

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/5/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Phenol extraction | Signature: |

SOP: Phenol extraction

Application:

This protocol enables the extraction of proteins from environmental samples. Extraction protocol is applicable also for samples containing high amounts of impurities, e.g. humic substances.

Remarks:

- Pay attention while working with phenol. It is toxic!
- Dispose contaminated materials and liquid waste into special containers. Check sucrose solution for any contaminations (flocculation). Urea buffer could crystallize during storage at 4°C. Hence, stir before usage.
- All incubation steps at -20 °C could be extended overnight in order to make a break.

Chemicals

Table 1: Used chemicals. Named manufacturer as well as order numbers are not mandatory and can be replaced by others with equal quality.

| Chemicals | Manufacturer | Order Numbers | Storage place |
|---------------------------------------|----------------------|---------------|---------------|
| Ammonium acetate | Roth Art. | 7869.1 | |
| 1,4-Dithiothreitol (DTT) | Carl Roth | 6908.2 | |
| Methanol, ≥ 99.9% (toxic ☠☠☠) | Carl Roth | T909.1 | |
| Phenol (toxic ☠☠☠) | Merck | 8.22296.1000 | |
| Sucrose | Merck | 1.07687.1000 | |
| Thiourea (toxic ☠☠☠) | Sigma-Aldrich | T8656 | |
| Urea | AppliChem | A1049.0500 | |
| 0.5mm Zirconia/ Silica Beads | BioSpec Products Inc | 1179105z | |

Devices

Table 2: Used devices. Devices and manufacturers are not mandatory and can be replaced by others with equal functionality.

| Device | Name | Manufacturer |
|-----------------|-----------------|--|
| Ball mill | FastPrep-96 | MP Biomedicals (Eschwege, Deutschland) |
| Distilled water | Millipore Q-POD | Merck, Darmstadt, Germany |
| Centrifuge | Micro Star 17 R | VWR International, Darmstadt, Germany |
| Centrifuge | Avanti J | Beckman Coulter, Brea, USA |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/5/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | Phenol extraction | Date: |
| Version: | 1.0.0. | | Signature: |

Buffer preparation

- 1,000% Phenol Solution: 10 g phenol (**toxic** ☠☠☠)
1 mL dest. water
(storage at 4 °C under the fume hood!)
- 0.1 M Ammonium Acetate in Methanol: 0.7708 g ammonium acetate
Fill up to 100 mL with methanol (storage at -20 °C)
- 2 M Sucrose: 68.46 g sucrose
Fill up to 100 mL with dest. water (storage at 4 °C)
- 1 M Sucrose / Saccharose Solution: 34.23 g Sucrose
Fill up to 100 mL with dest. water (storage at 4 °C)
- Urea Buffer: 8.41 g urea (7 M)
3.04 g thiourea (2 M) (**toxic** ☠☠☠)
0.2 g DTT (0.01 g/mL)
Fill up to 20 mL with dest. water
(storage at 4 °C)

Execution:

FASTPREP

- Weight out 5 g silica-beads into a 50 ml reaction tube
- Add 2 g resp. 2 mL sample
- Add 2 mL 2 M sucrose solution
- Add 3.5 mL phenol
- Close reaction tube (e.g. you may add also wrap the cap with parafilm)
- Place reaction tubes into the FASTPREP
- Cell lysis at 1,800 rpm for 5 min
- 10 min centrifugation with 10,000 g and RT
- Take upper phenol phase and collect it in a new 50 mL reaction tube
- Add same volume 1 M sucrose solution
- Shake (10 min, 60- 120 rpm, RT)
- Centrifuge (10 min, RT, 10,000 xg)
- Transfer upper phenol phase into a new 50 mL reaction tube
- Add the four-fold volume of icecold (4v/v) ammonium acetate in methanol
- Incubate for 20 min at -20 °C,

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/5/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | Phenol extraction | Date: |
| Version: | 1.0.0. | | Signature: |

- Centrifuge (10 min, 10,000 xg, 4 °C)
- Add the four-fold volume of icecold (4v/v) ammonium acetate in methanol
- Incubate for 20 min at -20 °C,
- Centrifuge (10 min, 10,000 xg, 4 °C)
- Discard supernatant

Ball mill (small 2 ml reaction tubes)

- Weight out 1 g silica-beads into a 2 ml reaction tube (**five times**)
- Add 400 mg/ μL sample
- Add 400 μL 2 M sucrose solution
- Add 700 μL phenol
- Place reaction tubes into the ball mill
- Cell lysis at 30 hertz for 10 min
- 10 min centrifugation with 10,000 g and RT
- Take upper phenol phase and pool them in a 15 mL reaction tube
- Add same volume 1 M sucrose solution
- Shake (10 min, 60- 120 rpm, RT)
- Centrifuge (10 min, RT, 10,000 xg)
- Transfer upper phenol phase into a new 15 mL reaction tube
- Add the four-fold volume of icecold (4v/v) ammonium acetate in methanol
- Incubate for 20 min at -20 °C,
- Centrifuge (10 min, 10,000 xg, 4 °C)
- Discard supernatant
- Add the four-fold volume of icecold (4v/v) ammonium acetate in methanol
- Incubate for 20 min at -20 °C,
- Centrifuge (10 min, 10,000 xg, 4 °C)
- Discard supernatant

Dissolve sample

- Dry pellet
- Dissolve pellet in e.g. 1 mL urea buffer and 0.1 g Silica Beads
- 2 min ball mill/ FASTPREP
- 5 min centrifugation with 10,000 xg and RT
- transfer supernatant into a new 2 mL reaction tube
- store at -20 °C

Encloser:

- not applicable

Abbreviations:

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/5/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Phenol extraction | Signature: |

| | |
|-------------|------------------|
| dest. water | deionized water |
| DTT | dithiothreitol |
| M | molare |
| RT | room temperature |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/25/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

6.9 SOP FASP Digest

Application:

Sample preparation of cell cultures for LC-MS/MS measurement, according to following references [1,2].

1. Wisniewski, J. R., Zougman, A., Nagaraj, N., and Mann, M. 2009. Universal sample preparation method for proteome analysis. *Nature Methods*, 6(5):359–362
2. Wiśniewski, J.R., Hein M.Y., Cox J., Mann M. *Mol Cell Proteomics*. 2014 Dec;13(12):3497-506. A "proteomic ruler" for protein copy number and concentration estimation without spike-in standards.

Remarks:

- The method provides protein digest that are free from nucleic acids and other cell components
- The method can be applied to samples containing high concentrations of detergents
- There is no precipitation and the concentration of sample is kept high
- In a single filter device 0.2-200 µg of total protein can be processed. Thus, FASP can be used upstream of separations of peptides such as OFFGEL and 2D- LC
- The yield and purity of peptides can be monitored by UV-spectrometry allowing QC of the digest
- Do not mix up the different urea buffers!

Chemicals

Table 1: Used chemicals. Named manufacturer as well as order numbers are not mandatory and can be replaced by others with equal quality.

| Chemicals | Manufacturer | Order Numbers | Storage place |
|--|------------------------|---------------|---------------|
| Acetic Acid ≥ 96% (corrosive!!!) | Carl Roth | T179.2 | |
| BSA (control) | Sigma-Aldrich | A3912 | |
| 1,4-Dithiothreitol (DTT) | Carl Roth | 6908.2 | |
| Methanol, ≥ 99.9% (toxic ☠☠☠) | Carl Roth | T909.1 | |
| Thiourea (toxic ☠☠☠) | Sigma-Aldrich | T8656 | |
| Urea | AppliChem | A1049.0500 | |
| Centrifugal Filter Units (MWCO 10 kDa) | Pall Nanosep 10K Omega | OD010C35 | |
| Acetonitrile (MS/MS grade) | Fluka | 34967 | |
| Iodacetamide | AppliChem, | A1666.0025 | |
| Ammoniumbicarbonat ultra >99.5% | Fluka | 09830 | |
| Trypsin, Premium grade | Serva | 111095 | |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/25/2019 |  6.9 FASP Protocol | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

| | | | |
|-----------------------------|-------------------------------|---------------|--|
| Formic acid 97% | Fluka | 5602 | |
| Trifluoressigsäure | Sigma Life Science | 73645 | |
| MilliQ | MilliQ, LC-MS Grade or MilliQ | | |
| Ethanol 96% (not denatured) | Merck | 1,009,832,511 | |

Devices

Table 2: Used devices. Devices and manufacturers are not mandatory and can be replaced by others with equal functionality.

| Device | Name | Manufacturer |
|-----------------|---------------------------------|---------------------------------------|
| Speed Vac | Digital Series SpeedVac SPD121P | Thermo Scientific, Waltham, USA |
| Distilled water | Millipore Q-POD | Merck, Darmstadt, Germany |
| Centrifuge | Micro Star 17 R | VWR International, Darmstadt, Germany |
| Centrifuge | Avanti J | Beckman Coulter, Brea, USA |

Buffer preparation

| | |
|-----------------------------|---|
| Urea Buffer: | 8.41 g urea (7 M) |
| | 3.04 g thiourea (2 M) (toxic ☠☠☠) |
| | 0.2 g DTT (0.01 g/mL) |
| | Fill up to 20 mL with dest. water |
| | (storage at 4 °C) |
| Ammonium bicarbonate buffer | 98.80 mg NH ₄ HCO ₃ (ABC) |
| 50 mM, pH 7.8 | 25 ml dest. water |
| | Prepare the buffer immediately before use. |
| | Keep it at room temperature until use. |
| 5 M NaOH | 20 g NaOH |
| | 100 ml dest. water |
| 0.1 M Tris-HCl pH 8.5 | 15.7 g Tris-HCl |
| | 800 mL dest. water |
| | Adjust pH to 8.5 by adding 5 M NaOH |
| | Fill up to 1 L |
| 8 M Urea buffer | 4.8 g Urea |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/25/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | 6.9 FASP Protocol | Signature: |

10 ml 0.1 M Tris-HCl pH 8.5

Fill up to 10 ml dest. water

0.40 M DTT Stock solution

24.68 mg DTT (M=154.25 g/mol)

400 µl 50 mM NH₄HCO₃

Prepare immediately before use

(store in the dark)

40 mM DTT Working Solution

Dilute 0.4 M DTT Stock solution 10fold with 8 M urea buffer

Immediately before use

(store in the dark)

0.55 M IAA Stock Solution

40.7 mg IAA (M=184.96 g/mol)

400 µl 50 mM NH₄HCO₃

Prepare immediately before use

(store in the dark)

55 mM IAA Working Solution

Dilute 0.55 M IAA Stock solution 10fold with 8 M urea buffer

Prepare immediately before use

(store in the dark)

Trypsin (25 µg/25 µl)

resuspend lyophilized Trypsin (Serva) in 25 µl 50 mM acetic

acid c = 1 µg/µl

optional: 1 mM (CaCl₂)_{aq}

Digestion buffer

1 ml 50 mM ABC buffer + 5% Acetonitrile (50 µl)

Execution:

A. FASP-DIGEST

- Add sample on the filter in maximum 200 µL of **urea buffer** vortex and incubate for 5 min on a thermomixer (recommended 100 µg)
- Transfer the protein solution to the filter unit (min vol. 50 µL / max vol. 500 µL)
- Centrifuge, 10,000 xg, 10 min at RT (**in case of remaining liquid on top of the filter extend centrifugation time!**)
- Add 200 µL of **urea buffer**
- Centrifuge, 10,000 xg, 10 min at RT (**in case of remaining liquid on top of the filter extend centrifugation time!**)

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/25/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | 6.9 FASP Protocol | Date: |
| Version: | 1.0.0. | | Signature: |

- Add 100 µL **DTT solution** to the filter unit, mix for 1 min at 800 rpm using a thermomixer, incubate at 56°C for 20 min with gentle agitation (300 rpm)
- Centrifuge, 10,000 xg, 5 min at RT,
- Add 100 µL **IAA solution** to the filter unit, mix for 1 min at 800 rpm using a thermomixer, Incubate for 20 min in the dark at RT
- Centrifuge, 10,000 xg, 5 min at RT
- Wash 3x with 100 µL **urea buffer**: incubate for 2 min at RT on a thermomixer, centrifuge for 5 min
- Wash 3x with 100 µL 50 mM **ABC buffer**: incubate for 2 min at RT on a thermomixer, centrifuge for 5 min
- Discard flow-through

Tryptic Digest

- Prepare enzyme solution (Trypsin in 50mM ABC buffer; 200 µL/sample recommended)
 - **Recommended enzyme:substrate ratio (E:S):** 1:100 for Trypsin
- Add 200 µl enzyme solution
- Incubate at 37 °C for 2h with gentle agitation (350 rpm)

Peptide Extraction

- Centrifuge, 10,000 xg, 5 min at RT, **DO NOT discard the flow-through**
- Add 50 µL **digestion buffer** (50mM ABC buffer + 5% Acetonitrile) to the filter unit
- Centrifuge, 10,000 xg, 5 min at RT, **DO NOT discard the flow-through**
- Add 50 µL **LC-MS grade dest. water** to the filter unit
- Centrifuge, 10,000 xg, 5 min at RT, **DO NOT discard the flow-through**
- Discard Filter Unit (Protein is in flow-through!)
- a.) acidify samples with TFA to same concentration as in the loading buffer of the MS and transfer the sample into an HPLC vial
- b.) as alternative you may dry the digest in a SpeedVac and store it at -20°C

For further preparation see protocols for MS measurements.

Encloser:

- NONE

Abbreviations:

| | |
|-------------|----------------------------------|
| BSA | bovine serum albumin |
| dest. water | deionized water |
| DMEM | Dulbecco`s modified eagle medium |
| DTT | dithiothreitol |
| FCS | fetal calf serum |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 10/25/2019 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | 6.9 FASP Protocol | Signature: |

M molar
IAA iodoacetamide
RT room temperature

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | 17/10/2018 | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 7.0.0. | Protein quantification with amido black | Signature: |

SOP: Protein quantification with amido black

Application:

The amido black assay enables the protein quantification in environmental samples. The protocol is compatible with urea buffer, other detergents and contaminants (see also the publications [1,2]).

1. Popov, N., Schmitt, M., Schulzeck, S., and Matthies, H. 1975. Eine störungsfreie Mikromethode zur Bestimmung des Proteingehaltes in Gewebehomogenaten. *Acta Biologica et Medica Germanica*, 34:1441–1446.
2. Schweikl, H., Klein, U., Schindlbeck, M., and Wieczorek, H. 1989. A vacuolar-type atpase, partially purified from potassium transporting plasma membranes of tobacco hornworm midgut. *Journal of Biological Chemistry*, 264(19):11136–11142.

Remarks:

- Amido black crosslinks proteins and dye molecules, causing their precipitation.
- Pay attention to your pellet during washing. Then you dissolve your pellet check whether the complete pellet is dissolved.
- Protein for the standard curve has to be dissolve into the same buffer as the sample.
- As blank use 0.1 M sodium hydroxide.
- For absorption above >2.0 or outside the calibration curve the sample has to be diluted with sodium hydroxide.

Chemicals

Table 1: Used chemicals. Named manufacturer as well as order numbers are not mandatory and can be replaced by others with equal quality.

| Chemicals | Manufacturer | Order Numbers | Storage place |
|---|---------------|---------------|---------------|
| Acetic Acid ≥ 96% (corrosive!!!) | Carl Roth | T179.2 | |
| BSA | Sigma-Aldrich | A3912 | |
| 1,4-Dithiothreitol (DTT) | Carl Roth | 6908.2 | |
| Methanol, ≥ 99,9% (toxic ☠☠☠) | Carl Roth | T909.1 | |
| Naphtol Blue Black 80 % (m/v) Dye Content (Amido Black) | Sigma-Aldrich | 195243 | |
| Sodium hydroxide, NaOH ≥ 98% (corrosive!!!) | Carl Roth | P031.1 | |
| Thiourea (toxic ☠☠☠) | Sigma-Aldrich | T8656 | |
| Urea | AppliChem | A1049.0500 | |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | 17/10/2018 | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 7.0.0. | Protein quantification with amido black | Signature: |

Devices

Table 2: Used devices. Devices and manufacturers are not mandatory and can be replaced by others with equal functionality.

| Device | Name | Manufacturer |
|-----------------|---|--|
| Photometer | Spectrophotometer Genesys 10S UV Vis | VWR International, Darmstadt, Germany |
| Distilled water | Millipore Q-POD | Merck, Darmstadt, Germany |
| Centrifuge | Micro Star 17 R | VWR International, Darmstadt, Germany |
| Centrifuge | Avanti J | Beckman Coulter, Brea, USA |

Buffer preparation

| | |
|-----------------------|---|
| Urea Buffer: | 8.41 g urea (7 M) 3.04 g thiourea (2 M) (toxic ☠☠☠) 0.2 g DTT (0.01 g/mL) Fill up to 20 mL with distilled water (storage at 4 °C) |
| Wash solution: | 180 mL methanol (toxic ☠☠☠) 20 mL acetic acid (storage at RT) |
| Dye solution: | 26 mg amido black Add 100 mL wash solution (storage at RT) |
| 0.1 M Sodium hydroxid | 0.4 g sodium hydroxyden Fill to 100 mL with distilled water |

Execution:

Measure the standard curve for BSA as triplicates:

- 0.0 µg/µL (just sample buffer)
- 0.2 µg/µL
- 0.4 µg/µL
- 0.6 µg/µL
- 0.8 µg/µL
- 1.0 µg/µL

| | | | |
|----------------------------|-------------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | 17/10/2018 | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 7.0.0. | Protein quantification with amido black | Signature: |

Prepare and measure the sample at least as triplicates. For samples with an expected high concentration use 1:5 dilutions (4 parts buffer and 1 part sample). For example biogas plant samples and waste water treatment plant samples.

- put 50 μ L sample/ standard into a 1.5 ml reaction tube
- add 300 μ l dye solution, vortex and centrifuge (16,400 g, 5 min, RT)
- Remove supernatant
- Add 500 μ L Washing solution, vortex and centrifuge (16,400 g, 5 min, RT)
- Remove supernatant
- Add 500 μ L Washing solution, vortex and centrifuge (16,400 g, 5 min, RT)
- Remove supernatant
- Dissolve pellet in 1 mL 0.1 M sodium hydroxide
- Place into a cuvette
- Measure at 615 nm wavelength
- Calculate sample concentration from standard curve

Encloser:

- Excel-Sheet

Abbreviations:

| | |
|-------------|----------------------|
| BSA | bovine serum albumin |
| dest. water | deionized water |
| DTT | dithiothreitol |
| M | molare |
| RT | room temperature |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

SOP: SDS-PAGE

Application:

SDS-PAGE enables the protein separation for quality control. Protocol is according to *Laemmli et al. [1]*.

1. Laemmli, U. K. (1970). "Cleavage of structural proteins during the assembly of the head of bacteriophage T4." *Nature* **227**(5259): 680-685.

Remarks:

- Acrylamide and mercaptoethanol are toxic. Do all steps under a fume hood and wear glasses.
- For pH adjustment of Tris-HCl-solutions different HCl concentrations could be used. However, to low concentrations result in high volumes, which may exceed the maximum volume.
- Check whether you want to work with 1 mm or 1.5 mm thick gels and use corresponding glass plates, combs and gel volumes. The current during electrophoresis could be set below the maximum current. Also duration of fixation or dyeing could be extended.
- Note down LOT number of the respective protein standard used since LOT specific molecular weights may vary compared to the LOT independent molecular weights (see figure below)
- The maximum/optimum loading volume per pocket for 1 mm gels is 30 µL/25 µL, 45 µL/40 µL for 1.5 mm gels, respectively.

Chemicals

Table 1: Used chemicals. Named manufacturer as well as order numbers are not mandatory and can be replaced by others with equal quality.

| Chemicals | Manufacturer | Order Numbers | Storage place |
|------------------------------------|---|-----------------------|---------------|
| Acetic Acid ≥ 96% | Carl Roth | T179.2 | |
| Acetone, ≥ 99%, | VWR International | 20063.296 | |
| Acrylamide solution 30% (toxic ☠☠) | Serva | 10688.01 | |
| Ammonium sulfate | Carl Roth | 3746.3 | |
| Ammonium persulfate (APS) | Merck | 1.01201.0500 | |
| Bromophenol blue | GE Healthcare | 17-1329-01 | |
| Coomassie BB G 250 | AppliChem | A3484.0100 | |
| Ethanol (70%) | Carl Roth | T913.3 | |
| Glycerol | Carl Roth | 3783.1 | |
| Glycine | VWR International | 444495D | |
| Hydrochloric acid (37%) | VWR International | 20252.420 | |
| Isobutanol | AppliChem | A1150.1000 | |
| Mercaptoethanol (toxic ☠☠☠) | Sigma | M3148 | |
| Methanol ≥ 99.9% (toxic ☠☠☠) | Carl Roth | T909.1 | |
| Protein standard | Thermo Scientific PageRuler Prestained | Protein Ladder #26616 | |
| Phosphoric acid ≥ 85% | Carl Roth | 6366.2 | |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

| | | | |
|---|-----------|------------|--|
| SDS (sodium dodecyl sulfate, (toxic ) | AppliChem | A2572.0250 | |
| TEMED | Carl Roth | 2367.1 | |
| Tris | AppliChem | A2264.1000 | |

Devices

Table 2: Used devices. Devices and manufacturers are not mandatory and can be replaced by others with equal functionality.

| Device | Name | Manufacturer |
|-------------------------|---------------------------|---------------------------------------|
| Electrophoresis chamber | Mini-Protean Tetra System | BioRad (Hercules, USA) |
| Power supply | PowerPac Basic | BioRad (Hercules, USA) |
| Distilled water | Millipore Q-POD | Merck, Darmstadt, Germany |
| Centrifuge | Micro Star 17 R | VWR International, Darmstadt, Germany |
| Centrifuge | Avanti J | Beckman Coulter, Brea, USA |

Buffer preparation

SDS-running buffer (5X):

- 15 g tris
- 72 g glycine
- 5 g SDS
- Fill to 1 L with dest. water
- (Store at 4 °C)
- Dilute with dest. water before usage

SDS-solution (0.1 g/mL):

- 1 g SDS (toxic )
- Fill to 10 mL with dest. water
- (Store at RT)

1.5 M Tris-HCl, pH 8.8:

- 100 mL dest. water
- 90.75 g Tris
- Adjust pH 8,8 with 4 M HCl (with 6M HCl about 41 ml for 500 mL buffer)
- Fill to 500 mL with dest water Note final pH value on the bottle
- (Store at 4 °C)

0.5 M Tris-HCl, pH 6.8:

- 100 mL dest. water
- 15 g Tris
- Adjust pH 6.8 with 1 M HCl

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | SDS-PAGE | Date: |
| Version: | 1.0.0. | | Signature: |

Fill to 250 mL with dest. water
 Note final pH value on the bottle
 (store at 4 °C)

Bromophenol blue-solution (5 mg/ml): 100 mL dest. water
 0.5 g bromophenol blue
 (Store at RT)

SDS-sample buffer: 50 mL dest. water
 12.5 mL 0.5 M Tris-HCl, pH 6.8
 10 mL glycerol
 20 mL SDS-solution (0.1 g/mL)
 5 mL mercaptoethanol (**toxic** ☠☠☠, fume hood)
 1 mL bromophenol blue-solution (5 mg/ml)
 (Store at 4 °C)

APS-solution (0.1 g/mL): 10 mL dest. water
 1 g APS
 Prepare aliquots à 1 mL
 (Store at -20 °C)

Polyacrylamide solution (30%): Buy ready to use (**toxic** ☠☠☠, fume hood)
 (Store at 4 °C)

Water-saturated butanol: 100 mL dest. water
 100 mL butanol
 (Top phase is butanol)

Fixation solution (1 L): 329 mL dest. water
 571 mL ethanol (70%)
 100 mL acetic acid (100%)

Coomassie Brilliant Blue Stock Solution: 5 g Coomassie Brilliant Blue G-250
 100 mL dest. water
 (store at RT)

Colloidale Coomassie Stock Solution: 50 g ammonium sulfate
 484 mL dest. water
 6 mL ortho-phosphoric acid (85%)
 10 mL Coomassie Brilliant Blue Stock solution

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

(Store at RT, acid cupboard)

Colloidale Coomassie Dye Solution: 200 mL Colloidale Coomassie Stock Solution
50 mL methanol
(Store at RT, solvent cupboard)

Execution:

- Clean glass plates and spacer with ethanol and a fuzz free wipe
- Insert both into the clips. Proof whether the plates terminate flat on the ground
- Assemble gel casting device
- Prepare **12% separation gel**

| 1 mm Separation Gel [ml] | 1 Gel | 2 Gels | 4 Gels | 6 Gels | 8 Gels |
|--------------------------|-------------|--------------|--------------|--------------|--------------|
| VE-Water | 2.23 | 4.47 | 8.93 | 13.4 | 17.87 |
| 1.5 M Tris-HCl pH 8.8 | 1.67 | 3.33 | 6.67 | 10 | 13.33 |
| SDS (10%) | 0.07 | 0.13 | 0.27 | 0.4 | 0.53 |
| Polyacrylamide | 2.67 | 5.33 | 10.67 | 16 | 21.33 |
| APS | 0.05 | 0.10 | 0.20 | 0.3 | 0.40 |
| TEMED | 0.005 | 0.01 | 0.02 | 0.03 | 0.04 |
| Total volume | 6.69 | 13.38 | 26.75 | 40.13 | 53.51 |

| 1.5 mm Separation Gel [ml] | 1 Gel | 2 Gels | 4 Gels | 6 Gels | 8 Gels |
|----------------------------|--------------|--------------|--------------|--------------|--------------|
| VE-Water | 3.35 | 6.7 | 13.4 | 20.1 | 26.8 |
| 1.5 M Tris-HCl pH 8.8 | 2.5 | 5 | 10 | 15 | 20 |
| SDS (10%) | 0.1 | 0.2 | 0.4 | 0.6 | 0.8 |
| Polyacrylamide | 4 | 8 | 16 | 24 | 32 |
| APS | 0.075 | 0.15 | 0.3 | 0.45 | 0.6 |
| TEMED | 0.0075 | 0.015 | 0.03 | 0.045 | 0.06 |
| Total volume | 10.04 | 20.07 | 40.13 | 60.20 | 80.26 |

- Overlay liquid gel with water-saturated butanol and let it polymerize for 30 min
- Remove butanol and wash it with dest. water, remove remaining water with a fuzzy free wipe
- Prepare **4% stacking gel**

| 1 mm Stacking Gel [ml] | 1 Gel | 2 Gels | 4 Gels | 6 Gels | 8 Gels |
|------------------------|-------|--------|--------|--------|--------|
| VE-Water | 2.03 | 4.07 | 8.13 | 12.2 | 16.27 |
| 0.5 M Tris-HCl pH 6.8 | 0.83 | 1.67 | 3.33 | 5 | 6.67 |
| SDS (10%) | 0.03 | 0.07 | 0.13 | 0.2 | 0.27 |
| Polyacrylamide | 0.43 | 0.87 | 1.73 | 2.6 | 3.47 |
| Bromophenol blue | 0.013 | 0.03 | 0.05 | 0.08 | 0.11 |
| APS | 0.025 | 0.05 | 0.10 | 0.15 | 0.20 |
| TEMED | 0.005 | 0.01 | 0.02 | 0.03 | 0.04 |

| | | | | |
|----------------------------|--------------|--|---------------------------------------|--|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg | |
| Creator: | Robert Heyer | | Bioprocess Engineering | |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 | |
| Update: | ---- | | 39106 Magdeburg | |
| Department: | BPT | | Date: | |
| Version: | 1.0.0. | SDS-PAGE | Signature: | |

| Total volume | 3.38 | 6.75 | 13.51 | 20.26 | 27.01 |
|--------------------------|--------------|--------------|--------------|---------------|--------------|
| 1.5 mm Stacking Gel [ml] | 1 Gel | 2 Gels | 4 Gels | 6 Gels | 8 Gels |
| VE-Water | 3.05 | 6.1 | 12.2 | 18.3 | 24.4 |
| 0.5 M Tris-HCl pH 6.8 | 1.25 | 2.5 | 5 | 7.5 | 10 |
| SDS (10%) | 0.05 | 0.1 | 0.2 | 0.3 | 0.4 |
| Polyacrylamide | 0.65 | 1.3 | 2.6 | 3.9 | 5.2 |
| Bromophenol blue | 0.02 | 0.04 | 0.08 | 0.12 | 0.16 |
| APS | 0.0375 | 0.75 | 0.15 | 0.025 | 0.3 |
| TEMED | 0.0075 | 0.15 | 0.03 | 0.045 | 0.06 |
| Total volume | 50.58 | 10.13 | 20.23 | 30.345 | 40.46 |

- Add comb airbubble free on the stacking gel (**Pay attention to splashing solution, wear glasses**)
- Remove comb after 30 min polymerization time and wash pockets with dest. water
- Assemble each 2 gels with the spacer outside into the electrophoresis chamber.
- Fill chamber with SDS-running buffer (1x). Remove airbubbles below the gel by pipetting
- Fill space into the chambers also with SDS-running buffer (**1x**)
- Fill 10-20 ml sample into each pocket (30 µl into 1.5 mm gels) and add 2 µL of the protein standard to one pocket (note name of the standard)
- Close the chamber and connect to power supply
- Adjust for each gel 10 mA current until the migration front entered the separation gel and then 20 mA current. Stop short before the migration front has left the gel.
- After disconnecting the power supply remove the gels, as well as fixate and dye them (see also SOP 5.1 Coomassie staining)

Sample preparation:

- Dilute your sample in at least the same amount of SDS-sample buffer
- Shake 5 min at 60 °C and 1.400 rpm on the
- Centrifuge at 16,400 xg and RT for 10 min
- Load 20 µL sample into each pocket

or

- Precipitate 110% of required sample amount
- Add same volume of dest. water to your sample
- Precipitate with fivefold of icecold acetone (100%)
- Incubate at least 1 h or overnight
- Centrifuge at 16,400 xg and RT for 10 min
- Discard supernatant and dry pellet

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | SDS-PAGE | Date: |
| Version: | 1.0.0. | | Signature: |

- Add 22 μL SDS-sample buffer to the dried protein pellet and shake 5 min at 60 °C and 1,400 rpm on the thermomixer \rightarrow adapt buffer volume and amount of precipitated protein to get 100%
- Centrifuge at 16,400 xg and RT for 10 min
- Load 20 μL sample into each pocket

Coomassie Staining

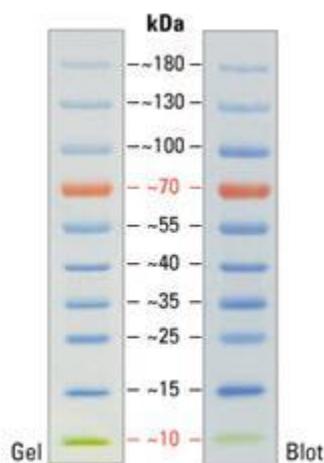
- Place gels after electrophoresis into marked bowls
- Add fixation solution for at least 1 h on a shaker with 20 rpm.
- Wash twice with dest. Water
- Add Colloidale Coomassie Dye Solution overnight at RT on a shaker with 20 rpm.
- Wash with dest. Water

Encloser:

- not applicable

Abbreviations:

| | |
|-------------|------------------------|
| APS | ammonium persulfate |
| dest. water | deionized water |
| DTT | dithiothreitol |
| M | molare |
| RT | room temperature |
| TEMED | tetramethylethyldiamin |
| SDS | sodium dodecyl sulfate |



| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

Figure 1: PageRuler Prestained Protein Ladder #26616, LOT independent molecular weights.

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  Peptide Electrophoresis | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

SOP: Peptide Electrophoresis

Application:

The peptide electrophoresis enables the quality control for the tryptic digestion. See also the publication of *Shägger et al. (2006)* [1].

1. Schägger H., 2006. Tricine-SDS-PAGE. Nat Protoc,1(1):16-22.

Remarks:

Acrylamide, mercaptoethanol and methanol are toxic! It is recommended to execute all steps under a fume hood. It is also advised to wear a pair of safety glasses.

For pH adjustment of the Tris/HCl-solutions different concentrations of HCl can be used. However, it has to be taken into account that a bigger volume is needed, when acids with smaller concentration are used. Do not exceed the maximum volume stated.

Before assembling the plates check the size of the gels plates (1 mm or 1.5 mm), combs and gel volumes.

The voltage of the electrophoresis can be set to values lower than the ones described. Keep in mind that this will lead to an increase in running time.

Important for the success of the peptide gel electrophoresis is a low concentration of SDS in the sample buffer. Therefore, do not forget to dilute the buffer 1:4 before use. Also do not exceed the recommended sample volume of 10 µl. To avoid diffusion of peptides after the run, use a fixation-solution containing methanol.

Gel preparation takes approx. 2h. The electrophoresis runs for about 3h!

Chemicals

Table 1: Used chemicals. Named manufacturer as well as order numbers are not mandatory and can be replaced by others with equal quality.

| Chemicals | Manufacturer | Order Numbers | Storage place |
|-----------------------------------|-------------------|---------------|---------------|
| Acetic Acid ≥ 96% | Carl Roth | T179.2 | |
| Acetone, ≥ 99%, | VWR International | 20063.296 | |
| Acrylamide solution 30% (toxic ☠) | Serva | 10688.01 | |
| Ammonium acetate | Carl Roth | 7869.1 | |
| Ammonium sulfate | Carl Roth | 3746.3 | |
| Ammonium persulfate (APS) | Merck | 1.01201.0500 | |
| Bromophenol blue | GE Healthcare | 17-1329-01 | |
| Coomassie BB G 250 | AppliChem | A3484.0100 | |
| Ethanol (70%) | Carl Roth | T913.3 | |
| Glycerol | Carl Roth | 3783.1 | |
| Glycine | VWR International | 444495D | |

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  Peptide Electrophoresis | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Signature: | |

| | | | |
|---|---|-----------------------|--|
| Hydrochloric acid (37%) | VWR International | 20252.420 | |
| Isobutanol | AppliChem | A1150.1000 | |
| Mercaptoethanol (toxic ☠☠☠) | Sigma | M3148 | |
| Methanol ≥ 99.9% (toxic ☠☠☠) | Carl Roth | T909.1 | |
| Protein standard | Thermo Scientific PageRuler Prestained | Protein Ladder #26616 | |
| Phosphoric acid ≥ 85% | Carl Roth | 6366.2 | |
| SDS (sodium dodecyl sulfate, (toxic ☠☠☠)) | AppliChem | A2572.0250 | |
| TEMED | Carl Roth | 2367.1 | |
| Tris | AppliChem | A2264.1000 | |
| Tricine | Sigma | T0377 | |

Devices

Table 2: Used devices. Devices and manufacturers are not mandatory and can be replaced by others with equal functionality.

| Device | Name | Manufacturer |
|-------------------------|---------------------------|---------------------------------------|
| Electrophoresis chamber | Mini-Protean Tetra System | BioRad (Hercules, USA) |
| Power supply | PowerPac Basic | BioRad (Hercules, USA) |
| Distilled water | Millipore Q-POD | Merck, Darmstadt, Germany |
| Centrifuge | Micro Star 17 R | VWR International, Darmstadt, Germany |
| Centrifuge | Avanti J | Beckman Coulter, Brea, USA |

Buffer preparation

Anode Buffer (pH 8.9) dissolve 12.11 g Tris in 500 mL MilliQ-Water
adjust pH value with 6M HCl (approx. 3 mL)
fill up to 1 L with MilliQ-Water
(store at 4 °C)

APS-Solution (10%) 10 mL MilliQ-Water
1 g APS
prepare aliquots of 1 mL
(store at -20 °C)

Cathode Buffer 12.11 g Tris
17.92 g Tricine
1 g SDS
fill up to 1 L with MilliQ-Water
(store at 4 °C)

Polyacrylamide-Solution (30%) buy ready to use (fume hood, **toxic** ☠☠☠)

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | Peptide Electrophoresis | Date: |
| Version: | 1.0.0. | | Signature: |

Sample Buffer (4x) (store at 4 °C)
6 g SDS (fume hood, toxic ☠☠☠)
3 mL Mercaptoethanol (fume hood, toxic ☠☠☠)
11.90 mL Glycerol
25 mg Coomassie BB G-250
fill up to 50 mL with 150 mM Tris/HCl
(Store at 4 °C)

150 mM Tris/HCl (pH 7.0) dissolve 1.28 g Tris in 50 mL MilliQ-Water
adjust pH value with 6 M HCl
fill up to 100 mL with MilliQ-Water

3 M Tris-Gel Buffer (pH 8.45) 90.86 g Tris
0.75 g SDS
dissolve in 200 mL MilliQ-Water
adjust pH value with 6 M HCl (> 40 mL)
fill up to 250 mL with MilliQ-Water
(Store at 4 °C)

Water-saturated Isobutanol: 100 mL MilliQ-Water
100 mL Isobutanol

Solution Preparation for Coomassie-staining:

Coomassie-Dye-Solution 270 mL MilliQ-Water
30 mL Acetic Acid (100%)
75 mg Coomassie BB G250

Destaining-Solution 450 mL MilliQ-Water
50 mL Acetic Acid (100%)

Fixation-Solution 200 mL MilliQ-Water
250 mL Methanol (100%) (fume hood, toxic ☠☠☠)
50 mL Acetic Acid (100%)
3.854 g Ammonium Acetate
(prepare fresh!, store at RT)
(Methanol **cannot** be replaced by Ethanol, because
Ethanol do not precipitate the peptides)

Execution:

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Peptide Electrophoresis | Signature: |

- Clean glass plates and spacer with ethanol and fuzz-free wipes and clamp them into the casting frames. Make sure the bottom of both plates lines up evenly.
- Assemble gel casting device.
- Prepare gels using the following table (sufficient for 4 gels):

| 1 mm Separation Gel [ml] | Separating gel (16%) | Spacer gel (10%) | Stacking gel (4%) |
|--------------------------|----------------------|------------------|-------------------|
| MilliQ-Water [mL] | 1.51 | 9.84 | 7.30 |
| 3 M Tris-Gel Buffer [mL] | 10 | 10 | 3 |
| Glycerol [mL] | 2.38 | – | – |
| Acrylamide-Solution [mL] | 16 | 10 | 1.6 |
| APS-Solution [mL] | 0.1 | 0.15 | 0.09 |
| TEMED [mL] | 0.01 | 0.015 | 0.009 |
| Total volume [mL] | 30 | 30 | 12 |

- Prepare 16% separating gel. Leave room (1-2 cm) for 10% gel and stacking gel!
- Cast 10% spacer gel on top of the still liquid 16% gel and overlay with water-saturated butanol.
- After polymerization (approx. 30 min) discard butanol and rinse gel surface with MilliQ-Water.
- Remove water with fuzz-free wipe.
- Pour 4% stacking gel on top of the 10% gel.
- Insert comb airbubble-free into the liquid stacking gel (**Beware of splashes: wear safety goggles!**)
- After polymerization (approx. 30 min) remove comb carefully and rinse pockets with MilliQ-Water.
- Assemble each two gels with the bigger plate to the outer side and place everything into the electrophoresis chamber. Fill inner chamber with Cathode Buffer and outer chamber up to the mark with Anode Buffer. Remove airbubbles under the gel with a 10 mL pipette.
- Load 10 µl of prepared sample per pocket and add 2 µl of a prestained protein or peptide standard to an empty pocket (note the name of the standard).
- Close the chamber and connect to power supply.
- Choose a constant voltage of 30 V until the migration front reached the 10% spacer gel. Then switch to 90 V (note the current [mA] at the beginning and at the end). Stop power, when the migration front reached the end of the gel. Avoid leakage.
- After disconnecting the power supply remove the gels. They can now be fixed and dyed (see below) or blotted (see SOP 7.1 for Western Blot).

Sample preparation:

- Use digested samples (see SOP 6.3 for in-gel digest or SOP 6.4 for FASP digest)
- Add 10 µL of the 1:4-diluted sample buffer to the protein pellet and incubate for 60 min at 37°C and 1,400 rpm on a thermomixer.

| | | | |
|----------------------------|--------------|--|---------------------------------------|
| Date: | 11/4/2017 |  | Otto-v.-Guericke-University Magdeburg |
| Creator: | Robert Heyer | | Bioprocess Engineering |
| Person responsible: | Dr. Benndorf | | Universitätsplatz 2 |
| Update: | ---- | | 39106 Magdeburg |
| Department: | BPT | | Date: |
| Version: | 1.0.0. | Peptide Electrophoresis | Signature: |

- Then, centrifuge at 16,400 xg and RT for 10 min
- Load 10 µl of sample per gel pocket.

Coomassie-staining for peptide gels:

- **Exclusively use the fixation-, staining-, and destaining-solutions described in this protocol!**
- Place gels after electrophoresis into marked bowls
- Add fixation solution for at least 1 h on a shaker with 20 rpm.
- Wash twice with dest. Water
- Add Colloidale Coomassie Dye Solution overnight at RT on a shaker with 20 rpm.
- For the destaining process incubate gels for 2x 15-60 min in destaining solution whilst shaking (30 rpm). Wash further in MilliQ-Water until desired contrast is attained.

Encloser:

- not applicable

Abbreviations:

| | |
|-------------|-------------------------|
| APS | ammonium persulfate |
| BSA | bovine serum albumin |
| dest. water | deionized water |
| DTT | dithiothreitol |
| M | molare |
| RT | room temperature |
| SDS | sodium dodecyl sulfate |
| TEMED | tetramethylethyldiamine |