

Pharmacokinetic/Pharmacodynamic Target Attainment Based on Measured Versus Predicted Unbound Ceftriaxone Concentrations in Critically Ill Patients with Pneumonia: An Observational Cohort Study

Supplementary Materials

Table S1

Table S1. Parameters of the protein binding models used to predict unbound ceftriaxone concentrations.

| | Fixed protein binding | Capacity Constant (nP) | Binding affinity constant (k_{aff}) | Maximum binding capacity (B _{max}) | Hill coefficient (h) | Dissociation constant (B ₅₀) |
|---|-----------------------|------------------------|---|--|----------------------|--|
| Fixed average protein binding | 89.5 % | - | - | - | - | - |
| Estimated saturable concentration-dependent protein binding, <u>Eq. 4</u> | - | 517 μ mol/L | 0.0367 L/ μ mol | - | - | - |
| Predicted protein binding, present study, <u>Eq. 2</u> | - | - | - | -0.64 mmol/L | 0.26 | 1.09 mmol/L |
| Predicted protein binding, <u>Bos</u> | - | - | - | 0.12 mmol/L | 1.3 | 0.0092 mmol/L |
| Predicted protein binding, <u>Leegwater</u> | - | - | - | 113 mg/L | 0.0399 | 11.5 mg/L |