

## Additional data file 1 - Chicken PNPLA and CGI-58 sequences.

cDNA and amino acid sequences of the identified chicken genes and their GenBank accession numbers. Start and stop codons are underlined.

### PNPLA1 (partial), cDNA: EU419876, protein: ACC91736

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1  M A A E E L R A P G T P F S L S F S G S  
1  ATGGCTGCAGAGGAGCTGCGTGCTCCGGGCACCCCTTTCTCGCTCTCCTTTTCGGGCAGT  
  
21  G F L V L Y Q V G V V Q S L L E L A P E  
61  GGGTTCCTCGTGCTGTATCAGGTTGGGGTGGTGCAGTCCCTCCTGGAGTTGGCCCCGAG  
  
41  L L K S A C K V Y G S S A G S L I A A A  
121  CTGCTCAAATCTGCCTGCAAGGTGTACGGATCGTCTGCCGGATCACTCATCGCCGCCGCC  
  
61  V V C G I S L D D L K E V F Y A N A R E  
181  GTGGTGTGCGGCATCAGCCTGGATGACCTGAAAGAAGTGTCTATGCAAACGCAAGGGAA  
  
81  A R K T L L G P L S P K C S L L A N I R  
241  GCCCGAAAACCTGCTGGGCCCCCTGTCCCCAAGTGCAGCCTGCTGGCCAACATCAGG  
  
101  A V L E R R L P E D S Y L V A S G R L H  
301  GCCGTGCTGGAGCGCAGGCTCCCGGAGGACTCCTACCTGGTGGCATCGGGGCGGCTGCAC  
  
121  I S L T R V V D G Q N V M V S E F S S N  
361  ATCTCTCTGACGCGGGTGGTGGACGGCCAGAACGTCATGGTGTCCGAGTTCAGCTCGAAT  
  
141  E E L I Q A L L C S C F L P I Y C G F I  
421  GAGGAGCTCATTCAGGCTCTCCTCTGTAGCTGCTTCCTTCCTATCTACTGCGGGTTCATC  
  
161  P P S Y R G V R Y V D G G F T G L Q P V  
481  CCTCCGTCTACCGAGGTGTGCGTTACGTTGATGGGGGATTACGGGCCTGCAGCCCGTC  
  
181  S S L E E  
541  TCCAGCCTGGAGGAA
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### PNPLA2/ATGL, cDNA: EU419874, protein: ACC91734

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1  M F P L D S A W N I S F A G C G F L G V  
1  ATGTTCCCTTTGGACTCCGCTTGGAAACATCTCCTTCGCCGGCTGCGGCTTCTAGGGGTC  
  
21  Y H I G V A S C L Q E H A P F L V A N A  
61  TACCACATCGGCGTGGCCAGCTGTCTCCAGGAGCATGCTCCTTTCTCGTCGCCAACGCC  
  
41  R K V Y G A S A G A L T A T A L V S G A  
121  CGGAAGGTGTACGGGGCCTCGGCCGGCGGCTCACCGCCACCGCCCTCGTCAGCGGGCGCC  
  
61  C L G E A G A S I I R V S K E A R K R F  
181  TGCCTCGGTGAGGCTGGTGCCAGCATTATTCGAGTGTCAAAGAAGCACGAAAGAGGTTCC  
  
81  L G P L H P S F N L V K I I R L C L S K  
241  CTGGGTCCGCTTCACCCCTCTTTCAACTTGGTGAAGATCATTCGGCTCTGCCTGTCCAAG  
  
101  T V P E N G H E V A A G R L G I S L T R  
301  ACTGTGCCAGAGAATGGGCATGAGGTGGCAGCAGGACGTTTGGGTATTTCCCTCACACGA  
  
121  V S D G E N V I L S D F H S K E E L I Q  
361  GTGTCTGATGGAGAAAACGTCATACTATCAGACTTCCATTCCAAGGAGGAGCTGATCCAG
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141 A C V C S T F I P V Y C G L I P P T L R  
421 GCCTGTGTCTGCAGCACCTTTATCCCTGTCTACTGTGGGCTGATACCTCCAACCTTTGCGT  
  
161 G V R Y V D G G I S D N L P R Y E L K N  
481 GGAGTGAGATATGTTGATGGAGGAATTTCTGACAACTTGCCACGATATGAGCTGAAGAAC  
  
181 T I T V S P F S G E S D I C P R D S S T  
541 ACAATCACGGTGTCTCCGTTCTCAGGAGAGAGTGATATCTGCCACGAGACAGTTCCACA  
  
201 N M H E L R V T N T S I Q F N L R N L Y  
601 AACATGCATGAGCTGAGAGTCACCAATACAAGCATCCAATTCAACCTTCGCAACCTCTAC  
  
221 R L S K A L F P P E P Q V L R D M C K Q  
661 CGCCTCTCAAAGGCCCTCTTTCCCTCCAGAGCCACAGGTGCTGCGGGATATGTGCAAGCAG  
  
241 G Y R D A L H F L K K N G L L H L Q R P  
721 GGCTATCGGGATGCGCTGCAC'TTCCCTGAAGAAGAATGGTCTCCTTCACCTTCAGCGTCCA  
  
261 N P A G P L L A I E A P P G E K K E E E  
781 AATCCTGCTGGTCTCTCCTTGCAATAGAAGCCCCTCCAGGAGAGAAGAAAGAGGAAGAA  
  
281 K E A E D Q M E D N T A L A V V E D H I  
841 AAAGAAGCTGAGGACCAGATGGAGGACAACACTGCCCTTGCAAGTTGTGGAAGACCACATC  
  
301 F E H L P P K L N Q A L L E A C A E R R  
901 TTCGAACACTTGCCCTCCCAAACCTGAACCAAGCTCTTTTGGAGGCATGTGCTGAAAGAAGA  
  
321 G L L S G I S N T L P I R V A T A M M V  
961 GGTCTCTTGAGTGGTATTAGCAACACGCTGCCTATACGTGTGGCCACTGCCATGATGGTC  
  
341 P Y L L P L E S A V S F T V R L L E W L  
1021 CCCTACCTGCTGCCTCTGGAGTCTGCTGTTTCCCTTCACTGTCAGATTGCTGGAATGGCTT  
  
361 P D I P E D I R W M R E Q I I E I C N Y  
1081 CCAGATATCCCTGAGGATATTAGATGGATGAGGGAGCAGATAATTGAAATCTGCAACTAT  
  
381 L V K K A K K K L G S H L S A R L Y Y H  
1141 CTTGTGAAGAAAGCCAAGAAGAACTGGGCAGTCATCTTTTCCAGCCAGGCTTTACTATCAC  
  
401 L E L G G P Q S L P I S S A S P C G E A  
1201 CTCGAGCTTGAGGGCCCCAGAGCCTGCCAATTTCTTCCAGCATCTCCTTGTGGCGAGGCA  
  
421 M P M W M R S N R S L S D V M L K W E E  
1261 ATGCCTATGTGGATGAGAAGCAACCGTTCCTGTCTGATGTCATGCTGAAGTGGGAGGAG  
  
441 Y Q R Q L V M G L L C I N V D M Q A S L  
1321 TACCAGCGTCAGCTTGTGATGGGCTTGCTTTGCATCAACGTGGACATGCAGGCATCCCTC  
  
461 F P W E G F Q M K L P P L D C A K E C L  
1381 TTCCCTTGGAAGGATTTTCAGATGAACTTCCACCTCTGGACTGTGCAAAAGAGTGCCTG  
  
481 P L F -  
1441 CCACTCTTCTGA

PNPLA3 (partial), cDNA: EU419875, protein: ACC91735

1 E A R K R N L G P L H P S F N V I K I I  
1 GAAGCTAGAAAGCGGAATCTTGGTCTCTTCATCCTTCATTTAATGTGATAAAGATAATA  
  
21 R D G L M R N L P E N T H L L S S G R L  
61 AGAGATGGATTGATGAGAAATCTGCCAGAAAACACTCACCTGTTGTCATCGGGCAGGCTG  
  
41 C I S L T R V S D G K N T L I S N F N S

121 TGCATTTCACTGACTAGAGTCTCAGATGGTAAAAACACACTGATATCTAATTTTAACTCT  
 61 K E E V V Q A L I C S S F V P I Y C G L  
 181 AAAGAAGAAGTTGTCCAGGCATTGATCTGTAGCTCATTGTCCCAATTTATTGTGGCCTC  
 81 I P P S F R G V R Y V D G G I S D N L P  
 241 ATTCCGCCATCATTTAGAGGTGTGCGCTACGTGGATGGAGGAATCAGTGACAACCTTGCCCT  
 101 Q Y E S K N T I T V S P F A G E C D I C  
 301 CAGTATGAATCTAAGAATACCATCACCGTTTCACCTTTTGGCTGGGGAGTGTGATATCTGT  
 121 P K G N S A N F H E M N V T N T S I Q L  
 361 CCAAAGGGGAATTCTGCCAACTTTCATGAAATGAATGTGACCAACACCAGCATTTCAGCTC  
 141 S L G N L Y R L T Q A L F P P E P K V L  
 421 AGTTTGGGGAACCTTTATCGTTTAACACAAGCACTCTTTCCTCCAGAACCTAAGGTACTA  
 161 G E I C E Q G Y S D A F K F L K E N G I  
 481 GGTGAGATCTGTGAGCAAGGATATTCAGATGCTTTTAAATTCCTGAAAGAGAATGGTATT  
 181 L N D S I Y V S L S F T K T N P H E A A  
 541 CTGAATGACTCAATTTATGTCAGCTTGTCTTCACCAAAAACAAATCCTCATGAAGCTGCA  
 201 Q H I D Y M K K R N K S E N S R M E T S  
 601 CAACACATTGACTATATGAAGAAAAGAAATAAGTCTGAAAACAGTAGAATGGAAACTTCA  
 221 Q V E V L G E Q M K Q N P W P L E K S I  
 661 CAAGTGAAGTACTCGGTGAGCAGATGAAGCAAATCCGTGGCCTCTGGAGAAGAGCATA  
 241 F E S L P P R L  
 721 TTTGAGAGTCTACCTCCTAGGCTT

PNPLA4, cDNA: EU419877, protein: ACC91737

1 M K R V N L S F A S C G F L G I Y H L G  
 1 ATGAAACGTGTCAATCTATCATTTCATCATGTGGGTTTCTGGGTATATACCACTTGGGG  
 21 A A A A L Y R H G K K L L K V V K D F A  
 61 GCAGCAGCTGCTCTTTACAGGCATGGTAAGAAGTTACTGAAAGTTGTGAAAGATTTTGCA  
 41 G A S A G S L A A T V L L A V P E N I E  
 121 GGAGCTTCTGCAGGATCCCTGGCTGCCACTGTCTTATTAGCAGTACCAGAAAATATAGAG  
 61 K C Q Q F T Y E F A E E V R K L D F G A  
 181 AAATGTCAGCAGTTTACCTATGAATTTGCTGAAGAAGTCAGAAAATTGGACTTTGGTGCA  
 81 V T P G Y D F M K R L R E G I E S I L P  
 241 GTAACCTCCTGGTTACGATTTTATGAAAAGACTTAGGGAAGGCATAGAATCTATTCTTCCT  
 101 S N A H E I A E N R L Y V S V T N V R N  
 301 TCTAATGCTCATGAGATAGCTGAGAATCGGCTCTATGTGTCTGTTACTAATGTGAGAAAT  
 121 G K N Y L F S N F A S R E D L I K V L L  
 361 GGGAAAAATTACTTGTCTCAAATTTTGCCTCCAGGGAGGACCTCATTAAGGTCCTGCTA  
 141 A S S F V P V Y A G M K P V E Y K G E K  
 421 GCAAGTAGTTTTGTACCAGTATATGCTGGAATGAAGCCAGTCGAGTATAAAGGAGAGAAG  
 161 W V D G G I T N G L P I L P F G R T I T  
 481 TGGGTTGATGGTGGCATTACCAATGGCCTTCTATCTTGCCTTTTGGACGAACGATTACG  
 181 I S P F S G R L D I C P Q D K G R V D L  
 541 ATTTCTCCTTTCAGTGGTCGATTAGATATCTGTCCACAAGATAAAGGACGTGTTGATCTG

201 Y V K F A K Q D I M L S L A N L V R F N  
 601 TATGTTAAATTTGCAAAACAAGATATAATGTTGTCTTTGGCCAACCTAGTAAGATTTAAT  
  
 221 Q A M F P P N Q E K M E S L Y Q N G F D  
 661 CAAGCTATGTTTCCACCAAACCAGGAGAAAATGGAATCACTGTACCAAATGGTTTTGAT  
  
 241 D A V Y F L L K E N W F E -  
 721 GATGCTGTATATTTTTTACTAAAAGAAAAGCTGGTTTGAATAG

PNPLA6 (partial), cDNA: EU419880, protein: ACC91740

1 V L G H F E K P L F L E L C K H M V F Q  
 2 GTGTTGGGACACTTTGAGAAGCCGCTGTTTCTGGAGCTCTGCAAGCACATGGTTTTCCAG  
  
 21 Q C Q Q G D Y V F R P G Q P D T S I Y V  
 62 CAGTGCCAGCAAGGGGATTACGTATTCGACCCGGGCAGCCCGACACCAGCATCTACGTG  
  
 41 L Q D G K L E L L L T E P D G K E T V M  
 122 CTGCAGGACGGCAAGCTGGAGCTGCTCCTCACCGAGCCGGATGGAAAGGAGACTGTGATG  
  
 61 K E V F P G D S V H S L L S I L D V I T  
 182 AAAGAGGTGTTTCTGGAGACAGCGTGCACAGCCTGCTCAGCATCCTCGATGTCATCAG  
  
 81 G H Q R P Y R T V C A R A A E D S T V L  
 242 GGCCACCAGCGGCCATACCGTACGGTGTGTGCGCGGGCAGCAGAGGATTCAACGGTTCTC  
  
 101 R L P V E A F S A V F E K Y P E S L V R  
 302 CGTTTGCCAGTTGAAGCCTTTTCAGCTGTCTTTGAGAAGTACCCCGAGAGCCTGGTGCGG  
  
 121 V V Q I I M V R L Q R V T F L A L H N Y  
 362 GTGGTGCAGATCATCATGGTGCCTTGCAGCGCTCACCTTCTGGCACTGCACAATTAC  
  
 141 L G L T N E L F S H E M Q P L R L F P Q  
 422 CTGGGGCTGACGAATGAGCTTTTCAGCCACGAGATGCAGCCACTGCGGCTCTTCCCGCAG  
  
 161 P S H A T R T S P V R H G K R G L G A A  
 482 CCCAGCCACGCCACCCGCACCAGCCCTGTCCGCCATGGCAAGCGGGGCTCGGCGCTGCT  
  
 181 E E G R E R P T E L I E P L K A G V L D  
 542 GAGGAGGAAGGGAGAGACCAACGGAGCTGATTGAGCCGCTGAAAGCCGGAGTTCTGGAT  
  
 201 A P A P P L L S R C I S M P V D I S G I  
 602 GCCCTGCACCACCCTGCTGAGCCGCTGCATCTCCATGCCAGTGGATATCTCTGGCATC  
  
 221 Q K G P R S D F D M A Y E R G R I S V S  
 662 CAGAAGGTCCCCGCTCTGACTTTGACATGGCCTACGAGCGCGGACGCATCTCAGTATCG  
  
 241 L Q E D S T S P L A A F S R S I S H E P  
 722 CTGCAGGAGGACAGCACCAGCCCCCTGGCTGCCTTCTCTCGGTCCATCTCACACGAGCCC  
  
 261 K E R K S V T V E E Q P S G I Y R Y S C  
 782 AAGGAACGTAAGTCGGTGACGGTGGAGGAGCAGCCATCGGGTATCTACAGGTACAGCTGT  
  
 281 E D E S A A V D C P F E P Y Q G R Q T S  
 842 GAGGACGAGTCGGCCGCGGTGGACTGTCCCTTCGAGCCCTACCAGGGCCGTCAAACCAGC  
  
 301 A I F E A A K Q E L V K L M K V E D P S  
 902 GCCATCTTCGAGGCTGCCAAGCAGGAGTTGGTCAAACCTGATGAAGGTGGAGGACCCTTCT  
  
 321 L L N N R V L L H H A K A G T V I A R Q  
 962 CTGCTCAACAACCGTGTCTTGCTTCATCAGCCAAAGCTGGGACGGTTATTGCCCGTCAA  
  
 341 G D Q D V S L H F V L W G C L H V Y Q R  
 1022 GGGGACCAGGACGTGAGCCTCCACTTCGTGCTGTGGGGCTGCCTACATGTCTACCAGAGG

361 M I D K A E D V C L F L T Q P G E M V G  
1082 ATGATTGACAAGGCCGAAGATGTCTGCCTCTTCCTGACACAGCCTGGTGAGATGGTGGGG  
  
381 Q L A V L T G E P L I F T I K A N R D C  
1142 CAGCTGGCCGTGCTCACTGGAGAGCCCCTCATCTTCACCATCAAGGCCAACCGAGACTGT  
  
401 T F L K I S K S D F Y E I M R E Q P S V  
1202 ACCTTCCTCAAGATCTCCAAGTCAGACTTCTACGAGATCATGCGGGAGCAGCCCAGCGTG  
  
421 V L S V A H T V V T R M S P F V R Q M D  
1262 GTGCTGAGCGTCGCCACACCGTGGTCACCCGCATGTCACCCTTCGTGCGCCAAATGGAC  
  
441 F A I D W M A V E A G R A L Y R Q G D K  
1322 TTTGCCATCGATTGGATGGCGGTGGAAGCCGGCCGGGCGCTCTACAGGCAGGGTGACAAG  
  
461 S D C T Y I A L N G R L R S V I Q K G S  
1382 TCAGACTGCACCTACATCGCGCTCAACGGGCGGCTCCGCTCCGTCATCCAGAAGGGCAGT  
  
481 G K K E L I G E Y G R G D L I G V V E A  
1442 GGCAAAAAGGAGCTCATTGGGGAGTACGGCCGCGGGACCTGATTGGCGTGGTGGAAGCA  
  
501 L T R Q P R A T T V H A V R D T E L A K  
1502 CTTACCCGGAACCCCGTGCCACCACGGTGCACGCGGTCCGGGACACGGAGCTGGCCAAG  
  
521 L P E G T L N N I K R R Y P Q V V T R L  
1562 CTTCCCGAAGGCACCTTGAACAACATCAAGCGTCGGTACCCTCAGGTTGTCACCCGTCTC  
  
541 I H L L S Q K I L G N L Q Q L R G P F A  
1622 ATCCACCTCCTGAGCCAGAAGATCTTGGGAAACCTCCAGCAGCTCCGCGGCCCTTCGCA  
  
561 G S G L G M A S S S E P T N P T S N L S  
1682 GGCTCTGGTTTGGGCATGGCCTCCAGCTCGGAGCCCACCAACCCACCAGCAACCTGTCA  
  
581 T V A V L P V C D D V P T A A F T L E L  
1742 ACGGTGGCGGTGCTGCCAGTGTGTGACGACGTGCCACGGCTGCCTTCACCTTGAGCTC  
  
601 K H A L N A I G P T L L L T S D I I R A  
1802 AAGCACGCGCTGAATGCCATCGGTCCCACACTGCTCCTCACCAGTGACATCATCCGCGCC  
  
621 R L G S S A L D S I H E Y R L S G W L A  
1862 CGACTTGGCTCCTCGGCACCTGGACAGCATCCATGAGTACCGCCTGTGCGGCTGGCTGGCC  
  
641 Q Q E D I H R I V L Y Q T D C T L T P W  
1922 CAGCAAGAAGACATCCATCGCATCGTGTCTACCAAACCGACTGCACTCTGACGCCGTGG  
  
661 T V R C I R Q A D C I L I V G L G D Q E  
1982 ACCGTGCGTGCATCCGGCAGGCGGACTGCATCCTCATTGTTGGGTTGGGTGACCAGGAG  
  
681 P A L G E L E Q M L E N T A V R A L K Q  
2042 CCAGCGCTCGGAGAGCTGGAGCAGATGCTGGAGAACACGGCGGTGCGTGCCTGAAGCAG  
  
701 L V L L H R E D G P S P S R T V E W L N  
2102 TTGGTTCTCCTGCACCGTGAGGATGGTCCCAGCCATCGCGCACCGTTGAGTGGCTCAAC  
  
721 M R S W C S G H L H I K C P R R V F S R  
2162 ATGCGGAGCTGGTGTCTCGGGCCACCTGCACATCAAGTGCCCGCGCCGCTCTTCTCCCGA  
  
741 R S P A K L R E M Y E K V F A K S A D R  
2222 CGCAGCCCCGCAAGCTGCGAGAGATGTACGAGAAGGTGTTTCGCAAGAGCGCCGATCGG  
  
761 H S D F S R L A R V L T G N T I A L V L  
2282 CACAGCGACTTCTCCCGCTTGGCGCGGGTGTCTACCCGGCAACACCATCGCCCTCGTTTTG  
  
781 G G G G A R G C S H I G V I K A M E E A

2342 GGTGGCGGCGGAGCCAGGGGCTGCTCCACATCGGGGTGATCAAGGCGATGGAGGAGGCG  
 801 G I P I D M V G G T S I G S F I G A L Y  
 2402 GGGATCCCCATCGACATGGTTGGCGGCACCTCCATCGGATCCTTCATCGGCGCGCTGTAC  
 821 A E E R S A V R T K Q R A R E W A K C M  
 2462 GCTGAGGAGCGCAGCGCCGTGCGCACCAAGCAGCGGGCAGCGAGTGGGCCAAGTGCATG  
 841 N S V F A T V L D L T Y P I T S M F S G  
 2522 AATTCGGTGTGTTGCGACCGTCTGGACCTCACTTACCCCATCACCTCCATGTTTTTCGGG  
 861 S A F N A S I N K V F Q D K Q I E D L W  
 2582 TCAGCCTTCAATGCCAGCATCAACAAAGTTTTCCAGGACAAGCAGATCGAGGACCTTTGG  
 881 L P Y F N V T T D I T A S A M R V H T D  
 2642 CTCCCTACTTCAACGTCACAACAGACATCACGGCCTCAGCCATGCGGGTGCACACGGAT  
 901 G S L W R Y V R A S M T L S G Y L P P L  
 2702 GGCTCGCTCTGGCGGTACGTGCGAGCCAGCATGACCCTATCTGGGTACCTGCCACCCCTC  
 921 C D P K D G N L L M D G G Y I N N L P A  
 2762 TGCGACCCCAAGGACGGCAACTTGCTGATGGACGGGGTTACATCAACAACCTGCCAGCT  
 941 D I A R N M G A K T V I A I D V G S Q D  
 2822 GACATCGCCCGCAACATGGGTGCCAAGACGGTGATTGCCATCGACGTGGGCAGCCAGGAC  
 961 E T D L C N Y G D S L S G W W L L W K R  
 2882 GAGACGGACCTGTGCAACTACGGGGACAGCCTGTGCGGGCTGGTGGCTGCTCTGGAAGCGC  
 981 L N P W A E K V K V P D M A E I Q S R L  
 2942 CTCAACCCTTGGGCTGAAAAAGTCAAGGTGCCCGACATGGCAGAGATCCAGTCGCGGTTG  
 1001 A Y V S C V R Q L E V V K S S S Y C E Y  
 3002 GCGTATGTGTCGTGCGTGCAGCAGCTGGAGGTGGTGAAGTCCAGCTCGTACTGTGAGTAC  
 1021 I R P P I D R F K T M D F G K F D E I Y  
 3062 ATCCGACCCCGATCGACCGCTTCAAGACGATGGATTTTCGGCAAGTTCGATGAGATCTAT

PNPLA7, cDNA: EU419881, protein: ACC91741

1 M E E E G N G T S L E A M P A S G I L Q  
 1 ATGGAAGAAGAAGGCAACGGCACCAGCCTTGAGGCCATGCCAGCAAGTGAATTCTTCAG  
 21 F V E D R I Q S T M L T G I A I G A A V  
 61 TTTGTAGAAGACAGAATACAGAGTACTATGCTGACTGGAATTGCCATTGGAGCTGCAGTT  
 41 A L F L I G I V V F V I Y R R V K Q S K  
 121 GCACTGTTCTGATAGGAATTGTTGTGTTTGTCAATTTACAGAAGAGTGAAACAATCCAAA  
 61 Q L Q P H G P Q Y R F R K R D K V M F Y  
 181 CAACTTCAGCCACATGGTCTCAATACAGATTTTCGCAAGAGAGACAAAGTGTGTTCTAT  
 81 G R K I M R K V S T L P N T L V G N T V  
 241 GGGCGGAAGATCATGAGAAAGGTTTCGACTCTTCCGAACACTCTGGTTGGGAACACTGTG  
 101 P R Q R M R K R A K V L N L A K R I L R  
 301 CCTCGCCAAAGGATGAGAAAACGGGCCAAAGTTTTAAATTTGGCTAAAAGGATTCTGCGT  
 121 I K K E C P T L Q P K E P P P S L L E A  
 361 ATTAAGAAAGAATGTCCAACCTGTCAGCCAAAAGAGCCACCTCCCTCTCTACTAGAGGCA  
 141 D L T E F D V K N S H L P S E V L Y M L  
 421 GATCTGACAGAATTTGATGTAAAGAATTTCTCATTTGCCGTGGAAGTCTTATACATGCTT

161 K N V R V L G H F E K P L F L E L C K H  
481 AAAAAATGTTAGGGTCTTGGTCACTTTGAGAAGCCTCTTTTTCTGGAATTGTGCAAGCAC  
  
181 M F F V Q L H E G E Y I F R P G Q L D N  
541 ATGTTTTTTGTGCAGTTGCATGAAGGAGAATACATCTTCCGTCCTGGGCAGCTGGATAAC  
  
201 S I Y V V Q D G K L E V C V Q E S D G T  
601 AGCATCTATGTTGTGCAAGATGGAAGCTGGAAGTTTGCCTTCAAGAAAGTGATGGCACA  
  
221 E V I V K E V L A G D S V H S L L S I L  
661 GAAGTGATTGTTAAGGAGGTGCTGGCAGGAGACAGTGTCCACAGTCTTCTCAGCATTCTA  
  
241 D V I T G H P A P Y K T V S A R A A T P  
721 GATGTCATCACGGGTCACCCTGCTCCATACAAAACAGTCTCAGCCCGGGCAGCCACTCCA  
  
261 S N I L R L P A S A F Q D V F Q K Y P E  
781 TCCAATATACTGCGACTTCCAGCAAGTGCCTTTCAAGATGTCTTCCAGAAATACCCTGAA  
  
281 T L V R V V Q I I M V R L Q R V T F L A  
841 ACTCTTGTTAGAGTGGTGCAGATCATCATGGTGGAGGCTGCAGAGAGTGACATTCCTTGCC  
  
301 L H N Y L G L T T E L F N C Q N Q A I P  
901 TTGCACAACCTACCTTGGGCTGACTACTGAGCTCTTCAATTGTGAGAACCAAGCCATCCCA  
  
321 L V S V A S V T S G G S S S K A A K R Q  
961 CTGGTCTCTGTGGCAAGTGTACATCTGGAGGAAGTTCAAGTAAAGCAGCAAAAAGACAA  
  
341 V S S V S E E E R G E K F E K S G E A S  
1021 GTGTCCAGTGTATCAGAGGAGGAGCGTGGAGAGAAGTTTGAGAAATCTGGGGAAGCATCA  
  
361 E M D T L K N S G T E N P E H I F R R S  
1081 GAAATGGATACATTGAAGAATTCTGGTACAGAAAACCCTGAGCATATTTTCAGGAGAAGC  
  
381 L S S P P S T E T S G T S S G A K S D M  
1141 CTTTCTTACCCCTTCTACAGAGACTTCTGGTACTTCCAGCGGTGCGAAGTCAGACATG  
  
401 D M A Y E R A R V H F S S E E A S C S P  
1201 GACATGGCATATGAGAGAGCCAGAGTGCCTTCCAGCTCAGAAGAGGCTTCTTGCAGTCCT  
  
421 V V G K S I L K K T V T V T R T P S V V  
1261 GTTGTGGGCAAGTCGATATTGAAGAAGACTGTGACAGTGACAAGAACCCTTTCAGTAGTT  
  
441 F R Y T D C E L T A Q E S C N G K P T D  
1321 TTCCGTTACACTGATTGTGAGCTGACTGCACAGGAATCCTGTAATGGCAAACCCACCGAT  
  
461 A I F E A A K K D L S T L M K L D D P S  
1381 GCCATCTTCAAGCAGCGAAGAAAGACCTTTCAACCCTGATGAACTTGATGATCCTTCC  
  
481 L L N D R V T L H Q V T A G T V L S R Q  
1441 CTGCTGAATGACAGAGTGACACTGCATCAGGTTACTGCTGGGACTGTGCTGTCAAGGCAG  
  
501 G D Q D V N V C F V V S G M L H V Y Q Q  
1501 GGAGATCAGGATGTTAATGTTTGGCTTTGTGGTCTCCGGGATGCTTACGTGTACCAACAG  
  
521 K V D S E E D T C L F I T H P G E L V G  
1561 AAGGTCGACTCCGAGGAGGACACCTGCCTGTTCACTACTCACCAGGAGAACTCGTGGGC  
  
541 Q L A V L T G E P L I F T I K A N R D C  
1621 CAGCTTGCTGTTCTCACTGGGGAACCACTGATTTTACCATCAAGGCCAATCGAGACTGT  
  
561 S F L S I S K S H F Y E I M R E Q P S V  
1681 AGCTTCCCTGTCTATTTCCAAGTCCCACTTCTACGAGATAATGCGAGAGCAGCCAAGTGTT  
  
581 V L G V A H T V V K R M S S F V R Q I D  
1741 GTGCTTGGTGTGGCCACACTGTTGTAAAGAGAATGTCCTCATTGTGAGGCAAATTGAC

601 F A L D W M E V E A G R A V Y R Q G D K  
1801 TTTGCCCTGGATTGGATGGAAGTTGAGGCTGGACGAGCTGTATACAGGCAGGGTGACAAG  
  
621 S D C T Y I V L N G R L R S V I R M D D  
1861 TCAGATTGCACATACATCGTCTTGAATGGACGACTGCGCTCAGTCATACGGATGGATGAT  
  
641 G K K H L T G E Y G R G D L I G V V E A  
1921 GGGGAAGAAGCACCTGACTGGTGAATATGGCCGAGGAGACTTAATTGGAGTGGTAGAGGCA  
  
661 L T H Q P R A T T V H A V R D S E L A K  
1981 CTAACCCATCAGCCTAGAGCCACAACAGTTCATGCCGTGAGAGATTTCAGAACTTGCCAAA  
  
681 L P E G G A L T S I K R K F P Q V V T R L  
2041 CTCCCAGAGGGAGCCCTGACATCTATCAAACGCAAATTCCCCCAGGTTGTGACTAGGCTT  
  
701 I H L L G E K I L G S L Q Q G G H P F G  
2101 ATTCACTTGCTGGGCGAGAAGATCCTTGGCAGCCTTCAGCAGGGAGGCCATCCTTTTGA  
  
721 L H S P S S K W D A G N P A S N L S T I  
2161 TTGCACAGCCCAAGCAGCAAATGGGATGCCGAAATCCTGCCAGCAATCTCTCCACAATA  
  
741 A I M P V S E E V P L T A F T L E L K H  
2221 GCAATTATGCCGGTGTCTGAAGAGGTGCCACTCACTGCTTTCACTCTGGAGCTCAAGCAT  
  
761 A L S A V G P A L L L T S D N I K Q R L  
2281 GCTCTTAGTGTGTGGGTCCCTGCCTTGCTGCTCACAAGTGATAACATCAAACAGCGGCTG  
  
781 G S A A L D S I H E Y R L T S W L G Q Q  
2341 GGTTCCTGCTGCACTGGACAGTATCCATGAGTACCGCCTGACGAGCTGGCTGGGCCAGCAG  
  
801 E D I H R I V L Y Q A D S T L T P W T Q  
2401 GAGGACATCCACCGCATCGTCCCTGTACCAGGCAGACAGCACCCCTTACTCCGTGGACTCAA  
  
821 R C I R Q A D C I L I V G L G D Q E P T  
2461 CGCTGCATCAGGCAGGCTGACTGCATCTTGATAGTGGGACTGGGAGACCAGGAGCCCACT  
  
841 V G E L E R M L E N T A V R A Q K Q L I  
2521 GTTGGAGAGCTGGAGAGGATGCTGGAGAACACAGCGGTCCGAGCCCAGAAGCAGCTGATT  
  
861 L L H K E D G P L P S R T V E W L N M R  
2581 CTGCTCCATAAGGAGGATGGACCTCTCCCTTCCCGAAGTGTGGAATGGCTCAATATGAGG  
  
881 S W C S A H L H L H C P R R V F S K R S  
2641 AGCTGGTGTCTGCTCATCTTCATCTCCACTGTCCACGAAGAGTGTTCCTCCAAAAGAAGC  
  
901 L P K L I E M Y E R V F Q K P P D R H S  
2701 TTGCCAAAGCTGATAGAGATGTATGAACGTGTGTTCCAGAAGCCACCAGACCCCACTCG  
  
921 D F S R L A R V L T G N A I A L V L G G  
2761 GACTTCTCTCGCCTGGCTCGTGTCTGACTGGAAATGCCATTGCCCTGGTCTTGGTGGT  
  
941 G G A R G C S Q V G L I R A L I E A G I  
2821 GGGGAGCCAGGGGTGCTCCCAGGTCGGGCTTATCAGGGCGCTGATTGAAGCTGGCATC  
  
961 P V D M I G G T S I G A F M S A L Y A E  
2881 CCCGTGGATATGATTGGAGGAACGTCCATCGGCGCTTTCATGAGCGCTCTGTACGCAGAA  
  
981 E R S Y N Q M R I K A R Q W A M V M N S  
2941 GAACGCAGCTACAATCAGATGAGGATCAAAGCCAGGCAGTGGGCCATGGTTATGAATTCA  
  
1001 V F K T I L D L T Y P I T S M F S G A A  
3001 GTGTTTAAGACTATCTAGACTTGACGTATCCAATAACCTCAATGTTTTCTGGAGCAGCT  
  
1021 F N N S I S N I F K D K Q I E D L W I P



3061 TTTAACAACAGCATCAGCAACATCTTCAAGGATAAGCAGATTGAGGATCTGTGGATTCT  
 1041 Y F T I T T D I T A S A M R V H T D G S  
 3121 TACTTCACAATCACAACCTGACATCACTGCCTCAGCAATGAGGGTCCACACCGATGGCTCT  
 1061 L W R Y I R A S M S L S G Y M P P L C D  
 3181 CTGTGGAGGTACATCCGTGCCAGCATGTCTCTCTCTGGGTACATGCCCCCGCTCTGCGAC  
 1081 P K D G H L L M D G G Y V N N L P A D V  
 3241 CCAAAGGATGGGCACCTCCTGATGGATGGAGGTTATGTCAACAACCTGCCTGCTGATGTG  
 1101 A R S M G A K V V I A I D V G S R D E T  
 3301 GCGAGGTCCATGGGTGCAAAGGTGGTGTATAGCAATCGATGTGGGGAGCCGGGATGAGACC  
 1121 N L T N Y G D C L S G W W L L W K R W N  
 3361 AACCTACCAACTACGGTGACTGCTTGTCCGGCTGGTGGCTGCTGTGGAAGAGGTGGAAT  
 1141 P L A E K V K V P N M A E I Q T R L A Y  
 3421 CCACTGGCTGAGAAAGTCAAGGTGCCGAACATGGCAGAGATCCAAACACGGCTCGCGTAC  
 1161 V C C V R Q L E M V K S S D Y C E Y I R  
 3481 GTGTGCTGCGTGCGGCAGCTGGAGATGGTGAAGAGCAGCGACTACTGCGAGTACATCCGG  
 1181 P P I D R Y G T L D F G K F D E I C E V  
 3541 CCACCCATCGACCGCTACGGCAGCTGGATTTTGGGAAGTTTGTATGAGATCTGTGAAGTG  
 1201 G Y Q H G K T V F G V W S R S G V L D K  
 3601 GGATATCAACATGGGAAGACTGTGTTTGGTGTCTGGTCCAGGAGCGGCGTCTTTGACAAG  
 1221 M L R D R Q E T H K T K T S D N V T Y P  
 3661 ATGCTACGAGACAGACAAGAGACACACAAAACAAAACCTTCTGATAACGTGACCTATCCC  
 1241 S T S F T D L A E I V S R I E P V K A A  
 3721 AGCACCTCCTTACAGACCTGGCAGAAATCGTGTCCAGGATCGAGCCAGTGAAGCTGCG  
 1261 V A D D E S D Y Q T E Y E E E V L D N Q  
 3781 GTGGCTGATGATGAGTCAGACTACCAGACTGAGTATGAGGAAGAAGTTCTGGACAACCAG  
 1281 K D D Y I H F I G N Q A E D D S D S D E  
 3841 AAGGATGATTATATTCATTTTCATAGGGAACCAGGCTGAAGACGACTCTGACTCGGATGAA  
 1301 D V Q I R K R K N L P K V D C Q A S S T  
 3901 GATGTACAGATAAGAAAGCGCAAGAATCTCCCAAAGGTGGACTGCCAGGCAAGCAGCACA  
 1321 G E P A -  
 3961 GGAGAGCCAGCCTAG

PNPLA8, cDNA: EU419878, protein: ACC91738

1 M T V H L S L D A Y L F F V I N P K S L  
 1 ATGACAGTTCATTTGTCTCTAGATGCATATTTGTTCTTTGTGATTAACCCAAAAAGTCTT  
 21 W W K Q R N K Y L C L Y R P K V C W R I  
 61 TGGTGAAGCAAAGAAACAAGTACCTGTGTTTGTATAGGCCTAAAGTCTGCTGGAGGATA  
 41 S H A I H L R V F H T G E P Q Y K W A R  
 121 AGTCATGCTATTCATCTTAGAGTTTTTCATACCGGTGAGCCTCAGTACAAATGGGCCAGA  
 61 S R T L W Y S K H I F S R D F L Y Y R V  
 181 AGCAGAACACTGTGGTATAGCAAGCACATTTTCAGTCGCGACTTTTTGTATTACAGAGTT  
 81 S K L L N S S S K G L T K V N N R M S R  
 241 TCTAAACTTTTAAATTCCTTCTTCCAAAGGACTTACAAAAGTGAACAATCGCATGTCACGA

101 I K N T I E S V S K A V S G T H S E L V  
301 ATTAAGAATACTATAGAATCTGTTTCAAAGGCAGTGTCTGGCACTCACAGTGAACGGTT  
  
121 S R I A R L K S H S G T L G K D T K S N  
361 TCGCGAATAGCTCGTTTAAAGTCACACTCAGGTACTCTAGGAAAGGATACTAAAAGTAAT  
  
141 A D E N N L N V N L E S G K Q V P D A R  
421 GCAGATGAAAATAACCTTAATGTGAATCTGGAAAGTGGTAAACAAGTCCCAGATGCCAGA  
  
161 T Q E D C N R G L A A K K S S N T N E N  
481 ACTCAGGAGGATTGCAACAGAGGCCTAGCTGCCAAGAAATCCAGTAACACAAATGAAAA  
  
181 L E F V L N S T S G T N Q D I P E D S A  
541 TTGGAGTTTGTGTTAAACAGTACAAGTGGCACTAATCAAGATATTCCAGAAGATTCCAGCA  
  
201 S A K N H L F H I S Y L S T S F G E T Y  
601 TCTGCTAAAAACCACCTTTTTTCATATAAGCTACCTTTCTACAAGTTTTGGAGAGACTTAT  
  
221 N F V A D H I N W Y F S N N F V M D Q E  
661 AACTTTGTTGCTGATCATATCAACTGGTACTTCAGTAATAATTTTTGTTATGGATCAAGAG  
  
241 K K K N A L L Q G S K S E T K L D S S E  
721 AAAAGAAGAATGCTTTGTTACAGGGCTCTAAAAGTGAACGAAGCTTGATTTCATCAGAG  
  
261 N T V I S E E K T V N S A A A L A P E T  
781 AATACTGTTATTAGTGAAGAAAAGACAGTGAATTCGGCAGCTGCTTTAGCTCCTGAAAA  
  
281 E T E G S E K S N A A L P V S T K K S I  
841 GAGACTGAGGGTTCTGAGAAGTCAAATGCTGCTCTTCCAGTTTCCACTAAAAAAGTATT  
  
301 A N F L S Y P S N S V Q A F V D S Y I G  
901 GCAAACCTTTCTTTTCCCTATCCCAGTAACAGTGTACAGGCTTTTGTAGACAGTTACATTGGT  
  
321 G L V P K L R S D T K V T A Q E K S K Q  
961 GGATTGGTTCCCAAGTTAAGATCGGATACAAAAGTTACTGCACAGGAGAAGAGTAAACAG  
  
341 L E Q E G S E K D E E D E I K E T K I A  
1021 CTAGAGCAAGAAGGGTCTGAAAAGGATGAGGAGGACGAAATCAAAGAGACTAAGATTGCA  
  
361 E E R E K H L S L Q R E K I I A R V S I  
1081 GAAGAGAGGAAAAACATCTGTCCCTTCAGAGAGAAAAGATCATAGCAAGAGTGAGTATC  
  
381 D N R T R A L V Q A L R R S S N R R V C  
1141 GATAACAGGACTCGAGCTTTAGTTCAAGCCCTTCGAAGATCCTCAAATCGGAGAGTCTGT  
  
401 I S R V E E L T Y H L L E F P E S R G V  
1201 ATCAGCAGGGTTGAAGAAGTACTTACCATCTTTTGGAAATTTCCGGAGAGCAGAGGAGTT  
  
421 A I K E K I I P C L L R L R Q A N D E S  
1261 GCAATTAAGGAGAAGATAATCCCGTGCCTACTGCGATTAAGACAAGCAAATGATGAAAGT  
  
441 L Q A A V R E T L A I I G Y T D P V K G  
1321 CTTCAGGCTGCTGTTAGAGAGACTTTAGCAATAATTGGATATACAGATCCAGTCAAAGGC  
  
461 W G V R V L A I D G G G T R G L V A L Q  
1381 TGGGGAGTTTCGAGTCTTGTCTATTGATGGTGGAGGAACAAGGGGTTTGGTTGCACTTCAA  
  
481 T L R K L E E L T G K P V H H L F D Y I  
1441 ACGCTACGGAAACTAGAAGAACTTACTGGAAAGCCAGTTCATCATCTTTTTGACTACATT  
  
501 C G V S T G A I L A F M L G L F H I P L  
1501 TGTGGTGTAAAGCACAGGAGCTATATTAGCTTTTTATGTTGGGGTTATTCCATATCCCTCTG  
  
521 D D C E E L Y H K L G S D V F K Q N V I  
1561 GATGATTGTGAAGAACTATATCACAAGTTGGGATCAGATGTTTTTAAGCAGAATGTTATT

541 V G T V K M G W S H A F Y D S D I W E K  
 1621 GTTGGAACAGTTAAGATGGGCTGGAGCCATGCCTTTTATGACAGTGATATCTGGGAAAAA  
  
 561 M L K E K M G S N L M I E T A R N S K C  
 1681 ATGCTCAAAGAAAAAATGGGCTCAAATCTAATGATTGAAACTGCACGAAATTCCAAATGT  
  
 581 P K V A A V S T I V N R G T P L K A F V  
 1741 CCAAAGGTAGCTGCAGTAAGCACCATTTGTGAACAGAGGAACACCACTGAAAGCATTGT  
  
 601 F R N Y N H F P G V K S H Y I G G C Q Y  
 1801 TTTAGAAACTACAATCACTTCCCTGGGGTTAAGTCTCATTATATTGGAGGCTGTCTAGTAT  
  
 621 K L W Q A I R A S S A A P G Y F Q E Y V  
 1861 AAAGTGTGGCAGGCCATTAGAGCATCATCTGCTGCACCAGGGTACTTCCAGGAATATGTT  
  
 641 L G N D L H Q D G G L L L N N P S A L A  
 1921 TTGGGCAATGATCTTCATCAGGATGGAGGCTTGCTTCTAAATAATCCTTCTGCACTGGCA  
  
 661 V H E C K C L W P D V P L Q C L V S L G  
 1981 GTTCACGAGTGCAAGTGTCTTTGGCCAGATGTTCCACTGCAGTGTCTGGTATCGCTGGGT  
  
 681 T G R Y E S A G K T N V T Y T S L K A K  
 2041 ACTGGCCGATATGAAAGTGCAGGGAAGACAAATGTCACATACACCAGTTTGAAGCCAAA  
  
 701 L T N V I S S A T D T E E V H T M L D A  
 2101 CTCACAAACGTTATCAGCAGTGCAACTGACACAGAAGAAGTTCACACCATGCTGGATGCA  
  
 721 L L P P D T Y F R F N P L M H E D I P L  
 2161 CTGTTACCGCCAGACACTTATTTTCAGATTTAACCCCTCTGATGCATGAAGACATACCTCTG  
  
 741 D E S R K E K L S Q L Q T D G I R Y L E  
 2221 GACGAAAGTCGGAAAGAGAAACTCAGTCAGCTGCAGACGGATGGAATTCGCTATTTAGAA  
  
 761 R N E E K L R K A A K I L T Q E K S T L  
 2281 CGAAATGAAGAAAAACTGAGAAAAGCTGCAAAGATATTAACACAAGAAAAATCAACTTTA  
  
 781 Q K F H D W I K L K A D M Y E G F P F L  
 2341 CAGAAATTTTCATGATTGGATAAAATTAAGGCTGATATGTATGAAGGGTTTCCTTTTCTT  
  
 801 S K L -  
 2401 TCCAAATTGTGA

PNPLA9, cDNA: EU419879, protein: ACC91739

1 M Q F L G R L L S Q A F S N P Y R V K E  
 1 ATGCAGTTCCTCGGGCGGCTTTTGAGCCAGGCGTTCAGCAACCCGTACCGGGTGAAGGAG  
  
 21 V S A A E Y S G Q S R L T E D G R V R L  
 61 GTGTCCGCCGCCGAGTACTCGGGGCAGAGCCGCTGACGGAGGACGGCCGGGTGCGGCTC  
  
 41 Y G N G R C W D G V L V N P Q S P G V A  
 121 TACGGGAACGGCCGCTGCTGGGACGGCGTGCTGGTCAACCCCCAGAGCCCGGGGGTGGCC  
  
 61 F R L F H L D D E A E A L V L F E R Y A  
 181 TTCCGGCTCTTCCACCTCGATGATGAAGCGGAAGCCCTGGTGTCTTTTGAGCGCTATGGC  
  
 81 G H L R P F Y E S S A Q P L S L E V L Q  
 241 GGCCACCTGCGGCCCTTCTACGAGAGCTCAGCCCAGCCCCTGTCGCTGGAAGTTCTGCAG  
  
 101 Q L T D C V R N H P S W S P A H V A V E  
 301 CAGCTCACTGACTGCGTCCGCAACCACCCAGCTGGTCCCCGGCACACGTAGCGGTGGAG  
  
 121 V G L R E T F R H N R V L S C V N S T D

361 GTTGGCCTGCGTGAGACCTTCCGGCACAACCGTGTGCTCAGCTGTGTGAATAGCACGGAC  
141 S E D G C T P L H L A C R K G D M A C L  
421 AGTGAGGATGGCTGCACCCCGCTGCACCTGGCGTGCCGCAAGGGAGACATGGCCTGCCTG  
161 Q E L L E C H A R V D I T D R K G E T V  
481 CAGGAGCTGCTGGAGTGCCACGCGGAGTGGATATCACAGACAGGAAAGGAGAGACGGTT  
181 F H Y A V R G S N P Y I I E L L S S A P  
541 TTCCACTATGCTGTGCGAGGAAGCAACCCCTATATCATTGAGCTCCTGAGCAGTGCCCCG  
201 T V G V N H L S H E G L T P L Y L A C Q  
601 ACTGTAGGTGTGAACCACCTGAGCCACGAAGGGTTGACCCCTCTGTATCTCGCTTGTGTCAG  
221 L G K E D M V R S L L K C R A S C N V M  
661 CTGGGCAAAGAGGACATGGTTCCGGTCTCTGCTGAAGTGCCGTGCCAGCTGTAATGTCATG  
241 G T V G Y P I H A A L K Y S Q K G C A Q  
721 GGGACGGTGGGCTACCCCATCCATGCAGCTCTGAAGTACTCCAGAAGGGGTGTGCCAG  
261 A I L E V D A S Q V H S R D P R H E A V  
781 GCCATCCTCGAGGTGGATGCCAGCCAGGTCCACTCCAGGGACCCACGCCATGAAGCCGTC  
281 P L H W A K K A E M T Q L L L K Y G S E  
841 CCGCTGCCTGGGCGAAGAAGGCAGAGATGACGCAGCTGCTGCTTAAGTATGGCTCTGAG  
301 V N L T S R T A D M A L H I A V K R G R  
901 GTGAACCTGACCAGCCGGACAGCTGACATGGCCCTGCACATTGCAGTCAAGAGAGGTCTGT  
321 F D C A M V L L T H G A D T N A K G Q D  
961 TTTGACTGTGCCATGGTACTGCTGACACACGGGGCTGACACCAATGCCAAGGGCCAGGAT  
341 G N T P L H L A M K H D H L D M I K A I  
1021 GGCAACACACCACCTGCATCTGGCCATGAAGCATGACCACCTGGATATGATCAAAGCAATT  
361 V V F G G D V E I P N D F G E T P G L L  
1081 GTTGTGTTCCGGAGGAGATGTTGAGATCCCTAATGATTTTCGGGGAGACGCCGGGGCTGCTG  
381 A A R N S K G A N R K V L L D L L Q T V  
1141 GCAGCCAGGAACAGCAAAGGTGCGAACCAGGAAAGTGCTCTTAGACCTGCTGCAAAGTGT  
401 G T E R C L P T I P A S Q S L A P S A A  
1201 GGGACCGAACGCTGCCTCCCAACCATTCCTGCCTCCCAAAGTCTGGCACCATCTGCCGCC  
421 S F L E G Q P S P R S S S N S L G Y K D  
1261 TCCTTCCTGGAAGGCCAACCTTCCCCGCGGAGCAGCTCCAACAGCTTAGGGTACAAGGAC  
441 L L Y V S A T L G Q F L K A P D V V D S  
1321 CTTCTGTATGTTTCTGCGACACTTGGGCAGTTCTTGAAGGCACCAGATGTTGTGGACTCA  
461 P R E G E R N Y D R L L C L D G G G I R  
1381 CCCAGAGAGGGTGAGAGAACTATGACCGTCTCCTGTGTCTGGATGGAGGGGGCATCCGA  
481 G L V L I Q L L L A I E K A A G R P I R  
1441 GGCTGGTGCTCATCCAGCTTCTTCTGGCCATCGAAAAAGCTGCGGGCCGTCCCATCCGT  
501 E I F D W I A G T S T G G I L A L A I V  
1501 GAGATCTTTGACTGGATCGCGGGGACCAGCACTGGGGGCATCTTGGCCTTGGCTATTGTA  
521 H G K S M D Y M R C L Y F R M K D M V F  
1561 CATGGGAAGTCCATGGACTACATGCGCTGCCTGTACTTCCGCATGAAGGACATGGTGTTC  
541 R G S R P Y E S E P L D E F L K K E F G  
1621 CGGGGTCTCGGCCCTACGAGTCAGAGCCCCTGGATGAGTTCTTGAAGAAGGAATTTGGG

561 E N T K M T D V Q K P K V I V T G T L C  
 1681 GAAAACACCAAAATGACAGATGTCCAAAACCCAAAGTGATTGTGACAGGGACTCTCTGT  
  
 581 D R Q P A E L H L F R N Y P A P E T K I  
 1741 GACCGACAGCCAGCTGAGCTCCATCTCTTCCGGAATTACCCTGCACCTGAGACAAAATC  
  
 601 S T E Y K T T A T F K P L T Q P E D Q L  
 1801 TCCACTGAATACAAGACAACCTGCGACTTTCAAACCACTCACTCAGCCTGAAGACCAGTTG  
  
 621 V W R A A R C S G A A P T Y F R P I G R  
 1861 GTATGGCGTGCTGCTCGCTGCAGTGGTGCAGCTCCCACTTATTTCCGACCGATAGGGCGC  
  
 641 F L D G G L L A N N P T L D A M A E I H  
 1921 TTTTTGGATGGGGGGCTGCTAGCAAACAACCAACCCCTTGATGCCATGGCGGAGATTTCAT  
  
 661 E Y N K T L I N K G Q R Q K V R K L G L  
 1981 GAGTACAACAAGACTCTGATCAACAAGGGTCAGAGGCAGAAAGTAAGAAAATTGGGGTTG  
  
 681 V V S L G T G K P P Q V P V S S V D V F  
 2041 GTGGTCTCCCTGGGGACAGGGAAGCCTCCACAGGTCCCGGTGTCCTCTGTGGATGTCTTC  
  
 701 R P T N P W E L A K T V F G A R E L G K  
 2101 CGCCCCACCAACCCCTGGGAACCTGGCAAAGACGGTCTTTGGGGCTAGGGAGCTCGGCAAG  
  
 721 M V V D C C T D A D G P A V N R A R A W  
 2161 ATGGTGGTGGACTGTTGCACTGACGCAGATGGCCAGCTGTGAATCGTGCCAGGGCCTGG  
  
 741 C E M T D I P Y F R L S P Q L H T D V M  
 2221 TGTGAGATGACAGATATCCCATATTTCCGGCTCAGCCCTCAGCTGCACACAGATGTGATG  
  
 761 L D E V N D S V L V N A L W D T Q L Y I  
 2281 CTGGACGAGGTGAATGACAGCGTGCTGGTGAACGCCCTCTGGGACACCCAGCTCTACATC  
  
 781 Y Q Q R E Q L E R L V Q Y L C R -  
 2341 TACCAGCAGCGGGAGCAGTTGGAGCGGCTGGTGCAGTATCTCTGCCGATGA

CGI-58: (lipase motif indicated in bold), cDNA: EU419873, protein: ACC91733

1 M A E E E A S S E R L G W L F S W L P A  
 1 ATGGCCGAGGAGGAGGCCCTCCAGCGAAAGGTTAGGATGGTTGTTTCAGCTGGCTTCCTGCT  
  
 21 W C P T S L L H L K E A E D K M L K C I  
 61 TGGTGGCCACGTCACCTACTGCACCTTAAAGAAGCTGAGGACAAAATGCTAAAATGTATT  
  
 41 T S T Y N K R Y V Y L A N G N K I W T L  
 121 ACAAGCACATAACAATAAGCGGTATGTGTATCTAGCTAATGGAAACAAGATATGGACACTG  
  
 61 T F S P D L S R K T P L V L L H G F G G  
 181 ACGTTCTCTCCAGACCTTTCACGTAAAACCTCACTTGTTCCTGCTTCATGGATTTGGAGGA  
  
 81 G V G M W A L N F E E L C E N R T V H A  
 241 GGTGTTGGAATGTGGGCTCTCAATTTTGAAGAGCTCTGTGAAAACAGGACCGTTTCATGCT  
  
 101 F D L L G F G R S S R P H F D T D A R E  
 301 TTCGACCTCTTGGGATTTGGACGAAGCAGTAGACCACACTTTGATACTGATGCTCGGGAA  
  
 121 A E N Q F V E S I E E W R K E M G L E K  
 361 GCAGAAAATCAGTTTGTGGAATCCATAGAAGAGTGGAGAAAGGAGATGGGGCTAGAAAAA  
  
 141 M I L L G H N L G G F L A A A Y S L K Y  
 421 ATGATTTTGGCTTGGACACAATCTGGGTGGATTCCCTGGCTGCTGCTTACTCGTTAAAATAC  
  
 161 P S R V K H L I L V E P W G F P E R P D  
 481 CCATCAAGGGTCAAACATCTTATCTTAGTGGAGCCATGGGGTTTTCCAGAAAGGCCTGAC

181 N A E H E R P I P I W I K A L G A I L S  
541 AATGCTGAACACGAAAGACCAATTCCAATCTGGATCAAAGCACTAGGAGCTATACTGAGT

201 P F N P L A G L R I A G P F G L S L V Q  
601 CCATTTAATCCATTAGCTGGGCTGAGGATAGCAGGACCCTTTGGTCTAAGCCTTGTTTCAG

221 R L R P D F K R K Y A S M F D D N T V T  
661 CGTTTAAGACCAGATTTCAAACGAAAATATGCATCGATGTTTGATGATAAACTGTGACT

241 E Y I Y H C N V Q S P S G E T A F K N M  
721 GAATATATCTATCACTGCAATGTGCAGTCGCCAGTGGTGAAACAGCTTTCAAGAACATG

261 T I P Y G W A K R P M L Q R I P Q M D Q  
781 ACTATTCCTTATGGATGGGCAAAAAGGCCAATGCTGCAACGGATTCCACAAATGGATCAA

281 D I P I T V V Y G A R S C I D G N S G S  
841 GACATTCCTATCACCGTGGTTTATGGAGCACGTTTCATGCATAGACGGCAATTCTGGCAGC

301 T I Q S L R P K S Y V K T I A I L G A G  
901 ACTATCCAGTCTCTGAGACCAAAGTCATATGTGAAGACAATAGCTATCCTTGGTGCAGGT

321 H Y V Y A D Q P E D F N Q K V K D I C D  
961 CATTACGTGTACGCTGATCAGCCTGAAGACTTCAATCAGAAAGTGAAAGACATCTGTGAT

341 S V D -  
1021 TCTGTGGACTGA