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-----QTDC-

VS-----

-----CA----SKSGCGWC-----SSGEQCLPNE-----
QECVDGP-----
-----GMLTSWE----
KCP-----
>PLXA1_MOUSE/516-562
-----YTSC-
EL-----

-----CLGSR-DPH-CGWC-----VLHSICSRQ-----
DACERAEE-----
-----PQRFASD-
LLQCV-----
>Q91823_XENLA/509-555
-----YESC-
DT-----

-----CLGSR-DPH-CGWC-----VLHNMCSRK-----
DKCERADE-----
-----LHRFTSD-
QRQCV-----
>PLXA3_HUMAN/494-540
-----YQSC-
AA-----

-----CLGSG-DPH-CGWC-----VLRHRCCRE-----
GACLGASA-----
-----PHGFAEE-
LSKCV-----
>PLXA4_MOUSE/512-558
-----YRSC-
GE-----

-----CLGSG-DPH-CGWC-----VLHNTCTRK-----
ERCERSRE-----
-----PRRFASE-
MKQCV-----
>PLXA2_HUMAN/514-560

-----YTTC-
GE-----

-----CLSSG-DPH-CGWC-----ALHNMCSRR-----
DKCQQAWE-----
-----PNRFAAS-
ISQCV-----
>PLXB1_HUMAN/485-534
-----HLDC-
AS-----

-----CLAHR-DPY-CGWC-----VLLGRCSRR-----
SECSRGQGPEQ-
-----WLWSFQP-
ELGCL-----
>PLXB2_HUMAN/472-519
-----YPTC-
TQ-----

-----CRDSQ-DPY-CGWC-----VVEGRCTRK-----
AECPRAE-----

ASHWLWSRSKSCV-----
>PLXB3_MOUSE/467-515
-----FPNC-
TT-----

-----CLQAR-DPL-CGWC-----ILQGRCTRR-----
GECGRAAQPN--
-----HWLWSYE-
DNHCP-----
>PLXB3_HUMAN/477-526
-----FPDC-
AS-----

-----CLQAQ-DPL-CGWC-----VLQGRCTRK-----
GQCGRAGQLNQ-
-----WLWSYEE-
DSHCL-----

>Q9YGM7_TAKRU/532-571

-----LTTC-

TS-----

-----CLVSS-RVTECGWC-----EGRCTRA-----

NQCPPSVWT---

QEYCT-----

>Q9VLT6_DROME/1123-1181

-----HRNC-

SS-----

-----CL----RTLSCGWCFDRDNPIEGI--CMQGDFSYSYSA-----

GNCSLALNSSSH

H-----DAEW--A-

YAQCP-----

>Q7Q434_ANOGA/2207-2251

-----FTQC-

SS-----

-----CLRHA----YCGWC--SRNGTDGDGVCTEGS-----

VDGPANHPA---

GATCA-----

>Q8T0D8_DROME/39-83

-----YTQC-

SS-----

-----CL----EHAHCGWC--AREGFNGDGICTEGA-----

LEHKQEHPS---

GSTCD-----

>Q8MJ16_BOVIN/976-1047

-----YCTC-

SH-----

-----CLEQP----GCGWC--TDPSNTGKGKCIEGSYKGPVKMP--

SQGPTGNSYPQP

LLNSSMCLE-----DSRYNWS-

FIHCP-----
>ATRN1_HUMAN/946-1012
-----LRTC-
GQ-----

-----CLEQP----GCGWC--
NDPSNTGRGHCIEGSSRGPMKLIGMHSEMVLDTNL
CPK-----EKNYEWS-
FIQCP-----
>TAG53_CAEEL/893-943
-----HKTC-
GE-----

-----CQRDP----GCGWL--ADDSKTGLGLCIRGT-----
STGGLEPK-----
-----PENSTWY-
FIDCP-----
>MEGF8_HUMAN/1009-1073
-----FLTC-
HE-----

-----CL----QSHCEGWC--GNEDNPTLGRCLQGDFSGPLGG--
GNCSLWVGEGLG
LPV-----ALPARWA-
YARCP-----
>A8B3H0_GIAIC/136-173
-----FTSC-
TD-----

-----CT----NNLLCVWC-----EENGSCIP-----
KDSQEDPQS---

SYYCK-----
>TAG53_CAEEL/831-878
-----RNNC-
SD-----

-----CTDLE----QCMWC-----PSTNRCINL-
EAYTLSFAYGQCHSWVTS---

GSGSV-----
>ATRN1_HUMAN/893-939
-----RTSC-
SN-----

-----CTS---NGMECMWC-----SSTKRCVDSNAYIIS-
FPYGQCLEWQ-----

TATCS-----
>Q8MJ16_BOVIN/922-969
-----RTAC-
GE-----

-----CTS---GSSECMWC-----SNMKQCVDSNAYVAS-
FPFGQCMEW-----
-----YT-
MSSCP-----
>Q7Q434_ANOGA/1071-1113
-----RTDC-
SS-----

-----CLN---DRDRCVWC-----EATSQCFSFSVYTSEYQF-
GMCREWLD-----

>MEGF8_HUMAN/953-1004
-----RLTC-
ED-----

-----CLA---NSSQCAWC-----QSTHTCFLFAAYLAR-
YPHGGCRG-----
-----WDDSVHS-
EPRCR-----
>Q960R8_DROME/734-780
-----LTNC-
QN-----

-----CTEDE-----CIWC-----QNEQRCVDRNAYTAS-

FPYGQCREWTTF----

TAKCR-----

>Q7QH41_ANOGA/835-881

-----LTSC-

GN-----

-----CTQEE-----CIWC-----QNEQRCVDKNAYTAS-

FPYGQCR-----

-----EWTG-

SSKCR-----

>PLXC1_HUMAN/595-635

-----LKEC-

PA-----

-----CVETG-----CAWC-----KSARRCIHPF-----

TACD-----

-----PSDYERN-

QECP-----

>PLXC1_MOUSE/594-634

-----LKEC-

PA-----

-----CIRSG-----CAWC-----KRDKKCIHPF-----

TPCE-----

-----PSDYERN-

QELCQ-----

>P90641_PARTE/278-323

-----LREC-

DS-----

-----CLSRE-----GCIWC-----TEEQTCQEGNARDGAFF--

NSCDIWVS-----

GSECP-----

>ATRN1_HUMAN/670-709

-----YADC-

AS-----

-----CTA---NTNGCQWC-----DDKKCISAN-----
SNCSMSVKN---

YTKCH-----

>ATRN1_HUMAN/719-760

-----LTSC-

KS-----

-----CS---LNLNCQWD-----QRQQECQALPA-----

HLC-----

-----GEGWSHI-

GDACL-----

>Q8MJ16_BOVIN/693-734

-----LTDC-

YS-----

-----CTA---NTNGCQWC-----NDHCVPTN-----

HSCTEGQ-----

-----ISIFK-

YDHCP-----

>Q9W650_XENLA/517-555

-----LKSC-

SH-----

-----CLSS---PSVNCGWS-----KNHCSTK-----

QECLNEEWI---

QETCP-----

>Q90975_CHICK/523-562

-----FQSC-

SQ-----

-----CLLAP-AFMRCGWC-----GQQCLRA-----

PECN-----

-----GGTWT-

QETCL-----

>MET_HUMAN/523-562

-----FQSC-

SQ-----

-----CLSAP-PFVQCGWC-----HDKCVRS-----
EECL-----
-----SGTWT-
QQICL-----
>MET_MOUSE/522-561
-----FQSC-
SQ-----

-----CLSAP-YFIQCGWC-----HNQCVRF-----
DECP-----
-----SGTWT-
QEICL-----
>Q08757_CHICK/525-563
-----FSTC-
DR-----

-----CLRAE-RFMGCGWC-----GNGCTRH-----
HECA-----
-----GPWV-
QDSCP-----
>Q9YGN0_TAKRU/516-554
-----FLTC-
AV-----

-----CLTAP-KFVGCGWC-----SGVCSWE-----
SDCDHHWR-----

NDSCP-----
>Q9YGM5_TAKRU/513-551
-----FRTC-
SM-----

-----CLMAP-RFMNCGWC-----SGVCSRQ-----
HQCDMQ-----
-----WE-
KDSCA-----
>P70003_XENLA/510-548
-----FLTC-
SR-----

-----CLRAP-RFMGCSWC-----KNVCCQQ-----
GECEGECA-----

QNTCL-----
>RON_HUMAN/530-568
-----FLTC-
GR-----

-----CLRAW-HFMGCGWC-----GNMCGQQ-----
KECP-----
-----GSWQ-
QDHCP-----
>PLX2_CAEEL/581-617
-----YGTC-
SS-----

-----CMS---SEYNCAWC-----SGLHKCS-----
NSCGALEK-----

SKACV-----
>Q9W2V9_DROME/425-477
-----YNDC-
NS-----

-----CINHN-TTFTCLWC-----
SVLNRCSTGDRKKHEWLQMGCEATAIHT--

SSLCP-----
>PXDC2_MOUSE/331-372
-----FNGC-
GP-----

-----CVSSQ-IGFNCSWC-----
SKLQRCSSGFD-----
-----RHRQDWV-
DSGCP-----
>PLDX1_MOUSE/308-349
-----HQSC-
DT-----

-----CVSSN-LTFNCSWC-----
HVLQRCSSGFD-----
-----RYRQEWL-
TYGCA-----
>PLDX1_HUMAN/307-348
-----HRSC-
DA-----

-----CMSSD-LTFNCSWC-----
HVLQRCSSGFD-----
-----RYRQEWM-
DYGCA-----
>Q8MJ16_BOVIN/638-680
-----HQSE-
AA-----

-----CLAAG-PGVRCMWD-----TGSSQCVSW-----
ELAPEAQEKI--

KSECF-----
>PLXB2_HUMAN/763-801
-----GRSDC-
SL-----

-----CRAAN-PDYRCAWC-----GGQSRCVYE-----
ALCNT-----

TSECP-----
>Q8CHG6_MOUSE/371-410
-----GRSDC-
SL-----

-----CLAAD-PAYRCVWC-----RGQNRCVYE-----
ALCSNV-----

TSECP-----
>PLXB3_HUMAN/791-833
-----GHPDC-
SH-----

-----CQAAN-RSLGCLWC-----ADGQPACRYG-----
PLCPPGAV-----

ELLCP-----
>PLXB1_HUMAN/1025-1068
-----GHGDC-
SR-----

-----CQTAM-PQYGCVWC-----EGERPRCVTR-----
EACGEAEAV---

ATQCP-----
>PLXA2_HUMAN/659-702
-----HQLC-
LS-----

-----CVN---SAFRCHWC-----KYRNLCTHDP-----
TTCSF-----
-----QEGRINI-
SEDCP-----
>PLXA3_HUMAN/641-684
-----LQSC-
MS-----

-----CVG---SPYPCHWC-----KYRHTCTSRP-----
HECSF-----
-----QEGRVHS-
PEGCP-----
>Q91823_XENLA/655-698
-----HQSC-
LS-----

-----CVN---GSFPCHWC-----KYRNVCTHNA-----
ADCSF-----
-----QEGRVNM-
SEDCP-----
>O96681_DROME/675-719
-----HSSC-

TR-----

-----CVS---SEFPCDWC-----VEAHRCTHDTA-----
ENCRN-----
-----DILVTGV-
SRIGP-----
>PLXD1_HUMAN/708-753
-----VYPHTAC-
TS-----

-----CLSAQ---WPCFWC-----SQQHSCVSN-----Q-----
SRCE-----
-----ASPNTS-
PQDCP-----
>Q7PSP2_ANOGA/602-645
-----HDTC-
RK-----

-----CLV---SNWGCHWC-----IYDNRCAFNT-----
TACRN-----
-----SANIVQN-
EASCP-----
>Q7QEM6_ANOGA/498-546
-----YTTC-
HA-----

-----CLSAK-DPF-CGWC-----SLENKCSRR-----
YECQDSSKDP--
-----LSWLSYK-
SGKCT-----
>096681_DROME/526-574
-----YKTC-
GD-----

-----CLGAR-DPY-CGWC-----SLENKCSPR-----
SNCQDDANDP--
-----FYWVSYK-
TGKCT-----
>PLXD1_HUMAN/552-601

-----HSTC-
GD-----

-----CVGAA-DAY-CGWC-----ALETRCTLQ-----
QDCTNSSQQHF-
-----WTSASEG-
PSRCP-----
>PLXA2_HUMAN/807-856
-----QRESC-
GL-----

-----CLKAD-RKFECGWC-----SGERRCTLH-----
QHCTSPSSP---
-----WLDWSSH-
NVKCS-----
>PLXA3_HUMAN/789-838
-----QRPSC-
GL-----

-----CLKAD-PRFNCGWC-----ISEHRCQLR-----
THCPAPKTN---
-----WMHLSQK-
GTRCS-----
>Q91823_XENLA/803-852
-----LRESC-
GL-----

-----CLKSD-RRFECGWC-----VSEKKCTLR-----
QNCPTLENP---
-----WMHASTA-
NSRCT-----
>Q9GLW2_BOVIN/150-199
-----MRESC-
GL-----

-----CLKAD-PDFECGWC-----QSQGQCTLR-----
QHCPVHESQ---
-----WLELSST-
NSKCT-----

>PLXA1_MOUSE/810-860
-----LRQSC-
GL-----

-----CLKAD-PRFECGWC-----VAERRCSLR-----
HHCPADSPAS--
-----WMHAHHG-
SSRCT-----
>PLXC1_MOUSE/458-507
-----RKSC-
SE-----

-----CLAAA-DPH-CGWC-----LPLQRCTFQ-----
GDCTHAGSFEN-
-----WLDISSG-
PKKCP-----
>PLXC1_HUMAN/458-507
-----HKSC-
SE-----

-----CLTAT-DPH-CGWC-----HSLQRCTFQ-----
GDCVHSENLEN-
-----WLDISSG-
AKKCP-----
>PLX2_CAEEL/450-488
-----HSSC-
TE-----

-----CLVSV-DPL-CQWC-----HPTQSCTTS-----
ARCTSPV-----

TSQCP-----
>Q9U631_DROME/489-534
-----HVSQ-
SS-----

-----CLNSM-DPY-CGWN-----ELVERCMPQP-----
QDSSV-----

LQHWDQAPQITCP-----

>SEM5A_HUMAN/490-533

YRTRST-----

-----CIGAQ-DPY-CGWD-----

VVMKKCTSLEESLS-----

-----MTQWEQS-

ISACP-----

>SEM5B_MOUSE/501-544

-----YHSQ-

GA-----

-----CLGAR-DPY-CGWD-----GKRQLCSTL-----

EDSSN-----

-----MSLWIQN-

ITTCP-----

>SEM2A_CAEEL/482-527

-----QPSC-

AL-----

-----CSL---DPY-CSWN-----AVNSKCSLKTKT-----

NEKSVG-----

-----WISSSWA-

GRISP-----

>SEM4A_MOUSE/500-547

-----YESC-

VD-----

-----CVLAR-DPH-CAWD-----PESRLCSLLS-----

GSTKPWKQ-----

-----DMERGNP-

EWVCT-----

>SEM4A_HUMAN/500-543

-----YESC-

VD-----

-----CVLAR-DPH-CAWD-----

PESRTCCLLSAPNLN-----

-----SWKQDM-
ERGNP-----
>SEM4B_HUMAN/529-573
-----YRSC-
GD-----

-----CLLAR-DPY-CAWS-----GSSCKHV-----
SLYQPQLA-----
-----TRPWIQD-
IEGAS-----
>SEM4B_MOUSE/516-560
-----YPTC-
GD-----

-----CLLAR-DPY-CAWT-----GSACRLA-----
SLYQPDLA-----
-----SRPWTQD-
IEGAS-----
>SEM4D_MOUSE/506-554
-----HGSC-
ED-----

-----CVLAR-DPY-CAWS-----PAIKACVTLHQEE-----
ASSRGW-----
-----IQDMSGD-
TSSCL-----
>SEM4D_HUMAN/506-554
-----HGTC-
ED-----

-----CVLAR-DPY-CAWS-----PPTATCVAL-----
HQTESPSRGL--
-----IQEMSGD-
ASVCP-----
>Q9J5F6_FOWPN/437-467
-----YGGTC-
DS-----

-----CLLSR-DPH-CGWT-----

NIDCVYG-----

GEKKL-----

>Q9BXR8_HUMAN/534-572

YSGCMKN-----

-----CIGSQ-DPY-CGWA-----

PDGSCIFL-----

-----SPGTRAA-

FEQDV-----

>SEM6D_HUMAN/518-569

YGSCKKS-----

-----CIASR-DPY-CGWL-----

SQGSCGRVTPGMLAEGYEQDTEFGNTAH--

LGDCH-----

>SEM6D_MOUSE/518-569

YGSCKKS-----

-----CIASR-DPY-CGWL-----

SQGVCEVTLGMLPGGYEQDTEYGNTAH--

LGDCH-----

>Q8BKG8_MOUSE/518-569

YGSCKKS-----

-----CIASR-DPY-CGWL-----

SQGVCEVTLGMLPGGYEQDTEYGNTAH--

LGDCH-----

>SEM4G_HUMAN/511-558

-----YRSC-

YD-----

-----CILAR-DPY-CGWD-----
PGTHACAAATTIANRTALIQDIERG-----

NRGCE-----

>SEM4E_DANRE/505-555

-----YQTC-

LD-----

-----CVLAR-DPH-CGWD-----LDTEHCATI-----

NSIHRTRSSTVI

-----QSLNDGD-

ASQCP-----

>SEM1A_TRICF/489-537

-----KTRC-

KD-----

-----CVELQ-DPH-CAWD-----

AKQNLCVSIDTVTSYRFLIQDVVRGD-----

DNKCW-----

>SEM4F_HUMAN/516-563

-----LQSC-

SE-----

-----CILAQ-DPV-CAWS-----FRLDECVAH--

AGEHRGLVQDIESADV-----

SSLCP-----

>SEM1A_DROME/550-601

-----KITSC-

SE-----

-----CVALQ-DPY-CAWD-----KIAGKCRS-----

HGAPRWLEENYF

Y-----QNVATGQ-

HAACP-----

>SEM1A_CAEEL/500-547

-----QTSC-

SK-----

-----CVQLQ-DPH-CAWD-----
SSIARCVHGGSWTGDQFIQNMVFGQ-----

SEQCP-----
>Q7PSP2_ANOGA/453-501
-----FGNC-
SA-----

-----CLESR-DPY-CGWC-----SLEKRCTVR-----
TACQKDTSA--
-----RWLSIGT-
GQQCI-----