DNA-binding domain within Brh2 N-terminus is the primary interaction site for association with DNA

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A

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gb|ACA39433.1| Endonuclease yhcR precursor [Lysinibacillus sphaericus C3-41]
Length=1379
Score = 32.7 bits (73), Expect = 8.1, Method: Composition-based stats.
Identities = 37/148 (25%), Positives = 61/148 (41%), Gaps = 10/148 (6%)

Query 1   TSQSSLHKRIHTTGSLPQALQSFG--NAPSMLSTVTRTPMQEIVPKQRTAAINESEKCAL 58
          T+ S+L K+I TGSL  +   S     +P+ +  V   P +   P      I E+   A
Sbjct 116 TNPSNLGKKIKITGSLDKYFGSHAGLKSPTSIEFVGSEPTEPTNPSVTEGTIAEAR--AA 173

Query 59  AEEDKVASVQATSQVTALPAAQAPTTRRIEPHP---FTTPKQTRNGRLPVRQNLASPMRT 115
             D++  +Q T  VTA P +       ++      + T      G L V +      +T
Sbjct 174 VGTDRIVQIQGT--VTATPGSWGGKAFYVQDESAGVYVFSNSTEAGSLAVGDIVKITGKT 231

Query 116 PATAPGLRFTTPQPSKRISLGMLPRAEI 143
             +  ++F +P   +RIS G  P  +I
Sbjct 232 SLFSGEVQFNSPT-IERISSGTAPAPQI 258
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B

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 No 1
>1eov_A ASPRS, aspartyl-tRNA synthetase; aminoacyl tRNA synthetase, tRNA ligase, APO-enzyme, OB-fold; 2.30A
  {Saccharomyces cerevisiae} SCOP: b.40.4.1 d.104.1.1
  Probab=95.49  E-value=0.051  Score=27.83  Aligned_cols=91  Identities=4%  Similarity=-0.150  Sum_probs=0.0

                                  β1          β2     β3                  β4
Q ss_pred            CCCCCCCCCCCEEEEEEEEEEECCCCCCCCCEEE-EECCCCCEECCCCCCCCE----------EECCCCEEEEEEEECCC
  Q ss_conf            26255554676036765488513688877627 8-86798731065788752 0----------23179757897620015
  Q brh2            53 SEKCALAEEDKVASVQATSQVTALPAAQAPTTR-RIEPHPFTTPKQTRNGRL----------PVRQNLASPMRTPATAP  120 (144)
  Q Consensus       53 ~~~~~~a~~~~~~~~~g~vt~~~~~~~~~~~~~~qd~s~gi~vy~~~~~~~~~~~~~~~~~~~~v~vGd~V~vtG~~~ey  120 (144)
                       +.....+...+..|++.|+|..-=..++.-.|+ ++|.++-+++....+...           .++.||.|.|+|.+..-
  T Consensus       26 ~~~~~~~~~~~~V~i~G~V~~~R~~G~~l~F~~lrD~~g~iQ~v~~~~~~~~~~~~~~~~~~~~l~~~~~v~v~G~v~~~  105 (487)
  T 1eov_A          26 FVDLDEAKDSDKEVLFRARVHNTRQQGATLAFLTLRQQASLIQGLVKANKEGTISKNMVKWAGSLNLESIVLVRGIVKKV  105 (487)
  T ss_dssp            GGGCCTTTTTTCEEEEEEEEEEEEECSSSEEEEEEEETTEEEEEEECCSSSSSCHHHHHHHTTCCTTCEEEEEEEEEC
  T ss_pred            HHCCCCCCCCCCEEEEEEEEEHHHCCCEEEEEEEECCCEEEEEEECCCCCCCCHHHHHHHHCCCCCCEEEEEEEEEEC
  T ss_conf            3124441227888999877521014874899999888607999983475333347999998518986189999899966

                                  β5
Q ss_pred            C--------CEEEECCCCEEEEECCCCCCCC
  Q ss_conf            6--------6155236724776367667777
  Q brh2           121 G--------LRFTTPQPSKRISLGMLPRAEI  143 (144)
  Q Consensus      121 ~--------G~tQi~~~S~~i~~~~~~paP~  143 (144)
                       .        |..+|....+++++.-..+-|.
  T Consensus      106 ~~~~~~~~~~~ei~~~~~~vls~~~~~~P~  136 (487)
  T 1eov_A         106 DEPIKSATVQNLEIHITKIYTISETPEALPI  136 (487)
  T ss_dssp            SSCCTTSSEEEEEEEEEEEEEEEECCCSSCSS
  T ss_pred            CCCCCCCCCCEEEEEEEEEEEECCCCCCCCC
  T ss_conf            8776567775078999998763147543785


No 2
>2pi2_A Replication protein A 32 kDa subunit; FULL-length RPA14/32, ssDNA binding protein, OB-fold, dioxane, DNA
  binding protein; 2.00A {Homo sapiens}
  Probab=93.53  E-value=0.1  Score=26.28  Aligned_cols=74  Identities=7%  Similarity=-0.208  Sum_probs=0.0

                        β1          β2      β3                  β4      β5
Q ss_pred            EEEEEEEECCCCCCCCCEEEEECCCC-CEECC------CCCCCCEEECCCCEEEEEEECCCCCEEEECCCCEEEEECCC
  Q ss_conf            676548851368887762788 67987-31065------788752023179757897620015661552367247763676
  Q brh2            66 SVQATSQVTALPAAQAPTTRRIEPHP-FTTPK------QTRNGRLPVRQNLASPMRTPATAPGLRFTTPQPSKRISLGML  138 (144)
  Q Consensus       66 ~~~~g~vt~~~~~~~~~~~~~qd~s~~gi~vy----------~~~~~~v~vGd~V~vtG~~~ey~G~tQi~~~S~~i~~~~~  138 (144)
                       |.+=|+|...-...-.-+|.|-|.++ .|-+.      ......-.+++|+-|+|.|.+..|+|..+|...+++.+...+
  T Consensus       74 V~iVG~Vr~v~~~~t~i~y~IdDgTG~~I~vr~W~d~~~~~~~~~~i~~g~YVrV~G~Lk~f~gkk~I~a~~IrpV~D~N  153 (270)
  T 2pi2_A          74 VTIVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVAFKIMPLEDMN  153 (270)
  T ss_dssp            EEEEEEEEEEEECCSSEEEEEEECSSSSCEEEEEECC-------CCCCCTTCEEEEEEEEEEEETTEEEEEEEEEECSCTH
  T ss_pred            EEEEEEEEECCCCCCEEEEEECCCCCEEEEEEECCCCCCCCCCCCCCCCEEEEEEEECCCCCCEEEEEEEEEECCCC
  T ss_conf            999989863223676689999879997379998516887643455655787899987873217841178999886267 56
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Fig S1. Bioinformatics analysis of Brh2^{NT} DNA-binding region.

A. BLAST alignment result using 144 residue from Brh2^{NT} as query.

B. Top two hits from HHpred server using both sequences in A as input query. Location of thepredicted five beta strands (E) are shown by the overhead lines.