

## SUPPLEMENTARY DATA

### The proofreading exonuclease subunit $\epsilon$ of *Escherichia coli* DNA polymerase III is tethered to the polymerase subunit $\alpha$ via a flexible linker

Kiyoshi Ozawa, Slobodan Jergic, Ah Young Park, Nicholas E. Dixon and Gottfried Otting

**Table S1.** PCR primers used in this study<sup>1</sup>

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975 <sup>2</sup>	5'-TTTGAATTCTTATGCTCGCCAGAGGCAAC-3' (29-mer)
974 <sup>3</sup>	5'-TTTTTTTTTCATATGAGCACTGCAATTACACG-3' (31-mer)
1131	5'-PO <sub>4</sub> -TTAGCTGGTCGATCCCGCGAAATTAATACG-3' (30-mer)
1132	5'-PO <sub>4</sub> -CCAGCTAACAAAAACCCCTCAAGACCCG-3' (29-mer)
1133	5'-PO <sub>4</sub> -TCGATCCCGCGAAATTAATACG-3' (22-mer)
1134	5'-PO <sub>4</sub> -CAAAAAACCCCTCAAGACCCG-3' (21-mer)
1145 <sup>2</sup>	5'-TTTTTTTTTCATATG <b>GCTT</b> CTGCAATTACACGCCAG-3' (35-mer)
1164 <sup>3</sup>	5'-TTTGAATTCTTACGCAAAAACAACGCGTAAC-3' (31-mer)
1167 <sup>4</sup>	5'-GGAAGGAGAG <b>GCA</b> CAACAGCAAC-3' (23-mer)
1168 <sup>4</sup>	5'-GTTGCTGTTG <b>TGC</b> CTCTCCTTCC-3' (23-mer)
1169 <sup>5</sup>	5'-GGTGAAGCA <b>GCA</b> ATTCAGCGC-3' (21-mer)
1170 <sup>5</sup>	5'-GCGCTGAATT <b>GCT</b> GCTTCACC-3' (21-mer)
1179 <sup>6</sup>	5'-CAAACGTCGATGG <b>GT</b> TTTTCGATGG-3' (25-mer)
1180 <sup>6</sup>	5'-CCATCGCAAA <b>ACC</b> ATCGACGTTTG-3' (25-mer)
1181 <sup>7</sup>	5'-GATGGCTTTT <b>GG</b> ATGGAAGGAGAG-3' (25-mer)
1182 <sup>7</sup>	5'-CTCTCCTTCCAT <b>CCC</b> AAAAGCCATC-3' (25-mer)
1183 <sup>8</sup>	5'-CAAGGTGAAG <b>GAA</b> ACAATTCAGCGC-3' (24-mer)
1184 <sup>8</sup>	5'-GCGCTGAATTG <b>TTC</b> CTTCACCTTG-3' (24-mer)
1185 <sup>9</sup>	5'-CTCTGGCGAG <b>GAT</b> AATACTGTG-3' (24-mer)
1186 <sup>9</sup>	5'-CACAGGTATTTAT <b>CCT</b> CGCCAGAG-3' (24-mer)

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<sup>1</sup> Codons of mutated amino acids are underlined. Mutated bases are shown in bold.

<sup>2</sup> Forward and reverse primers to generate the S2A/T3S double mutant of  $\epsilon$ .

<sup>3</sup> Forward and reverse primers to generate the C-terminal deletion mutant  $\epsilon$ 217.

<sup>4</sup> Forward and reverse primers to generate the T193A mutant of  $\epsilon$ .

<sup>5</sup> Forward and reverse primers to generate the T201A mutant of  $\epsilon$ .

<sup>6</sup> Forward and reverse primers to generate the A186G mutant of  $\epsilon$ .

<sup>7</sup> Forward and reverse primers to generate the A188G mutant of  $\epsilon$ .

<sup>8</sup> Forward and reverse primers to generate the A200G mutant of  $\epsilon$ .

<sup>9</sup> Forward and reverse primers to generate the A243G mutant of  $\epsilon$ .

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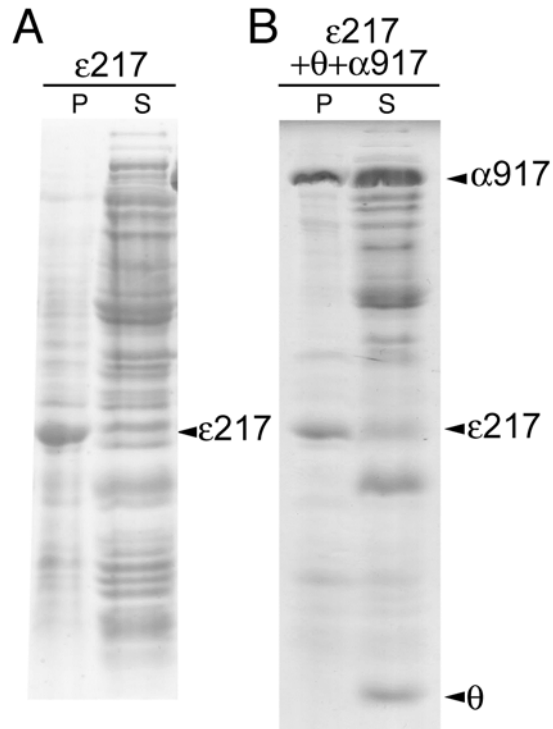
### Preparation of C-terminally truncated $\alpha$ subunit of the *E. coli* DNA polymerase III

A construct of C-terminally truncated (after residue 917) subunit  $\alpha$  with an N-terminal His<sub>6</sub> tag ( $\alpha$ 917) was prepared by insertion of the corresponding part of the *dnaE* gene as a PCR-generated NdeI-EcoRI fragment between the corresponding sites in the T7 promoter vector pETMCSI (S1), to generate the plasmid pKO1342 that encodes  $\alpha$ 917.

*E. coli* cells (BL21:: $\lambda$ DE3/plysS) harboring pKO1342 were grown aerobically for two days at room temperature in an auto-induction medium (S2); 2 litres of cell culture yielded about 14 g of cells. The French press lysate was loaded onto a 5 ml column of Ni-NTA resin (Pharmacia) in a buffer of 50 mM Hepes-KOH, pH 7.5, 300 mM NaCl, 5% glycerol, and 20 mM imidazole. Bound  $\alpha$ 917 was eluted with an gradient of 20–500 mM imidazole in the same buffer. The elute was dialyzed and subjected to chromatography on a DEAE-Toyopearl column (2.6  $\times$  3.5 cm) in a buffer of 20 mM Tris.HCl, pH 7.6, 1 mM EDTA, 1 mM dithiothreitol, and 5% glycerol. The bound  $\alpha$ 917 was eluted with a gradient of 0–1M NaCl, yielding about 11 mg of pure  $\alpha$ 917. Its concentration was determined spectrophotometrically at 280 nm, using the calculated  $\epsilon_{280}$  value of 73820 M<sup>-1</sup>cm<sup>-1</sup> (S3).

### References

- S1. Neylon, C., Brown, S.E., Kralicek, A.V., Miles, C.S., Love, C.A. and Dixon, N.E. (2000) Interaction of the *Escherichia coli* replication terminator protein (Tus) with DNA: a model derived from DNA-binding studies of mutant proteins by surface plasmon resonance. *Biochemistry*, **39**, 11989–11999.
- S2. Studier, F.W. (2005) Protein production by auto-induction in high-density shaking cultures. *Protein Express. Purif.*, **41**, 207–234.
- S3. Gill, S.C. and von Hippel, P.H. (1989) Calculation of protein extinction coefficients from amino acid sequence data. *Anal. Biochem.*, **182**, 319–326.



**Figure S1.** Cell-free synthesis of  $\epsilon 217$  in the absence and presence of  $\theta$  and  $\alpha 917$ .  $\epsilon 217$  was synthesized at  $30^{\circ}\text{C}$  from PCR-amplified DNA as described in the main text. The gels were stained with Coomassie brilliant blue. P and S denote the insoluble (pellet) and soluble (supernatant) fractions, respectively. **(A)**  $\epsilon 217$  synthesized in the absence of  $\theta$  and  $\alpha 917$  is insoluble. **(B)**  $\epsilon 217$  synthesized in the presence of  $0.5\text{ mg/ml}$   $\theta$  and  $5\text{ mg/ml}$   $\alpha 917$  results in co-precipitation of  $\alpha 917$  with  $\epsilon 217$  (lane 1) but also in  $\epsilon 217$  in the soluble fraction (presumably in the  $\epsilon 217:\theta$  or  $\alpha 917:\epsilon 217:\theta$  complex). The co-precipitation demonstrates binding of  $\epsilon 217$  to  $\alpha 917$ . Whereas the  $\alpha 917:\epsilon:\theta$  complex prepared in the same way could be purified by Ni-NTA chromatography, the  $\alpha 917:\epsilon 217:\theta$  complex could not, indicating limited stability (data not shown).