

*ngf-1* 1 CCCCCCCCCCCCCCCCCCCCCCGGCCACCCACGGAACCACTGACACTTTGTTTGTCAATGTCTACAGATACCAAGCGCAAGGCTACCGAGGAGCCT  
 NGF-1 1 M S T D T K R K A T E E P

*ngf-1* 101 ACCTCTCCTTCGTCGGCGAAACGAATCAAGCATAGCGACTCGAACGAGGAGAATGAGGACACCAAGAAGCCAAAAATCCCCGCCATTCCCTTCCCAGAAA  
 NGF-1 14 T S P S S A K R I K H S D S N E E N E D T K K P K I P A I P F P E  
 L L

*ngf-1* 201 AGGCCGCGTTATCGAAGAAAGCGACGGCGAAATCGAATTCGGTGTGGTCAACATGATGGCGAACGCGAAAGCCTGATCATTCTCACGGGTCTCAAGTG  
 NGF-1 47 K A A V I E E R D G E I E F R V V N N D G E R E S L I I L T G L K C  
 C F

*ngf-1* 301 CATCTTCCAGAAACAATACCCAAGATGCCAAAGACTACATCGCCCGCCTTGTCTACGACCGGACCCATTTGTGGATGGCCATCGTCAAAAAGCCGCTC  
 NGF-1 81 I F Q K Q L P K M P K D Y I A R L V Y D R T H L S I A I V K K P L  
 Q L F

*ngf-1* 401 GAGGTAGTGGGTGGCATCACATACCGACCATTCAAGGGCCGCCAGTTCGCCGAAATCGTCTTTTGGCCATTTCTCCGACAGCAGGTCAAGGGCTACG  
 NGF-1 114 E V V G G I T Y R P F K G R Q F A E I V F C A I S S D Q Q V K G Y  
 I C \*

*ngf-1* 501 GTGCTCATCTCATGTACATTTGAAGGACTATGTCAAGGCTACCTCGGACGTCATGCACCTCCTCACATACGCCGACAATTATGCCATTGGCTACTTCAA  
 NGF-1 148 G A H L M S H L K D Y V K A T S D V M H F L T Y A D N Y A I G Y F K  
 I L

*ngf-1* 601 AAAACAAGGCTTCAAAAGGAAATCACTCGACCAAGTCGTATGGATGGGCTACATCAAGGATTATGAAGGGCGCACTATCATGCAGTGCAGCATGCTTC  
 NGF-1 182 K Q G F T K E I T L D K S V W M G Y I K D Y E G G T I M Q C S M L  
 I L

*ngf-1* 701 CACGAGTACGCTACCTCGAGATGGGCGCATGCTTCTCAAGCAAAGGAATGTGTTGAGGCAGAGATCCGTGCCTACAGCAAATCTCACATTGTCCACCA  
 NGF-1 215 P R V R Y L E M G R M L L K Q K E C V Q A K I R A Y S K S H I V H Q  
 L \* \* F Y Y

*ngf-1* 801 GCCCCCCAAGCAGTGAAGAAGCGGCTAAACCCATCGACCCCTCTTTCAGTCGAGGCATCCGCGCTTCAGGATGGAGCCAGATATGGACGAGCTCGCC  
 NGF-1 249 P P K Q W K N G V T P I D P L S V E A I R A S G W S P D M D E L A  
 \* L

*ngf-1* 901 CGTCAGCCACGCCACGGGCCAAATTACAACAGCTGCTGCACCTCCTCAATGATTTACAGAATCATGCCAGTAGTTGGCCCTTCTTGGTACCCGTC AAC  
 NGF-1 282 R Q P R H G P N Y N Q L L H L L N D L Q N H A S S W P F L V P V N  
 L Y L \* Y Y

*ngf-1* 1001 AAGGACGAGGTACATGACTACTACGATGTATCAAGAGCCTATGGACTTGAGTACCATGGAGGACAAGCTTGAGAAAGATCAATACAAACGCCCCGAGG  
 NGF-1 315 K D E V H D Y Y D V I K E P M D L S T M E D K L E K D Q Y N T P E  
 F

*ngf-1* 1101 ATTTTCATCAAGGACGCCAAGCTCATATTTCGACAACTGCCGAAAGTACAAACACGAAAAACCCCATATGCAAAGTGCGCCAACAGCTCGAGAAGTACAT  
 NGF-1 348 D F I K D A K L I F D N C R K Y N N E N T P Y A K C A N K L E K Y M  
 L F

*ngf-1* 1201 GTGGCAGCAAATTAAGGCGATTCCCGAGTGGTACACCTCGAGCCTTAGAAGGGTGAAAGTCGTGAGGACCGTCAGATGGAGGAGCAAGATGTGGA CAAT  
 NGF-1 382 W Q Q I K A I P E W S H L E P \*  
 L F L

*ngf-1* 1301 GACAAAGCTGTACACATGGCACATATGAGAACGCTGTTGCCATGTCGATAATGACAATGCTGATGCTGATCCAGATTGGAGTGAAATTGGTCTTGCTA

*ngf-1* 1401 CTAAGGCTGGCCGCGTGGTCAACTCCCAAAACGTGGGCGTGGTAGGCCAAGGATCCACTGAGAGGGGGAAAATTAAACAGCGGCCGTAGCACACGGAC

*ngf-1* 1501 ACAACCCCAAGCTCAGAAGGAACCAAAAGCATTCGATCAACCCTCTGGAGAGAAAAGACGGTCACTCCATGCTTTGAACCCAGGAAAACCCGAGCCACC