ^K E ^E M ^L S ^Q D ^F R ^Q C ^K L ^N E ^L K	434
CeACTN	A ^F L ^P R ^D G ^H L ^I K ^D I ^N A ^A W ^A G ^L E ^D S ^E K ^G F ^E E ^W L ^L S ^E I ^M R ^L E ^R L ^E H ^L A ^E K ^F R ^R K ^C A ^L H ^E E ^W A ^H G ^K E ^D A ^L R ^S N ^D W ^R S ^C G ^L Y ^K I ^K	462
DdACTN	P ^F V ^A P ^A G ^L T ^P N ^E I ^D S ^T W ^S A ^L E ^K A ^E Q ^E H ^A E ^A L ^R I ^E L ^K R ^Q K ^I A ^V L ^L O ^K Y ^N R ^I L ^K K ^L E ^N W ^A T ^T K ^S V ^L G ^S N ^E T ^G D ^S -I ^T A ^V Q	422
SpACTN	K ^Y E ^P P ^A G ^L K ^I V ^D L ^E R ^Q W ^K D ^F L ^S E ^E A ^N Q ^S K ^L I ^N T ^H M ^R -----	367



	ACTN2 T495M ↴	
HsACTN1	ALLKKHEAFES ^D LAAH ^Q DR-VE ^Q IAAIA ^Q ELN ^E LDY ^D YD ^S PSV ^N AR-C ^O KI ^C D ^O W ^D N ^L G ^A L ^T Q ^K R ^R E ^A L ^E R ^T E ^K L ^L E ^T I ^D Q	509
HsACTN4	ALIRKHEAFES ^D LAAH ^Q DR-VE ^Q IAAIA ^Q ELN ^E LDY ^D YD ^S H ^N V ^N TR-C ^O KI ^C D ^O W ^D A ^L G ^S L ^T H ^S R ^R E ^A L ^E K ^T E ^K Q ^L E ^A I ^D Q	528
HsACTN2	ALLRKHEAFES ^D LAAH ^Q DR-VE ^Q IAAIA ^Q ELN ^E LDY ^H D ^A V ^N V ^N DR-C ^O KI ^C D ^O W ^D R ^L G ^T L ^T Q ^K R ^R E ^A L ^E R ^M E ^K L ^L E ^T I ^D Q	516
HsACTN3	ALLRRHEAFES ^D LAAH ^Q DR-VE ^H IAA ^L A ^Q ELN ^E LDY ^H E ^A S ^V NS ^R -C ^O A ^I C ^D O ^W D ^N L ^G T ^L T ^Q K ^R R ^D A ^L E ^R M ^E K ^L L ^E T ^I D ^Q	523
DmACTN	ALKKKHEAFES ^D LAAH ^Q DR-VE ^Q IAAIA ^Q ELN ^T L ^E Y ^H D ^C V ^S V ^N AR-C ^O R ^I C ^D O ^W D ^R L ^G A ^L T ^Q R ^R R ^T A ^L D ^E A ^E R ^I L ^E K ^I D ^I	512
CeACTN	ALRRKHEAFES ^D LG ^A H ^Q DR-VE ^Q IAA ^I A ^R E ^L N ^N L ^R Y ^P D ^I G ^P I ^N AR-C ^O A ^I C ^S O ^W D ^R L ^G O ^L S ^K R ^R E ^T L ^E D ^A E ^R I ^A E ^R L ^D S	540
DdACTN	AKLKNLEAFD ^G C ^O S ^L E ^G O ^S N ^S D ^L L ^S I ^L A ^Q L ^T E ^L N ^Y N ^G V ^P E ^L T ^E R ^K D ^T F ^A Q ^O W ^T G ^V K ^S S ^A E ^T Y ^K N ^T L ^L A ^E L ^E R ^L O ^K I ^E D	502
SpACTN	-----E ^I K ^E S	372



	ACTN3 R577X ↴	ACTN2 E583A ↴	
HsACTN1	L ^Y L ^E Y ^A K ^R A ^A P ^F N ^N W ^M E ^G A ^M E ^D L ^O D ^T F ^I V ^H T ^I E ^E I ^Q G ^L T ^T A ^H E ^O F ^K A ^T L ^P D ^A D ^K E ^R L ^A I ^L G ^I H ^N E ^V S ^K I ^V Q ^T Y ^H V ^N M ^A G ^T	589	
HsACTN4	L ^H L ^E Y ^A K ^R A ^A P ^F N ^N W ^M E ^S A ^M E ^D L ^O D ^M F ^I V ^H T ^I E ^E I ^E G ^L I ^S A ^H D ^O F ^K S ^T L ^P D ^A D ^R E ^R E ^A I ^L A ^I H ^K E ^A Q ^R I ^A E ^S N ^H I ^K L ^S G ^S	608	
HsACTN2	L ^H L ^E F ^A K ^R A ^A P ^F N ^N W ^M E ^G A ^M E ^D L ^O D ^M F ^I V ^H S ^I E ^E I ^Q S ^L I ^T A ^H E ^O F ^K A ^T L ^P E ^A D ^R E ^R G ^A I ^M G ^I O ^G E ^I O ^K I ^C O ^T Y ^G L ^R P ^C S ^T	596	
HsACTN3	L ^Q L ^E F ^A R ^R A ^A P ^F N ^N W ^L D ^G A ^V E ^D L ^O D ^V L ^V H ^S V ^E E ^T O ^S L ^L T ^A H ^D O ^F K ^A T ^L P ^E A ^D R ^R E ^G A ^I M ^G I ^O G ^E I ^O K ^I C ^O T ^Y G ^L R ^P C ^S T	603	
DmACTN	L ^H L ^E F ^A K ^R A ^A P ^F N ^N W ^L D ^G T ^R E ^D L ^V D ^M F ^I V ^H T ^M E ^E I ^Q G ^L I ^Q A ^H D ^O F ^K A ^T L ^G E ^A D ^K E ^F N ^L I ^V N ^L V ^R E ^V E ^S I ^V K ^O H ^I P ^G G ^L E	592	
CeACTN	L ^Y L ^D F ^A K ^R A ^A P ^F N ^N W ^L D ^G A ^R E ^D L ^A D ^L V ^I V ^H E ^M R ^E I ^E E ^L V ^N A ^H D ^O F ^K S ^T L ^G D ^A D ^R E ^F S ^S I ^N Q ^I E ^H E ^V E ^H L ^V T ^S H ^G L ^D R ^E L ^L	620	
DdACTN	S ^L V ^E F ^A K ^R A ^A Q ^L N ^V W ^I E ^A A ^D D ^H V ^F D ^P I ^N V ^D S ^V O ^G V ^O E ^I O ^E K ^F D ^A F ^L H ^D O ^S Q ^O F ^A E ^L E ^A L ^A A ^L T ^Q L ^R E ^L G ^R S ^E -----	575	
SpACTN	M ^R I ^A F ^A D ^R A ^N S ^F S ^K M ^L S ^T I ^S N ^E I ^T N-----	397	



	ACTN2 E628G ↴	
HsACTN1	-N ^P Y ^T T ^I T ^P Q ^E I ^N G ^K W ^D H ^V R ^O L ^V P ^R R ^D Q ^A L ^T E ^H A ^R O ^O H ^N E ^R L ^R K ^O F ^G A ^Q A ^N V ^I G ^P W ^I O ^T K ^M E ^E I ^G R ^I S ^I E ^M H ^G T ^L E ^D O ^L	668
HsACTN4	-N ^P Y ^T T ^V T ^P Q ^I I ^N S ^K W ^E K ^V Q ^O L ^V P ^K R ^D H ^A L ^L E ^E O ^S K ^O O ^S N ^E H ^L R ^R O ^F A ^S Q ^A N ^V V ^G P ^W I ^O T ^K M ^E E ^I G ^R I ^S I ^E M ^N G ^T L ^E D ^O L	687
HsACTN2	-N ^P Y ^S T ^V T ^M D ^E L ^R T ^K W ^D K ^V Q ^L V ^P I ^R D ^Q S ^L Q ^E E ^L A ^R O ^H A ^N E ^R L ^R R ^O F ^A A ^Q A ^N A ^I G ^P W ^I O ^N K ^M E ^E I ^A R ^S S ^I O ^I T ^G A ^L E ^D O ^M	675
HsACTN3	-N ^P Y ^I T ^L S ^P O ^D I ^N T ^K W ^D M ^V R ^K L ^V P ^S R ^D Q ^T L ^Q E ^E L ^A R ^O V ^N E ^R L ^R R ^O F ^A A ^Q A ^N A ^I G ^P W ^I O ^A K ^V E ^E V ^G R ^L A ^G L ^A G ^S L ^E E ^O M	682
DmACTN	-N ^P Y ^T T ^L T ^A N ^D M ^T R ^K W ^S D ^V R ^O L ^V P ^O R ^D Q ^T L ^A N ^E L ^R K ^O O ^N N ^E M ^L R ^R O ^F A ^E K ^A N ^I V ^G P ^W I ^E R ^O M ^D A ^V T ^A I ^G M ^G L ^O S ^L E ^D O ^L	671
CeACTN	R ^N P ^Y T ^D L ^S A ^S D ^I R ^R K ^W G ^E V ^O N ^S V ^P R ^R D ^S O ^L Q ^A E ^L K ^R O ^O N ^N E ^R L ^R T ^I F ^A E ^K A ^N O ^V G ^P W ^L E ^R E ^L E ^Q V ^L A ^I G ^L G ^R R ^L E ^D A ^I	700
DdACTN	-N ^D Y ^S V ^I S ^Y D ^E L ^S A ^K W ^N N ^L L ^A G ^I E ^E R ^K V ^O L ^A N ^E L ^T T ^O T ^N D ^V L ^C O ^S F ^S V ^K A ^N E ^I S ^D Y ^V R ^V T ^L D ^A I ^S O ^N ---T ^S S ^D P ^O E ^O L	651
SpACTN	-----L ^O G ^D W ^R D ^O L	406



	ACTN1 T737N ↴	ACTN1 R738W ↴	
HsACTN1	S ^H L ^R Q ^Y E ^K S ^I V ^N Y ^K P ^K I ^D Q ^L E ^G D ^H O ^L I ^Q E ^A L ^I F ^D N ^K H ^T N ^Y T ^M E ^H I ^R V ^G W ^E Q ^L L ^T I ^A R ^T I ^N E ^V E ^N O ^I L ^T R ^D A ^K G ^I S ^O E ^O M	748	
HsACTN4	S ^H L ^K Q ^Y E ^R S ^I V ^D Y ^K P ^N L ^D L ^L E ^Q O ^H Q ^L I ^Q E ^A L ^I F ^D N ^K H ^T N ^Y T ^M E ^H I ^R V ^G W ^E Q ^L L ^T I ^A R ^T I ^N E ^V E ^N O ^I L ^T R ^D A ^K G ^I S ^O E ^O M	767	
HsACTN2	N ^O L ^K Q ^Y E ^H N ^I N ^Y K ^N N ^I D ^K L ^E G ^D H ^O L ^I Q ^E A ^L V ^F D ^N K ^H T ^N Y ^T M ^E H ^I R ^V G ^W E ^L L ^L T ^T I ^A R ^T I ^N E ^V E ^T O ^I L ^T R ^D A ^K G ^I T ^O E ^O M	755	
HsACTN3	A ^G L ^R Q ^O E ^Q N ^I N ^Y K ^T N ^I D ^R L ^E G ^D H ^O L ^L Q ^E S ^L V ^F D ^N K ^H T ^V Y ^S M ^E H ^I R ^V G ^W E ^Q L ^L T ^S I ^A R ^T I ^N E ^V E ^N O ^V L ^T R ^D A ^K G ^L S ^O E ^Q L	762	
DmACTN	H ^R L ^K E ^Y Q ^A V ^Y A ^Y K ^P N ^I E ^E L ^K I ^H O ^A V ^O E ^S M ^I F ^E N ^R Y ^T N ^Y T ^M E ^T L ^R V ^G W ^E Q ^L L ^T S ^I N ^R N ^I N ^E V ^E N ^O I ^L T ^R D ^S K ^G I ^S O ^E Q ^L	751	
CeACTN	Q ^O L ^R S ^I Q ^R N ^V L ^G Y ^K P ^N L ^D E ^L E ^R V ^H O ^E M ^E N ^F V ^F E ^N R ^K S ^R Y ^S M ^S E ^L R ^V G ^W E ^T L ^L T ^S I ^N K ^T I ^N E ^F E ^N O ^V L ^L R ^D S ^K G ^I S ^E E ^Q I	780	
DdACTN	N ^N I ^R A ^I I ^T A ^H A ^E K ^K P ^E L ^D E ^L Y ^T I ^A S ^O L ^E A ^Q V ^D N ^K H ^T O ^H S ^L E ^S I ^K L ^K W ^D K ^L N ^T L ^A K ^K N ^E O ^V V ^E G ^E I ^L A ^K O ^L T ^G V ^T A ^E E ^L	731	
SpACTN	D ^H V ^E F ^L Q ^E H ^L G ^P L ^E V ^E L ^A S ^V K ^V L ^Y D ^N C ^F Q ^A G ^I E ^E N ^D Y ^T M ^F S ^Y E ^D L ^E H ^E F ^G I ^T A ^N I ^A N ^K I ^K Y ^L E ^N E ^L L ^E R ^E K ^R T ^L S ^K O ^E L	486	



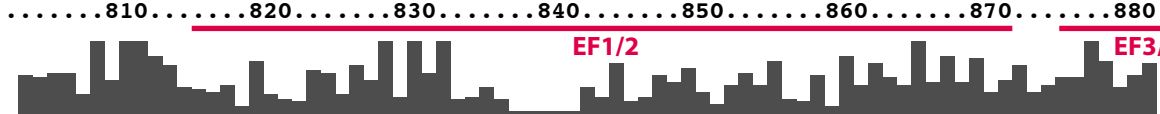
ACTN2 R759T ↴

ACTN1 R752Q ↴

ACTN1 G764S ↴

ACTN1 E769K ↴

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HsACTN1	NEFRASFNHFDRDHSGLGPEEFKACLISLGYDIGNDPQGEAEFARIMSIVDPNRLGVVTFQAFIDFMSRETTADTDTADQ	828	
HsACTN4	QEFRASFNHFDKDHGGALGPEEFKACLISLGYDVENDROGEAEFNRMISLVDPNHSGLVTFQAFIDFMSRETTDITDADQ	847	
HsACTN2	NEFRASFNHFDRRKNGLMDHEDFRACLISMGYDLG-----EAEFARIMTLVDPNGQGTVTFQSFIDFMTRETTADTDTAEQ	830	
HsACTN3	NEFRASFNHFDRKRNGMMEPDDFRACLISMGYDLG-----EVEFARIMTMVDPNAAGVVTFQAFIDFMTRETTAETDTTEQ	837	
DmACTN	NEFRSFFNFHFDKNRTGRLSPEEFKSCVLSLGYSIGKDROGDLDFQRILAVVDPNNTGYVHFDAFLDFMTRESTDITDTAEQ	831	
CeACTN	AEFRASFSHFDKERAG-LDPEQLRSCLISVGYTIRPGREGDAELHRVLAHVDPNRMGRVVFQAFIDFMTKENSQDTVEQ	859	
DdACTN	SEFKACFSHFDKDNDNKLNRLEFSSCLKSIGDELT-----EEQLNOVISKIDTDGNGTISFEFEIDYMVSSRKGTDVSVES	806	
SpACTN	DGITKVFRRHFEEKKSNMLNEVEFYAALASLGLVYD-----TEEGTALFHRAANSEEGVTYERFTEIVMEELEDSDSARQ	560	



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HsACTN1	VMASFKILAGDKNYITMDELRRRLP-PDQAEYCIARMAPYTGPDSPGALDYMSFSTALYGESDL--	892	
HsACTN4	VIAAFKVLADGKNFITAEELRRRLP-PDQAEYCIARMAPYQGPDAVPGALDYKSFSTALYGESDL--	911	
HsACTN2	VIAAFRILASDKPYILAEELRRRLP-PDQAEYCIKRMPSYSGPGSPGALDYAAFSSALYGESDL--	894	
HsACTN3	VVASFKILAGDKNYITPEELRRRLP-AKQAEYCIKRMVYKGGSGAPAGALDYVAFSSALYGESDL--	901	
DmACTN	VIDSFRILAADKPYILPDELRRRLP-PDQAEYCIQRMPPYKGPNGVPGALDYMSFSTALYGETDL--	895	
CeACTN	MIDSFRILASGKTFITADELERRLP-RDQAAVCMARMAPSREPGAPPRSFYVTFSSRSLYSQ-----	920	
DdACTN	TKAAFVMAEDKDFITEAQIRAAISDSKQIDYLLASMP-----AVEGGFDYNSFAEKLYQ-----	861	
SpACTN	VLYAFCDVADGKSYVSDDLLRSQVRNIVKFLCENMN-----KHSEGLDYLTIKQLLAEDKEIV	621	

