

gi|32528301|ref|NP_004435.3| MELRVLWCWASLAAALE-----ETLLNNTKLEADLKWVTFPPQVDGQWEELSGLDEEQHSVRTYEVCDVQAPGQAHWLRIGWVPRRGAVHVVYALRFMTMLECLSLPRAGRSCKETFTVFYFESDADTAHAFPAWMPNPIYIK 150
gi|114615050|ref|XP_519269.2| MELRVLWCWASLAAALE-----ETLLNNTKLEADLKWVTFPPQVDG----- 150
gi|73957950|ref|XP_546948.2| MELRALLCWASLAAALELVTLVHLFTCLSVLEETLLNNTKLEADLKWVTFPPQVDGQWEELSGLDEEQHSVRTYEVCDVQAPGLAHWLRIGWVPRRGAVHVVYALRFMTMLECLSLTRAGRSCKETFTVFYFESDADTAHAFPAWMPNPIYIK 150
gi|194678442|ref|XP_874493.3| MELRALLCWASLAAALE-----ETLLNNTKLEADLKWVTFPPQVDGQWEELSGLDEEQHSVRTYEVCDMQRAPGLAHWLRIGWVPRRGAVHVVYALRFMTMLECLSLPRAGRSCKETFTVFYFESDADTAHAFPAWMPNPIYIK 150
gi|47059093|ref|NP_034274.3| MELRALLCWASLAAALE-----ETLLNNTKLEADLKWVTFPPQVDGQWEELSGLDEEQHSVRTYEVCDMQRAPGLAHWLRIGWVPRRGAVHVVYALRFMTMLECLSLPRAGRSCKETFTVFYFESDADTAHAFPAWMPNPIYIK 150
gi|18858599|ref|NP_571489.1| MELFSRNVAAFVWVILLEFLLSGV-----AEEVLMNTEITSDLRKTHRSKPEWELSGLDDEENNSVRTYICQADGS--SSHCVRSLKLIERRGASQVYVLEFFIMVCSRNTHHRSCKETFNLYYQSDTDDATAHAFPAWMPNPIYIK 150
gi|18859329|ref|NP_571492.1| MDRVCMIMALSWFMVMSGLVLS-----AEEVLMNTEITSDLRKTHRSKPEWELSGLDDEENNSVRTYICQADGS--SSHCVRSLKLIERRGASQVYVLEFFIMVCSRNTHHRSCKETFNLYYQSDTDDATAHAFPAWMPNPIYIK 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|32528301|ref|NP_004435.3| VDTVAAEHLTRKRPGAEATGKVNVTLLRGLPLSKAGFYLAFOGACMALLSLHLFYKCAQLTVNLIRFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
gi|114615050|ref|XP_519269.2| VDTVAAEHLTRKRPGAEATGKVNVTLLRGLPLSKAGFYLAFOGACMALLSLHLFYKCAQLTVNLIRFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
gi|73957950|ref|XP_546948.2| VDTVAAEHLTRKRPGAEATGKVNVTLLRGLPLSKAGFYLAFOGACMALLSLHLFYKCAQLTVNLIRFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
gi|194678442|ref|XP_874493.3| VDTVAAEHLTRKRPGAEATGKVNVTLLRGLPLSKAGFYLAFOGACMALLSLHLFYKCAQLTVNLIRFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
gi|47059093|ref|NP_034274.3| VDTVAAEHLTRKRPGAEATGKVNVTLLRGLPLSKAGFYLAFOGACMALLSLHLFYKCAQLTVNLIRFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
gi|18858599|ref|NP_571489.1| VDTVAADFLLRK--GGEK--KVNVTLLRGLPLSKAGFYLAFOGACMALLSVRFFKCPALTRSLVFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
gi|18859329|ref|NP_571492.1| VDTVAADFLLRK--GGEK--KVNVTLLRGLPLSKAGFYLAFOGACMALLSVRFFKCPALTRSLVFPETVPRELIVPVVAGSCVVDVAVPAG--PSPSLYCREDDGQWAEQVPTGCSAPGFEEAEGNTKCRACAQGFKPLSGEGSC 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|32528301|ref|NP_004435.3| QPCPANSNSNTIGSAVCCRVGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
gi|114615050|ref|XP_519269.2| QPCPANSNSNTIGSAVCCRVGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
gi|73957950|ref|XP_546948.2| QPCPANSNSNTIGSAVCCRVGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
gi|194678442|ref|XP_874493.3| QPCPANSNSNTIGSAVCCRVGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
gi|47059093|ref|NP_034274.3| LPCPANSNSNTIGSAVCCRVGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
gi|18858599|ref|NP_571489.1| SVCPENSQTEGSAACVRCGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
gi|18859329|ref|NP_571492.1| RVCPCNSNTIGSAVCCRVGYFRARIDPRGAPCTTTPSAPRSVVRNLGSSLLHLEWAPLESGGREDLTYALRCRECR--PGGSCAPCGGDLTFDPGPRDLVPEVWVVRGLRPLDFTYTFEVTALNGVSSLATGPVFPFVAVVTTDREVP 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|32528301|ref|NP_004435.3| PAVSDIRVTRSSPSSLSLAWAVPRAPSGAVLDYEVKYHEKG--AEGPSSVRFKLTSENRAELRGLKRGASYLVOVRARSEAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
gi|114615050|ref|XP_519269.2| PAVSDIRVTRSSPSSLSLAWAVPRAPSGAVLDYEVKYHEKG--AEGPSSVRFKLTSENRAELRGLKRGASYLVOVRARSEAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
gi|73957950|ref|XP_546948.2| PPVSDIRVTRSSPSSLSLAWAVPRAPSGAVLDYEVKYHEKG--AEGPSSVRFKLTSENRAELRGLKRGASYLVOVRARSEAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
gi|194678442|ref|XP_874493.3| PPVSDIRVTRSSPSSLSLAWAVPRAPSGAVLDYEVKYHEKG--AEGPSSVRFKLTSENRAELRGLKRGASYLVOVRARSEAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
gi|47059093|ref|NP_034274.3| PAVSDIRVTRSSPSSLSLAWAVPRAPSGAVLDYEVKYHEKG--AEGPSSVRFKLTSENRAELRGLKRGASYLVOVRARSEAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
gi|18858599|ref|NP_571489.1| VLVSGLRKETAHESLTLKWNFTQSHYRILQYQIRYCEKERGSEENSCHYMESNVEVLLSDLRRAQYEVQVRRARFAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
gi|18859329|ref|NP_571492.1| VLVSGLRKETAHESLTLKWNFTQSHYRILQYQIRYCEKERGSEENSCHYMESNVEVLLSDLRRAQYEVQVRRARFAGYGFPGQEHHSQTLDESEGWREOLALIACTAVVGVLVVLVVIIVAVLCLRKQSNGREAEYSDKHGQOYLI 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|32528301|ref|NP_004435.3| GHGTVYIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
gi|114615050|ref|XP_519269.2| GHGTVYIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
gi|73957950|ref|XP_546948.2| GHGTVYIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
gi|194678442|ref|XP_874493.3| GHGTVYIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
gi|47059093|ref|NP_034274.3| GHGTVYIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
gi|18858599|ref|NP_571489.1| GQGVKVIIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
gi|18859329|ref|NP_571492.1| GQGVKVIIDPFTYEDPNEAVREFAKEIDVSVKIEEVIAGGEGVCRGRLKAPGKKECVAIKILKGGYTERORREFLSEASIMGQFHPNIIIRLEGVVTNSMPVMILTFEMENGALDSFLRLNDGQFVIQLVGMRLGIASGMRYLAE 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



