

Jun 14, 2024

Purification of recombinant Tau Repeat Domain (TauRD) from Escherichia coli

DOI

dx.doi.org/10.17504/protocols.io.x54v9p6p1g3e/v1

Patricia Yuste-Checa¹, F Ulrich Hartl¹

¹Department of Cellular Biochemistry, Max Planck Institute of Biochemistry

ASAP Collaborative Rese...



Patricia Yuste-Checa

MPI Biochemistry

OPEN ACCESS



DOI: dx.doi.org/10.17504/protocols.io.x54v9p6p1g3e/v1

Protocol Citation: Patricia Yuste-Checa, F Ulrich Hartl 2024. Purification of recombinant Tau Repeat Domain (TauRD) from Escherichia coli. **protocols.io** https://dx.doi.org/10.17504/protocols.io.x54v9p6p1g3e/v1

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: February 12, 2024

Last Modified: June 14, 2024

Protocol Integer ID: 95194

Keywords: ASAPCRN

Funders Acknowledgement: Aligning Science Across

Parkinson's

Grant ID: ASAP-000282



Abstract

This protocol details how to efficiently purify the recombinant Tau repeat domain from Escherichia coli.

Attachments



1.7MB

Guidelines

NOTE: This protocol was optimized for purification of the cysteine-free TauRD (Tau residues 244-371, C291A/P301L/C322A/V337M), but in principle any Tau isoform or mutant could be purified following this method if it is tagged with a His 6 -ubiquitin tag. If cysteines are present, reducing agent should be added to buffers to avoid the formation of disulphide bonds.



Materials

Terrific Broth (TB) media:

A	В
Yeast extract	24 g/L
Tryptone	20 g/L
Glycerol	4 mL/l
KH2PO4	0.017 M
K2HPO4	0.072 M

Lysis buffer:

A	В
PIPES-NaOH pH 6.5	50 mM
NaCl	250 mM
Imidazole	10 mM
β-mercaptoethanol (β-ME)	2 mM

Ni-NTA high salt buffer :

A	В
PIPES-NaOH pH 6.5	50 mM
NaCl	500 mM
lmidazole	10 mM
β-ΜΕ	2 mM

Ni-NTA wash buffer:

	A	В
Г	PIPES-NaOH pH 6.5	50 mM
Г	NaCl	250 mM
Г	Imidazole	50 mM
Г	β-МЕ	2 mM

Ni-NTA elution buffer:

A	В
PIPES-NaOH pH 6.5	50 mM
NaCl	50mM
Imidazole	250 mM
β-ΜΕ	2 mM

PIPES buffer or Cation exchange Buffer A:



A	В
PIPES-NaOH pH 6.5	50 mM
β-ΜΕ	2 mM

Cation exchange Buffer B:

	A	В
Г	PIPES-NaOH pH 6.5	50 mM
Г	NaCl	1 M
	β-МЕ	2 mM



TauRD expression

1d 4h 37m 45s

- 1 Thaw RbCl-competent Escherichia coli Bl21 cells (DE3) & On ice.
- Add Δ 1 μL of pHUE-TauRD plasmid (His 6 -ubiquitin-TauRD) and incubate 00:30:00



30m

3 Heat shock 00:00:45 at \$\mathbb{8} 42 \cdot C\$.

45s

Incubate On ice 00:02:00, then add $4850 \, \mu L$ Lysogeny broth (LB) or Super Optimal broth with Catabolite repression (SOC) medium.

2m

5 Shake for 5 01:00:00 at \$ 37 °C.

1h

6 Centrifuge for 60 00:05:00 at 60 3000 x g and remove most of the supernatant.

5m

Resuspend the pellet with the remaining supernatant and plate the bacteria on LB/Ampicillin agar plates and incubate Overnight at 37 °C.

8h

Prepare preculture: Scrap all colonies with the scraper and inoculate 25 mL - 50 mL LB/Ampicillin. Shake at 37 °C for 4- 60 06:00:00 .

6h

9 Measure OD_{600} of the preculture and inoculate two flasks with $\boxed{\bot}$ 1 L of TB media each to an OD_{600} = 0.05.

4h

10 Shake flasks at 37 °C until approx. OD₆₀₀ = 0.5-0.8. (2 -) 04:00:00)

71



- 11 Add isopropyl β-D-1-thiogalactopyranoside (IPTG) at final concentration of [M] 0.4 millimolar (mM) .
 - 12 Shake flasks Novernight at \$37 °C. 8h
 - 13 Centrifuge bacterial culture at 4000 rpm for 01:00:00 Discard supernatant. Cell 1h
 - pellets can be stored at 4 -80 °C.

Ni-NTA chromatography

1h 32m

69

- 14 Resuspend the cell pellets with lysis buffer (\bot 50 mL lysis buffer/ \bot 2 L bacteria culture) supplemented with Complete EDTA-free protease inhibitor cocktail (Merck) and benzonase.
- 15 Add A 1 undetermined lysozyme and incubate gently shaking for 00:30:00 at 4°C.

30m

16 Sonicate lysate On ice , 5 cycles 00:00:30 ON, 00:01:30 OFF.

2m

17 Centrifuge lysate at 4 °C .

- 1h
- 18 Prepare Ni-NTA column by transferring 🚨 10 mL Ni-NTA resin slurry to a column (🚨 5 mL column bed). Wash Ni-NTA column with 10 column volumes (CV, A 50 mL) water and equilibrate with 10 CV (\perp 50 mL) lysis buffer.

- 19 Load lysate supernatant to Ni-NTA column.
- 20 Wash Ni-NTA column with 10 CV (\$\rm 50 mL \) high salt buffer and 10 CV (\$\rm 50 mL \) wash buffer.



21 Elute His 6 -ubiquitin-TauRD with \(\begin{aligned} \Lambda 20 \text{ mL} \end{aligned} elution buffer and collect everything.

Note

Prepacked or any other Ni column can be used for His 6 -ubiquitin-TauRD purification.

His 6 -ubiquitin cleavage

8h

- 22 Dilute eluted protein 1:5 with PIPES buffer to reduce the amount of salt (🚨 20 mL eluted protein + 4 80 mL PIPES buffer).
- 23 Incubate diluted His 6 -ubiquitin-TauRD protein with 4 0.5 mg Usp2 ubiquitin protease at 4 °C Overnight





Note

Dilution of eluted protein is not needed for protease cleavage but recommended to avoid protein precipitation during incubation. Salt dilution is needed for the next purification step, cation exchange chromatography.

Cation exchange chromatography

- 24 Load the cleavage mixture onto a Source S cation exchange column previously equilibrated with cation exchange buffer A.
- 25 Wash the column with 5 CV of cation exchange Buffer A.



26 Elute TauRD with a 0- [M] 500 millimolar (mM) linear NaCl gradient in [M] 50 millimolar (mM) PIPES-NaOH 6.5 , [M] 2 millimolar (mM) β-ME (0-50% gradient from cation exchange



buffer A to cation exchange buffer B over 10 CV).

27 Analyze eluted fraction by SDS-PAGE and Coomassie blue staining.



Size exclusion chromatography

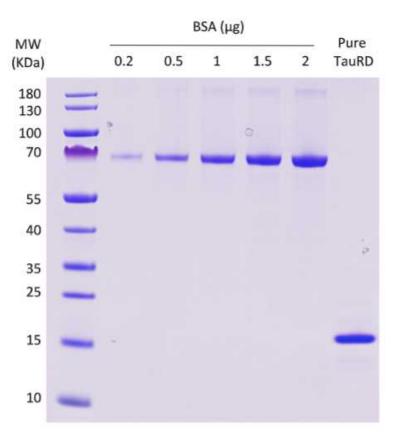
- 28 Load TauRD-containing fractions onto a Superdex-75 column previously equilibrated with PBS.
- Analyze eluted fraction by SDS-PAGE and Coomassie blue staining.



Pool fractions containing TauRD, aliquot and flash-freeze in liquid nitrogen for storage at $-80 \, ^{\circ}\text{C}$.

Note

- Due to the intrinsic disordered nature of Tau protein, the apparent size observed by size exclusion chromatography is larger than expected.
- TauRD protein contains few Tyr and Trp residues, and therefore the determination of pure protein concentration by OD _{280nm} is not reliable. We recommend to determine protein concentration of purified TauRD by BCA assay or Coomassie blue staining including a BSA standard curve. Rapid commercial Coomassie protein stain buffers are not recommended since sensitivity for the TauRD is very low. Standard Coomassie blue staining buffer should be used.



Note

- For TauRD thiol labelling, the mutation I260C could be introduced in the cysteine-free TauRD. The same purification protocol can be followed but [M] 1 millimolar (mM) tris(2-carboxyethyl)phosphine (TCEP) should be added to the size exclusion chromatography buffer in order to prevent the formation of disulfide bonds.
- Approximate yield: from 🚨 2 L of bacterial culture around 🚨 8 mg of pure TauRD are obtained.