Table S1a (The hemostatic system entities interaction KCs)**, Table S1b** (The complement system entities interaction KCs), **Table S1c (**The hemostatic system and complement system cross-talk KCs), **Table S1d** (The hemostatic and complement systems entities and SARS-CoV-2 structure proteins interaction KCs), and **Table S1e** (Drug-Target interaction KCs).

Table S1a. The hemostatic system entities interaction KCs

Meaning	Rate constant	Value adopted	Source
Association rate for TF and F7 Disassociation rate for TF:F7	k^{+}_{TFF7} k^{-}_{TFF7}	$3.2 \times 10^{6}\ M^{-1}s^{-1}$ $3.1 \times 10^{-3}\ s^{-1}$	[1], [2]
Association rate for TF and F7a Disassociation rate for TF:F7a	k^{+}_{TFF7a} k^{-}_{TFF7a}	$2.3 \times 10^{7}\ M^{-1}s^{-1}$ $3.1 \times 10^{-3}\ s^{-1}$	[1], [2]
Activation of F7 by TF:F7a	k^{TFF7a}_{catF7}	$4.4 \times 10^{5}\ M^{-1}s^{-1}$	[2]
Activation of F7 by F10a	k^{F10a}_{catF7}	$1.3 \times 10^{7}\ M^{-1}s^{-1}$	[2]
Activation of F7 by F2a	k^{F2a}_{catF7}	$2.3 \times 10^{4}\ M^{-1}s^{-1}$	[2]
Association rate for F7a and F9 Disassociation rate for F7a:F9	k^{+}_{F7aF9} k^{-}_{F7aF9}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $0.9\ s^{-1}$	[2]
Production of F9a by F7a	k^{F7a}_{catF9a}	$3.6 \times 10^{-5}\ s^{-1}$	[2]
Association rate for F7a and F10 Disassociation rate for F7a:F10	k^{+}_{F7aF10} k^{-}_{F7aF10}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $210.0\ s^{-1}$	[2]
Production of F10a by F7a	$k^{F7a}_{catF10a}$	$1.6 \times 10^{-6}\ s^{-1}$	[2]
Association rate for TF:F7a and F9 Disassociation rate for TF:F7a:F9	$k^{+}_{TFF7aF9}$ $k^{-}_{TFF7aF9}$	$1.0 \times 10^{7}\ M^{-1}s^{-1}$ $2.4\ s^{-1}$	[2]
Activation of F9 by TF:F7a	k^{TFF7a}_{catF9}	$1.8\ s^{-1}$	[2]

Association rate for TF:F7a and F10 Disassociation rate for TF:F7a:F10	$k^{+}_{TFF7aF10}$ $k^{-}_{TFF7aF10}$	$2.5 \times 10^{7}\ M^{-1}s^{-1}$ $1.05\ s^{-1}$	[2]
Activation of F10 by TF:F7a	k^{TFF7a}_{catF10}	$6.0\ s^{-1}$	[2]
Association rate for TF:F7a and F10a Disassociation rate for TF:F7a:F10a	$k^{+}_{TFF7aF10a}$ $k^{-}_{TFF7aF10a}$	$2.2 \times 10^{7}\ M^{-1}s^{-1}$ $19.0\ s^{-1}$	[2]
Association rate for F10a and TFPI Disassociation rate for F10a:TFPI	$k^{+}_{F10aTFPI}$ $k^{-}_{F10aTFPI}$	$9.0 \times 10^{5}\ M^{-1}s^{-1}$ $3.6 \times 10^{-4}\ s^{-1}$	[2]
Binding of TF:F7a:F10a and TFPI Disassociation of TF:F7a:F10a	$k^{+}_{TFF7aF10aTFPI}$ $k^{-}_{TFF7aF10aTFPI}$	$3.2 \times 10^{8}\ M^{-1}s^{-1}$ $1.1 \times 10^{-4}\ s^{-1}$	[2]
Binding of F10a:TFPI and TF:F7a	$k^{+}_{F10aTFPITFF7a}$	$5.0 \times 10^{7}\ M^{-1}s^{-1}$	[2]
Association rate for F11a and F9 Disassociation rate for F11a:F9	k^{+}_{F11aF9} k^{-}_{F11aF9}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $41.0\ s^{-1}$	[2], [3]
Generation of F9a by F11a	k^{F11a}_{catF9a}	$7.7\ s^{-1}$	F11a can generate F9a [2], [3].
Inhibition of F11a by AT3	$k^{+}_{F11aAT3}$	$3.2 \times 10^{2}\ M^{-1}s^{-1}$	Destruction of F11a by inhibitor AT3 [2], [3].
Binding of F12a and F11 Disassociation of F12a:F11	$k^{+}_{F12aF11}$ $k^{-}_{F12aF11}$	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $200.0\ s^{-1}$	[2], [3].
Production of F11a by F12a	$k^{F12a}_{catF11a}$	$5.7 \times 10^{-3}\ s^{-1}$	F12a can produce F11a [3].
Binding of F12 and F12a Disassociation of F12:F12a	$k^{+}_{F12F12a}$ $k^{-}_{F12F12a}$	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $750.0\ s^{-1}$	[2], [3]

Autocatalysis of F12a amplification by F12:F12a	$k_{catF12a}^{F12F12a}$	$3.3 \times 10^{-2}\ s^{-1}$	The product of F12 and F12a autocatalysis of F12a and increase it expression level [2], [3].
Association rate for P-KAL and F12a Disassociation rate for P-KAL:F12a	$k_{PKALF12a}^{+}$ $k_{PKALF12a}^{-}$	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $3.6 \times 10^{3}\ s^{-1}$	Binding of P-KAL with F12 and disassociation of their product P-KAL:F12 [2], [3].
Association rate for KAL and F12 Disassociation rate for KAL:F12	k_{KALF12}^{+} k_{KALF12}^{-}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $45.3\ s^{-1}$	Binding of KAL with F12 and disassociation of their product KAL:F12 [2], [3].
Production of F12a by KAL	$k_{catF12a}^{KAL}$	$5.7\ s^{-1}$	[2], [3]
Association rate for F9a and F10 Disassociation rate for F9a:F10	k_{F9aF10}^{+} k_{F9aF10}^{-}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $0.64\ s^{-1}$	[2], [3]
Production of F10a by F9a	$k_{catF10a}^{F9a}$	$7.0 \times 10^{-4}\ s^{-1}$	[2], [3]
Association rate for F9a and F8a Disassociation rate for F9a:F8a	k_{F9aF8a}^{+} k_{F9aF8a}^{-}	$1.0 \times 10^{7}\ M^{-1}s^{-1}$ $5.0 \times 10^{-3}\ s^{-1}$	[2], [3]
Binding of F9a and AT3	k_{F9aAT3}^{+}	$4.9 \times 10^{2}\ M^{-1}s^{-1}$	Inhibition of F9a by AT3 [2], [3].
Association rate for F9a:F8a and F10 Disassociation rate for F9a:F8a:F10	$k_{F9aF8aF10}^{+}$ $k_{F9aF8aF10}^{-}$	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $1.0 \times 10^{-3}\ s^{-1}$	[2], [3]
Activation of F10 by F9a:F8a	k_{catF10}^{F9aF8a}	$8.2\ s^{-1}$	[2], [3]
Association rate for F10a and F8 Disassociation rate for F10a:F8	k_{F10aF8}^{+} k_{F10aF8}^{-}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $2.1\ s^{-1}$	[2], [3]
Production of F8a by F10a	k_{catF8a}^{F10a}	$2.3 \times 10^{-2}\ s^{-1}$	F10a produce F8a [2], [3].

Binding of F10a and F5a Disassociation of F10a:F5a	$k^{+}_{F10aF5a}$ $k^{-}_{F10aF5a}$	$4.0 \times 10^{8}\ M^{-1}s^{-1}$ $0.2\ s^{-1}$	[2], [3]
Inhibition of F0a by AT3	$k^{+}_{F10aAT3}$	$1.5 \times 10^{3}\ M^{-1}s^{-1}$	Binding of F10a and AT3 [2], [3].
Binding of F10a:F5a and F2 Disassociation of F10a:F5a:F2	$k^{+}_{F10aF5aF2}$ $k^{-}_{F10aF5aF2}$	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $103.0\ s^{-1}$	[2], [3]
Activation of F2 by F10a	k^{F10a}_{catF2}	$7.5 \times 10^{3}\ M^{-1}s^{-1}$	Binding of F10a and F2 [2], [3].
Inhibition of F2a by A2M	k^{+}_{F2aA2M}	$2.5 \times 10^{3}\ M^{-1}s^{-1}$	Association rate of A2M and F2a [4].
Association rate for TF:F7a and AT3	$k^{+}_{TFF7aAT3}$	$2.3 \times 10^{2}\ M^{-1}s^{-1}$	Inhibition of TF:F7a by AT3 [2].
Binding of F11 and F2a Disassociation of F11:F2a	k^{+}_{F11F2a} k^{-}_{F11F2a}	$1.0 \times 10^{8}\ M^{-1}s^{-1}$ $5.0\ s^{-1}$	[2], [3]
Generation of F11a	k^{F11}_{catF2a}	$1.3 \times 10^{-4}\ s^{-1}$	[2], [3]
Inhibition of F2a by AT3	k^{+}_{F2aAT3}	$7.1 \times 10^{3}\ M^{-1}s^{-1}$	Binding of AT3 and F2a [2], [3].
Activation of F5 by F2a	k^{F2a}_{catF5}	$2.0 \times 10^{7}\ M^{-1}s^{-1}$	[2], [3]
Binding of F2a and F1 Disassociation of F2a:F1	k^{+}_{F2aF1} k^{-}_{F2aF1}	$1.17 \times 10^{7}\ M^{-1}s^{-1}$ $84.0\ s^{-1}$	[5], [6]
Production of F1a	k^{F2a}_{catF1a}	$84\ s^{-1}$	[5], [6]
Activation of F8 by F2a	k^{F2a}_{catF8}	$2.0 \times 10^{7}\ M^{-1}s^{-1}$	F2a binds with F8 [2], [3].
Inhibation of F12a by AT3	$k^{+}_{F12aAT3}$	$21.6\ M^{-1}s^{-1}$	AT3 is associated with F12a and inhibits it [2], [3].
Production of KAL by F12a	k^{F12a}_{catKAL}	$40\ s^{-1}$	F12a can generates KAL) [2], [3].

Activation of KAL by P-KAL	$k^{+}_{KALPKAL}$	$2.7 \times 10^{4}\ M^{-1}s^{-1}$	KAL auto-activation [2], [3].
Generation of Lys-Pg by Glu-Pg	$k^{Glu-Pg}_{catLys-Pg}$	$0.1\ s^{-1}$	Pg variants are Lys-Pg and Glu-Pg [7]. Lys-Pg can be generated by Pn hydrolysis of Glu-Pg [8]. Conversion of Glu- to Lys-Lys-Pg [9]–[11]. In literature the generation rate of Lys-Pg not available. Assume a small value for it.
Activation of Glu-Pg by tPA	k^{F1a}_{cattPA} k^{F1a}_{mtPA}	$4.1 \times 10^{-7}\ s^{-1}$ 0.073 M	tPA activates Glu-Pg in the presence of F1a [8].
Activation of Lys-Pg by tPA	k^{F1a}_{cattPA} k^{F1a}_{mtPA}	$2.0 \times 10^{-8}\ s^{-1}$ 0.064 M	tPA activates Lys-Pg in the presence of F1a [8].
Association rate for Glu-Pg and FDPs Disassociation rate for Glu-Pg:FDPs	$k^{+}_{Glu-PgFDPs}$ $k^{-}_{Glu-PgFDPs}$	$5.71 \times 10^{5}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	Native Plasminogen (Glu-Pg) binds to FDPs with affinity ($k_d = 175 \times 10^{-9}$M) [12]. The Association rate (k^{+}) can be computed from the formula $k_d = \frac{k^{-}}{k^{+}}$. Assume a small value for $k^{-} = 0.1s^{-1}$.
Association rate for Lys-Pg and FDPs Disassociation rate for Lys-Pg:FDPs	$k^{+}_{Lys-PgFDPs}$ $k^{-}_{Lys-PgFDPs}$	$1.11 \times 10^{6}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	Lys-Pg binds to FDPs with affinity ($k_d = 90 \times 10^{-9}$M) [12]. The Association rate (k^{+}) can be computed from the formula $k_d = \frac{k^{-}}{k^{+}}$. Assume a small value for $k^{-} = 0.1s^{-1}$.
Inhibition of Glu-Pg:FDPs by TAFIa	$k^{+}_{Glu-PgFDPsTAFIa}$	$1.7133 \times 10^{7}\ M^{-1}s^{-1}$	Glu-Pg is degraded by TAFIa in the presence of FDPs. Treatment of the FDPs with TAFIa removes Glu-Pg binding sites. When FDPs are treated with TAFIa the k_d increases to 1×10^{-6} M, $k_{cat} = 2.35\ s^{-1}$, $k_m = 0.143\mu$M [12]. The Association rate (k^{+}) can be computed from the formula $k^{+} = \frac{k^{-} + k_{cat}}{k_m}$. Assume a small value for $k^{-} = 0.1s^{-1}$.
Inhibition of Lys-Pg:FDPs by TAFIa	$k^{+}_{Lys-PgFDPsTAFIa}$	$1.051 \times 10^{7}\ M^{-1}s^{-1}$	Lys-Pg is degraded by TAFIa in the presence of FDPs. Treatment of the FDPs with TAFIa removes Glu-Pg binding sites. When FDPs are treated with TAFIa the k_d increases to 1.55×10^{-6}M, $k_{cat} = 0.888\ s^{-1}$, $k_m = 0.094\mu$M [12]. The Association rate (k^{+}) can be computed from the formula $k^{+} = \frac{k^{-} + k_{cat}}{k_m}$. Assume a small value for $k^{-} = 0.1s^{-1}$.

Association rate for F1a and Lys-Pg Disassociation rate for F1a:Lys-Pg	$k^{+}_{F1aLys-Pg}$ $k^{-}_{F1aLys-Pg}$	$1.0 \times 10^{-7}\ M^{-1}s^{-1}$ $3.8\ s^{-1}$	Lys-Pg binds to F1a [7], [8]. The binding rate constant for Pg to F1 and the unbinding rate constant for Pg from F1 [13].
Activation of F1 by Lys-Pg	k^{Lys-Pg}_{catF1}	$1.0 \times 10^{-7}\ M^{-1}s^{-1}$	Lys-Pg can binds to F1a, the binding rate measured $1.0 \times 10^{-7}\ M^{-1}s^{-1}$ [7], [8]. Assumption for activation rate of F1 to F1a by Lys-Pg.
Inhibition of tPA by PAI-1	$k^{+}_{tPAPAI-1}$	$2 \times 10^{7}\ M^{-1}s^{-1}$	PAI-1 is an efficient inhibitor of tPA [14].
Production of tPA by F1a:Lys-Pg	$k^{F1aLys-Pg}_{cattPA}$	$0.1\ s^{-1}$	Assumption for the rate of tPA production by F1a: Lys-Pg, as in propagation phase of fibrinolysis, F1a can generates tPA in the presence of Lys-Pg [15].
Generation of Lys-Pg by Pn	$k^{Pn}_{catLys-Pg}$	$0.1\ s^{-1}$	Assumed a small value for the rate of Lys-Pg production by Pn. As in propagation phase of fibrinolysis, Lys-Pg can be produced by Pn [15].
Association rate for P-KAL and HK Disassociation rate for P-KAL:HK	k^{+}_{PKALHK} k^{-}_{PKALHK}	$8.3 \times 10^{7}\ M^{-1}s^{-1}$ $1s^{-1}$	P-KAL binds to HK with high specificity and affinity ($k_d = 1.2 \times 10^{-8}$M) [16]. The Association rate (k^{+}) can be computed from the formula $k_d = \frac{k^{-}}{k^{+}}$. Assumed a small value for $k^{-} = 1s^{-1}$.
Activation of HK by KAL	k^{KAL}_{catHK}	$8.3 \times 10^{7}\ M^{-1}s^{-1}$	Estimated based on association rate of P-KAL and HK.
Generation of BK by P-KAL:HK	k^{PKALHK}_{catBK}	$0.1\ s^{-1}$	The product of P-KAL and HK can release BK [17]. The generation rate is unknown, estimated a small value for it.
Association rate for BK and B2R Disassociation rate for BK:B2R	k^{+}_{BKB2R} k^{-}_{BKB2R}	$3.4 \times 10^{8}\ M^{-1}s^{-1}$ $1\ s^{-1}$	BK binds to B2R with a high affinity ($k_d = 2.90 \times 10^{-9}$) [18]. The disassociation rate (k^{-1}) is unknown, assumed a small value for $k^{-1} = 1\ s^{-1}$. Using the formula $k_d = \frac{k^{-}}{k^{+}}$, determined k^{+}.
Association rate for HK and F11 Disassociation rate for HK:F11	k^{+}_{HKF11} k^{-}_{HKF11}	$0.40 \times 10^{7}\ M^{-1}s^{-1}$ $1\ s^{-1}$	F11 can binds to HK with an affinity $k_d = (2-3) \times 10^{-7}$M [19], [20]. Considered $k_d = 2.5 \times 10^{-7}$M. The disassociation rate (k^{-1}) is unknown, assumed $k^{-1} = 1\ s^{-1}$. Using the formula $k_d = \frac{k^{-}}{k^{+}}$, determined k^{+}.
Production of F11a by HK:F11	$k^{HKF11}_{catF11a}$	$0.1\ s^{-1}$	The association of HK and F11 can generate F11a. Assumed, a small value for the production of F11a by product of HK and F11.

Production of tPA by BK:B2R	k_{cattPA}^{BKB2R}	$0.1\ s^{-1}$	The product of BK:B2R stimulates tPA [20]. Assumed, a small value for the production of tPA by BK: B2R.
Activation of the F1 by F2a	k_{catF1}^{F2a} k_{mF1}^{F2a}	$59\ s^{-1}$ 3.16×10^{-6}M	Enzyme reactions between F2a and F1 [1].
Cleavage of TAFI by Pn	$k_{catTAFI}^{Pn}$ k_{mTAFI}^{Pn}	$4.0 \times 10^{-4} s^{-1}$ 5.5×10^{-8}M	Pn cleaves TAFI at Arg92, generating TAFIa. Pn-mediated TAFI activation [9].
Cleavage of TAFI by F2a	$k_{catTAFI}^{F2a}$ k_{mTAFI}^{F2a}	$0.17\ s^{-1}$ 8.3×10^{-7}M	F2a can cleaves TAFI and generates active TAFIa [21].
Inhibition of Glu-Pg by TAFIa	$k^{+}_{Glu-PgTAFIa}$	$1.69 \times 10^{7}\ M^{-1}s^{-1}$	TAFIa inhibits the activation of Glu-Pg and the conversion of Glu- to Lys-Pg [9]–[11]. $k_{cat} = 2.30\ s^{-1}$, $k_m = 0.142\mu M$ [22], [23]. The disassociation rate (k^-) is unknown, assumed a small value for $k^- = 0.1 s^{-1}$. Using the formula $k^+ = \frac{k^- + k_{cat}}{k_m}$, determined the association rate (k^+).
Inhibition of Lys-Pg by TAFIa	$k^{+}_{Lys-PgTAFIa}$	$1.051 \times 10^{7}\ M^{-1}s^{-1}$	Assumption for association rate of Lys-Pg and TAFIa based on inhibition of Lys-Pg:FDPs by TAFIa.
Inhibition of C3a by TAFIa	$k^{+}_{C3aTAFIa}$	$2.36 \times 10^{5}\ M^{-1}s^{-1}$	TAFIa can inhibit C3a. $k_{cat} = 8.4\ s^{-1}$, $k_m = 35.9\mu M$ [22], [23]. Assume a small value for $k^- = 0.1 s^{-1}$. Using the formula $k^+ = \frac{k^- + k_{cat}}{k_m}$, determined k^+.
Inhibition of C5a by TAFIa	$k^{+}_{C5aTAFIa}$	$1.35 \times 10^{5}\ M^{-1}s^{-1}$	TAFIa can inhibit C5a. $k_{cat} = 29.5\ s^{-1}$, $k_m = 219.0\ \mu M$ [22], [23]. Assume a small value for $k^- = 0.1 s^{-1}$. Using the formula $k^+ = \frac{k^- + k_{cat}}{k_m}$, determined k^+.
Inhibition of BK by TAFIa	$k^{+}_{BKTAFIa}$	$2.8 \times 10^{5}\ M^{-1}s^{-1}$	TAFIa can inactivate BK. $k_{cat} = 19.7\ s^{-1}$, $k_m = 70.6\ \mu M$ [22], [23]. Assume a small value for $k^- = 0.1 s^{-1}$. Using the formula $k^+ = \frac{k^- + k_{cat}}{k_m}$, determined k^+.
Activation of F12 by Pn	k_{catF12}^{Pn}	$1.0 \times 10^{3}\ M^{-1}s^{-1}$	Pn can cleave and activate F12 [24]. Estimated a small value for activation of F12 by Pn.

Cleavage of F1 by Pn	k_{catF1}^{Pn} k_{mF1}^{Pn}	$7.1\ s^{-1}$ 6.5×10^{-6}M	Pn can activates and cleaves F1 [25].
Cleavage of F1a by Pn	k_{catF1a}^{Pn} k_{mF1a}^{Pn}	$6.4\ s^{-1}$ 0.14×10^{-6}M	Degradation of F1a by Pn which cleaved F1a [26].
Cleavage of Glu-Pg by Pn	$k_{catGlu-Pg}^{Pn}$ $k_{mGlu-Pg}^{Pn}$	$0.1\ s^{-1}$ 1.0×10^{-4}M	Plasmin also enhances fibrinolysis by converting native Pg (Glu-Pg) to Lys-Pg. Pn cleaves Glu-Pg at lysine 77/78 result in Lys-Pg generation [12]. Assumption for the cleavage of Glu-Pg by Pn.
Cleavage of Glu-Pg by KAL	$k_{catGlu-Pg}^{KAL}$ $k_{mGLu-Pg}^{KAL}$	$1.6 \times 10^{-4}\ s^{-1}$ 5.6×10^{-7}M	[27]
Cleavage of Glu-Pg by tPA	$k_{catGlu-Pg}^{tPA}$ $k_{mGlu-Pg}^{tPA}$	$4.1 \times 10^{-7}\ s^{-1}$ 0.073 M	[8]

Table S1b. The complement entities interaction KCs

Meaning	Rate constant	Value adopted	Source
Binding rate for C1r and C1s Disassociation rate for C1r:C1s	k^{+}_{C1rC1s} k^{-}_{C1rC1s}	$0.61 \times 10^{6}\ M^{-1}s^{-1}$ $3.44 \times 10^{-3}\ s^{-1}$	Association and disassociation rates of C1r and C1s are measured with respect to different modules such as x-ray structure of the N-terminal CUB-epidermal growth factor (EGF) marked by different residues. Among the high affinity sites at $C1rCUB_1$–Y56A, binding rates and disassociation rates measured as $k^{+} = 0.61 \times 10^{6}\ M^{-1}s^{-1}$ and $k^{-} = 3.44 \times 10^{-3}\ s^{-1}$ [28].
Binding rate for C1q and C1r:C1s Disassociation rate for C1q :C1r:C1s	k^{+}_{C1qrs} k^{-}_{C1qrs}	$0.82 \times 10^{6}\ M^{-1}s^{-1}$ $1.2 \times 10^{-3}\ s^{-1}$	[28]–[31]
Binding rate for C1s and C4 Disassociation rate for C1s:C4	k^{+}_{C1sC4} k^{-}_{C1sC4}	$7.9 \times 10^{5}\ M^{-1}s^{-1}$ $4.8 \times 10^{-1}\ s^{-1}$	[32]
Binding rate for MASP2 and C4 Disassociation rate for MASP2:C4	$k^{+}_{MASP2C4}$ $k^{-}_{MASP2C4}$	$7.9 \times 10^{5}\ M^{-1}s^{-1}$ $4.8 \times 10^{-1}\ s^{-1}$	Estimation based on MASP2 functionally homologous of C1q [32], [33].
Binding rate for C3W and FB Disassociation rate for C3W:FB	k^{+}_{C3WB} k^{-}_{C3WB}	$1.1 \times 10^{4}\ M^{-1}s^{-1}$ $1.4 \times 10^{-3}s^{-1}$	[30], [31], [34]
Binding rate for C3W and Factor H (FH) Disassociation rate for C3W:FH	k^{+}_{C3WH} k^{-}_{C3WH}	$1.1 \times 10^{6}\ M^{-1}s^{-1}$ $6.0 \times 10^{-2}s^{-1}$	Estimation structurally/functionally homologous protein C3b and FH [30], [31], [34].
Binding rate for fC3b and FB Disassociation rate for fC3b:FB	k^{+}_{fC3bFB} k^{-}_{fC3bFB}	$21.3 \times 10^{4}\ M^{-1}s^{-1}$ $15.5 \times 10^{-2}s^{-1}$	[29]–[31].

Binding rate for fC3b:C4b:P and FB Disassociation rate for fC3b:C4b:P:FB	$k^{+}_{fC3bC4bPFB}$ $k^{-}_{fC3bC4bPFB}$	$21.3 \times 10^{4}\,M^{-1}s^{-1}$ $15.5 \times 10^{-2}s^{-1}$	[29]–[31], [35].
Binding rate for lgG:fC3b and FB Disassociation rate for lgG:fC3b:FB	$k^{+}_{lgGfC3bFB}$ $k^{-}_{lgGfC3bFB}$	$21.3 \times 10^{4}\,M^{-1}s^{-1}$ $15.5 \times 10^{-2}s^{-1}$	Estimation functionally homologous protein fC3b and FB.
Binding rate for C3b and P Disassociation rate for C3b:P	k^{+}_{C3bP} k^{-}_{C3bP}	$1.5 \times 10^{5}\,M^{-1}s^{-1}$ $15.5 \times 10^{-5}\,s^{-1}$	[29]–[31], [36]
Binding rate for fC3b:C4b and P Disassociation rate for fC3b:C4b:P	$k^{+}_{fC3bC4bP}$ $k^{-}_{fC3bC4bP}$	$1.5 \times 10^{5}\,M^{-1}s^{-1}$ $15.5 \times 10^{-5}\,s^{-1}$	[29]–[31]
Binding rate for C3b and FH Disassociation rate for C3b:FH	k^{+}_{C3bFH} k^{-}_{C3bFH}	$1.1 \times 10^{6}\,M^{-1}s^{-1}$ $5.9 \times 10^{-2}\,s^{-1}$	[29]–[31], [37]
Binding rate for fC3b:Bb and FH Disassociation rate for fC3b:Bb:FH	$k^{+}_{fC3bBbFH}$ $k^{-}_{fC3bBbFH}$	$1.1 \times 10^{6}\,M^{-1}s^{-1}$ $5.9 \times 10^{-2}\,s^{-1}$	Estimation functionally homologous protein C3b and FH.
Binding rate for C3b:Bb:C3b and FH Disassociation rate for C3b:Bb:C3b:FH	$k^{+}_{C3bBbC3bFH}$ $k^{-}_{C3bBbC3bFH}$	$1.1 \times 10^{6}\,M^{-1}s^{-1}$ $5.9 \times 10^{-2}\,s^{-1}$	Estimation functionally homologous protein C3b and FH.
Binding rate for C4b and C4BP Disassociation rate for C4b:C4BP	$k^{+}_{C4bC4BP}$ $k^{-}_{C4bC4BP}$	$2.0 \times 10^{5}\,M^{-1}s^{-1}$ $1.6 \times 10^{-2}\,s^{-1}$	[29]–[31], [38]–[40].
Binding rate for C4b:C2a and C4BP Disassociation rate for C4b:C2a:C4BP	$k^{+}_{C4bC2aC4BP}$ $k^{-}_{C4bC2aC4BP}$	$2.0 \times 10^{5}\,M^{-1}s^{-1}$ $1.6 \times 10^{-2}\,s^{-1}$	Estimation functionally homologous protein C4b and C4BP.

Binding rate for C3b and CR1 Disassociation rate for C3b:CR1	k^{+}_{C3bCR1} k^{-}_{C3bCR1}	$4.4 \times 10^{6}\ M^{-1}s^{-1}$ $5.7 \times 10^{-2}\ s^{-1}$	[29]–[31], [37]
Binding rate for C3b:Bb and CR1 Disassociation rate for C3b:Bb:CR1	$k^{+}_{C3bBbCR1}$ $k^{-}_{C3bBbCR1}$	$4.4 \times 10^{6}\ M^{-1}s^{-1}$ $5.7 \times 10^{-2}\ s^{-1}$	Estimation functionally homologous protein C3b and CR1.
Binding rate for fC3b:Bb:C3b and CR1 Disassociation rate for fC3b:Bb:C3b:CR1	$k^{+}_{fC3bBbC3bCR1}$ $k^{-}_{fC3bBbC3bCR1}$	$9.8 \times 10^{4}\ M^{-1}s^{-1}$ $2.1 \times 10^{-3}\ s^{-1}$	[29]–[31], [37]
Binding rate for fC3b:Bb and DAF Disassociation rate for fC3b:Bb:DAF	$k^{+}_{fC3bBbDAF}$ $k^{-}_{fC3bBbDAF}$	$1.4 \times 10^{3}\ M^{-1}s^{-1}$ $1.2 \times 10^{-3}\ s^{-1}$	[29]–[31], [41]
Binding rate for C4b:C2a and DAF Disassociation rate for C4b:C2a:DAF	$k^{+}_{C4bC2aDAF}$ $k^{-}_{C4bC2aDAF}$	$1.4 \times 10^{3}\ M^{-1}s^{-1}$ $1.2 \times 10^{-3}\ s^{-1}$	Estimation functionally homologous protein C3 convertase (fC3b:Bb) and DAF.
Binding rate for C4b:C2a:C3b and DAF Disassociation rate for C4b:C2a:C3b:DAF	$k^{+}_{C4bC2aC3bDAF}$ $k^{-}_{C4bC2aC3bDAF}$	$1.4 \times 10^{3}\ M^{-1}s^{-1}$ $1.2 \times 10^{-3}\ s^{-1}$	Estimation functionally homologous protein C3 convertase (C4b:C2a) and DAF.
Binding rate for fC3b:Bb:C3b and DAF Disassociation rate for fC3b:Bb:C3b:DAF	$k^{+}_{fC3bBbC3bDAF}$ $k^{-}_{fC3bBbC3bDAF}$	$1.4 \times 10^{3}\ M^{-1}s^{-1}$ $1.2 \times 10^{-3}\ s^{-1}$	Estimation functionally homologous protein C3 convertase (fC3b:Bb) and DAF.
Binding rate for C4b:C2a and CR1 Disassociation rate for C4b:C2a:CR1	$k^{+}_{C4bC2aCR1}$ $k^{-}_{C4bC2aCR1}$	$3.8 \times 10^{6}\ M^{-1}s^{-1}$ $4.2 \times 10^{-2}\ s^{-1}$	[29]–[31].
Binding rate for C3W:Bb and FH Disassociation rate for C3W:Bb:FH	$k^{+}_{C3WBbFH}$ $k^{-}_{C3WBbFH}$	$1.1 \times 10^{6}\ M^{-1}s^{-1}$ $5.9 \times 10^{-2}\ s^{-1}$	Estimation functionally homologous protein C3b and FH.
Binding rate for C5b and C6 Disassociation rate for C5b:C6	k^{+}_{C5bC6} k^{-}_{C5bC6}	$6.0 \times 10^{4}\ M^{-1}s^{-1}$ $9.0 \times 10^{-8}\ s^{-1}$	[29]–[31], [38], [42]

Binding rate for C5b:C6 and C7 Disassociation rate for C5b:C6:C7	$k^{+}_{C5bC6C7}$ $k^{-}_{C5bC6C7}$	$7.3 \times 10^{5}\ M^{-1}s^{-1}$ $1.5 \times 10^{-7}\ s^{-1}$	[29]–[31], [38], [42]
Binding rate for C5b:C6:C7 and C8 Disassociation rate for C5b:C6:C7:C8	$k^{+}_{C5bC6C7C8}$ $k^{-}_{C5bC6C7C8}$	$1.1 \times 10^{6}\ M^{-1}s^{-1}$ $9.8 \times 10^{-7}\ s^{-1}$	[29]–[31], [38], [42]
Binding rate for C5b:C6:C7:C8 and C9 Disassociation rate for C5b:C6:C7:C8:C9	$k^{+}_{C5bC6C7C8C9}$ $k^{-}_{C5bC6C7C8C9}$	$2.8 \times 10^{6}\ M^{-1}s^{-1}$ $2.8 \times 10^{-6}\ s^{-1}$	[29]–[31], [38], [42]
Association of fC3b to H_2O	k^{+}_{fC3b}	$4.2 \times 10^{8}\ M^{-1}s^{-1}$	[29]–[31]
Binding rate for fC3b and IgG	$k^{+}_{IgGfC3b}$	$4.2 \times 10^{8}\ M^{-1}s^{-1}$	[29]–[31]
Activation rate of C1	k^{+}_{C1}	$2.1 \times 10^{-5}\ s^{-1}$	[29]–[31]
Binding rate for C1 and inhibitor C1INH	$k^{+}_{C1C1INH}$	$4.3 \times 10^{5}\ M^{-1}s^{-1}$	[29]–[31], [43]
Binding rate of C1INH and MASP1	$k^{+}_{C1INHMASP1}$	$6.3 \times 10^{3}\ M^{-1}s^{-1}$	[14], [29]–[31], [44]
Binding rate of C1INH and MASP2	$k^{+}_{C1INHMASP2}$	$2.2 \times 10^{7}\ M^{-1}s^{-1}$	[29]–[32]
Disassociation of initial C3-convertase C3W:Bb Disassociation of C3-convertase fC3b:Bb	k^{-}_{C3WBb} k^{-}_{fC3bBb}	$9.0 \times 10^{-3}\ s^{-1}$ $7.70 \times 10^{-3}\ s^{-1}$	Estimation is based on the increases in decay rate of fC3b:Bb. The enzyme C3W:Bb is less active and less stable compared to C3bBb [29]–[31], [43].
Binding rate for C4b and C2 Disassociation rate for C4b:C2	k^{+}_{C4bC2} k^{-}_{C4bC2}	$1.6 \times 10^{6}\ M^{-1}s^{-1}$ $4.2 \times 10^{-3}\ s^{-1}$	[29]–[31], [34].
Binding rate for fC3b:C4b and C2 Disassociation rate for fC3b:C4b:C2	$k^{+}_{fC3bC4bC2}$ $k^{-}_{fC3bC4bC2}$	$1.6 \times 10^{6}\ M^{-1}s^{-1}$ $4.2 \times 10^{-3}\ s^{-1}$	[29]–[31].

Binding rate for C4b and C2a Disassociation rate for C4b:C2a	k^{+}_{C4bC2a} k^{-}_{C4bC2a}	$4.4 \times 10^{3}\ M^{-1}s^{-1}$ $5.8 \times 10^{-3}\ s^{-1}$	In Quasi steady-state approximation (QSSA), rapid equilibrium leads to $k_m \approx k_d$, QSSA leads to $k_m \approx \frac{k_{cat}}{k^{+}}$ [45]. $\frac{k_{cat}}{k_m} = 4.4\times 10^{3}\ M^{-1}s^{-1}$ [46] , $k^{-} = 5.8\times 10^{-3}s^{-1}$ [38].
Binding rate for C4b:C2a and C3b Disassociation of C5-convertase C4b:C2a:C3b	$k^{+}_{C4bC2aC3b}$ $k^{-}_{C4bC2aC3b}$	$1.5 \times 10^{7}\ M^{-1}s^{-1}$ $5.0 \times 10^{-3}\ s^{-1}$	In Quasi steady-state approximation (QSSA), rapid equilibrium leads to $k_m \approx k_d$, QSSA leads to $k_m \approx \frac{k_{cat}}{k^{+}}$ [45]. $\frac{k_{cat}}{k_m} = 1.5\times 10^{7}\ M^{-1}s^{-1}$ [46] , $k^{-} = 5.0\times 10^{-3}s^{-1}$ [30].
Binding rate for fC3b and C3b:FB Disassociation of fC3b:C3b:FB	$k^{+}_{fC3bC3bFB}$ $k^{-}_{fC3bC3bFB}$	$21.3 \times 10^{4}\ M^{-1}s^{-1}$ $15.5 \times 10^{-2}s^{-1}$	Estimation functionally homologous protein fC3b and FB.
Binding rate for fC3b and C3b:FB Disassociation of fC3b:C3b:FB	$k^{+}_{fC3bC4bFB}$ $k^{-}_{fC3bC4bFB}$	$21.3 \times 10^{4}\ M^{-1}s^{-1}$ $15.5 \times 10^{-2}s^{-1}$	Estimation functionally homologous protein fC3b and FB.
Decay of C3-convertase (fC3b:Bb) by down-regulator Factor H (FH)	$k^{-}_{dfC3bBbFH}$	$1.7 \times 10^{-2}\ s^{-1}$	[47]
Binding rate for fC3b and C4b	$k^{+}_{fC3bC4b}$	$4.2 \times 10^{8}\ M^{-1}s^{-1}$	[29]–[31]
Decay of initial C3-convertase (C3W:Bb) by inhibitor FH	$k^{-}_{dC3WBbFH}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C3-convertase (fC3b:Bb) by inhibitor DAF	$k^{-}_{dfC3bBbDAF}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C3-convertase (fC3b:Bb) by inhibitor CR1	$k^{-}_{dfC3bBbCR1}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Disassociation of C3-convertase (fC3b:Bb) and properdin (P) complex (fC3b:Bb:P)	$k^{-}_{fC3bBbP}$	$7.7 \times 10^{-4}\ s^{-1}$	[29]–[31], [48]

Disassociation of C5-convertase (C3b:Bb:C3b) and properdin (P) complex (C3b:Bb:C3b:P)	$k^{-}_{C3bBbC3bP}$	$5.7 \times 10^{-4}\ s^{-1}$	[30], [31], [48]
Decay of C5-convertase (C3b:Bb:C3b) by inhibitor FH	$k^{-}_{dfC3bBbC3bFH}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C5-convertase (fC3b:Bb:C3b) by inhibitor CR1	$k^{-}_{dfC3bBbC3bCR1}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C5-convertase (C3b:Bb:C3b) by inhibitor DAF on host cell	$k^{-}_{dC3bBbC3bDAF}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C5-convertase (C4b:C2a:C3b) by inhibitor CR1on host cell	$k^{-}_{dC4bC2aC3bCR1}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C5-convertase (C4b:C2a:C3b) by inhibitor DAF on host cell	$k^{-}_{dC4bC2aC3bDAF}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C3-convertase (C4b:C2a) by down-regulator C4BP on host cell	$k^{-}_{dC4bC2aC4BP}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C3-convertase (C4b:C2a) by down-regulator CR1 on host cell	$k^{-}_{dC4bC2aCR1}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C3-convertase (C4b:C2a) by down-regulator CR1 on host cell	$k^{-}_{dC4bC2aDAF}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein fC3b:Bb down-regulated by FH.
Decay of C5-convertase (C4b:C2a:C3b) by down-regulator CR1 on host cell	$k^{-}_{dC4bC2aC3bCR1}$	$1.7 \times 10^{-2}\ s^{-1}$	It is assumed based on the decay of functionally homologous protein C4b:C2a down-regulated by CR1.

Disassociation of C5-convertase C4b:C2a:C3b	$k^{-}_{C4bC2aC3b}$	$5.0 \times 10^{-3}\ s^{-1}$	[29]–[31], [46]
Binding rate for CR1 and fC3b:C4b Disassociation rate for fC3b:C4b:CR1	$k^{+}_{fC3bC4bCR1}$ $k^{-}_{fC3bC4bCR1}$	$9.8 \times 10^{4}\ M^{-1}s^{-1}$ $2.1 \times 10^{-3}\ s^{-1}$	[29]–[31], [49]
Binding rate for fC3b:C4b and FH Disassociation rate for fC3b:C4b:FH	$k^{+}_{fC3bC4bFH}$ $k^{-}_{fC3bC4bFH}$	$1.1 \times 10^{6}\ M^{-1}s^{-1}$ $5.9 \times 10^{-2}\ s^{-1}$	Estimation functionally homologous protein fC3b and FH.
Binding rate for CR1 and fC3b:C4b:C2a Disassociation rate for fC3b:C4b:C2a:CR1	$k^{+}_{fC3bC4bC2aCR1}$ $k^{-}_{fC3bC4bC2aCR1}$	$9.8 \times 10^{4}\ M^{-1}s^{-1}$ $2.1 \times 10^{-3}\ s^{-1}$	Estimation functionally homologous protein fC3b:C4b and CR1.
Binding rate for fC3b:Bb and P Disassociation rate for fC3b:Bb:P	$k^{+}_{fC3bBbP}$ $k^{-}_{fC3bBbP}$	$1.5 \times 10^{5}\ M^{-1}s^{-1}$ $15.5 \times 10^{-5}\ s^{-1}$	Estimation functionally homologous protein fC3b and P.
Binding rate for fC3b:Bb:C3b and P Disassociation rate for fC3b:Bb:C3b:P	$k^{+}_{fC3bBbC3bP}$ $k^{-}_{fC3bBbC3bP}$	$1.5 \times 10^{5}\ M^{-1}s^{-1}$ $15.5 \times 10^{-5}\ s^{-1}$	Estimation functionally homologous protein fC3b and P.
Binding rate for fC3b:FB and P Disassociation rate for fC3b:FB:P	$k^{+}_{fC3bFBP}$ $k^{-}_{fC3bFBP}$	$1.5 \times 10^{5}\ M^{-1}s^{-1}$ $15.5 \times 10^{-5}\ s^{-1}$	Estimation functionally homologous protein fC3b and P.
Binding rate for lgG:fC3b:FB and P Disassociation rate for lgG:fC3b:FB:P	$k^{+}_{fC3bFBP}$ $k^{-}_{fC3bFBP}$	$1.5 \times 10^{5}\ M^{-1}s^{-1}$ $15.5 \times 10^{-5}\ s^{-1}$	Estimation functionally homologous protein fC3b and P.
Synthesis rate of FB	k^{+}_{sFB}	$0.013 \times 10^{-9}\ Ms^{-1}$	[50]
Degradation rate of FB	k^{-}_{dFB}	$5.5 \times 10^{-6}\ s^{-1}$	[50]
Synthesis rate of FH	k^{+}_{sFH}	$0.0117 \times 10^{-9}\ Ms^{-1}$	[50]
Degradation rate of FH	k^{-}_{dFH}	$3.7 \times 10^{-6}\ s^{-1}$	[50]

Synthesis rate of properdin (P)	k_{sP}^{+}	$1.17 \times 10^{-12}\ Ms^{-1}$	[50]
Degradation rate of properdin (P)	k_{dP}^{-}	$2.7 \times 10^{-7}\ s^{-1}$	[50]
Synthesis rate of C3	k_{sC3}^{+}	$0.053 \times 10^{-9}\ Ms^{-1}$	[50]
Degradation rate of C3	k_{dC3}^{-}	$6.5 \times 10^{-6}\ s^{-1}$	[50]
Hydrolysis of C3W	k_{C3W}^{+}	$4.5 \times 10^{-6}\ s^{-1}$	[29]–[31]
Binding rate for MBL and MASP1 Disassociation rate for MBL:MASP1	$k_{MBLMASP1}^{+}$ $k_{MBLMASP1}^{-}$	$2.1 \times 10^{5}\ M^{-1}s^{-1}$ $6.8 \times 10^{-4}\ s^{-1}$	[31], [51]
Binding rate for MBL and MASP2 Disassociation rate for MBL:MASP2	$k_{MBLMASP2}^{+}$ $k_{MBLMASP2}^{-}$	$2.3 \times 10^{5}\ M^{-1}s^{-1}$ $5.5 \times 10^{-4}\ s^{-1}$	[31], [51]
Cleavage of C3 by initial C3-convertase (C3W:Bb)	k_{catC3}^{C3WBb} k_{mC3}^{C3WBb}	$0.78\ s^{-1}$ $11.6 \times 10^{-6}\ M$	The C3b:Bb have a half-life ($t_{\frac{1}{2}}$) of $90 \pm 2s$ and $\frac{k_{cat}}{k_m}$ of $31.1 \times 10^{4} \pm 0.8 \times 10^{4}$ $M^{-1}\ s^{-1}$. The C3b:Bb structurally/functionally homologous C3W:Bb [31] is found slightly less stable than C3b:Bb. It is known that C3W:Bb have $t_{\frac{1}{2}}$ of $77 \pm 3s$ and presented only half the activity of C3b:Bb ($\frac{k_{cat}}{k_m}$ is $16.3 \times 10^{4} \pm 16.3 \times 10^{4}$ $M^{-1}\ s^{-1}$) [43]. Assumption k_m of C3W:Bb found from increasing k_m of C3b:Bb [31].
Cleavage of C3 by C3-convertase (C3b:Bb)	k_{catC3}^{C3bBb} k_{mC3}^{C3bBb}	$1.78\ s^{-1}$ $5.86 \times 10^{-6}M$	[29]–[31], [43]
Cleavage of C3 by C3-convertase (C4b:C2a)	k_{catC3}^{C4b2a} k_{mC3}^{C4b2a}	$3.17\ s^{-1}$ $1.8 \times 10^{-6}\ M$	[29]–[31], [38]
Cleavage of C5 by C3-convertase (C3b:Bb)	k_{catC5}^{C3bBb} k_{mC5}^{C3bBb}	$1.1 \times 10^{-2}\ s^{-1}$ $24.0 \times 10^{-6}\ M$	[29]–[31], [38]

Cleavage of C5 by C3-convertase (C4b:C2a)	k_{catC5}^{C4b2a} k_{mC5}^{C4b2a}	$2.2 \times 10^{-2}\ s^{-1}$ 8.9×10^{-6} M	[29]–[31], [38]
Cleavage of C5 by C5-convertase (C4b:C2a:C3b)	$k_{catC5}^{C4b2a3b}$ $k_{mC5}^{C4b2a3b}$	$2.0 \times 10^{-2}\ s^{-1}$ 5.1×10^{-9} M	[38]
Cleavage of C5 by C5-convertase (C3b:Bb:C3b)	$k_{catC5}^{C3bBbC3b}$ $k_{mC5}^{C3bBbC3b}$	$3.0 \times 10^{-3}\ s^{-1}$ 48.0×10^{-9} M	[29]–[31], [38]
Activation of the product/complex C3W:FB by Factor D (FD)	$k_{catC3WFB}^{FD}$ k_{mC3WFB}^{FD}	$5.0\ s^{-1}$ 2.5×10^{-6} M	[29]–[31]
Down-regulation/inhibition of the complex fC3b:FH by negative regulator Factor I (FI)	$k_{catfC3bFH}^{FI}$ $k_{mfC3bFH}^{FI}$	$1.32\ s^{-1}$ 2.52×10^{-7} M	It is assumed based on the FI inhibition of functionally homologous protein C3b:FH.
Down-regulation of the complex C3b:FH by inhibitor FI	$k_{catC3bFH}^{FI}$ k_{mC3bFH}^{FI}	$1.32\ s^{-1}$ 2.52×10^{-7} M	[29]–[31]
Down-regulation of the complex C3W:FH by FI	$k_{catC3WFH}^{FI}$ k_{mC3WFH}^{FI}	$1.32\ s^{-1}$ 2.52×10^{-7} M	It is assumed based on the FI inhibition of functionally homologous protein C3b:FH.
Down-regulation of the complex fC3b:C4b:FH by FI	$k_{catfC3bC4bFH}^{FI}$ $k_{mfC3bC4bFH}^{FI}$	$1.32\ s^{-1}$ 2.52×10^{-7} M	It is assumed based on the FI inhibition of functionally homologous protein C3b:FH.
Up-regulation of the complex fC3b:FB by FD	$k_{catfC3bFB}^{FD}$ $k_{mfC3bFB}^{FD}$	$1.32\ s^{-1}$ 2.52×10^{-7} M	Estimation structurally/functionally homologous protein C3W and Factor B [29]–[31], [34].

Inhibition of the complex fC3b:CR1 by FI	$k^{FI}_{catfC3bCR1}$ $k^{FI}_{mfC3bCR1}$	1.32 s^{-1} 2.52×10^{-7} M	It is assumed based on the FI inhibition of functionally homologous protein C3b:FH.
Inhibition of the complex C3b:CR1 by FI	$k^{FI}_{catC3bCR1}$ $k^{FI}_{mC3bCR1}$	1.32 s^{-1} 2.52×10^{-7} M	It is assumed based on the FI inhibition of functionally homologous protein C3b:FH.
Inhibition of the complex fC3b:C4b:CR1 by FI	$k^{FI}_{catfC3bC4bCR1}$ $k^{FI}_{mfC3bC4bCR1}$	1.32 s^{-1} 2.52×10^{-7} M	It is assumed based on the FI inhibition of functionally homologous protein C3b:FH.
Activation of the complex fC3b:FB:P by FD	$k^{FD}_{catfC3bFBP}$ $k^{FD}_{mfC3bFBP}$	5.0 s^{-1} 2.5×10^{-6} M	It is assumed based on the FD upregulation of functionally homologous protein C3W:FB.
Activation of the complex lgG:fC3b:FB by FD	$k^{FD}_{catlgGfC3bFB}$ $k^{FD}_{mlgGfC3bFB}$	5.0 s^{-1} 2.5×10^{-6} M	It is assumed based on the FD upregulation of functionally homologous protein C3W/FB.
Activation of the complex lgG:fC3b:FB:P by FD	$k^{FD}_{catlgGfC3bFBP}$ $k^{FD}_{mlgGfC3bFBP}$	5.0 s^{-1} 2.5×10^{-6} M	It is assumed based on the FD upregulation of functionally homologous protein C3W:FB.
Activation of the complex fC3b:C4b:FB by FD	$k^{FD}_{catfC3bC4bFB}$ $k^{FD}_{mfC3bC4bFB}$	5.0 s^{-1} 2.5×10^{-6} M	It is assumed based on the FD upregulation of functionally homologous protein C3W:FB .
Activation of the complex C3b:FB by FD	$k^{FD}_{catC3bFB}$ k^{FD}_{mC3bFB}	5.0 s^{-1} 2.5×10^{-6} M	It is assumed based on the FD upregulation of functionally homologous protein fC3b:FB [29]–[31].
Activation of the complex fC3b:C4b:P:FB by FD	$k^{FD}_{catfC3bC4bPFB}$ $k^{FD}_{mfC3bC4bPFB}$	5.0 s^{-1} 2.5×10^{-6} M	It is assumed based on the FD upregulation of functionally homologous protein C3W:FB [29]–[31].

Cleavage rate of MASP fragment (MASP1) on C2 substrate	k_{catC2}^{MASP1} k_{mC2}^{MASP1}	$0.1\ s^{-1}$ 4.8×10^{-6} M	[31], [52]
Cleavage rate of MASP fragment (MASP2) on C2 substrate	k_{catC2}^{MASP2} k_{mC2}^{MASP2}	$5.6\ s^{-1}$ 5.2×10^{-6} M	[31], [53]
Cleavage rate of MASP fragment (MASP1) on C4 substrate	k_{catC4}^{MASP1} k_{mC4}^{MASP1}	$2.0 \times 10^{-3}\ s^{-1}$ 5.2×10^{-6} M	[31], [53]
Cleavage rate of MASP fragment (MASP2) on C4 substrate	k_{catC4}^{MASP2} k_{mC4}^{MASP2}	$1.9\ s^{-1}$ 8.5×10^{-8} M	[31], [53]
Cleavage rate of C2 by C1	k_{catC2}^{C1} k_{mC2}^{C1}	$5.1\ s^{-1}$ 6.1×10^{-6} M	[31], [53]
Cleavage rate of C4 by C1	k_{catC4}^{C1} k_{mC4}^{C1}	$5.4\ s^{-1}$ 6.10×10^{-6} M	[31], [53]
Cleavage rate of fC3b:C3b:FB by FD	$k_{catfC3bC3bFB}^{FD}$ $k_{mfC3bC3bFB}^{FD}$	$5.0\ s^{-1}$ 2.5×10^{-6} M	[29]–[31]
Binding rate for C3a and C3aR1 Disassociation rate for C3a:C3aR1	$k_{C3aC3aR1}^{+}$ $k_{C3aC3aR1}^{-}$	$2.6 \times 10^{8}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	Disassociation constant (k_d) is 3.85×10^{-9}M [54]. Assume $k^- = 0.1\ s^{-1}$, Estimation for k^+ by formula $k_d = \frac{k^-}{k^+}$.
Binding rate for C5a and C5aR1 Disassociation rate for C5a:C5aR1	$k_{C5aC5aR1}^{+}$ $k_{C5aC5aR1}^{-}$	$2.2 \times 10^{8}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	Disassociation constant (k_d) for the product C5a:C5aR1 is $\approx 4.5 \times 10^{-9}$M and free energy of association (ΔG_{bind}) is -13.6 ± 4.1 kcalmol^{-1} [55]. Assumed $k^- = 0.1\ s^{-1}$, estimated for k^+ by formula $k_d = \frac{k^-}{k^+} = e^{\frac{\Delta G_{bind}}{RT}}$.

Inhibition of C1s by C1INH	$k^{+}_{C1INHC1s}$	$9.5 \times 10^{4}\ M^{-1}s^{-1}$	C1 inhibitor binds to C1s [56].
Degradation rate of FD	k^{-}_{dFD}	$2.2 \times 10^{-4}\ s^{-1}$	[57], [58]
Synthesis rate of FD	k^{+}_{sFD}	$1.3 \times 10^{-11}\ Ms^{-1}$	[57]
Synthesis rate of C5	k^{+}_{sC5}	$2.2 \times 10^{-12}\ Ms^{-1}$	[57]
Degradation rate of C5	k^{-}_{dC5}	$5.6 \times 10^{-6}\ s^{-1}$	[57]
Synthesis rate of C6	k^{+}_{sC6}	$1.8 \times 10^{-10}\ Ms^{-1}$	[57]
Degradation rate of C6	k^{-}_{dC6}	$2.9 \times 10^{-4}\ s^{-1}$	[57]
Synthesis rate of C7	k^{+}_{sC7}	$1.9 \times 10^{-12}\ Ms^{-1}$	[57]
Degradation rate of C7	k^{-}_{dC7}	$3.2 \times 10^{-6}\ s^{-1}$	[57]
Synthesis rate of C8	k^{+}_{sC8}	$1.4 \times 10^{-12}\ Ms^{-1}$	[57]
Degradation rate of C8	k^{-}_{dC8}	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Synthesis rate of C9	k^{+}_{sC9}	$3.4 \times 10^{-12}\ Ms^{-1}$	[57]
Degradation rate of C9	k^{-}_{dC9}	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of Ba	k^{-}_{dBa}	$7.7 \times 10^{-5}\ s^{-1}$	[57]
Degradation rate of Bb	k^{-}_{dBb}	$7.7 \times 10^{-5}\ s^{-1}$	[57]
Degradation rate of C3W	k^{-}_{dC3W}	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of C3WFB	k^{-}_{dC3WFB}	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of C3WBb	k^{-}_{dC3WBb}	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of fC3b	k^{-}_{dfC3b}	$4.01 \times 10^{-6}\ s^{-1}$	[57]

Degradation rate of fC3bFB	$k^{-}_{dfC3bFB}$	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of fC3bBb	$k^{-}_{dfC3bBb}$	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of C5b	k^{-}_{dC5b}	$5.0 \times 10^{-3}\ s^{-1}$	[57], [59]
Degradation rate of C5a	k^{-}_{dC5a}	$1.15 \times 10^{-2}\ s^{-1}$	[57], [60]
Degradation rate of C3b	k^{-}_{dC3b}	$4.01 \times 10^{-6}\ s^{-1}$	[57]
Degradation rate of C3a	k^{-}_{dC3a}	$1.15 \times 10^{-2}\ s^{-1}$	[57]
Binding rate for C1q and gC1qR Disassociation rate for C1q:gC1qR	$k^{+}_{C1qgC1qR}$ $k^{-}_{C1qC1qR}$	$4.0 \times 10^{2}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	C1q binds to gC1q-receptor (gC1qR) with an affinity ($k_d = 250 \times 10^{-6}$) [61][50]. The disassociation rate (k^{-1}) is unknown, assumed a small value for $k^{-1} = 0.1\ s^{-1}$. Using the formula $k_d = \frac{k^{-}}{k^{+}}$, determined k^{+}.
Inhibition of MAC by CD59	$k^{+}_{MACCD59}$	$1.0 \times 10^{6}\ M^{-1}s^{-1}$	The terminal complement complex (TCC), C5b-9 (MAC) bind to CD59 glycoprotein, also known as MAC-inhibitory protein (MAC-IP) [29].

Table S1c. The hemostatic system and complement system cross-talk KCs

Meaning	Rate constant	Value adopted	Source
Inhibition of F12a by C1INH	$k^{+}_{C1INHF12a}$	$3.6 \times 10^{3}\ M^{-1}s^{-1}$	C1INH suppresses F12a [62], [63].
Inhibition of KAL by C1INH	$k^{+}_{C1INHKAL}$	$1.7 \times 10^{4}\ M^{-1}s^{-1}$	C1INH suppresses KAL [62], [63]. Association rate of C1INH and KLK [64].
Inhibation of F2a by FH	k^{+}_{FHF2a}	$3.367 \times 10^{7}\ M^{-1}s^{-1}$	For FH and F2a the disassociation constant (k_d) is measured 29.9nM. Binding affinity of FH and F2a range (3.1 - 200 nM) [65]. Estimation for association rate (k^{+}_{FHF2a}) based on k_d.

Inhibation of F1a by FH	k^{+}_{FHF1a}	$2.62 \times 10^{7}\ M^{-1}s^{-1}$	FH and F1a disassociation constant (k_d) is measured 38.2nM. Binding affinity of FH and F2a range (3.1 - 200 nM) [65]. Estimation for association rate (k^{+}_{FHF1a}) based on k_d.
Cleavage of C5 by Pn	k^{Pn}_{catC5} k^{Pn}_{mC5}	$0.056\ s^{-1}$ 2.4×10^{-6}	Pn can cleaves C5 generating C5a with a catalytic efficiency ($\frac{k_{cat}}{k_m}$) of 2.3×10^{4} $M^{-1}s^{-1}$ [66], [67].
Cleavage of C5 by F2a	k^{F2a}_{catC5} k^{F2a}_{mC5}	$0.56\ s^{-1}$ 2.4×10^{-6}	F2a is less effective than Pn in cleaving C5 to generates C5a [66]. We could estimate catalytic efficiency ($\frac{k_{cat}}{k_m}$) of $2.3 \pm 0.6 \times 10^{3}\ M^{-1}s^{-1}$ based on Pn catalytic efficiency.
Cleavage of C3 by Pn	k^{Pn}_{catC3} k^{Pn}_{mC3}	$0.056\ s^{-1}$ 2.4×10^{-6}	Pn can cleaves C3. The cleavage of C3 by Pn is assumed based on functionally homologous C5.
Cleavage of C3 by F2a	k^{F2a}_{catC3} k^{F2a}_{mC3}	$0.56\ s^{-1}$ 2.4×10^{-6}	The cleavage of C3 by F2a is assumed based on functionally homologous C5.
Cleavage of C3 by F10a	k^{F10a}_{catC3} k^{F10a}_{mC3}	$0.056\ s^{-1}$ 2.4×10^{-5}	F10a is less effective than Pn in cleaving C3 to generates C3a [66]. We could estimate catalytic efficiency ($\frac{k_{cat}}{k_m}$) of $2.3 \times 10^{3}\ M^{-1}s^{-1}$ based on Pn catalytic efficiency.
Cleavage of C5 by F10a	k^{F10a}_{catC5} k^{F10a}_{mC5}	$0.056\ s^{-1}$ 2.4×10^{-5}	F10a is less effective than Pn in cleaving C5 to generates C5a, respectively [66]. We could estimate catalytic efficiency ($\frac{k_{cat}}{k_m}$) of $2.3 \pm 0.6 \times 10^{3}\ M^{-1}s^{-1}$ based on Pn catalytic efficiency.
Production of TF by C5a	k^{C5a}_{catTF}	$0.01 \times 10^{-3}\ s^{-1}$	C5a can increase the activity and expression of TF [68]. C5a stimulate the expression of TF on neutrophils via C5aR [62], [69]. Estimated a small value.
Production of TF by C3a	k^{C3a}_{catTF}	$0.01 \times 10^{-3}\ s^{-1}$	C3a increases the expression of TF [68]. Assumption based on C3a functional homologous C5a.
Inhibition of F11a by C1INH	$k^{+}_{C1INHF11a}$	$1.8 \times 10^{3}\ M^{-1}s^{-1}$	CIINH binds with F11a and inhibit it [2], [3].
Inhibition of F2a by C1INH	$k^{+}_{C1INHF2a}$	$1.0 \times 10^{2}\ M^{-1}s^{-1}$	C1-INH can inhibit F2a. Assumption.

Inhibition of Plasmin by C1INH	$k^{+}_{C1INHPlasmin}$	$5.5 \times 10^{3}\ M^{-1}s^{-1}$	Kinetic analysis for inhibition experiment with Pn, generated an association rate for plasma C1INH [70].
Generation of F1 by IL6	k^{IL6}_{catF1}	$0.01 \times 10^{-6}\ s^{-1}$	IL6 induces the expression of F1. IL-6 correlated positively with F1 concentration [71]. Assume a small random value for generation of F1 by IL6.
Activation rate of F2 by MASP1	k^{MASP1}_{catF2}	$141.0 \times 10^{3}\ M^{-1}s^{-1}$	MASP1 activates and cleaves F2 to F2a [63], [72], [73]. Activation of F2 wildtype by MASP1 computed via kinetic analysis [74].
Activation rate of F2 by MASP2	k^{MASP2}_{catF2}	$141.0 \times 10^{3}\ M^{-1}s^{-1}$	MASP2 activates and cleaves F2 into F2a [63], [73]. Activation rate of F2 by MASP2 estimated based on functionally homologous MASP1.
Activation rate of F1 by MASP1	k^{MASP1}_{catF1}	$141.0 \times 10^{3}\ M^{-1}s^{-1}$	MASP1 activate F1 to F1a [63], [72], [73]. Assumed based on the activation rate of F2 by MASP1.
Activation rate of F1 by MASP2	k^{MASP2}_{catF1}	$141.0 \times 10^{3}\ M^{-1}s^{-1}$	MASP1 activate F1 to F1a [63], [72], [73]. Activation rate of F1 by MASP2 estimated based on functionally homologous MASP1.
Generation of F2 by MAC	k^{MAC}_{catF2}	$0.1\ s^{-1}$	Estimation for MAC (C5b-C9) can generate F2 [62].
Activation of C1r by F12a	k^{F12a}_{catC1r}	$1.0 \times 10^{2}\ M^{-1}s^{-1}$	F12a can activate the C1r [62], [68], [75]. Assumed a small value for the activation of C1r by F12a.
Association rate for gC1qR and F12 Disassociation rate for gC1qR:F12	$k^{+}_{gC1qRF12}$ $k^{-}_{gC1qRF12}$	$8.3 \times 10^{13}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	gC1qR binds to F12 with disassociation constant $k_d = 120 \times 10^{-9}$M [76]. Assumed a small value for $k^{-1} = 0.1\ s^{-1}$. Using formula $k_d = \frac{k^{-}}{k^{+}}$, estimated for k^{+}.
Production of F12a by gC1qR:F12	$k^{gC1qRF12}_{catF12a}$	$0.1\ s^{-1}$	The complex of gC1qR and F12 can generates F12a [77].
Association rate for gC1qR and HK Disassociation rate for gC1qR:HK	$k^{+}_{gC1qRHK}$ $k^{-}_{gC1qRHK}$	$5.3 \times 10^{11}\ M^{-1}s^{-1}$ $0.1\ s^{-1}$	gC1q-receptor (gC1qR) binds to HK with disassociation constant $k_d = 1.9 \times 10^{-9}$M [76]. Assumed a small value for $k^{-1} = 0.1\ s^{-1}$. Using formula $k_d = \frac{k^{-}}{k^{+}}$, estimated k^{+}.
Production of BK by gC1qR:HK	$k^{gC1qRHK}_{catBK}$	$0.1\ s^{-1}$	The product of gC1qR and HK can release BK [77]. The generation rate is unknown, estimated a small value for it.

Cleavage of FB by KAL	k_{catFB}^{KAL} k_{mFB}^{KAL}	$0.01\ s^{-1}$ $1.0 \times 10^{-12}\ M$	KAL can cleaves FB [68], [77]. Assumed small values for the catalytic rate constant and Michaelis constant. FB co-exist with hydrolyzed C3 (C3W) and fC3b.
Cleavage of C3 by KAL	k_{catC3}^{KAL} k_{mC3}^{KAL}	$0.01\ s^{-1}$ $1.0 \times 10^{-12}\ M$	KAL can cleaves C3 [68], [77]. Assumed small values for the catalytic rate constant and Michaelis constant.
Cleavage of C5 by KAL	k_{catC5}^{KAL} k_{mC5}^{KAL}	$0.01\ s^{-1}$ $1.0 \times 10^{-12}\ M$	Kallikrein can cleaves C5 [68]. Assumed small values for the catalytic rate constant and Michaelis constant.
Degradation rate of IL-6	k_{dIL6}^{-}	$0.01 s^{-1}$	Assumption.
Production of IL6 by BK:B2R	k_{IL6}^{BKB2R}	$0.1\ s^{-1}$	BK via B2R can stimulate the production of IL6 [78] Estimation for the production rate of IL6 by BK and B2R complex.
Production of IL6 by C3a:C3aR	$k_{IL6}^{C3aC3aR1}$	$0.1\ s^{-1}$	C3a via C3aR1 can induce IL6 [79]. Estimation for the production rate of IL6 by C3a and C3aR complex.
Production of IL6 by C5a:C5aR	$k_{IL6}^{C5aC5aR1}$	$0.1\ s^{-1}$	C5a via C5aR1 can induce interleukin 6 (IL6) [79]. Estimation for production rate of IL6 by C5a and C5aR complex.
Activation of Pro-FD by MASP1	$k_{catPro-DF}^{MASP1}$	$3.9 \times 10^{3}\ M^{-1}s^{-1}$	Activation and cleavage of Pro-FD by MASP1 that can be converted into active FD [80].
Activation of Pro-FD by MASP2	$k_{catPro-FD}^{MASP2}$	$7.2 \times 10^{3}\ M^{-1}s^{-1}$	Activation and cleavage of Pro-FD by MASP2 that can be converted into active FD [80].
Activation of Pro-FD by F2a	$k_{catPro-FD}^{F2a}$	$4.6 \times 10^{2}\ M^{-1}s^{-1}$	The activation rates of pro-FD by thrombin (F2a) [80].
Cleavage of TAFI by MASP1	$k_{catTAFI}^{MASP1}$ k_{mTAFI}^{MASP1}	$0.1\ s^{-1}$ $3.9 \times 10^{-8}\ M$	MASP-1 directly activates/ cleaves TAFI [72], [77].

Table S1d. The hemostatic and complement systems entities and SARS-CoV-2 structure proteins interaction KCs

Meaning	Rate constant	Value adopted	Source
Association rate for gC1qR and CoV2S	$k^{+}_{gC1qRCoV2S}$	$1.1 \times 10^{10} M^{-1}s^{-1}$	Binding of S protein of SARS-CoV-2 (termed as CoV2S) on the surface of wild-type gC1qR of classical pathway of the complement system. The binding affinity is $k_d = 91 \times 10^{-12}$M [81]. The disassociation rate (k^{-}) is unknown, assume $k^{-} = 1s^{-1}$. Using $k_d = \frac{k^{-}}{k^{+}}$ determined k^{+}.
Association rate for gC1qR and CoV2N	$k^{+}_{C1qRCoV2N}$	$1.7 \times 10^{5} M^{-1}s^{-1}$	Binding of N protein of SARS-CoV-2 (termed as CoV2N) on the surface of wild-type gC1qR of classical pathway of the complement system. The binding affinity is $k_d = 6 \times 10^{-6}$M [81]. Assume $k^{-} = 1s^{-1}$. Using $k_d = \frac{k^{-}}{k^{+}}$ determined k^{+}.
Association rate for gC1qR and CoV2M	$k^{+}_{C1qRCoV2M}$	$2.4 \times 10^{9} M^{-1}s^{-1}$	Binding of the M protein of SARS-CoV-2 (termed as CoV2M) on the surface of wild-type C1qR of classical pathway of the complement system. The binding affinity is $k_d = 410 \times 10^{-12}$ M [81]. Assume $k^{-} = 1s^{-1}$. Using $k_d = \frac{k^{-}}{k^{+}}$ determined k^{+}.
Association rate for gC1qR and CoV2E	$k^{+}_{C1qRCoV2E}$	$2.4 \times 10^{9} M^{-1}s^{-1}$	Binding of the E protein of SARS-CoV-2 (termed as CoV2E) on the surface of wild-type C1qR classical pathway of the complement system. The binding affinity $k_d = 410 \times 10^{-12}$ M [81]. Assume $k^{-} = 1s^{-1}$. Using $k_d = \frac{k^{-}}{k^{+}}$ determined k^{+}.
Association rate for F12 and CoV2S	$k^{+}_{CoV2SF12}$	$1.0 \times 10^{6} M^{-1}s^{-1}$	S protein of SARS-CoV-2 (termed as CoV2S) binds to inactive coagulation factor F12 of contact pathway that is intrinsic pathway of the coagulation cascade [81]. Assumed for binding rate of F12 and CoV2S.
Association rate for F12 and CoV2N	$k^{+}_{CoV2NF12}$	$1.0 \times 10^{4} M^{-1}s^{-1}$	N protein of SARS-CoV-2 (termed as CoV2N) binds to coagulation factor F12 [81]. Assumption for binding rate of F12 and CoV2N.
Association rate for F12 and CoV2M	$k^{+}_{CoV2MF12}$	$1.0 \times 10^{4} M^{-1}s^{-1}$	M protein of SARS-CoV-2 (termed as CoV2M) binds to coagulation factor F12 [81]. Assumption for binding rate of F12 and CoV2M.

Association rate for F12 and CoV2E	$k^{+}_{CoV2EF12}$	$1.0 \times 10^{4} M^{-1} s^{-1}$	E protein of SARS-CoV-2 (termed as CoV2E) binds to coagulation factor F12 [81]. Assumption for binding rate of F12 and CoV2S.
Association rate for HK and CoV2S	$k^{+}_{HKCoV2S}$	$1.0 \times 10^{3} M^{-1} s^{-1}$	S protein of SARS-CoV-2 (termed as CoV2S) binds to HK of the system KKS [81]. Assumption for binding rate.
Association rate for HK and CoV2N	$k^{+}_{HKCoV2N}$	$1.0 \times 10^{3} M^{-1} s^{-1}$	N protein of SARS-CoV-2 (termed as CoV2N) binds to HK of the system KKS [81]. Assumption for binding rate.
Association rate for HK and CoV2M	$k^{+}_{HKCoV2M}$	$1.0 \times 10^{3} M^{-1} s^{-1}$	M protein of SARS-CoV-2 (termed as CoV2M) binds to HK of the system KKS [81]. Assumption for binding rate.
Association rate for HK and CoV2E	$k^{+}_{HKCoV2E}$	$1.0 \times 10^{3} M^{-1} s^{-1}$	E protein of SARS-CoV-2 (termed as CoV2E) binds to HK of the system KKS [81]. Assumption for binding rate.
Association rate for MASP2 by CoV2N protein	$k^{+}_{MASP2CoV2N}$	$6.9 \times 10^{4} M^{-1} s^{-1}$	The N protein of SARS-CoV-2 (termed as CoV2N) can cleaved/ activate MASP2 [82]. $k_{cat} = 3.64\, s^{-1}$ and $k_m = 5.437 \times 10^{-5}$ M. Assume a small value for disassociation rate $k^{-} = 0.1 s^{-1}$. Using the formula $k^{+} = \frac{k^{-} + k_{cat}}{k_m}$, determined k^{+}.
Binding rate for lgG and CoV2S Disassociation rate for the complex lgG/CoV2S	$k^{+}_{CoV2SlgG}$ $k^{-}_{CoV2SlgG}$	$2.14 \times 10^{5} M^{-1} s^{-1}$ $1.70 \times 10^{-2} s^{-1}$	Association rate for lgG via Fab (ID-1F4) bind with spike (S) protein of SARS-CoV-2 [83].
Association rate of CoV2S/lgG and C1q	$k^{+}_{CoV2SlgGC1q}$	$2.3 \times 10^{5} M^{-1} s^{-1}$	S protein of SARS-CoV-2 binding by antibody lgG mediated C1q activate complement system through classical pathway [44]. An antibody IgG1 subclass antibodies Rituximab (RTX) and Ofatumumab (OFA) bind with C1q. Association rates of C1q and RTX, C1q and OFA are $5.2 \times 10^{4} M^{-1} s^{-1}$ and $2.3 \times 10^{5} M^{-1} s^{-1}$ [84]. Estimation for lgG based on structurally/ functionally homologous lgG1 subclass.
Cleavage rate of CoV2S by F10a	$k^{F10a}_{catCoV2S}$ k^{F10a}_{mCoV2S}	$1.79 \times 10^{-1} s^{-1}$ $4.035 \times 10^{-5} M$	Cleavage rate of S protein by active coagulation factor F10a [85].
Cleavage rate of CoV2S by F2a	$k^{F2a}_{catCoV2S}$ k^{F2a}_{mCoV2S}	$5.20 \times 10^{-2} s^{-1}$ $16.34 \times 10^{-6} M$	Cleavage rate of S protein by activated coagulation factor F2a [85].

Table S1e. The Drug-Target interaction KCs

Meaning	Rate constant	Value adopted	Source
Association of Heparin to C2	k^{+}_{HepC2}	$4.13 \times 10^{3} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C2	k^{-}_{HepC2}	$1.32 \times 10^{-3}\ s^{-1}$	
Association of Heparin to C3	k^{+}_{HepC3}	$1.83 \times 10^{4} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C3	k^{-}_{HepC3}	$5.73 \times 10^{-4}\ s^{-1}$	
Association of Heparin to C4	k^{+}_{HepC4}	$9.64 \times 10^{4} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C4	k^{-}_{HepC4}	$3.46 \times 10^{-3}\ s^{-1}$	
Association of Heparin to C5	k^{+}_{HepC5}	$2.43 \times 10^{5} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C5	k^{-}_{HepC5}	$1.35 \times 10^{-3}\ s^{-1}$	
Association of Heparin to C6	k^{+}_{HepC6}	$1.72 \times 10^{4} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C6	k^{-}_{HepC6}	$5.58 \times 10^{-4}\ s^{-1}$	
Association of Heparin to C7	k^{+}_{HepC7}	$6.25 \times 10^{4} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C7	k^{-}_{HepC7}	$9.60 \times 10^{-4}\ s^{-1}$	
Association of Heparin to C8	k^{+}_{HepC8}	$4.17 \times 10^{4} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C8	k^{-}_{HepC8}	$5.74 \times 10^{-3}\ s^{-1}$	
Association of Heparin to C9	k^{+}_{HepC9}	$3.43 \times 10^{4} M^{-1} s^{-1}$	[86]
Disassociation of Heparin:C9	k^{-}_{HepC9}	$4.51 \times 10^{-3}\ s^{-1}$	

Activation of AT3 by Heparin	k^{+}_{HepAT3}	$1 \times 10^{2} M^{-1} s^{-1}$	Heparin as potentiator of AT3 [87]. Assumption.
Inhibition of C5aR1 by Avdoralimab	$k^{+}_{AvdC5aR1}$	$1.0 \times 10^{3} M^{-1} s^{-1}$	Avdoralimab (IPH5401) is a therapeutic antibody that specifically binds and blocks C5a receptors (C5aR1). It is safely used in COVID-19 patients [88]. Assumption.
Inhibition of tPA by Tranexamic acid (TXA)	k^{+}_{TXAtPA}	$1.0 \times 10^{2} M^{-1} s^{-1}$	Assumption.

Abbreviations

MBL, Mannose binding lectin; MASP1 and MASP2 stand for MBL associated Mannan-binding lectin serine protease MASP-1 and MASP-2;

C2, Complement component 2; C2a, Complement component 2a; C2b, Complement component 2a; C3aR1, C3a anaphylatoxin Receptor 1;

C4BP, Complement component 4 binding protein; CR1, Complement receptor 1; DAF, Decay Accelerating Factor;

FB, FD, FH and FI stand for Complement factor B, D, H and I, respectively;

P, Properdin; IgG, Immunoglobulin G; C1q, C1r, C1s Complement components C1q, C1r, C1s; C1, Activated Complement component 1;

Ba, cleavage fragment of FB; Bb, cleavage fragment of FB; MAC, Membrane attack complex (MAC); IL6, Interleukin 6;

F1 stand for Coagulation factor 1 (Fibrinogen); F1a, Coagulation factor 1a (Fibrin); F2, Coagulation factor 2 (Pro-Thrombin);

F2a, Coagulation factor 2a (Thrombin); F5, Coagulation factor 5 (Labile factor, Proaccelerin);

F5a, Activated coagulation factor 5; F7, Coagulation Factor 7 (Proconvertin); F7a, Activated coagulation factor 7;

F8, Coagulation factor 8 (Antihemophilic factor A); F8a, Activated coagulation factor 8; F9, Coagulation factor 9 (Antihemophilic factor B);

F9a, Activated coagulation factor 9; F10, Coagulation factor 10 (Thrombokinase); F10, Activated coagulation factor 10;

F11, Coagulation factor 11 (Plasma thromboplastin antecedent); F11, Activated coagulation factor 11; F12, Coagulation factor 12 (Hageman factor);

F12a, Activated coagulation factor 12; KAL, Kallikrein; P-KAL, Pre-Kallikrein;

Pn, Plasmin; Pg, Plasminogen; TF, Tissue factor (Tissue thromboplastin); TFPI, Tissue factor pathway inhibitor;

TAFI, Thrombin-activatable fibrinolysis inhibitor; TAFIa, Activated Thrombin-activatable fibrinolysis inhibitor; BK, Bradykinin;

C3a and C5a stand for complement anaphylatoxins;

HK, High-molecular-weight kininogen; tPA, Tissue-type plasminogen activator; A2M, Association rate of Alpha-2 macroglobulin;

AT3, Anti-Thrombin 3 (Serpin); PAI-1, Plasminogen activator inhibitor-1; B2R, B2-receptor.

S stand for Spike protein; N, Nucleocapsid; M, Membrane; E, Envelope;

KKS, Kallikrein-kinin system.

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