```
                                 *  .         *                                                                  *:  ...:.  .::.. *                                  .*
gi|153791414|ref|NP_001093161.1| MVPSA-----GQLA-------------------------------------------------------------------------LFALGIVLAACQALENSTSPLS--------------------------------DPP    34
gi|114577952|ref|XP_001142892.1| MVPSA-----GQLA-------------------------------------------------------------------------LFALGIVLAACQALENSTSPLSA-------------------------------DPP    35
gi|194671362|ref|XP_593710.4|   MVTSA-----GQLA-------------------------------------------------------------------------LFALGIFLAVCQALENSTSALSA-------------------------------DPP    35
gi|73970269|ref|XP_855490.1|    MDPDADWGLLGRLAPLPLPTRSGDGAVSLWSRGEPDAGRGTGVDVVGLLPTLSLKHPLLSVLTNVPDDGVGRAGVWDGSLPSPVRRPGRLLRALGLPPPASQPPPGSAQSRSRRKPGPFPGALLSVEKAGSAPTLTPDDALRPRDASRPP   150
gi|13654266|ref|NP_112476.1|    MVPAT-----GQLA-------------------------------------------------------------------------LLALGILLAVCQALENSTSPLSD--------------------------------SP    34
gi|6981646|ref|NP_036803.1|     MVPAA-----GQLA-------------------------------------------------------------------------LLALGILVAVCQALENSTSPLSD--------------------------------SP    34
gi|118101429|ref|XP_001234468.1| MGPAG-----VIQA-------------------------------------------------------------------------RQEQGVLVAVCHALENTTSALSD--------------------------------PP    34
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

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                                 ***** ****.***** *:************:*****
gi|153791414|ref|NP_001093161.1| VAAAVVSHFNDCPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLAVVAASQKKQAITALVVVSIVALAVLIITCVLIHCCQVRKHCEWCRALICRHEKPSALLKGRTACCHSET-------VV------------------   159
gi|114577952|ref|XP_001142892.1| VAAAVVSHFNDCPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLAVVAASQKKQAITALVVVSIVALAVLIITCVLIHCCQVRKHCEWCRALICRHEKPSALLKGRTACCHSET-------VV------------------   160
gi|194671362|ref|XP_593710.4|   VAAAVVSHFNDCPDSHSQFCFHGTCRFLVQEEKPACVCHSGYVGARCEHADLLAVVAASQKKQAITALVVVSIVALAVLIITCVLIHCCEVRKHCEWCRALICRHEKPSALLKGRTACCHSET-------VV------------------   160
gi|73970269|ref|XP_855490.1|    VAAAVVSHFNDCPDSHSQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLAVVAASQKKQAITALVVVSIVALAVLIIACVLIHCCQVRKHCEWCQALLCRHEKPSALLKGRAACCHSETDARVRATVVPVELRGRSGQLRLRDGPG   300
gi|13654266|ref|NP_112476.1|    VAAAVVSHFNKCPDSHTQYCFHGTCRFLVQEEKPACVCHSGYVGVRCEHADLLAVVAASQKKQAITALVVVSIVALAVLIITCVLIHCCQLRKHCEWCRALVCRHEKPSALLKGRTACCHSET-------VV------------------   159
gi|6981646|ref|NP_036803.1|     VAAAVVSHFNKCPDSHTQYCFHGTCRFLVQEEKPACVCHSGYVGVRCEHADLLAVVAASQKKQAITALVVVSIVALAVLIITCVLIHCCQVRKHCEWCRALVCRHEKPSALLKGRTACCHSET-------VV------------------   159
gi|118101429|ref|XP_001234468.1| VAAAVRSHFNECPDSHRQFCFHGTCRFLVQEDKPACV-------------------------------------------------------------------------------------------------------------   71
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

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gi|153791414|ref|NP_001093161.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   159
gi|114577952|ref|XP_001142892.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   160
gi|194671362|ref|XP_593710.4|   ------------------------------------------------------------------------------------------------------------------------------------------------------   160
gi|73970269|ref|XP_855490.1|    RTAGQCPQAAPPPAPRLTGSPQPSQEAPGEPGDAAAPVLVHTSDTKPADAEGNTSTQSLPPGNRGLAETLTQKVALDQVKQGSPCPQCTGLVAALQQSPQPLLGPKGQPHLHLVLPPPLGPVPSRRLGAAPPPLYPVGASPGATPPASLI   450
gi|13654266|ref|NP_112476.1|    ------------------------------------------------------------------------------------------------------------------------------------------------------   159
gi|6981646|ref|NP_036803.1|     ------------------------------------------------------------------------------------------------------------------------------------------------------   159
gi|118101429|ref|XP_001234468.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   71
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
```

```
gi|153791414|ref|NP_001093161.1| ----------------------------   159
gi|114577952|ref|XP_001142892.1| ----------------------------   160
gi|194671362|ref|XP_593710.4|   ----------------------------   160
gi|73970269|ref|XP_855490.1|    PSRGGPGVHGALGCRDPGPGGALGCPLLR   479
gi|13654266|ref|NP_112476.1|    ----------------------------   159
gi|6981646|ref|NP_036803.1|     ----------------------------   159
gi|118101429|ref|XP_001234468.1| ----------------------------   71
                                 .......460.......470.........
```