

1 10 20 30 40 50 60 70 80 90 100 110 120 130
 |-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
 Mp10 MFSTQSQAMDSRIAVVCCYVLAYFAYDQTYGAPQKDAYRASGPAYTTKYDHIDIDQVLGSKRLVNSYYQCLLDKKPCTPEGAELRKILPDALKTQCVKCNATQKNAALKYVDRQLRDYDKEWKQLDKWDP
 ACYPI000097 MDSRIAVVCCYVLAYFAYDQTYGAPQKDAYRASGTAYTTKYDHIDIDQVLASKRLVNSYYQCLLDKKPCTPEGAELRKILPDALKTQCAKCNATQKNAALKYVDRQLRDYDKEWKQLDKWDP
 BPHOGS10008228 MYYPYRYGYSLCLADDQYTTSKYDNIDLDKILDSDKRLVSNYYQCLLGTKGCPPEGLELKRILPDALKTQCSKCTCYQRQGAYKAIQRLQKDYPDEWKLLDKWDA
 BPHOGS10002786 MSNYIIKCYLLVSYSVSLCLADDQYTTSKYDNIDLDKILDSDKRLVSNYYQCLLGTKGCPPEGLELKRILPDALKTQCSKCTCYQRQGAYKAIQRLQKDYPDEWKLLDKWDA
 RAJJ0269C MIPLIAIAGILAVSAAAPAEFYESRYDHLDYESILNNRRMVNYYAACLLSKGPCPPQGVDLKRYLPICALQTNCAKCTEKQRTAAYRSIKRLKKEYPKIWEQLRAYWDP
 RAJJ0269B MIKRKFRFIPVHDFVNGKTLHRSTRDDKYTTRYDNYDVDRILHSKRLLLNYINCLLEKGPCSPEGREKKILPDALVTNC SKCSEVQKKQAGKILTFVLLNYRNEWNQLYAKYDP
 DP0006842 MHCAASVFFVYVSALLYLISAQSSPYTSKYDNYDVDKILKNDRVLTNYIKCLMEEGPCTPEGRELRTLPDALASGCSKCNEKQKSTTEKVIRHLQTRRAKDWDRLSKKYDP
 XP_012166268 MRTEETAQVYCYTAEDYTTKYDNYDVDRILQNGRILTNYIKCMLDEGPCTNEGRELKKILPDALSTGCSKCNEKQKHTANKVYNYLRTKRPKDWERLSAKYDS
 HMELO10990 MKTYLC--LFALYAYACALPSSTYTDKYDNIDLDEILSNKRLLTPYYKCMLDEGKCSPEGKELKSHVREALENECSKCTENQKAGSRKYIGHLINNEQEYHSKLTRAKYDP
 CSUOGS107535 MKAILLIGLSVVVTIAWRPGNTYTDKWDHINVDEILESNRLLKGYYDCLLERGRCTPDGKALKETLPDALHECSKCTEKQKTASDKYIRHLVNKRPDWLTELAKYDP
 Bta06193 MNLLSVVYLVCCLFAAVLSAPADEFYTTSQFDNIDIESILNNEKLLDNYFKCLMDEGPCTLEGRTLKSVPDALNTSCAKCTDKQKQIARRYITFYLOKYPANSARIKKYDP
 PYENscaf20457 KLFVLAFCATAATVLAYPEPAYTTKYDNVNIDEILGNDRLF-----LPDALENDCKGCSEKQKEGAERIIKHLIDNKPDWTKLEEKYDP
 Consensusa.p...YT.k%Dn!#.#.IL.n.R11..g...c11..gpc.peg.elk..1P#AL.t.CskC.ekQk..a.kv!..1...yp..H..L..KyDp

131 140 150 160 170 180 190 200 210 220 230 240 250 260
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 Mp10 KREYFQKFQQFLAEEKKKGVVKF
 ACYPI000097 KREQFQKFQQFLAEEKKKGVVKF
 BPHOGS10008228 KRESLAKFDDYYKKGGKIC
 BPHOGS10002786 KRESLAKFDDYYKKGGKIC
 RAJJ0269C DDYFIRKFETSFESGKPSGYISTNTSPPS PILSNRGENEEDARASNYISSTPLPPTTSTTRTLTTKFTTKPSTKPTNKPVYVYTKPPQAPPFATYGANLQATYSFGTNLYGGIVRSLGTLGSRYVESG
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 DP0006842 EGYYKQKYTAELKTETTA
 XP_012166268 SGEYKKRYENYLQPTKNS
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 CSUOGS107535 DNMYQQRYDKKIEEVKGKQ
 Bta06193 ENKFKDGIEKALLGSR
 PYENscaf20457 TG
 Consensus
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 Mp10
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 RAJJ0269B
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 Bta06193
 PYENscaf20457
 Consensus