Figure 2 - source data 3:

Quantitative time-resolved analysis reveals intricate, differential regulation of standard and immuno-proteasomes.

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Table 1: List of mathematical model species

peptide-bond hydrolysis	
E_0	initial proteasome concentration
S	substrate inside the chamber
P	product inside the chamber
transport	
S_{out}	substrate outside the chamber
P_{out}	product outside the chamber
G_1	proteasome gate for influx
G_2	proteasome gate for efflux
$[G_1 S_{out}]$	substrate bound to proteasome gate for influx
$[G_1 P_{out}]$	product bound to proteasome gate for influx
$[G_2 S]$	substrate bound to proteasome gate for efflux
$[G_2 P]$	product bound to proteasome gate for efflux
transport regulation	
E_{reg}	enhancing regulator site
$[E_{reg} S_{out}]$	substrate bound to enhancing regulator site outside the chamber
$[E_{reg} P_{out}]$	product bound to enhancing regulator site outside the chamber
$[E_{reg} S]$	substrate bound to enhancing regulator site inside the chamber
$[E_{reg} P]$	product bound to enhancing regulator site inside the chamber
I_0	initial concentration of inhibiting regulator site outside the chamber
I_{free}	inhibiting regulator site outside the chamber
$[IS]$	substrate bound to inhibiting regulator site outside the chamber
$[IP]$	product bound to inhibiting regulator site outside the chamber