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32-6290: ACVR1 Human

Alternative Name :	ACVR1A, ALK2, ACVR1, ACTRI, ACTR-I, ACVRLK2, FOP, SKR1, TSRI, Activin receptor type I, Activin receptor-like kinase 2, ALK-2, TSR-I, Serine/threonine-protein kinase receptor R1, TGF-B superfamily receptor type I.

Description

Source: Sf9, Baculovirus cells.
Sterile filtered colorless solution.
Activin A Receptor Type 1 (ACVR1) is a member of TGF-beta serine/threonine kinase receptor family. ACVR1 forms a receptor complex contains2 type II and 2 type I transmembrane serine/threonine kinases. Type II receptors phosphorylate and activate type I receptors which autophosphorylate,bind and activate SMAD transcriptional regulators. ACVR1 takes part in left-right pattern formation during embryogenesis and is also essential in the BMP pathway which is responsible for the development and repair of the skeletal system.ACVR1 is linked to Fibrodysplasia Ossificans Progressiva which isknown for the formation of heterotopic bone throughout the body.
ACVR1 produced in Sf9 Baculovirus cells is a single, glycosylated polypeptide chain containing 342 amino acids (21-123a.a.) and having a molecular mass of 38.4kDa. ACVR1 is expressed with a 239 amino acid hIgG-His-Tag at C-Terminus and purified by proprietary chromatographic techniques.

Product Info

Amount :	2 µg / 10 µg
Purification :	Greater than 90.0% as determined by SDS-PAGE.
Content :	ACVR1 protein solution (0.25mg/ml) contains Phosphate Buffered Saline (pH 7.4) and 10% glycerol.
Storage condition :	Store at 4°C if entire vial will be used within 2-4 weeks.Store, frozen at -20°C for longer periods of time. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA).Avoid multiple freeze-thaw cycles.
Amino Acid :	MEDEKPKVNP KLYMCVCEGL SCGNEDHCEG QQCFSSLSIN DGFHVYQKGC FQVYEQGKMTCKTPPSPGQA VECCQGDWCN RNITAQLPTK GKSFPGTQNF HLELEPKSCD KTHTCPPCPAPELLGGPSVF LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTLPPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLTVDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGKHHHH HH.

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