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Originally published as Genetics Published Articles Ahead of Print on January 11, 2010.

Genetics, Vol. 184, 899-913, April 2010, Copyright © 2010 doi:10.1534/genetics.109.111591

EOR-2 Is an Obligate Binding Partner of the BTB-Zinc Finger Protein EOR-1 in *Caenorhabditis elegans*Kelly Howell\*, Swathi Arur\*, Tim Schedl\* an Meera V. Sundaram

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Manuscript received November 2, 2009. Accepted for publication January 3, 2010.



## ABSTRACT

BTB-zinc finger transcription factors play many important roles in metazoan development. In these proteins, the BTB domain is critical for dimerization and for recruiting cofactors to target genes. Identification of these cofactors is important for understanding how BTB-zinc finger proteins influence transcription. Here we show that the novel but conserved protein EOR-2 is an obligate binding partner of the BTB-zinc finger protein EOR-1 in *Caenorhabditis elegans*. EOB-1 at EOR-2 function together to promote multiple Ras/ERK-dependent cell fates during deprending and we show that EOR-1 is a robust substrate of ERK in vitro A point mutal and (E8TF) in the EOR-1 BTB domain reduces both ERK phosphorylation at 1EOR-2 aroung and eliminates all detectable biological function without affecting EOR-1 expression revers, ocalization, or dimerization. This

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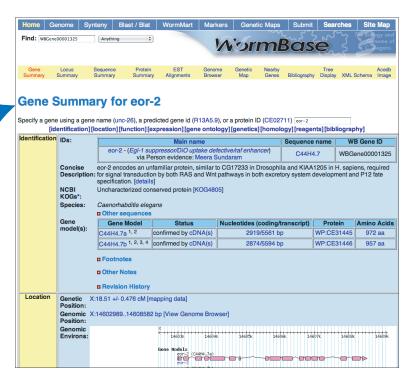
ACKNOWLEDGEMENTS

LITERATURE CITED

point mutation lies near the predicted charged pocket region of the EOR-1 BTB dimer, a region that, in other BTB-zinc finger proteins, has been proposed to interact with corepressors or coactivators. We also show that a conserved zinc finger-like motif in EOR-2 is required for binding to EOR-1, that the interaction between EOR-1 and EOR-2 is direct, and that EOR-2 can bind to the human BTB-zinc finger protein PLZF. We propose that EOR-2 defines a new family of cofactors for BTB-zinc finger transcription factors that may have conserved roles in other organisms.

THE BTB (or POZ) domain, named for founding members *br*io-à-brac, *t*ramtrack, and *br*oad complex, is a protein—protein interaction domain evolutionarily conserved from yeast to humans (reviewed in PEREZ-TORRADO *et al.* 2006). While some proteins such as Skp1 and Elongin C are made up almost entirely of the BTB domain, most BTB proteins consist of the BTB domain in the N terminus and other functional domains in the C terminus by which they are classified. These different classes of BTB domains all share a well-conserved tertiary structure termed the "core BTB loid"

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