

CLUSTAL O(1.2.4) multiple sequence alignment

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rh.10      MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
AAV8       MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
*****

rh.10      KGEFVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQ 120
AAV8       KGEFVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQ 120
*****

rh.10      AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPTSSTGIGKKGQPPAKKRLNFGQTGDS 180
AAV8       AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPTSSTGIGKKGQPPAKKRLNFGQTGDS 180
*****

rh.10      ESVPDPQPIGEPPAGPSGLSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDVR 240
AAV8       ESVPDPQPPLGEPPAAPSGVGPTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDVR 240
*****

rh.10      ITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYDFNRFHCHFSPRDWQ 300
AAV8       ITTSTRTWALPTYNNHLYKQISNGTSGGATNDNTYFGYSTPWGYDFNRFHCHFSPRDWQ 300
*****

rh.10      RLINNNGWFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA 360
AAV8       RLINNNGWFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA 360
*****

rh.10      HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFEEFSYQFED 420
AAV8       HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFED 420
*****

rh.10      VPFHSSYAHSQSLDRLMNPLIDQYLYLSRTQSTGGTAGTQQLLFSQAGPNNMSAQAKNW 480
AAV8       VPFHSSYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTANTQTLGFSQGGPNTMANQAKNW 480
*****

rh.10      LPGPCYRQQRVSTTSLQNNNSNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSS 540
AAV8       LPGPCYRQQRVSTTTGQNNNSNFAWTAGTKYHLNGRSLANPGIAMATHKDDEERFFPSN 540
*****

rh.10      GVLMEFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVNS 600
AAV8       GILIFGKQNAARDNADYSDVMLTSEEEIKTTNPVATEEYGVVADNLQQQNTAPQIGTVNS 600
*:*:*****:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:

rh.10      QGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPMLGGFGLKHPPPQILIKNTPVPADP 660
AAV8       QGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPMLGGFGLKHPPPQILIKNTPVPADP 660
*****

rh.10      PTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDFAVNTD 720
AAV8       PTTFNQSKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTSVDFAVNTE 720
*****:*:** *****:*****

rh.10      GTYSEPRPIGTRYLTRNL 738
AAV8       GUYSEPRPIGTRYLTRNL 738
*:*****

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#  
#  
# Percent Identity Matrix - created by Clustal2.1  
#  
#
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1: rh.10	100.00	93.50
2: AAV8	93.50	100.00