

PRODUCT INFORMATION

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| Tag | C-Flag Tag |
| Target | BEST3 |
| Synonyms | VMD2L3 |
| Description | Human BEST3 full length protein-synthetic nanodisc |
| Delivery | 6~8weeks |
| Uniprot ID | Q8N1M1 |
| Expression Host | HEK293 |
| Protein Families | Ion Channels: Other |
| Protein Pathways | N/A |
| Molecular Weight | The human full length BEST3 protein has a MW of 76.1kDa |
| Formulation & Reconstitution | Lyophilized from nanodisc solubilization buffer (20 mM Tris-HCl, 150 mM NaCl, pH 8.0). Normally 5% - 8% trehalose is added as protectants before lyophilization. Please see Certificate of Analysis for specific instructions of reconstitution. |
| Storage&Shipping | Store at -20°C to -80°C for 12 months in lyophilized form. After reconstitution, if not intended for use within a month, aliquot and store at -80°C (Avoid repeated freezing and thawing). Lyophilized proteins are shipped at ambient temperature. |
| Background | BEST3 belongs to the bestrophin family of anion channels, which includes BEST1 (MIM 607854), the gene mutant in vitelliform macular dystrophy (VMD; MIM 153700), and 2 other BEST1-like genes, BEST2 (MIM 607335) and BEST4 (MIM 607336). Bestrophins are transmembrane (TM) proteins that share a homology region containing a high content of aromatic residues, including an invariant arg-phe-pro (RFP) motif. The bestrophin genes share a conserved gene structure, with almost identical sizes of the 8 RFP-TM domain-encoding exons and highly conserved exon-intron boundaries. Each of the 4 bestrophin genes has a unique 3-prime end of variable length (Stohr et al., 2002 [PubMed 12032738]; Tsunenari et al., 2003 [PubMed 12907679]).[supplied by OMIM, Mar 2008] |
| Usage | Research use only |
| Conjugate | Unconjugated |

