

FIGURE 1

LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR 60
LGYYPYIDSIITGVTVNGGIPQKISLQDHLDKAKKDIIFYMPVDNLGMAVIDWEEWRPTWA 120
RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGLLRPNHL 180
WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDDLSWLWNNESTALYPsiYLNtQQSPVAAT 240
LYVRNRVREAIRVSKI^{PD}AKSP^{LP}VFA^YTR^{IV}FTDQ^{VL}KFLSQDEL^{VY}TFGET^{VAL}GASG 300
IVIWGTL^{SI}MRSMKSC^{LL}LDNYMETILNPYIINVT^{LA}AKMCSQ^{VL}CQEQGVCIRKNWNSS 360
DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCYCSTLSCKEKADV^{KD}TD^{AV} 420
DVCIADGV^CIDAFLKPPMETE^{EP}QIFYN^{AS}PS^{TL}SATMFIV^{SI}LFLIISSVASL 474

FIGURE 2B

SEQIDNO_3	LNFRAPPVIPNVFPLWAWNAPSEFCGLGFDEPLDMSLFSFIGSPRINATGQGVTFIFYVDR 60
Rhesus_SEQIDNO_12_	LNFRAPPVIPNVFPLWAWNAPSEFCGLGFNEPLDMSLFTLMGSPRINITGQGVTFIFYVDR 60
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	LGYYPYIDSLTGTVTVNGGIPQKISLQDHLDKAKKIDITFYMPVDNLGMAVIDWEEWRPTWA 120
Rhesus_SEQIDNO_12_	LGYYPYIDSLTGTVTVHGIPQKVSLQDHLDKSKQDILFYMPVDNLGMAVIDWEEWRPTWA 120
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	RNWPKPDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKGLLRPNHL 180
Rhesus_SEQIDNO_12_	RNWPKPDVYKNRSIELVQQQNVQLSLPQATDKAKQEFKAGKDFMLETIKLGRSLRPNHL 180
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	WGYLFPDCYNHHYKPGYNGSCFENVEIKRNDLWSLWNESTALYPSIYLNTOQSPVAAT 240
Rhesus_SEQIDNO_12_	WGYLFPDCYNHHYKPGYNGSCFDEVEIKRNDLWSLWNESTALYPSIYLNTOQSVVAT 240
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	LYVRNRVREAIRVSKIPDAKSLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG 300
Rhesus_SEQIDNO_12_	LYVRNRVREAIRVSKIPDAKNPLPVFVYARLVFTDQVLKFLSREELVSTLGETVALGASG 300
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCQVLCQEQGVCIRKNWNSS 360
Rhesus_SEQIDNO_12_	IVIWGSLSTRSMKSCLLLDTYMETILNPYIINVTLAAKMCQVLCQEQGVCIRKDNSS 360
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV 420
Rhesus_SEQIDNO_12_	DYLHLNPDNFDIRLEKGGKFTVHGKPTVEDLEEFSEKFCSCYTNLSCKEKADVKTDAV 420
	*****:*****:*****:*****:*****:*****:*****
SEQIDNO_3	DVCIADGVCIDAFLKPPMETE-EPQIFY----- 447
Rhesus_SEQIDNO_12_	DVCIADGVCIDASLKPPVETEGSPPIFYNTSSSTVSTTMFIWRLEVWDQGISRIGFF 477
	*****:*****:*****:*****:*****:*****:*****

4/13

FIGURE 2C

```
SEQIDNO_3
Cyno_SEQIDNO_14_
LNFRAPPVIPNVPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR 60
LNFRAPPVIPNVPFLWAWNAPSEFCLGKFNEPLDMSLFTLMGSPRINVTGQGVTFYVDR 60
*****:*****:*****:*****:*****:*****:*****
LGYYPYIDSLITGTVTNGGIPQKISLQDHLDKAKDITFYMPVDNLGMAVIDWEEWRPTWA 120
LGYYPYIDSLITGTVTNGGIPQKISLQDHLDKSKQDILFYMPVDNLGMAVIDWEEWRPTWA 120
*****:*****:*****:*****:*****:*****:*****
RNWPKPDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGLLRPNHL 180
RNWPKPDVYKNRSIELVQQQNVQLSLPQATDKAKQEFKAGKDFMLETIKLGRSLRPNHL 180
*****:*****:*****:*****:*****:*****:*****
WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLWLNWNESTALYPSIYLNTOQSPVAAT 240
WGYLFPDCYNHHYRKPGYNGSCFDVEIKRNDLWLNWNESTALYPSIYLNTOQSVVAT 240
*****:*****:*****:*****:*****:*****:*****
LYVRNRVREAIRVSKIIPDAKSPLPVFAVYTRIVFTDQVLKFLSQDELVYTFGETVALGASG 300
LYVRNRVREAIRVSKIIPDAKNPLPVFYARLVFTDQVLKFLSREELVSTLGETVALGASG 300
*****:*****:*****:*****:*****:*****:*****
IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS 360
IVIWGSLITRSMKSCLLLDTYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKDNSS 360
*****:*****:*****:*****:*****:*****:*****
DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCYSCYSTLSCKEKADVKTDAV 420
DYLHLNPDNFDIRLEKGGKFTVHGKPTVEDLEEFSEKFCYSCYTNLSCKEKADVKTDAV 420
*****:*****:*****:*****:*****:*****:*****
DVCIADGVCIDAFLLKPPMETE-EPQIFY----- 447
DVCIADGVCIDASLKKPPVETEGSPPIFYNTSSSTVSTTMFIVNILFLIISSVASL 475
*****:*****:*****:*****:*****:*****:*****
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8/13

FIGURE 2G

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SEQIDNO_3
Rabbit_SEQIDNO_24_
LNFRAPPVIPNVPFLWAWNAPSEFFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR 60
ANFRAPPVIPNVPFLWAWNAPTEFFCLGKSGEPLDMSLFSFGSPRKNKTGQGITIFYVDR 60
*****:*****.*****.*****.*****.*****.*****
LGYYPYIDSIITGVTVNGGIPQKISLQDHLDKAKKIDTFYMPVDNLGMAVIDWEEWRPTWA 120
LGYYPYIDPHTGAIVHGRIPOGLPQLQOHLTKLRQEILYMPKDNVGLAVIDWEEWLPTWL 120
*****.***.***.***.***.***.***.***.***.***.***.***.***
RNWPKDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL 180
RNWPKDIYRIKSIELVKSQHPQYNHSHYATEKAKRDFEAKGKDFMEETLKLGRLLRPNHL 180
*****:***.*****.***.***.*****:*****.*****:*****
WGYLFPDCYNHHYKKP-GYNGSCFNFVEIKRNDLWSLWNESTALYPSIYLTQQ---SP 236
WGYLFPDCYNHHYDKPNLYKGSCFEDIEKKRNDLWSLWNESTALFPSVLTSRARSATA 240
*****:***.*****.***.*****:*****:*****:***.***.***.***
VAATLYVRNRVREAIRVSKIPDAKSPLPVFAIYTRIVFTDQVFLKFLSQDELVYTFGETVAL 296
LSKLYVRNRVHEAIRVSKIPDDKSPLPNFYTRIVFTDQIFQFLSHHDLVYTTIGEIVAL 300
:***.*****:*****.*****.*****.*****:*****:***.***
GASGIVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIKRN 356
GASGIVVWGSQSLARSMKSCLLHDNYMKTILNPYILNVTLAAKMCNQVLCQEQGVCTRKN 360
*****:***.*****.*****:*****:*****.*****:*****.***
WNSSDYLHLNPDNFALQLEKGGKFTVRGKPTLEDLEQFSEKFYCSYSTLSCKEKADVCD 416
WNPNDYLHLNPGNFALQLGSGNGTYKVDGKPTLTDLEQFSKNFQCSCTNLNCKERTDMNN 420
**..*****.*****.***.***.*****.*****:***.*****:***:***
TDÄVDVCIADGVCIADFLKPPMETEEPQ----- 444
VRTVNVCAVENVCIDTNVGPQAVTYAPKEKKDVAHILSNSTTSINSSTMSLPFPRKHVSG 480
.***.***.***:***.***.***.***.***.***.***.***.***.***.***
-----IFY----- 447
CLLVLCMYSQYLNICYRLVAIGIQHGYLYLK 510
* *

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FIGURE 2H

SEQIDNO_3	LNFRAPPVIPNVPFLWAWNAPSEFCLGKFEPLDMSLFSFIGSPRINATG	50
GuineaPig_SEQIDNO_29_	-DKRAPPLIPNVPFLWAWNAPTEFCIGGTNQPLDMSFFSIVGTPRKNITG	49
	: ****:****:*. ****:****:*. ****:****:****:****:*. ****:*. *	
SEQIDNO_3	QGVTFYVDRGLGYPYIDISITGVTVNGGIPQKISLQDHLDAKAKDITFYM	100
GuineaPig_SEQIDNO_29_	QSITLYVDRGLGYPYIDPHTGAI VHGGLPQLMNLQQHLRKSQRDILFYM	99
	.::*****. *. *:***:*. *:***:*. *:***:*. *:***:*. *	
SEQIDNO_3	PVDNLGMAVIDWEEWRPTWARNWPKDVYKNRSIELVQQQNVQLSLTEAT	150
GuineaPig_SEQIDNO_29_	PTDSVGLAVIDWEEWRPTWTRNWRPKDIYRNKSIELVKSQHPQYNHSYAV	149
	.::*****. *:***:*. *:***:*. *:***:*. *:***:*. *:***:*. *	
SEQIDNO_3	EKAKQEFKAGKDFLVETIKLGKLLRPNHLWGYYLFPDCCYNHHYKKPGYN	200
GuineaPig_SEQIDNO_29_	AVAKRDFERTGKAFMLETLKLGKSLRPSSLGYYLFPDCYNTHFTKPNYD	199
	.::* *:***:*. ****. *****. *:***:*. *	
SEQIDNO_3	GSCFNVEIKRNDLWSLWNESTALYPSIYLNTQQ-SPVAATLYVRNRVRE	249
GuineaPig_SEQIDNO_29_	GHCPIELQRNDLQWLNDSTALYPSVYLTSRVRSSQNGALYVRNRVHE	249
	* *:***:*. ****:*****. *:***:*. *:***:*****. *	
SEQIDNO_3	AIRVSKIPDAKSPLPVFAYTRIVFTDQVLFKLSQDELVYTFGETVALGAS	299
GuineaPig_SEQIDNO_29_	SIRVSKLMDDKNPLPIYVIRLVFTDQVLTTFLELDDLVSVEIPLGVS	299
	:*****: * *.***:*. *:***:*. *. *.***:*. *.***:*. *	
SEQIDNO_3	GIVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQ	349
GuineaPig_SEQIDNO_29_	GIIIWGSLSTRSLVSCIGLENYMKGTLLPYLINVTLAAKMCGQVLCQKQ	349
	.:*:***:*. **:***:*. *:***:*. *:***:*****. *:***:*. *	
SEQIDNO_3	GVCIRKNWNSSDYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFY	399
GuineaPig_SEQIDNO_29_	GICTRKDWNTNTYLHLNATNFDIELQQNGKFVVGKPSLEDLQEFSSKNFH	399
	: *:***:*. *****. ** *:***:*. *****:*****:***:***:*	
SEQIDNO_3	CSCYSTLSCKEKADVKTDAVDVCIADGVCIDAF-----KPPMET	440
GuineaPig_SEQIDNO_29_	CSCYTNVACKDRILDVHNVRSVNVCTANNICIDAVLNFPSLDDDDDEPPITD	449
	*****:***:*. **:***:*. *:***:*. *****. *:***:*	
SEQIDNO_3	EEPQ-----IFY----- 447	
GuineaPig_SEQIDNO_29_	DTSQNQDSISDITSSAPSSHILPKDLSWCLFLLSIFSQHWKYL 494	
	: . *	

FIGURE 2J

SEQIDNO_3	LNFRAPPVIPNVPFLWAWNAPSEFCGLKFDEPLDMSLFSFIGSPRINATQGVTIFYVDR	60
GIBBON_SEQIDNO_857	LNFRAPPVIPNVPFLWAWNAPSEFCGLKFDEPLDMSLFSLTGSPRINVTGQGVTFIFYVDR	60
	*****; *****	
SEQIDNO_3	LGYYPIYDSITGVTNNGGIPQKISLQDHLDDKAKKDI TFYMPVDNLGMAVIDWEEWRPTWA	120
GIBBON_SEQIDNO_857	LGYYPIYDSITGVTNNGGIPQKISLQDHLDDKAKQDITFYPVPVDNLGMAVIDWEEWRPTWA	120
	*****; *****	
SEQIDNO_3	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180
GIBBON_SEQIDNO_857	RNWKPKDVYKNRSIELVQQQNVQLSLAEATEKAKQEFKAGKDFMVFETIKLGKLLRPNHL	180
	*****; *****	
SEQIDNO_3	WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLDSLWNNESTALYPSIYLNTOQSPVAAT	240
GIBBON_SEQIDNO_857	WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLDSLWNNESTALYPSIYLNTOQSPVAAT	240

SEQIDNO_3	LYVRNRVREAIRVSKI PDAKSPLPVFA YTRI VFTDQVLKFLSQDELVYTFGETVALGASG	300
GIBBON_SEQIDNO_857	LYVRNRVREAIRVSKI PDAKSPLPVFYAR VFTDQVLKFLSRDELVYTLGETVALGASG	300
	*****; *****; *****	
SEQIDNO_3	IVIWGTLSIMRSMKSCLLLDNYMETILNPYI INVTLAAKMCSQVLCQE QGVCIRKNWNSS	360
GIBBON_SEQIDNO_857	IVIWGSLSVIRSMKSCLLLDNYMETILNPYI INVTLAAKMCSQVLCQE QGVCIRKDNSS	360
	*****; *****; *****	
SEQIDNO_3	DYHLNPNDFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV	420
GIBBON_SEQIDNO_857	DYHLNPNDFAIQLEKGGKFTVRGKPTPEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV	420

SEQIDNO_3	DVCIADGVCIDAF LKPPMETEEPQIFY----- 447	
GIBBON_SEQIDNO_857	DVCIADGVCIDAF LKPPKETEESEQIFYNASPSTLSATMFIVSILFLIISSVSL 474	

FIGURE 2K

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SEQIDNO_3
MARMOSSET_SEQIDNO_859
LNFRAPPVIPNPVFLWAWNAPSEFCLGKDFEPLDMSLFSFIGSPRINATGQGVTFYVDR 60
LNFRAPPVIPNPVFLWAWNAPSEFCLGKDFEPLDMSLFSFIGSPRINVTGQGVTFYVDR 60
*****:*****:*****:*****:*****:*****:*****
LGYPYIDSIITGVTVNGGIPQKISLQDHLDKAKKDIIFYMPVDNLGMAVIDWEEWRPTWA 120
LGYPYIDPTTGAVVNGGIPQKIALQDHLDKVRKDIIFYMPVDNLGMGVIDWEEWRPTWA 120
*****. **. *****:*****:*** *****:*****:*****
RNWPKDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL 180
RNWPKDIYKNKSIEMVQQRVQLNLTQATDIAKQEFKAAKDFMLETIKLGKALRPNHL 180
*****:*****:*****:***: *****:*****:*****
WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLWSLWNESALYPSIYLNTOQSPVAAT 240
WGYLFPDCYNHHYKKPDYNGSCFNIEIKRNDLWSLWNESALYPSIYLNTOQSAVAA 240
*****:*****:*****:*****:*****:*****:*****
LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG 300
LYVRNRVQEAIRVSKTPNANSPLPVFYARLVFTDQVLRFLSQDELVYTLGETVALGASG 300
*****:***** *:*****:*****:*****:*****:*****
IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTAAKMCQVLCQEQGVCIRKNWNSS 360
IVIWGSLSIMRSMKSCLLLDTYMETVLNPYIINTTAAKMCQVLCQEQGVCIRKDNWSS 360
*****:*****:*****:*****:*****:*****:*****
DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV 420
DYLHLNPDNFAIETEKGGKFTVRGKPTYEDLEQFSEKFYCSCYSTLSCKVKADVKTDAV 420
*****:*****:*****:*****:*****:*****:*****
DVCIADGVCIDAFKPPMETEEP-QIFY----- 447
DVCIADGVCIDASLKPPKETEESQIFYNPSSSTPSAAIFIVAILFFISCVVSL 474
*****:*****:*****:*****:*****:*****

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FIGURE 2L

```
SEQIDNO_3
ORANGUTAN_SEQIDNO_861
LNFRAPPVIPNVPFLWAWNAPSEFCLGKDFDEPLDMSLFSFIGSPRINATGQGVTFYVDR 60
LNFRAPPVIPNVPFLWAWNAPSEFCLGKDFDEPLDMSLFSFIGSPRINATGQGVTFYVDR 60
*****:*****:*****:*****:*****:*****:*****:*****
LGYYPIIDSIITGVTVNGGIPQKISLQDHLDKAKDITFYMPVDNLGMAVIDWEEWRPTWA 120
LGYYPIIDSIITGVTVNGGIPQKISLQDHLDKAKDILFYMPVDNLGMAVIDWEEWRPTWA 120
*****:*****:*****:*****:*****:*****:*****:*****
RNWPKPDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL 180
RNWPKPDVYKNRSIELVQQNVQLNLTEATEKAKQEFKAGKDFMVFETIKLGKLLRPNHL 180
*****:*****:*****:*****:*****:*****:*****:*****
WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLDSLWNFESTALYPSIYLNTOQSPVAAT 240
WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLDSLWNFESTALYPSIYLNTOQSPVAAT 240
*****:*****:*****:*****:*****:*****:*****:*****
LYVRNRVREAIRVSKIIPDAKSPVPFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG 300
LYVRNRVREAIRVSKIIPDAKSPVPFYARIVFTDQVLKFLSQDELVYTFGETVALGASG 300
*****:*****:*****:*****:*****:*****:*****:*****
IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTAAKMCQVLCQEQGVCIRKNWNSS 360
IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTAAKMCQVLCQEQGVCIRKNWNSS 360
*****:*****:*****:*****:*****:*****:*****:*****
DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV 420
DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV 420
*****:*****:*****:*****:*****:*****:*****:*****
DVCIADGVCIDAFKPPMETEEPQIFY----- 447
DVCIADGVCIDAFKPPMETEESQIFYNASPTLSATMFIWRLEVWDQGISRMGFF 476
*****:*****:*****:*****:*****:*****:*****:*****
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