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gi |197276661|ref|NP_006183.2| MKFTLGLGSRRAWRSWEGAAAAAAG-PGAGGSAALRCRAQRVSSPRLGRRGSRSLGALPLCLERGGGGAQALPDCAGPSPGHPGHPGARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 149
gi |114681249|ref|XP_514547.2| MKFTLGLGSRRAWRSWEGAAAAAG-PGAGGSAALRCRAQRVSSPRLGRRGSRSLRALPLCLERGGGGAQALPDCAGPSPGHPGHPGARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 149
gi |6679209|ref|NP_032806.1| MKFTLGLGSRRAWRSWEGAAAAAAG-PGAGGSAALRCRAQRVSSPRLGRRGSRSLGALPLCLERGGGGAQALPDCAGPSPGHPGHPGARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 55
gi |109468929|ref|XP_230663.4| MKFTLGLGSRRAWRSWEGAAAAAAG-PGAGGSAALRCRAQRVSSPRLGRRGSRSLGALPLCLERGGGGAQALPDCAGPSPGHPGHPGARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 141
gi |73991105|ref|XP_542866.2| MSEGMYRLTRQSRARHAGLKRAAPPPLGGS-----RRGPRLARALPLCLERX-GGGARALPDCAGPSPRRS---GARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 113
gi |119905393|ref|XP_617873.3| MSEGMYRLTRQSRARHAGLKRAAPPPLGGS-----RRGPRLARALPLCLERX-GGGARALPDCAGPSPRRS---GARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 68
gi |123704971|ref|NP_001074061.1| MSEGMYRLTRQSRARHAGLKRAAPPPLGGS-----RRGPRLARALPLCLERX-GGGARALPDCAGPSPRRS---GARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 60
gi |189533396|ref|XP_700877.3| MSEGMYRLTRQSRARHAGLKRAAPPPLGGS-----RRGPRLARALPLCLERX-GGGARALPDCAGPSPRRS---GARQLAGPLAMEQTYGEVNQLGGVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLRVSHGCVSK 57
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |197276661|ref|NP_006183.2| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 299
gi |114681249|ref|XP_514547.2| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 299
gi |6679209|ref|NP_032806.1| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 205
gi |109468929|ref|XP_230663.4| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 291
gi |73991105|ref|XP_542866.2| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 263
gi |119905393|ref|XP_617873.3| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 218
gi |123704971|ref|NP_001074061.1| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 210
gi |189533396|ref|XP_700877.3| ILARYNETGSILPGAIGGSKPRVTTPNVVKHIRDYKQDGPFIWEIRDRLLDAGVCDKYNVPSVSSISRILRNKIGSLAOPGPEYASKOPPSOPTLPYNHIIQYPPSPVSPITGAKMGSHPGVPGTAGHVSIPRSWPSAHSVSNILGIR 199
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |197276661|ref|NP_006183.2| TFMEQTGALAGSECTAYSPKMEDWAGVNRATFAPPAVAVNGLEKPALEADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 446
gi |114681249|ref|XP_514547.2| TFMEQTGALAGSECTAYSPKMEDWAGVNRATFAPPAVAVNGLEKPALEADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 446
gi |6679209|ref|NP_032806.1| TFMEQTGALAGSECTAYSPKMEDWAGVNRATFAPPAVAVNGLEKPALEADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 334
gi |109468929|ref|XP_230663.4| TFMEQTGALAGSECTAYSPKMEDWAGVNRATFAPPAVAVNGLEKPALEADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 422
gi |73991105|ref|XP_542866.2| TFMEQTGALAGSECTAYSPKMEDWAGVNRATFAPPAVAVNGLEKPALEADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 413
gi |119905393|ref|XP_617873.3| TFMEQTGALAGSECTAYSPKMEDWAGVNRATFAPPAVAVNGLEKPALEADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 366
gi |123704971|ref|NP_001074061.1| AFMDPT-AIAGSAE---GVYAPKMEDW-GVNRATFQSG-HGVNGIDKSSIDADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 332
gi |189533396|ref|XP_700877.3| AFMDPT-AIAGSAE---GVYAPKMEDW-GVNRATFQSG-HGVNGIDKSSIDADIKYQASASTLSAVGGFLPACAYPASNOHGVSAPGGGYLAPGPPWPPAQPPLAPPAGVAVHGGELAAAMTFKHPREGSLE---APAARPRTPSVAYTD 316
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |197276661|ref|NP_006183.2| CPSRPRPPRGSSPRTARRERQADPGAQVCAAPPAIGTGRIGGLAEAEASAGPRGARPPAQAPCLWDPDPHFLYWSGFLGFSLELWF 534
gi |114681249|ref|XP_514547.2| CPSRPRPPRGSSPRTARRERQADPGAQVCAAPPAIGTGRIGGLAEAEASAGPRGARPPAQAPCLWDPDPHFLYWSGFLGFSLELWF 534
gi |6679209|ref|NP_032806.1| ---RKPPSPGGK-----ATDALGS---LHGLSIPASTS 361
gi |109468929|ref|XP_230663.4| ---RKPPSPGGK-----ATDALGS---LHGLSIPASTS 449
gi |73991105|ref|XP_542866.2| CPSRPPPPRGSSAS-----PSASS-----MAAETLVSARRSPRALREGSGT 453
gi |119905393|ref|XP_617873.3| YPSRPPPPRAAPPRAEPELE-----PGSGGARTRGFVAAAEVPTSLASLCPALGGRASSILPGFRLL 428
gi |123704971|ref|NP_001074061.1| ---KPPSPLSKQK-----HEALSGLHGLSLSLTS 359
gi |189533396|ref|XP_700877.3| ---KPLSPLSKHQ-----HEGLSAVHGLSD 339
.....460.....470.....480.....490.....500.....510.....520.....530

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