

# Nucleotide sequence of the F<sub>1</sub>-ATPase $\alpha$ subunit gene of sunflower mitochondria

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Mitochondrial DNA of the sunflower (*Helianthus annuus* L.) line Baso was cloned into pUC18 vector after digestion with SalI and probed with the *atpA* gene of *Oenothera* (1). Sequence analysis of the *atpA* gene revealed a region of 1530 nucleotides encoding a polypeptide with a predicted molecular weight of 55474 Da. The DNA sequence was 94.1% homologous to the *Oenothera* (1) and 92.4% homologous to the maize (2) *atpA* gene. The deduced amino acid sequence and the molecular weight were estimated assuming no mRNA editing (3, 4, 5). An imperfect inverted repeat of 25 bp downstream of the *atpA* gene (underlined) might play a role in transcription termination or processing. A homology to the *orfB* of *Oenothera* (6) is indicated by a line above the sequence.

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GAGCTCTTTGAAATTGAAAGCGGTATCCCCCTTATATCCAAAAATCAGTAGAATC

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1  ATGGAATCTCTCCGAGAGCTGCTGAACCTAACGACTCTATTAGAAAAGTAGAATTAGCAACTTTTACACGAATTTCAAGTGGATGAGATTGGTCGAGTGGTCTCAGTTGGAGATGGGATT
1  M E P S P R A A E L T T L L E S R I S N F Y T N F Q V D E I G R V V S V G D G I
121 GCACGTGTTTATGGGTTGAACGAGATTCAAGCTGGGAAATGGTTGAATTTGCCAGCGGTGTGAAAGGAATAGCCTTGAATCTTGAGAATGAGAATGATAGGGATTGTGTCTTTGGTAGT
41  A R V Y G L N E I Q A G E M V E F A S G V K G I A L N L E N E N V G I V V P G S
241 GATACGTCTATTAAGGAAGGAGATCTGTCAAGCGCACTGGCTCTATTGTGGATGCTCCCTGGCGGAAAGGCTATGTCTAGCGCGTGTGGTCGACGCCCTGGGAGTACCTATTGATGGAAGA
81  D T A I K E G G D L L V K R T G S I V D V P A G K A M L G R V V D A L G V P I D G R
361 GGGCTCTAAGCGATCAGCAGCGAAGACGTGTCGAAGTGAAGCCCTGGGATTATTGAACGTAAATCTGTGCACGAGCCTATGCAAACTGGGTTAAAAGCGGTAGATAGCCTGGTTCCT
121  G A L S D H E R R R V E V K A P G I I E R K S V H E P M Q T G L K A V D S L V P
481 ATAGCCGCTGGTCAACGAGAATTTAATCGGGACCGCAAACTGGAAAAACAGCTATTGTATCGATACCATATTAACCAAAAGCAAAATGAACTCAAGGAGCACCCTCTGAGAGTGAG
161  I G R G Q R E L I I G D R Q T G K T A I A I D T I L N Q K Q M N S R S T S E S E
601 ACATTGTATTGTCTATGTAGCGATTGGACAGAAACCGCTCAACTGTGGCACAATTAGTTCAAATTTTCAGAAGCGAATGCTATGGAATATCCACTTCTGTAGCAGCCACCGCTTCG
201  T L Y C V Y V A I G Q K R S T V A Q L V Q I L S E A N A M E Y S I L V A A T A S
721 GATCCTGCTCCTCTGCAATTTCTGGCCCGTATTCTGGCTGTGCCATGGGGAAATATTTCCCGGATAATGGAATGCACGCATTAAATCTATGATGATCTTAGTAAACAGGCAGTGGCA
241  D P A P L Q P L A P Y S G C A M G E Y P R D N G M H A L I I Y D D T S K Q A V A
841 TATCGCAAAATGTCATTATTGTTACGCCGACCACCGCCGAGGCTTTCCAGGGGATGTTTTCTATTACATTCGGTCTTTAGAAAAGAGCCCTAAACGATCGGACCGACAGCAGGC
281  Y R Q M S L L L R R P P G R E A P P G D V F Y L H S R L L E R A A K R S D Q T G
961 GCAGGTAGCTTACCCGCTTACCCGCTCAATGAAACACAAGCTGGAGAGCTATCAGCCTATATTCCTACTAATGTGATCCGCATTACTGATGGACAAATCTGTTCCGAAAACAGAGCTCTTT
321  A G S L T A L P V I E T Q G S I D V S A Y I P T N V I P I T D G Q I C S E T E L F
1081 TATCGCGAATTAGACCTGCTATTAACGTCGGCTTACTGTGTCAGTCGTGTTGGTCTGCCGCTCAGTTGAAAACTATGAAACAAGTCTCCGCTAGTTCAAACTCGAATTCGGCACAATAT
361  Y R G I R P A I N V G L S V S R V G S A A Q L K T M K Q V C G S S K L E L A Q Y
1201 CGCGAAGTGGCCGCTTGGCTCAATTTGGGTGAGCCTGGATGCTGGGACTCAGGCAATTAAGTCAATAGAGGTGGCAAGGCTTACAGAAGTACCGAAACAACCACAATATGCCACTTCCA
401  R E V A Q L A L P F G S D L D A A T Q A L L N R G A R L T E V P K Q P Q Y P I D L P
1321 ATTGAAAAACAATTTTATGCTTTTATGAGCTGTCAATGGATTCTGTGATCGAATGCCACTAGACAGAATTTCTCAATATGAGAGAGCCATTTTAAAGAGTATAAAAAACAGAATTACTA
441  I E K Q I L V I Y A A V N G P C D R M P L D R I S Q Y E R A I L K S I K T E L L
1441 CAATCCCTTTTAGAAAAGTGGCTTAACTAACGAAAGAAAATGGAACAGATACATTTTAAAGGAATCGCTTTGCCCTTACACAATATAAAAAAGAAAAGAGAATAAAAAATAGAAA
481  Q S L L E K G G L T N E R K M E P D T P L K E C A L P Y T I *
1561 GATGAAGAACAAAGTTGACACAATCCCTTCTTCCGTTGGTCAACAACCAACAAAACAAATCGTTTAGTTCCTCACTACTCGTACAGGAAGGCCTCTCTTTCTGTATGGGGGAATC
1681  CTTTATTCTCAATCAAGATGCCCTCAACTGATAAATTCACCTATTCTTTCCGTTTACTATTTTGCCTATTTTCCACAATGCTACTCGGAGCTTTTCTAGGAACCGGCTGCCCGGGGATT
1801 CCACCTATTGACTTTATTTTTTAAATAGTACCCTCCTCCTGATTATTCGAATGAGAGTTTTCGAAAGAGAAGAGACTTCTTTCTTCTTCGTAATCTCATTCTCATCTACGTGT
1921  TATGTACTTCTCTAGGCTTTTTTTCATTTTTATGCTGGCAGGAATGCCAAGTGCAATCGCTTTGAAAGTCTCTCCGAAAGTGGAGATGCAACAAGTCTTCCCGCTTTGGAGTCTTCTCT
2041  CAAGCAGTGAATCATTGGCTACGTTTAGAGCCGAAATAGCAGCCGAGAACGAGGCTGAAATTTTTACTCGCATACGCAATCTTGAGACCAGGATTACTACAACCTTCTCCCGAGAATA
2161  ATCCTGGGAGTATGAGGTTCTTGTAGGGAAGAATTC

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