

H.sapien 1 -----MESSTGPRMPLLKYSVATS LKAPGWDGAAP
G.gorilla 1 -----MESSTGPRMPLLKYSVATS LKAPGWD SAAP
P.abelii 1 -----MPLLKYSVATS LKAPGWD SAAP
N.schauinslandi 1 -----MESSAGEGTPLPKYCSVAT TLKSPSRTGAAP
L.vexillifer 1 -----MPLPKYCSVAT TLKAPAWAGTAP
E.przewalskii 1 -----MESSAGEGMPLPKYCSVAT LRAPAWAGAAP
H.armiger 1 -----MESTAEPGMPLPKYCSVAT LEAPAWTSTAS
C.lanigera 1 MAAVTSEQVDGCHGPEVSAQP GPPELVPPH SPPAMQPAMPLPKYCSVAT ILQDPGWGCDAG
C.mydas 1 -----MENPGRSLFTEHRYCRAMTALDKLSCSNFLT
B.gibbericeps 1 -----
consensus 1 mess p mplpkycsvatslkapgw aap

H.sapien 32 PWDLSFTYPFALQAPWLTGHKPLARHASSCPCLHVADPAWQGP-GWLGRAGDAANTWVLA
G.gorilla 32 PWDLSFTYPFALQAPWLTGHKPLARHASSCPCLHIADPAWQGP-GWLGRAGDAANTWVLA
P.abelii 24 PWDLSFPYPFALQAPWLTGHKPLARHASSCPCLHIADPAWQGP-GWLGRAGDAANTWVLA
N.schauinslandi 32 PWGLSFTCPFATQAPWLSRHNP LSRYSYHPCLHIADSAWQGP-GWLGRVGDAAADTWVLA
L.vexillifer 24 PWE LSEACPLASQGPWLTROSPLTRYASYDPCLHIADPAWQGP-GWLRRGGDAADAWVLA
E.przewalskii 32 RWNLSFACPFALQAPWLPGHSA LTSYAAYPPCLHVADPAWQGP-GWLGRVGDAAADTWVLA
H.armiger 32 PWDLSFTCPFALRVPWHN--PLTRCSCYHPYLHSADPAWQGP-GWLGGV RGAADTWVLA
C.lanigera 61 PGDI SEACPF AHRAPGLPRAHALTRYALHLPCLHIADPAWQDP-GWMGRVRDAANAWVLA
C.mydas 32 NIDPFSSGSEFMVHPAWVT RLLIPQRCSWIGHCPHFDP TACKGLKVWEKSVDI AH-DPVLA
B.gibbericeps 1 -----CVPSPGPAWKRLSAPGISVGLGCNVPVLV
consensus 61 pwdlsftcpfalqapwlt h plsr as pclhiadpAwqgp gwlgrv gdaantwVLa

H.sapien 91 RREADG FYYRAQIKATPELEROGVLLVEFEAPLVA GPKLPAQOQORVVLEEDVIPLSPSVG
G.gorilla 91 RREADG FYYRAQIKAPELEROGVLLVEFEAPLVA GPKLPAQOQORVVLEEDVIPLSPSVG
P.abelii 83 RKEADG FYYRAQIKAPELEROGVLLVEFEAPLVA GSKLPAQOQORVVLEEDVIPLSPSVG
N.schauinslandi 91 RRGPDG FYYWAQIKAPELERRGALLVEFEVPLVTDPKRPAQRONVVLEDDVIOFLPSTE
L.vexillifer 83 RREADG FYYRAQIKAPELEROGFLLVEFEAPLVTCPGLPAQRXSMAL EEDVIOFSPSVE
E.przewalskii 91 RREP DGFYRAQIKAPELEROGALLVEFEAPLVTGLKLP AQOQOSVVLEDDVIOFSPSME
H.armiger 88 RREP DGFYWAQIKAPELEROGALLVEFEAPLVTGPKLP AQOWOSVVLEDDVIOFSPFTQ
C.lanigera 120 RKEP DGLYRAQIKAPELEROGTLLVEFEAPLVTGPRLP AQOROSVSVVEDVIOFSPYVE
C.mydas 91 RRES DGFYLLGTIKOEIEGER-GTFLVEFDKPPASGD KYSVCVQ-KTARDDILEYVNGMR
B.gibbericeps 30 RGEODG FYYRGTVKEEIESE R-GMFLVEFAEPLVSRGSHPV RVQ-KTAKDDILECVNGMK
consensus 121 Rre DGfYYraqiKaapElERqG llVEFeaPlvtgpklp aq q vvleeDviqf spsv

H.sapien 151 YSLRPGDKVLALWEPGQQOYGP GTVLLGLEMRDPQRASKEKEITVHF WNGKAAKVPLGGV
G.gorilla 151 YSLRPGDKVLALWEPGQQOYGP GTVLLGLEMRDPQRASKEKEITVHF WNGKAAKVPLGGV
P.abelii 143 YSLRPGDKVLALWEP RQQOYGP GTVLLGLEMRDPQRASKEEEEITVHF WNGKAAKVS LGGV
N.schauinslandi 151 CSLRPGD TVLAPWEPDRORYGPGTVLLG LEARDPQRASKEGEITVHF WNGKTA SVPRGGV
L.vexillifer 143 YSLRLGDKVLALWGP HQRYGPGT PLGLEARDPQRASKEEEEITVHF WNGKTAHVPLGGV
E.przewalskii 151 YSLQPGDKVLAPWEPDRORYGPGTVLLGLEARDPQRASKEEEEITVHF WNGKIAVPPLGGV
H.armiger 148 YSLQPGDKVLAPWEPDQORYGPATV LG-LEAREPQRASKEEEEITVHF WNGKMATVPLGGV
C.lanigera 180 YSLRPGDKVLAAWEPGRORYGPGTVLLGLDMRDSQRASKEEEEITVHF WNGKTAQVPLGGV
C.mydas 149 HSLLPGDKVLAPWEPDLVRYGPGT LLGIE TRDPLRASEDEEIMVYFWNDKKVKVPLGVA
B.gibbericeps 88 HSLLPGDKVLAPWESDMARYGPGTVLTGIE TRDPLRASEDEEIMI QFWNDKKVKLQRGVA
consensus 181 ySlrpGdKvLApWepdqqrYGPgTvl lgle RdpqRASkeeEitvhFWNgk akvplGgv

H.sapien 211 QSVSLT IWKKAVERLHKSEFTR-----EHP RPLHWAPCCSLLGPITGRITNELP--PDA
G.gorilla 211 QSVSLA IWKKAVERLHKSEFTR-----EHP RPLHWAPCCSLLGPITGCIANELP--PDA
P.abelii 203 QSVSLA IWKKAVERLHKSEFTR-----EHP RPLHWAPCCSLLGPITGRITNELP--PDA
N.schauinslandi 211 RWVPPAVWKKAGGR LHKPSIK-----EHAGALLWAPCCSFRGPAAGWVTNGLS--PGT
L.vexillifer 203 RWVPPAVWKKAVDR LHKAFTT-----EHP RPLLWAPCCS IAGPVAGCVTGGLP--LST
E.przewalskii 211 RWVPPAVWKKKAVERLHKPFTR-----EHP SPLLWAPCCP LLGPVTGYVSNGLP--LGT
H.armiger 207 RWVSPA VWKKKAVERLHNPFTR-----EHP SPLLWAPCCS PLGPVTGCVTYGLP--LGT
C.lanigera 240 RWVPPTEWKKKAVERLSKSHTS-----EHP SALLWAPCCS LLGTVTGGITNRLP--PDT
C.mydas 209 LWIPPD MWERIVEMIHMPFT SRLKFMNPHNTTSSYTS PCRF LRAPIHSCALDDGLSKYRW
B.gibbericeps 148 LWIPPSL WERIVEMIHMPFT SRAKPRES PDAN-SCTFSCSPNTALIPVCAVHS---LAKH
consensus 241 rWvppaiWkkaverlhkpftr eh p pllwapCcsllgpitgcitn lp p t

H.sapien 262 PFLCPLCHH-----HACCOLLCQGCLCGCPPCGT TWWPLTRTSEVMARELP----ELE
G.gorilla 262 PFLCPLCHP-----HACCOLLCQGCLCGCPPCGT TWWPLTRTSEVMARELP----ELE
P.abelii 254 PFLYPLCHP-----HTCCOLLGQGLCGCPPCGT TWWPLTRTSEVMARELP----ELE
N.schauinslandi 262 PFLCPPCVP-----OACCOLLGQGLCPCPLAGPTWWPLTR-----AKEHPE--VELK
L.vexillifer 254 PFLCPPCHP-----HTCCOLLGQGLCRRPLAGPTWWPLTRTSGVTAREHPE--AELK
E.przewalskii 262 PFLCPPCHP-----YACCOLLCQGRGCCPLVGP TWWPLTRTSGVTATERPE--AELK
H.armiger 258 PFLCPPCHP-----NVCCOLLGQGLCCCPPLAGSTWWPLTRSSGATARRYPE--VELK
C.lanigera 291 AFLCPPCHS-----HACCOLLCQSSLLCCCPSSMSA WWRLLTRTFDTTARELPE--PELK
C.mydas 269 PRPCPLPCPFHGHCHSVCCSPVHVGCICCSHPKFNAWWPLLSTLLSORGRTKPKQESNNK
B.gibbericeps 204 CLLCSECWPRRLHYHCDGICCCSSAYVRCICCCYPHVDAWWPLPSRSLVFORETEEAESSGK
consensus 301 pflcppchp haCCqllcqqclCccpp gttWWpLtrts vtare pe elk

H.sapien 311 PTAQLLPLEGPKEEKVAMHAPLAVSSSS--SSSCEODGVENDLEMGP PQRMLVNSAVNTDP
G.gorilla 311 PTAQLLPLEGPKEEKVAMHAPLAVSSSS--SSSCEODGVENDLEMGP PQRMLVNSAVNTDP
P.abelii 303 PTAQLLPLEGPKEEKVAMHALLAVSSSS--SSSCEODGVENDLEMGP PQRMLVNTAVNTDP
N.schauinslandi 308 PTAPRLPLEGPKEEGAVQAP-LGVSSSS--SSSSSEEDLENDLQIGLPQRMLVDS TVNTDP
L.vexillifer 305 PTAQLLPLEGPKEEVVQAPXAVSSSSAS--SSSSAEEDLENDLELELGLPQRPAVDSTANTAP
E.przewalskii 313 PTAQLLPLEGPKEEEVAVQAPMAVPS--SSSEEDLENDLEMGLPQRMLVDS TVNTDP
H.armiger 309 PVAQLLPLEGPKEEEATVQAPMAVCPSS--STSQEEEDLEKDLLEMGLPQRMLVDS TVNTDP
C.lanigera 342 PAAQLLPLEGAKKEPVAVHVAPAVSSSS--SSSFCEDLEDNLEVLGLPQRMLVNSAVNTDP
C.mydas 329 PTAQFLLELESPKENE-----PAAAAASSSSSSSSSDLEKSEEMCLTQSTMVDSAVNTDS
B.gibbericeps 264 PSPHLLLELEGPNOEQ-----PAVVAASSPSSDSEWDLEPPF-----AKSTVDSAVNTAS
consensus 361 PtaqlLpLEgpkeeevav aplavssSS sSsse ddlendlemglpqrmlVdsavNTdp

H.sapien 370 IFLEMLPLR-OSGLCOPEWRYWKRNGPEPC LGKPGTRY-----
G.gorilla 370 ILLETPLR-OSGLCOPEWRYWKRNGPEPC LGKPGTRY-----
P.abelii 362 ILLKTPLR-OSGLCOPEWRYWKRNGPEPC PGKSGTRY-----
N.schauinslandi 367 ILLEKSPRRQGGLCOPEWRYWRRNGSKLPGKPGTRH-----
L.vexillifer 365 ALLEESPGROGGLCOPEWRYWRRNGSKPHPRKPGTRL-----
E.przewalskii 371 ILLEKSPRRQSGLCOPEWRYWRRNGPEPHPGKPGTRG-----
H.armiger 367 MLPGTSLRRQGDLCOPEWRYWRRNGPEPRPGKSGTRG-----
C.lanigera 400 ILPE-RPLMQSGPROPEWRYWKRNGPEPRPGKPGIRC-----
C.mydas 384 SLFEKPKLKDAAAR--PEWKYWKRSHPKSHPRNPGISIPSSKCTKGKAESRTIFCFDMYPV
B.gibbericeps 314 VCLEKPRPKDSAR--PEGKYWKRS-----
consensus 421 ille p rrqsglcqPEwrYWkrngpephpgkpgtr

H.sapien 406 -----
G.gorilla 406 -----
P.abelii 398 -----
N.schauinslandi 404 -----
L.vexillifer 402 -----
E.przewalskii 408 -----
H.armiger 404 -----
C.lanigera 436 -----
C.mydas 442 APTNQSAMFETIEQSPRRHFTPKDVLIIHDFKPSLGLQATPCLEKLGENQIERERQKAC
B.gibbericeps -----
consensus 481 -----

H.sapien 406 -----SNIKKEEKDHKQORAQTAVVGT
G.gorilla 406 -----SNIWKEEKDHKQORAQTVVGT
P.abelii 398 -----SNIWKEEKDHKRORAQTVVGT
N.schauinslandi 404 -----GTIWREKRGNKQORVQSVVLGN
L.vexillifer 402 -----SNIKKEEKGNKQOTVKTAAAGS
E.przewalskii 408 -----GNIQKE--KGNKPOQOTTVVG
H.armiger 404 -----CNIRKEDTGNKRORQHTVVVGS
C.lanigera 436 -----HNMOKEDDNEQE-KAQAAVLGT
C.mydas 502 MEQKRKKKFLQQTWEHEREQQAEEKYTAQEHQRKKLLQHFENEDKKVKEODIKQNQTMK
B.gibbericeps -----
consensus 541 -----ni keek k qr qt vvgt

H.sapien	428	TKELVSKATHMKPPRTPEGEAEHRKRSQSLAICQWNKNSR-----
G.gorilla	428	TKELVSKATHTKPPRTPPREAEHRKRSQSLAICQRNKNSR-----
P.abelii	420	TKELVSKATHTKPPQTPPEAEHRKRSQSLAIRKWNKNSR-----
N.schauinslandi	426	TKELVLEASGVKPPQILPEEDGEHREWSPGTATHORDONALRLKAPRSQER-----
L.vexillifer	424	PRELVLEATGMKPLQILPEEAEHKKLSRGTAHQEXQNSPXTKSPKDLGKADGWEGASEG
E.przewalskii	428	TKELVLEATDMKPLQVLPKAERRKLSQVRHIRGTRIPLSLKLALRI-----
H.armiger	426	TKELVLEAANRKPLOILPEEAEHGLSWCATACQSDSNSS-----
C.lanigera	457	TKELALKATNVKPPQTLREGAQHRKPGNEKAVIVRI-----
C.mydas	562	TKQLAQORTNLKMQTMAEEDRQKGQORLAHLQQVRETHDQREFNKCIAEEIKKKQSQEAR
B.gibbericeps		-----
consensus	601	tkelvl at mkppqilpeeaehrks a qr ns

H.sapien		-----
G.gorilla		-----
P.abelii		-----
N.schauinslandi		-----
L.vexillifer	484	LLPWFFDLLGPYHF-----
E.przewalskii		-----
H.armiger		-----
C.lanigera		-----
C.mydas	622	RRRVETQYKLMAEKIFQDEKQKGG
B.gibbericeps		-----
consensus	661	