

```

NTF4rp_Callorhinchus HQ174788 -----MIILLYAVVIS-----LGRHRGWCCPEQRGSG
NTF4_Callorhinchus HQ174787 -----MIILLYAMAVSYFGGVETAPV-----
NTF4_Scylliorhinus FR693756 -----MITLLYTMVVLHLSIKAAPP-----
NTF4_Homo NM_006179.1 -----MLPLPSCSLPILLLFLLPSPVPIESQPLQPNST-----
BDNF_Callorhinchus HQ174786 -----MTILFLTMTVISYFGCLKAAPMKEAGGRGQGSLSYPALR
BDNF_Homo AF400438 -----MTILFLTMTVISYFGCMKAAPMKEANIRGQGLAYPGVR
NTF3_Callorhinchus HQ174789 -----MSILFYGMLLTYLGGIQTATPPTDRK---SLSENSVNSL
NTF3_Scylliorhinus FR693755 -----MVSSVTLLQVNKVM SVLFYGMLLTYLGGIQTATMDKRR---SSEDSVNSI
NTF3_Homo BC107075 -----MSILFYVIFLAYLRGIQGNMMDQR---SLPEDSLNSL
NGF_Callorhinchus HQ174790 -----MNEVMSILCVLLITYLSATQASPKEGYV-----
NGF_Homo NM_002506.2 -----MSMLFYTLITAFLLIGIQAEPHSES NV-----
NT2_Petromyzon BN001521 -----MRFVLLTMLTMFIKGPAAAP IHEQHAV-VISDD SARTL
NT2_Lampetra FR693754 -----
NT1_Petromyzon BN00150 -----MRGLIEKGNDEEDDDREDDTEGLDEVKEAQNKAMEEEEEEPVAVLDEV DGQKTTI KDLVDEAAVDKKAVSKVEVDQEE
NT1_Lampetra AF071432 -----?REHDTEDGYDEVKEVQNKAM--EEEEPVAVLDEV DGQKTTI TDLVDEPAVDKKAVTKKVQDQEE
NTz_Petromyzon BN001522 -----?????

```

```

NTF4rp_Cm      FPGERLPARQ-----PEGGEKEQDLYSLRVMWASEPPVNSPLPFIGEESQS---RADMG
NTF4_Cm        -----NLSVAMPGPQAE-----QRAAGTNDLSGSDFHQVSPESWEKEWDLYSPRVMLASEPPGIPPLLFIMEASLS---QAEVA
NTF4_Sc        -----LLNHRSPQDELGRESRLNDEEAAGREYLLDDMPVDIQDLGDLAGSGREWDFYSPRVTLAARPGGVPPLLFIMEELS---QADVA
NTF4_Hs        -----PSTLPDPAPEWDLLSPRVVLSRGAPAGPPLLFLLAAGAFRESAGAPA
BDNF_Cm        PHGTLTDLNISGGGGGGGRRGGGAGGGGGGGNGELSGSLANTFEHVLEELLEVEQEP--PSEGKGDVDLYSRVMSGQVPLEPPLLFMLEEYRN---YLBAA
BDNF_Hs        THGTLGVNNGPKAGSR-----GLTSLADTFEHVIEELLEDQKVRVEMENKNDADLYTSRVMLSQQVPLEPPLLFLLIEEYKN---YLDAA
NTF3_Cm        IIKIIQADILKAKLSKQTEGVKEKYQDTRYKSDALKTSEMGNTMSDFQPIISVNAELLRKQKRYHSRVLLSERPPLPPPLLYIDDFIG---DSRMG
NTF3_Sc        IIKILQADILKGLRAKQSEVVEKQYDQTKQKDDTHRNTNSLNGTISDFQPIVLVDAELLRQKKRYHSRVLLSDRPLPQPPPLYIEDFA---SLEMD
NTF3_Hs        IIKLIQADILKKNLSKQMVDVKENYQSTLPKAEAPREPERRGGPAKSAFQPIVAMDTELLRQQRYSRVLSSDTPLEPPLLYMLDYVG---SPVVA
NGF_Cm         -----TVG-VSFSPLNHQSQSRVPQSGREMGHSSNNVNGLHFTVEPKLFFK--RRLYSSRCFVRNRSPPGLAGSLDQSRN---DAQE-
NGF_Hs        -----PAGHTIPQVHWTKLQHSLDTALRRARSAPAAAIAARVAGQTRNITVDPRLFFK--RRLSRPRVLFSTQPPREAADTQDLDFEVG---GAAPF
NT2_Pm        LIPLLRTEMLKEVLLKTLQEEVVGWGDShPRRRARDTGSQQQQQQQPPRPRISVIDAGLLSHVDEEELFSSRVLISQLPPSGPPLLPVDDFSA---SVVSA
NT2_Lf        -----
NT1_Pm        ANKVVDTNALLEQEGVMFDKGGKEAAVAPGAGGET--IRGASGKEAADRHYYAADHEEPAKNSGEPETEKVLGPFEREALSNApSTR-----ASGMS
NT1_Lf        ADKVVDTDALVEQEDHVMFDKGGEEAAVAPGAGGETHHHGASGKEAADRPAAADHEEPAKNSGELETEKVGVPFEREGLSAPSHR-----ASGRS
NTz_Pm        MAPRRPMPDVLQDLMLKRGASAATAPRWGADPEGNATRPGRAPRGSDATLAGAESPTR--SEPEPARAGRLDGGDGDGDEYDEEYEEEGDAEPFEA

```

NTF4rp_Cm	-DGTERRARRKADNP-----TFIIGNLAI CNS INSWVL--DKKTALDQYGETVTVLDMAPE-----SPS
NTF4_Cm	--NRTERARRRQAGGE-----QVKPTRRGELSV CDS INFWWT--DKRTAVDINGWVVSVLNEVP-----TSK
NTF4_Sc	--NRTWRARQRAGAG-----GVDPSSRRGDL SVCDSFS RWWT--DRRAVDVHGKMVTVMIEVP-----TST
NTF4_Hs	--SRSGRGVSETAPA-----SRRELAVGDAVSGWWT--DRRTAVDLRGREVEVLGEVPA-----AGG
BDNF_Cm	--NMSARVRRHSDP-----ARRGELSV CDSISQ WTA EAKK TAVDMGGQTVTVLLEKIL-----VPN
BDNF_Hs	--NMSMRVRRHSDP-----ARRGELSV CDSISE WTTAA DKK TAVDMGGQTVTVLEKVP-----VSK
NTF3_Cm	--NRTFARRKKYADHK-----GHRGEYS CDSESR WWT--DKTAATDIRGRQTVTLGEIK-----TGT
NTF3_Sc	--NRTARRKKYADRR-----GHRGEYS CDSESR WWT--DKTAAIDIRGQTVTLGEIK-----TGN
NTF3_Hs	--NRTSRRKKRYAEHK-----SHRGEYS CDSES LWWT--DKSSAIDIRGHQTVTLGEIK-----TGN
NGF_Cm	--NHGKRSRRVRRRVS-----GLRHRLGS VCDSV HWNQ--NKKS AIDIRG REVTLTSEFY-----MNN
NGF_Hs	--NRTHSRKRSSSH-----PIFH RGEF SV CDSV SVVVWG--DKTTATDIKGKEVMVLGEVN-----INN
NT2_Pf	--NSTHHRDRRRHASSSSSSS--SSSSSSSSSLSSSSGDPHRADRGELSV CDS ESVWWT--DKSTAVDIKGNRVTVLDEMR-----TST
NT2_Lf	--NSTHHRDRRRHASSSSSSS--SSSSSSSSSSSGDPHRADRGELSV CDS ESVWWT--DKSTAVDIGKNRVTVLEEMR-----TST
NT1_Pf	KGNARRRSRSAAPQQQQKQQ-----KQQQP PRRPHRGEYPACDSESR WVS--DRDTAFDITGMVRVVLGELSLSSSSSASSSSSSSSSSSQSSS
NT1_Lf	KGKARRRSRSAAPQQQQKQQQQKQQQQKQQQPSR PHRGEYPACDSESR WVS--DRKHAFTDITGMVRVVLGELSLSSSSSAS--SSSSSSSSSQSSS
Nt2_Pm	GHPRRRPPRARROAER--PPHRAELAV CDS ENVVWT--DKAHAVDVGKHNVTVLSDIR-----VEE

NTF4rp_Cm GPTKQIFFEVTCP-----NPTPSR--CGGTDEKNRTFCEKPRQSLVKAMTMSKKKKKGWLRLRVNTTCV¹CALKE*-----
NTF4_Cm GPMKQFFFYETKCN-----NNTSTARSRCRGVDKRRHWVSECKTKQSFVRALTVDRHKQAGWRWRIRIDTACV²CALNNRTTRT*
NTF4_Sc SPLKQYFFYETKCN-----ERSTTAAGGCRGVDRKRWISECKTKQSYVRALTVDTQKRGWRWRIRIDTSCV³TLNRTGR1*
NTF4_Hs GPKRQYFFETRCCK-----ADNAEEGGPGAGGGCRGVDRRHWVSECKAKQSYVRALTVDAQRGVGRWRIRIDTACV⁴CTLLSRTGRA*
BDNF_Cm GQLKQYFFYETKCN-----PKGFTNEGCRGIDKHHWNSQCKTTSQSYVRALTMSDKRKIGWRFRIRIDTSCV⁵CTLTFKRGR*--
BDNF_Hs GQLKQYFFYETKCN-----PMGYTKEGCRGIDKRRHWNSQCRTTQSYVRALTMSDKKRIGWRFRIRIDTSCV⁶CLTLTIKGR*--
NTF3_Cm TAIKQYFFYETRCR-----EAKPVKNGCRGIDDKHHWNSQCKTQTYVRALSTENKKYLGRWRIRIDTSCV⁷CLSRKLGRS*--
NTF3_Sc SAIKQYFFYETRCR-----EAKPVKNGCRGIDDKHHWNSQCKTTSQTYVRALSTENKKYVGRWRIRIDTSCV⁸CLALSRLKGK*--
NTF3_Hs SPVKQYFFYETRCCK-----EARPVKNGCRGIDDKHHWNSQCKTTSQTYVRALSTENKKLVGRWRIRIDTSCV⁹CALSRLIGRT*
NGF_Cm TGIRQYFFYETRCR-----SRKPSHGGCRGVDRRWHEVSHCDTDSQVRLVLDNN-QVKWNFRIRIKTACV¹⁰CVLTKTGT*--
NGF_Hs SVFKQYFFETRCCK-----DNPVDSGCRGIDSKHHWNSYCTTHTHTFVKALTMDG-KQAARWFRIRIDTACV¹¹CVLSRKAVRRA*
NT2_Pm VPLRQYFFETRCCK-----ATGNTDRGCRGVDDKHHWNTCRTTQSYVRALTMEGTRHVGRWRIRIDTSCA¹²CALSSKSGRAY*
NT2_Lf VPLRQYFFETRCCK-----ATGNTRDGCRGVDDKHHWNTCRTTQSYVRALTMEGTRHVGRWRIRIDTSCA¹³CALSSKSGRA*
NT1_Pm TSVKQYFFYETRCKPAAAAAGAAAGSRTREAPSRFASGTGTGAACRGADELRWRSQCKTTSQSFVRALTEDARGRLAWRWIRLDTACV¹⁴CTLTRYGGA*
NT1_Lf TSVKQYFFYETRCKPAAAAAGT---GIRSREAPSRFASGTGTGSCARGADELRWRSQCKTTSQSFVRALTEDARGRLAWRWIRLDTACV¹⁵CTLTRYGGA*
NTz_Pm TALRQYFFETRCCK-----ASRHTRDGCRGIDRAHWNSQCRTVOSFVOLTSGKGNLGRWRIRIDTACV¹⁶CALSORRP*--