

## *MRC PPU REAGENTS*

### Standard Operating Procedure

#### Preparation of MINDY1 [1 - 469]

**Enzyme description:-** MINDY1 [1 – 469]

**Clone number:-** DU 59325

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal MBP

**Purification method:-** Amylose resin

**Calculated molecular mass:-**

Monoisotopic 95, 984.03 daltons

Average Mass 96, 044.08 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 4.81

**Purity:-** >80 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** -70 deg C

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## Clone Data Sheet

### MINDY1 [1 – 469]

**Protein** MINDY1 [1 – 469]

**Clone number** DU 59325

**Species** Human

**Accession number** Q8N5J2.2

**Tags** N-terminal MBP

**Bacterially  
expressed protein**

MKIEEGKLVIIWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLEEKF  
PQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPKAFQDKLYPFTWD  
AVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKG  
KSALMFNLQEPYFTWPLIAADGGYAFKYENKDYDIKDVGVNAGAKAG  
LTFVLVDLIKKNHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSK  
VNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTD  
EGLEAVNKDKPLGAVALKSYEEELVKDPRIAATMENAQKGEIMPNIPO  
MSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNLGD  
DDDKVPEFLEVLFGQPLGSMEYHQPEDPAPGKAGTAEAVIPENHEVLA  
**GPDEHPQD**TDARDADGEAREREPADQALLPSQCGDNLESPLPEASSAP  
**PGPTL**GLTPEVETIRACSMPOELPQSPRTRQPEPDFYCVKWIPWKGEQ  
**TP**IITQSTNGPCPLLAIMNILFLQWKVKLPPQKEVITSDELMAHLGNC  
**LLS**IKPQEKSEGLQLNFQONVDDAMTVLPKLATGLDVNVRFTGVSDFE  
**YT**PECSVFDLLGIPLYHGWLVDPOSPEAVRAVGKLSYNQLVERIITCK  
**HSS**DTNLVTEGLIAEQFLETTAAQLTYHGLCELTAAKEGELSVFFRN  
**NHF**STMTKHKSHLYLLVTDQGFLOEEQVWESLHNVDGSDCFCDSDFH  
**LSH**SLGKGPAGEGSGSPEKQLQVDQDYLIALSLOQQQPRGPLGLTDL  
**ELA**QQLQEEYQQQAAQPVRMRTRVLSLQGRGATSGRPAGERRORPK  
**HESDCILL**

**Native sequence** Amino acids M1 – L469 (end) of human MINDY1.  
Residue M404 of the fusion protein is equivalent to M1 of the native  
enzyme. The MBP tag is located at residues 1 – 392.

**Protease cleavage** PreScission (LEVLFGQP) residues 393 – 400

**Cloning sites** *Bgl*II / *Not*I into *Bam*H1 / *Not*I sites of pMEX3C

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### Nucleotide Sequence Of Insert

agatctATGGAATACCATCAGCCTGAGGATCCAGCCCCTGGTAAGGCCGGGACTGCAGAAGCAGT  
CATCCCTGAAAACCATGAGGTTCTGGCAGGCCAGATGAGCACCCCTCAGGACACAGATGCAAGAG  
ATGCTGATGGGGAGGCTAGAGAACGGGAGCCAGCAGACCAAGCTTTGCTGCCCTAGCCAGTGTGGG  
GACAACCTTGAGTCCCTCTGCCTGAAGCTAGCTCAGCTCCACCGGGGCCAACCCCTGGGGACACT  
GCCTGAAGTAGAGACAATAAGGGCATGCTCCATGCCCCAGGAGCTTCCTCAGTCCCCCAGGACCC  
GACAGCCTGAGCCAGATTTCTACTGTGTCAAGTGGATCCCTTGAAAGGAGAACAGACACCCATC  
ATCACCCAGAGCACTAACGGCCCTTGCCCTCTCCTTGCCATCATGAACATCCTCTTTCTTCAGTG  
GAAGGTGAAGCTCCCCCGCAGAAGGAAGTGATCACATCGGATGAGCTCATGGCCCATCTTGAA  
ACTGCCTCCTGTCCATCAAGCCCCAGGAGAAGTCAGAGGGACTTCAGCTTAATTTTCAGCAGAAT  
GTGGATGATGCAATGACAGTGCTGCCTAAACTGGCCACAGGTCTGGATGTCAATGTGCGATTAC  
AGGCGTCTCTGATTTTGGAGTATACACCCGAGTGCAGTGTCTTTGACCTGCTAGGCATACCTCTGT  
ACCATGGCTGGCTTGTTGATCCACAGAGTCTTGAGGCTGTGCGTGCAGTTGGGAAACTGAGTTAC  
AACCAGCTGGTGGAGAGGATCATCACCTGCAAACACTCCAGTGACACCAACCTCGTGACAGAAGG  
CCTGATTGCAGAGCAGTTCCTGGAGACCACCGCGGCCAGCTGACCTACCACGGACTGTGTGAGC  
TGACAGCAGCTGCTAAGGAGGGTGAACTTAGCGTCTTTTTCCGAAACAACCACTTTAGCACCATG  
ACTAAGCATAAGAGTCACTTATACCTACTGGTCACTGACCAGGGCTTTCTACAGGAGGAGCAAGT  
CGTATGGGAGAGCCTGCACAATGTGGATGGAGACAGCTGCTTTTGTGACTCTGACTTTCACCTGA  
GTCATTCCCTGGGCAAGGGGCTGGAGCAGAAGGTGGGAGTGGCTCCCCAGAAAAGCAGCTGCAG  
GTAGACCAGGACTACCTGATTGCTCTGTCCCTGCAGCAGCAACAGCCACGAGGCCCGCTGGGGCT  
TACCGACTTGGAGCTGGCCCAGCAGCTTCAGCAAGAGGAGTATCAACAGCAGCAGGCAGCGCAGC  
CAGTGCGGATGCGGACGCGGGTCTGTCACTGCAGGGGAGAGGAGCCACATCTGGACGCCAGCC  
GGGAGCGTTCGGCAGAGGCCGAAGCACGAGTCAGACTGCATTCTGCTGtaggcggccgc