

SUPPLEMENTARY INFORMATION

A

BL107_FoiA1-342 1 MKARKAKEYFVNDLLSMESYCIDHYSDDYYSKSNFSCNVTLQSKGELVTSICAPINDAHLEIFKSNQTLIYEEEAQNQNSVAF... 115
CC9902_FoiA1-342 1 MKARKAKEYFVNDLLSMESYCIDHYSDDYYSKSNFSCNVTLQSKGELVTSICAPINDAHLEIFKSNQTLIYEEEAQNQNSVAF... 115
RCC307_FoiA1-343 1 MRAKKAKEYYFSDLLGMEAYCRSHYAEYYSKSNFSCNVTLQSKGELLTSSICAPINDVHLELIFKSNQTLIYEEEAQNQNSVAF... 115
RS9916_FoiA1-342 1 MRSKKAKEYIFSDLLGMEYCRSHYAEYYSKSNFSCNVTLQSKGELLTSSICAPINNVHLEIFKSNQTLIYEEEAQNQNSVAF... 115
CC9311_FoiA1-344 1 MKARKAKEYFVNDLLGMEYCRSHYAEYYSKSNFSCNITQLSKGELQTSICAPINNVHLEIFKSNQTLIYEEEAQNQNSVAF... 115
WHB020_FoiA1-344 1 MKARKAKEYFVNDLLGMEYCRSHYAEYYSKSNFSCNITQLSKGELQTSICAPINNVHLEIFKSNQTLIYEEEAQNQNSVAF... 115
WHB109_FoiA1-343 1 LKRRSRNRYVSDTLEMEEFCAHFEYHSTSFSGCNVTQLSTGLLETKTTCSPIDQVHLEIFKSNQTLIYEEEAQNQNSVAF... 116
MINOS11_FoiA1-346 1 VLRKPASHYSFTDLEMEECCHAFSEYYQGSFAFDCNVTLQSGSLLTKTICSPVVDIHLFEFESNQALLYEEEAQNQNSVAF... 116
PROS-U1_FoiA1-343 1 LRRKRSRNYVFCDTLEMEEFCAHFEYHSTSFSGCNVTQLSTGILETQTTCSPIDQVHLEIFKSNQTLIYEEEAQNQNSVAF... 116
WHB016_FoiA1-343 1 MKARKAKEYFVNDLLGMEYCRSHYAEYYSKSNFSCNITQLSKGELQTSICAPINNVHLEIFKSNQTLIYEEEAQNQNSVAF... 115
MVIR-18-1_FoiA1-344 1 MKARKAKEYFVNDLLGMEYCRSHYAEYYSKSNFSCNITQLSKGELQTSICAPINNVHLEIFKSNQTLIYEEEAQNQNSVAF... 115
A15-62_FoiA1-343 1 LRRKRSRNYIFSDTLEMEEFCAHFEYHSTSFSGCNVTQLSTGLLETKTTCSPIDQVHLEIFKSNQTLIYEEEAQNQNSVAF... 116
RS9915_FoiA1-344 1 LRRKRSRNYVFCDTLEMEEFCAHFEYHSTSFSGCNVTQLSTGILETQTTCSPIDQVHLEIFKSNQTLIYEEEAQNQNSVAF... 116
BIOS-U3-1_FoiA1-343 1 MKARKAKEYFVNDLLGMEYCRSHYAEYYSKSNFSCNITQLSKGELQTSICAPINNVHLEIFKSNQTLIYEEEAQNQNSVAF... 115
WHB103_FoiA1-343 1 LRRKRSRNYVFCDTLEMEEFCAHFEYHSTSFSGCNVTQLSTGILETQTTCSPIDQVHLEIFKSNQTLIYEEEAQNQNSVAF... 116

Consensus

MK KKAKEYYFSD LLGME YCK Hy EYYSKSNFSCNVTLQSKGELTSSICAPINDVHLEIFKSNQTLIYEEEAQNQNSVAF...
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BL107_FoiA1-342 116 KTGGNVWDIVGANTQLCCMS-LKWEKMKKIKDMNAYNAFALEECIGIDSNSSASIQLSLFRHFHTKG-LREAEAFYDLAIATLEED... 228
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CC9311_FoiA1-344 116 KTGGNVWDIVGANTQLCCMS-LKWKIMKEKIKDMNAYNAFALEECIGIDSKSAASIQLRFLDKHFHKG-MTSADEFYDLAIATLEED... 229
WHB020_FoiA1-344 116 KTGGNVWDIVGANTQLCCMS-LKWKIMKEKIKDMNAYNAFALEECIGIDSNSSASIQLRFLDKHFHKG-MTSADEFYDLAIATLEED... 229
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WHB103_FoiA1-343 117 KTGGNVWDIVGANEELCCMS-LKWNKLGKIQDKMNAAYARLEECIGIDSDHASTQLKLFYHFFHKG-VAKANGFYDLAIATLEED... 231

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CC9311_FoiA1-344 230 REGLPPLTIGEITKYLNSKESVGVQVCRSTFNMNILDILKSIRLEQVKKSYLNPHVPGKLNFTKKNALYYGFKNWITFQKLYQTFQESPEET... 344
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PROS-U1_FoiA1-343 232 RAGMPPITLDEITEYLNSENTESLNTICRKNFNMVDIELVRRIRLEQTRKAFRLTPHSSTGLKDFTKKRTALYYGFKNWITFQKLYQTFQESPEET... 343
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RS9915_FoiA1-344 233 RAGMPPITLDEITEYLNSENTESLNTICRKNFNMVDIELVRRIRLEQTRKAFRLTPHSSTGLKDFTKKRTALYYGFKNWITFQKLYQTFQESPEET... 344
BIOS-U3-1_FoiA1-343 230 RLGLPPLSISDITKFLNSKESVGVQVCRSTFNMNILDILKSIRLEQVKKSYLNPHVPGKLNFTKKNALYYGFKNWITFQKLYQTFQESPEET... 343
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Consensus

RGLPPLTISEITKYLNSKESVGVQVCRSTFNMNILDILKSIRLEQVKKSYLNPHVPGKLNFTKKNALYYGFKNWITFQKLYQTFQESPEET...
RAGL PPLTI+EITKYLNSKESLNTACRSTFNM+ILELILKSIRLEQVKKSYLNPHVPGKLNFTKKNALYYGFKNWITFQKLYQTFQESPEET...
IDKSSK+SVLVSCLKRER++

PFAM PF12833

SMART SM00342

PROFILE PS01124

B

RCC307_FeiB/1-315 1 - MKLSLSYKDPQLQSETLAEELGQNTTRITQLDLGEGTYSMSHAMSSGVSIAEIKASKTLLYEGWGTGWSVDFNWI TPIKATTDPFYCEGYEMRNSISGGLNTINSAPGSSWG 111
 CC9902_FeiB/1-318 1 - MKLELSYSDHLQLSESLNELGQTRITQLPEGEGKYTMSFKQSTGIALAEIQSTQPLLYEGWGTGWSVDFNWI TPTCHLNDPFYCEGYEMKETS LGGFNTLNTSPGNSWG 111
 CC9311_FeiB/1-318 1 - MKLQLAYTDPQLQSETLQAYGGVTRITQLESEGEGYSMSHKKSSMAIAEICASKPLLYEGWGTGWSVDFNWI TPMRKSNYPFYCEGYDMMLNSLGGKFTHSNSGDSWG 111
 PROS-U-1_FeiB/1-321 1 - MKTTFEFRDPLEISEELAKLGLTKITQLDGGNGIYTMQAATANKVSLAEISANKTLLYEGWGTGWSVDFNWI TPKIDIQDAFGYCDGFKMAKNSLAGFTINSIPGNAWG 111
 MVIR-18-1_FeiB/1-318 1 - MKIKFAYTDPQLQSETLQEQYGGVTRISQLESEGEGYSMSHQKSTGMAIAEISASKPLLYEGWGTGWSVDFNWI TPIRKANSFPFYCEGFDMMNDSLGGFNTFHSNPGDSWG 111
 WHB016_FeiB/1-316 1 - MKVKFSYTDPLQLSETLQKQYDFRITQLETEGEGYSMAHERSSGMAIAEISASKPLLYEGWGTGWSVDFNWI TPIQKASYPHGYCDGFDMSDNLGGKFTFRNSPGDSWG 111
 WHB020_FeiB/1-318 1 - MKLQFAYTDPQLQSETLQAYGGVTRITQLESEGEGYSVSHKSSMAIAEISASKPLLYEGWGTGWSVDFNWI TPMRKTTPFYCEGYDMKTNLGGKFTINSIPGNAWG 111
 WHB109_FeiB/1-321 1 - MKTSEYRDPLEISEELAKLGLTKITQLDGGNGIYTMQAANTNKVALAEISANKTLLYEGWGTGWSVDFNWI TPKANTQGVFGYCDGFKMTKNSLAGFTINSIPGNAWG 111
 RS9916_FeiB/1-316 1 MIKLSLSYKDPHLSETLAEELGQNTTRITQLDRGEGTYSMSHAIASGVSIAEIKASKTLLYEGWGTGWSVDFNWI TPLKSSADPLFYCEGYEMRNSISGGLNTLNTSTASSWG 112
 BL107_FeiB/1-318 1 - MKLELAYSDDHQLSESLNELGQTRITQLEPEGKYTMSFKQSSAGIALAEIQSTQPLLYEGWGTGWSVDFNWI TPTCOFNDPFYCEGYEMKEASLGGFNTLNTSPGNSWG 111
 WHB103_FeiB/1-321 1 - MNKTFDYRDPLEISEELAKLGLTKITQLDGGNGIYTMQAATANKVSLTEISANKTLLYEGWGTGWSVDFNWI TPKIDIQDAFGYCDGFKMEKNSLAGFTINSIPGNAWG 111
 A15-62_FeiB/1-321 1 - MKTSEYRDPLEISEELAKLGLTKITQLDGGNGIYTMQAANTNKVTLAEISANKTLLYEGWGTGWSVDFNWI TPKANTQGAFGYCDGFKMTKNSLAGFTINSIPGNAWG 111
 BIOS-U3-1_FeiB/1-315 1 - MKLSPYSDDLQSETLNLGQLTRITQFDGAGSYSMTHSMASGSIASIAEKASKTLLYEGWGTGWSVDFNWI TPLKNSVAPMGLECYEMKANSIGGLNTYNSPGSSWG 111
 MNOS11_FeiB/1-332 1 - MSIIIEYKDPNLSEELQKLGQSTRITQFENGGGYTKISPLQYKTVSVAQIESSTKLLYEGWGTGWSVDFNWI TPLGRKVEGLRCDGGRMTNSLAGFATISPPFRNSWG 111
 RS9915_FeiB/1-321 1 - MNKTFDYRDPLEISEELAKLGLTKITQLDGGNGIYTMQAATANKVSLTEISANKTLLYEGWGTGWSVDFNWI TPKIDIQDAFGYCDGFKMKRNSLAGFTINSIPGNAWG 111

Consensus

MKLS+YDPLQLSE-L LGQTRITQLDGGEGYS+MSHA++SGV++AEISASKTLLYEGWGTGWSVDFNWI TPK+KTQDPFYCEGY+MNSLGGFT+NSPGNSWG
 -MKLS++YRDPQLQSETLAKLGLTKITQLEGGEGYS+MSHA++SGV++AEISASKTLLYEGWGTGWSVDFNWI TPK+KTQDPFYCEGY+MKNKSLGGFNTINS+PGNSWG

RCC307_FeiB/1-315 112 KYSEACSSSTACMLDKAVLIDSLKACNAQTALENLTKRGLDVFHFAALQLRKLASDMSKGI VNAA - KYDDLITACLEEGTVRHYKKSSELKNLGLLSEIVLSLHSDVMQSP 222
 CC9902_FeiB/1-318 112 KYSNCCSSSTACMLDKNILMKLKECNAQAIDNLSKARGLDVSSLSYQLKLLTRKDLVRGIMNPT - KYDDLIVACLEEGDKRGRYKGLTKNYRLLGEIVQLSHDSRRMSSP 222
 CC9311_FeiB/1-318 112 KYSECCSSSTACMLDKTILLNLRDCNASHAIDNLSQSSGLDIDHEAFALRLLRRLRELKVGISDPS - KYDDLMTIACLEEGSKRQYKQKQVKNQRLLGEIVNLSHDLDKMSSP 222
 PROS-U-1_FeiB/1-321 112 KYSECCSSSTACMLDKIILLELQNKAYDGLERLSDQGGVYNNNALGQLKRLARKEVSSGIQTP - KYFDLVIACLEEGMSEQNS-HGEKNIQGLREIINLAHSQKSMSSP 221
 MVIR-18-1_FeiB/1-318 112 KYSECCSSSTACMLDKKILLDKLQEKASHAIDNLSQSMGLVIDHEAFTLRKLRDLVKGISNPS - KYDDLMTIACLEEGNRRLFKKKQAKNQRLLGEIVDLAHDLDQMSSP 222
 WHB016_FeiB/1-316 112 KYSECCSATACMLDKIILLDKLEECCANRALIHLQSIGLVIDHEAFTLRLLRDLVQGISNPS - KYDDLMTIACLEEGHRLYKQKQAKNQRLLGEIVNLSHDPDKMSSP 222
 WHB020_FeiB/1-318 112 KYSECCSSSTACMLDKIILLNLRDCNASHAIDSLRSIGLDIDHEAFAALRLLRDLVKGISNPS - KYDDLMTIACLEEGIHRGYKQKQVKNQRLLAEIVNLSHDSKSMSSP 222
 WHB109_FeiB/1-321 112 KYNNECCSSSTACMLDKQLLFELLENCKAYDGLERLSDQGGIYCNNTALNQLKRLAAREVSAGIQNPE - KYFDLVIACLEEGPMTQNS-QDPHIDQLREIIDLASEKTMSSP 221
 RS9916_FeiB/1-316 112 KYSECCSSSTACMLDKALLIDSLKACNAQVALDNLNKRGLDVHHPAALQLRKLARKEVSSGIQTP - KYDDLITACLEEGTVRHYRKAELRQGLLSEIVLSLHSDVMQSP 223
 BL107_FeiB/1-318 112 KYSNCCSSSTACMLDKNILMKLKECNAQAIDNLSKARGLDVHNSLHQLKLLTRKDLVKGIMNPT - KYDDLIVACLEEGSNKRGYKGLTKNYRLLGEIVLSHDSRRMSSP 222
 WHB103_FeiB/1-321 112 KYSECCSSSTACMLDKIILLELLENCKAYDGLERLSDQGGVYNNNALGQLKRLARKEVSSGIQTP - KYFDLVIACLEEGPMSDQNS-HGQKNIQGLREIINLAHSQKSMSSP 221
 A15-62_FeiB/1-321 112 KYNNECCSSSTACMLDKQLLELLENCKAYDGLERLSDQGGIYCNNTALNQLKSLAAKEVSSGIQTP - KYFDLVIACLEEGPMTAQS-QDPHIDQLREIIDLASEKTMSSP 221
 BIOS-U3-1_FeiB/1-315 112 KYSRCCSSSTACMLDKASLMEAMICNAQVIGLNDGKGLVSDQLNQLKRLARKEVSSGIQTP - KYDDLITACLEEGRSRAIKKGETKNHTLLSEIVRLAHDTEKMSAP 222
 MNOS11_FeiB/1-332 112 RYTNNCTSTACMVRKSDFDYLHECKAYNALERIDGIDGMECEPKHLAQLKRLVERNIRROEESIDSKYFEILTACLEEQITVSDSIQSPKNVDLLREIVKLAHSDVMTKP 223
 RS9915_FeiB/1-321 112 KYSECCSSSTACMLDKIILLELLENCKAYDGLERLSDQGGVYNNNALGQLKRLARKEVSSGIQTP - KYFDLVIACLEEGPMSDQNS-HGQKNIQGLREIINLAHSQKSMSSP 221

Consensus

KYS CSSTACMLDK LLE L CNA LE L G L AL QL KR R K D L G I N P KY DL A C L E E G Y KN L L E I V L H D M S P
 KYSE+CSSTACMLDKKILLELLE+CNAQYDLENLSD+GLDI++EAL+QLKRLARKDLSSGIQTP+KYDDLITACLEEGMRSRQYKQKQ+KN+GLLREIVNLAHSD+MSSP

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 CC9902_FeiB/1-318 223 MTLSDVCCQYLDTGQASLYRVCQYFFGMG IEMMTQIRLEEARRALLMFQKNEKNHALTVRDVALGYGFKHGRFRSRRYFTSFGELPSQTLDRSQEL 318
 CC9311_FeiB/1-318 223 LSLSDVCKLLNSGQASLYRVCQYFFGMG IEMMTQIRLEEARRAMIFQSTSSQDNNTIREIAIRYGFKHQGRFRSRRYFTSFGELPSQTLRRSKLV 318
 PROS-U-1_FeiB/1-321 222 LSLLEVCKHINTSQASLYRVCQYFFGMG IELMTHIRLEESRRMMLNKEARQKLKLYSIRDAIKYGFKHQGRYARRYTAFFGELPSQTIKSSRRYKLPF 321
 MVIR-18-1_FeiB/1-318 222 MSLSDVCRHLNSGQASLYRVCQYFFGMG IEMMTQIRLEEARSMIYYSTTSDDNNTIREIAIRYGFKHQGRFRSRRYFTSFGELPSQTLKRSKLL 318
 WHB016_FeiB/1-316 223 MSLSDVCRHLNVAQASLYRVCQYFFGMG IEMMTQIRLEEARSLDQCS-ADQNTKTIREIAIRYGFKHQGRFRSRRYFTSFGELPSHTVKHSESL 316
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 WHB103_FeiB/1-321 222 LSLLEVCKHINTSQASLYRVCQYFFGMG IELMTHIRLEESRRMMLNKEARQKLKLYSIRDAIKYGFKHQGRYARRYTAFFGELPSQTIKSSRRYKLPF 321
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 BIOS-U3-1_FeiB/1-315 223 MTLSDVCCQHLDTGQASLYRVCQYFFGMG IEMMTQIRLEESRRALLRQCYQSVAESMIREVAIRYGFKHQGRYARRYTAFFGELPSQTLNNA 315
 MNOS11_FeiB/1-332 224 LTLAEVCRQIHTSQASLYRVCQYFFGMG IEMMTQIRLEESRRVLLNSALRYELKLSIRIEAIFHGFKHQGRYARRYTAFFGELPSQTIKSSRRYKLPF 332
 RS9915_FeiB/1-321 222 LSLLEVCKHINTSQASLYRVCQYFFGMG IELMTHIRLEESRRMMLNKEARQKLKLYSIRDAIKYGFKHQGRYARRYTAFFGELPSQTIKSSRRYKLPF 321

Consensus

LSLSDVCKHLNLSQASLYRVCQYFFGMG IEMMTQIRLEESRRMLNQSARSKL+LYTIR+IAIRYGFKHQGRYARRYFTSFGELPSQTIKSSRRYKLPF
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 PS01124

PFAM PF12833
 SMART SM00342
 PROFILE PS01124

C

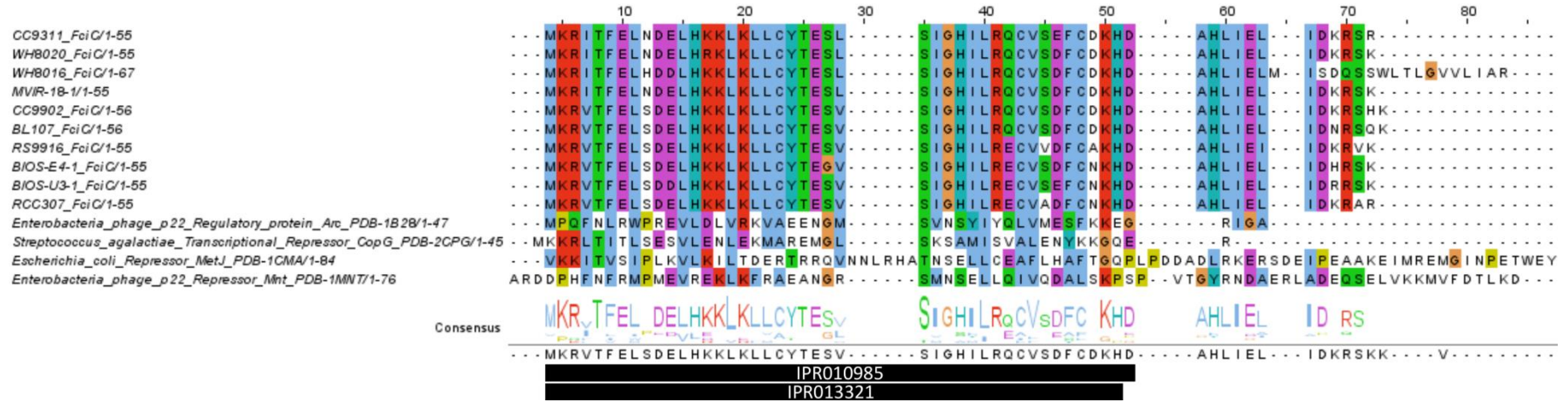


Figure S1. Multiple sequence alignments of putative transcriptional regulators FciA (A) and FciB (B), both containing an AraC-like α -helix-turn- α -helix (HTH, IPR018060) domain, and FciC (C) with a predicted ribbon-helix-helix (IPR010985 and IPR013321). Shading represents identical amino acid in at least 70% of the sequences. Protein domains, framed by a black rectangle, were determined using InterProScan against *Synechococcus* sp. RS9916 sequences, used as reference. *Ab initio* modeling using Phyre2 indicated that 77% of FciA (263 of 342 residues) and 50% of FciB (158 of 316 residues) from *Synechococcus* sp. RS9916 could be modeled with >90% confidence to the AraC/XylS family. Furthermore, 78% of FciC (42 of 55 residues) were modeled based on the CopG-like family (Gomis-Rüth et al., 1998).

Gomis-Rüth, F.X., Solà, M., Acebo, P., Párraga, A., Guasch, A., Eritja, R. et al. (1998) The structure of plasmid-encoded transcriptional repressor CopG unliganded and bound to its operator. *EMBO J* 17(24): 7404-7415.