

FIGURE 1

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value	Description
7tm_2	23	214	1	268	-179.1	0.76	7 transmembrane receptor (Secretin family)
!! 7tm_1	40	296	1	259	109.7	2.8e-35	7 transmembrane receptor (rhodopsin family)

7tm_1 40-296

7tm_1: domain 1 of 1, from 40 to 296: score 109.7, E = 2.8e-35
 +->GNILVilvilrtkkklrtptnifilNLAvADLLfltltpwalyylvg
 N L+++v++ +++ i++ N vADL ++l lp+ +l+ ++
 query 40 LNTLALWVFVH-IPSSSTFIILKNTLVADLINTFLMLPFKILSDSHL 85
 gsedWpfGsalCklvtaldvvnmyaSillltaISiDRYLAivhPlryrrr
 W++ ++C+++ ++ +my++i lL +I++DK+l I++Plr +
 query 86 --APWQLRAFVCRFSSVIFYETHYVGIVLLGLIAFDRFLKIIRPLRNIFL 133
 rtsprrrAkvvillvWvlalllslPpllfswvktveegngtlnvntvCli
 p Ak v+++W++ + +sLP ++s+ + +++ + C
 query 134 KK-PVFAKTVSIFIWFFLFFISLPNTILSNKEATPSSVKK-----CAS 175
 dfpeestasvstwlrsyvlstlvgFlL..PllvilvoYtrIlrtlr...
 l++++ + +++ F++ + +++lv+Y +I++++++
 query 176 LKSPLG-----LKWHQMYYNNICQFIFwtVFILMLVFYVVIKKVYdsy 218
kaaktllvvvvFvLCWLPyfiivllldtlc.lsiimss
 ++++++++k+ +vvv vF++C++P++ + + t+ +++ +
 query 219 rkskskdrknnkKLEGKVFVVVAVFFVCFAPFHFAFVPYTHSQTN--NKT 266
 tCelervlptallvtlwLayvNscLNpIiY<-+
 +C l ++l ++t tl+La +N o++P+IY
 query 267 DCRLQNQLFIAKETTLFLAATNICMDPLIY 296

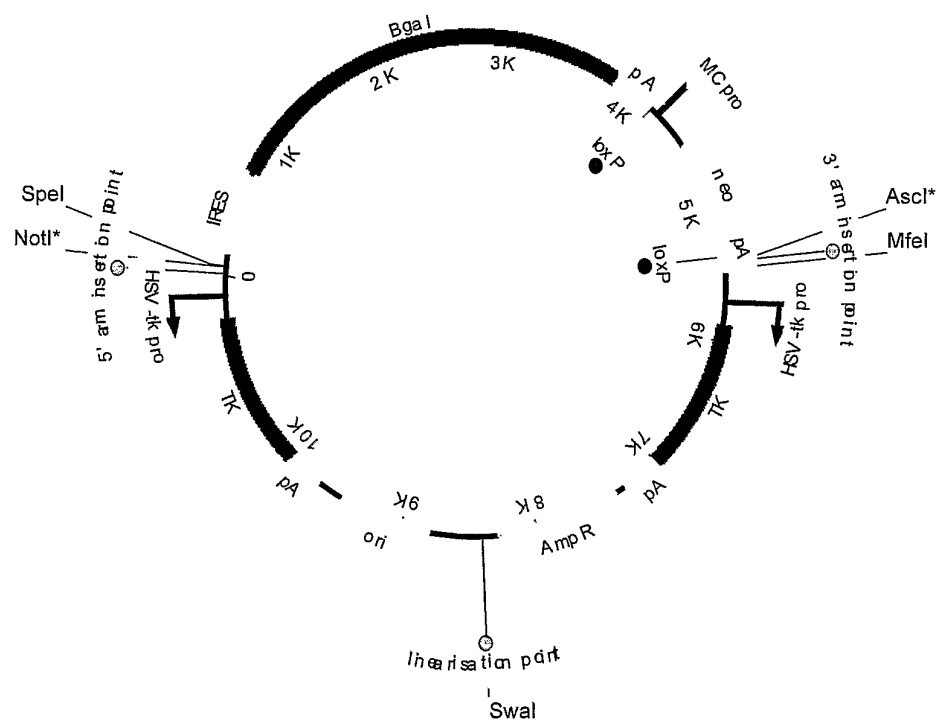
FIGURE 2

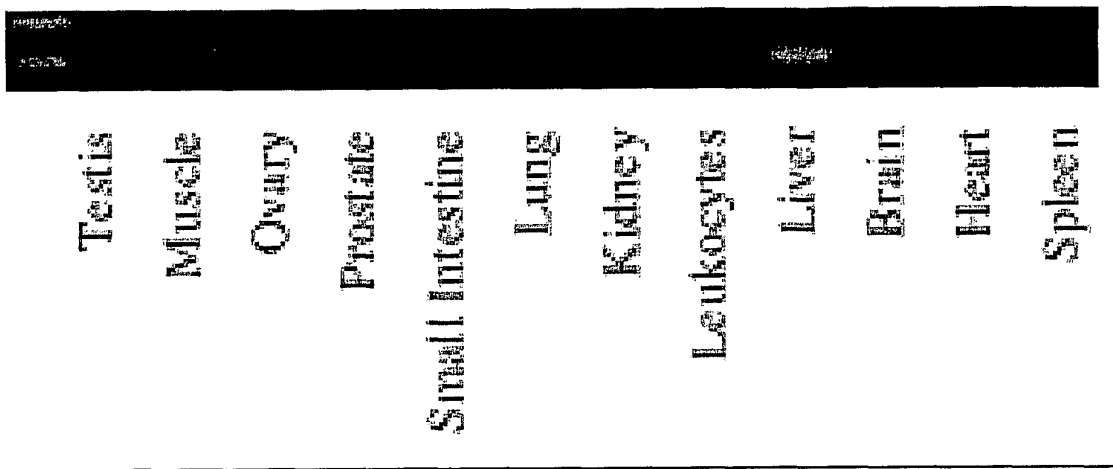
FIGURE 3

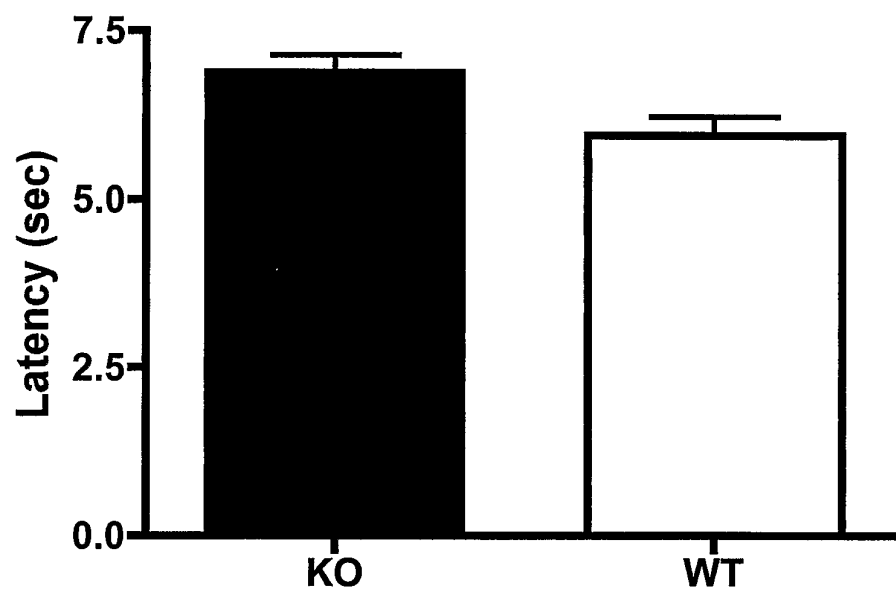
FIGURE 4

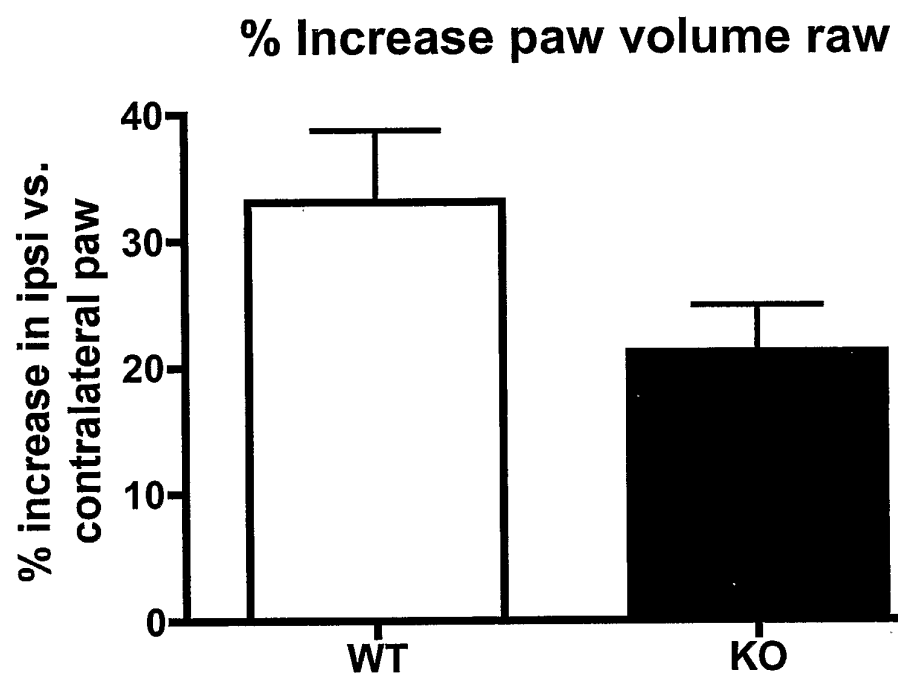
FIGURE 5

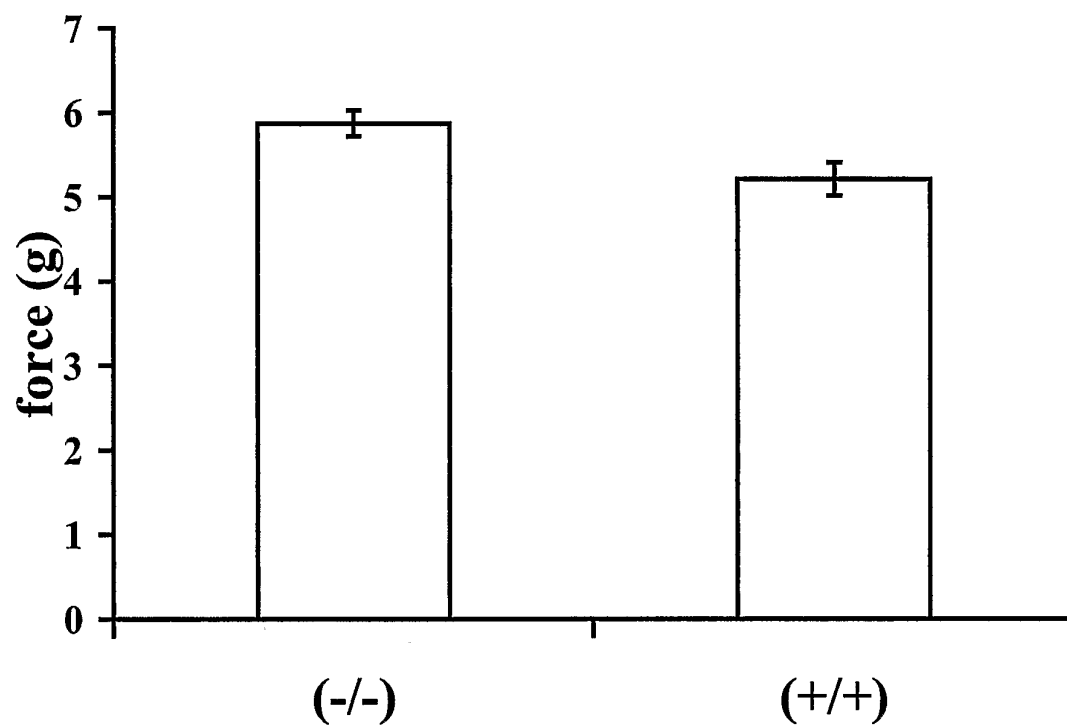
FIGURE 6

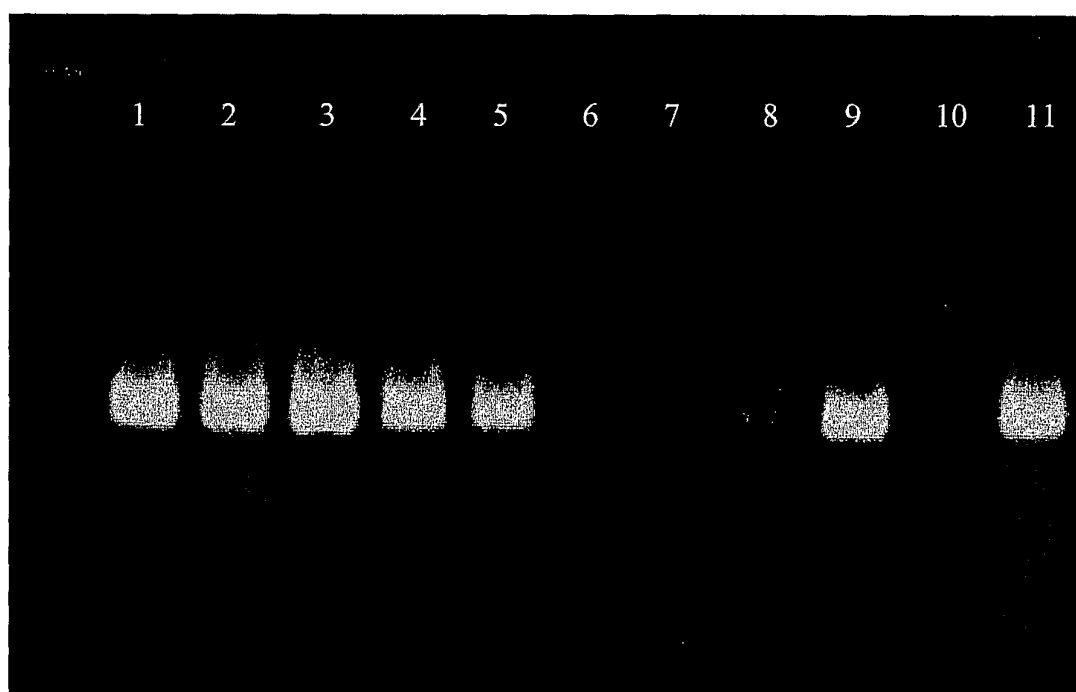
FIGURE 7

FIGURE 8