

**Nucleotide sequence of the *Hansenula anomala* gene encoding flavocytochrome b<sub>2</sub> (L-lactate:cytochrome c oxidoreductase)**

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We present here the nucleotide sequence of the flavocytochrome b<sub>2</sub> gene from *Hansenula anomala*, which encodes a 573 aa protein. The mature protein starts at amino acid 74 (1) suggesting the existence of a presequence, as previously detected for *Saccharomyces cerevisiae* flavocytochrome b<sub>2</sub> (2), (80 aa for the latter (3)). 135 aa of the mature enzyme were previously determined (1,4).

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- 303                                     ttgtacttctccagc
- 288 atcaattctcccactataatgaaagctctgtccccaccgctttcccactgagaccacaactctcgtggggga
- 216 ctcttttactactccacagattacgtaacacagtgcttattttaaagtacttgggataggcaggtttca
- 144 ctaaaaccgaaaagttttggtgaaagcctcgaggattcatcattcttggatataatattcaaggactgac
- 72 ctcccacaaactttcccttctacttttaaatattcataaatacataacgagtgccaattccactgtctca
  1  ATGTTTAAAAGCCAATTGAGAACAGCAACTGCTAGATCAAGCTTTAGATCTTTAGCTAGCAAGCTAAACCCC
  73  CAGAGATTCAATCTTCAAAGACTCCAATTCTCAATGCTACAGGGGTTCAAATCGTTCCAAAAATTCATTA
 145  ATCGCATAGCCATCTCATTATCAGCTGTTTCATCTTCTTATTATCTATACCAAAAGGACAAATTCATTAGT
 217  GCAGATGTTTCCCTCATTGGAAAGATATAGAACTAACACCAGAAATTGTTTCTCAGCATAACAAAAAGATGAT
 289  CTATGGGTGTCTTGAACCGTCAAGTTTATGACTTAACAGATTTCTTGCCAAATCATCCAGGTGGTCAAAAA
 361  ATCATTATTAGATATGCTGGCAAAGATGCTACAAAGATCTTTGTACCAATTCATCCACTGATACTATTGAA
 433  AAATTTATCCCACTGAAAAGCATCTTGGTCCATTAGTTGGTGAGTTTGAACAGGAAGAAGAAGAAATTGAGT
 505  GATGAAGAAATTGATAGATTGGAAGAATCGAAAAGAAACCACCATTATCCAAATGATAAATCTTCATGAT
 577  TTTGAACTATTGCTAGACAAATCTACCACCACCTGCATTAGCTTATTACTGTTCCGCTGCAGACGATGAA
 649  GTCACACTAAGAGAAAATCATAATGCTTATCATAGAATCTTTTCAACCAAAAATCTTGATTGATGTTAAA
 721  GATGTTGATATTTCCACTGAATCTTTGGTGAAGACATCAGCACCATTTTATATATCTGCCACTGCATTG
 793  GCGAAATGGGCCATCCAGAAGTGAAGTCGCTATTGCAAAAGGTGCAGGTCGTAAGATGTCGTCCAAATG
 865  ATTTCTACATTAGCTTCATGTTTCATTTGATGAAATAGCCGATGCAAGAATCCAGGCCAACCAAAATGGTAT
 937  CAATTGTATGTTAATGCAGATAGATCAATCACCGAGAAAGCTGTGAGACACCCAGAGGAAGAGGATGAAA
1009  GGTTTATTCATAACAGTTGATGCGCCATCCTTAGGACGTCGTA AAAAGATATGAAGATGAAATTCGAAGT
1081  GATAGTGATGCCAGGTGATGATGAAGATATGATAGAAGTCAAGGTGCTTTCGCTGCTTTAGCTCCTTC
1153  ATTGATCCTTCTTTATCTTGGAAAGATATCGCTTTTATTAATCCATTACAAGATGCCTATTGTTATTA
1225  GGTGTTCAAAGAAAAGAGATGTTACTTGCTGCTGAACATGGATTACAAGGTGTTGCTTTATCAAACAT
1297  GGTGGTGCATTAAGATTATACAGAGCCCAGTGGAAAGTTTAGCTGAAGTTATGCCAATCTTGAAGAA
1369  AGAGGTTTAGATCAAAGATTGACATCTTTGTTGATGGTGGTGTAGAAGAGGTAAGTGTCTTGAAGCT
1441  TTGTGCTTGGTGCTAAAGGTGTTGGTTTAGGTAGACCTTCTTGTATGCAATGAGTTTCATATGGTGATA
1513  GGTGTTACTAAAGCTATTCAATTTGTTAAAAGATGAAATGAAATGAATATGAGATTATTAGGTGTAATA
1585  ATTGAAGAATTGACTCCTGAATTTATTGGATAGTAAAGTATTCATAACAGAGCCGTTCCAGTTGCTAAAGAT
1657  TATCTATATGAACAAAATTAACAAGATGAGCGGTGCTGAATTTAGACCAGGTATAGAGGATTAACAcaaat
1729  ttgtacattatgaaataaataacttgcatttattttaaaggacatagtacatcaatttgttgcact
1801  tgtggaagaacattataggtttcttc

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