bs-12205R

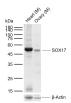
[Primary Antibody]

SOX17 Rabbit pAb

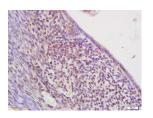


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– DATASHEFT –		400-901-9800	
Host: Rabbi Clonality: Polycl		Applications: WB (1:500-2000) IHC-P (1:100-500)	
GenelD: 64321	SWISS: Q9H6I2	IHC-F (1:100-500) IF (1:100-500)	
Target: SOX17 Immunogen: KLH co 71-180	onjugated synthetic peptide derived from Human SOX17:		
Concentration: 1mg/r Storage: 0.01M Glycer Shipp	TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50%	Reactivity: Mouse, Rat (predicted: Human, Pig, Cow, Chicken) Predicted MW.: 44 kDa	
Background: Sox genes comprise a family of genes that are related to the mammalian sex determining gene SRY. These genes similarly contain sequences that encode for the HMG-box domain, which is responsible for the sequence-specific DNA-binding activity. Sox genes encode putative transcriptional regulators implicated in the decision of cell fates during development and the control of diverse developmental processes. The highly complex group of Sox genes cluster at least 40 different loci that rapidly diverged in various animal lineages. At present, 30 Sox genes have been identified. Members of this family have been shown to be conserved during evolution and to play key roles during animal development. Some are involved in human diseases, including sex reversal.		Subcellular Location: Nucleus	
- VALIDATION IMAGES			



Sample: Lane 1: Mouse Heart tissue lysates Lane 2: Mouse Ovary tissue lysates Primary: Anti-SOX17 (bs-12205R) at 1/1000 dilution Secondary: IRDye800CW Goat Anti-Rabbit IgG at 1/20000 dilution Predicted band size: 44 kDa Observed band size: 48 kDa



Tissue/cell: rat uterus tissue; 4% Paraformaldehyde-fixed and paraffinembedded; Antigen retrieval: citrate buffer (0.01M, pH 6.0), Boiling bathing for 15min; Block endogenous peroxidase by 3% Hydrogen peroxide for 30min; Blocking buffer (normal goat serum,C-0005) at 37°C for 20 min; Incubation: Anti-SOX17 Polyclonal Antibody, Unconjugated(bs-12205R) 1:200, overnight at 4°C, followed by conjugation to the secondary antibody(SP-0023) and DAB(C-0010) staining

- SELECTED CITATIONS -

• [IF=7.5] Xie Tianqin. et al. Dysregulated lncRNAs regulate human umbilical cord mesenchymal stem cell differentiation into insulin-producing cells by forming a regulatory network with mRNAs. STEM CELL RES THER. 2024 Dec;15(1):1-17 IF ;Human. 38273351

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