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>HumanIn
MPRSRPPPTAQRAAEPKSEGVVAMTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPEDSGFYATIVAVVGLHVVLIAIFVFIVWKEGLP
>MouseIn
MPRSRQPPPAPRAPEPKSDGVLAMTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPEDSAFYATIVSVVGLHVVLIAIFVFIVWKEGLP
>RatIn
MPCSHRQPPPVPRAPEPKSDGVLAMTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPEDSAFYATIVSVVGLHVVLATFVFIWWEGLP
>DogIn
MPRSRPPPTAQRPRAEPKPEGSLATTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPEDSAFYATIVAVVGLHVVLAVFVFIWKEGMP
>CowIn
MPRSRPPPTAQRPRAEPKPEGSLATTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPEDSAFYATIVAVVGLHVVLAVFVFIWKEGMP
>ElephIn
MPRSRHPPAAPRTEEPKSDGVLPMTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPDDSGFYATIVAVVGLHVVLAFFFIIVWKEGLP
>ArmIn
MPRSRPPPVQAQRPAEPKSDGVLAMTFKIFLLFAGLMVKPVGLYFSCKLLLQSLMLSPEDSAFYATIVAVVGLHVVLIAIFVFIVWKEGLL
>HumanTmem
MERPDKAALNALQPPEFRNESSLASTLKTLFFTALMITVPIGLYFTTKSYIFEGALGMSNRDSYFYAAIVAVVAVHVVLALFVYVAWNECSR
>MouseTmem
MERLDKAALNALQPPEFRNENSLAATLKTLFFTALMITVPIGLYFTTKSYIFEGALGMSNRDSYFYAAIVAVVAVHVVLALFVYVAWNECSR
>CowTmem
MERLDKAALNALQPPEFRNESSLASTLKTLFFTALMITVPIGLYFTTKSYVFEAGFGMSNRDSYFYAAIVAVVAVHVVLALFVYVAWNECSR
>ElephTmem
MERLDKAALNALQPPEFRSESSLASTLKTLFFTALMITVPIGLYFTTKSYVFEAGFGMSNRDSYFYAAIVAVVAVHVVLALFLYVAWNECSR
>ArmTmem
MERFDKAALNALQPPEFRTESSLASTLKTLFFTALMITVPIGLYFTTKSYLFEGALGMSNRDSYFYAAIVAVVAVHVVLALFVYVAWNECSR
>OpMTmem
MERLEKTTQSALQPPEQRNEGSLTSTLKTLVFTALMITLPIGLYFSSKSYVFEGFLGMSNGDSYFYAAIVAVIAHVVLALFVYVAWNECSR
>OpTTmem
MERLEKTTLSVLQPPELRNEGSLTSTLKTLVFTALMITLPIGLYFSSKSYVFEGTLGLSNRDSYFYAAIVAVVAVHVVLALFVYVAWNECSR

| | | | | |
|-----------|--|---|----------------------|-----|
| HumanIn | MPRSHRPPPPTAQRAAEPKSEGVVAMTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSGFYATIVAVVGLHVVLAI | FVFIVWKEGLPQWRENKNEX | 102 |
| MouseIn | MPRSHRQPPPAPRAPEPKSDGVLAMTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSAFYATIVSVVGLHVVLAI | FVFIVWKEGLPQWRENKNDX | 102 |
| RatIn | MPCSHRQPPPPTAQRAEPEPKSDGVLAMTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSAFYATIVSVVGLHVVLAT | FVFIVWEEGLPQWRENKNDX | 102 |
| DogIn | MPRSHRPPPPTAQRPAEPKPEGSLATTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSGFYATIVAVVGLHVVLAVFVIVWKEGMPDWQENKSEX | 102 | |
| CowIn | MPRSHRPPPPTAQRQAEPKPEGSLATTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSGFYATIVAVVGLHVVLAVFVIVWKEGMPDWREEKNEX | 102 | |
| ElephIn | MPRSHRHPPAAPRTEEPKS DGVLPMTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSAFYATIVAVVGLHVVELAFFFIIVWKEGLPHWRENKNEX | 102 | |
| ArmIn | MPRSHRPPPVAQRPAEPKSDGVLAMTFKIFLLFAGLMVKVPVGLYFSCKLLLLFQS | LMLMSPEDSAFYATIVAVVGLHVVLAI | FVFIVWKEGLLOWRENKNDX | 102 |
| HumanTmem | MERPDKAALNALQPPEFRNESSLASTLKTLFFTALMITVPIGLYFTTKSYIFEGALGM | SNRDSYFYAAIVAVVAVHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| MouseTmem | MERLDKAALNALQPPEFRNENSLAATLKTLFFTALMITVPIGLYFTTKAYIFEGALGM | SNRDSYFYAAIVAVVAVHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| CowTmem | MERLDKAALNALQPSDFRNESSLASTLKTLFFTALMITVPIGLYFTTKSYVFE | GAFGMSNRDSYFYAAIVAVVAVHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| DogTmem | MERLDKAALNALQPFDFRNESSLASTLKTLFFTALMITVPIGLYFTTKSYVFE | GAFGMSNRDSYFYAAIVAVVAAHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| ElephTmem | MERLDKAALNALQPPDFRSESSLASTLKTLFFTALMITVPIGLYFTTKSYVFE | GAFGMSNRDSDYFYAAIVAVVAVHVVLALFLYVANNEGSRQWREGKQDX | 102 | |
| ArmTmem | MERPDKAALNALQPPEFRTESSLASTLKTLFFTALMITVPIGLYFTTKSYVLF | EALGMSSRDSYFYAAIVAVVAVHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| OpMTmem | MERLEKTTOSALQPPEQRNEGSLTSTLKTLLVFTALMITLPIGLYFSSKS | VVFEGPLGMSNGDSYFYAAIVAVIAVHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| OpTTmem | MERLEKTTLSVLOPPELRNEGSLTSTLKTLLVFTALMITLPIGLYFSSKS | VVFEGTLGLSNRDSDYFYAAIVAVVAVHVVLALFVYVANNEGSRQWREGKQDX | 102 | |
| ruler | 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.. | | | |

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>ElephantMcts1
MGKGRFDEKENVSNCIQLKTSVIKGIKNQLVEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>GorillaMcts1
--KGRFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
EILTVNGELLFFRQREGPFYPTLRLHCKYPFILPHQQVDKGAIKFVLSGANIMCPGLTSP
GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>HedgehogMcts1
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>PlatypusMcts1
-SFDRFDEKENVSNCIQLKTSVIKGIKNQLIDQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAASDTVVAIMAEGKQHALCVGVMKMSADDIEKVNGIGIENIHYNGLWLMKT
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YKX
>ChimpMcts1
MGKGRFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>CowMcts1
-MFKKFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
EILTVNGELLFFRQREGPFYPTLRLHCKYPFILPHQQVDKGAIKFVLSGANIMCPGLTSP
GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>DogMcts1
MGKGRFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>GuineaMcts1
MGKGRFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAADTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>HumanMcts1
-MFKKFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
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-MFKKFDEKENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>MouseMcts1
-MFKKFDEKENVSNCIQLKTSVIKGIKNQLLEQFPGIEPWLNQIMPKKDPVKIVRCHEHI
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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNGIGIENIHYNGLWLMKT
YKX
>OpossumMcts1

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-MFKKFDEKESEVINCIQLKNSVIKGIGIKNQLTSLFPEIKPWLNOIIPKKDLIKIVRCHEHI
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>RatMcts1

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GAKLYPAAVDTIVAIMAEGKQHALCVGVMKMSAEDIEKVNKIGIENIHYLNDGLWHMKT
YKX

>RhesusMcts1mRNA

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YKX

>ChimpMcts2

-MFKKFDEKESEVSNCIQLKTSVIKGIGISQLVEQFPGIEPWLNQIMPKKDPVKIVRCHEHT
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GAKLYPAAVDTIVAVTAEGKQHALCVGVMKMSAEDIEKVNKIGIENIHYLNDGLWHMKT
YKX

>MarmosetMcts2

-MFKKFDEKESEVSNCIQLKTSVIKGIGISQLIEQFPGIEPWLNQIMPKKDPVKIVRCHEHT
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GAKLFPAAVDTIVAVTAEGKQHALCVGVMKMSAEDIEKVNKIGIENIHYLNDGLWHMKT
YKX

>MouseMcts2

-MFKKFDEKESEVSNCIQLKTSVIKGIGISQLTEQFPGIEPWLNQIMPKKDPVKIVRCHEHM
EILTVNGELLFFRQRKGPFYPTLRLHKGYPFILPHQOVDKGAIKFVLSGANIMCPGLTSP
GAKLYTAAVDTIVAVMAEGKEHALCVGVMKMAAADIEKINKGIGIENIHYLNDGLWHMKT
YKX

>OrangutanMcts2

-MFKKFDEKESEVSNCIQLKTSVIKGIGISQLTEQFPGIEPWLNQIMPKKDPVKIVRCHEHT
EILTVSGELLFFRQRKGPFCP TLRLHKGYPFILPHQOVDKGAIKFVLSGANIMCPGLTSP
GAKLYPAAVDTIVAVTAEGKQHALCVGVMKMSAEDIEKVNKIGIENIHYLNDGLWHMKT
YKX

>RatMcts2

-MFKKFDEKESEVSNCIQLKTSVIKGIGISQLTEQFPGIEPWLNQIMPKKDPVKIVRCHEHM
EILTVNGELLFFRQRKGPFYPTLRLHKGYPFILPHQOVDKGAIKFVLSGANIMCPGLTSP
GAKLYTAAVDTIVAVMAEGKEHALCVGVMKMAAADIEKINKGIGIENIHYLNDGLWHMKT
YKX

>newhumanMcts2

-MFKKFDEKESEVSNCIQLKTSVIKGIGISQLVEQFPGIEPWLNQIMPKKDPVKIVRCHEHT
EILTVSGELLFFRQRKGPFCP TLRLHKGYPFILPHQOVDKGAIKFVLSGANIMCPGLTSP
GAKLYPAAVDTIVAVTAEGKQHALCVGVMKMSAEDIEKVNKIGIENIHYLNDGLWHMKT
YKX

*****. * *****. *****. ** . ** *:*****:***** ;*****. *****. *****. *****: * * *****. *****:*****;*****. *****: * . *:****: * :****:****: * :*****. *****

EleMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLVEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 GorMcts1 --KGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 181
 HedMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 PlatMcts1 -SFDRDEKENVSNCQQLKTSVKGIKNQLIDQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGTFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAASDTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 ChickMcts1 -MFKKDEKENVSNCQQLKTSVKGIKNQLIDQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGTFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 ChimpMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 CowMcts1 -MFKKDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 DogMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 GuinMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 HuMcts1 -MFKKDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 MarMcts1 -MFKKDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 MoMcts1 -MFKKDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 OpMcts1 -MFKKDEKEHSVNCQQLKNSVKGIKNQLTSIFPEKPMNQIIPKKDLKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLSPAEEADTIVAVMAEGKQHALSVGIMKMSSEEIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 RatMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 RheMcts1 MGKGRDEKENVSNCQQLKTSVKGIKNQLIEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIILTVNGELLFFRQREGPFYPTILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAIMAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 183
 ChimpMcts2 -MFKKDEKEHSVNCQQLKTSVKGIKSQLVEQFPGEPEMLNQIMPKKDPVKIVRCHEHETEILTVSGELLFFRQRKGPICPTIRLLHKYPFILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAVTAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 MarmMcts2 -MFKKDEKEHSVNCQQLKTSVKGIKSQLVEQFPGEPEMLNQIMPKKDPVKIVRCHEHETEILTVSGELLFFRQRKGPICPTIRLLHKYPFILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAVTAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 MoMcts2 -MFKKDEKEHSVNCQQLKTSVKGIKSQLTEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIELTVNGELLFFRQRKGPICPTIRLLHKYPFILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLYAAADTIVAVMAEGKQHALCVGVVKMSAEDIEKINKKGIGJENHYLNDGLNHMKTYKK 182
 OranMcts2 -MFKKDEKEHSVNCQQLKTSVKGIKSQLVEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIELTVSGELLFFRQRKGPICPTIRLLHKYPFILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAVTAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182
 RatMcts2 -MFKKDEKEHSVNCQQLKTSVKGIKSQLTEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIELTVNGELLFFRQRKGPICPTIRLLHKYPFILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLYAAADTIVAVMAEGKQHALCVGVVKMSAEDIEKINKKGIGJENHYLNDGLNHMKTYKK 182
 HuMcts2 -MFKKDEKEHSVNCQQLKTSVKGIKSQLVEQFPGEPEMLNQIMPKKDPVKIVRCHEHEIELTVSGELLFFRQRKGPICPTIRLLHKYPFILPQDQVDKGAIKFVLSGANIMCPGLTSPGAKLPAADTIVAVTAEGKQHALCVGVVKMSAEDIEKVNKGIGJENHYLNDGLNHMKTYKK 182

ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150.....160.....170.....180....

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>P.troglodytesNap115

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-----GAKHDDA

HAEMPDDAKKX-----

>B.taurusNap115

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RVLALKKLQKRC~~DKIEAKFDKEFQALEKKYNDIYKPLLAKIQL~~ELT-----GEMEGCAWTL
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HSAVPDDAKKX-----

>C.l.familiarisNap115

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-----AAAKDEGP

HSAVPDDAKK-----

>H.sapiensNap115

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EGEEE-----EEEYED~~EEGEDEEEEE~~AAA~~AAA~~AAA-----

-----GAKHDDA

HAEMPDDAKK-----

>C.jacchusNap115

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RVLALKKLQKRC~~DKIEAKFDKEFQALERKYNDIYKPLLAKIQL~~ELT-----GEMEGCAWTL
EGEEE-----GGR-----

-----GVRGX-----

>M.musculusNap115

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MADPEKQGPAE-----SRAEDEVME--GAQGGE-DAATG-----
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EGEDDE-----DDEEEEDEEEEEEEAAAGATG-----

-----GPNFAKKX-----

>P.pygmaeusNap115

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EGEEEE-----EEEYEDDEEEGEEEEEEEAAAEEAAA-----

-----GAKHDDA
HAEMPDDAKKX-----

>R.noverticulusNap115

MADPEKQGPAE-----SRAEDEVME--GAQGGE-DAATG-----
-----DSATAPAAEPPQAPAENAPKPKNDIESLPNPVKC
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EGEDDE-----DDEEEDEEEEEE-AAAGATG-----

-----GPDSAEKKX-----

>M.mulattaNap115

MADSENQGPAEPSQAAAA-----AEAAAEEVMAEGGAQGGDCDSAAGDP-----
-----DSAAGQMAEEPQTPAENAPKPKNDIESLPNSVKC
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-----GAKHDDA
HAEMPDDAKKX-----

>H.sapiensNap113

MAEAD-FKMVSEPVAHGVAEEEMASSTS DS GEES DSSSSS ST DS SSSS ST SG SSSS -- G
SG SSSSSSGS ----- TSSRSRLYRKRVPEPSRRARRA -- PLGTNFVDR LPQAVRN
RVQALRN IQDEC DVDT LFLKAIHD LER KYA ELNK PLYD RRF QII IN AYE PT EEE CEW NS
EDEEFSS DEEV QDNT PSEM PPLEGE -EE ENPKEN PEVKA EEE KEP VKE IPEV K D E E K EP V K
EIPEVK -----
-----AEEKADSKDCMEATPEVKEDPKEVPKQVKADDKEQPKATEAKARA
AVRETHKRVPEERLQDSV D LKR ARKGKP KR E DP K GIP DYWLIVLK NVDKL GPMI QKY DEP
ILKFLSDVSLKF SKPGQPV SYT FEF HFLPNPYFRNEVLVKT YII KAKPDHNDPFF SWGWE
IEDCKGCKIDWRRGKDVT VTTTQSRT -- TATGEIEI QPRV VPNA SFN FFSPPEI PMIGK
---LEPRE DAI LDED FEI GQIL HDN VILK SI YYYY TGEVN -- GTYY QFGK HYGN K KYR KX --

>C.jacchusNap113

MAEAD-FKEVSEPVAQSV AEEEMASSAS DS GEES DSSSSS ST DS SSSS SSSSSSSSSSSSS -- S

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SGSSSTSSGS-----GLYRKRVPEPSRRARRA--PWRTDFVIKLPQAVRN
RVQALRNIQDECDKVDTMFLKAIHDLERKYAELNKPPLYDRRFQIINAELYEPTEEECEWNS
EDEEFSSDEEVQDDTLSEMPPLEGE-EEEKPKENPEVKAAEEKEVPKEIPEVKDEEKEVPK
EIPEVKDEEKEVPKEIPEVKDEEKEVPKEIAEVMDEEKVIPKEIAEVMDEEKVIPKEIAE
VMDEEKVVVPKEIAEVKAEEKADSEDGMEAIPVKEDPKEAPQAKAEDKEQPKATEAKPRA
GVREAHKRVPEERLPERVSLKRARRGKPKREDPKGIPDYWLIVLKVNVDKLGPMLQYDEP
ILKFLSDVNLKFSKPGQPVSYTFEFHFLPNPYFRNEVLVKTIIIKSKPDHNDPFFSWGWE
IEDCKGCKIDWRRGKDVTQTSR--TATG--EIOPRVPNSSFNPPEIPMIGK
---LEPQEDAILDEDFEIGQILHDNVILKSIYYYTGEVNEYGSYYVGKDYGNRKYRXX-

>M.musculusNap113

MAEAD-PKMVTEPGAHVAAEEMASTACDSGDESDSNSSSNTNSCSSGSSSSGSSSSSS
SSSSSSSSSSSSGSSGSSNGSHLNRRKRVPEPSRRARRA--PSGKLFLDKLPQAVRN
RVQALRNIQNECDKVDTLFLRAIHDLERKYAELNKPPLYDKRFQIINAELYEPTEEECEWNS
E-EFGDEEMQDDTPNEMPPLEGEEEEESCNEKAEVKEEGTHVPEEVPEAKVEEEEAPK
ETPEVKTEEKDIPKEGAEKAEEQESSKE-----

-----IPEVKGEEKADSTDCIDIAPEEKEDVKEVTQANTENKDQP-TEEFTPRA
PAREAQKRVPETRPEEGVNIKRARKGPKKEDPKGIPDYWLTVLKVNVDKLGPMLQKCDEP
ILKFLSDVSLKFSNPGQPIGYTFEFHFLPNPYFRNELLMKTYIIRSKPDHYDPFFAWGWE
IEECKGCKIDWRRGKDVTVTTRSRP--GITGEIEVOPRVPNASFFNPPEIPLIGK
---LEPREDAILDEDFEIGQILHDNVILKSIYYFTGEIN--DPYYHDFRDYGNRKYYKX-

>P.pygmaeusNap113

MAEAD-FKMVSEPVAHVAAEEMASSTS DS GEESDSSSSSTSGSSSSSTGSSSSG
SGSSSSSSGSGS-----TSSRSRLYRKRVPEPSRRARRA--PLGTNFVDR LPQAVRN
RVQALRNIQDECDKVDTLFLRAIHDLERKYAELNKPPLYDKRFQIINAELYEPTEEECEWNS
EDEEFSSDEEVQDNTPSEMPPLEGE-EENPKENPEVKAAEEKEVPKEIPEVKDEEKEVPK
EIPQVK-----

-----AEEKADSKDCMEATPEVNEDPKEAPQVKADDKEQPKATEAKARA
AVREAHKRVPEERLQDSV рлкRARKGPKREDPKGIPDYWLIVLKVNVDKLGPMLQYDEP
ILKFLSDVSLKFSKPGQPVSYTFEFHFLPNPYFRNEVLVKTIIIKSKPDHNDPFFSWGWE
IEDCEGCKIDWRRGKDVTVTTRSRP--GITGEIEVOPRVPNASFFNPPEIPLIGK
---LEPREDAILDEDFEIGQILHDNVILKSVYYYTGEVN--GTYYQFGKHYGNKKYRXX-

>R.noverticusNap113

MAEAD-PKMVTEPGAHVAAEEMASTACDSGDESDSNSSSNTNSCSSGSSSSGSSSSSS
SSSSSSSSSSSSGSSGSSNGSHLNRRKRVPEPSRRARRA--PSGKLFLDKLPQAVRN
RVQALRNIQNECDKVDTLFLRAIHDLERKYAELNKPPLYDKRFQIINAELYEPTEEECEWNS
E-EFGDEEMQDDTPNEMPPLEGEEEEESCNEKAEVKEEGTHVPEEVPEAKVEEEEAPK
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-----IPEVKGEEKADSTDCIDIAPEEKEDVKEVTQANTENKDQP-TEEFTPRA
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ILKFLSDVSLKFSNPGQPIGYTFEFHFLPNPYFRNELLMKTYIIRSKPDHYDPFFAWGWE
IEECKGCKIDWRRGKDVTVTTRSRP--GITGEIEVOPRVPNASFFNPPEIPLIGK
---LEPREDAILDEDFEIGQILHDNVILKSIYYFTGEIN--DPYYHDFRDYGNRKYYKX-

>P.troglodytesNap113

MAEAD-FKMVSEPVARVAAEEMASSTS DS GEESDSSSSSTSDSSSSSTGSSS--G
SGSSSSSSG-----TSSRSRLYRKRVPEPSGRARRA--PLGTNFVDR LPQAVRN
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EDEEFSSDEEVQDNTPSEMPPLEGE-EENPKENPEVKAAEEKEVPKEIPEVKDEEKEVPK
EIPEVK-----

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ILKFLSDVSLKFSKPGQPVSYTFEFHFLPNPYFRNEVLVKTIIIKSKPDHNDPFFSWGWE
IEDCKGCKIDWRRGKDVTVTTRSRP--TATGEIEIOPRVPNASFFNPPEIPLIGK
---LEPREDAILDEDFEIGQILHDNVILKSIYYYTGEVN--GTYYQFGKHYGNKKYRXX-

>C.l.familiarisNap113

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SGRS-----RLYRKRVSGPSRGARGA--PLGKS FVDR LPQAVRN

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ILKFLSDISLKFSKPGQPISYTTFEFYFLPNPYFRNEMLTKTYIIKSKPDHNDPFFSWGWE
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---LEPREDAILDEDFEIGQILHDNVILKSIYYYYTGEVK--GTYDD-GKDYGNRKRYRKKX-

>P.troglodytesNap112

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DSEDCDDEEMCH---EEMYGNEGMVHEYVDEDGYEDYYDYAVEEEEEEE-----

-----EEEE--DIEATGEENKEEEDPKGIPDFWLTVLKNVDTLTPLIKKYDEP
ILKLLTDIKVKLSDPGEPLSFTLEFHFKPNEYFKNELLTKTYVLKSCLAYDHPYRGTA
IEYCTGCEIDWNEGKNVTLKTICKKQKHRIWGTIRTVTEDFPKDSFFNFFSPHGITSNGR
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>C.l.familiarisNap112

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RVLALKKLQTRVANLESKFMREFHGIERKFAEMYQPLLEKRRQIINAIYEPTKEECEYKS
DSEDYDD-EMYDE---EEMYGNEGLVHEYMDGGYEGDYYDYAVEEDDGD-----

-----DDDDNGDDIEATGENKEEQDPKGIPDFWLTVLKNVDTLTPLIKKYDEP
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IEYCTGCEIDWNEGKNVTLKTICKKQKHRIWGTIRTVTEDFPKDSFFNFFTPQGISSNGK
---DGND-----DFLLGHNLRTYIIPRSVLFFSGDALE-SQEGVVREVNDAIYDKII
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>E.caballusNap112

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RVLALKKLQTRVANLESKFLREFHDIERKFAELYQPLLEKRRQIINAIYEPTKEECAYKS
DSEDYDEEMYDE---EEMYGNEESLVHEYMDGGYEDYYDYDVEEEEDDE-----

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>H.sapiensNap112

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>C.jacchusNap112

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>M.musculusNap112

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DCEDYFEEEMDEE---EETNGNEDGMVHEYVDEDGYEDCYYDYDDEEEEEE----------EDD-SAGATGGEEVNEEDPKGIPDFWLTVLKNVEALTPMIKKYDEP
ILKLLTDIKVKLSDPGEPLSFTLEFHFKPNEYFKNELLTKTYVLKSKLACYDHPYRGTA
IEYATGCDIDWNEGKNVTLRTIKKKQRHRVWGTVRTVTEDFPKDSFFNFFSPHGISLNGG
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>R.noergicusNap112

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>M.mulattaNap112

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ILKLLTDIKVKFSDPGEPLSFTLEFHFKPNEYFKNELLTKTYVLKSKLAYDHPYRGTA
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>P.troglodytesNap111

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RVNALKNLQVKCAQIEAKFYEEVHDLERKYAVLYQPLFDKRFEIINAIYEPTEECEWKP
D-----EDEISEELKEKAKIEDEKKDEEKE----------DPKGIPFWLTVFKNVDLLSDMVQEHDEP
ILKHLKDIKVFKFSDAGQPMFSVLEFHFEPEYFTNEVLTCKTMRSEPDDSDPFSFDGPE
IMGCTGCQIDWKKGKNVTLKTIKKQKHGRGTWVTKTVSNDSFFNFFAPPEVPESGD
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>H.sapiensNap111

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-----DPKGIPPEFWLTVFKNV DLLSDMVQEHD
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>P.troglodytesNap114

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-----NP KGIPEFWFTIFRN VDMLSELVQEYD E P
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IVDCDGCTIDWKKGKNVTVK TIKKKQKHKGRTV RTITK QVPN E SFFNPLKGNS GD
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>M.domesticusNap114

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-----ECVPHAFELH XNL T QSGQETH XC FETAAGEV CTH
RSQVLRG SAXFGAKIRSP LPAS LX-XETGFCHWX CXTYRC RIMA QX--EXGGGETGWR S
EKQSGDS-----REGSSC RAKS QRD SRILV YNLX KRG Y AER-----

-----ISAGVXXA
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>H.sapiensNap114

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-----NPRVLAALQERLDNVP--HTPSSYIETLPKAVKR
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IVDCDGCTIDWKKGKNVTVK TIKKKQKHKGRTV RTITK QVPN E SFFNPLK--ASGD
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>ChimpU2af1-rs2

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LQCEFCPVTWKMAICGLFEIQQCPRGKHCVNLFHVFRNPNEWEANRDIYLSPDRTGSS
FGKNSERRERMGHHDYYSLRGRR-NPSPDHSYKRNGESERKR-SHHRGKK-SHKRTSK
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>DogU2af1-rs2

----MAAPEKMMFPEKPSHKKYRAALKKAKRKKRQELARLRDGLLQKEEE-DAFIEEQ
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LQCEFCPVTWKMAICGLFEIHQCPRGKHCVNLFHVFRNPNEWEANRDIYLSPDRTGSS
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>HumanU2af1-rs2

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>MarmosetU2af1-rs2

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>MouseU2af1-rs2

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GSRDKTTQSPSKX-----

>OpossumU2af1-rs2

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KSASRSRSRDRKRSTS RD RNTX-----

>RatU2af1-rs2

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KERESEEQKQQEKRERE-----LENGGTWQNPEPPTDIRVLEKDRANCPFYS
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FAKS SERRERASHYDEYYGRSRRR-SPSPGLSYKRNGESDRKSSSNHRVKK-SHKGMK
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>RhesusU2af1-rs2

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>platypusU2af1-rs2

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>mouseU2af1-rs1

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KOREEEEQKLOKEKREREAVQKMLDQA---ENERIWQNPEPPPKDLR-LEKYRPSCP FYN
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LDFYHDVLPEFKNVGVKVIQFKVSCNLEPHLRGNVYVQYQSEEECQAALSLFVN GRWYAGRQ
LOCEFCPVTRWVAICGLFEMQKCPKGKHCNFLHVFRNPNEFWEANRDYLMSPPAWTGS
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DSSPGPQS QSHRTX-----

>RatU2af1-rs1

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KOREEEEQKLOKEKKEREAVQKMLDQA---ENE GTWQNPEPPPKDLR-LEKYRPSCP FYN
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SHERHSSR-RGRE-----E
GSSPGPQS QSHRTX-----

