

# Importins promote high-frequency NF- $\kappa$ B oscillations increasing information channel capacity

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## Computational model description

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**Supplementary information: Additional file 1**

# 1 Parameters and reactions

**Table A.** Notation guide

<i>Symbol</i>	<i>Description</i>
TNF	TNF $\alpha$ trimers
TNFR <sub>i</sub>	inactive TNFR receptors
TNFR <sub>a</sub>	active TNFR receptors
IKKK <sub>n</sub>	neutral form of IKKK
IKKK <sub>a</sub>	active form of IKKK
IKK <sub>i</sub>	inactive form of IKK
IKK <sub>ii</sub>	inactive intermediate form of IKK
IKK <sub>n</sub>	neutral form of IKK kinase
IKK <sub>a</sub>	active form of IKK
A20 <sub>mRNA</sub>	A20 transcript
A20	A20 protein
I $\kappa$ B $\alpha$ <sub>mRNA</sub>	I $\kappa$ B $\alpha$ transcript
I $\kappa$ B $\alpha$ <sub>c</sub>	cytoplasmic I $\kappa$ B $\alpha$
I $\kappa$ B $\alpha$ <sub>c,p</sub>	phosphorylated cytoplasmic I $\kappa$ B $\alpha$
I $\kappa$ B $\alpha$ <sub>n</sub>	nuclear I $\kappa$ B $\alpha$
I $\kappa$ B $\alpha$ <sub>n,e</sub>	nuclear I $\kappa$ B $\alpha$ bound to an exportin
NF $\kappa$ B <sub>c</sub>	cytoplasmic NF- $\kappa$ B
NF $\kappa$ B <sub>c,i</sub>	cytoplasmic NF- $\kappa$ B bound to an importin
NF $\kappa$ B <sub>n</sub>	nuclear NF- $\kappa$ B
NF $\kappa$ B <sub>c</sub> ·I $\kappa$ B $\alpha$ <sub>c</sub>	cytoplasmic NF- $\kappa$ B·I $\kappa$ B $\alpha$ complexes
NF $\kappa$ B <sub>c</sub> ·I $\kappa$ B $\alpha$ <sub>c,p</sub>	phosphorylated I $\kappa$ B $\alpha$ complexed with NF- $\kappa$ B in the cytoplasm
NF $\kappa$ B <sub>n</sub> ·I $\kappa$ B $\alpha$ <sub>n</sub>	nuclear NF- $\kappa$ B·I $\kappa$ B $\alpha$ complexes
NF $\kappa$ B <sub>n</sub> ·I $\kappa$ B $\alpha$ <sub>n,e</sub>	nuclear complex of NF- $\kappa$ B and I $\kappa$ B $\alpha$ bound to an exportin
$g_{I\kappa B\alpha}^i$	state of the $i^{\text{th}}$ I $\kappa$ B $\alpha$ gene copy, discrete random variable: $g_{I\kappa B\alpha}^i \in \{0, 1\}$
$g_{A20}^i$	state of the $i^{\text{th}}$ A20 gene copy, discrete random variable: $g_{A20}^i \in \{0, 1\}$

**Table B. Cell parameters**

<i>Parameter</i>	<i>Symbol</i>	<i>Value</i>	<i>Remarks</i>	<i>Refs</i>
C:N ratio = $\frac{\text{Volume of cytoplasm}}{\text{Volume of nucleus}}$	$k_v$	5	—	[L07]
Number of TNFRs	$R$	735	The median number of receptors is assumed equal 735, and this value was used in deterministic simulations. In stochastic simulations, the number of TNFRs is drawn from log-normal distribution with mean = $2 \times 10^3$ and $\sigma = \sqrt{2}$ , which gives median = mean $\times \exp(-1) \approx 7 \times 10^2$ . $R = TNFR_a(t) + TNFR_i(t)$	[T10]
Number of IKKK molecules	$K_N$	$10^5$	$K_N = IKKK_n(t) + IKKK_a(t)$	[T10]
Number of IKK molecules	$K_{NN}$	$2 \times 10^5$	$K_{NN} = IKK_n(t) + IKK_a(t) + IKK_i(t) + IKK_{ii}(t)$	[L07]
Number of NF- $\kappa$ B molecules	$NF\kappa B_{tot}$	$10^5$	The median number of NF- $\kappa$ B molecules that can be imported into the nucleus is assumed equal 70 000, whereas the median number of inert (non-translocatable) NF- $\kappa$ B molecules (that are bound to inhibitors other than I $\kappa$ B $\alpha$ and in response to TNF are very slowly degraded or not degraded) is assumed 30 000. These numbers are used for deterministic simulations. In stochastic simulations, both molecule numbers are drawn independently from an experimental distributions of NF- $\kappa$ B levels (shown in Fig. 2b in the main text) which has been rescaled so that the median number of translocable NF- $\kappa$ B molecules is 70 000 and median of non-translocatable NF- $\kappa$ B molecules is 30 000.	[this study]
Number of I $\kappa$ B $\alpha$ gene copies	$N_I$	2	—	[T10]
Number of A20 gene copies	$N_A$	2	—	[T10]

(For references, see page 4.)

Table C. List of reactions

<i>Reaction</i>	<i>Rate</i>	<i>Coefficients</i>	<i>Value</i>	<i>References</i>
<i>TNFR activation and signal transduction cascade</i>				
$TNF \rightarrow \emptyset$	$c_{\text{deg}}$	$c_{\text{deg}}$	$10^{-4} \text{ s}^{-1}$	[this study]
$TNFR_i \rightarrow TNFR_a$	$\frac{k_b \cdot TNF}{TNF_{\text{cell}}}$	$k_b$ $TNF_{\text{cell}}$	$1.2 \times 10^{-5} \text{ s}^{-1}$ $6 \times 10^4$ (*)	[T10] (see footnote)
$TNFR_i \leftarrow TNFR_a$	$k_f$	$k_f$	$1.2 \times 10^{-3} \text{ s}^{-1}$	[T10]
$IKKK_n \rightarrow IKKK_a$	$\frac{k_a \cdot k_{A20}}{k_{A20} + A20} \cdot TNFR_a$	$k_a$ $k_{A20}$	$2 \times 10^{-5} \text{ s}^{-1}$ $10^5$	[this study] [T10]
$IKKK_n \leftarrow IKKK_a$	$k_i$	$k_i$	$10^{-2} \text{ s}^{-1}$	[T10]
$IKK_n \rightarrow IKK_a$	$k_1 \cdot IKKK_a^2$	$k_1$	$6 \times 10^{-10} \text{ s}^{-1}$	[T10]
$IKK_a \rightarrow IKK_i$	$\frac{k_3}{k_2} \cdot (k_2 + A20)$	$k_2$ $k_3$	$5 \times 10^3$ $2 \times 10^{-3} \text{ s}^{-1}$	[this study] [T10]
$IKK_i \rightarrow IKK_{ii}, \quad IKK_{ii} \rightarrow IKK_n$	$k_4$	$k_4$	$2 \times 10^{-3} \text{ s}^{-1}$	[this study]
<i>I<math>\kappa</math>B<math>\alpha</math> and A20 gene expression</i>				
$(g_{A20}^i = 0) \rightarrow (g_{A20}^i = 1)$ $(g_{I\kappa B\alpha}^i = 0) \rightarrow (g_{I\kappa B\alpha}^i = 1)$	$q_1 \cdot NF\kappa B_n$	$q_1$	$10^{-7} \text{ s}^{-1}$	[this study]
$(g_{A20}^i = 0) \leftarrow (g_{A20}^i = 1)$ $(g_{I\kappa B\alpha}^i = 0) \leftarrow (g_{I\kappa B\alpha}^i = 1)$	$q_2 \cdot I\kappa B\alpha_n$	$q_2$	$5 \times 10^{-7} \text{ s}^{-1}$	[this study]
$\emptyset \rightarrow A20_{\text{mRNA}}$	$c_1 \cdot g_{A20}^i$	$c_1$	$0.2 \text{ s}^{-1}$	[this study]
$\emptyset \rightarrow I\kappa B\alpha_{\text{mRNA}}$	$c_1 \cdot g_{I\kappa B\alpha}^i$			
$\emptyset \leftarrow A20_{\text{mRNA}}$	$c_{3a}$	$c_{3a}$	$1.5 \times 10^{-3} \text{ s}^{-1}$	[this study]
$\emptyset \leftarrow I\kappa B\alpha_{\text{mRNA}}$	$c_{3i}$	$c_{3i}$	$7.5 \times 10^{-4} \text{ s}^{-1}$	[L07]
$\emptyset \rightarrow A20$	$c_4 \cdot A20_{\text{mRNA}}$	$c_4$	$0.5 \text{ s}^{-1}$	[L07]
$\emptyset \rightarrow I\kappa B\alpha$	$c_4 \cdot I\kappa B\alpha_{\text{mRNA}}$			
<i>Protein interactions and lifetime</i>				
$NF\kappa B_c + I\kappa B\alpha_c \rightarrow NF\kappa B_c \cdot I\kappa B\alpha_c$	$a_1$	$a_1$	$10^{-7} \text{ mlcl}^{-1} \text{ s}^{-1}$	[this study]
$NF\kappa B_n + I\kappa B\alpha_n \rightarrow NF\kappa B_n \cdot I\kappa B\alpha_n$	$a_1 \cdot k_v$	$k_v$	5	[L07]
$I\kappa B\alpha_c \rightarrow I\kappa B\alpha_{c,p}$	$a_2 \cdot IKK_a$	$a_2$	$10^{-7} \text{ s}^{-1}$	[L07]
$NF\kappa B_c \cdot I\kappa B\alpha_c \rightarrow NF\kappa B_c \cdot I\kappa B\alpha_{c,p}$	$a_3 \cdot IKK_a$	$a_3$	$5 \times 10^{-7} \text{ s}^{-1}$	[L07]
$A20 \rightarrow \emptyset$	$c_5$	$c_5$	$5 \times 10^{-4} \text{ s}^{-1}$	[L07]
$I\kappa B\alpha_{c,p} \rightarrow \emptyset$ $NF\kappa B_c \cdot I\kappa B\alpha_{c,p} \rightarrow NF\kappa B_c$	$t_p$	$t_p$	$10^{-2} \text{ s}^{-1}$	[L07]
$I\kappa B\alpha_c \rightarrow \emptyset$	$c_{5a}$	$c_{5a}$	$3 \times 10^{-4} \text{ s}^{-1}$	[this study]
$NF\kappa B_c \cdot I\kappa B\alpha_c \rightarrow NF\kappa B_c$	$c_{6a}$	$c_{6a}$	$2 \times 10^{-5} \text{ s}^{-1}$	[L07]
<i>Karyopherins and transport</i>				
$I\kappa B\alpha_c \rightarrow I\kappa B\alpha_n$	$i_{1a}$	$i_{1a}$	$7 \times 10^{-4} \text{ s}^{-1}$	[this study]
$NF\kappa B_c \rightarrow NF\kappa B_{c,i}$	$b_{iN}$	$b_{iN}$	$0.1 \text{ s}^{-1}$	[this study]
$NF\kappa B_n \cdot I\kappa B\alpha_n \rightarrow NF\kappa B_n \cdot I\kappa B\alpha_{n,e}$ $I\kappa B\alpha_n \rightarrow I\kappa B\alpha_{n,e}$	$b_{e1}$	$b_{e1}$	$5 \times 10^{-3} \text{ s}^{-1}$	[this study]
$NF\kappa B_{c,i} \rightarrow NF\kappa B_n$	$i_{iN}$	$i_{iN}$	$10^{-2} \text{ s}^{-1}$	[this study]
$NF\kappa B_n \cdot I\kappa B\alpha_{n,e} \rightarrow NF\kappa B_c \cdot I\kappa B\alpha_c$ $I\kappa B\alpha_{n,e} \rightarrow I\kappa B\alpha_c$	$e_{e1} \cdot k_v$	$e_{e1}$ $k_v$	$10^{-2} \text{ s}^{-1}$ 5	[this study] [L07]

(\*)  $TNF_{\text{cell}}$  – number of TNF trimers/cell at 1 ng/ml TNF stimulation at the cell density of  $2 \times 10^5$ /ml.

## 2 Methods and protocols of numerical simulations

### Deterministic model

The model, provided in Additional file 2, is specified in BIONETGEN language, which is intended for defining regulatory networks of high combinatorial complexity [F09]. BIONETGEN software is capable of performing both deterministic and stochastic simulations of model dynamics. BIONETGEN allows for rule-based specification of the model; the rules are used to build a system of ODEs which are solved by an integrated CVODE solver.

### Stochastic simulations

The stochastic simulations were performed using the Gillespie direct Stochastic Simulation Algorithm [G77] as implemented in BIONETGEN. The simulator allows for expressing reaction rates through functions of the system state, i.e., current number of molecules of given species. This allows for defining propensities not necessarily following the mass action kinetics. At every time step between consecutive reaction events, reaction propensities calculated using such functions remain constant.

To ensure random initial conditions at time  $t = 0$ , each stochastic simulation was started at time  $t$  drawn at random uniformly from the interval  $[-110 \text{ hr}, -100 \text{ hr}]$ . The population average was obtained from 300 simulations.

### Supplementary references

- [T10] Tay S, Hughey J, Lee T, Lipniacki T, Covert M, Quake M (2010) Single-cell NF- $\kappa$ B dynamics reveal digital activation and analogue information processing. *Nature* **466**:267–271.
- [L07] Lipniacki T, Puszynski T, Paszek P, Brasier AR, Kimmel M (2007) Single TNF $\alpha$  trimers mediating NF- $\kappa$ B activation: Stochastic robustness of NF- $\kappa$ B signaling. *BMC Bioinformatics* **8**:376.
- [F03] Faeder JR, Blinov ML, Hlavacek WS (2009) Rule-based modeling of biochemical systems with BioNetGen. *Methods Mol. Biol.* **500**:113–167.
- [G77] Gillespie DT (1977) Exact stochastic simulations of coupled chemical reactions. *J. Phys. Chem.* **81**:2340–2361.