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Data Article

Data on optimization of expression and purification of AIMP2-DX2 protein in *Escherichia coli*

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ABSTRACT

AIMP2-DX2 is a splicing variant of AIMP2 protein which has been implicated in human lung cancer and chemoresistance of ovarian cancer (J.W. Choi, D.G. Kim, A.E. Lee, H.R. Kim, J.Y. Lee, N.H. Kwon, et al., 2011; J.W. Choi, J.W. Lee, J.K. Kim, H.K. Jeon, J.J. Choi, D.G. Kim, et al., 2012) [1,2]. We have shown, here, the data for the expression of AIMP2-DX2 protein in *Escherichia coli* and optimization of the critical steps in purification of AIMP2-DX2. The data described here has been successfully used to get a maximum yield of highly pure AIMP2-DX2 for subsequent characterization of its biophysical property in: "Purification and biophysical characterization of the AIMP2-DX2 protein" (R. Jha, H.Y. Cho, A. Ul Mushtaq, K. Lee, D.G. Kim, S. Kim, et al., 2017) [3].

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Abbreviations: AIMP2, Aminoacyl-tRNA synthetase interacting multifunctional protein 2; AIMP2-DX2 or DX2, splicing variant of AIMP2 lacking exon 2; DTT, dithiorietol; IPTG, isopropyl β-D-1-thiogalactopyranoside; SDS-PAGE, Sodium dodecyl sulfate polyacrylamide gel electrophoresis; SUMO, Small Ubiquitin-like modifier

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Specifications Table

Subject area	*Biochemistry, Structural Biology*
More specific subject area	*Protein Expression and purification*
Type of data	*Table and figures*
How data was acquired	*Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)*
Data format	*Raw, analyzed*
Experimental factors	*Common laboratory practices for production of recombinant proteins from E.Coli, Common protocol for SDS-PAGE analysis*
Experimental features	*Optimization of protein expression in E.Coli, optimization of protein purification, Yield of protein*
Data source location	*Korea University, Sejong, South Korea*
Data accessibility	*Data is within this article*

Value of the data

- The data includes a process for screening the expression system and optimizing the purification steps for human AIMP2-DX2 protein. This data provides an efficient method to get a high yield of AIMP2-DX2 protein.
- The data on SUMO-tag cleavage shows that the protease activity of SUMO-proteases is efficient even at a salt concentration of 500 mM NaCl.
- The data on screening the optimal condition for protein purification and stabilization shows that EDTA can be a good additive to prevent aggregation of protein by chelating residual nickel and other metallic impurities from Nickel affinity chromatography.

1. Data

Fig. 1 shows the SDS-PAGE image of the expression and the solubility trial of the AIMP2-DX2 protein with a SUMO-tag in various *E. coli* cell lines. The *E. coli* cells were expressed at 37 °C and 18 °C with 1 mM IPTG. These cells were harvested, lysed and separated as pellet and supernatant before subjecting to SDS-PAGE. The variation in the solubility of SUMO-DX2 at different temperature and cell lines is easily comparable with relative protein band intensity.

Fig. 2 shows the SDS-PAGE image comparing the improvement in the stability of the SUMO-tagged AIMP2-DX2 between the optimized and unoptimized buffer conditions. The protective effect of 500 mM NaCl and 10 mM EDTA has been shown here for two critical processes, dialysis and SUMO-tag cleavage, during the purification of AIMP2-DX2.

2. Experimental design, materials and methods

2.1. Cloning and expression of protein

Full length human AIMP2 isoform C (hereafter referred as AIMP2-DX2 or DX2) protein was amplified from a PGEX-4T-1 plasmid containing human DX2, reported previously by Choi and Lee et al. [1,2]. The splicing variant of AIMP2 (NCBI nucleotide accession number NM_006303 and Genbank code U24169) lacking exon2 was generated as described by Choi et al. [1]. To get a high yield of soluble DX2 protein, we designed a cloning strategy to express DX2 with a SUMO protein tag. For this purpose, the yeast SUMO protein (Smt3; Genbank ID BK006938) was cloned into the pET-28a plasmid