

**Clone sample ID:** WHSC1:JMC027-A07:C212867

**Construct ID:** WHSC1-32

**Vector:** pET28-MHL

**N-terminal tag:** Mhhhhhssgrenlyfqg      **C-terminal tag:** N/A

**Residues (from-to):** 208- 368

**Uncut:**

MhhhhhssgrenlyfqgPNTGRDKDHLLKYNVGDVWSKVSGYPWWPCMVSADPLLHSYTKLKG  
QKKSARQYHVQFFGDAPERAWIFEKSLVAFEGEGQFEKLCQESAKQAPTKAEKIKLLKPISGKL  
RAQWEMGIVQAEAAASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAE

**Cut:**

gPNTGRDKDHLLKYNVGDVWSKVSGYPWWPCMVSADPLLHSYTKLKGQKKSARQYHVQFF  
GDAPERAWIFEKSLVAFEGEGQFEKLCQESAKQAPTKAEKIKLLKPISGKLRAQWEMGIVQAE  
AASMSVEERKAKFTFLYVGDQLHLNPQVAKEAGIAAE

**Host:** *E. Coli*, BL21 (DE3)

**Yield:** >10 mg/L

**Storage buffer:** 20 mM Tris-HCl pH 7.4, 500 mM NaCl, 5% Glycerol

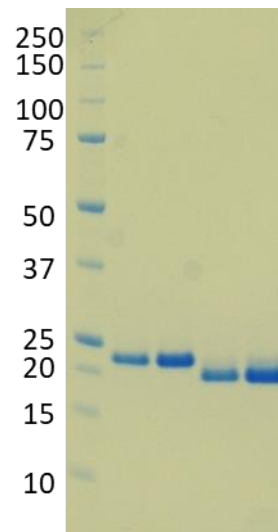
**Purity cut and uncut protein:** >95%

**Purity assessment:** SDS-PAGE on 4-12% Bis-Tris Gel (Life technology)

Lane 1: Precision Plus Protein standard, Bio-Rad

Lanes 2- 3: 1 and 2 µg uncut

Lanes 4- 5: 1 and 2 µg cut



### **Construct and Expression:**

DNA fragment encoding human NSD2 (residues 208- 368) was amplified by PCR and sub-cloned into a pET28-MHL vector, downstream of the poly-histidine coding region. Following transformation into E. Coli BL21 (DE3) the cells were amplified at 37°C by inoculating Terrific Broth with overnight culture, both supplemented with 50 µg/ml Kanamycin and 35 µg/ml chloramphenicol. When the OD600 of the culture reached 0.8- 1.5, the temperature was lowered to 16°C and the target protein was over-expressed by inducing cells with 0.5 mM IPTG (isopropyl-1-thio-D-galactopyranoside) and incubated overnight before being harvested (7000 rpm for 10 min at 4°C) using a Beckman Coulter centrifuge.

### **Harvest and cell lysis:**

Harvested cells were re-suspended in 20 mM Tris-HCl, pH 7.5, 500 mM NaCl, 5 mM imidazole and 5% glycerol, 1X protease inhibitor cocktail (100 X protease inhibitor stock in 70% ethanol (0.25 mg/ml Aprotinin, 0.25 mg/ml Leupeptin, 0.25 mg/ml Pepstatin A and 0.25 mg/ml E-64) or Pierce™ Protease Inhibitor Mini Tablets, EDTA-free. The cells were lysed chemically by rotating 30 min with 0.5% CHAPS, 1 mM TCEP, 1 mM PMSF and 15 µL Benzonase Nuclease (In-House) followed by sonication at frequency of 7 (5" on/7" off) for 5 min (Sonicator 3000, Misoni). The crude extract was clarified by high-speed centrifugation (60 min at 36,000 xg at 4°C) by Beckman Coulter centrifuge.

### **Purification:**

The clarified lysate was then loaded onto an open column containing pre-equilibrated Ni-NTA (Qiagen). The column was washed and eluted by running 20 mM Tris-HCl, pH 7.5, 500 mM NaCl, 5% glycerol, containing 5 mM, 20 mM, and 250 mM imidazole, respectively. The eluted protein was analyzed for purity by SDS-PAGE. Since it was quite pure after Ni-NTA, the protein was split into two portions for dialysis overnight in 20 mM Tris-HCl pH 7.4, 500 mM NaCl, 5% glycerol. One portion had TEV protease added to facilitate tag cleavage. This portion was subjected to a second Ni-NTA column to remove TEV, tag and uncut protein. After tag removal, both uncut and cut WHSC1 was concentrated, aliquoted and flash frozen.

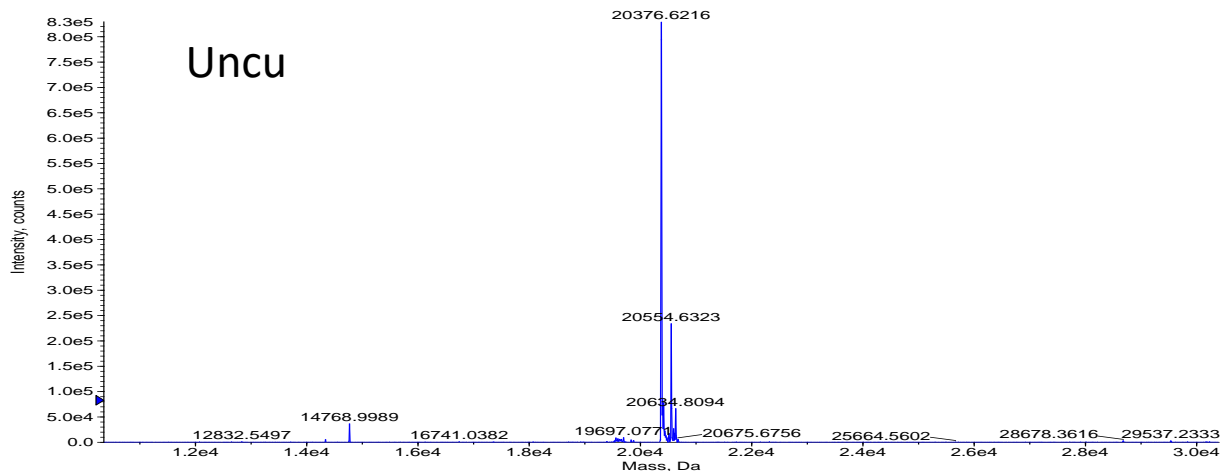
**Expected size Uncut:** 20376.21 Da

**Mass Spec Uncut:** 20376.62 Da

**Expected size Cut:** 18239.91 Da

**Mass Spec Cut:** 18240.33 Da

Mass reconstruction of +TOF MS: 4.494 to 4.712 min from 00008-C3\_RAPID-1-32UN.wiff Agilen... Max. 8.3e5 cps.



Mass reconstruction of +TOF MS: 4.458 to 4.676 min from 00020-C3\_RAPID-CUT2.wiff Agilent Max. 7.9e5 cps.

