<html><head><style type="text/css"></style></head><body>CLUSTAL 2.1 multiple sequence alignment

humanCLN3	MGGCAGSRRRFSDSEGEETVPEPRLPLLDHQGAHWKNAVGFWLLGLCNNFSYVVMLSAAH	60
mouseCLN3	MGSSAGSWRRLEDSEREETDSEPQAPRLDSRSVLWKNAVGFWILGLCNNFSYVVMLSAAH	60
zebrafishCLN3	MDRSVNSG-TASTSDTEGRCQRWRNCVAFWLLGLCNNFAYVVMLSAAH	47
drosophilaCLN3	MTATKQQEAEAEHDPQVVVTPGDASRSSRQDRGLWRDLTSYWILGLCNNYGYVVMLSAAH	60
celegansCLN3	VAFWLLGLCNNFAYVVMLSAAK	
yeastCLN3	MSDKSHQIYCYFWLFGLINNVLYVVILSAAV	
уеавссииз	**************************************	31
humanCLN3		115
•	DILSHKRTSGNQSHVDPGPTPIPHNSSSRFDCNSVSTAAVLLADILPTLVIKLLA	
mouseCLN3	DILKQEQASGNQSHVEPGPTPTPHNSSSRFDCNSISTAAVLLADILPTLVIKLLA	
zebrafishCLN3	DILQ-KQESQN <mark>T</mark> TAPSPAPNGTNIEFRNSSNSS <mark>R</mark> YDCNPVSTAAVLLADILPTLLIKLTA	
drosophilaCLN3	DIIKQFNPNDE <mark>S</mark> EESSS <mark>G</mark> RNCHLVSTGAILLADVLPSLFVKILM	
celegansCLN3	DILEKDAKHIE <mark>K</mark> PCREHVT <mark>T</mark> RECQMMSTGSV <mark>L</mark> LADIIPALLIKITA	
yeastCLN3	DIVGDTLPKSLVLLADIFPSLAIKLCS	58
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humanCLN3	PLGLHLLPY <mark>S</mark> PRVLVSGI <mark>C</mark> AAGSFVLVAFSHSVGTSLCGVVF <mark>A</mark> SI <mark>S</mark> SGLGEVTFLSLTAF	175
mouseCLN3	PLGLHLLPY <mark>S</mark> PRVLVSGV <mark>C</mark> SAGSFVLVAFSQSVGLSLCGVVL <mark>A</mark> SI <mark>S</mark> SGLGEVTFLSLTAF	175
zebrafishCLN3	PFYIHKVPYGFRVLVCFFTAVVSFLMVSFSSTISMSIIGVIFASVSSGLGELSFLSLSVF	166
drosophilaCLN3	PFFPFWVNFRIALAVAFSAAGFLLVGFANAEWMALLGVIITSASSGIGETTFLAYSSR	162
celegansCLN3	PMF1HRVPFGIRHSIVVLLQASSFLIVGISDSTALALFGVVLASFGSGLGEISYLALSSN	
yeastCLN3	PFFIDRIKYSYRIWSLITMSCLGMFLVSFKN-LFVCLLGISFASISSGFGEVTFLQLTHY	
yeascchis		11/
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humanCLN3	YPRAVISWWSSGTGGAGLLGALSYLGLTQAGLSPQQTLLSMLGIPALLLASYFLLLT	232
mouseCLN3	YPSAVISWWSSGTGGAGLLGSLSYLGLTQAGLSPQHTLLSMLGIPVLLLASYFLLLT	
zebrafishCLN3	FSSDVLSGWGSGTGAAGVAGALLYSALTQAGLTPQVTLWIMLVVPVILAVSYFVLLV	
drosophilaCLN3	YNKNVISTWSSGTGGAGVIGSLSYASLRSLDFSPRDTMLIMLIFPAIEAFAFWLLLR	
celegansCLN3	YPSTVVASWSSGTGGAGLIGASAYALLTDSKLLAISPK <mark>H</mark> TMFIMLTLPALFSVSYWSILK	
yeastCLN3	YKQISLNGWSSGTGGAGIIGGASYMFLTSIFKVPVK <mark>L</mark> TLLVFSLLPFAFLFYFKLESN	175
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humanCLN3		274
	SPEAQDPGGEEEAESAARQPLIRTEAPESKPGSSSSLSLRER	
mouseCLN3	SPEPLDPGGENEAETAARQPLIGTETPESKPGASWDLSLQER	
zebrafishCLN3	FPHSFPQWRCPEVSQSLSRGLNSEERRALIEEDTDTDEDSEPALEDQDDKHIGPLTFTEK	
drosophilaCLN3	RPQDEKPLVGFKEK	
celegansCLN3	IPHSVQRAHFLQPSTWLVTGDFIPADDMRREEVEEEGLLGIRED	
yeastCLN3	DTNLTYQSLQQIDEAEDDQLVPFPVAFTHTNASQSLYSTRQHILQTVKR	224
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humanCLN3	WTVFKGLLWYIVPLVVVYFAEYFINQGLFELLFFWNT	
mouseCLN3	EYTVFKGLLWYIIPLVLVYFAEYFINQGLFELLFFRNT	311
zebrafishCLN3	KYIIKGLLKFIFPLALVYFAEYFINQGLMELLYFPDS	320
drosophilaCLN3	EYIKHLFKYMLPLCLVYFFEYFINQGLFELVYFED	286
celegansCLN3	RENSVDVTSRRRQTSTTLERVLPLLKFMIPLISVYLAEYYINQGLLELLEFDCSHG	304
yeastCLN3	LRRLVFPYMVPLTTVYLFEYLINQAVAPTLLFPINGDERSK	
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humanCLN3	SLSHAQQYRWYQMLYQAGVFASRSSLRCCRIRFTWALALLQCLNLVFLLADVW	364
mouseCLN3	SLSHAQQYRWYQMLYQAGVFASRSSLQCCRIRFTWVLALLQCLNLALLLADVC	364
zebrafishCLN3	RLSHAEQYRWYQTVYQIGVFVSRTSLFCFKIRKIFLMSLLQCANAVLLVFAVY	
drosophilaCLN3	IFLDKDSQYRWLNVDYQIGVFISRSSVNLFQLDKIWLMSIFQFVNVVYFLTEVI	
celegansCLN3	FSMSSESQYRWFQVTYQLGVFISRSSSNYVTIPTQYLKSLAVLQIFNAGFFTITAI	
yeastCLN3	SMPFFFHKYRDIYVTYGTLYQLGVFISRSFGHLMRMRSLYILAFLQGVNLCITVLQSW	
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humanCLN3	FGFLPSIYLVFLIILYEGLLGGAAYVNTFHNIAL <mark>E</mark> TSDEHREFAMAATCIS <b>D</b> TLGISL <mark>S</mark> G 424		
mouseCLN3	LNFLPSIYLIFIIILYEGLLGGAAYVNTFHNIAL <mark>E</mark> TSDKHREFAMEAACIS <mark>D</mark> TLGISL <mark>S</mark> G 424		
zebrafishCLN3	YQFLPNISVVFVIIAFEGLLGGAAYVNTFFFIRE <mark>E</mark> SVEREREFAMATATVG <mark>D</mark> SLGIAF <mark>S</mark> A 433		
drosophilaCLN3	WWYTPSIWIVFAIVLWEGLLGGGAYVNTFYRMSK <mark>E</mark> ISPERQQFAMAMVVQS <mark>D</mark> SYGIAL <mark>A</mark> G 400		
celegansCLN3	YSFLPHILIAFLVILFEGLLGGASYVNTFRAVHK <mark>E</mark> IPADSREFSMGVVSIS <mark>D</mark> TIGIVF <mark>A</mark> G 420		
yeastCLN3	FYVTHSPWAVMILIFYEGFLGGASYVNTFLNILE <mark>Q</mark> EDPDETEFAMGAVSIA <mark>D</mark> SFGVFL <mark>A</mark> A 383		
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humanCLN3	LLALPLHDFLCQLS 438		
mouseCLN3	VLALPLHDFLCHLP 438		
zebrafishCLN3	AAAFPVHHYFCSL 446		
drosophilaCLN3	FLAIPVHNAICGLPAAARSLVW 422		
celegansCLN3	FLAMPVHNRICSMPM 435		
yeastCLN3	LLGLGLEPKLCRHQIADDRPWCRME 408		
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