

gi | 6755779 | ref | NP_035711.1 | 150
gi | 34854062 | ref | XP_214778.2 | 150
gi | 73946255 | ref | XP_541204.2 | MDRQPPGPGQMLFADDDKLLGVECGQGWMEGQRRLLDAERGLCSHTDLSPITITICLTFSCVTPGCRVHDASCCGILGATHLNPOOQLLGLGQVVEGAARSNGEKPATLTAVGHAGTLPSSLHPQPRGPGQGRFLADQASLGLAPSSGPIRER 150
gi | 28875793 | ref | NP_789861.1 | 150
gi | 40317628 | ref | NP_003238.2 | 150
gi | 48976107 | ref | NP_001001755.1 | 150
gi | 292619572 | ref | XP_694690.4 | 150
gi | 292620269 | ref | XP_001919848.2 | 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi | 6755779 | ref | NP_035711.1 | AGDH 300
gi | 34854062 | ref | XP_214778.2 | AGDH 300
gi | 73946255 | ref | XP_541204.2 | WLLCVDEAPRRPPEHIKORLLPGGQCGADPSSPAGRAEPPPAVVPVAPALHRPERRRHLPHRSLIPPGQSAVDGRMLGALVLLALWASSAAGECCGPHSRSSGLLGPQSRREASSVNOQLSRGPHVKGQPKERITVLHNSIHEHPAGDQ 300
gi | 28875793 | ref | NP_789861.1 | AGDQ 300
gi | 40317628 | ref | NP_003238.2 | AGHQ 300
gi | 48976107 | ref | NP_001001755.1 | DDAK 300
gi | 292619572 | ref | XP_694690.4 | QL 300
gi | 292620269 | ref | XP_001919848.2 | LV 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 6755779 | ref | NP_035711.1 | 450
gi | 34854062 | ref | XP_214778.2 | 450
gi | 73946255 | ref | XP_541204.2 | VEDTAFDLFSISNINRKTIGAKQFRGPDPGVPAYRFVRFDIYPPVNDLNRIVKLARRKEGFFLTAQLKQDRKSRGTLILVLEGPSTSORQFEIVSNGPGDILDLNFWVE-GHGHNFLEDVGLADSQWKNVTVQVADTYSLVVGCDLI 450
gi | 28875793 | ref | NP_789861.1 | DEDMAFDLFRISNINRKTIGAKQFRGPDPSVPAYRFVRFDIYPPVADYLSRIKIVRQKEGFFLTAQLKQDPKSRGTLILALEGPGA-QRQFEIVSNGPADILDLTWVD-GTQHVISLEDVGLADSQWKNVTVQVGTDTYSLVVGCDLI 450
gi | 40317628 | ref | NP_003238.2 | DEDTAFDLFSISNINRKTIGAKQFRGPDPSVPAYRFVRFDIYPPVADYLSRIKIVRQKEGFFLTAQLKQDRKSRGTLILALEGPGA-QRQFEIVSNGPADILDLTWVD-GTQHVISLEDVGLADSQWKNVTVQVGTDTYSLVVGCDLI 450
gi | 48976107 | ref | NP_001001755.1 | DKDTTFDLFSISNINRKTIGAKQFRGPDPGVPAYRFVRFDIYPPVNDLNRIVKLARRKEGFFLTAQLKQDRKSRGTLILALEGPGA-QRQFEIVSNGPADILDLTWVD-GTQHVISLEDVGLADSQWKNVTVQVGTDTYSLVVGCDLI 450
gi | 292619572 | ref | XP_694690.4 | ESENTFDLFSISNINRKTIGAKLFRGPDPAIPAYRFVRFDIYPPVADYLSRIKIVRQKEGFFLTAQLKQDRKSRGTLILALEGPGA-QRQFEIVSNGPADILDLTWVD-GTQHVISLEDVGLADSQWKNVTVQVGTDTYSLVVGCDLI 450
gi | 292620269 | ref | XP_001919848.2 | EDETFDLFESSGITRKTIGVLFKGLSDAPAYRFVRFDIYPPVADYLSRIKIVRQKEGFFLTAQLKQDRKSRGTLILALEGPGA-QRQFEIVSNGPADILDLTWVD-GTQHVISLEDVGLADSQWKNVTVQVGTDTYSLVVGCDLI 450
EDESVDLFKISGISRKTIGAKLFRGPDPAIPAYRFVRFDIYPPVADYLSRIKIVRQKEGFFLTAQLKQDRKSRGTLILALEGPGA-QRQFEIVSNGPADILDLTWVD-GTQHVISLEDVGLADSQWKNVTVQVGTDTYSLVVGCDLI 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 6755779 | ref | NP_035711.1 | 600
gi | 34854062 | ref | XP_214778.2 | 600
gi | 73946255 | ref | XP_541204.2 | 600
gi | 28875793 | ref | NP_789861.1 | 600
gi | 40317628 | ref | NP_003238.2 | 600
gi | 48976107 | ref | NP_001001755.1 | 600
gi | 292619572 | ref | XP_694690.4 | 600
gi | 292620269 | ref | XP_001919848.2 | 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 6755779 | ref | NP_035711.1 | 750
gi | 34854062 | ref | XP_214778.2 | 750
gi | 73946255 | ref | XP_541204.2 | 750
gi | 28875793 | ref | NP_789861.1 | 750
gi | 40317628 | ref | NP_003238.2 | 750
gi | 48976107 | ref | NP_001001755.1 | 750
gi | 292619572 | ref | XP_694690.4 | 750
gi | 292620269 | ref | XP_001919848.2 | 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



