

Gene: NCU03013

intron

10 20 30 40 50 60 70 80 90 100 110 120

N_crassa AAGGCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGATTCCCTAATGGCGGCAACATCAAGGGC
K A L P T A A A V T N N P S C L I A E A V L P E N A W Q K N G F P N G G N I K G

N_c_B_8772 AAGGCTCTCCCCACTGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGATTCCCTAATGGCGGCAACATCAAGGGC
K A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_c_C_8863 AAGGCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGATTCCCTAATGGCGGCAACATCAAGGGC
K A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_dis_8780 AAGCTCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
K P L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_dis_8827 AAGCTCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
K P L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_i_A_8901 AAGGCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
K A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_i_B_8768 ---GCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_his_8815 -----CTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_met_8853 ---CCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
P L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_per_8835 AAGGCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGATTCCCTAATGGCGGCAACATCAAGGGC
K A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

N_sit_0412 ACGGCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCCGAGAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGTGGCAACATCCAGGGC
T A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I Q G

N_tetraspe AAGGCTCTCCCCACAGCTGCAGCTGTGACCAACAATCCCTCTTGTCTCGTTGCGGAGCGGTCTTCCAGAAAACGCCTGGCAAAAAGAACGGCTTCCCTAATGGCGGCAACATCAAGGGC
K A L P T A A A V T N N P S C L V A E A V L P E N A W Q K N G F P N G G N I K G

130 140 150 160 170 180 190 200 210 220 230 240

N_crassa AAGGTGGTAGCCAAGTCGGGCGATGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_c_B_8772 AAGGTAGTTGCCAAGTCGGGCGATGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_c_C_8863 AAGGTGGTAGCCAAGTCGGGCGATGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_dis_8780 AAGGTGGTAGCCAAGTCGGGCGAGGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G E G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_dis_8827 AAGGTGGTAGCCAAGTCGGGCGAGGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G E G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_i_A_8901 AAGGTGGTAGCCGAGTCGGGCGACGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A E S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_i_B_8768 AAGGTGGTAGCCAAGTCGGGCGACGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_his_8815 AAGGTGGTAGCCAAGTCGGGCGACGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_met_8853 AAGGTGGTAGCCAAGTCGGGCGACGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_per_8835 AAGGTGGTAGCCAAGTCGGGCGATGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

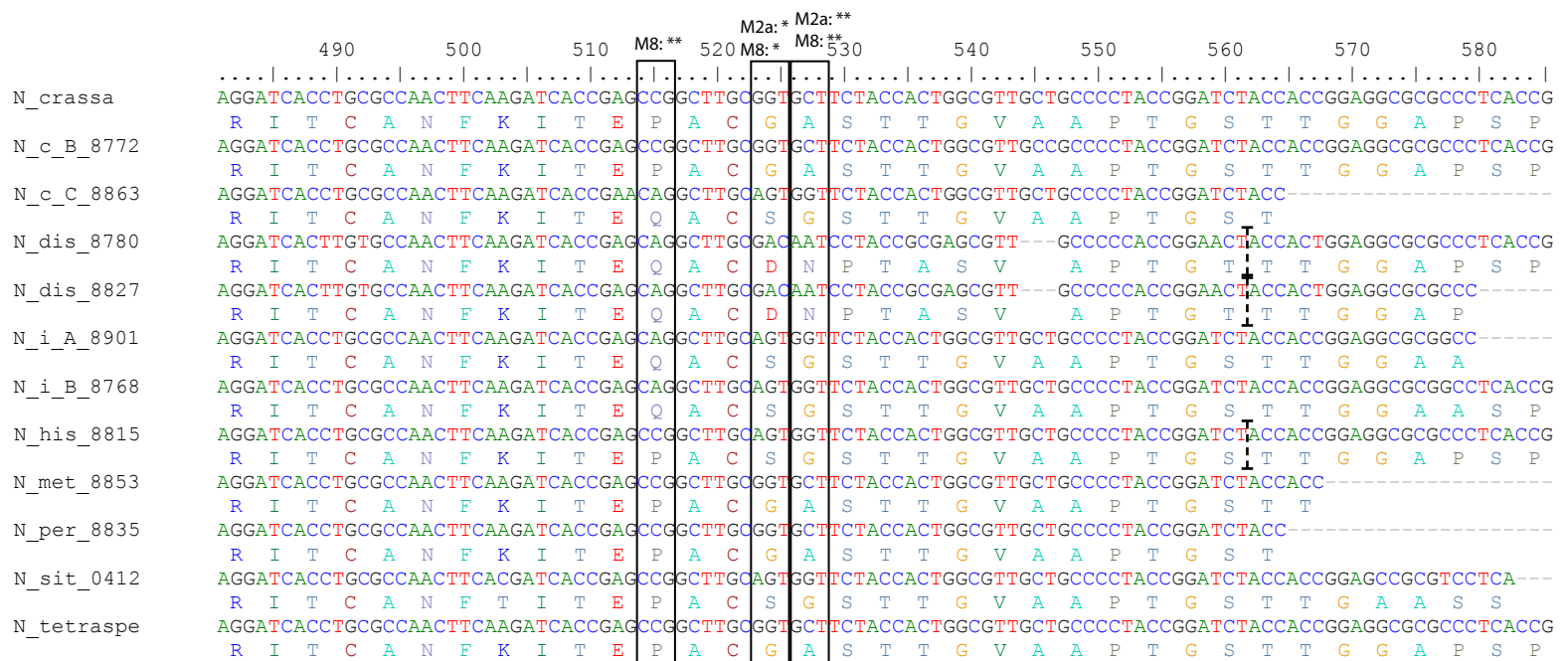
N_sit_0412 AAGGTAGTAGCCAAGTCGGGCGATGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

N_tetraspe AAGGTGGTAGCCAAGTCGGGCGACGGCGGTGTTGGAGTGCAGTTCAATGTTGAAGTGAGCGGCGCTGAGGGTGGCCCTTTTCACTTACCACATTCAGCCAAACCCGTCCCCGAGAAC
K V V A K S G D G G V G V Q F N V E V S G L P E G G P F F Y H I H A K P V P E N

intron

250 260 270 280 290 300 310 320 330 340 350 360
N_crassa GGCAACTGCACAGCAACC...
N_c_B_8772 G N C T A T G A H F D P T E R G E D P A C D K S K P E T C Q I G D L A G K H G A
N_c_C_8863 GGCAACTGCACAGCAACC...
N_dis_8780 G N C T A T G A H F D P T E R G E D P A C D K S K P E T C Q I G D L A G K H G A
N_dis_8827 GGCAACTGCACGGCAACC...
N_i_A_8901 G N C T A T G A H L D P T E R G E D P V C D K S K P E T C Q I G D L A G K Y G A
N_i_B_8768 GGCAACTGCACAGCAACC...
N_his_8815 G N C T A T G A H F D P T E R G E D P A C D K S K P E T C Q I G D L A G K H G A
N_met_8853 GGCAACTGCACAGCAACC...
N_per_8835 G N C T A T G A H F D P T E R G E D P V C D K S K P E T C Q I G D L A G K H G A
N_sit_0412 GGCAACTGCACAGCAACC...
N_tetraspe G N C T A T G A H F D P T E R G E D P V C D K S K P E T C Q I G D L A G K Y G A

370 380 390 400 410 420 430 440 450 460 470 480
N_crassa ATTCTGCGGGCAACACC...
N_c_B_8772 I P A G N T T F S A S Y V D K Y A S L V E G S D A Y F L D R S I V F H F P N K T
N_c_C_8863 ATTCTGCGGGCAACACC...
N_dis_8780 I P A G N T T F S A S Y V D K Y A S L V E G S D A Y F L D R S I V F H F P N K T
N_dis_8827 ATTCTGCGGGCAATACC...
N_i_A_8901 I P A G N T T F S A S Y V D K Y A S L V E G S D A Y F L D R S I V F H F P N K T
N_i_B_8768 ATTCTGCGGACAATACC...
N_his_8815 I P A G N T T F S A S Y V D K Y A S L V E G S D A Y F L D R S I V F H F P N K T
N_met_8853 ATTCTGCGGACAATACC...
N_per_8835 I P A G N T T F S A S Y V D K Y A S L V E G S D A Y F L D R S I V F H F P N K T
N_sit_0412 ATTCTGCGGACAATACC...
N_tetraspe I P A D N I T F S A S Y V D K Y A S L V E G S D A Y F L D R S I V F H F P N K T



⋮ the sequence has been cut due to
| length differences between taxa

Gene: NCU03013

Compared to the annotated sequence for N. crassa, the alignment is missing the first 20 codons and the last 35 codons.
The sequence N_crassa is the annotated gene sequence for NCU03013.
The sequence N_tetraspe is the gene sequence from the N. tetrasperma genome sequence.

Gene: NCU06387

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      10      20      30      40      50      60      70      80      90     100     110     120
N_crassa  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AGGCATGCCGCCCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATCGACTGAGAAATCATGGAGGAGAACC GAAGGAGGAGTATCATGACAGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S I M T A N G M G M
N_c_B_8772 -----
N_c_C_8858 AGGCATGCCGCCCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATCGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGTTCATGACAGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S V M T A N G M G M
N_dis_8780 -----GAGGCCGATCGACTCAGGATCATGGAGGAGAACC GAAGGAGGGGTACCATGACAGCAAATGGCATGGGCATG
E A D R L R I M E E N R R R G T M T A N G M G M
N_dis_8827 -----GCTCTAATGGGTGGTCCGACGGGCTGGAAGGAGGCCGATCGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGCCATGACAGCAAATGGCATGGGCATG
A L M G G P T G W K E A D R L R I M E E N R R R S A M T A N G M G M
N_his_8815 AGGCATGCCGCCCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATCGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGTTCATGACAGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S V M T A N G M G M
N_i_A_8901 -----
N_i_B_8768 AGGCATGCCGCTCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATAGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGTTCATGACGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S V M T A N G M G M
N_met_8853 -----AGGAGGAGTGTTCATGACAGCAAACGGCATGGGTATG
R R S V M T A N G M G M
N_per_8835 AGGCATGCCGCCCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATCGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGTTCATGACAGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S V M T A N G M G M
N_sit_0412 AGGCATGCCGCCCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATCGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGTTCATGACAGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S V M T A N G M G M
N_tetraspe AGGCATGCCGCCCTCGATGCTCTCATGGGTGGTCCAAACAGGCTGGAAGGAGGCCGATCGACTCAGAATCATGGAGGAGAACC GAAGGAGGAGTGTTCATGACAGCAAACGGCATGGGTATG
R H A A L D A L M G G P T G W K E A D R L R I M E E N R R R S V M T A N G M G M

      130     140     150     160     170     180     190     200     210     220     230     240
N_crassa  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CCGAGCGGACTTTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATACAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S Y N N P S G Y A T P V P P I P R
N_c_B_8772 -----
N_c_C_8858 CCGAGCGGACTGTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATACAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S Y N N P S G Y A T P V P P I P R
N_dis_8780 CCGAGCGGACTTTCAACTCCAGTCCACGCCGGTGTCTTTACCGCGCAACAGCAGCCTCACGCATGTTTCATTAGCAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G V S T P V H A G V F T R A N S S L T H V S F S N P S G Y A T P V P P I P R
N_dis_8827 CCGAGCGGACTTTCAACTCCAGTCCACGCCGGTGTCTTTACCGCGCAACAGCAGCCTCACACATGTTTCATTAGCAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S F S N P S G Y A T P V P P I P R
N_his_8815 CCGAGCGGACTTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATACAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S Y N N P S G Y A T P V P P I P R
N_i_A_8901 -----CCCGTCCCTCCGATTTCCCCGA
P V P P I P R
N_i_B_8768 CCGAGCGGACTTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATTCAACAACCCCAAGCGGCTCCGTCACACCCGTCCCTCCGATTTCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S F N N P S G S V T P V P P I P R
N_met_8853 CCGAGCGGACTGTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATACAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S Y N N P S G Y A T P V P P I P R
N_per_8835 CCGAGCGGACTGTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATACAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S Y N N P S G Y A T P V P P I P R
N_sit_0412 CCGAGCGGACTGTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATTCAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S S N N P S G Y A T P V P P I P R
N_tetraspe CCGAGCGGACTTCAACTCCAGTCCACGCCGGTGTCTTTACGCGCGCAACAGCAGCCTCACGCACGTTTTCATATAACAACCCCAAGCGGCTACGCCACACCCGTCCCTCCAAATCCCCGA
P S G L S T P V H A G V F T R A N S S L T H V S Y N N P S G Y A T P V P P I P R
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250 260 270 280 290 300 310 320 330 340 350 360
N_crassa GCATACAGCTACCACGGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATCAAGGGAAAAGAAAAG
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_c_B_8772 -----GGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCAATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATTAAGGGAAAAGAAAAG
G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_c_C_8858 GCATACAGCTACCACGGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGCCAGCAGCGGAACATCGATAAAGGGAAAAGAAAAG
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_dis_8780 GCATACAGCTACCACGGCCCGTCCCGGGTGGAGCCATCATGGCGTGAGATCAGCTATCTCTCAATCGACATGGCGGGAGCTGCCAGCAGTGGAAATCGATAAAGGGAAAAGAGAAA
A Y S Y H G S V P G W S H H G G E I S Y L S I D M A G A A S S G T S I K G K E K
N_dis_8827 GCATACAGCTACCACGGCCCGTCCCGGGTGGAGCCATCATGGCGTGAGATCAGCTATCTCTCAATCGACATGGCGGGAGCCGCCAGCAGTGGAAATCGATAAAGGGAAAAGAGAAA
A Y S Y H G P V P G W S H H G G E I S Y L S I D M A G A A S S G T S I K G K E K
N_his_8815 GCATACAGCTACCACGGCTCGATCCCGGATGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGACATGGCTGGAGCTGCCAGCAGTGGAAATCGATCAAGGGAAAAGAAAAG
A Y S Y H G S I P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_i_A_8901 GCATACAGCTACCACGGCTCAGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCTATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATAAAGGGAAAAGAGAA
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_i_B_8768 GCATACAGCTACCACGGCTCAGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATAAAGGGAAAAGAGAA
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_met_8853 GCATACAGCTACCACGGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATAAAGGGAAAAGAAAAG
A Y S Y H G S V P G W S Y H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_per_8835 GCATACAGCTACCACGGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGTCCAGCAGTGGAAATCGATAAAGGGAAAAGAAAAG
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A V S S G T S I K G K E K
N_sit_0412 GCATACAGCTACCACGGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATAAAGGGAAAAGAAAAG
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K
N_tetraspe GCATACAGCTACCACGGCTCGGTCCCGGGTGGAGCCATCATGGCGTGAAGTCAGCTATCTCTCGATCGATATGGCTGGAGCTGCCAGCAGTGGAAATCGATAAAGGGAAAAGAAAAG
A Y S Y H G S V P G W S H H G G E V S Y L S I D M A G A A S S G T S I K G K E K

370 380 390 400 410 420 430 440 450 460 470 480
N_crassa GAACTTCGGCGCCCGAGGCTCGAATCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGGGATCTGGCTCAGCCCTCGAACCCAGGGAC
E L R R P R L E S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_c_B_8772 GAACTTCGGCGCCCGAGGCTCGACTTCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGGGATCTGGCTCAGCCCTCGAACCCAGGGAC
E L R R P R L D F G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_c_C_8858 GAACTTCGGCGTCCCAAGCTCGACTCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGAGGATCCGGCTCTGCCCTCGAACCCAGGGAC
E L R R P R K L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_dis_8780 GAAATTCGGCGTCCCGAGGCTCAACTCTGGCCGAGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAGCTGGTGGACGAATTCACCTATGAAGGAGTATCCGGCTCTGCCCTCCAACCCAGGGAC
E I R R P R L N S G R A S W S S S R L S A A G G R F H Y E G V S G S A L P T R D
N_dis_8827 GAAATTCGGCGTCCCGAGGCTCAACTCTGGCCGAGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAGCTGGTGGACGAATTCACCTATGAAGGAGTATCCGGCTCTGCCCTTAGAACCCAGGGAC
E I R R P R L N S G R A S W S S S R L S A A G G R F H Y E G V S G S A L R T R D
N_his_8815 GAACTTCGGCGTCCCAAGCTCGACTCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGAGGATCTGGCTCTGCCCTCGAACCCAGGGAC
E L R R P R K L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_i_A_8901 GAACTTCGGCGTCCCGAGGCTCGACTCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGAGGATCTGGCTCTGCCCTCGAACCCAGGGAC
E L R R P R L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_i_B_8768 GAACTTCGGCGTCCCGAGGCTCGACTCCGGCCGAGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGAGGATCTGGCTCTGCCCTCGGACCAGAGAC
E L R R P R L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_met_8853 GAACTTCGGCGTCCCGAGGCTCGACTCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGAGGATCTGGCTCTGCCCTCGAACCCAGGGAC
E L R R P R L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_per_8835 GAACTTCGGCGTCCCAAGCTCGACTCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTCGAAGGAGGATCCGGCTCTGCCCTCGAACCCAGGGAC
E L R R P R K L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D
N_sit_0412 GAACTTCGGCGTCCCAAGCTCGACTCCGGCCATGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGACGATCTGGCTCTGTCCCTCGAACCCAGGGAC
E L R R P R K L D S G H A S W S S S R L A A T G G R I H F E G R S G S V P R T R D
N_tetraspe GAACTTCGGCGTCCCAAGCTCGACTCCGGCCGTGCCAGCTGGTCTTCAAGCAGGCTTGCAGCAACTGGTGGACGAATTCACCTTTGAGGGAGGATCTGGCTCTGCCCTCGAACCCAGGGAC
E L R R P R K L D S G R A S W S S S R L A A T G G R I H F E G G S G S A P R T R D

490 500 510 520 530 540 550 560 570 580 590 600
N_crassa GGCTCGAGTTCACCCCGTCCAGAGCTCAAGCAACTCCAGCAGCTCAGAAGACGATTTGGAGATCACTCCCGTAAAGAAATTTACCAGCGGGTGACAACTCAAGTCCACTCGCGGGAGTA
G S S S P V Q S S S N S S S S E D D L E I T P V K K F T S A V T T S S P L A G V
N_c_B_8772 GGCTCGAGTTCACCCCGTCCAGAGATCAAGCAACTCCAGCAGCTCAGAAGACGATTTGGAGATCAAGCCGTGTAAGAAATTTACCAGCGGGTGACAACTCAAGTCCACTCGCGGGAGTA
G S S S P V Q R S S N S S S S E D D L E I T P V K K F T S A V T T S S P L A G V
N_c_C_8858 GGCTCGAATTCACCCCGTCCAGAGCTCCAGCAACTCCAGTAGCTCAGAAGACGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGTAGTGACAACTCAAGTCCACTCGCGGGAGTA
G S N S P V Q S S S N S S S S E D D L E I T P V R K F T S V V T T S S P L A G V
N_dis_8780 GGCTCGAGTTCACCCCGTCCAGAGCTCCAGCAACTCCAGCAGCTCGGAAGACGATTTGGAGATCAAGCCCGTGAAGAACTTTACCAGCGCCGTGACAACTCCAGTCCCTTCGCAGAACTA
G S S S P V Q S S S N S S S S E D D L E I K P V K N F T S A V T I S S P L A E V
N_dis_8827 GGCTCGAGTTCACCCCGTCCAGAGCTCCAGCAACTCCAGCAGCTCGGAAGACGATTTGGAGATCAAGCCCGTGAAGAACTTTACCAGCGCCGTGACAACTCCAGTCCCTTCGCAGAACTA
G S S S P V Q S S S N S S S S E D D L E I K P V K N F T S A V T I S S P L A E V
N_his_8815 GGCTCGAATTCACCCCGTCCAGAGCTCCAGCAACTCCAGCAGCTCAGAAGACGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGCAGTGACAACTCAAGTCCCGTTCGCAGAACTA
G S N S P V Q S S S N S S S S E D D L E I T P V R K F T S A V T T S S P L A G V
N_i_A_8901 GGCTCGAATTCACCCCGTCCAGAGCTCAAGCAACTCCACCAGCTCAGAAGATGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGGGTGACAACTCAAGTCCCGTTCGCAGAACTA
G S N S P V Q S S S N S T S S E D D L E I T P V R K F T S A V T T S S P L A G V
N_i_B_8768 GGCTCGAATTCACCCCGTCCAGAGCTCCAGCAACTCCAGCAGCTCAGAAGACGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGGGTGACAACTCAAGTCCCGTTCGCAGAACTA
G S N S P V Q S S S N S S S S E D D L E I T P M R K F T S A V T T S S P L A G V
N_met_8853 GGCTCGAATTCACCCCGTCCAGAGCTCCAGCAACTCCAGCAGCTCCGAAGACGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGGGTGACAACTCAAGTCCCGTTCGCAGAACTA
G S N S P V Q S S S N S S S S E D D L E I T P V R K F T S A V T T S S P L A G V
N_per_8835 GGCTCGAATTCACCCCGTCCAGAGCTCCAGCAACTCCAGTAGCTCAGAAGACGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGTAGTGACAACTCAAGTCCACTCGCGGGAGTA
G S N S P V Q S S S N S S S S E D D L E I T P V R K F T S V V T T S S P L A G V
N_sit_0412 GGCTCAAAATTCACCCCGTCCAGAGCTCCAGCAGCTCCAGCAGCTCAGAAGACGATTTGGAGATCAAGCCCGTGGGAAATTTACCAGCGCAGCGACAACTCAAGTCCCGTTCGCAGGAGTA
G S K S P V Q S S S S S S S E D D L E I T P V G K F T S A A T T S S P L A G V
N_tetraspe AGCTCGAATTCACCCCGTCCAGAGCTCCAGCAACTCCAGCAGCTCAGAAGACGATTTGGAGATCAAGCCCGTGAGGAAATTTACCAGCGCAGTGACAACTCAAGTCCCGTTCGCAGGAGTA
S S N S P V Q S S S N S S S S E D D L E I T P V R K F T S A V T T S S P L A G L

610 620 630 640 650 660 670 680 690 700 710 720
N_crassa CCCAGCCGGCCGACAAGCGACGCCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAAGTGTCAAACCTCATCATACAAACAAGCCGGACAGTCCCTCATCGCCAGTCAAGTCAATCC
P S R P T S D A D S V H R L H P G H A R K V S N S S Y K Q A G Q S S S P S Q S S
N_c_B_8772 CCCAGCCGGCCGACAAGCGACGCCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAAGTGTCAAACCTCA---TACAAACAAGCCGGACAGTCCCTCATCGCCAGTCAAGTCAATCC
P S R P T S D A D S V H R L H P G H A R K V S N S Y K Q A G Q S S S P S Q S S
N_c_C_8858 CCCAGTCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCC---CGAAAAGTGTCAAACCTCATCTACAAACAAGCCGGACAGTCCCTCATCGCCAGTCAAGTCAATCC
P S R P T S D T D S V H R L H P R K V S N S S Y K Q A G Q S S S P S Q S S
N_dis_8780 TCGAGTCCGGCCGACAAGCGATACCGACTCCGTTCCACCGTCTTTCATCCGTTGTCATGCCGAAAATGTGTCAAACCTCATCAAACAACAAGCCGGACCACTCCCTCATCGCCAGTCAAGTATTTC
S S R P T S D T D S V H R L H P G H A R N M S N S S N K Q D G P S S S P S Q L F
N_dis_8827 TCGAGTCCGGCCGACAAGCGATACCGACTCCGTTCCACCGTCTTTCATCCGTTGTCATGCCGAAAATGTGTCAAACCTCATCAAACAACAAGCCGGACCACTCCCTCATCGCCAGTCAAGTATTTC
S S R P I S D T D S V H R L H P G H A R N M S N S S N K Q D G P S S S P S Q L F
N_his_8815 CCCAGCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAATGTGTCAAACCTCATCATACAAACAAGCCGGACAACTCCCTCATCGCCAGTCAAGTCAATCC
P S R R A S D T D S V H R L H P G H A R N V S N S S Y K Q A G Q S S S P S Q S S
N_i_A_8901 CCCAGCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAATGTGTCAAACCTCATCATACAAACAAGCCGGGCAATCCCGTTCGCCAGTCAAGTCAATCC
P S R P T S D T D S V H R L H P G H A R N V S N S S Y K Q A G Q S A S P S Q S S
N_i_B_8768 CCCAGTCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAATGTGTCAAACCTCATCATACAAACAAGCCGGACAACTCCCGTTCGCCAGTCAAGTCAATCC
P S R P T S D T D S V H R L H P G H A R N V S N S S Y K Q A G Q S A S P S Q S S
N_met_8853 CCCAGCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAATGTGTCAAACCTCATCATACAAACAAGCCGGACAACTCCCGTTCGCCAGTCAAGTCAATCC
P S R P T S D T D S V H R L H P G H G R N V S N S S Y K Q A G Q S A S P S Q S S
N_per_8835 CCCAGTCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAAGTGTCAAACCTCATCATACAAACAAGCCGGACAACTCCCTCATCGCCAGTCAAGTCAATCC
P S R P T S D T D S V H R L H P G H A R K V S N S S Y K Q A G Q S S S P S Q S S
N_sit_0412 CCCAGCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAATGTGTCAAACCTCATCATACAAACAAGCCGGACAACTCCCTCATCGCCAGTCAAGTCAATCC
P S R R T S D T D S V H R F H P G H A R N V S N S S Y K Q A G Q S S S P S Q S S
N_tetraspe CCCAGCCGGCCGACAAGCGACACCGACTCTGTTCACCGTCTTTCATCCCGGTCATGCCGAAAATGTGTCAAACCTCATCATACAAACAAGCCGGACATTCCTCATCGCCAGTCAAGTCAATCC
P S R R T S D T D S V H R L H P G H A R N V S N S S Y K Q A G H S S S P S Q S S

730 740 750 760 770 780 790 800 810 820 830 840

N_crassa C C A C A G A G T A G T C C G A C C A A A T T A G G A G G A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T T G G C G G A A C C C T C G T
P Q S S P T K L G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_c_B_8772 C C A A A G A G T A G T C C G A C C A A A G T A G G A G T A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G T
P K S S P T K V G G V G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_c_C_8858 C C A A A G A G T A G T C C G A C C A A A G T A G G A G G A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G T
P K S S P T K V G G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_dis_8780 T C G A A G A G T A G T C C G A C T A A A G T A G G A G G G G T T T A A G T A G C A G C A G C G T T C A C T G A G T G C C G C A G G C A T C C C A C C G T T C C G C A A T C C C T C C C A T G
S K S S P T K V G G G L S S S S A S L S A A G I P P V P A I P P M

N_dis_8827 T C G A A G A G T
S K S

N_his_8815 C C A A A G A G T A G T C C G A C C A A A G T A G G A G G A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G T
P K S S P T K V G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_i_A_8901 C C A A A G A G T A G T C C G A C C A A A G G A G G A G A A G T T T A A C C A G C A G T A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G
P K S S P T K G G G S L T S S S A S L S A A G I P P V P A I P P M

N_i_B_8768 C C A A A G A G T A G T C C G A C C A A A G G A G G A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C A T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G T
P K S S P T K G G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_met_8853 C C A A A G A G T A G T C C G A C C A A A G G A G G A G G T T T A A C C A G C A G T A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G T
P K S S P T K G G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_per_8835 C C A A A G A G T A G T C C G A C C A A A G T A G G A G G A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G T
P K S S P T K V G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_sit_0412 C C A A A G A G T A G T C C G A C C A A A G T A G G A G G A G G T T T A G C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G C C
P K S S P T K V G G G L A S S S A S L S A A G I P P V P A I P P M Q F G G T L A

N_tetraspe C C A A A G A G T A G T C C G A C C A A A G T A G G A G G A G G T T T A A C C A G C A G C A G C G T T C A C T G A G T G C C G C C G G C A T C C C A C C G T T C C A G C A A T C C C T C C C A T G C A A T T C G G C G G A A C C C T C G C C
P K S S P T K V G G G L T S S S A S L S A A G I P P V P A I P P M Q F G G T L A

850 860 870 880 890 900 910 920 930 940 950 960

N_crassa C T T C C C A C A G C T C C C C C T T C G C A C A A G A G T T C G C A C C C A T T G C A C C G T C C G T G G T G G T A G A A G A A G A T G G C C C A G A C C T C T C A G A A G A C A A C A G C T T G C A A T T C T C T G C C G G C A C C G G C
L P T A P P S H K S S H P I A P S V V V E E D G P D L S E D N S L Q I S A G T G

N_c_B_8772 C T T C C C A C A G C T C C C C C T T C G C A C A A G A G T T C G C A C C C A T T G C A C C A T C C G T G G T G G T A G A A G A G A T G G C C C A G A C C T C T C A G A A G A C A A C A G C T T C C A A T T C T C T G C C G G C A C C G G C
L P T A P P S H K S S H P I A P S V V V E E D G P D L S E D N S L Q F S A G T G

N_c_C_8858 C T T C C C A C A G C T C C C C C T T C G C A C A A G A G T T C G C A C C C A T T G C A C C G T C C G T A G T G G T A G A A G A A G A T G G C C T A G A C C T C T C A G A A G A C A A C A G C T T C C A A T T C T C T G C C G G C A C C G G C
L P T A P P S H K S S H P I A P S V V V E E D G L D L S E D N S F Q F S A G T G

N_dis_8780

N_dis_8827

N_his_8815 C T T C C C A C A G C T C C C C C T T C G C A C A A G A G T T C G C A C C C A T T G C C C G T C C G T G G T G G T A G A A G A A G A T G G C C C A G A C C T C T C A G A A G A C A A T A G C C T C C A A T T C T C T G C C G G C A C C G G C
L P T A P P S H K S S H P I A P S V V V E E D G P D L S E D N S L Q F S A G T G

N_i_A_8901

N_i_B_8768 C T T C C C A C A G C T C C C C C T T C G C A C A A G A A T T C G C A C C C A T T G C A C C G T C C G T G G T G G T A G A A G A A G A T G G C C C A G A C C T C T C A G A A G A C A A C A G C T T T C A A T T C T C T G C C G G C A C C G G C
L P T A P P S H K N S H P I A P S V V V E E D G P D L S E D N S F Q F S A G T G

N_met_8853 C T T C C C A C A G C T C C C C C T T C G C A C A A G A A T T C G C A C C C A T T G C A C C G T C C G T G G T G G T A G A A G A A G A T A C C C C G A C C T C T C A G A A G A C A A C A G C T T T C A A T C C T C C A C C G G C A C T G G C
L P T A P P S H K N S H P I A P S V V V E E D N S F Q S S A G T G

N_per_8835 C T T C C C A C A G C T C C C C C T T C G C A C A A G T T T C A C A C C C A T T G C A C C G T C C G T G G T G G T A G A A G A A G A T G G C C T A G A C C T C T C G G A A G A C A A C A G C T C C C A A T T C T C T G C C G G C A C C G G C
L P T A P P S H K C S H P I A P S V V V E E D G L D L S E D N S S Q F S A G T G

N_sit_0412 C T T C C C A C A G C T T C C T C T T C G C A C A A G A T T C G C A C C C A T C G C A C C T C C G T G G T G G T A G A A G A A G A T G G C C C A G A C C T C T C A G A A G A C A A C A G C T T T C A A T C C T C C A C C G G C A C C G G C
L P T A S S S H K H S H P I A P S V V V E E D G P D L S E D N S F Q S S T G T G

N_tetraspe C T T C C C A C A G C T T C C T C T T C G C A C A A G A A T T C G C A C C C A T C G C A C C A T C C G T G G T G G T A G A A G A A G A T G G C C C A G A C T T C T C A G A A G A C A A C A G C T T T C A A T C C T C C A C C G G C A C C G G C
L P T A S S S H K N S H P I A P S V V V E E D G P D F S E D N S F Q S S T G T G

M2a: *
M8: **


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                1210      1220
N_crassa      ....|....|....|....|.
              ACAACTGGGAAGTTGGGGAAA
              T T G K L G K
N_c_B_8772    -----
N_c_C_8858    GCAACTGGGAAG-----
              A T G K
N_dis_8780    -----
N_dis_8827    -----
N_his_8815    GCAACTGGGAAGTTGGGGAAA
              A T G K L G K
N_i_A_8901    -----
N_i_B_8768    GCAACTGGGAAGTTGGGGAAA
              A T G K L G K
N_met_8853    GCAACTGGGAAG-----
              A T G K
N_per_8835    ACAAGTGGAAAG-----
              T S G K
N_sit_0412    GCAACTGGGAAGTTGGGGAAA
              A T G K L G K
N_tetraspe    GCAACTGGGAAGTTGGGGAAA
              A T G K L G K

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Gene: NCU06387

Compared to the annotated sequence for *N. crassa*, the alignment is missing the first 37 codons and the last 36 codons.

The sequence *N_crassa* is the annotated gene sequence for NCU06387.

The sequence *N_tetraspe* is the gene sequence from the *N. tetrasperma* genome sequence.

Gene: NCU07311

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      10      20      30      40      50      60      70      80      90      100     110     120
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N_crassa  CCATTTCCATCATGGCTCCTTTACATTCCGATCGCCATCCTCGTGCTCTCCTTGTTCCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W L L Y I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_c_C_8863 CCATTTCCCTCATGGATCCTTTACATTCCGATCGCCATCCTCGTGCTGTCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_c_B_8772 CCATTTCCATCATGGCTCCTTTACATTCCGATCGCCATCCTCGTGCTGTCTCCTTGTTCCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W L L Y I R I A I L V L S L V L L G V A A W A V S M F A R G G S A A Y G
N_dis_EST  CCATTTCCATCATGGATCCTTTACATTCCGATCGCCATCCTCGTACTGTCTCCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_his_8815 -----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
S L V L L G V A A W A V S M F A G G G S A A Y G
N_i_A_8901 CCATTTCCATCATGGATCCTTTACATCCGGATCGCCATCCTTTGTCTGTCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_i_B_8768 CCATTTCCATCATGGATCCTTTACATCCGGATCGCCATCCTCGTGCTGTCTCCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A I L V L S L A L L G V A A W A V S I I A G G
N_met_8853 CCATTTCCATCATGGATCCTTTACATTCCGATCGCCATCCTCGTGCTGTCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCAATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_per_8835 CCATTTCCCTCATGGATCCTTTACATTCCGATCGCCACCTCGTGCTGTCTCCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A T L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_sit_0412 -----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
ATTCGGATCGCCATCCTCGTGCTGTCTGGTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G
N_tetraspe CCATTTCCATCATGGATCCTTTACATTCCGATCGCCATCCTCGTGCTGTCTCCTTCTTCTGGGGGTTGCCGCGTGGGCTGTCTCGATGTTTGCCGGAGGAGGGTCTGCGGCTTATGGA
P F P S W I L Y I R I A I L V L S L V L L G V A A W A V S M F A G G G S A A Y G

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      130     140     150     160     170     180     190     200     210     220     230     240
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N_crassa  TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G L Q F G A P H L F Y R I V G L I
N_c_C_8863 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G L Q F G A P H L F Y R I V G L I
N_c_B_8772 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G L Q F G A P H L F Y R I V G L I
N_dis_EST  TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAAATTCGGGGCACCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G F Q F G A P H L F Y R I V G L I
N_his_8815 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCATCGGCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G F Q F G A P H L F Y R I I G L I
N_i_A_8901 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGGGCGCCACATCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L L V Y G G S L G F Q F G A P H L F Y R I V G L I
N_i_B_8768 -----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGGGCGCCACATCTCTTCTATCGCATCGTCCGGTCTTATT
A S G M M I F V T I W S L L V Y G G S L G F Q F G A P H L F Y R I V G L I
N_met_8853 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G L Q F G A P H L F Y R I V G L I
N_per_8835 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G L Q F G A P H L F Y R I V G L I
N_sit_0412 TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G V Q F G A P H L F Y R I V G L I
N_tetraspe TATACGGGCGCTAGTGGGATGATGATCTTTGTGAATAATTTGGAGTCTTGTGTTTACGGCGGCTCCCTCGGGTCCAGTTTGGAGCGCCACATCTCTTCTATCGCATCGTCCGGTCTTATT
Y T G A S G M M I F V T I W S L V V Y G G S L G F Q F G A P H L F Y R I V G L I

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intron

M8:*

250 260 270 280 290 300 310 320 330 340 350 360

M2a:**
M8:**
M8:*

N_crassa
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTCGTGCTCGACTATTCTAGCGGTTACTACGGTGCAGTTCATGACTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D Y S S S G Y Y G A V H D Y G S A

N_c_C_8863
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTCGTGCTCGACTATTCTAGCGGTTACTACGGTGCAGTTCATGATTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D Y S S S G Y Y G A V H D Y G S A

N_c_B_8772
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTCGTGCTCGACTATTCTAGCGGTTACTATGGTGCAGTTCATGACTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D Y S S S G Y Y G A V H D Y G S A

N_dis_EST
 CTTTATAGTCTCGCAGTATCTTCTGGCTTGTGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTGGTGCTCGACTGGCTGGCGGTTACGGTGGTGCAGTTCGTGACTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D Y S S G G Y Y G A V R D Y G S A

N_his_8815
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGTGGGCTGGGCGTATGCGGCTAGCGAGGCAGCTGTCCGCTCGACTATTCTGGCGGTTACTATGGTGCAGTTCATGACTATGGCTCGGCC
 L Y S L A V I F W L V G W A Y A A S E A A V A L D Y S G G Y Y G A V H D Y G S A

N_i_A_8901
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCTAGCGAGGCAGCTGTCCGCTT-----GGC---TACTACTATTAT---CATGACTATGGCTCAGCC
 L Y S L A V I F W L A G W A Y A A S E A A V A L D Y S G G Y Y Y Y G A V H D Y G S A

N_i_B_8768
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCTAGCGAGGCAGCTGTCCGCTT-----GGC---TACTACTATTAT---CATGACTATGGCTCAGCC
 L Y S L A V I F W L A G W A Y A A S E A A V A L D Y S G G Y Y Y Y G A V H D Y G S A

N_met_8853
 CTTTACAGTCTCGCAGTATCTTCTGGCTCGCGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTCGTGCTCGACTGGTCTGGCGGTTACTATGGTACAGTTCATGACTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D W S G G Y Y G T V H D Y G S A

N_per_8835
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTCGTGCTCGACTATTCTAGCGGTTACTATGGTGCAGTTCATGACTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D Y S S S G Y Y G A V H D Y G S A

N_sit_0412
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGGGGCTGGGCGTATGCGGCAAGCCAGGCAGCTCTCGTACTCGACTATTCTGGCGGTTACTATGGTGCAGTTCATGACTATGGCTCGGCC
 L Y S L A V I F W L A G W A Y A A S Q A A L V L D Y S S G G Y Y G A V H D Y G S A

N_tetraspe
 CTTTACAGTCTCGCAGTATCTTCTGGCTTGTGGGCTGGGCGTATGCGGCTAGCGAGGCAGCTGTCCGCTTGACTGGCTGGCTACTACTATGGTGCATTTCATGACTATGGCTCGGCT
 L Y S L A V I F W L V G W A Y A A S E A A V A L D W S G Y Y Y G A I H D Y G S A

370 380 390 400 410 420 430 440 450 460 470 480

N_crassa
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTTGCTTGGCTTCGCGAAGCTACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L A C V R E A T A P K L S Q A E L

N_c_C_8863
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTTGCTTGGCTTCGCGAAGCCACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I V D L V F F I L A C V R E A T A P K L S Q A E L

N_c_B_8772
 TTGGCTGTGTGCGCAGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTTGCTTGGCTTCGCGAAGCTACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L A C V R E A T A P K L S Q A E L

N_dis_EST
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTTGCTTGGCTTCGCGAAGTCACGGCGCCAAAGCTCAAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L S C V R E V T A P K L N Q A E L

N_his_8815
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGCTACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L A C V R E A T A P K L S Q A E L

N_i_A_8901
 ATGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGCCACGGTGCCTCAAGCTCAGCCAGGCCGAACCTT
 M A V C A G L G A V A W V L S V V D L V F F I L A C V R E A T V P K L S Q A E L

N_i_B_8768
 ATGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGCCACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 M A V C A G L G A V A W V L S I V D L V F F I L A C V R E A T A P K L S Q A E L

N_met_8853
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGTCACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L A C V R E V T A P K L S Q T E L

N_per_8835
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGCTACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L A C V H E A T A P K L S Q A E L

N_sit_0412
 TTGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGCTACGGCGCCAAAGCTCAGCCAGGCCGAACCTT
 L A V C A G L G A V A W V L S I I D L V F F I L A C V R E A T A P K L S Q A E L

N_tetraspe
 ATGGCTGTGTGCGCTGGTCTAGGTGCCGTTGCCCTGGTCTGTCAATCATCGATCTTGTCTTCTTCATCCTCGCTTGGCTTCGCGAAGCTACGACGCCAAAGCTCAGCCAGGCCGAACCTT
 M A V C A G L G A V A W V L S I I D L V F F I L A C V R E A T T P K L S Q A E L

intron

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          490      500      510      520
...|...|...|...|...|...|...|...|...|...|...|...|...
N_crassa  GGACAAGTACAGCCAACCGCCTCCGTTGCGCCCGCCACTGCT
          G  Q  V  Q  P  T  A  S  V  A  P  A  T  A
N_c_C_8863 GGACAAGTACAACCAACCGCCTCCGTT-----
          G  Q  V  Q  P  T  A  S  V
N_c_B_8772 GGACAAGTACAACCAACCGCCTCCGTTGCGCCCGCCACTGCT
          G  Q  V  Q  P  T  A  S  V  A  P  A  T  A
N_dis__EST GGACAAGTACAGCCAACCGCCTCTGTTGCGCCCGCCACTGCT
          G  Q  V  Q  P  T  A  S  V  A  P  G  T  A
N_his_8815 GGACAAGTA-----
          G  Q  V
N_i_A_8901 GGACAAGTACAGCCAACCGCCTCCGTTACGCCCGCCACT---
          G  Q  V  Q  P  T  A  S  V  T  P  A  T
N_i_B_8768 GGACAAGTACAGCCAACCGCCTCCGTTACGCCCGCCACTGCT
          G  Q  V  Q  P  T  A  S  V  T  P  A  T  A
N_met_8853 GGACAATACAGCCAACCGCCTCCGTTGCGCCCACTGCT
          G  Q  I  Q  P  T  A  S  V  A  P  T  T  A
N_per_8835 GGACAAGTACAACCAACCGCCTCCGTTACGCCCACTGCT
          G  Q  V  Q  P  T  A  S  V  T  P  T  T  A
N_sit_0412 GGACAAGTACAGCCAACCGCCTCC-----
          G  Q  V  Q  P  T  A  S
N_tetraspe GGACAAGTACAGCCAACCGCCTCCGTTGCGCCCGCCACTGCT
          G  Q  V  Q  P  T  A  S  V  A  P  A  T  A

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Gene: NCU07311

Compared to the annotated sequence for *N. crassa*, the alignment is missing the first 13 codons and the last 17 codons.

The sequence *N_crassa* is the annotated gene sequence for NCU07311.

The sequence *N_tetraspe* is the gene sequence from the *N. tetrasperma* genome sequence.