Recombinant BIVM protein (His tag)

Catalog Number	549006
Species	Human
Expression System	E. coli
Accession	Q86UB2
Molecular Weight	Predictes a molecular mass of 28.86 kDa. In SDS-PAGE under reducing conditions, it migrates as an approximately 29 kDa band.

Product Information

Sequence Region	187-422
Form	Lyophilized powder
Formulation	Lyophilized from sterile PBS, pH 7.4
Purity	>86%, 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 187-422 aa (Q86UB2) 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 BIVM Protein Fragment (aa 187-422) - A highly stable and soluble fragment of the Basic immunoglobulin-like variable motif-containing protein, specifically engineered for structural and biochemical research applications. The full-length Basic immunoglobulin-like variable motif-containing protein (BIVM) is localized to both the cytoplasm and nucleus, as evidenced by experimental data. While specific functional details are not fully characterized, its dual subcellular localization suggests potential roles in cellular processes that may involve nucleocytoplasmic shuttling. The selected fragment (amino acids 187-422) represents a computationally optimized region designed to maintain structural integrity and solubility for experimental studies.