protein order 99194

Organization	**ATUM**
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Start date	**01/25/2018**
Confirmed date	**01/25/2018**

sample summary

Protein ID	Protein Name	Conc. (mg/ml)	Yield (mg)	Culture Volume (ml)	Endotoxin (EU/mg)	Titer (mg/L)	Aliquots	Aliquot Volume (ml)
29833.23.a	Herceptin	2.20	48.68	100	< 0.50	486.82	1	22.13

29833.23.a

Protein Name	**Herceptin**
Molecular Weight	**145337 Da**
Extinction Coefficient	**215380**
Isoelectric Point	**8.45**
Date of Manufacture	**12/03/2018**

production notes

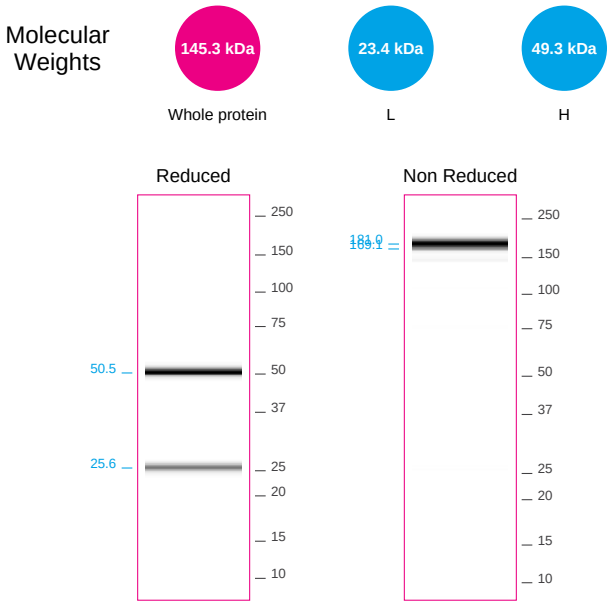
Expression Host:	**HEK SUS**
Culture Volume:	**100 ml**
Purification resins:	**MabSelect Sure PCC**
Endotoxin:	**< 0.50 EU/mg**
Yield:	**48.68 mg**
Formulation Buffer:	**PBS**

productivity data

Titer: **486.82 mg/L**

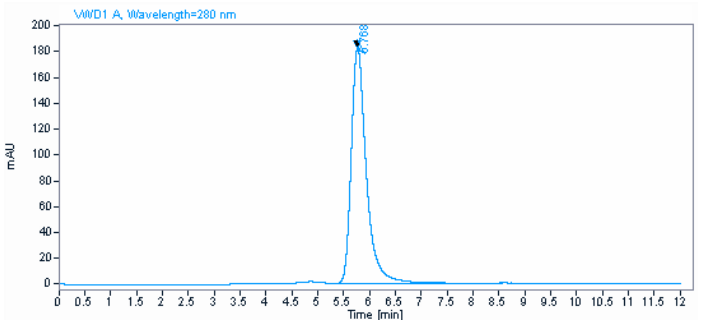
identity

SDS-PAGE - Product Identity



biophysical data

SEC - Product Characterization



Retention time (min)	Area %	Peak symmetry
5.77	100.00	0.64

ATUM production report

1. Protein expression vectors transfected into HEK293.sus using standard ATUM methods.

2. Protein A resin was used to capture proteins.

3. Resin was washed, protein was eluted and immediately neutralized.

4. Proteins were buffer exchanged into PBS.

5. Proteins were quantified by OD280, quantity and concentration was determined using calculated extinction coefficient.

6. Perkin Elmer GXII capillary electrophoresis system or SDS-PAGE (Biorad criterion Tris/Glycine/SDS, 4-20%) was used to determine purity and approximate molecular mass.

7. Charles River Endotoxin Kit was used to determine endotoxin levels- if requested.

8. Aggregation status was determined by HPLC-SEC with a column of 300A pore size, detection at 280 nm and PBS as the running buffer.

9. Proteins were shipped as aliquots after filter sterilization, snap frozen in liquid nitrogen.

protein information

Molecular Weight and Extinction Coefficient are estimated for the sum of the contributing protein chains in the quaternary structure. By default the calculation assumes equal and monomeric contribution from each chain.

Extinction Coefficient is the predicted absorbance at 280nm per molar protein in units of $M^{-1}cm^{-1}$.

Potential post-translational modifications such as glycosylation, phosphorylation, and proteolysis are not considered in Molecular Weight or Extinction Coefficient estimates.

protein analytics

SDS-PAGE gels are run under reducing and non-reducing conditions to determine purity and approximate molecular mass. Digital data results are collected, reviewed and exported into our LIMS system. The data is then displayed and exported as virtual gels.

Size Exclusion Chromatography (SEC) – HPLC separates molecules based on molecular mass and hydrodynamic volume. Larger molecules elute first i.e. earlier retention time, followed by smaller sized molecules i.e. later retention time. The table shows retention time, area % and peak symmetry. Area % of each peak is calculated based on total area of the peaks. Peak symmetry is calculated to determine the peak fronting (<1) or tailing (>1).