

CLUSTAL 2.0.12 MULTIPLE SEQUENCE ALIGNMENT

File: C:/Program Files/ClustalX2/protein-homo/11163.ps
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Date: Sat Jun 26 12:31:59 2010

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*: .:** :*:* :** :* *:: ..***** ** *****:*****.* :*****:***:: : :*****:***:*.****: :*:** *****:.*: :***** ** :***** *****:
gi |27894319|ref|NP_776214.1| MEICRGLRSHLIT-LLLFLFSEETICRPSGRSSSKMQAFRIWDVNQKTFYLRNNQLVAGYLGPNVNLEEKIDVVPTEPHALFLGIHGGKMCSCVKSQDETRLEAVNITDLENRQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 149
gi |114579655|ref|XP_001147954.1| MEICRGLRSHLIT-LLLFLFSEETVCRPSGRSSSKMQAFRIWDVNQKTFYLRNNQLVAGYLGPNVNLEEKIDVVPTEPHALFLGIHGGKMCSCVKSQDETRLEAVNITDLENRQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 149
gi |27805939|ref|NP_776782.1| MDIV--IHGYLIC-LLLFLFSEETACHPLGKRRCEMQAFRIWDVNQKTFYLRNNQLVAGYLGPNVTKLEEKIDVVPTEPHALFLGIHGGKMCSCVKSQDETRLEAVNITDLENRQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 147
gi |50978786|ref|NP_001003096.1| METCRCLSVYLIS-FLLFLFSEETACRPLGKRPCRMAAFRIWDVNQKTFYLRNNQLVAGYLGSPNTKLEEKIDVVPTEPHAVFLGIHGGKMCSCVKSQDETRLEAVNITDLENRQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 149
gi |89257344|ref|NP_001034790.1| MEICWGPYSHLIS-LLLILLFSEEAACRPSGKRPCRMAAFRIWDVNQKTFYLRNNQLVAGYLGPNVTKLEEKIDVVPTEPHAVFLGIHGGKMCSCVKSQDETRLEAVNITDLENRQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 150
gi |11559964|ref|NP_071530.1| MEICRGPYSHLIS-LLLILLFSEEAAGHPAGKRPCRMAAFRIWDVNQKTFYLRNNQLVAGYLGPNVTKLEEKIDVVPTEPHAVFLGIHGGKMCSCVKSQDETRLEAVNITDLENRQDKRFAFIRSDSGPTTSFESLACPGWFLCTA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150
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:***.*** ** * *****:
gi |27894319|ref|NP_776214.1| MEADQPVSLTNPDEGVMVTKKFVQEDD 177
gi |114579655|ref|XP_001147954.1| MEADQPVSLTNPDEGVMVTKKFVQEDD 177
gi |27805939|ref|NP_776782.1| LEADQPVGLTNPTEALKVTKKFVQEDD 174
gi |50978786|ref|NP_001003096.1| LEADRPVSLTNRPEEAMMVTKKFVQKE- 176
gi |89257344|ref|NP_001034790.1| LEADRPVSLTNPPEELIVTKKFVQEDD 178
gi |11559964|ref|NP_071530.1| LEADHPVSLTNTPKKPCVTKKFVQEDD 178
.....160.....170.....
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