Human LRIG1 Protein

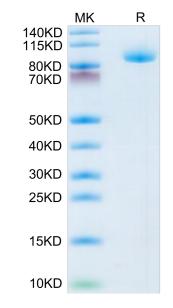
Cat. No. LRI-HM101

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Description	
Source	Recombinant Human LRIG1 Protein is expressed from HEK293 with His tag at the C-Terminus.
	It contains Ala35-Ser779.
Accession	Q96JA1-1
Molecular Weight	The protein has a predicted MW of 83 kDa. Due to glycosylation, the protein migrates to 85-105 kDa based on Bis-Tris PAGE result.
Endotoxin	Less than 1 EU per μg by the LAL method.
Purity	> 95% as determined by Bis-Tris PAGE
Formulation and S	Storage
Formulation	Lyophilized from 0.22µm filtered solution in 50mM MES, 150mM NaCl, 1mM EDTA (pH 5.0). Normally 8% trehalose is added as protectant before lyophilization.
Reconstitution	Dissolve the lyophilized protein in 50mM MES, 150mM NaCl, 1mM EDTA (pH 5.0). Please refer to the Certificate of Analysis for detailed instructions.
Storage	-20 to -80°C for 12 months as supplied from date of receipt80°C for 3 months after reconstitution.Recommend to aliquot the protein into smaller quantities for optimal storage. Please minimize freeze-thaw cycles.
Background	
	The leucine-rich repeats and immunoglobulin-like domains (LRIG)-1 is a tumor suppressor gene that belongs to the LRIG family. LRIG1 expression has prognostic significance in various human cancers. Somatic mutations, which are associated with a certain rate of response to targeted therapies, are ubiquitously found in human non- small cell lung cancer (NSCLC). LRIG1 was an independent prognostic factor for OS of NSCLC patients. LRIG1 in combination with other clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stronger prognostic model than clinicopathological risk factors was a stron
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Bis-Tris PAGE

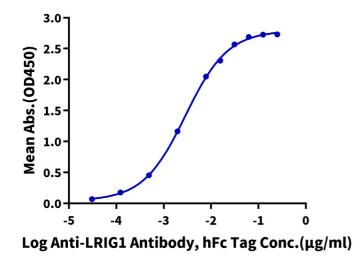


Human LRIG1 on Bis-Tris PAGE under reduced condition. The purity is greater than 95%.



Human LRIG1, His Tag ELISA

0.2µg Human LRIG1, His Tag Per Well



Immobilized Human LRIG1, His Tag at 2µg/ml (100µl/well) on the plate. Dose response curve for Anti-LRIG1 Antibody, hFc Tag with the EC50 of 2.9ng/ml determined by ELISA.