

CLUSTAL O(1.2.4) multiple sequence alignment

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rh46      MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD  60
rh10      MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD  60
          *****

rh46      KGEFVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQ  120
rh10      KGEFVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQ  120
          *****

rh46      AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQSRSPDSSTGIGKKGQQPARKRLNFGQTGDS  180
rh10      AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQSRSPDSSTGIGKKGQQPARKRLNFGQTGDS  180
          *****

rh46      ESVPDPQPIGEPPAAPSSVSGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDVR  240
rh10      ESVPDPQPIGEPPAGPSGLSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDVR  240
          *****

rh46      ITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSRWDWQ  300
rh10      ITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSRWDWQ  300
          *****

rh46      RLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA  360
rh10      RLINNNWGFPRKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA  360
          *****

rh46      HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFSSFSYTFED  420
rh10      HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFSSFSYTFED  420
          *****

rh46      VPFHSSYAHSQSLDRLMNPLIDQYLYLSRTQSTGGTAGTQQLLFSQAGPSNMSAQARNW  480
rh10      VPFHSSYAHSQSLDRLMNPLIDQYLYLSRTQSTGGTAGTQQLLFSQAGPNMSAQAKNW  480
          *****

rh46      LPGPCYRQQRVSTTSLQNNSNFAWTGATKYHLNGRDSLVPNGVAMATNKDDEDRFFPSS  540
rh10      LPGPCYRQQRVSTTSLQNNSNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSS  540
          *****

rh46      GILMFGKQGAGKDNVDYSNVMLTSEEEIKATNPVATEQYGVVADNLQQQNTAPIVGAVNS  600
rh10      GVLNFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVNS  600
          *.:*****

rh46      QGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPMLMGGFGLKHPPPQILIKNTPVPADP  660
rh10      QGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPMLMGGFGLKHPPPQILIKNTPVPADP  660
          *****

rh46      PTAFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDFAVNTE  720
rh10      PTTFNQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDFAVNTD  720
          *:.*.*****

rh46      GYSEPRPIGTRYLTRNL  738
rh10      GYSEPRPIGTRYLTRNL  738
          *.*****

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#  
#  
# Percent Identity Matrix - created by Clustal2.1  
#  
#
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1: rh46	100.00	97.29
2: rh10	97.29	100.00