

1 10 20 30 40 50 60 70 80 90 100 110 120 130
|-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Mp10 MFSTQSQAMDSRIAYVCYVLAVFAYDQTVGAPQKDAYAASGPAYTTKYDHIDIDQVLGSKRLVNSYVQCLLDKKPCTPEGAELRKILPDALKTQCYKCNATQKNAAALKVVDRLQRDYDKEWKQLLDKWDP
ACYPI000097 MDSRIAYVCYVLAVFAYDQTVGAPQKDAYAASGTAYTTKYDHIDIDQVLASKRLVNSYVQCLLDKKPCTPEGAELRKILPDALKTQCAKCNATQKNAAALKVVDRLQRDYDKEWKQLLDKWDP
BPHOGS10008228 MYVPYRVGYSLCLADDQYTSKYDNIDLKILDSKRLVSNYVQCLLGTKGCPPEGLELKRILPDALKTQCSKCTCVQRQGAVKAIQRLQKDYPDEWKL LLDKWDA
BPHOGS10002786 MSNYIICKVLLYSVSYSLSLCLADDQYTSKYDNIDLKILDSKRLVSNYVQCLLGTKGCPPEGLELKRILPDALKTQCSKCTCVQRQGAVKAIQRLQKDYPDEWKL LLDKWDA
AAJJ0269C MIPLIAIAGILAYSAPAFAEFYESRYDHLDESILNRRHMVNYAACLLSGPCPPQGVDLKRYLPEARLTNCAKCTEKQRTAAYRSIKRLKKEYPKIEWEQLRAYWDP
AAJJ0269B MIKKRFRFIPYHDFVNGKTLHRSTRDDKYTRYDNVDYDRILHSKRLLLNYINCLLEKGPCSPEGRELKKILPDALVTNCSKCSEVQKKQAGKITFTVLLNRYNEWNQLVAKYDP
DP0006842 MHCASYFFVYSALLYLISAQSSPYTSKYDNVDYDKILKNDRLTNHYIKCLMEEGPCTPEGRELKRTL PDALASGCSKCNEKQKSTTEKVIIRHLQTRRAKDWDRLSKKYDP
XP_012166268 MRTEETAQVVCYTAEITYTKYDNVDYDRILQNGRILTNYIKCHLDEGPCTNEGRELKKILPDALSTGCSKCNEKQKHTANKVYNYLRTRKPKDWERLSAKYDS
HMELO10990 MKTVLC--LFALVAVACALPSSTYTDKYDNIDLDEL SNKRLLTPLYVKCHLDEGKCSPEGKELKSHVREALENECSKCTENQKAGSRKVIGHLINNEQEYWSKLTAKYDP
CSUOGS107535 MKAIILIGLSVVYTIAWARPGNTYTDKWDHINYDEILES NRLLKGYYDCLLERGRCTPDGKALKETLPDALEHECSKCTEKQKTASDKVIRHLYNKRPDLWTELAAKYDP
Bta06193 MNLLSVVYLVCCLFAYLSAPAEFYTSQFDNIDIESILNNEKLLDNYFKCLMDEGPCTLEGRTLKSLVPDALNTSCAKCTDKQKQIARRVITFYLDKYPANSARIK KYDP
PVENScaf20457 KLFYLAFLATAATYVLAVPAPAYTTKYDNVNIDEILGNDR LF-----LPDALENDCKGCSEKQKEGAERI IKHLIDNKPDMWTKLEEKYDK
Consensusa.p...YT.k%N!#. #. IL.n.Rll..y..c ll..gpc.peg.elk..lp#AL.t.CskC.ekQk..a.kv!..l...yp..W..L..KyDp

	261	270	274
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Mp10			
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AAJJ0269B			
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Consensus			