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[Primary Antibody]

Rabbit Anti-BBS12 antibody

Catalog Number: SL11505R

FOR RESEARCH USE ONLY

[DATASHEET]

Host:	Rabbit
Isotype:	IgG
Clonality:	Polyclonal
Target:	BBS12
Immunogen:	KLH conjugated synthetic peptide derived from human BBS12: 25-100/710
Purification:	affinity purified by Protein A
Concentration:	1mg/ml
Storage:	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol. Shipped at 4℃. Store at -20 °C for one year. Avoid repeated freeze/thaw cycles.
Applications:	WB=1:500-2000 ELISA=1:5000-10000 not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
Reactivity:	(predicted:Human,Mouse,Cow,Horse,Rabbit)
Predicted MW.:	79kDa
Subcellular Location:	cytoplasmic
Background:	The protein encoded by this gene is part of a complex that is involved in membrane trafficking. The encoded protein is a molecular chaperone that aids in protein folding upon ATP hydrolysis. This protein also plays a role in adipocyte differentiation. Defects in this gene are a cause of Bardet-Biedl syndrome type 12. Two transcript variants encoding the same protein have been found for this gene. **Function:** Probable molecular chaperone. Assists the folding of proteins upon ATP hydrolysis. As part of the BBS/CCT complex may play a role in the assembly of BBSome, a complex involved in ciliogenesis regulating transports vesicles to the cilia. Involved in adipogenic differentiation. **Subunit:** Component of the BBS/CCT complex composed at least of MKKS, BBS10, BBS12, TCP1, CCT2, CCT3, CCT4, CCT5 AND CCT8. **Subcellular Location:** Cell projection, cilium. **Note:** Located within the basal body of the primary cilium of differentiating

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	preadipocytes. DISEASE: Defects in BBS12 are the cause of Bardet-Biedl syndrome type 12 (BBS12) [MIM:209900]. Bardet-Biedl syndrome (BBS) is a genetically heterogeneous, autosomal recessive disorder characterized by usually severe pigmentary retinopathy, early onset obesity, polydactyly, hypogenitalism, renal malformation and mental retardation. Secondary features include diabetes mellitus, hypertension and congenital heart disease. A relatively high incidence of BBS is found in the mixed Arab populations of Kuwait and in Bedouin tribes throughout the Middle East, most likely due to the high rate of consaguinity in these populations and a founder effect. BBS12 seems to be rarely involved in oligogenic inheritance. **Similarity:** Belongs to the TCP-1 chaperonin family. BBS12 subfamily. **Database links:** **Entrez Gene:** 166379 Human Omim: 610683 Human **SwissProt:** Q6ZW61 Human **Unigene:** 400698 Human

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