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CYB5_3 -----MGGDGKVFTLSEVSOHSSAKDCWIVIDGKVVYDVTKFLDDHPGGDEVILLTSTGKDATDDF
CYB5_4 -----MGDEAKIFTLSEVSEHNOAHDCWIVINGKVVYNTKFLEDHPGGDDVLLSSTGKDATDDF
CYB5_2 -----MSSDRKVLSFEEVSKHNKTKDCWLIISGKVYDVTPFMDDHPGGDEVLLSSTGKDATNDF
CYB5_1 -----MANLISFHDVAKHKCKNDCWLIISGKVYDISTFMDEHPGGDNVLLAVTGKDASIDF
CYB5_6 -----MPTLTKLYSMEFAATHNKQDDCWVVIDGKVVYDVSSYMDEHPGGDDVLLAVAGKDATDDF
CYB5_5 MIAVIGLLLGLFVLSALFLIQKRRRTNDNQEKRSSEPEVDVVRPKSYSKSEVAVHNRNDCWIITKDKVYDITSYVEEHPGGD-ATLDHAGDSDTDGF
consensus .....*.....*.....*.....*.....*.....*.....*.....*.....*
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....
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CYB5_3 EDVGHSSTAKAMLDEYYVGDIDTATVPKAKFVPPTSTKAVATQDKSSDFVIKLLQFLVPLLILGLAFGIRIYTKTKAPSS
CYB5_4 EDVGHSESAREMMEQYYVGEIDPTIPKKVKYTPPK--QPHYNQDKTSEFIIKLLQFLVPLAILGLAVGIRIYTKSG----
CYB5_2 EDVGHSDIARDMMDKYFIGEIDSSVPATRYVAPQ--QPAYNQDKTPEFIIKLLQFLVPLLILGLALVVRHYTKD----
CYB5_1 EDVNHSKDAKELMKKYCIGDVDQSTVPVTQYIPPEWEKESTAAETTKESGKLLIYLIPLLLILGVAFALRFYNNK----
CYB5_6 EDAGHSKDARELMEKYFIGELDESSLPEIPELKIYKQDQSVQKLFDLTKQYWVVPVSIITTSVASVLFSRKT----
CYB5_5 FGPQHATRVFDMIEDFYIGELH-----
consensus .....*.....*.....*.....*.....*.....*.....*.....*.....*
101.....110.....120.....130.....140.....150.....160.....170.....
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