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EOR-2 Is an Obligate Binding Partner of the BTB-Zinc Finger Protein EOR-1 in *Caenorhabditis elegans*

Kelly Howell^{*}, Swathi Arur[†], Tim Schedl[†] and **Meera V. Sundaram**

^{*} Department of Genetics, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania 19104 and [†] Department of Genetics, Washington University School of Medicine, St. Louis, Missouri 63110

^{*} Corresponding author: Department of Genetics, University of Pennsylvania School of Medicine, 415 Curie Blvd., 445 Clinical Research Bldg., Philadelphia, PA 19104.
 E-mail: sundaram@mail.med.upenn.edu

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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*. **EOR-1** and **EOR-2** function together to promote multiple Ras/ERK-dependent cell fates during *D. elegans* development, and we show that **EOR-1** is a robust substrate of ERK *in vitro*. A point mutation (L81F) in the **EOR-1** BTB domain reduces both ERK phosphorylation and **EOR-2** binding and eliminates all detectable biological function without affecting **EOR-1** expression levels, localization, or dimerization. This 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 *bric-à-brac*, *tramtrack*, and *broad* 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 fold"

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Meera Sundaram

Name	First name: Meera Middle name: Vedavalli Last name: Sundaram Standard name: Meera Sundaram Full name: Meera Vedavalli Sundaram Also known as: Meera Sundaram, Meera V. Sundaram, MV Sundaram, M Sundaram, Meera V Sundaram
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Gene Summary Locus Summary Sequence Summary Protein Summary EST Alignments Genome Browser Genetic Map Nearby Genes Bibliography Tree Display XML Schema Image

Gene Summary for eor-2

Specify a gene using a gene name (unc-26), a predicted gene id (R13A5.9), or a protein ID (CE02711) eor-2
 [identification][location][function][expression][gene ontology][genetics][homology][regents][bibliography]

Identification	IDs:	Main name	Sequence name	WB Gene ID
		eor-2 (<i>Egl-1 suppressor/DIO uptake defective/rat enhance</i>) via Person evidence: Meera Sundaram	C44H4.7	WBGene0001325

Concise Description: eor-2 encodes an unfamiliar protein, similar to CG17233 in *Drosophila* and KIAA1205 in *H. sapiens*, required for signal transduction by both RAS and Wnt pathways in both excretory system development and P12 fate specification. [details]

NCBI KOGs*: Uncharacterized conserved protein [KOG4805]

Species: *Caenorhabditis elegans*

- Other sequences

Gene model(s)	Gene Model	Status	Nucleotides (coding/transcript)	Protein	Amino Acids
	C44H4.7a	1, 2 confirmed by cDNA(s)	2919/5561 bp	WP:CE31445	972 aa
	C44H4.7b	1, 2, 3, 4 confirmed by cDNA(s)	2874/5594 bp	WP:CE31446	957 aa

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Location

Genetic Position: X:18.51 +/- 0.476 cM [mapping data]

Genomic Position: X:14602989..14608582 bp [View Genome Browser]

Genomic Environments: