**Biomasses**

**HumanGEM Model was modified prior to reconstruction of cell-type/tissue specific reconstruction of T-cells:**

- A biomass reaction from the macrophage model iAB-AMØ-1410 was added (named *biomass\_macrophage\_iABAM01410*). Thus, two different biomasses will be available to test: *biomass\_human* (biomass from HumanGEM) and *biomass\_macrophage\_iABAM01410* .

- With this, we have 2 generic HumanGEM models, the original one (*HumanGEM-1.4.1*), which will be used in cancer reconstruction models and the one that will be used in T-cell reconstruction models (HumanGEM-1.4.1*\_forTcells*)

- Since the only difference between these two models is the presence of one more biomass reaction in one of them:

- HumanGEM was tested for the ability to perform tasks that all cells should be able to perform (adapted to a json file from *metabolicTasks\_full.xlsx* from HumanGEM: <https://github.com/SysBioChalmers/Human-GEM/tree/master/data/metabolicTasks>).

- The capacity to carry flux through the biomasses reactions was also tested, using the Plasmax and SMDB\_Blood media (both as converting the concentrations to ub fluxes and open bounds) and the default open medium from *HumanGEM*.

**Units:** mmol gDW-1 h-1 -> mmol of metabolite per gram of dry weight of cell per hour

**Biomass reaction from the macrophage model iAB-AMØ-1410:**

|  |  |  |  |
| --- | --- | --- | --- |
| **Reactants** | **Metabolite ID** | **Metabolite Name** | **Stoichiometry** |
|  | m01307c | L-Alanine | 0.396559456 |
| alpa\_hs\_c | Lysophosphatidic Acid | 0.011499127 |
| m01334c | Adenosine monophosphate | 0.048664064 |
| m01365c | L-Arginine | 0.325724532 |
| m01369c | L-Asparagine | 0.215407845 |
| m01370c | L-Aspartic acid | 0.282759085 |
| m01371c | ATP | 25.17352552 |
| m01450c | Cholesterol | 0.020930954 |
| m01590c | CMP | 0.042373167 |
| m01628c | L-Cysteine | 0.127154496 |
| m00240c | Diglyceride (1,2.diacylglycerol-LD-TAG pool) | 0.0036682 |
| m01639c | dAMP | 0.021495345 |
| m01644c | dCMP | 0.014937443 |
| m01686c | dGMP | 0.014937443 |
| m01752c | dTMP | 0.021495345 |
| m01975c | L-Glutamine | 0.280436629 |
| m01974c | L-Glutamic acid | 0.424428935 |
| m01986c | Glycine | 0.366948135 |
| m03161c | Glycogen | 0.528027894 |
| m02016c | GMP | 0.043710887 |
| m02040c | H2O | 25.17352552 |
| m02674c | Palmitic acid | 0.004850777 |
| m02675c | Palmitoleic acid | 0.001222285 |
| m02125c | L-Histidine | 0.153862747 |
| m02184c | L-Isoleucine | 0.25953452 |
| m02360c | L-Leucine | 0.580614138 |
| m02426c | L-Lysine | 0.351852168 |
| m02471c | L-Methionine | 0.126573882 |
| m02938c | Stearic acid[cytoplasm] | 0.004736708 |
| m02646c | Oleic acid[cytoplasm] | 0.003853116 |
| m02750c | 1-Phosphatidyl-1D-Myo-Inositol (PI pool) | 0.003741686 |
| m02684c | Phosphatidylcholine (PC-LD pool) | 0.031527146 |
| m02685c | Phosphatidylethanolamine (PE-LD pool) | 0.021107135 |
| m02715c | Phosphatidylglycerol (PG-CL pool) | 0.008918017 |
| m02724c | L-Phenylalanine | 0.214246617 |
| m02770c | L-Proline | 0.346626641 |
| m02808c | Phosphatidylserine (PS-LD pool) | 0.001024655 |
| m02896c | L-Serine | 0.476684207 |
| m02908c | Sphingomyelin (SM pool) | 0.007049706 |
| m02959c | TAG-LD pool **\*** | 0.002742439 |
| m02993c | L-Threonine[cytoplasm] | 0.303661194 |
| m03089c | L-Tryptophan[cytoplasm] | 0.069673697 |
| m02494c | Myristic acid[cytoplasm] | 0.00136164 |
| m03101c | L-Tyrosine[cytoplasm] | 0.156185203 |
| m03114c | Uridine 5'-monophosphate[cytoplasm] | 0.04602478 |
| m03135c | L-Valine[cytoplasm] | 0.347207255 |
| **Products** | **Metabolite ID** | **Metabolite Name** | **Stoichiometry** |
|  | adp[c] | ADP[cytoplasm] | 25.17352552 |
| h[c] | Hydrogen Ion[cytoplasm] | 25.17352552 |
| pi[c] | Phosphate[cytoplasm] | 25.17352552 |
| **Lower Bound** | 0 | | |
| **Upper Bound** | 1000 | | |

**\*** In the macrophage model (iAB-AMØ-1410), Triglyceride was considered as TAG-VLDL pool. However, it was changed to TAG-LD pool (due to unability to produce biomass from either Plasmax or SMDB\_Blood media).