# Supplement for: Correlation Between Binding Rate Constants and Individual Information of *E. coli* Fis Binding Sites

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This document contains:

1. Fis binding sequences used in EMSA experiments - Fig. 1

2. Graphs of Fis binding rates *vs.* information - Fig. 2

**Computation of $K_{\mathrm{D}}$ values**
See reference [1] for definitions of symbols, methods and the equations used. The competitor EMSA experiments were repeated three times with different competitor concentrations ($C_0$). $K_{\mathrm{D}w}$ and $R_0$ were simultaneouly adjusted to fit two criteria. First, the $K_{\mathrm{D}}$ of the Hin-180 oligo was made to match the published value of Hin-D, $2 \times 10^{-9}$ M [2]. Second, the $K_{\mathrm{D}w}$ constant was made to match the computed $K_{\mathrm{D}}$ of the **con** oligo. The top and bottom bands (Figure 5) were quantitated using the ImageQuant program (Molecular Dynamics, Sunnyvale, CA). The $K_{\mathrm{D}c}$s were computed using the method given in [1] and the average $K_{\mathrm{D}c}$s and standard deviations were computed from the three values.

Additional supplementary files are:

- Fis-koff-raw-data.xls - The raw SPR data.
- Fis-kd-raw-data.xls - The raw EMSA data.
- Fis-kon-koff-kd-ri.xls - Combination of SPR and EMSA data, graphed in Fig. 2.

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# References

[1] I. G. Lyakhov, P. N. Hengen, D. Rubens, and T. D. Schneider. The P1 Phage Replication Protein RepA Contacts an Otherwise Inaccessible Thymine N3 Proton by DNA Distortion or Base Flipping. *Nucleic Acids Res.*, 29(23):4892–4900, 2001. http://www.ccrnp.ncifcrf.gov/˜toms/paper/repan3/.

[2] C. Q. Pan, S. E. Finkel, S. E. Cramton, J. A. Feng, D. S. Sigman, and R. C. Johnson. Variable structures of Fis-DNA complexes determined by flanking DNA-protein contacts. *J. Mol. Biol.*, 264:675–695, 1996.

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Sequences used for EMSA Experiments

#              Ri (bits)      Name   Sequence

1            -30.6          anti-con
CTGACCCCGGGTCAGGCGAAGCCTGACCCGGGGTCAG

3              4.9          cin-336
GTCTAACTTCCATACGCGAAGCGTATGGAAGTTAGAC

2              5.4          hin-1096
GAACAAATCCCAGTCGCGAAGCGACTGGGATTTGTTC

4              6.6          lacP-560
GCTCACTCATTAGGCGCGAAGCGCCTAATGAGTGAGC

6              8.2          ndhII-188
GCCTATCTTTTCAGCGCGAAGCGCTGAAAAGATAGGC

7              8.2          comp-ndhII-188
GCTGAAAAGATAGGCGCGAAGCGCCTATCTTTTCAGC

9             10.1          fis-333
GGTCAAAGTTTGGCCGCGAAGCGGCCAAACTTTGACC

8             10.2          tgt-1824
GCTAAAAAATTCATCGCGAAGCGATGAATTTTTTAGC

5             10.4          hin-180
GGTCACAATTTGCACGCGAAGCGTGCAAATTGTGACC

10            10.9          thrU-87
GGTCACATTTTATGCGCGAAGCGCATAAAATGTGACC

11            12.7          ndhI-137
GCTCAAATAATAAACGCGAAGCGTTTATTATTTGAGC

12            12.8          mut-con
GGTTAAATGTTAACCGCGAAGCGGTTAACATTTAACC

13            14.9          con
GGTTAAATTTTAACCGCGAAGCGGTTAAAATTTAACC
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Figure 1: Fis binding sequences used in EMSA experiments.

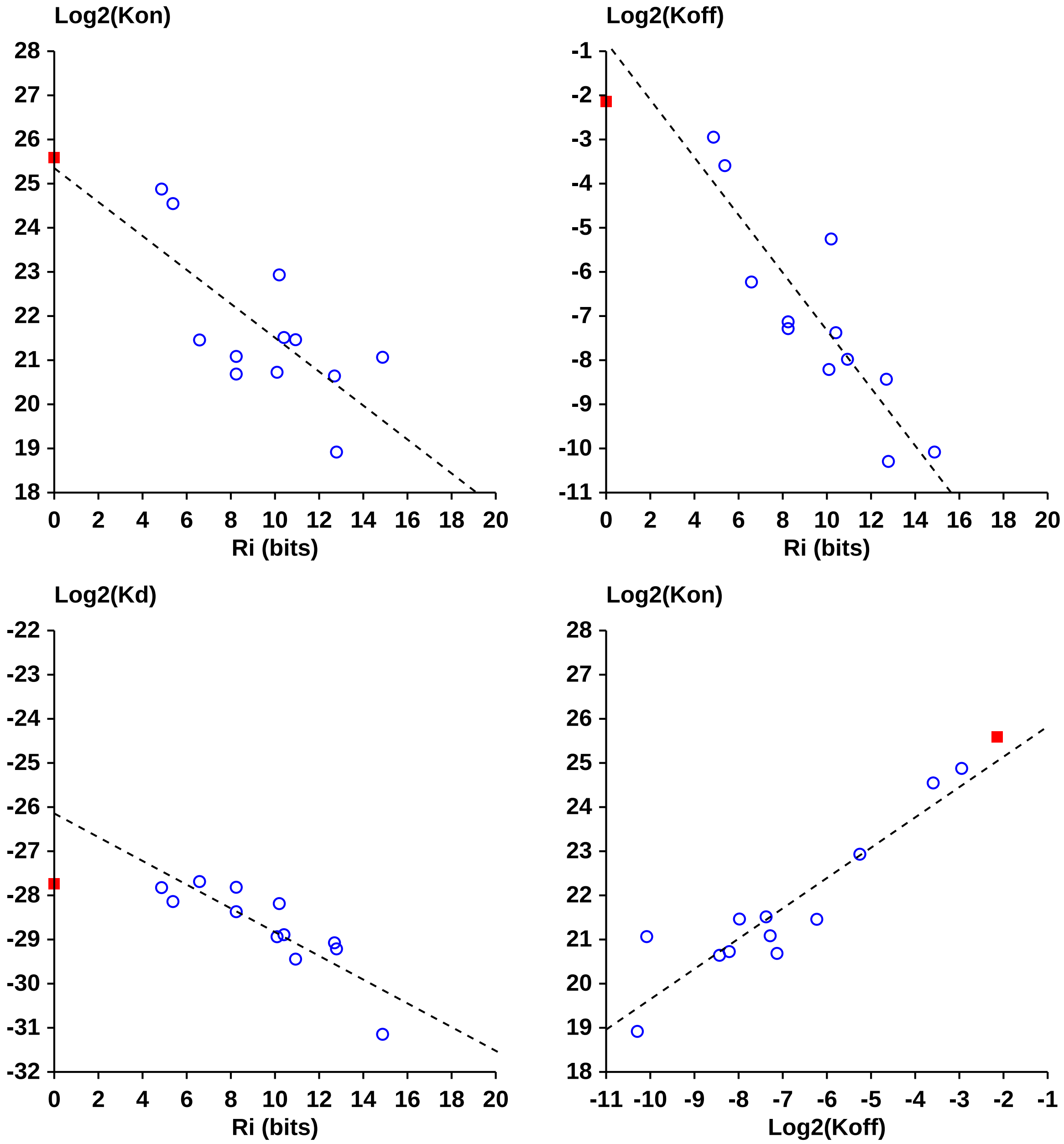

Figure 2: Fis binding rates versus information.

The axes of each rate graph always covers 10 powers of 2 so that the slopes of the regression lines can be compared. $k_{\text{off}}$ values were averaged for each oligo. The anti-con oligo is plotted at 0 bits as a square but was not included in the regressions.