# **AVIDD ASAP: EVD68 & EVA71 3C protease expression and purific ation**

PAGE22-01976

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Experiment Started:

Projects: Expression; Purification; ASAP

Related Pages:

Referenced by: PAGE23-00563

Tags:

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D68EV3CPROA-c001/D68EV3CPROA-k001/D68EV3CPROA-e001/D68EV3CPROA-p001

MGPGFDFAQAIMKKNTVIARTEKGEFTMLGVYDRVAVIPTHASVGEIIYINDVETRVLDACALRDLTDTNLEITIVKLDRNQKFR DIRHFLPRCEDDYNDAVLSVHTSKFPNMYIPVGQVTNYGFLNLGGTPTHRILMYNFPTRAGQCGGVVTTTGKVIGIHVGGNGA QGFAAMLLHSYFTDTQKHHHHHH

21283.3 Da

10430 mM-1cm-1

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A71EV3CPROA-c001/A71EV3CPROA-k001/A71EV3CPROA-e001/A71EV3CPROA-p001

MGPSLDFALSLLRRNIRQVQTDQGHFTMLGVRDRLAVLPRHSQPGKTIWVEHKLINILDAVELVDEQGVNLELTLVTLDTNEKF RDITKFIPENISAASDATLVINTEHMPSMFVPVGDVVQYGFLNLSGKPTHRTMMYNFPTKAGQCGGVVTSVGKVIGIHIGGNG RQGFCAGLKRSYFASEQLEHHHHHHH

21331.5 Da

9970 mM-1 cm-1

From

https://doi.org/10.1107/S0907444913002862

The protein was stored in 25 mM Tris-HCl pH 8.0, 150 mM NaCl, 1 mM TCEP at 277 K.

crystallization example

The droplets were prepared by a 1:1 mix of the complex (12 mg/ml) and the reservoir solution containing 100 mM Tris-HCl pH 8.5, 25% PEG4000, and 0.8 M lithium chloride. The crystals were ready for data collection at 16 °C for about 1 week. (https://doi.org/10.1002/jmr.2551)

Score Expect Method Identities Positives Gaps
214 bits(544) 4e-76 Compositional matrix adjust. 99/184(54%) 128/184(69%) 0/184(0%)
Query 1 MGPGFDFAQAIMKKNTVIARTEKGEFTMLGVYDRVAVIPTHASVGEIIYINDVETRVLDA 60
Sbjct 1 ...SL..LSLLRR.IRQVQ.DQ.H....R.L.L.R.SQP.KT.WVEHKLINI... 60

```
Query 61 CALRDLTDTNLEITIVKLDRNQKFRDIRHFLPRCEDDYNDAVLSVHTSKFPNMYIPVGQV 120

Sbjct 61 VE.V.EQGV...L.I.T..T.E....TK.I.ENISAAS..T.VIN.EHM.S.FV...D. 120

Query 121 TNYGFLNLGGTPTHRILMYNFPTRAGQCGGVVTTTGKVIGIHVGGNGAQGFAAMLLHSYF 180

Sbjct 121 VQ.....S.K...TM.....K....SV....I...R...C.G.KR... 180

Query 181 TDTQ 184

Sbjct 181 ASE. 184
```

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15 mL o/n in SOC + Kan 50

Use to inoculate 1L AIM-TB

grow 4h 37C/20h 17C 250 rpm shaking

Harvest 4000 g (grew 2L of each protease, around 100 g of cells total for each protease)

Lyse in base buffer + 1 % TX-100 and 0.5 mg/mL HEWL + 1 ug/mL benzonase + 30 mM Imidazole

Centrifuge 30,000g 1h 4C

Pour SN over 15 mL Ni Sepharose FF

Wash 3 x 100 mL Base Buffer + 30 mM Imidazole

Elute 3 x 30 mL Base Buffer + 30 mM Imidazole (protein predominantly in 1st 2 fractions)

#### D68EV3CPROA

Fraction 1 = 30 mL A280 of 9

Fraction 2 = 30 mL A280 of 6

Fraction 3 = 30 mL A280 of 1.3

## A71EV3CPROA

Fraction 1 = 30 mL A280 of 3.4

Fraction 2 = 30 mL A280 of 3.1

Fraction 3 = 30 mL A280 of 1.2

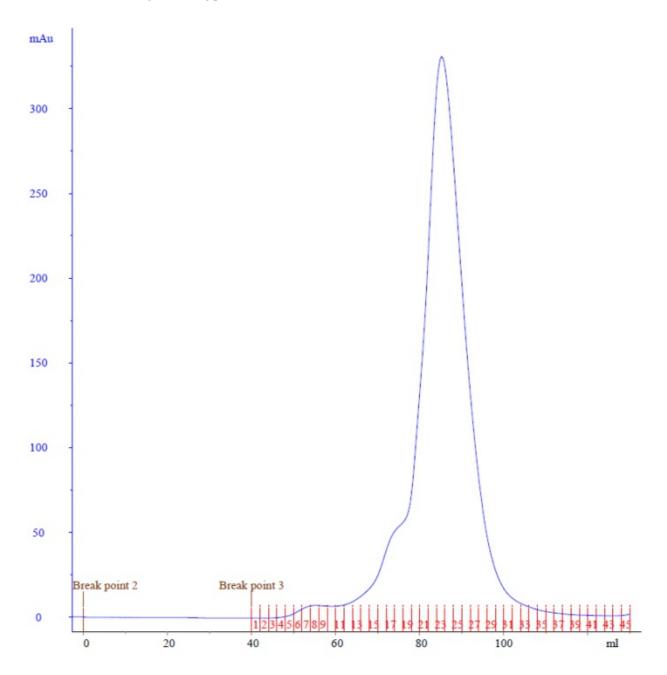
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Dialyze o/n into base buffer + 0.5 mM TCEP

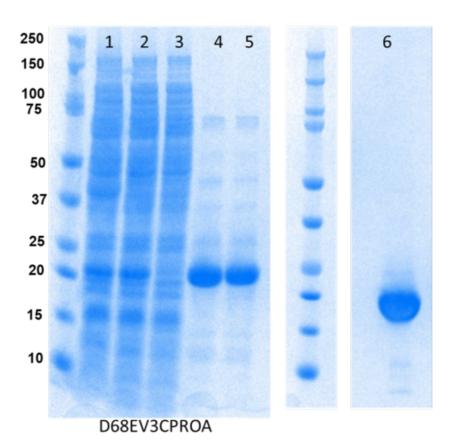
Very very slow to concentrate in both cases about 30 mL was the best I could do in both cases (about 10 mg/mL of EVD68 and 5 mg/mL for EV71)

Run 5 mL aliquots over 125 mL superose 12 pg column using base buffer + 0.5 mM TCEP as mobile phase

EVD68 3CL Protease superose 12 pg column

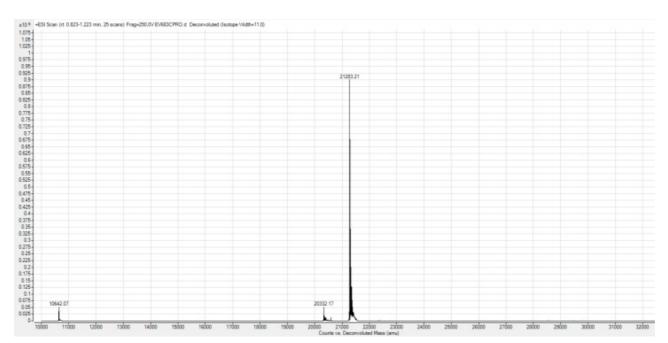


SDS PAGE D68EV3CPROA

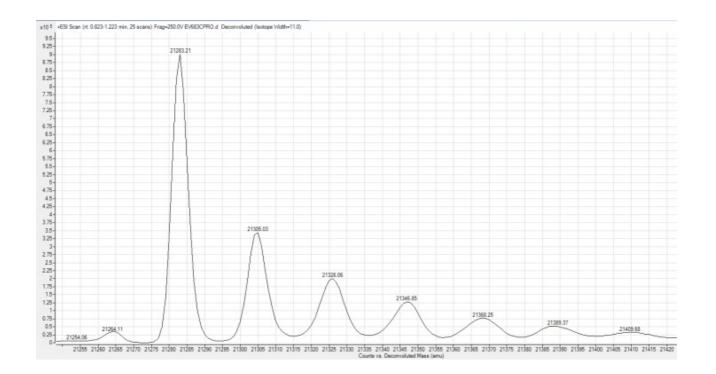


- 1 = Lysate
- 2 = Soluble fraction
- 3 = Flow through
- 4 = IMAC fraction 1
- 5 = IMAC fraction 2
- 6 = Final pool after SEC

## D68EV3CPROA-p001 MS confirmation Z:\Agilent\_SGC\_QTOF\Rod\221124\_MS424C



D68EV3CPROA-p001 MS confirmation Z:\Agilent\_SGC\_QTOF\Rod\221124\_MS424C



#### **EVD68 3CL Protease**

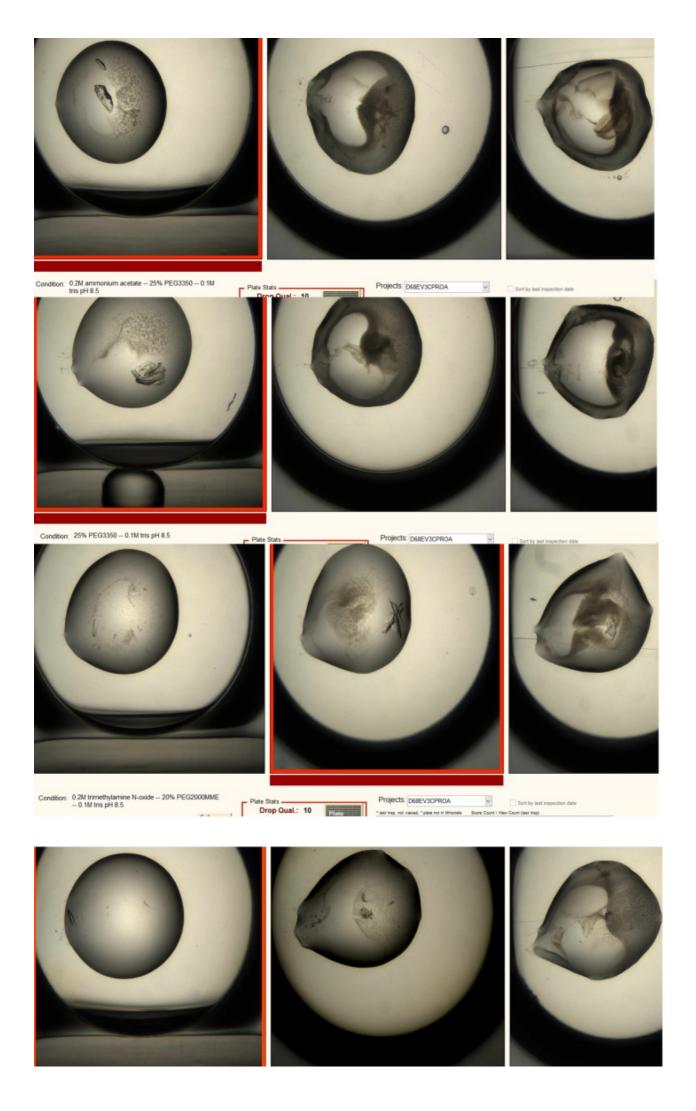
EVD68 pool concentrates ok to 8.2 (786 uM) 16.7 mg mL just over 1.2 mL per run so about 20 mg can do 6 runs in total so about 120 mg from 2 L or 60 mg/L final Did three runs

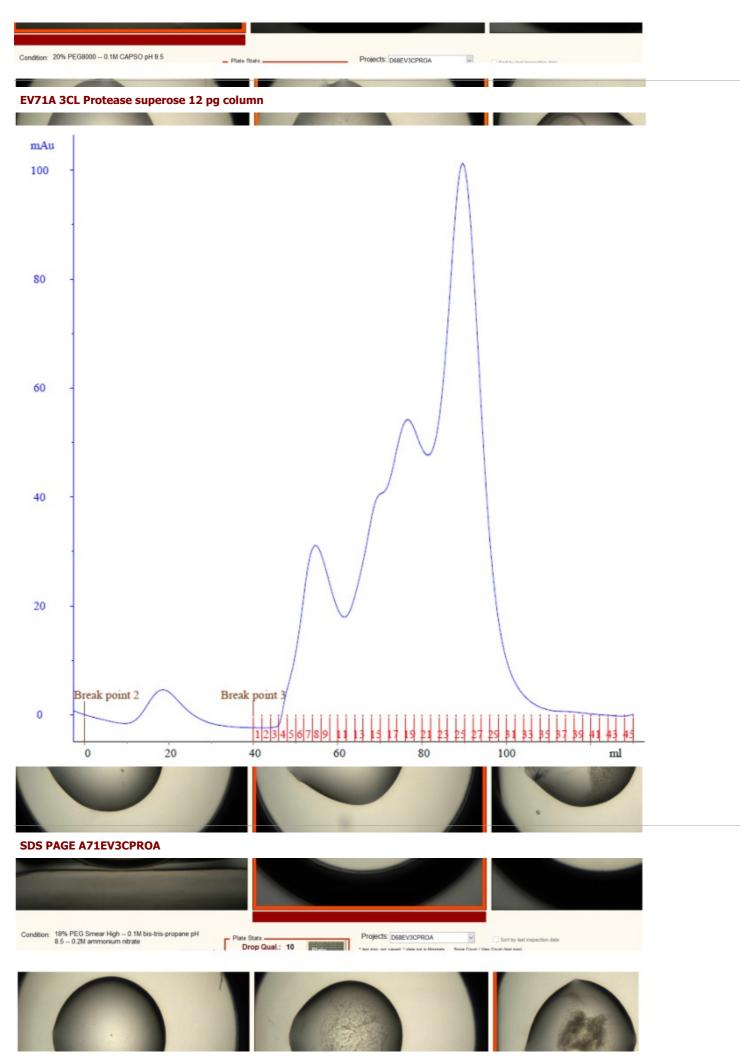
Mass-Spec shows MW 21283.21 Da observed versus 21283.3 Da expected

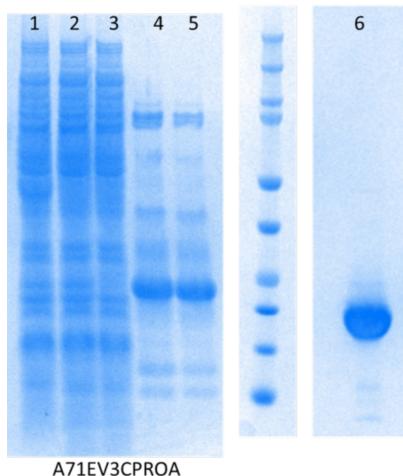
D68EV3CPROA-p001 1 mM 31 x 50 uL aliquots after making plates 300 nL drops in

CI084721 HCS CI084722 BCS CI084723 LFS CI084724 MORPHEUS CI084725 JCSG CI084726 HIN

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1 = Lysate

2 = Soluble fraction

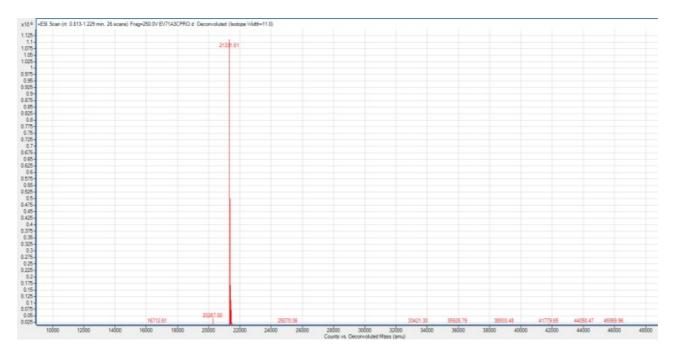
3 = Flow through

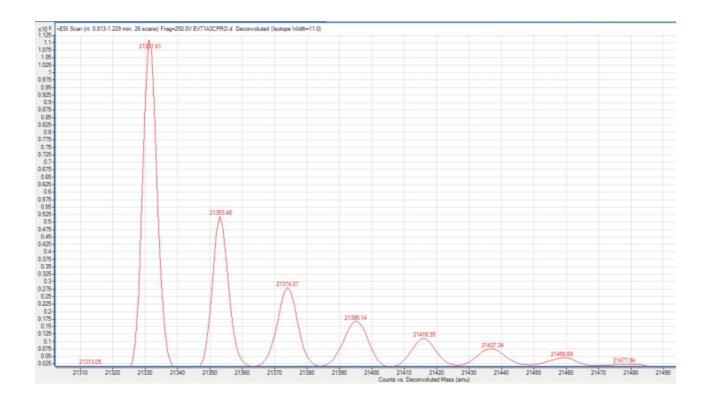
4 = IMAC fraction 1

5 = IMAC fraction 2

6 = Final pool after SEC

## A71EV3CPROA-p001 MS confirmation Z:\Agilent\_SGC\_QTOF\Rod\221124\_MS424C





#### **EVD71A 3CL Protease**

Took peak centered around 90 mL and concentrated as much as possible did a total of 4 runs Final yield after much concentrating is 2mL at A280 of 3.4 (341 uM) 7.3 mg/mL

Mass-Spec shows MW 21331.61 Da observed versus 21331.5 Da expected

A71EV3CPROA-p001 0.34 mM 55 x 50 uL aliquots after making plates 300 nL drops in

CI084990 LFS6 CI084991 BCS CI084992 MORPHEUS CI084993 HIN3 CI084994 JCSG7 CI084995 HCS3

Difficulty in cocentrating to 1mM in base buffer so I took a 50 uL aliquot and added either 0.5 mL of 50 mM Bicine pH 8.5, 500 mM NaCl, 5 % Glycerol, 0.5 mM TCEP or

0.5 mL of 50 mM MES pH 6.5, 500 mM NaCl, 5 % Glycerol, 0.5 mM TCEP

Added to 0.5 mL 10000 MWCO cocentrator and reconcentrated

MES one would not go beyond original concentration of 0.34 mM Bicine concentrated nicely to 1 mM

Thawed several more aliquots and repeated at scale to get enough to repeat original coarse screen plates

Buffer of protein now 10 mM Bicine pH 8.5, 500 mM NaCl, 5 % Glycerol, 0.5 mM TCEP and protein at 1 mM (21.3 mg/mL)

CI084900 BCS CI084901 LFS6 CI084902 HIN3 CI084903 JCSG CI084904 HCS3

## After 4 days clear xtals

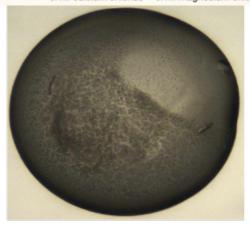
Condition: 30% PEG Smear Low -- 0.1M citrate/phosphate pH 5.5



Condition: 25% PEG Smear Medium -- 0.1M citrate/phosphate pH 5.5



Condition: 22.5% PEG Smear Medium -- 0.1M PIPES pH 7.0 -- 0.1M calcium chloride -- 0.1M magnesium chloride



Condition: 30% PEG4000 - 0.2M magnesium chloride - 0.1M tris pH 8.5

