

Supplementary File 2: Pairwise alignments of human ALS-linked proteins with yeast homologs

Yellow highlight: identical amino acid

Blue highlight: similar amino acid

Red text: dissimilar amino acid, ALS-linked in human

2-1: ALS1 (*SOD1*)

2-2: ALS4 (*SETX*)

2-3: ALS8 (*VAPB*)

2-4: ALS11 (*FIG4*)

2-5: ALS13 (*ATXN2*)

2-6: ALS14/FTD-ALS6 (*VCP*)

2-7: ALS15 (*UBQLN2*)

2-8: ALS16 (*SIGMAR1*)

2-9: ALS17/FTD-ALS7 (*CHMP2B*)

2-10: ALS18 (*PFN1*)

2-11: ALS20 (*HNRNPA1*)

2-12: ALS22 (*TUBA4A*)

2-13: ALS25 (*KIF5A*)

2-14: ALS26 (*TIA1*)

2-15: ALS27 (*SPTLC1*)

2-16: FTD-ALS2 (*CHCHD10*)

2-17: FTD-ALS5 (*CCNF*)

2-1: CLUSTAL O(1.2.4) multiple sequence alignment [ALS1]

hsSOD1	MATKAVCVLKGDPVQGIINFEQKESNGPVKVGWSIKG-LTEGLHGFIHVEFGDNTAGCT	59
scSOD1	-MVQAVAVLKGDAGVSGVVKFEQASESEPTTVSYEIAGNSPNAERGFHIEHFGDATNGCV	59
	.:.*.*****.*.:::***. . . *. . * . * :. :.***:***** * **.	
hsSOD1	SAGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVAIVSIEDSVISLSGDHCIIGRTLIV	119
scSOD1	SAGPHFNPFKKTHGAPTDEVHRHVGDMGNVKTDENGVAKGSFKDSLILKLGPTSVVGRSVV	119
	*****.:.:.*. . *. * * * * * .***.:.:.***. *:***.*. * .:.**: *	
hsSOD1	VHEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ	154
scSOD1	IHAGQDDLGKGDTEESLKTGNAGPRPACGVIGLTN	154
	:* *****.*** ***** * *****:..	

2-2: CLUSTAL O(1.2.4) multiple sequence alignment [ALS4]

hsSETX	MSTCCWCTPGGASTIDFLKRYASNTSPSGE----FQTA--DEDLC--YCLECVAEYHKARD	52
scSEN1	-----MNSNNPDNNNSNNINNNNNKDKDIAPNSDVQLATVYTKAKS	40
	**.*...: :: *:~:~ :: .: * *~:~.	
hsSETX	ELPFLHEVLWELETLRRLINHFEEKSMKAEIGDDDELYIVDNNGEMPLFDITGQDFENKLRV	112
scSEN1	YIPQIEQVYQG-----	51
	:* .:~*	
hsSETX	PLLEILKYPYLLLHERVNELCVEALCRMEQANCSEFQVFDKHPGIYLFVHPNEMVRRWAI	172
scSEN1	-----TNPN-----I	56
	.:~* *	
hsSETX	LTARNLGKVDRDDYYDLQEVLLCLFKVIELGLLESPDIYTSSVLEKKGKLILLPSHMYDTT	232
scSEN1	QEAKLLG-----ELLQVL-A---EVPKGTHLFCPILEPISIFSLTIFSFNE-	99
	*: ** *:~* * : .: .:~. .:~* .:~* .:~.	
hsSETX	NYKSYWLGICML--LTILEEQAMDSLGLGSDKQNDFMQSILHTMEREADDD-----SVD	284
scSEN1	EATATWLKNHFNPILSVCD-KCILNFARGKCK---MLQH--FATQRHVPHEHVAKFNDIV	153
	: .: ** : *:~: : .:~. .: * * :~* .:~*:~. .: .:~.	
hsSETX	PFWPALHCFMVIL-----DRLG-----SKVWGQLMDPIVA-----FQTIINNA	322
scSEN1	CQWRVEAVFPILRNISVNDNTGINITNEIETAMYECLCNPHMLRLNKQLKATFEAIF-KF	212
	* . * :~ * * : .:~ * *:~ *:~*:~: .	
hsSETX	SYNREIRHIRNSSVRTKLEPESYLDMMVTCSEQIVYNNPEKTKKDSGWRTAICPDYCPNM	382
scSEN1	FYDTKHR--LLDVTNPLSIKTFISGVIFC-----W-CEGSKEENEWSRAFLKDLYSRN	262
	*: : * .* * .:~:~:~:~:~* : * *:~:~. * *:~* .	
hsSETX	YEEMETLASVLQSDIGQDMRVHNSTFLWFIPFVQSLMDLKDGLGVAYIAQVNVNHLHYSEVKE	442
scSEN1	FHI-----NL-----	267
	:. *:~	
hsSETX	VLNQTDVAVCDKVTEFFLLILVSVIELHRNKKCLHLLWV-SSQQWVEAVVKC-----	492
scSEN1	---SNLTPDIIIEVY-----IHILFLQNPANWTEIVVSQFWSRLLPVF	307
	:~. * :~*:~ *:~*:~. .:~* *~.	
hsSETX	AKLPTTAFTSRSEKSSG-NCSEKGTAMISLHSMPSNSVQLAYVQLIRSLKKEGYQLGQ	551
scSEN1	NLFDKDVFIIEYFQVQPNVESLKKTFKFPLEPIFKMWYNHLSKSYHDKPLDFLRLGLTMFL	367
	: .:~* .: .:~. * * : .:~* * .:~*:~ .:~* * :	
hsSETX	QSLCKRFWDKLNLFRLGNLSLWQLTSQETHELQSCCLKIIRNIKFKAPPCNTFVDLTSA	611
scSEN1	NKFGSEFWSKIIEPFTFHSI-----LDIIIFNR-----	393
	:~:~ .:~*~*~*~*~*~* .: * *~:~.	
hsSETX	CKISPASYNKEESEQMGKTSRKDMHCLEASSPTFSKEPMKVDSVLIKADNTIEGDNNEQ	671
scSEN1	-----DSFPIKLIKIQDNPIVEH-----QTE-	414
	:~ :~:~*~. .:~ .:~*	
hsSETX	NYIKDVKLEDHLLAGSCLKQSSK--NIFTE-RAEDQIKISTRKQ-KSVKEISSY-----T	722
scSEN1	VYFQ-----LTGSVTDLLSWTLFPYHALSPSKRIQMVRKVSMAFLRIIANYPCLKSI	466
	*~:~ *~*~* * .:~ .:~*~:~:~ .: .:~*~*~.	
hsSETX	PKDCTSRNGPERGCDRGIIVSTRLLTDSSTDALEKVSTS---NEDFSLKDDALAKTSKRK	779
scSEN1	PKACLMNSA-----TALLRAVLTIKENERAMLYKNDEF-----	500
	** * ... * *~. * * .:~ :~ *~*~:~	
hsSETX	TKVQKDEICAKLSHVIAKQHRKSTLVDNTINLDEN-LTVSNIESFYSRKDTGVQ--KGD	835
scSEN1	-----TVLLTKTDSRALLNNPLIQDIIIRSASNPNDFYPGLGAASASVATST	547
	:~ .: .:~:~*~:~ * .:~*~*~*~*~ .:~ .:~.	

[illegible]

hsSETX	TFETVAQEWLNSPNRENFYQLQV----RKFPADYIKYWE-F-AVYLEECEELAKQLYPKEN	1808
scSEN1	SWQGLCS----SRDREDYKPFISIIVGNRTAVSDFYDVYASVAKQVIQDCGISE-----S ::: .. * :*: : : * . :*: . : . :*: : : .	1214
hsSETX	DLVFLAPERINEEEKDTERNDIQDLHEYHSGYVHKFRRTSVMRNGKTECYLSIQTQENFP	1868
scSEN1	DLIVMAYLPDFRP---DKRLSSDDFKKAQHTCLAKVRTLKNTKGGNVDTVLRHNRHSFS *: :*: . :* . :*: : : :* . . :*: : * : :*:	1271
hsSETX	AN--LNELVNCIVISSLVTTQRKLKAMSLGSRNQLARAVLNPNPMDFCTKDLLTTTTER	1926
scSEN1	KFLTLRSEIYCVKVMQMTTIEREYSTLEGLEYD-LVGQILQAKPSPPVNVD-----AAE * . : * : : :*: :*: :*: * :* . :*: :* . *	1325
hsSETX	IIAYLRDFNEDQKKAJETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRLLTENQR	1986
scSEN1	IETVKKSYKLN-----TSQAEIIVNSVSKEGFSLIQGPPTGKTKTILGIIGYFLSTKNA * : :*: : : : :* * :*: :*: :*: :* :* :* :*	1380
hsSETX	KG-----HSDENSNAKIKQNRVLVCAPSNAAVDELMMKIIIEFKEKCKDKKNPLGN	2037
scSEN1	SSSNVIKVPLEKNSSNTEQLLKKQKILICAPSNAAVDEICLRKSGVYDKQ-----GH .. :*: :* :*: :*: :*: :* :* :* :*	1433
hsSETX	CGDINLVRLGPEKSINSEVLKFSLDSQVNRHMKE-----LPSHV-QAMHKRKEFL	2087
scSEN1	QFKPQLVRVGRSDVNVVAIKDLTLEELVDKRIGERNYEIRTDPELERKFNNNAVTKRREL . :*: :* . :* : :*: . :*: : : * . :* :*: :	1493
hsSETX	DYQLDELSRQRALCRGGR----EIQRQELDENISKVSKERQELASK----IKEVQGR	2138
scSEN1	-GKLDSESGNPESPMSTEDISKLQLKIRELSKIINELGRDRDEMREKNSVNYRNRDLDRR :*. * : . : :*: :* :*: :*: :* . * : : :	1552
hsSETX	KTQSIIILESHIICCTLSTSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHR	2198
scSEN1	NAQAHILAVSDIICSTLGSAGHDL----ATMGIKFDTVIIDEACQCTELSSIIPLRYG :*. * : *. :*. :*. * :* . * :* . :*. :*. * :*: :* :	1607
hsSETX	CNKLILVGDPKQLPPTVISMKAQEYGYDQSMARFCRLLEENVEHNMISRLPILQLTVQY	2258
scSEN1	GKRCIMVGDPNQLPPTVLSGAASNFKYNQSLFVRMEKN-----SSPYLLDVQY : :*: :*: :* :* :* :* :* :* :* :* :* :* :* :*	1655
hsSETX	RMHPDICLFPSNYVYNRNLKTNRQTEAIRC---SSDWPFQPYLVFDVGDGSERR--DNDS	2313
scSEN1	RMHPSISKFPSSEFYQGRKDGPGMDILNKRPPHQLPLAPYKFDFIISGRQEQNAKTMS ***. * . :*. :*. :* :* :* :* :* :* :* :* :* :*	1715
hsSETX	YINVQEIKLVMIEIKLIKDKR-KDV-SFRNIGIITHYKAQKTMIQKDLKDFDRK--GPA	2369
scSEN1	YTNMEEIRVAIELVDYLFRKFDNKIDFTGKIGIISPYREQMKMRKEFARYFGGMINKSI * :*: :*: :*: :* :* :* :* :* :* :* :* :* :*	1775
hsSETX	EVDTVDAFQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSFILGHLRTL	2429
scSEN1	DFNTIDGFQGEKEIILISCVRADDTKSSVGFLKDFRNMNVALTRAKTSIWVLGHQRLA :*. :*. :*. :* :* :* :* :* :* :* :* :* :* :* :*	1835
hsSETX	ENQHWNQLIQDAQRGAIKTCCKNYRHDVAVKILKLPVLQRLTHPTIAPEGSRPQGG	2489
scSEN1	KSKLWRDLIEDAKDRSCLAYACSGFLDPRNNRAQSI--L-RKFNVFV--PSEQEDDYK : :* :*: :*: :* :* :* :* :* :* :* :* :* :*	1888
hsSETX	LPSSKLDSGFAKTSVAAS--LYHTPSDSKEITLTVTSKDPER-----PPVHDQLQDP--	2539
scSEN1	LPMEYITQGPDEVKSNKDTKKRRVVDEGEEADKAVKKKKKKKKKKSKADDKKKNNKK ** . : * :* . :* :* :* :* :* :* :* :* :* :*	1948
hsSETX	--RLLKRMGIEVKGIGFLWDPQPSPPQHPGATPPTGEPGFVHVHQLSHIQQPAAVVAAL	2597
scSEN1	AESPSTSSGTTKKSSIFGGMSP-----SAVVPK---TFPDVD-----SNKKAADVVGKK . * :* :* :* :* :* :* :* :* :* :* :* :*	1995
hsSETX	SS-----HKPPVRGEPFAASPEASTCQSKCDD	2624
scSEN1	KNNKHVCFSDDSFIPRNDPEIKVTRSLSSVLKEQLGLKETRTISPPEISNNE--DDD .. : : :* * . : *	2053

hsSETX	PEEELCHRREARAF----SEGEQEKCGSETHHTRNSRWDKRTLEQEDSSS-----	2671
scSEN1	DEDDYTPSISDSSLMKSEANGRNRRVASHNQ-NFSASIYDDPQVSQAKQTQVPAAITKHR	2112
	:: . :: ::.:*: . * :*. :.* ...	
hsSETX	-----KKRKLL-----	2677
scSEN1	SSNSVLSGSSRIILTASDYGEPNQNGQNGANRTLSQHVGNANQYSTAPVGTGELHETLPA	2172
	. ::*	
hsSETX	-----	2677
scSEN1	HPQDSYPAEAEDPYDLNPHPQPQSSAFKGP GSGPTGTRNSSRRNASSSPFIPKKRKPRS	2231

2-3: CLUSTAL O(1.2.4) multiple sequence alignment [ALS8]

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hsVAPB      MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTDRNVCFKVKTTAPRRYCVRPNSGI      60
scSCS2      MSAV----EI-SPDVLVYKSPLTEQSTEYASISNNSDQTIAFKVKTAPKFYCVRPNAAV      55
              *: *      .:      . * :.:*: *: *      .:.* :.:.:*****: *****: :.:
              .:      . * :.:*: *: *      .:.* *: *      .:      *: .: : *

hsVAPB      IDAGASINVSVMQLQPFDDYDPNE--KSKHKFMVQSMFAPTD--SDMEAVWKEAKPEDL--      114
scSCS2      VAPGETIQVQVIFLGLTEEPAADFCKRDKFLVITLPSPYDLNGKAVADVWSDLEAEFKQQ      115
              : * :*:*.*: : : *      *.:*:*: : : * *      . :      **: .: : *

hsVAPB      -MDSKLRVCFELPAENDKPHDVEINKIISTTASKTETPIVSKSLs----SSLDDETEVKV      169
scSCS2      AISKIKVKYLISPDVHPAQNQNIQE-----NKETVEPVVQDSEPKEVPVAVNEKEVPAAE      170
              :..*:: : : : . : :*: :      .:* **:..*      : :.:.*

hsVAPB      MEECKRLQGEVQRLREENKQ-----FKEEDGLR-MRKTVQSNSPI--SALAPTGKEEGLS      221
scSCS2      P---ETQPPVQVKKEEVPVQKTVPHENEKQTSNSTPAPQNQIKEAATVPAENE-SSS      225
              . * ** :**      . .*: : ..*      . * :* .*: :* . *

hsVAPB      TRLLAL-VVLFFIVGVIIGKIAL      243
scSCS2      MGIFILVALLILVLGWFYR----      244
              :: * .:***** :

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CLUSTAL O(1.2.4) multiple sequence alignment [ALS8]

```

hsVAPB      MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTDRNVCFKVKTTAPRRYCVRPNSGI      60
scSCS22      -----MRI-VPEKLVFKAPLNKQSTEYIKLENDGEKRVIFKVRTSAPTKYCVRPNVAI      52
              : :      .:* **:..* * :** *      :.* ***:*:** :*****.*

hsVAPB      IDAGASINVSVMQLQPFDDYDP---NEKSKHKFMVQSMFAPTD-----TSDMEAVWKEAKP      111
scSCS22      IGAHESVNVQIVFLGLPKSTADDEMDQKRDKFLIVTLPIPAAYQNVEDGELLSDWPNLEE      112
              *. * :*:*.*: : .      :.:.**: : : * :      .: : * : :

hsVAPB      E---DLMSKLRVCFELPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDETEVKK      168
scSCS22      QYKDDIVFKKIKI-FH-----SAPTKYCVRPNVAI      127
              : *:: .*: : *.

hsVAPB      VMEECKRLQGEVQRLREENKQFKEEDGLRMRKTVQSNSPISAL-APTGKEEGLSTRLLA-      226
scSCS22      -----SVL-----PKRKPSGNHDAESARAPSAGNGQSLSSRALLI      162
              . :      **      .:. **      :*: :.**: *

hsVAPB      LVVLFFIVGVIIGKIAL      243
scSCS22      ITVIALLVGWIYY---      175
              :.*: :*: *

```

2-4: CLUSTAL O(1.2.4) multiple sequence alignment [ALS11]

hsFIG4	-----MPT---AAPIISSVQKLVLYETRARYFLVGSNNAETKYRVLKID	42
scFIG4	MNNDAMEHTLGGGILTTSGSKQRKTSKFVMGKYTLIYETKDRMYIVGSNKRETMFRILEID	60
	: * : * . * * * : * : * * * : * : * : * *	
hsFIG4	RTEPKDLV-IIDRHHVYTQQEVRELLGRDLGNRTKMGQKGSSGLFRAVSAFGVVGFEVRF	101
scFIG4	LTVPRGELTVLEDNVFFTRNEIMNVLASLE-----EATEDGLHKKITGYGLLGFIKF	112
	* * . : : * . . * * * : * . * : : * * . * : * * * * *	
hsFIG4	LEGYYIVLITKRRKMADIGGHAIYKVEDTNMIYIPNDSVR-VTHPDEARYLRIFQNVDLS	160
scFIG4	TCWYYLIMVTKYSQVAVIGGHGIYHIDGIDIIPITNNYKKPEKSSDEARLLNIFKDLDT	172
	* * : * * : * * * * * . : * * * : : . * * * * * . * * : * * :	
hsFIG4	SNFYFSYSYDLSHSLQYNLTVLMPLEMLKSEMTQNRQESFDIFEDEGLITQGGSGVFGI	220
scFIG4	KTFYFSYTYDITNTLQTNILREKLK--AV-----DRCDITIPC-----GI	210
	. * * * * : * * : * : : * : : : : * : : * * * * *	
hsFIG4	CSEPYMKYVWNGELLDIIKST--VHRDWLLYIIHGFQGSKLLIYGRPVYVTLIARRSSK	278
scFIG4	-TDYNEMFVWNNLLSPIFACIDTVDFWFQCIHGFIDQVNVSVLGKSIYITLIARRSHH	269
	: : : * * . * * . * : . * * : * * * * . * : : * : * : * * * * *	
hsFIG4	FAGTRFLKRGANCEGDVANEVETEQLCDASVMSF-----TAGSYSSYVQVRGSVPL	330
scFIG4	FAGARFLKRGVNNKGHVANEVETEQLVTDMLTPFHQPGNGFFDSDRYTSFVQHRGSIPL	329
	* * : * * * * . * : * . * * * * * * : * : * : : * : * : * * : * *	
hsFIG4	YWSQDISTMMPKPPITLDQADPFHAHVAALHFDQMFQRFQSP-IIILNLVKEREKRKHERI	389
scFIG4	YWTQDASNLTTKPPIRINVDPFFSPAALHFDNLFQRYGGGTIQILNLIKTKKEKTPRET	389
	* * : * * . : * * * : : * * * * * : * * : * * : * * : * * : *	
hsFIG4	LSEELVAAVTYLNQFLPPEHTIVYIPWDMAKYTKSKLCNVLDRLNVIAESVVKKTGFFVN	449
scFIG4	LLWEFEQCIDYLNFLPTLKKLDYTSWDMRSASKQDQGQVIEFLEKYAVNTVTTTGIFHN	449
	* * : . : * * : * * * : : * * * : : * . . . : * : * * . * * : * *	
hsFIG4	RPDSYCSILRPDEKWNELGGCVIPTGRLQTGILRTNCVDCLDRTNTAQFMVGKCALAYQL	509
scFIG4	GPDF-----ASTKIQEGICRSNCIDCLDRTNAAQFVIGKRALGCQL	490
	* * : : * * * : * * : * * * * * : * * : * * . * *	
hsFIG4	YSLGLIDKPNLQFDTDAVRLFEELYEDHGDTLISLQYGGSQLVHRVKTYRKIAPWTQHSKD	569
scFIG4	KSLGIIDNSYLEYDSDIVNLTFLHDLGDTIALQYGGSHLVNTMETYRKINQWSSHSRD	550
	* * : * * : * * : * * : * * : * * * * : * * : * * * * : * : * *	
hsFIG4	IMQTLSTRYYSNAFSDADRQDSINLFLGVFHPTEGKPHLWELPTDFYLHHKNTMRLLPTRR	629
scFIG4	MIESIKRFYSNSFVDAQRQDAINLFLGHYSWREGFPSLWEMNTDFYLHNAYSL--NMPKR	608
	: : : : * : * * : * * : * * * * : * * * * * : * * : * * : *	
hsFIG4	SYTYWWTPPEVIKHLPLPYDEVICAVNL--KKLIVKKFKHYEEI-DIHNEFFRPYELSS	685
scFIG4	SYIHHWWDYNIKSVKELINEELIATGNDVTREKIIKNVRGYPGAFDNYWNEYYPERSVTW	668
	* * : * * . * * : : * : * . : : * : * : * : * : : * * : * : *	
hsFIG4	FDDTFCLAMTSSARDFMPK-TVGIDPSPFTVRKPDETGKSVLG---NKS-N-REEAVLQR	739
scFIG4	IRDLFAYNMNSTRRYHNALSQDKAMSPFTSRKQSWLNNKLKMITSSKSLEKAEGRVVET	728
	: * * . * * : * . . * * * * . . : : . * * : * * :	
hsFIG4	KTAASAPPPPSEEAVS---SSSEDDSGTDREEGSVSQRSTPVKMTDAGDSAKVTENVV	795
scFIG4	TDLDRDTSKQLELELYEHLHIISDRSQKLEEKMNSFSYSKYPIFISH-----ESSEI	781
	. * * : . * * . * : . * * . * : : * . . . :	
hsFIG4	QPMKELYGINLSDDLSEEDFSIYSRFVQLGQSQHKQDKNSQQPCSRCSGDGVIKLTPISAF	855
scFIG4	PPMRKVIGEPLVDIA-----EDFTDVYDDDDGDDE---NDEMTTEALLIAPDHVS	829
	* * : : * * * . * : : : . . * : . . : : * : *	

hsFIG4	SQDNIYEVQ-----PPRVDRKSTEIFQAHIQASQGIMQPLGKEDSSMYREYIRNRYL--	907
scFIG4	VDEKFYEKVLNVDDYKPALDDYS-----AVI-----HIKPDNLQLYRDLCFSKDIQL	876
	::::** * :* * * * : :: .:**:* .: :	

hsFIG4	---	907
scFIG4	DFQ	879

hsATXN2	MRSAAAAPRSPAVATESRRFAAARWPGRWSLQRPARRSGRGGGGAAPGPYPSPAAPPPPGP	60
scPBP1	-----	0
hsATXN2	GPPPSRQSSPPSASDCFGSNGNGGGAFRPGSRRLGLGGPRPFVVLLPLASPGAPPAA	120
scPBP1	-----	0
hsATXN2	PTRASPLGARASP PRSGVSLARPAGCPRFACEPVYGPLTMSLKPRQQQQQQQQQQQQQQ	180
scPBP1	-----	0
hsATXN2	QQQQQQQPPPAANVRKPGGSGLLASPAAAPSPSSSVSSSSSATAPSSVAATSGGGRPG	240
scPBP1	-----MKG NFRKR D-----SS-TNSRKGG----	18
	. * . ** . ** . : . **	
hsATXN2	LGRGRNSNKGLPQSTISFDGIYA-----NMRMVHILTSVVGSKCEVQVKNGGIYEGV	292
scPBP1	NSDSNYTNGGVPNQNNS-SMFYENPEITRNDDRQDYLLANSIGSDVTVTVTSGVKYTGL	77
	. .. : * *:*. . * . : * : * ::*: . **: . * *. . * * :	
hsATXN2	FKTYS PKCD---LVLDAAH--EKSTESSGPKREEIMESILFKCSDFVVVQFKDMDSSY	346
scPBP1	LVSCNLESTNGIDVLRFP RVADSGVSVD DLAKTLGETLLIHGEDVAE LELKNIDL SL	137
	: : . . . : ** : :* . : : *::*: . *. . ::*:.* *	
hsATXN2	AKR-----DAFTDSAISA KVN GEHK EKDL E PWD AG EL	378
scPBP1	DEKWEN SKAQ ETTPARTNIEKER VNG ESNE VT KFRTDV DIS GSGREI KER KLE KW TP EE G	197
	: : * .. : . * **:.*** * *	
hsATXN2	TANE ELE--ALENDV SNGWDPND MF R Y NE EN Y GV STYDSSL SSYTV PLERDNSEEF LKR	436
scPBP1	AEHF DI NK GA LED DS AS W ---D Q F AV NE KK FG VK S TF DE HLY TTK IN KDD P ---NY SKR	251
	: : ::: :* * .* * * **:::** **:. * : . : :: **	
hsATXN2	EARANQLAE EI ESS AQYKA-----R VALENDR SEEEKYTA VQRNSSERE-----GH	483
scPBP1	LQE AERI AK EIES QGT SGNIH I AE DR GI IIDDS GLDEEDLYSGVD RR GD ELLA ALKS NSK	311
	. *:.:*:****.. : :.... **. *:.*:*. . . *	
hsATXN2	SINTRENKYIP PGQRNR EVISWGSGRQNSPRMGQP GS GSMPSRSTSHT SD FN PNSGSD QR	543
scPBP1	PNSN KG NR Y VPPT LR QQPH ----- M-D----- PAI ISS ---- NSN KN EN	347
	.. : *:*:* * : : * : * : * **.....	
hsATXN2	VVNGGVPW PS PC PSP SR PP SRY QS GP NSLP RA ATPTR PPPSRPPSRPSRPPSH PSAHGS	603
scPBP1	AVSTD TSTP AAAGAPEG KP PQKTSKNK KSLS-----	378
	*. . . . * : . :*...**: . . . : **	
hsATXN2	PAPVSTM PK RMS SEGPPRM SP KAQRHP RNHR VSAGRGIS SG LEFV SHNP PSEAATPPVA	663
scPBP1	-----SKEAQ IEELKKFSEK-----FKVP--	397
	: ...*.. :* .: . *	
hsATXN2	RTSPSGGTWSSV SVGP RLSPKTHRPRS PRQNSIGNTPSG PV LASPQA GI IPT EA VAMPI	723
scPBP1	-----YDI PKDMLEV LKRSS STLKSN SSLPPK PI SKTPSAK-----	433
	.*: . . : * :* .. * * : :*.*	
hsATXN2	PAASPTPAS PAS NRA VTPS SEA KDSLQDQRONS--PAGNKENIKPNETSP SF S KAENKG	781
scPBP1	-----TVSPTTQ ISAGKSESRRSGSNSIQQSSTGH TTRSSTSLRRR-NHG	478
	:*:*::: . . . :*:*. * *.... : . :.* *: : *.*	
hsATXN2	ISPVVSEHRKQ IDDLK--KFKNDFRLQPSSTSES MDQLLNKNREG EKSRDL IKDKIEPSA	839
scPBP1	--SFFGAK NP HTNDA KRVLFGKSFNMFIKSKE-A----HDEKKKGDD----ASE NM EP --	525
 : * * * :* : * : :***: :***	

hsATXN2	KDSFIENSSSNTSGSSKPNSPSISPSILSNTEHKRGPEVTSQGVQTSSPACKQEKDDKE	899
scPBP1	--FFIEKPYF-----TAPTWLNTIEESY-----KTFFP----DED--T	555
	***: *: *..*.. :* * ::*	
hsATXN2	EKKDAAEQVRKSTLNP---NAKEFNPRSFSQPKPSTTPTSPPRQAQPSPSMVGHQQP---	953
scPBP1	AIQEAQTRFQQRQLNSMGNAPGMNPAMGMNMGMMGFPMGGPSASPNPMMNGFAAGSMG	615
	::* ::: ** . :** : *.*.*.* * *.	
hsATXN2	--TPVYTQPVCFAPNMMYPVPVSPGVQPLYPIPMTPMPVNQAKT--YRAVPNMPQQRQDQ	1009
scPBP1	MYMPFQPPMFYHPSMPQMPVM-----GSNGAEEGGNISPHVP-----	655
	*. **.: *.* :** * *: . *::*	
hsATXN2	HHQSAMMHPASAAGPPIAATPPAYST-----QYVAYSPQQFPNQPLVQ----HVPHYQ--	1058
scPBP1	---AGFMA--AGPGAPMGAF--GYPGGIPFQGMMSGPSGMPANGSAMHSHGHSRNYHQT	708
	:::* :. * *:. * .* :. *.: * : * :**	
hsATXN2	SQHPHVYSPVIQGNARMMAPPTHAQPGLVSSSATQYGAHEQTHAMYACPKLPYNKETSPS	1118
scPBP1	SHHGHHNSS-TSGHK-----	722
	: * * .*:	
hsATXN2	FYFAISTGSLAQQYAHPNATLHPHTPHQPSPATPTGQQQSQHGGSHPAPSPVQHHQHQA	1178
scPBP1	-----	722
hsATXN2	QALHLASPQQQSAIYHAGLAPTPPSMTPASNTQSPQNSFPAAQQTVFTIHPSHVQPAYTN	1238
scPBP1	-----	722
hsATXN2	PPHMAHVPAHVQSGMVPSHPTAHAPMMLMTTQPPGGPQAALAQSAIQPIPVSTTAHFPY	1298
scPBP1	-----	722
hsATXN2	MTHPSVQAHHQQL	1312
scPBP1	-----	722

[illegible]

hsUBQLN2	MAENGESSGPPRSPRGPAAAQGSAAAPAEPKIIKVTVPKEKEEFVAVPENSSVQQFKEA	60
scDSK2	-----MSLNIIHKSGQDKWEVNVAPESTVLQFKEA :: : * : * . * :* * *****	30
hsUBQLN2	I SKRFKSQTDLVLIFAGKILKDQDTLIQHGIHDGLTVHLVIKSQNRPQGQSTQPSNAAG	120
scDSK2	INKANGIPVANQRLLIYSGKILKDDQTVESYHIQDGHSVHLVKSQ-PKPQTASAAGANNAT *. * : ** ::*****: *: .: ***: ***** .. :** *: : * *	89
hsUBQLN2	TNTTSASTPRSNSTPISTNSNPFGLSLGGLAGLSSLGL--SSTNFSELQSQMQQQLMA	177
scDSK2	ATG---AAAGTGATPNMSSGQSAGFNPLADLTSAFYAGLYNMPSADMFGPDGGALNNDSN :. :: .:** :..: *: . *.**.. * *::: :. ::	146
hsUBQLN2	SPEMMIQIMENPFVQ----SMLSNPDLMRQLIMANPMQMQOLI-----QRNPEISHLLNN	227
scDSK2	NQDELLRMENPI FQSQMNEMLSNPQMLDFMIQSNPQLQAMGPQARQMLOSPMFRQMLTN . : :::****.* .*****::: : * :***:* : :. * : :*. *	206
hsUBQLN2	PDIMRQTLEIARNPAMMQEMMRNQDLALSNLSEIPGGYNALRRMYTDIQEPMLNAAQE QF	287
scDSK2	PDMIRQSMQFARMMDPNAGMG-----SA **::**::::** *	229
hsUBQLN2	GGNPFASVGSSSSSGEGTQP SR TENRDLPNPWAPP PAT QSATTSTTTSTGSGSGNSSS	347
scDSK2	GGA-----ASAFPAPGGDAPEE GS N T N T S S N T G N N A G T N A G ** . : * * . * * . . * : : . . * . . *	267
hsUBQLN2	NATGNTVAAAANYVASI-----FSTPGMQSL LQ QITENPQLIQNMLSAPYMRSM MQ SL S	400
scDSK2	TNAGANTAANPF-ASLLNPALNPFANAGNAASTGM PAFDPALLASMFP FP VQA----- . :* ..** : **: *: . * : : * * : .*: . *	319
hsUBQLN2	QNPDLAAQMMLNSPLFTANPQLQEQMRPQLPAFLQQMQNP D T L S A M S N P R A M Q A L M Q I Q Q	460
scDSK2	-----	319
hsUBQLN2	GLQTLATEAPGLIPSFTP GVGV GLTAIGPVGP VT P IG PI GP IV P FT P IG PI GP IPTG	520
scDSK2	-----	319
hsUBQLN2	PAAP PG STGSGGPTGPTVSSAAPSETTSPTS ESG PN QQ FI QQ MV QAL AG AN AP QL NP EV	580
scDSK2	-----SQAEDTRPTEE :: * : **	330
hsUBQLN2	RFAQQLEQLNAMGFLNR EANLQ ALI ATGGDINA AIER LLGSQ PS	624
scDSK2	RYEHQLRLND MGFFDFDRNVAA LR SG SVQ GALDSL NGDV-	373
	:::*.*** ****:: : * : * * :*.**:*: : * . :	

2-8: CLUSTAL O(1.2.4) multiple sequence alignment **[ALS16]**

```

hsSIGMAR1      MQWAVGRRWAWAALLLAVAAV-LTQVVWLWLGTQSFVFQREEIAQLARQYAG--LDHEL 56
scERG2         -----MKFFPLLLLLIGVVGYIMNVLFTTWLPT-NYMFDPKTLNEICNSVISKHNAEGL 53
                ::      **:.*. . . . .  ** * .::*: : : : : . . . . .  . *

hsSIGMAR1      AFSRLIVELRRLHPG-----HVLPEELQWVFVNAGGWMGAMCLLHASLSEYVLLFGTAL 111
scERG2         STEDLLQDV RDALASHYGDEYINRYVKEEWVFNNAGGAMGQMIILHASVSEYLILFGTAV 113
                : . *: ::* . . . . . : : : : *** ** ** * :***:***:***:***:
                : . *: ::* . . . . . : : : : *** ** ** * :***:***:***:***:

hsSIGMAR1      GSRGHSGRYWAEISDTIISGTFHQWREGTTKSEVFYPGETVVHGPGEATAVEWGPNTWMV 171
scERG2         GTEGHTGVHFADDYFTILHGTQIAALPYATEAEVYTPGMTHHLKKG YAKQYSMPGGSFAL 173
                *:***:***:***:***:***:***:***:***:***:***:***:***:***:***:
                *:***:***:***:***:***:***:***:***:***:***:***:***:***:

hsSIGMAR1      EYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLRLELTT-YLFGQDP 223
scERG2         ELAQGWIPCM L PFGFLDTFSSTLDLYTLRTVYLTARDMGKNLLQNKKF---- 222
                * .: * ** . * *: ** . ** *: ** *: *: **.: : * *

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2-9: CLUSTAL O(1.2.4) multiple sequence alignment [ALS17/ALS-FTD7]

hsCHMP2B	---MASLFKK-KTVDDVIKEQNRELRGTRAIIRDRAALEKQEKQLELEIKKMAKIGNKE	56
scDID4	MSLFEWVFGKNVTPQERLKKNQRALERTQRELEREKKLELQDKKLVSSEIKKSAKNGQVA	60
	: : * * * : : : : * * . *** : * : : * * * : * : * * * * * :	
hsCHMP2B	ACKVLAKQLVHLRKQKTRTFVSSKVTSMSTQTKVMNSQMKMAGAMSTAKTMQAVNKKM	116
scDID4	AAKVQAKDLVTRNYIQKFDNMKAQLQAISLRIQAVRSSDQMTRSMSEATGLLAGMNRTM	120
	* . ** ** : ** : * : : : : : * : : . . * . : * : ** : : : . : * . *	
hsCHMP2B	DPQKTLQTMQNFQKENMKMEMTEEMINDTLDDIFD-GSDDEEESQDIVNQLVDEIGIEIS	175
scDID4	NLPQLQRISMFEFEKQSDLMGQRQEFMDEAIDNVMGDEVDEDEEAEIVNKVLDEIGVDLN	180
	: : : : * : * : . * : * : : : * : : . * : * : : : * * . * * * * : : .	
hsCHMP2B	GKMAKAPSAARSLPSASTSKATI-----SDEEIERQLKALGVD-	213
scDID4	SQLOSTPQNLVSNAPIAETAMGIPEPIGAGSEFHGNPDDDLQARLNTLKKQT	232
	. : : . : * . * : : * * : : : : * : * : * : :	

2-10: CLUSTAL O(1.2.4) multiple sequence alignment **[ALS18]**

hsPFN1	MAGWNAYIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGVLVGK--DRSS	58
scPFY1	-MSWQAYTDNLIGTGKVDKAVIY-SRAGDAVWATSGGLS---LQPNEIGEIVQGFDNPAG	55
	.*: ** ***:. *. :.*.* :. :. :***: * : : * *:* :* : :.	
hsPFN1	FYVNGLTLLGGQKCSVIRDSLLQDGEFSMDLRTKSTGGAPTFNVTVTKTDLVLLMGKEG	118
scPFY1	LQSNGLHIQQQKFMLLRADDR-----SIYGRHDA-----EGVVCVVRTKQTVIIAHYPPT	104
	: *** : *** :.* . * : * .: .*. .:*.*:*:::	
hsPFN1	VHGGLINKKCYEMASHLRRSQY	140
scPFY1	VQAGEATKIVEQLADYLIGVQY	126
	*:. * .* :.*.* **	

Sequence	Score
hsHNRNPA1 sCHRP1	0 60
hsHNRNPA1 sCHRP1	0 120
hsHNRNPA1 sCHRP1	35 180
hsHNRNPA1 sCHRP1	95 239
hsHNRNPA1 sCHRP1	155 293
hsHNRNPA1 sCHRP1	215 339
hsHNRNPA1 sCHRP1	253 399
hsHNRNPA1 sCHRP1	281 459
hsHNRNPA1 sCHRP1	330 508
hsHNRNPA1 sCHRP1	372 534

hsTUBA4A	MRECISVHVQGAGVQMGNACWELYCLEHGIQPDGQMPSDK-TIGGGDDSFSTFFFCETGAG	59
scTUB1	MREVISINVGQAGCQIGNACWELYSLEHGIKPDGHLEDGLSKPKGGEFGSTFFFHETGYG	60
	*** **::***** *:*****.*****:***::.. . *:::*:*** ** *	
hsTUBA4A	KHVPRAVFDLEPTVIDEIRNGPYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDPVL	119
scTUB1	KFVPRAIYVDLEPNVIDEVRNGPYKDLFHPEQLISGKEDAANNYARGHYTVGREILGDVL	120
	*.****::*****.*****:*****:*****:*****:*****:*****:***:*. **	
hsTUBA4A	DRIRKLSDQCTGLQGFLVFHSGGGTSGSFTSLLMERLSVDYGKSKLEFSIYPAPQVST	179
scTUB1	DRIRKLADQCDGLQGFLFTHSLGGGTSGSLGSLLEELSAEYGGKSKLEFAVYPAPQVST	180
	*****:*** *****. **:*** ***: ***:*.**.:*****:*****	
hsTUBA4A	AVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRNLNLDIERPTYTNLNRLISQIVSSIT	239
scTUB1	SVVEPYNTVLTTHTTLEHADCTFMVDNEAIYDMCKRNLDIRPSPFANLNLIQVSSVT	240
	:*** ***: :*****: **:*****:*. ***: ***: ***: ***: ***: *	
hsTUBA4A	ASLRFDGALNVDLTFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEP	299
scTUB1	ASLRFDGSLNVDLNEFQTNLVPYPRIHFPLVSYSPLSKSKAFHESNSVSEITNACFEP	300
	*****.*****.*****:*****:***:*. ***: ***: ***:*****.	
hsTUBA4A	NQMVKCDPRHGKYMACCLLYRGDVPKPDVNAAIAIKTKRSIQFVDWCPTGFKVGINYQP	359
scTUB1	NQMVKCDPRDGKYMATCLLYRGDVTTRDQRAVEQVKNKKTQVLVDWCPTGFKIGICYEP	360
	*****.***** ***** ***: ***: :*.**.:*:*****:*** *:*	
hsTUBA4A	PTVVPGGDLAKVQRAVCMLSNNTTIAIEAWARLDHKFDLMYAKRAVHVYVGEEMEEGEFS	419
scTUB1	PTATPNSQLATVDRAVCMLSNNTTSIAEAWKRIDRKFDMYAKRAVHVYVGEEMEEGEFT	420
	*. *.**.:**.:*****. ***** *:*.*****:*****:*****:	
hsTUBA4A	EAREDMAALEKDYEEVGIDSYEDEDEGEE	448
scTUB1	EAREDLAALERDYIEVGADSYAEEEEF--	447
	*****:***** *** *** *** ***: *	

2-12 (continued): CLUSTAL O(1.2.4) multiple sequence alignment **[ALS22]**

hsTUBA4A	MRECISVHVGQAGVQMGNACWELYCLEHGIQPDGQMPSDK-TIGGGDDSFSTFFCETGAG	59
scTUB3	MREVISINVGQAGCQIGNACWELYSLEHGIKEDGHLEDGLSKPKGGEFGSTFFHETGYG	60
	*** **.:***** *:*****.*****: **: :. . **.:*:* ** *	
hsTUBA4A	KHVPRAVFVDLEPTVIDEIRNGPYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDPVL	119
scTUB3	KFVPRAIYVDLEPNVIDEVRTGRFKELFHPEQLINGKEDAANNYARGHYTVGREIVDEVE	120
	*.*****.:*****.*****:*.* :.:*****.*****:***:* *	
hsTUBA4A	DRIRKLSdqCTGLQGFLVFHSGGGTSGSFTSLMERLSVDYGKKSKEFSIYPAPQVST	179
scTUB3	ERIRKMADQCDGLQGFLFTHSLGGGTGSGLSLLENLSYEYGKKSKEFAVYPAPQLST	180
	:****.:*** *****. **:*** ***: **:*.* ** :*****.:*****:***	
hsTUBA4A	AVVEPYNSILTHTTLEHSDCAFMVDNEAIYDICKRNLDIRPTYTNLNRLISQIVSSIT	239
scTUB3	SVVEPYNTVLTHTTLEHADCTFMVDNEAIYDICKRNLGISRPSFSNLNGLIAQVISSVT	240
	:*****.:*****.***:*****:***.*.* **.:*** ***:***:***:*	
hsTUBA4A	ASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEP	299
scTUB3	ASLRFDGSLNVDLNEFQTNLVPYPRIHFPLVSYAPILSKKRATHESNSVSEITNACFEP	300
	*****:*****.*****:*****:***:* **.* ***:*****.	
hsTUBA4A	NQMVKCDPRHGKYMACCLLYRGDVVPKDVNAIAAIAIKTKRSIQFVDWCPTGFKVGINYQP	359
scTUB3	NQMVKCDPTKGKYMANCELYRGDVVTRDVQRAVEQVKNKKTVMVDWCPTGFKIGICYEP	360
	***** :***** *****:***: *: :*.***:***:*****:*** *:*	
hsTUBA4A	PTVVPGGDLAKVQRAVCMLSNNTAIAEAWARLDHKFDLMYAKRAVHWYVGEEMEEGEFS	419
scTUB3	PSVIPSSSELANVDRAVCMLSNNTAIAADAWKRIDQKFDLMYAKRAVHWYVGEEMEEGEFT	420
	:.*.:***:***:*****:***.**:***:*****:*****:*****:	
hsTUBA4A	EAREDMAALEKDYEVEGIDSYEDEDEGEE	448
scTUB3	EAREDLAALERDYIEVGADSYAEFF----	445
	*****:*****.* ** *	

2-13: CLUSTAL O(1.2.4) multiple sequence alignment [ALS25]

hsKIF5A	-----MAETNNECSIKVLCRFRPLNQAEIL----RGDKF--IPIFQG	36
scSMY1	MHWNIISKEQSSSVSLPTLDSSEPCHIEVILRAIPEKGLQNNESTFKIDPYENTVLFRT	60
	::: * *: * * : : : * : :::	
hsKIF5A	D----DSVVIGGKPYVFDVFPNTTQEQVYHACAMQIVKDVLAGYNGTIFAYGQTSSGK	92
scSMY1	NNPLHETTKETHSTFQFDKVF DANATQEDVQKFLVHPIINDVLNGYNGTVITYGPSFSGK	120
	: ::. : *: ** *: ***: * : * : ** * : ** * : ** *	
hsKIF5A	THTMEGKLHDPQLMGIIPRIARDIFNHIYSMDE--NLEFHIKVSFYFEIYLDKIRDLLDVT	150
scSMY1	SYSLIGSK---ESEGILPNICKTLFDTLEKNEETKGDSFSVSVLAFEIYMEKTYDLLVPL	177
	::: * : *: *. * : : : : : * . * : * * : * : * *	
hsKIF5A	KTN--LSVHEDKNR--VPFVKGCTERFVSSPEEILDVIDEGKSNRHVAVTNMNEHSSRSRSH	206
scSMY1	PERKPLKLRSSSKMDLEIKDICPAH-VGSYEDLRSYIQAVQNVGNRMACGDKTERSRSRSH	236
	. *: *. * : : : . * : * * * : . * : : . : : . * * *	
hsKIF5A	SIFLINIKQENMETEQKLSGKLYLVDLAGSEKVSKTGAEGAVLDIAKNINXLSLSALGNVI	266
scSMY1	LVFQLHVEQRNRKDDILKNSSLYLVDLHGAEKFDKRTESTLSQDALKKLNQSIEALKNTV	296
	: * : : : * * : : . . * * * * * * : * * . * * : * : * * * * : :	
hsKIF5A	SALA-----EGTKSYVPYRDSKMTRILQDSLGGNCRTTMFICCSPPSSYNDAETKST	317
scSMY1	RSLSMKERDSAYSAGKSHSSAYRESQLTEVLKDSLGGNRKTKVILTCFLSNVP--TTLST	354
	: * : . *: * : : : * : * * * * : * : : : * * * *	
hsKIF5A	LMFGQRAKTIKNTAS-----VNLELTAEQWKKKYEKEKEKTKAQKETIAKLEAELSRWR-	371
scSMY1	LEFGDSIRQINNKVTDNTTGLNLKKKMDLFIQDMKIKDDNYV---AQINILKAEIDSLKS	411
	* * * : : * * * : : * * : . : : : . : : : * * * * : . :	
hsKIF5A	-NGENVPETERLAGEEAALGAELCEETPVNDNSSIVVRIAPEERQKYEEE---IRRLYKQ	427
scSMY1	LHNKSLPEDDE-----KKMLN-TKKENIKLKLQLD SITQLLSS	449
	: : : : * * : . . : : . : : * . * : : * * * . .	
hsKIF5A	LD--DKDDEINQQ-SQLIEKLKQQMLDQEELLVSTRGDNEKVQREL SHLQSENDAAKDEV	484
scSMY1	STNEDPNNRIDEEVSEILTKRCEQIAQLELSFDRQMNSNSKLQOELEYKKSKEEA----	504
	* : . * : : : * : : : * : . . * . * : * : : : * : : : *	
hsKIF5A	KEVLQALEELAVNYDQ---KSQEVEEKSQQNQLLVDELSQKV-----ATMLSLESEL	533
scSMY1	-----LESMNVRLLLEQIQLOEREIQELLTNAILKGELETHTKLTETRSEIRIKSLESSV	558
	* * : * . : : : : : * * * * . * * : . : * * * : :	
hsKIF5A	QRLQEVSGHQKRKRIAEVLNGLMKDLSEFSVIVNGEIKLPVEISGAIEEEFTVARLYISK	593
scSMY1	KELSL---NKSALPSPRRGSMSS-----SSGNTMLHIEEGSEISNSP-----WSAN	601
	: . * : : . * . * * * . . . * : * * * . . * : . : : :	
hsKIF5A	IKSEVKS VVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQHEAKIRSLTEYMQSVELK	653
scSMY1	--TSSKPLVWGARKVSSSS-----IATTGSQES----F-----VAR---PFKKGL---	637
	: . * * * * : : . . : . * * : * : * : : :	
hsKIF5A	KRHLEESYDSLDELAKLQAQETVHEVALKDKEPDTQDADEVKALELQMES HREAHHRQ	713
scSMY1	-----NLHSIKVTSSTPKSPSSGS-----	656
	. : * : : . . . * : . : . .	
hsKIF5A	LARLRDEINEKQKTIDELKDLNQKLQLELEKLQADYEKCLKSEHEKSTKLQELTFLYERH	773
scSMY1	-----	656
hsKIF5A	EQSKQDLKGLEETVARELQTLHNLKFLVQDVTRVKKSAEMEPEDSGGIHSQKQKISFL	833
scSMY1	-----	656

hsKIF5A	ENNLEQLTKVHKQLVRDNADLRCELPKLEKRLRATAERVKALEGALKEAKEGAMKDKRRY	893
scSMY1	-----	656
hsKIF5A	QQEVDRIKEAVRYKSSGKRAHSAQIAKPVRPGHYPASSPTNPYGTRSPECISYTNSLFQN	953
scSMY1	-----	656
hsKIF5A	YQNLYLQATPSSTSDMYFAN ^S CTSSGATSSGGPLASYQKANMDNG ^N ATDINDNRSDLPCG	1013
scSMY1	-----	656
hsKIF5A	YEAEDQAKLFPLHQETAAS	1032
scSMY1	-----	656

2-14: CLUSTAL O(1.2.4) multiple sequence alignment **[ALS26]**

hsTIA1	-----	0
scPUB1	MSENNEEQHQQQQQQPVAVETPSAVEAPASADPSSEQSVAVEGNSEQAEDNQGENDP	60
hsTIA1	-----MEDEMPKTLVYVGNLSRDVTEALILQLFSQIGPCKNCKMIMDTA-GNDPYCFV	51
scPUB1	VPANAITGGRETSDRVLYVGNLDKAITEDILKQYFQVGPIANIKIMIDKNNKNVNYAFV	120
	.: :.*****.: **: :. * *. ** * *: :. * *.**	
hsTIA1	EFHEHRHAAAALAAMNGRKIMGKEVKVNWATTPSSQKKTSSSTVVSTQRSQDHFHVFVG	111
scPUB1	EYHQSHDANIALQTLNGKQIENNIVKINWAFQSQQ-----SSDDTFNLFVG	167
	.: :.* ** :*: :. :. **:*** .. . *.* *: :***	
hsTIA1	DLSP EITTEDIKAAFAPFGRISDARVVKDMATGKSKGYGFVSFFNKWDAENAIQQMGGQW	171
scPUB1	DLNVNVDDETLRNAFKDFPSYLSGHVMWDMQTGSSRGYGFVSFTSQDDAQNAMDSMQGD	227
	.: : * :. * * ..*: ** *.*:***.: **:***:.* **	
hsTIA1	LGGRQIRTNWATRKPPAPKSTYESNTK-----	198
scPUB1	LNGRPLRINWAAKRDNNNNNNYQQRNRYGNNNRGGFRQYNSNNNNNMGMNMNMNMNMN	287
	. : * ***: : :..*.: :	
hsTIA1	-----QLSYDEVVNQSSPSNCTVYCGG	220
scPUB1	NSRGMPPSSMGMPIGAMPLPSQGQPQQSQTIGLPPQVNPQAVDHIIRSAPPRVTAYIGN	347
	: *. : : : * *. * *	
hsTIA1	VTSGLTEQLMRQTFSPFGQIMEIRVFPDKGYSFVRFNHESAAHAIVSVNGTTIEGHVVK	280
scPUB1	IPHFATEADLIPLFQNFQFILDFFKHYPEKGCCFIKYDTHEQAAVCIVALANFPFQGRNLR	407
	: ** : *. ** *: : : :*:** .*: : : :*.** .*: : . :*: : :	
hsTIA1	CYWGETLDMINPVQQNQIGYPQPYGQWGQWYGNAQQIGQYMPNGWQVPAYGMYGQAWN	340
scPUB1	TGWGKERSNFMPQQQQQGG--QPLIMNDQ-----QQPVMSEQQQQQQ	447
	**** : : : ***. * .: * *. . * :	
hsTIA1	QQGFNQTSAPWMGPNYGVQPPQGQNGSMLPNQPSGYRVAAGYETQ	386
scPUB1	QQ--QQQQ-----	453
	** : * *	

2-15: CLUSTAL O(1.2.4) multiple sequence alignment **[ALS27]**

hsSPTLC1	-----MATATEQWVLVEMVQA-----LYEAPAYHLILE	28
scLCB1	MAHIPEVLPKSIPIPAFIVTTSSYLWYYFNLVLTQIPGGQFIVSYIKKSHHDDPYRTTVE	60
	::*: * .:*: :	
hsSPTLC1	GILILWIIRLLEFSK---TYKLQERSDLTVKEKEELIEEWQPEPLVPPVPKDHPALNYNI	84
scLCB1	IGLILYGIIYYLSKPQQKSLQAQKPNLSPQEIDALIEDWEPEPLVDPSATDEQSWRV--	118
	: * .:** .:*: *: : ***:*.** * .*. : .	
hsSPTLC1	VSGPPSHK-----T-----VVNGKECINFASFNFLGLLDNPRVKAAALASLKKYGVG	131
scLCB1	AKTPVTMEMPIQNHITITRNNLQEKYTNVFNLASNNFLQLSATEPVKEVVKTTIKNYGVG	178
	.. * : : * : .: :*.** *** * . ** .. :*:**.*	
hsSPTLC1	TGPRGFYGTFDVHLDLEDRLAKFMKTEEAIISYGFATIASAIPAYSKRGDIVFVDRAA	191
scLCB1	ACGPAGFYGNQDVHYTLEYDLAQFFGTQGSVLYGQDFCAAPSVLPFAFTKRGDVIVADDQV	238
	:*** ***. ** ** **.*: *: :*:*. .*: *.:***:***:..* .	
hsSPTLC1	CFAIQKGLQASRSDIKLFKHNDMADLERLLKEQEIEDQKNPRKARVTRRFIVVEGLYMNT	251
scLCB1	SLPVQNALQLSRSTVYYFNHNDMNSLECLLNELTE-QEKLEKLPaiprkFIVTEGIFHNS	297
	.: :*:** *** : *:***. ** **.* :~* : : *:***.**:~* :	
hsSPTLC1	GTICPLPELVKLKYKYKARIFLEESLSFGVLGEHGRGVTEHYGINI-DDIDLISANMENA	310
scLCB1	GDLAPLPELTKLKNKYKFRLFVDETFSIGVLGATGRGLSEHFNMDRATAIDITVGSMTA	357
	* .:*****.*** *** *:~*:~*:~*:~* ***:~*:~*:~* **~* ..* .*	
hsSPTLC1	LASIGGFCCGRSFVIDHQRLSGQGYCFSASLPPLAAAAIEALNIMEENPGIFAVLKEKC	370
scLCB1	LGSTGGFVLGDSVMCLHQRIQSNAYCFSACLPAITVTSVSKVLKLMSNNDVQTLQKLS	417
	. *** * *.~* ***:~*:~*:~* ... :~*:~*:~* ..*~* .	
hsSPTLC1	GQIHKALQGISGLK---VVGESLSPAFHLQLEESTGSREQ-----	407
scLCB1	KSLHDSFASDDSLRSYVIVTSSPVSAVLHLQLTPAYRSRKFGYTCEQLFETMSALQKKSQ	477
	.:~*:~* . .~*: *... :~* .:***~* : **~*	
hsSPTLC1	-----DVRLLQEIVDQCMNR-SIALTQARYLEKEEKCLPPPSIRVVVTVEQTEEE	456
scLCB1	TNKFIEPYEEEEKFLQSIVDHALINYNVLITRNTIVLKQETLPIVPSLKICNAAMSPEE	537
	: :~*:~*.***:~* . .:~*: :~*:~* ***:~* .. :~*~*	
hsSPTLC1	LERAASTIKEVAQAVLL----	473
scLCB1	LKNACESVKQSILACCQESNK	558
	:~..:~*:~* *	

2-16: CLUSTAL O(1.2.4) multiple sequence alignment **[FTD-ALS2]**

```
hsCHCHD10      MP--RGSRSAA--SRPASRPAAP----SAHPPAHPPPSAA---APAPAPSGQPGLMAQMA 49
scMIX17        MARSRGSSRPISRSRPTQTRSASTMAAPVHPQQQQPNAYSHPPAAGAQTROPGMFAQMA 60
               *   ***           ***:.   :*           .**   :   *. *           * *   :   ***.:****

hsCHCHD10      TTAAGVAVGSAVGHVMGSSALTGAFSGGSSEPSQPAVQQAPTPA-----APQPLQMGPCAY 104
scMIX17        STAAGVAVGSTIGHTLGAGITGMFSGSGSDSAPVEQQQQNMANTSGQTQTDQQLGRTCEI 120
               :*****GS:**.:GS:.:** ***..*: :   **           :           *

hsCHCHD10      EIRQFLDCSTT-QSDLSLCEGFSEALKQCKYYHGLSSLP           142
scMIX17        DARNFTRCLDENNGNFQICDYQLQQLKACQEAAARQY---           156
               :  *: *   *   :.:.:.*: : :  ** *:
```


2-17: CLUSTAL O(1.2.4) multiple sequence alignment [FTD-ALS5]

hsCCNF	-----MGSGGVVHCRCAKCFCYPTKRRIRRRPRNLTILSLPEDVLFHILKWLSVEDILAV	55
scCLN1	MNHSEVKTGLIVT---AKQTYYPIELS-----NAELLTHY---E-----TI	35
	: :* :* ** ** : : * *	
hsCCNF	RAVHSQLKDLVDNHASVWACASFQELWPSPGNLKLFERAAEKGNFEEAVKLGIAIYLYNEG	115
scCLN1	QEYHEEISQ-----NVLVQS-SKTKPDIKLIDQQPEMNPQH-TREAIVTFYQLS	83
	: * : . * . : : * * : : * . : : : : : * * : .	
hsCCNF	LSVSDEARAEVNG--LKASRFF-----SLAERLNVGAAPFIWLFIRPPWSVSGSCK	165
scCLN1	VMTRV-----SNGIFFHAVRFYDRYCSKRVLKQAKLVVGTCLWLAA-KTW---GGCNH	134
	: . ** : * * : * : : . . : * * * * *	
hsCCNF	AVVHESLRAECQLQRTHKASILHCLGRVLSLFEDEEKQQQAHDLFEEAAHQGC--LTSSY	223
scCLN1	IINNVS IPTGGRFYGPNPRARIPRLSELVH-----YCGGSDLFDESMFIQMERHILDT	187
	: : * : : : : : * * * * * * . .	
hsCCNF	LLWESDRR---TDVSDPGRCLHSFRKLRDY-----AAKGCWEAQLSLAKACANANQLGL	274
scCLN1	LNWDVYEPMINDYILNVDENCLIQELYKNQLQNNNSNGKEWSCK-----RKSQSSD	239
	* * : . : . * * . . : : : * . . : . * *	
hsCCNF	EVRASSE-IVCQLFQASQAVSKQQVFSVQKGLNDTMYIILIDWLVEVATMKDFTSLCLHL	333
scCLN1	DSDATVEEHISSPQSTGLDGDTTTMDDEDEELNSKIKLINL-----	280
	: * : * . . * : : : * * . . : * :	
hsCCNF	TVECVDRLRRRLVPRYRLQLLGIACMVICTRFISKE--ILTIREAVWLTD--NTYKYE	388
scCLN1	-----KRFLIDL--SCWQYNLLKFELYEICNGMFSIINKFTNQDQGPFLSMPIGNDINSN	333
	. * * : : * * : * * . : * : . . : * : *	
hsCCNF	DLVFMGEIVSALEGKIRV-PTVVDYKEVLLTLVPVELRTQHLC-----SFLCELSLL	440
scCLN1	TQTQVFSII---INGIVNSPPSLVEVYKEQYGIVPFILQVKDYNLELQKKLQLASTIDLT	390
	. : . . * : * : . * * * : : * * . * . . . : . . : *	
hsCCNF	-----HTSLSAYAPARLAAA---ALLLARLTHGQTQPWTTQ	473
scCLN1	RKIAVNSRYFDQNASSSSVSSPSTYSSGTNYTPMRNFSAQSDNSVFSTTNIDHSSPITPH	450
	: * : * * * * : : : * * :	
hsCCNF	LWDLTGFSYEDLIPCVLSLH---KKCFHDDAP--KDYRQVSLTAVKQRFEDKRYGEISQE	528
scCLN1	MYTFNQFKNESACDSAISVSSLPNQQTQNGNMPLSSNYQNMME---ERNKENRIPN---	503
	: : . . * . * . . : * : : : * . : * : : * : *	
hsCCNF	EVLSYSQALCAALGVTQDSPDPPTFLSTGEIHAFLSSPSGRRTKRKRENSLQEDRGSFVTT	588
scCLN1	-----SSSAEIPQRAKEMTTGIFQ-----	522
	. : : * : . * : * * : :	
hsCCNF	PTAELSSQEETLLGSFLDWSLDCCSGYEGDQSEGEKEGDVTAPSGILDVTVVYLNPEQH	648
scCLN1	-----	522
hsCCNF	CCQEESDEEACPEDKGPQDPQALALDTQIPATPGPKPLVRTSREPDKDVTTSYSSVSTA	708
scCLN1	-----	522
hsCCNF	SPTSSVDGGLGALPQPTSVLSLSDSHTQPCHHQARKSCLQCRPPSPPESSVPQQQVKRI	768
scCLN1	-----NTGELTNRASSISLSLRNHNSSQL-----	546
	. * * : : * * * . * . .	
hsCCNF	NLCIHSEEDMNLGLVRL	786
scCLN1	-----	546

2-17 (continued): CLUSTAL O(1.2.4) multiple sequence alignment **[FTD-ALS5]**

hsCCNF	MGSGGVVHCRCAKCFCYPTKRRIRRRPRNLTL-SLPEDVLFHILKWLSVEDILAVRAVH	59
scCLN2	-----MASAEPRPRMGLVINAKPDYYPIE-----	24
	. *** : : * : : .	
hsCCNF	SQLKDLVDNHASVWACASFQELWSPGNLKLFERAAEKGNFEEAVKLGIAIYLYNEGLSVS	119
scCLN2	-----	24
hsCCNF	DEARAEVNLKASRFFSLAERLNVGAAPFIWLFIRPPWSVSGSCCKAVVHESLRAECQLQ	179
scCLN2	-----	24
hsCCNF	RTHKASILHCLGRVLSLFEEDEEKQQQAHDLFEEAAHQGCLTSSYLLWESDRRTDVSDPGR	239
scCLN2	-----LSNAE	29
	. . .	
hsCCNF	CLHSFRKLRDYAAKGCWEAQSLAKACANANQLGLEVRASSEIVCQLFQASQAVSKQQVF	299
scCLN2	LLSHFEMLQEYHQEIST--NVIAQ-----SCKFKPNPKLIDQ----	64
	* * . * : * : . : * : * : : :	
hsCCNF	SVQKGLN-DTMRYLIDWLVEVATMKDFTSLCLHLTVECVDRLRRRLVPRYRLQLLGIA	358
scCLN2	--QPEMNPVETRNSNIITFLFELSVVTRVTNGIFFHSVRLYDRYCSKRIVLRDQAKLVVAT	122
	* : * * : * : * . : . : * . * : * * : : * : :	
hsCCNF	CMVICTRFISKEILTIREAVWLTNTYKYEDLVMMGEIVSALEGKIRVPTVVDYKEVLL	418
scCLN2	C-----LWLAAKTWGGCN--HIINNVVIPTGGRFYGPNPARR-----	157
	* : * : * : : : * : * : *	
hsCCNF	TLVPVELRTQHLCNFLCELSLLHTSLSAYAPARLAAAALLLARLTHGQTQPWTTQLWDLT	478
scCLN2	--IPRLSELVHYCGD--GQVFDE-----SMFLQ-M--ERHILDTLNWNIIY	195
	: * . * * . : . : : * : : : * * : :	
hsCCNF	GFSYEDLIPCVLSLHKKCFHDDAP-----KDYRQVSLTAV-KQRFEDKRYGEIS	526
scCLN2	EPMIND--YVLNVDENCLMQYELYENQVTYDKQCSEKRQSLSQSDATVDERPYQNEE	252
	: * * . : : * : : : : * : * . * : . : : * : :	
hsCCNF	-----QEEVLSYSQLCAALGVTQDSPDPPTFLSTGEIHAF	561
scCLN2	EEEEDLKLKIKLINLKKFLIDVSAWQYDLLRYELFEVSHGIF-----S-	295
	* : * * . : : * : :	
hsCCNF	LSSPSGRRTKRKRENSLQEDRGSFVTTPTAELSSQEETLLGSFLDWSLDCCSGYEGDQES	621
scCLN2	-----IINQFTNQDHGPFLLTTPMTSESKNGEIL-STLM-----	327
	: : : * * * : * : . * : * * . : :	
hsCCNF	EGEKEGDVTAPSGILDVT-----VVYLNPEQH	648
scCLN2	---NGIVSIPNSLMEVYKTVNGVLPFINQVKEYHLDLQRKLQIASNLNISRKLTISTPS	383
	: * * : * . : : *	
hsCCNF	CCQESSDEEACPEDK-----GPQDPQALALDTQIP--	678
scCLN2	CSFENSNSTSIPSPASSQSHTPMRNMSSLSDNSVFSRNMEQSSPITPSMYQFGQQQSNS	443
	* . * . * . : * . : * * . : . *	
hsCCNF	-----ATPGPKPLVRTSREPGKDVTTSGYSSV-----STA	708
scCLN2	ICGSTSVSVNSLVNTNNKQRIYEQITGPNSSNATNDYIDLNLNESNKENQNPATAHYLNG	503
	* . : : . * . : * . * . : .	
hsCCNF	SPTSSVDGGLGALPQPTSVLSLSDSDSHTQPCHHQARKSCLQCRPPSPPESSVPQQQVKRI	768
scCLN2	GPPKTSFINHGMFSPPTGTINSGKSSSASSL-----I	535
	. * . : . * : * . * . : . . * : . *	

hsCCNF	NLCIHSEEDMNLGLVRL-	786
scCLN2	-----SFGMGNTQVI	545
	.:.:* .:.	

2-17 (continued): CLUSTAL O(1.2.4) multiple sequence alignment **[FTD-ALS5]**

hsCCNF	MGSGGVVHCRCAKCFCYPTKRRIRRRPRNLTILSLPEDVLFHILKWLSVEDILAVRAVHS	60
scCLN3	-----	0
hsCCNF	QLKDLVDNHASVWACASFQELWPSPGNLKLFERAAEKGNFEEAAVKLGIAYLYNEGLSVSD	120
scCLN3	-----	0
hsCCNF	EARAEVNLKASRFFSLAERLNVGAAPFIWLFIRPPWSVSGSCCKAVVHESLRAECQLQR	180
scCLN3	-----	0
hsCCNF	THKASILHCLGRVLSLFEDEEKQQQAHLFEEAAHQGCLTSSYLLWESDRRTDVSDPGRC	240
scCLN3	-----MAILK-----DTIIRYANARYATASGTST- ::: .: : . * : . * .	24
hsCCNF	LHSFRKLRDYAAKGCWEAQLSLAKAC-----ANANQLGLEVRASS-----EI	282
scCLN3	----ATAASVSAASCPNLPPLLQKRRAIASAKSKNPNLVKRELQAHHSAISEYNNDQLDH . . : * . * : * * * * * : * : * :	80
hsCCNF	VCQLFQASQAVSKQQVFSVQKGLNDTMRYYILIDWLVEVATMKDFTSLCLHLTVECVDRYL	342
scCLN3	YFRLSHTERPLYNLTNFNSQPQVNPKMRFILFDFIMYCHTRLNLSTSTLFLTFTILDKYS :* : : : : : * . * : * . * : : : : : * : : : * . * . : : *	140
hsCCNF	RRRLVPRYRLQLLGIACMVICTRFISKEIL--TIREAVWLTDNTYKYEDLV R MMGEIVSA	400
scCLN3	SRFIKSYNYQLLSLTALWISSKFWDKSNRMATLKVQLNCCNQYSIKQFTTMMHFLFKS * : : * . * . * : : : * : : * * : : * * * . : : . * . . . :	200
hsCCNF	LEGKIRVP-TVVDYKEVLLTL-----VPVELRTQ-----	428
scCLN3	LDWSICQSATFDSYIDIFLFQSTSPSPGVLSAPLEAFIQQLALLNNAAGTAINKSSS * : . * * . . * : : * * : * *	260
hsCCNF	-----HLCSFLCELSLLHTSLSA-YAPARLAAAALLARLTHGQTQPWTTQLW	475
scCLN3	SQGPSLNINEIKLGAIMLCELASFNLELSFKYDRSLIALGAINLI--KLSLNYYNSNLW . : * * * : : . * * * : : * . * : . . : : : * *	317
hsCCNF	DLTGFSYEDLIPCVLSLHKKCFHDDAPKDYRQVSLTAVKQRFEDKRYGEISQEEVLSYSQ	535
scCLN3	ENINLAL EE-----NCQDL DIK-----LSEISNT----- : . : : * : * . * . * * :	341
hsCCNF	LCAALGVTQDSPD-PPTFLSTGEIHAFLSSPSGRRTKR----KRENSLQEDRGSFVTTPT	590
scCLN3	---LLDIAMDQNSFPSSFKS-----KYLNSNKTSLAKSLDALQNYCIQLKLEEFYRS-- * : : * . . * : * * : * . . * : : : * . . * : :	391
hsCCNF	AELSSQEETL-LGSFLDWSLDCCSGYEGDQES E GE R KEGDVTAPSGILDVTVVYLNPEQHC	649
scCLN3	QELETMYNTIFAQSFDSDSLTCVYSNATTPKS-----A-----TVSSAATDYFSDHHTL ** : : : : * * . * * . : . : . . . * : . . *	440
hsCCNF	CQESSDEEACPEDKGPQDPQALALDTQIPATPGPKPLVRTSRE-----PGK---DVTTS	700
scCLN3	RRLTKDISPPFAFTP-----T--SSSSSPSPFNSPYKTSSSMTTPDSASHHSHSG : . : * : * * : : . * : : : * . . . : . :	489
hsCCNF	GYSSVSTASPTSSVDGGLGALPQPTSVLSLSDSDSHTPCHHQAR-----KSCLQC	750
scCLN3	SFSST----QNSFKRSL-SIPQNSSIFWPSPLTPTPSLMSNRKLLQNLVRSKRLFPV .: * . . * . . * : : * : : . : * * . . * : :	543
hsCCNF	RPPSPPE-SSVPQQQVKRINLCIHSE-EEDMNLGLVRL	786
scCLN3	RPMTAHPCSAPTQLKKRSTSSVDCDFNDSSNLKKTR- * * : . . * . * * * . : : : : : : : * * . *	580