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1CJW_5107555 PANEFRCLTF-----EDAAGVFEIEREAFI-----SVSGNCPNLNDEVQH-FLTLCPELSLGWV--EGRLVAFIIGSLWDEERLQPSL----- 77
1BOB_4929920 EEFVVYKSSLV-----DDFARRMHRVQIFSLFI-----EAANYIDETD---PSWQIYVLLNKKTKELIGFVTTYKWHYLGAKSF----- 74
1QSM_6730553 SEDNITVRFVTE---NDKEGWQLWKSYPDFYVVSFF-----DLDLDFNFGRLDPLNI---KMW-AAVAVESSEKIIIGMINFFNMTTWD----- 79
1FY7_11513348 PGNEIYRDDYVSFF--EIDGRKRTWCRNLCLLKLFL-----DHKLLYDVD---PFLFYCMTRRDELGHHLVGYFSKEKESA----- 74
5GCN_5822577 GLLDFDILTND---DGTNRNMKLLIDLKNIFSRQLP-----KMPKEYIVKLVFD---RHESMVILKN-KQKVIIGICFRQYKPKQ----- 72
1YGH_5822444 -KIEFRVNN-----DNTKENMMVLTGLKNIFQKQLP-----KMPKEYIARLVYD---RSHLSMAVIRK-PLTVVGGIITYRPFDKR----- 71
1CM0_5542194 KVIEFHVVGNLNLQ--KPNKKILMWLVGLQNVFSHQLP-----RMPKEYITRLVFD---PKHKTALALIK-DGRVIGGICFRMFPFSQ----- 75
1BO4_3745773 GIIRICRLGPD-----QVKSMRAALDLGREFG-----DVATYSQHQPDSDYLNLLRSKTFIALAAFD--QEAVVGALAAAYVLPKFEQ----- 77
1B87_5542089 --MIISEF-DRN---NPLVKDQLSLLRLTWP-----EYGDSSA-EEVEE-MMNPER-IAVAADV-QDELVGFIGAIPOYGI----- 68
Ecol_Sc --KIVYVR--PDKSNGEVRAMTETMTL-----VNNELNAPHDENVIWNST-----TEEKGAFFVIR--NDRAVGIIIEENLYGGNGKTSRRGRVMV----- 81
Ecol_Sp --CIYSIN--SESSLIDQRKAEALS-----VNNELSSPETETIGV-----DKYTTFLFIS--DKKCVGLLLAERISSAYIVDELELNNNNST-----S 79
Ecol_Trypanosoma_brucei --CIHDAS-RTAMP-----RAREGCKIVGLC-VARELSAPH-----RMHCESNWSHE-KSEASVGAAVQEGLGDCWEHDATR----- 68
Ecol_Ce --KVYYLA--TFADGPFKKLFNHMKK-----INEELGYCDEKNDLWSP-----EKRIFLV-LSVRE-ERMLIGLIVIEKISRAWNVGKME----- 77
Ecol_Dm --RIIRIN--ERAPTARLDRLDLIGV-----VDKELGYSSYIV-----PKIFVAFIATR--KQIVGFCLVQPLSQAHRFIVDGT----- 71
Ecol_At_new --RIVMVS--ENDSPAHRNKVQEVVKM-----MEVELGEDWIL-----HQCKVYLFIS--SQRISGCLVAEPKKEAFKLIASPDDERQL----- 74
Ecolb_Hs_fragment --KIVLVL--PHDPSFAIKKVEDVQEL-----VDNLEGFQQVVPKC-----YSR-TKTLFLFISN-DKKVVGCLIAEHIQWGYRVIIEKLPVIRSEEKVRFE----- 70
Ecola_Hs_fragment --KIVLVL--PHDPSFAIKKVEDVQEL-----VDNLEGFQQVVPKC-----PNK-IKTLFLFISD-EKRVVGCILIAEPIKQAFRVLSEPIGPESSP-----TE 82
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120

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1CJW_5107555 -----ALHRFRGHS AHLHALAVHRSFRQQGKGVLLWRYLHHVG-AQP-----AVRRAVLMCED-----ALVPPYQRFQ- 140
1BOB_4929920 -----DEDIDKKFRAKISQFLIFPPYONKGGHSCLYEAIQSWL-EDK-----SITEITVEDP-----NEAFDDLRD- 135
1QSM_6730553 -----FKDKIYINDLVVDENS RVKGGKLIQFVYDEAD-KLG-----TPSVYWCIDE----- 126
1FY7_11513348 -----DGINVACILILPQYRMGYGKLLIEFSYELSK-KENKVGSPPEKPLSDLGLLSYRAYWSDTL----- 134
5GCN_5822577 -----RFAEVAVLAVTANEGVRGYGIRLMNFKDHHMQ-KQN-----IEYLLTYADN-----FAIGYFKKQG- 127
1YGH_5822444 -----EFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSN-----IKYFLTYADN-----YAIGYFKKQG- 127
1CM0_5542194 -----GFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHI-KHD-----ILNFLTYADE-----YAIGYFKKQG- 130
1BO4_3745773 -----PRSEIYIDLAVS GEHRRQGIATALINLLKHEAN-ALG-----AYVIYVQADY-----GDDP- 128
1B87_5542089 -----TGWELHPLVVESSRRKNQIGTRLVNYLEKEVA-SRG-----GITIYLGITDLDHGITLSTQTDLYEHTFDKVASIQNLRHPEYEFYEKLG- 151
Ecol_Sc YDSRRLVQNVYPDFKIGISRIWVCRTARKLGIAIKLIDVAREN-----IVY-GEVIPRY-----QVAW--SQPTDS--GGKLASKYNG 154
Ecol_Sp SAVYIKNENLRKCFVLGISRIWVSASRRKQGIASLLLDNALKK-----FIY-GYVISPA-----EVAF--SQPSES--GKQFIISWHR 152
Ecol_Trypanosoma_brucei ----VGCTNNVRKAFCGVQLVWVADCYRRHGVAKVLVDIARRH-----ISY-GFVVPVE-----RVAF--SEPTSL--GKLFAKSYSG 137
Ecol_Ce ----VTDNNDINDWIVGVDRIVWDSHCRMKGVANSLLDAAATQ-----DRQMEFRSRRL-----RIAF--CDPTDD--GIKLARRFIE 147
Ecol_Dm ----DYFSEESYPASCVSRIVVSPLORRSGIAIKLLRVVQCH-----TVL-GQEIARE-----CIAF--STPTDD--GRALARQFTG 140
Ecol_At_new DNGVIVCEEAKPAVCGIRAIWVSPSNRRKGIASWLLDTRES-----FCNNGMLES-----OLAF--SQPSI--GRSFGSKYFG 148
Ecolb_Hs_fragment RQKAWCCSTLPEPAICGISRIWVFSMMRRKKIARMIIECLRSN-----FIY-GSYLSKE-----EIAF--SDPTPD--GKLFATQYCG 143
Ecola_Hs_fragment CPRAWQCSDVPEPAVCGISRIWVFRLLKRRKRIARRLVDTLRNC-----FMF-GCFLSTD-----EIAF--SDPTPD--GKLFATKYCN 155
ruler .....130.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230...

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