

hCELA3B, His-tag (S217A)

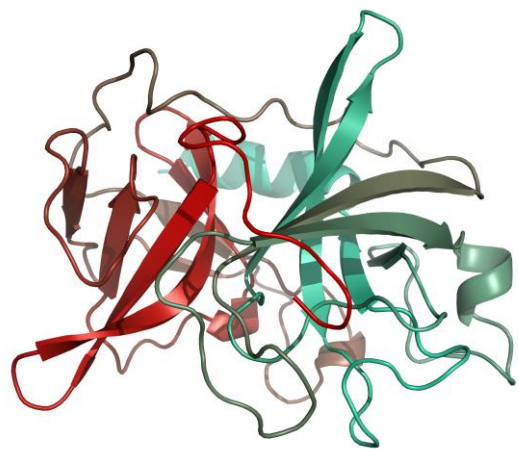
Cat. no. P2020-132

Product Information

Protein:	hCELA3B-His (S217A) (29.8 kDa)
Uniprot#:	P08861
Sequence:	YGPPSSRPSSRVVNGEDAVPYSWPWQVSLQYEKSGSFYHTCGGSLIAPDWVVTAGHCISSSRTYQV VLGEYDRAVKEGPEQVIPINSGDLFVHPLWNRSCVACGNIDIALIKLSRSAQLGDAVQLASLPPAGDIL PNETPCYITGWGRLYTNGPLPDKLQEALLPVVDYEHCSRWNWWGSSVKKTMVCAGGDIRSGCNGD AGGPLNCPTEDEGGWQVHGVTSEVSAFGCNTRRKPTVFTRVSAFIDWIEETIASH
	C-terminal His-tag not shown in sequence.
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	His-tag, C-terminal
Purification:	Purified by affinity chromatography and subsequent buffer exchange.
Formulation:	PBS; pH 7.4 Liquid, stored and shipped at -80 °C.
Purity:	> 95 % (will be determined by densitometry of Coomassie stained gel, example next page)
Concentration:	Will be determined by BCA-Assay.
Long-term storage:	No recommendations.
Comment:	Protein migrates at higher molecular weight during SDS-PAGE due to posttranslational modifications.

Background Information:

Chymotrypsin-like elastases (CELAs) are pancreatic serine proteinases, which belong to the peptidase S1 family, a subfamily of serine proteases. The human CELA3B is a member of the elastase family, which consists of six human elastase genes encoding the proteins elastase 1, 2, 2A, 2B, 3A, and 3B, all of which are structurally similar. Typically, elastases hydrolyze many proteins in addition to elastin. However, CELA3B has only little elastolytic activity. CELA3B is secreted by the pancreas and characterized by a digestive function in the intestine, very similar to other serine proteases such as trypsin, chymotrypsin and kallikrein. The amino acid S217 of CELA3B is part of the catalytic triade typical for all serine proteases. By substitution of this amino acid by a different one (S217A), the enzyme is loosing its catalytic activity. In clinical assays, pancreatic function is analyzed by excretion of CELA3B in fecal material.



Structural model of the CELA3B protein generated by AlphaFold (<https://alphafold.ebi.ac.uk>)

- Jumper, J et al. Highly accurate protein structure prediction with AlphaFold. *Nature* (2021).

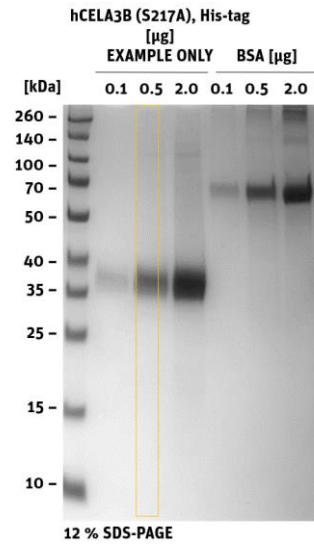
- Varadi, M et al. AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models. *Nucleic Acids Research* (2022).

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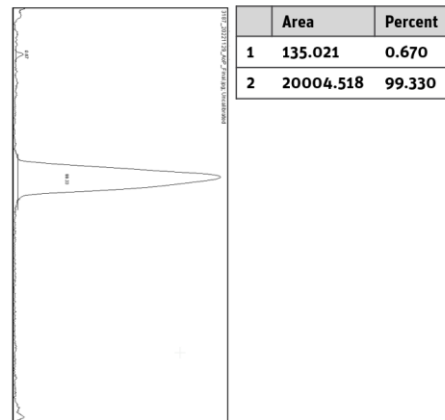
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Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)