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gi|17647691|ref|NP_523811.1|
gi|158296464|ref|XP_316867.4|
gi|12667808|ref|NP_075370.1|
gi|58865478|ref|NP_001011950.1|
gi|4758118|ref|NP_004623.1|
gi|194665288|ref|XP_001787885.1| MRVCGSGEEGAAARLLRFPWSTADPFRSLSGGGQRVSLAEEMRERRGERRGAKRGLRGGGSRNRDGDLLPLRKANPKWRRRERRRQSGGGGSSLGGRERRAPRAPPPPTPPSSRFPPSSSPLRLGRRSAHARPHAPECIWACKSLLPP 150
gi|57089109|ref|XP_537250.1|
gi|118102186|ref|XP_422859.2|
gi|148922922|ref|NP_001092207.1|
gi|17532723|ref|NP_496280.1|
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|17647691|ref|NP_523811.1|
gi|158296464|ref|XP_316867.4|
gi|12667808|ref|NP_075370.1|
gi|58865478|ref|NP_001011950.1|
gi|4758118|ref|NP_004623.1|
gi|194665288|ref|XP_001787885.1| IAFGRRLARPPASTHSLNGALWHSPLPLGPCQASSGAGPHAYLQOREPKSGGEDDRRSGLSLPLGHELPRATERNLWLFSLAAAPWRRSFLFWPRPGRGERVGGGLAPLRWRVVGCGGCALSFLPYDPSLLLRCTRGVEIALDSVC 300
gi|57089109|ref|XP_537250.1|
gi|118102186|ref|XP_422859.2|
gi|148922922|ref|NP_001092207.1|
gi|17532723|ref|NP_496280.1|
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|17647691|ref|NP_523811.1|
gi|158296464|ref|XP_316867.4|
gi|12667808|ref|NP_075370.1|
gi|58865478|ref|NP_001011950.1|
gi|4758118|ref|NP_004623.1|
gi|194665288|ref|XP_001787885.1| RLPGRGSWFVVRTGIMLKGMRILVSRVHKLDPGRFSLHGTQAPCPVAHLDNQVPTERTRAISRLENDPAKHGEQHVQHYNISIQELKTVFPHG-LPPRFVMOVKIFNEACLMVRKPALELLHVKLNTNFAHPAVRYVLY 441
gi|57089109|ref|XP_537250.1|
gi|118102186|ref|XP_422859.2|
gi|148922922|ref|NP_001092207.1|
gi|17532723|ref|NP_496280.1|
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|17647691|ref|NP_523811.1|
gi|158296464|ref|XP_316867.4|
gi|12667808|ref|NP_075370.1|
gi|58865478|ref|NP_001011950.1|
gi|4758118|ref|NP_004623.1|
gi|194665288|ref|XP_001787885.1|
gi|57089109|ref|XP_537250.1|
gi|118102186|ref|XP_422859.2|
gi|148922922|ref|NP_001092207.1|
gi|17532723|ref|NP_496280.1|
WNTDGMQAGEYRVGDGERGFGKMTMLCHVVFHFCARQGWLVLHHPDAHLWVKNCKELMQSSYNKERLDPLOASFWLRNFRITNEHFLK-EIKTQOKYVWVKRDSIEOGRPLGEVVEQGLTRVRNATDAVGIVLKEIKQOC-CLG- 276
GDTGSGKSIISLCHTLHYCYTCQWLILHVPDAHLWVKNCKEMLPSTYNPLRFDQPVQATQWLKDFKITNEHFLS-KIKTRRYVWTKRESTEGRITLGEILDQGVNRMKSSSDVVGAVLRRLQAGATTEGEB 258
GAFCTGKSVTLNQAVHHAYNNKWAIVHLRSAMELITRRVKEIEMSSFVQGRINDPNSVSILONFQONQHMKILGELLTERDYENKSERLTKGKPIETIEMGIEAPFLASDCVGAIFRRLRRHAK---DD 227
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi |17647691|ref|NP_523811.1| QCKVMVAIDGFNAFFHPTIRIFSDNKQLVTPDRVLTQFFLDITNYDWTNGVCILSVDKIAMTEGHMDSYMPR---YLLGKEGFELDPFVPIHVENYTDKFEHSYISYYLDRHWINKTPOGFEE---GLKFMSENKIPYSIMGLVKAL 392
gi |158296464|ref|XP_316867.4| RARAMVVIDGYNAFFQPHTRLLTEAKARITPDQITLTKPFLSITRNDWTNGVCVTVD--QMVKEFKDTAAGR---SSASRECFEHLDPFVPIHVENYTDKFEHSYISYYLDRHWINKTPOGFEE---ELKLLSCQNPYQLMLQCASL 392
gi |12667808|ref|NP_075370.1| LFHLLVAVDGVNALWG-RTTLKKEDRTLIAP EELSLVHNLRKMKVNDWHGGAIVLSLSQTGSLFKSRRTAYLPH---ELLGKEGFNALEPFLPILIPNYNPKFEFESSFOYYLENNWLOHEKASTE EGRKELRFLSNCPBQLERLCASL 391
gi |58865478|ref|NP_001011950.1| LFHLLVAVDGVNALWG-RTTLKKEDRTLIAP EELALVHNLRKMKVNDWHGGAIVLSLSQTGSLFKSRRTAYLPH---ELLGKEGFNALEPFLPILIPNYNPKFEFESSFOYYLENNWLOHEKASTE EGRKELRFLSNCPBQLERLCASL 391
gi |4758118|ref|NP_004623.1| MFHLLVAVDGINALWG-RTTLKKREDKSP IAP EELALVHNLRKMKVNDWHGGAIVSALSQTGSLFKPRKAYLPQ---ELLGKEGFDAIDPFIPILVSNYNPKFEFESSFOYYLENNWLOHEKAPTE EGGKELFLSNANPSLLERHCAYL 398
gi |194665288|ref|XP_001787885.1| VFHLLVAVDGVNALWG-RTTLKKREDKSP ITP EELALVHNLRKMKVNDWHGGAIVLSVTSQTGSLFKPRKAYLPQ---ELLGKEGFDAIDPFIPILVSNYNPKFEFESSFOYYLENNWLOHEKAPTE EGGKELFLSNANPSLLERHCAYL 712
gi |57089109|ref|XP_537250.1| AFHLLVAVDGVNALWG-RTSLKKEDKSLIAP EELALVCSLRKMKVNDWHGGAIVLSLSQTGSLFKPRKAYLPQ---ELLGKEGFDAIDPFIPILVSNYNPKFEFESSFOYYLENNWLOHEKAPTE EGGKELFLSDANPGQLERLCAYL 393
gi |118102186|ref|XP_422859.2| SFHLLVAVDGVNALWG-RTTLKKEDKSP VSP EELALVHNLRKMKVNDWHGGAVVTSLSQTGSLFKPSSAHLPH---ELLGKEGFDAIDPFIPILVSNYNPKFEFESSFOYYLENNWLOHEKAPTE EGGKELFLSNANPSLLERHCAYL 420
gi |148922922|ref|NP_001092207.1| VFHLLVAVDGVNALWG-NTTLKKEDRTMCEPEELILVHNLRKMKVNDWHGGAILTALSQTGSLFKPRKAYLPQ---ELLGKEGFDEMEPFVPCVSGYNEKFEFGCYLYLDRNWLQHPRE EGGKELFLSNANPSLLERHCAYL 402
gi |17532723|ref|NP_496280.1| KLVVLAIDDANSLWG-KLVVLRADRTYAPPSDLILVHVRMMIENDWTNGCVLMVADKKEVADARDHLGVSRHPLLELFGEEGFYVEFVPIETSNYTEAETDAIYNYVVKVNLASKAARSE EGRKELRFLSNANPSLLERHCAYL 375
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....

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