

EBF/MmCOE1 1 **M**FGIQESIQRSGSS**M**KKEEPLGSG**M**NNAVRT**W**MQAGVLDANTAAQSGVGLA
Col/DmCOE 1 **M**EWGRKLYPSAVSGPR**S**AGGL**M**FGLPPTAAVD**M**NQPRGP**M**TSLKKEEPLGSR**W**A**M**QPVVDQSNLIG

RAHFEKQPPSNLRKSNFFHFVLAYDR**Q**Q**P**VEI**E**RTAFV**G**F**V**E**K**E**K**E**A**N**S**E**K**T**N**N**G**I**H**Y**R**I**Q**LL**S**N**G**I**R**T**E**Q**D**F**V**R**L**
RAHFEKQPPSNLRKSNFFHFVIALYDR**Q**P**I**E**I**ERTAF**I**G**F**I**E**K**D**S**E**S**D**A**T**K**T**N**N**G**I**Q**Y**R**L**Q**L**L**Y**A**N**A**R**Q**E**Q**D**I**F**V**R**L

IDSM**T**K**Q**A**I**V**E**G**Q**D**K**N**P**E**M**C**R**V**L**L**T**H**E**I**M**C**S**R**C**D**K**K**S**C**G**N**R**N**E**T**P**S**D**P**V**I**I**D**R**F**F**L**K**F**L**K**C**N**Q**N**C**L**K**N**A**G**N**P**R**D**M**R**R**
IDS**V**T**K**Q**A**I**I**V**E**G**Q**D**K**N**P**E**M**C**R**V**L**L**T**H**E**V**M**C**S**R**C**D**K**K**S**C**G**N**R**N**E**T**P**S**D**P**V**I**I**D**R**F**F**L**K**F**L**K**C**N**Q**N**C**L**K**N**A**G**N**P**R**D**M**R**R**

FQV**V**S**T**T**V**N**V**D**G**H**V**L**A**A**P**D**N**M**F**V**H**N**S**K**H**G**R**R**A**R**R**L**D**P**S**E**G**T-----PSYLEH-----**A**T**P**C**I**K**A**I**S**P
FQV**V**I**S**T**Q**V**A**V**D**G**P**L**L**A**I**S**D**N**M**F**V**H**N**S**K**H**G**R**R**A**K**R**L**D**T**T**E**G**T**G**N**T**S**L**S**I**S**G**H**P**L**A**D**S**T**Y**D**G**L**Y**P**L**P**V**A**T**P**C**I**K**A**I**S**P

SEG**W**T**T**G**G**A**T**V**I**I**I**G**D**N**F**F**D**G**L**Q**V**I**F**G**T**M**L**V**W**S**E**L**T**G**P**H**S**I**R**V**Q**T**P**P**R**H**I**P**G**V**V**E**V**T**L**S**Y**K**S**Q**F**C**K**G**T**P**G**R**F**I**Y**
SEG**W**T**T**G**G**A**T**V**I**I**V**G**D**N**F**F**D**G**L**Q**V**V**F**G**T**M**L**V**W**S**E**L**I**T**S**H**A**I**R**V**Q**T**P**P**R**H**I**P**G**V**V**E**V**T**L**S**Y**K**S**Q**F**C**K**G**S**P**G**R**F**V**Y**

Helix 1 **Linker** **Helix 2d** **Helix 2a**
- **TALNEPTIDYGFQRLQKVI****PRHPGDPERL****PKEVILKRAADLVEALYGM****PH****NNQEIILKRAADIAEALYSVPRNHNLQ**LPA
V **SALNEPTIDYGFQRLQKLI****PRHPGDPEK**L**Q**-----**KEIILKRAADLVEALYSMP**RSPGGSTG

----**Col/EBFΔH1**-----

-----**ColΔH2**-----

--**ColΔLH2**-----

--**EBFΔ**³⁷⁰⁻³⁸³--

EBF* (1-429)

L**A**N**T**S**V**H**A**G**M**M**G**V**N**S**F**S**G**L**A**V**N**V**S**E**A**S**Q**A**T**N**Q**G**F**T**R**N**S**S**V**S**P**H**G**Y**V**P**S**T**T**P**Q**T**N**Y**N**S**V**T**T**S**M**N**G**Y**G**S**A**A**M**S**N**L**G**G**S**P
FN**S**Y**S**G**Q**L**A**V**S**V**Q**D**G**S**G**W**E**D**D**Y**Q**R**A**Q**S**S**S**V**S**P**R**G**G**Y**C**S**S**A**S**T**P**H**S**S**G**S**G**Y**G**A**T**A**S**A**A**V**A**A**T**A**N**G**Y**A**P**A**P**N**M**G**T**L**S**S

Col* (1-449)

T**F**L**N**G**S**A**A**N**S**P**Y**A**I**V**P**S**S**P**T**M**A**S**T**S**L**P**S**N**C**S**S**S**S**G**I**F**S**F**S**P**A**N**M**V**S**A**V**K**Q**K**S**A**F**A**P**V**V**R**P**Q**T**S**P**P**T**C**T**S**T**N**G**N**S**L**Q**A**I**
PG**S**V**F**N**S**T**S**M**S**A**V**S**T**W**H**Q**A**F**V**Q**H**H**H**A**A**T**A**H**P**H**H**H**Y**P**H**P**H**Q**P**W**H**N**P**A**V**S**A**A**T**A**A**V **557**

SGMIVPPM **591**

Figure S4

Diagrammatic alignment of EBF (top) and Col protein amino-acid sequences. Conserved residues in the DBD (red), IPT (yellow) and HLH (italics) domains, including the H1-H2 linker (green) are in bold. The extent of the H1 and H2 deletions introduced in the modified versions of EBF and Col (Fig. 2) are shown by dashed lines. The position of the EBF internal deletion (residues 370 to 383) described in Hagman et al., 1995 is also indicated. In frame Methionine initiator codons are underlined. The position of the C-terminal valine of truncated EBF* and Col* (Fig. 2) is indicated by a star. Position of the putative zinc finger (Hagman et al., 1995) in the DBD is red underlined.