Recombinant ERIC4 protein (His tag)

Catalog Number	551781
Species	Human
Expression System	E. coli
Accession	A6NGS2
Molecular Weight	Predictes a molecular mass of 16.13 kDa. In SDS-PAGE under reducing conditions, it migrates as an approximately 19 kDa band.

Product Information

Sequence Region	1-130
Form	Lyophilized powder
Formulation	Lyophilized from sterile PBS, pH 7.4
Purity	>90%, by SDS-PAGE with Coomassie Brilliant Blue staining.
Endotoxin	Not tested.
Activity	Not tested.
Stability	Samples are stable for up to twelve months from date of receipt at -70℃
Protein Construction	DNA encoding 1-130 aa (A6NGS2) were fused with 6His tag.

Storage & Handling

Reconstitution	Reconstitute at 0.25 μg/μl in sterile water for short-term storage. Reconstitution with 50% glycerol solution is recommended for longer term storage (see Stability and Storage for more details). If a different concentration is needed for your purposes please adjust the reconstitution volume as required (please note: the ion concentration of the final solution will vary according to the volume used). Note: Centrifuge vial before opening. When reconstituting, gently pipet and wash down the sides of the vial to ensure full recovery of the protein into solution.
Storage	Store it under sterile conditions at -20℃ to -80℃. It is recommended that the protein be aliquoted for optimal storage. Avoid repeated freeze-thaw cycles.
Shipping	In general, recombinant proteins are provided as lyophilized powder which are shipped at ambient temperature. Bulk packages of recombinant proteins are provided as frozen liquid. They are shipped out with blue ice unless customers require otherwise.

Description

Description	Recombinant Human Glutamate-rich protein 4 (ERICH4) Fragment (aa 1-130). This high-quality, soluble protein fragment is designed for structural biology and functional studies, offering a stable and well-folded unit ideal for biochemical characterization and interaction analyses. Glutamate-rich protein 4, encoded by the ERICH4 gene, is a human protein of significant research interest. While specific functional and subcellular localization data are still under investigation, its classification and gene context suggest potential roles in cellular processes that are the focus of ongoing discovery. The provided fragment (amino acids 1-130) represents a computationally selected, stable domain predicted to maintain structural integrity, making it a valuable tool for elucidating the protein's fundamental properties and molecular interactions.