Supporting Information

Article

Designability of Aromatic Interaction Networks at *E. coli* Bacterioferritin B-type Channels

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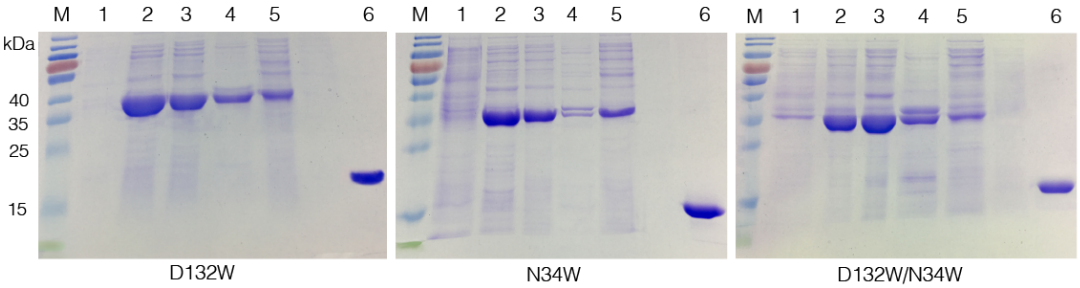

Figure S1 Electrophoretic monitoring of the purification of the BFR-derived proteins. Lane M: ladder. Lane 1: before induction. Lane 2: post induction. Lane 3: soluble fraction. Lane 4: insoluble fraction. Lane 5: flow through. Lane 6: purified protein after cleavage.

D132W

D132W-F（5'-3'）: *TGG*TGGCTGGAAACCGAACTG

D132W-R（5'-3'）: GATATGACCTTCTTCATCACGC

N34W

N34W-F（5'-3'）: CCA*CCA*TTTGAACATACGTGCATGCAG

N34W-R（5'-3'）: CGTATGTTCAAA*TGG*TGGGGTCTGAAACGTCTG

D132W/N34W was performed on the basis of plasmid D132W.

Figure S2. Primers used in QuikChange mutagenesis for D132W, N34W and D132W/N34W using the BFR construct as a template.

Sequencing Results

The sequencing results were aligned with the BFR gene using BLAST (NCBI). The mutant codon is highlighted in red.

D132W: (D-GAT; W-TGG)

Query is BFR native, Sbjct is the sequencing result.

```
Query 1    .....ATGAAAGGTGATACCAAAGTGATCAACTACCTGAACAAACTGCTGGGTAACGAAC
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1    ACAAGATGAAAGGTGATACCAAAGTGATCAACTACCTGAACAAACTGCTGGGTAACGAAC

Query 56   TGGTGGCAATCAACCAGTACTTCCTGCATGCACGTATGTTCAAAAACTGGGGTCTGAAAC
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61   TGGTGGCAATCAACCAGTACTTCCTGCATGCACGTATGTTCAAAAACTGGGGTCTGAAAC

Query 116  GTCTGAACGATGTGGAATACCATGAAAGCATCGATGAAATGAAACATGCAGATCGTTACA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  GTCTGAACGATGTGGAATACCATGAAAGCATCGATGAAATGAAACATGCAGATCGTTACA

Query 176  TCGAACGTATCCTGTTCCTGGAAGGTCTGCCGAACCTGCAGGATCTGGGTAAACTGAACA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TCGAACGTATCCTGTTCCTGGAAGGTCTGCCGAACCTGCAGGATCTGGGTAAACTGAACA

Query 236  TCGGTGAAGATGTGGAAGAAATGCTGCGTAGCGATCTGGCACTGGAACTGGATGGTGCAA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  TCGGTGAAGATGTGGAAGAAATGCTGCGTAGCGATCTGGCACTGGAACTGGATGGTGCAA

Query 296  AAAACCTGCGTGAAGCAATCGGTTACGCAGATAGCGTGCATGATTACGTGAGCCGTGATA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  AAAACCTGCGTGAAGCAATCGGTTACGCAGATAGCGTGCATGATTACGTGAGCCGTGATA

Query 356  TGATGATCGAAATCCTGCGTGATGAAGAAGGTCATATCGATTGGCTGGAAACCGAACTGG
           ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Sbjct 361  TGATGATCGAAATCCTGCGTGATGAAGAAGGTCATATCTGGTGGCTGGAAACCGAACTGG

Query 416  ATCTGATCCAGAAAATGGGTCTGCAGAACTACCTGCAGGCACAGATCCGTGAAGAAGGT
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  ATCTGATCCAGAAAATGGGTCTGCAGAACTACCTGCAGGCACAGATCCGTGAAGAAGGTT
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N34W: (N-AAC; W-TGG)

Query is BFR native, Sbjct is the sequencing result.

```
Query 1    ..............ATGAAAGGTGATACCAAAGTGATCAACTACCTGAACAAACTGCTGG
                          ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1    ATGACGACGACAAGATGAAAGGTGATACCAAAGTGATCAACTACCTGAACAAACTGCTGG
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query 47  GTAACGAACTGGTGGCAATCAACCAGTACTTCCTGCATGCACGTATGTTCAAAAACTGGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||
sbjct 61  GTAACGAACTGGTGGCAATCAACCAGTACTTCCTGCATGCACGTATGTTCAAATGGTGGG

query 107 GTCTGAAACGTCTGAACGATGTGGAATACCATGAAAGCATCGATGAAATGAAACATGCAG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
sbjct 121 GTCTGAAACGTCTGAACGATGTGGAATACCATGAAAGCATCGATGAAATGAAACATGCAG

query 167 ATCGTTACATCGAACGTATCCTGTTCCTGGAAGGTCTGCCGAACCTGCAGGATCTGGGTA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
sbjct 181 ATCGTTACATCGAACGTATCCTGTTCCTGGAAGGTCTGCCGAACCTGCAGGATCTGGGTA

query 227 AACTGAACATCGGTGAAGATGTGGAAGAAATGCTGCGTAGCGATCTGGCACTGGAACTGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
sbjct 241 AACTGAACATCGGTGAAGATGTGGAAGAAATGCTGCGTAGCGATCTGGCACTGGAACTGG

query 287 ATGGTGCAAAAAACCTGCGTGAAGCAATCGGTTACGCAGATAGCGTGCATGATTACGTGA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
sbjct 301 ATGGTGCAAAAAACCTGCGTGAAGCAATCGGTTACGCAGATAGCGTGCATGATTACGTGA

query 347 GCCGTGATATGATGATCGAAATCCTGCGTGATGAAGAAGGTCATATCGATTGGCTGGAAA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
sbjct 361 GCCGTGATATGATGATCGAAATCCTGCGTGATGAAGAAGGTCATATCGATTGGCTGGAAA

query 407 CCGAACTGGATCTGATCCAGAAAATGGGTCTGCAGAACTACCTGCAGGCACAGATCCGTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
sbjct 421 CCGAACTGGATCTGATCCAGAAAATGGGTCTGCAGAACTACCTGCAGGCACAGATCCGTG

query 467 AAGAAGGT
          ||||||||
sbjct 481 AAGAAGGT
```

D132W-N34W： (D-GAT; N-AAC; W-TGG)

Query is BFR native, Sbjct is the sequencing result.

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Query  1   ..ATGAAAGGTGATACCAAAGTGATCAACTACCTGAACAAACTGCTGGGTAACGAACTGG
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1   AGATGAAAGGTGATACCAAAGTGATCAACTACCTGAACAAACTGCTGGGTAACGAACTGG

Query  59  TGGCAATCAACCAGTACTTCCTGCATGCACGTATGTTCAAAAACTGGGGTCTGAAACGTC
           ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Sbjct  61  TGGCAATCAACCAGTACTTCCTGCATGCACGTATGTTCAAATGGTGGGGTCTGAAACGTC
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Query 119TGAACGATGTGGAATACCATGAAAGCATCGATGAAATGAAACATGCAGATCGTTACATCG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TGAACGATGTGGAATACCATGAAAGCATCGATGAAATGAAACATGCAGATCGTTACATCG

Query 179AACGTATCCTGTTCCTGGAAGGTCTGCCGAACCTGCAGGATCTGGGTAAACTGAACATCG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AACGTATCCTGTTCCTGGAAGGTCTGCCGAACCTGCAGGATCTGGGTAAACTGAACATCG

Query 239GTGAAGATGTGGAAGAAATGCTGCGTAGCGATCTGGCACTGGAACTGGATGGTGCAAAAA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 GTGAAGATGTGGAAGAAATGCTGCGTAGCGATCTGGCACTGGAACTGGATGGTGCAAAAA

Query 299ACCTGCGTGAAGCAATCGGTTACGCAGATAGCGTGCATGATTACGTGAGCCGTGATATGA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ACCTGCGTGAAGCAATCGGTTACGCAGATAGCGTGCATGATTACGTGAGCCGTGATATGA

Query 359TGATCGAAATCCTGCGTGATGAAGAAGGTCATATCGATTGGCTGGAAACCGAACTGGATC
         |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Sbjct 361 TGATCGAAATCCTGCGTGATGAAGAAGGTCATATCTGGTGGCTGGAAACCGAACTGGATC

Query 419 TGATCCAGAAAATGGGTCTGCAGAACTACCTGCAGGCACAGATCCGTGAAGAAGGT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421 TGATCCAGAAAATGGGTCTGCAGAACTACCTGCAGGCACAGATCCGTGAAGAAGGT
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