

# *Supplementary Material*

# **Using quantitative systems pharmacology modeling to optimize combination therapy of anti-PD-L1 checkpoint inhibitor and T cell engager**

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## **Supplementary Information**

### **1- TCE binding module**

The dynamics of TCE binding to cancer calls and T cells are described in this section following equations 1-3. In summary, TCE can bind either to CEA on cancer cells or CD3 on T cells (Teff or Treg) cells to form the dimers CEA\_TCE or CD3\_TCE respectively (Eqs. 1, 2-1, 2-2). For simplicity, we assume that cibisatamab has only one binding arm for CEA. After the dimers are formed, they can subsequently bind to CD3 and CEA to form the final molecule, CEA\_TCE\_CD3 (Eqs. 3-1, 3-2). A summary of all parameters used in these equations with their units and description are provided in Table S1.



**Table S1 : Summary of the parameters and variables used in the TCE binding module**



Following other models of bispecific antibodies (Vauquelin and Charlton 2013; Schropp et al. 2019), a parameter called *f* is added to count for avidity of TCE to two targets, which implies that binding to the first target affects the binding affinity to the second target (Eqs. 3-1, 3-2). The formation of CEA\_TCE\_CD3 in the immunological synapse will cause enhanced cancer killing by Teff since more Teff cells are triggered by TCE in an MHC-independent manner. Treg will also be activated by TCEs to exhibit an immunoregulatory function as was suggested by experimental data (Koristka et al. 2015, 2012), which is achieved by suppressing the activity of Teff cells in this model.

$$
\frac{d(CEA\_TCE)}{dt} = k_{on,CEA\_TCE} \cdot D_{CEA} \cdot TCE - k_{off,CEA_{TCE}} \cdot D_{CEA_{TCE}} - \frac{k_{on,CD3_{TCE}}}{D_{syn}*N} \cdot D_{CEA_{TCE}} \cdot D_{TEffCD3} + k_{off,CD3_{TCE}} \cdot D_{CEA_{TCE_{TregCD3}}} \tag{1}
$$
\n
$$
\frac{d(TeffCD3\_TCE)}{dt} = k_{on,CD3\_TCE} \cdot D_{TeffCD3} \cdot TCE - k_{off,CD3\_TCE} \cdot D_{TeffCD3\_TCE} - \frac{k_{on,CEA_{TCE}}}{D_{syn}*N} \cdot D_{TeffCD3\_TCE} \cdot D_{TeffCD3\_TCE} \tag{2-1}
$$

$$
\frac{d(TregCD3\_TCE)}{dt} = k_{on,CD3\_TCE} \cdot D_{TregCD3} \cdot TCE - k_{off,CD3\_TCE} \cdot D_{TregCD3\_TCE} - k_{on,CEA\_TCE} \cdot D_{TregCD3\_TCE} \cdot D_{CEA} + k_{off,CEA\_TCE} \cdot D_{CEA\_TCE\_TregCD3}
$$
(2-2)  
\n
$$
\frac{d(CEA\_TCE\_TeffCD3)}{dt} = \frac{k_{on,CEA\_TCE}}{f * D_{syn} * N} \cdot D_{TeffCD3\_TCE} \cdot D_{CEA} - k_{off,CEA\_TCE} \cdot D_{CEA\_TCE\_TeffCD3} + k_{on,CD3\_TCE} \cdot D_{CEA\_TCE} \cdot D_{CEA\_TCE\_TeffCD3}
$$
(3-1)  
\n
$$
\frac{d(CEA\_TCE\_TregCD3)}{dt} = \frac{k_{on,CEA\_TCE}}{f * D_{syn} * N} \cdot D_{TregCD3\_TCE} \cdot D_{CEA} - k_{off,CEA\_TCE} \cdot D_{CEA\_TCE\_TregCD3} + k_{on,CD3\_TCE} \cdot D_{CEA\_TCE} \cdot D_{TEgCD3} - k_{off,CD3\_TCE} \cdot D_{CEA\_TCE\_TregCD3}
$$
(3-2)

The number of bound CEA\_TCE\_CD3 was translated to cancer cell killing rate by activation of Teff cells using a Hill equation. The Hill function coefficient was calculated by fitting the T cell activation as a function of average number of CEA\_TCE\_TeffCD3 per Teff cell to experimental data of MKN45 published in the study by Van De Vyver et. al. (van de Vyver et al. 2021) (Figure 2). The equations of cancer killing by TCE induced Teffs are provided by Ma et. al. (Ma, Wang, Sové, et al. 2020)

#### **2- Pharmacokinetics**

Pharmacokinetic of both cibisatamab and atezolizumab were modelled following the same physiologically-based pharmacokinetic model as described by (Jafarnejad et al. 2019). The equations describing drug PK has presented below, equations 4-7. A<sup>i</sup> indicate antibody (either cibisatamab or atezolizumab) concentration.  $V_i$  is the compartment volume,  $Q_i$  is the volumetric flow rate between the central and the corresponding compartment,  $q_{LD}$  is the rate of lymphatic drainage from tumor to TDLNs and from TDLNs to central, and CL is clearance rate. Subscripts C, P, LN, and T represent the central, peripheral, tumor-draining lymph node, and tumor compartments, respectively.

The PK parameters of cibisatamab and atezolizumab in this model has been previously estimated by Ma et. al. 2020 fitted to standard pharmacokinetic two-compartment model. Cibisatamab PK parameters were fitted to reported plasma concentration at dose levels of 80, 160, 200, 300, 400 mg. Atezolizumab PK parameters were fitted to reported plasma concentration at dose levels of 1, 3, 10, 15 mg/kg and 1200mg. The parameters are provided in the Table S4. The simulated concentrations of atezolizumab (1200mg Q3W) and cibisatamab (60mg QW) in each compartment are presented in Fig. S1.

$$
V_C \frac{dA_C}{dt} = Q_P(A_P - A_C) + Q_{LN}(A_{LN} - A_C) + Q_T(A_T - A_C) + q_{LD} * V_T * A_{LN} - CL * A_C
$$
 (4)

$$
V_P \frac{dA_P}{dt} = Q_P (A_C - A_P) \tag{5}
$$

$$
V_T \frac{dA_T}{dt} = Q_T (A_C - A_T) - q_{LD} * V_T * A_T \tag{6}
$$

$$
V_{LN}\frac{dA_{LN}}{dt} = Q_{LN}(A_C - A_{LN}) + q_{LD} * V_T * A_T - q_{LD} * V_T * A_{LN}
$$
\n(7)



Figure S1. The concentration of A) atezolizumab (1200mg Q3W) and B) cibisatamab (60mg QW) in central, Tumor, Tumor Draining Lymph Node (TdLN), and Peripheral compartments.



Figure S1. The partial rank correlation coefficient, PRCC, between input parameters and tumor volume after treatment with (A) cibisatamab monotherapy and (B) combination therapy.

### **References**

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