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CLUSTAL 2.1 multiple sequence alignment


RdpA            MHAALSPLSQRFERIAVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
FT_5            MHAALSPLSQRFERIAVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
FT_C            MHAALTPLTNKYRFIDVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
FT_R            MHAALTPLTNKYRFIDVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
FT_T            MHAALTPLTNKYRFIDVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
FT_Tv3          MHAALTPLTNKYRFIDVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
FT_Tv7          MHAALTPLTNKYRFIDVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQ
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RdpA            AITNEQHIAFSRRFGPVDPVPLLKSIEGYPEVQMIRREANESGRVIGDDWHTDSTFLDAP
FT_5            AITNEQHIAFSRRFGPVDPVPLLKSIEGYPEVQMIRREANESGRVIGENWHTDSTFLDAP
FT_C            AITNEQHIAFSRRFGPVDPVPLLKSIEGYPEVQMIRREANESGRVIGDDWHTDSTFLDAP
FT_R            AITNEQHIAFSRRFGPVDPVPLLKSIEGYPEVQMIRREANESSRVIGDDWHSDSTFLDAP
FT_T            AITNEQHIAFSRRFGPVDPVPILKSIEGYPEVQMIRREANESSRFIGDDWHTDSTFLDAP
FT_Tv3          AITNEQHIAFSRRFGPVDPVPILKSIEGYPEVQMIRREANESSRYIGDDWHADSTFLDAP
FT_Tv7          AITNEQHIAFSRRFGPVDPVPILKSIEGYPEVQMIRREANESSRYIGDDWHADSTFLDAP
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RdpA            PAAVVMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNR
FT_5            PAAVVMYAKEIPPYGGDTLFTSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNR
FT_C            PAAVVMRAIEVPEYGGDTGFLSMYSAWETLSPTMQATIEGLNVVHSATKVFGSLYQATNW
FT_R            PAAVVMRAIEVPEYGGDTGFLSMYSAWETLSPTMQATIEGLNVVHSATKVFGSLYQATNW
FT_T            PAAVVMRAIEVPEYGGDTGFLSMYSAWETLSPTMQATIEGLNVVHSATKVFGSLYQATNW
FT_Tv3          PAAVVMRAIEVPEYGGDTGFLSMYSAWETLSPTMQATIEGLNVVHSATKVFGSLYQATNW
FT_Tv7          PAAVVMRAIEVPEYGGDTGFLSMYSAWETLSPTMQATIEGLNVVHSATKVFGSLYQATNW
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RdpA            RFSNTSVKVMDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFL
FT_5            RFSNTSVKVMDVDAGDRETVHPLVVTHPETGRKGLYVNQVYCQRIEGMSEKESEPLLSFL
FT_C            RFSNTSVKVMDVDAGDRETVHPLVVTHPVTGRRALYCNQVYCQKIQGMTDAESKSLLQFL
FT_R            RFSNTSVKVMDVDAGDRETVHPLVVTHPVTGRRALYCNQVYCQKIQGMTDAESKSLLQFL
FT_T            RFSNTSVKVMDVDAGDRETVHPLVVTHPVTGRRALYCNQVYCQKIQGMTDAESKSLLQFL
FT_Tv3          RFSGTSVKVMDVDAGDRETVHPLVVTHPVTGRRALYCNQVYCQKIQGMTDAESKSLLQFL
FT_Tv7          RFSNTSVKVMDVDAGDRETVHPLVVTHPVTGRRALYCNQVYCQKIQGMTDAESKSLLQFL
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RdpA            YEHATRFDFTCRVRWKKDQVLVWDNLCTMHRAVPDYAGKFRYLTRTTVGGVRPAR
FT_5            FAHATKPEFTCRVRWQEGDVLVWDNLCTQHYAVPDYAGKFRYLTRTTVGGVRPAR
FT_C            YEHATKFDFTCRVRWKKDQVLVWDNLCTMHRAVPDYAGKFRYLTRTTVAGDKPSR
FT_R            YEHATKFDFTCRVRWKKDQVLVWDNLCTMHRAAPDYAGKFRYLTRTTVAGDKPSR
FT_T            YEHATKFDFTCRVRWKKDQVLVWDNLCTMHRAVPDYAGKFRYLTRTTVAGDKPSR
FT_Tv3          YEHATQFDFTCRVRWKKDQVLVWDNLCTMHRAVPDYAGKFRYLTRTTVAGDKPSR
FT_Tv7          YEHATQFDFTCRVRWKKDQVLVWDNLCTMHRAVPDYAGKFRYLTRTTVAGDKPSR
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