



Jun 04, 2025

Version 2

Zika NS2B-NS3 fusion construct for assay small scale expression and purification protocol V.2



Version 1 is forked from [Dengue virus serotype 2 NS2B-NS3 protease fusion construct small scale expression and purification for Creoptix and biochemical assaysprotocol](#)

DOI

<https://dx.doi.org/10.17504/protocols.io.eq2lyw6jpvx9/v2>

Korvus Wang¹, Michael Fairhead¹, Eleanor Williams¹

¹Centre for Medicines Discovery, University of Oxford, ASAP Discovery Consortium

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.eq2lyw6jpvx9/v2>

Protocol Citation: Korvus Wang, Michael Fairhead, Eleanor Williams 2025. Zika NS2B-NS3 fusion construct for assay small scale expression and purification protocol. **protocols.io** <https://dx.doi.org/10.17504/protocols.io.eq2lyw6jpvx9/v2> Version created by **Mary-Ann Xavier**

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 04, 2025

Last Modified: June 04, 2025

Protocol Integer ID: 219552

Keywords: expression, purification, ASAP, CMD, AViDD, Zika Virus, NS2B-NS3 protease, purification of zika virus ns2b, zika virus ns2b, zika ns2b, ns3 protease fusion, ns3 protease fusion construct, zika, ns3 protease, ns3 fusion, purified enzyme, purification protocol this protocol, purification protocol, purification, enzyme, qq01zvns2b, ns3, biochemical assay, ns2b

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 Zika virus NS2B-NS3 protease fusion construct bearing a N-terminal His-StrepII tag at small scale (<6L). The purified enzyme is active and suitable for use in biochemical assays. Construct used here is (internal id: QQ01ZVNS2B-cC001). In this version we added the Addgene Id of the construct used.

Attachments



PAGE24-01001-

QQ01Z...

244KB



Guidelines

- **Construct / plasmid resource-name:** Zika NS2B-NS3 protease fusion construct bearing TEV-cleavable N-terminal His tag.

Materials

Plasmid details:

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


```
MHHHHHHSSGASWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSVDLG TENLYFQSMGKSVD MYIERAGDITWEKD
AEVTGNSPRLDVALDESGDFSLVEDDGPPMREGGGGSGGGGGSGALWDVPAPKEVKKGETTDGVYRVMTRRLLGSTQ
VGVGVMQEGVFHTMWHVTKGSALRSGEGR LDPYWGDVKQDLVSYCGPWKLDAAWDGHSEVQLLAVPPGERARNIQT
LPGIFKTKDGDIGAVALDYPAGTSGSPILDKCGRVIGLYGNGVVIKNGSYVSAITQGRREEETPVE
```

Expression

TB media, 0.5mM IPTG

Purification

Chicken hen egg white lysozyme

Benzonase

Imidazole

Ni Sepharose 6 FF resin

Gravity flow column, 2.5cm diameter

Centrifugal concentrators, 10kDa MWCO

Thermo Slide-A-Lyzer Dialysis Cassette, 3.5kDa 15mL (or equivalent snakeskin tubing)

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



	A	B
	Benzonase	0.05 mg/mL

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

Elution buffer: base buffer, add 200mM imidazole

Gel filtration buffer: base buffer

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

Run in MES buffer, 200V 35mins.



Protocol materials



ZIKV VE_Ganxian2016 NS2B-NS3 protease fusion (non-cleavable linker, N-term Twin-Strep-tag) **addgene Catalog #228661**



Abbreviations

- 1 CV - column volume, total volume of resin in a column
IMAC - immobilised metal affinity chromatography
FT - flow through
ZVNS2B3 - ZV NS2B-NS3 protease

Plasmid Transformation

1d

- 2 ZVNS2B3 N-terminal His-StrepII tagged fusion construct was inoculated from its BL21(DE3)-RR glycerol stock. Using the plasmid

 ZIKV VE_Ganxian2016 NS2B-NS3 protease fusion (non-cleavable linker, N-term Twin-Strep-tag) **addgene Catalog #228661**

Note

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

Protein expression

2d 10h

- 3 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.
- 4 Use  10 mL starter culture to inoculate every  1 L TB media (see Materials) supplemented with  50 Mass Percent kanamycin in a baffled flask.
 200 rpm, 37°C

4h

6h



Note

For this protocol 4L of pellet was grown for purification



- 5 When the OD₆₀₀ approximately 1.8, add [m] 0.5 millimolar (mM) IPTG. Lower the temperature and shaker speed to [🔄] 180 rpm, 18°C . Incubate overnight. 1d
- 6 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

Protein Purification

2d

7 Lyse cell pellet

2h 30m

7.1

1h

Note

See Materials tab for buffer compositions.

Note

Zika NS2B-NS3 His6-StrepII fusion protein properties

Before tag cleavage:

MW = 31250.5 Da

E (assume all Cys reduced)= 55920 mM-1cm-1

PI = 5.35

After tag cleavage:

MW = 25556.5 Da

E (assume all Cys reduced)= 43430 mM-1cm-1

PI = 4.85

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.



7.2 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.

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

1h

8 Perform IMAC to extract target protein from the lysed cell mixture

8.1 Dispense 4 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

8.2 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 otherwise mixing gently at 4 °C

30m

8.3 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.

8.4 Wash the column with 10 µL of base buffer, followed by 10 µL of wash buffer twice. 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

8.5 Elute the protein with 2.5 µL of elution buffer.

20m

8.6 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

- 8.7 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)

- 9 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.

10 Elution de-salting, tag cleavage and reverse IMAC

1d

- 10.1 Pool and desalt the two elutions by dialysis, using Thermo Slide-A-Lyzer Dialysis Cassette, 3.5kDa 15mL (or equivalent), into 4L of base buffer.

30m

Note

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

Dialysis cassettes were used due to equipment availability. Dialysis using snake skin tubing or desalting using pre-packed columns are also acceptable.

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

1d

🌡 4 °C

🕒 Overnight

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

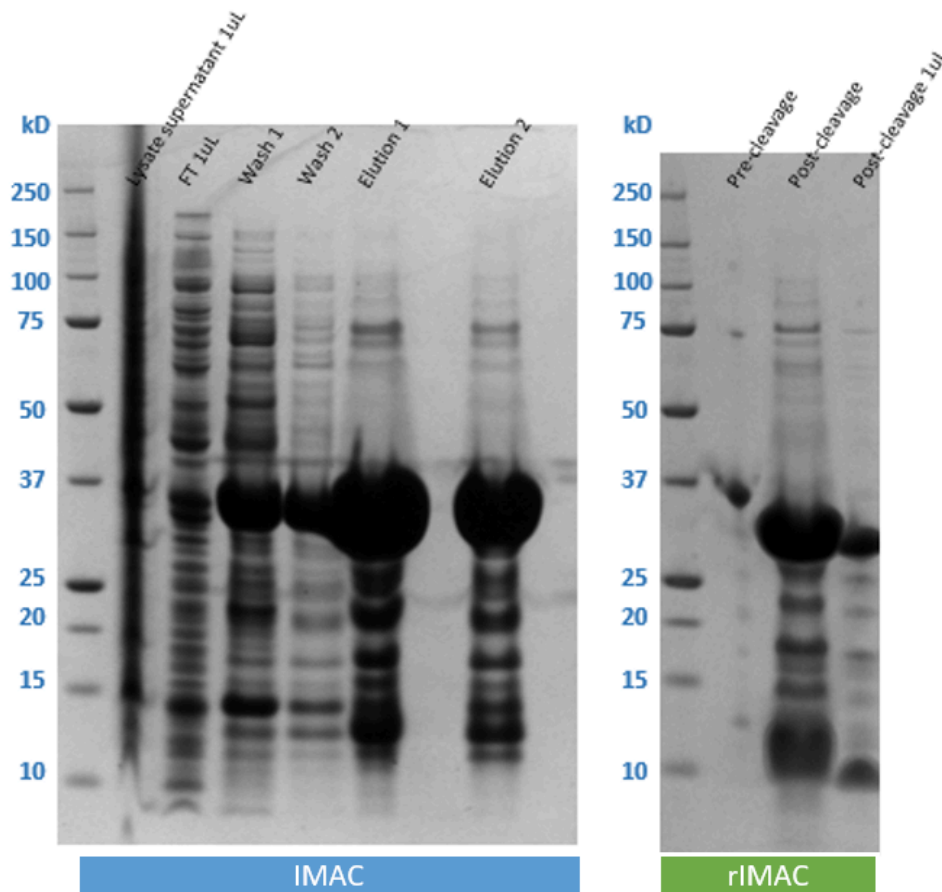
30m

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.

- 10.4 Wash rIMAC resin with 2 μ L wash buffer 1 and 2 to remove any target protein still bound to the resin. Take samples of the FT and wash, characterise content by SDS-PAGE

30m



SDS-PAGE analysis of IMAC and cleavage fractions. The major band in rIMAC FT agrees with the size of the cleaved fusion construct (25.556 kDa)

- 10.5 (Optional) elute rIMAC resin with 2 μ 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.

11 Purify sample further by size exclusion chromatography.

6h

11.1 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

11.2 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. This can also be done by filtering the sample through a 0.22 micron syringe filter.

12 Using the AKTA Pure system:

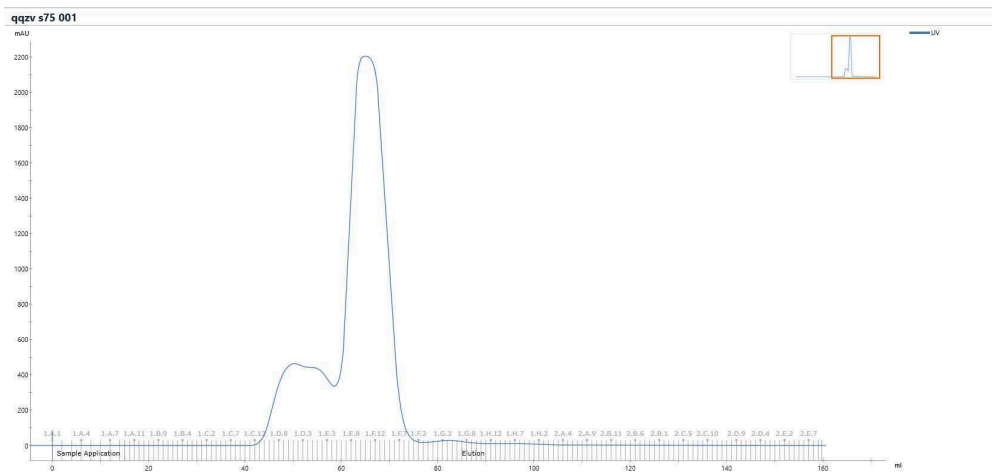
2h

Inject the sample onto a 5mL sample loop.

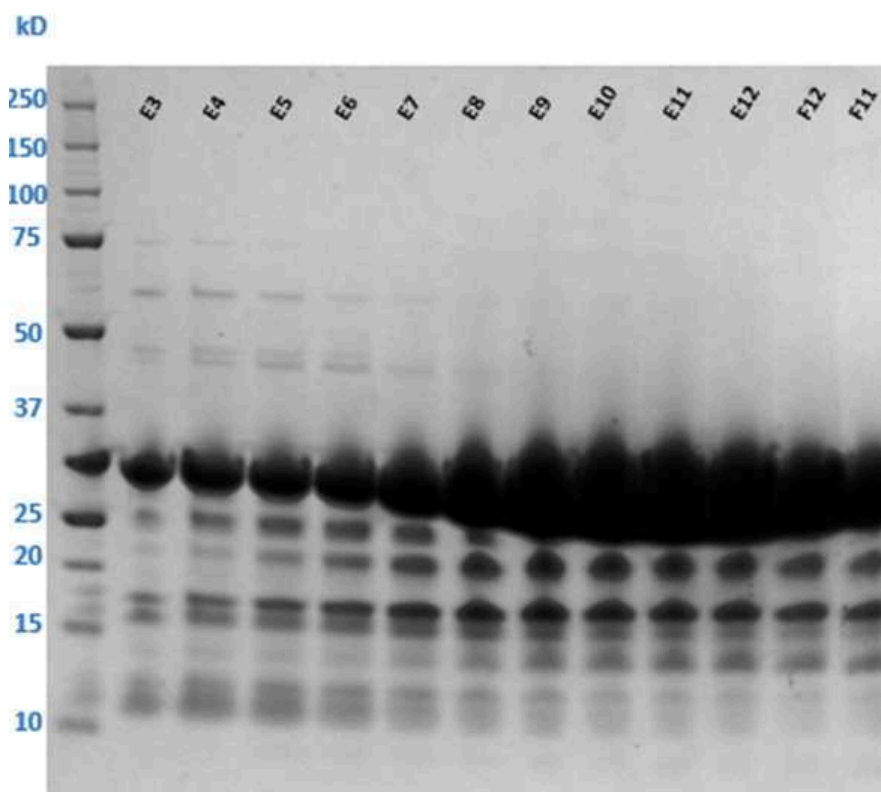
Run the sample down HiLoad 16/60 Superdex 75 pg gel filtration column at 1mL/min in gel filtration buffer, collecting 1mL aliquots.

13 From the chromatogram, fraction E3-F11 were analysed by SDS-PAGE.

1h



Chromatogram of the Zika NS2B3 fusion construct SEC run. Fractions E3-F11 were analyzed by SDS-PAGE to see which contained the target protein.

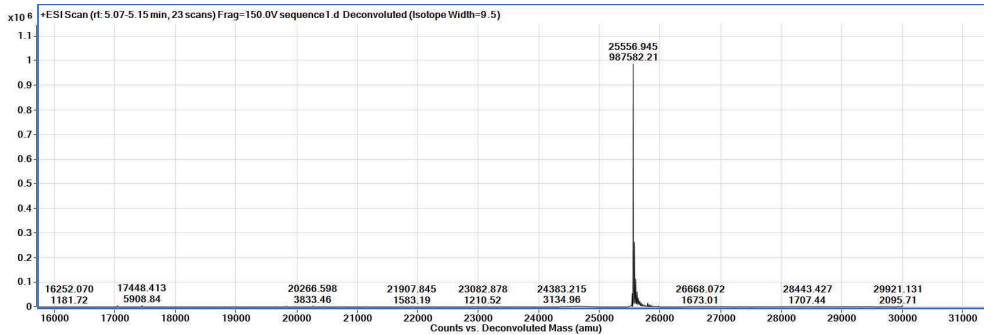


SDS-PAGE analysis of SEC fraction E3-F11. Fraction E8-F10 were pooled as they contain majority target protein in comparison to contaminants.

- 13.1 Take the fractions that contain the target protein, which in this case are fraction E8-F10. Concentrate the final sample in Vivaspın 500 10kda MWCO centrifugal concentrator until the concentration reaches approximately **20 mg/mL**.

30m

Take **1 μ L** of the final sample for SDS-PAGE (result not shown here), and another **1 μ L** for mass spectroscopy (MS) analysis.



Intact MS result of the final sample. Major peak molecular weight (25556.945 Da) agrees with the expected weight (25556.5 Da), confirming the target protein as the major species in the sample.

- 13.2 Aliquot into appropriate volumes for future usage to minimise freeze/thaw cycles. Flash-freeze in liquid nitrogen, and store at **-80 °C** until required.

10m

Protocol references

ZIKV isolate VE_Ganxian2016 NS2B-NS3 protease fusion with non cleavable linker (N-terminal Twin-Strep-tag) was a gift from ASAP Discovery & Frank von Delft (Addgene plasmid # 228661 ; <http://n2t.net/addgene:228661> ; RRID:Addgene_228661)