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West Nile virus NS2B-NS3 protease fusion construct small scale expression and purification protocol V.3

Version 1 is forked from Zika NS2B-NS3 fusion construct for assay small scale expression and purification protocol

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CMD

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We use this protocol and it's working

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Abstract

This protocol details the co-expression and purification of West Nile virus NS2B-NS3 protease fusion construct bearing a N-terminal His-StrepII tag at small scale (<6L). This protocol produces enzymatically active product that is suitable for biochemical assays. In this version we added the Addgene id.

Attachments

PDF

PAGE23-01159 - Purif...

530KB

Guidelines

- **Construct / plasmid resource-name:** WNV NS2BNS3 protease fusion construct bearing TEV-cleavable N-terminal His-StrepII tag.

Materials

Plasmid details:

The construct used was internal id (QQ01WNVNS2B-c003).

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

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
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

WNV NY99 NS2B-NS3 protease fusion (non-cleavable linker) K→A mutation anti-autoproteolysis **addgene Catalog #**228660

Abbreviations

1 CV - column volume, total volume of resin in a column
IMAC - immobilised metal affinity chromatography
FT - flow through
WNVNS2B3 - WNV NS2B-NS3 protease

Plasmid Transformation

1d

2 The plasmid encodes WNVNS2B and NS3 protease with a non-cleavable flexible linker and a N-terminal His6-StrepII tag fusion.

WNV NY99 NS2B-NS3 protease fusion (non-cleavable linker) K→A mutation anti-autoproteolysis **addgene Catalog #**228660

Pre-culture was inoculated from its BL21(DE3)-RR glycerol stock.

Note

The WNV 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 [M] 50 Mass Percent kanamycin. Grow the starter culture at 37 °C Overnight with 200 rpm shaking.

4h

4 Use 10 mL starter culture to inoculate every 1 L TB media (see Materials) supplemented with [M] 50 Mass Percent kanamycin in a baffled flask.

200 rpm, 37°C

6h

5 When the OD_{600} approximately 1.8, add [M] 1 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 Purifcation 2d

7 **Lyse cell pellet** 2h 30m

7.1 1h

Note

See Materials tab for buffer compositions.
The expression scale for this protocol is 2L.

Note

WNV NS2B-NS3 His6-StrepII fusion protein properties

Before tag cleavage:
MW = 32038.6 Da
E (assume all Cys reduced)= 66920 mM-1cm-1
PI = 5.34

After tag cleavage:
MW = 26344.5 Da
E (assume all Cys reduced)= 54430 mM-1cm-1
PI = 4.83

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 00:00:05 On 00:00:10 Off for a total 'on' time of 00:15:00 at 50% amplitude to fully rupture the cells. Ensure pellet is 0 °C 45m

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 4 °C — 1h

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

8.1 Dispense 8 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, incubate on resin for 00:10:00 before eluting. — 10m

8.6 Repeat step 8.5 two more times, collecting a total of 3 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.

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 Coomasssie 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.

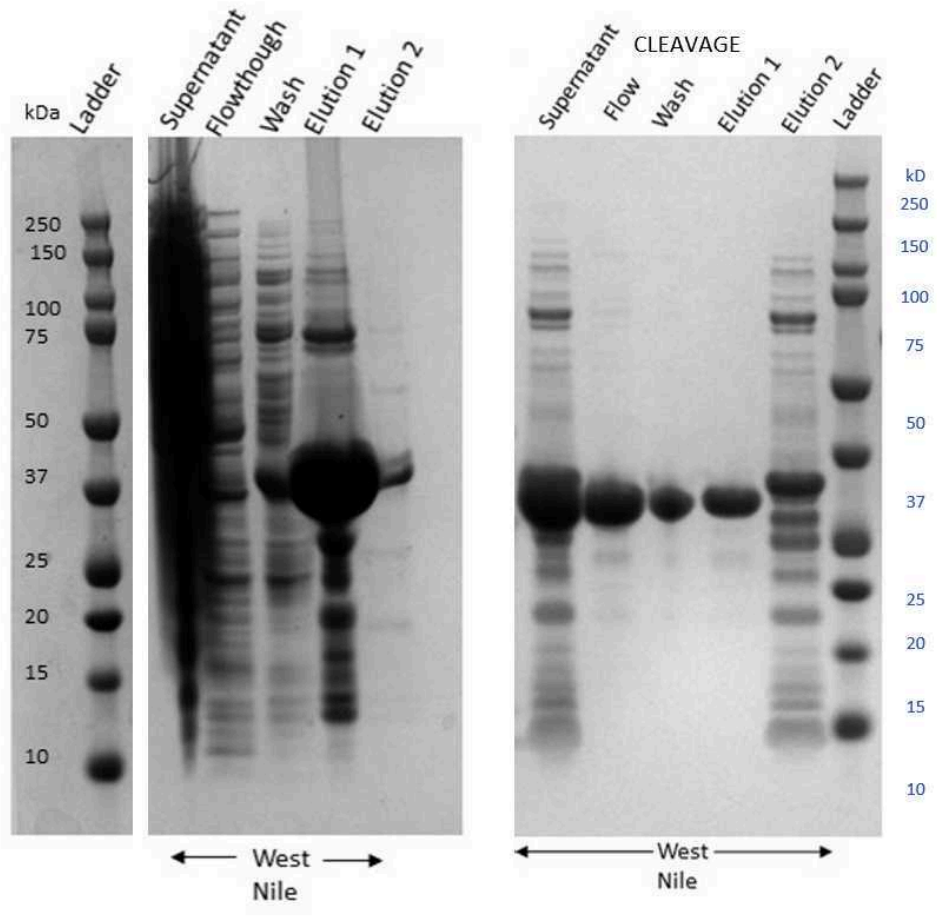
10.2 For tag removal, His-TEV was added in 1:20 ratio to the total protein content of the dialysis sample, as determined by nanodrop. The mixture was left in the cold room at 4 °C Overnight 1d

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 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 major band in rIMAC FT agrees with the size of the cleaved fusion construct (26.345 kDa) The gel on the left contains sample taken from IMAC, and the right contains samples from rIMAC. In rIMAC, cleaved target protein is also present in the wash and elution 1 fractions. One possible cause is that the target is "sticky" and contains some intrinsic affinity for the resin used.

10.5 (Optional) elute rIMAC resin with 2 µL 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

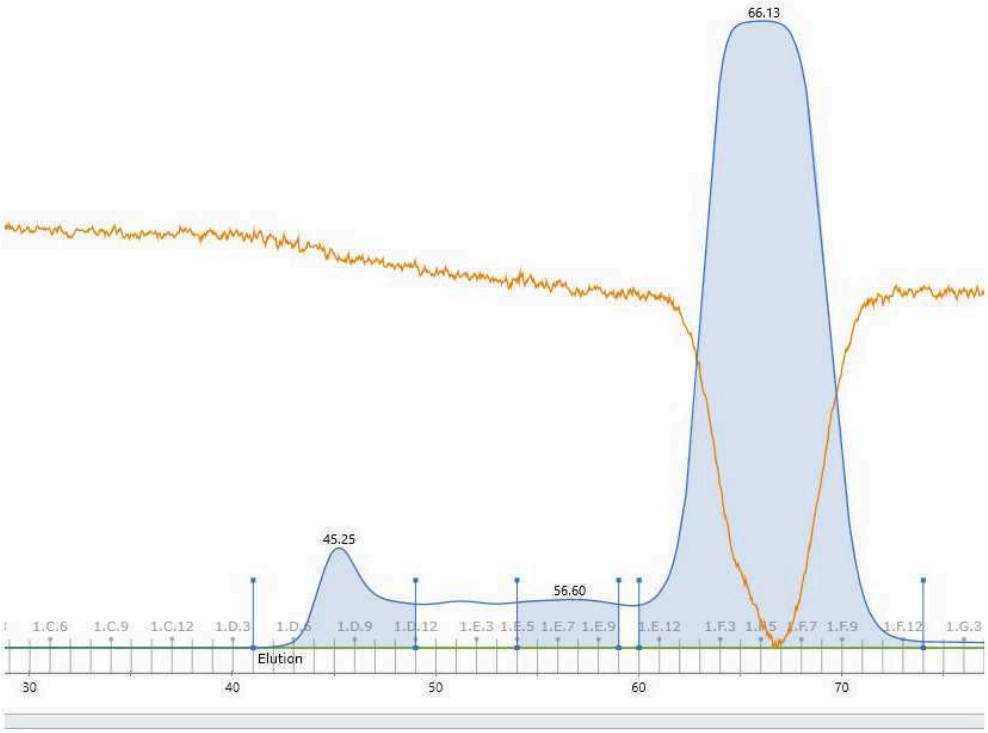
This is to remove as much solid particles from the injection sample as possible, so as to not clog the in-line filter or frit of the column.
Sample can also be passed through a 0.22 micron syringe filter instead.

12 Using the AKTA Pure system: 2h

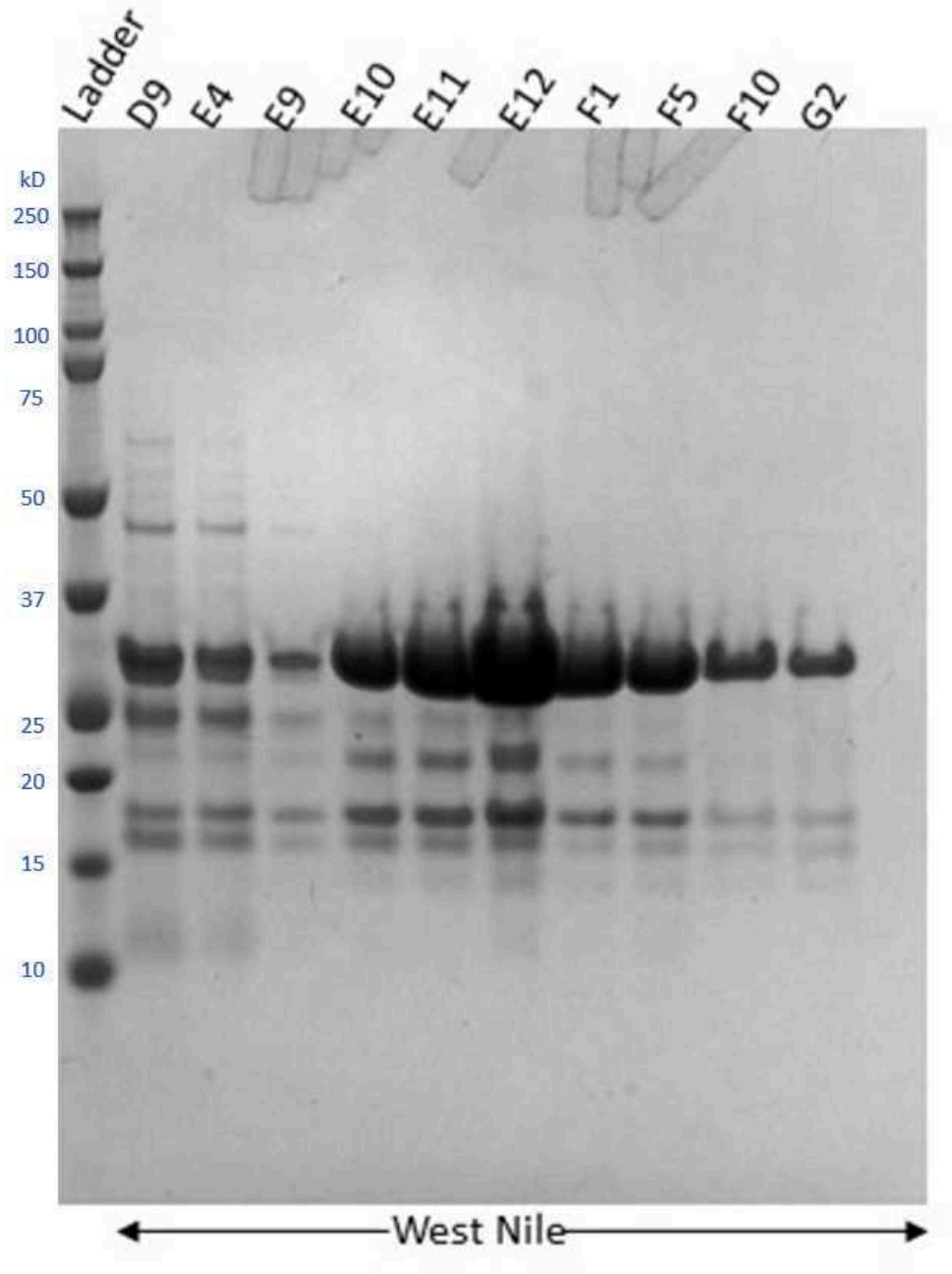
Inject the sample onto a 5mL sample loop.

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 E10-G2 were analysed by SDS-PAGE. 1h



Chromatogram of the WNV NS2B3 fusion construct SEC run. Fractions D9, E4, E9-G2 were analyzed by SDS-PAGE to see which contained the target protein.



SDS-PAGE analysis of SEC fraction D9, E4, E9-G2. Fraction E10-G2 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 E10-G2. Concentrate the final sample in Vivaspin 500 10kda MWCO centrifugal concentrator until the concentration reaches approximately [M] 10 mg/mL . 30m

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

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