



Jun 03, 2024

Version 2

## DENV2 NS2B-NS3 protease co-expression construct small scale expression and purification protocol V.2



Version 1 is forked from [Enterovirus coxsackievirus A16 2A protease small scale expression and purification protocol](#)

DOI

[dx.doi.org/10.17504/protocols.io.rm7vzj362lx1/v2](https://dx.doi.org/10.17504/protocols.io.rm7vzj362lx1/v2)

Korvus Wang<sup>1</sup>, Michael Fairhead<sup>1</sup>, Eleanor Williams<sup>1</sup>

<sup>1</sup>Centre for Medicines Discovery, University of Oxford

ASAP Discovery



Korvus Wang

CMD

### Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.rm7vzj362lx1/v2>

**Protocol Citation:** Korvus Wang, Michael Fairhead, Eleanor Williams 2024. DENV2 NS2B-NS3 protease co-expression construct small scale expression and purification protocol. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.rm7vzj362lx1/v2> Version created by **Korvus Wang**

**License:** This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

**Protocol status:** Working

**We use this protocol and it's working**

**Created:** June 03, 2024

**Last Modified:** June 03, 2024

**Protocol Integer ID:** 101135

**Keywords:** expression, purification, ASAP, CMD, AViDD, Dengue 2, Dengue Virus, Dengue Virus NS3 protease, NS3 protease, DENV2 NS2B-NS3 protease, purification of deng2 ns2b, ns3 protease, deng2 ns2b, purification protocol this protocol, purification protocol, purification, small scale expression

**Funders Acknowledgements:**

**National Institutes of Health/National Institute Of Allergy and Infectious Diseases (NIH/NIAID)**

Grant ID: U19AI171432

## Disclaimer

Research was supported in part by NIAID of the U.S National Institutes of Health under award number U19AI171399. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

## Abstract

This protocol details the co-expression and purification of DENV2 NS2B-NS3 protease construct bearing a N-terminal His-GST tag at small scale (<6L).

## Attachments



PAGE23-01988 - SRF-

B...

439KB



## Guidelines

- **Construct / plasmid resource-name:** A71EV2A protease construct bearing a N-terminal SUMO-His tag.
- **Construct Addgene ID**

# Materials

## Plasmid details:

- Vector: pNIC
- Cell line: E. coli Rosetta strain BL21(DE3)-RR
- Tags and additions: N-terminal GST-His tag
- Construct protein sequence: `
 

```
MHHHHHHSSMSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAII
RYIADKHNMLGGCPKERAIEISMLEGAVLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPD
FMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSGGGSENLYFQSM
GKSVD MYIERAGDITWEKDAEVTGNSPRLDVALDESGDFSLVEE
```

## Expression

TB media, 1mM IPTG

## Purification

Chicken hen egg white lysozyme

Benzonase

Imidazole

Ni Sepharose 6 FF resin

Gravity flow column, 2.5cm diameter

Centrifugal concentrators, 10kDa MWCO

On an FPLC system:

Cytiva HiLoad 16/600 Superdex 75 pg

5mL sample loop

SDS-PAGE sample buffer, gel, and gel tank

## Lysis buffer:

	A	B
	Hepes (pH 7.5)	50 mM
	NaCl	500 mM
	Glycerol	5%
	TCEP	1 mM
	Lysozyme	0.5 mg/mL
	Benzonase	0.05 mg/mL



	A	B
	TX-100	1%

Prepare 100L per 1L E.coli expression

**Base buffer:**

	A	B
	Hepes (pH 7.5)	50 mM
	NaCl	50 mM
	Glycerol	5%
	TCEP	1 mM

Prepare 2L per 6L E.coli expression. Used to prepare the following buffers

**Binding buffer:** base buffer + 20mM imidazole

**Wash buffer 1:** base buffer + 30mM imidazole

**Wash buffer 2:** base buffer + 50mM imidazole

**Elution buffer:** base buffer, add 500mM imidazole

**Gel filtration buffer:** base buffer + 20mM imidazole

**SDS-PAGE gel:** NuPage 4-12%, Bis-Tris protein gel, 27 well.

Run in MES buffer, 200V 35mins.

## Troubleshooting



## Changes

- 1 Corrected ELN mistake

## Abbreviations

- 2 CV - column volume, total volume of resin in a column  
IMAC - immobilised metal affinity chromatography  
FT - flow through  
DVNS2B3 - DENV2 NS2B-NS3 protease

## Plasmid Transformation

1d










- 3 DVNS2B3 N-terminal His-GST tagged co-expression construct was inoculated from its BL21(DE3)-RR glycerol stock.

### Note

The DENV2 NS2B-NS3 co-expression construct encodes the NS2B and NS3 protease with a N-terminal His6-GST tag fusion on a kanamycin resistant plasmid backbone with a T7 promoter.

## Protein expression

2d 10h

- 4 Scrape off some of the glycerol stock with a sterile loop and use this to inoculate a 50 mL falcon tube containing  10 mL of LB supplemented with  50 Mass Percent kanamycin. Grow the starter culture at  37 °C  Overnight with 200 rpm shaking.
- 5 Use  10 mL starter culture to inoculate every  1 L  Sample (see Materials) supplemented with  50 Mass Percent kanamycin in a baffled flask.  
 200 rpm, 37°C

4h

6h




**Note**

For this protocol 2L of pellet was grown for purification



**Note**

Media and expression condition are especially important for the production of this construct, as it is prone to auto-cleavage of the affinity tag during expression.

- 6 When the OD<sub>600</sub> approximately 1.8, add 1mM IPTG. Lower the temperature and shaker speed to  180 rpm, 18°C . Incubate overnight.

1d



- 7 Harvest the cell by centrifugation at  4000 x g, 4°C, 00:30:00 . Discard supernatant and store pellet by freezing at  -80 °C .

30m

**Note**

For reference: total pellet weight from 2L TB media was 33g

**Protein Purification**

2d

- 8 **Lyse cell pellet**

2h 30m

8.1

1h

**Note**

See Materials tab for buffer compositions.



**Note**

DENV2 NS2B-NS3 His6-GST fusion protein properties

**Before tag cleavage:**

MW = 32.812 kDa

E (assume all Cys reduced) = 51340 mM-1cm-1

PI = 5.47

**After tag cleavage:**

NS2B

MW = 5.0635 kDa

E(assume all Cys reduced) = 6990

PI = 3.98

NS3

MW = 18.096 kDa

E(assume all Cys reduced) = 30940

PI = 6.73

These values are determined by Expasy ProtParam

Thaw and resuspend the pellet in ~7mL of lysis buffer per g of pellet. Stir gently with magnetic stir bar at Room temperature for 00:30:00 to allow lysozyme and bezonase to start breaking down cell components.


- 8.2 Lyse by sonication 00:00:04 On 00:00:12 Off for a total 'on' time of 00:07:00 at 50% amplitude to fully rupture the cells. Ensure pellet is 0 °C during sonication to prevent overheating. 7m 16s

- 8.3 Centrifuge the lysed cells for 38000 x g, 4°C, 01:00:00 to remove insoluble cell debris, and collect supernatant in a bottle 4 °C 1h

## 9 Perform IMAC to extract target protein from the lysed cell mixture

- 9.1 Dispense 3 mL Nickle affinity resin Ni Sepharose 6 FF - Cytiva into a gravity flow column. Equilibrate resin by first rinsing with ~ 10 µL distilled water, then ~ 10 µL binding buffer to remove the storage solution. 10m
- 9.2 Resuspend the equilibrated resin with some binding buffer and add to the supernatant bottle. Incubate the resin with the supernatant for 00:30:00 while rotating or 30m





otherwise mixing gently at  4 °C

- 9.3 Load the resin/supernatant mix back onto the gravity flow column, retaining the FT separately for SDS-PAGE analysis.


30m

#### Note

For SDS-PAGE samples, mix 15uL sample with 5uL 4x sample buffer, supplemented with 10mM DTT.

- 9.4 Wash the column with  10 µL of base buffer, followed by  10 µL of wash buffer 1 and 2. Allow wash buffer to pass through completely between washes. This is to remove non-specific, weak binding of contaminant proteins from the resin for a cleaner elution. Collect washes separately for SDS-PAGE analysis.

30m

- 9.5 Elute the protein with  2.5 µL of elution buffer.

20m

- 9.6 Repeat step 8.5 one more time, collecting a total of 2 separate elution fractions. This is to ensure maximum retrieval of protein from the resin.

20m

Measure the total protein concentration of the elutions by Nanodrop. Although still a mixture, A280 value can give an estimate of the protein content, which will determine how much protease need to be added to remove the affinity tag.

For example, E1 = 18.28 mg/mL, E2 = 13.02 mg/mL at 1 A280 unit = 1 mg/mL

- 9.7 Wash used IMAC resin with 10CV of base buffer, and leave in the column submerged in a small amount of base buffer such that the resin is kept moist.  
This washed IMAC resin will later be reused for reverse IMAC (rIMAC)

- 10 Run SDS-PAGE of all samples from total lysis supernatant to final elution. Stain gel with protein staining solution Coomassie Blue and determine which fractions contain the target protein by finding the band corresponding to the target molecular weight.

40m

#### Note

The target protein is expected to be present mostly in the elution samples, although small amounts may be found in the FT and washes.  
If that is not the case, then further troubleshooting is required.



## 11 Elution de-salting, tag cleavage and reverse IMAC

1d

- 11.1 Pool and desalt the two elutions using HiPrep 26/10 desalting columns, run on AKTA pure at the maximum flow rate of 10mL/min.

30m

### Note

This is to reduce imidazole concentration in the sample. High concentration of imidazole will inhibit protease activity during tag cleavage and removal.

- 11.2 For tag removal, His-TEV was added in 1:100 ratio to the total protein content of the desalted sample, as determined by nanodrop. The mixture was left in the cold room at

1d

4 °C

Overnight

- 11.3 In morning, pour the cleavage mixture over the washed resin three times and collect final FT.

30m

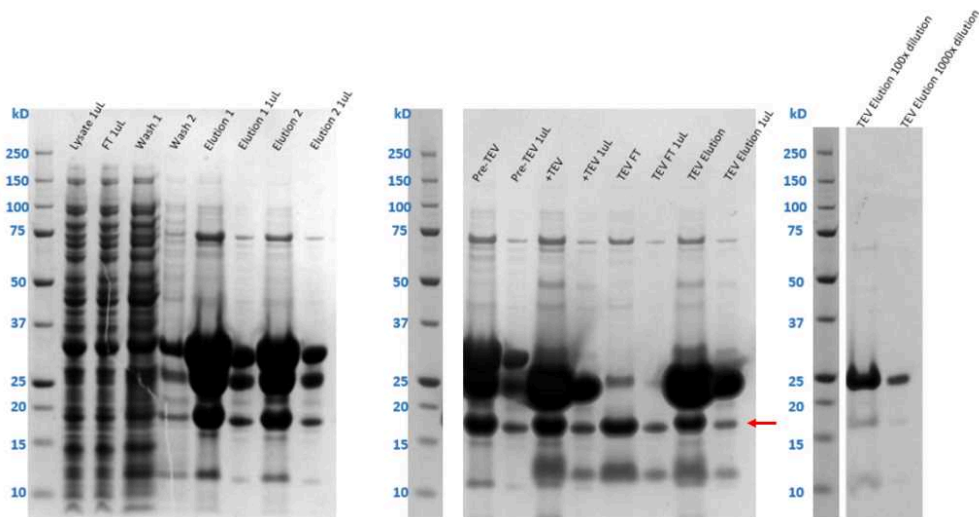
### Note

This step will remove the cleaved tag and any uncleaved target from the sample. If the protease used is His-tagged, then the protease is removed from sample too.

- 11.4 Wash rIMAC resin with 2 µL wash buffer 1 and 2 to remove any target protein still bound to the resin.

30m

Take samples of the FT and wash, characterise content by SDS-PAGE



**SDS-PAGE analysis of IMAC and cleavage fractions.** The band highlighted by red arrow agrees with the size of the cleaved NS3 construct (18.095 kDa)

- 11.5 (Optional) elute rIMAC resin with 2  $\mu$ L elution buffer to confirm if the protein shows non-specific binding to the resin used.

5m

#### Note

This will help determine if the protein is "sticky" to the Ni resin matrix material, and help in further troubleshooting if the final yield is lower than expected.

## 12 Purify sample further by size exclusion chromatography.

6h

- 12.1 Using 10,000 MWCO spin concentrators, concentrate the rIMAC step containing fractions of the target protein to a final volume of under 5 mL .

1h

- 12.2 Remove any solid aggregates from the sample by centrifugation at 17200 x g, 4°C, 00:10:00 , then immediately draw up the supernatant with a 5mL syringe and a blunt-tip fill needle, taking care not to disturb the pellet.

15m

### Note

This is to remove as much solid particles from the injection sample as possible, so as to not clog the in-line filter or frit of the column.

## 13 Using the AKTA Pure system:

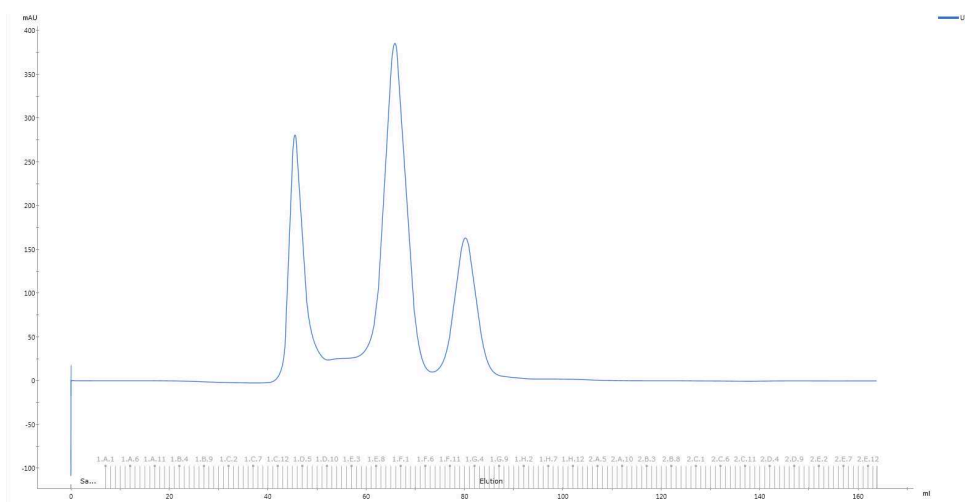
2h

Inject the sample onto a 5mL sample loop.

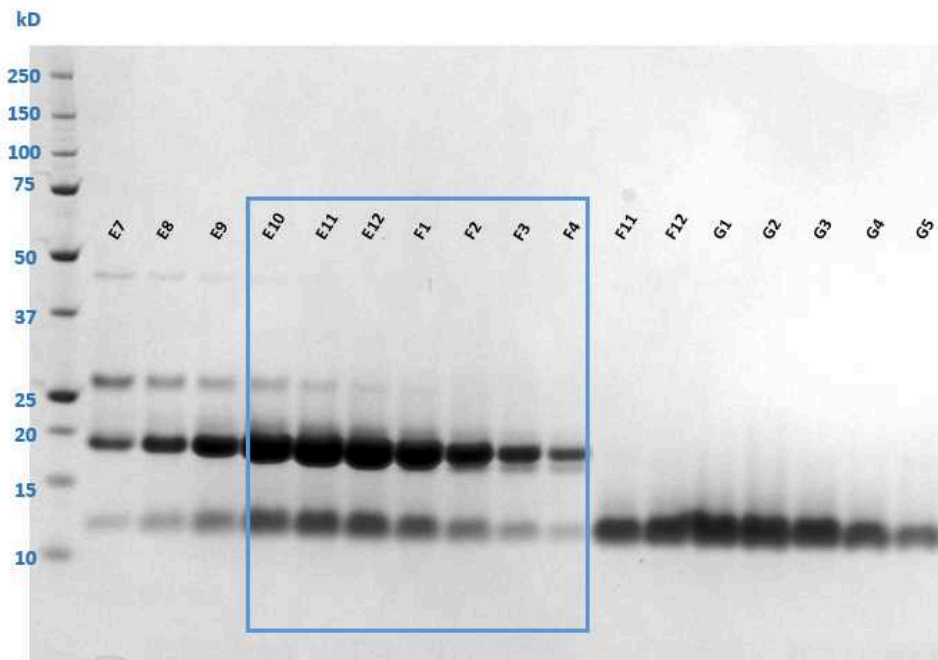
Run the sample down HiLoad 16/60 Superdex 75 pg gel filtration column at 1mL/min in gel filtration buffer, collecting 1mL aliquots.

## 14 From the chromatogram, fraction E9-H8 analyse by SDS-PAGE.

1h



**Chromatogram of the DVNS2B3 SEC run.** Fractions E7-G5 were analyzed by SDS-PAGE to see which contained the target protein



**SDS-PAGE analysis of SEC fraction E7-G5.** Fractions E10-F4 were pooled as they contain majority target protein in comparison to contaminants.  
Red arrow indicated the position of bands corresponding to the target protein.

- 14.1 Take the fractions that contain the target protein, which in this case are fraction E10-F4. Concentrate the final sample in Vivaspın 500 10kda MWCO centrifugal concentrator until the concentration reaches > [IM] 23 mg/mL or [IM] 1 millimolar (mM) .

30m

Take 1  $\mu\text{L}$  of the final sample for SDS-PAGE, and another for mass spectroscopy (MS).

- 14.2 Aliquot into appropriate volumes for future usage to minimise freeze/thaw cycles. Flash-freeze in liquid nitrogen, and store at  $-80\text{ }^{\circ}\text{C}$  until required.

10m