FIGURE LEGENDS SUPPLEMENTAL FIGURES

SUPPLEMENTAL FIGURE S1: The expression level of NLRC4 is reduced by co-expression with flagellin. Western blot analysis of the cleared lysate of HEK293E cells transfected with *Nlrc4* and flagellin. Cells were harvested 48h post transfection. The blot was probed with anti-His-tag antibody. The asterisk denotes a protein that interacts non-specifically with the antibody.

SUPPLEMENTAL FIGURE S2: Amino acid sequence alignment of the terminal regions of flagellin from different bacterial species. Sequences of full length flagellin from the indicated bacterial species were aligned using ClustalW2 (Larkin, Blackshields et al. 2007); only the regions corresponding to the *S. typhimurium* $D0_L$ fragment are depicted. Subdivision of the terminal fragments into the N- and C-terminal parts of the D0 domain, D1 domain, and the N- and C-terminal spokes (NS and CS, respectively) is indicated. Their domain boundaries are according to Fig. 2*A*. The boxed regions indicate amino acids absent in the $D0_S$ fragment. Numbers at the bottom refer to the amino acid sequence of *S. typhimurium* flagellin. The threshold for coloring is set to 90% similarity based on the BLOSUM62 matrix. Flagellin sequences were taken from the following bacterial species: *Salmonella typhimurium* (*S.typh*., UniProt entry P06179), *Salmonella enteritidis* (*S.Ent*., Q06972), enterohaemorrhagic *Escherichia coli* (*E.coli* EHEC, C8TTK4), *Escherichia coli* K12 (*E.coli K12*, P04949), *Legionella pneumophila* (*L.pneu*, Q5ZVV0), *Listeria monocytogenes* (*L.mono*, Q02551), *Photorhabdus luminescens* (*P.lumi*., Q7N5J4), *Pseudomonas aeruginosa* (*P.aer*., P72151), *Yersinia enterocolitica* (*Y.ent*., D3JZT5).

SUPPLEMENTAL FIGURE S3: Symmetry analysis of NAIP5-NLRC4 inflammasomes. The rotational autocorrelation function (left) calculated for sub-tomograms that were reprojected along the symmetry axis (middle) identifies inflammasome symmetry. An example of particles with 11-fold (A; also depicted in Fig. 8F) and 12-fold symmetry (B) are shown, together with the symmetry averaged projection (right). Vertical lines in the auto-correlation graphs indicate the expected location of correlation maxima for 11- and 12-fold symmetry, respectively.

Figure S1

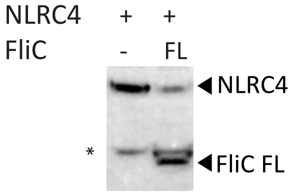
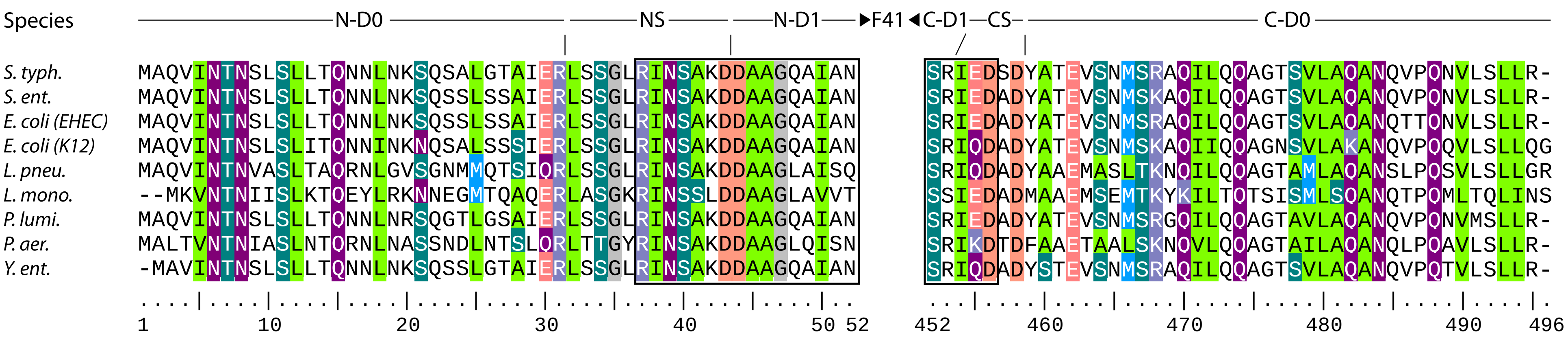


Figure S2


Species
N-D0
NS
N-D1
▶F41◀
C-D1
CS
C-D0
S. typh. MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIAN SRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR-
S. ent. MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIAN SRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR-
E. coli (EHEC) MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIAN SRIEDADYATEVSNMSRAQILQQAGTSVLAQANQTTQNVLSLLR-
E. coli (K12) MAQVINTNSLSLITQNNINKNQSALSSSIERLSSGLRINSAKDDAAGQAIAN SRIQDADYATEVSNMSKAQIIQQAGNSVLAKANQVPQQVLSLLQG
L. pneu. MAQVINTNVASLTAQRNLGVSGNMMQTSIQRLSSGLRINSAKDDAAGLAISQ SRIQDADYAAEMASLTKNQILQQAGTAMLAQANSLPQSVLSLLGR
L. mono. --MKVNTNIISLKTQEYLRKNNEGMTQAQERLASGKRINSSLDDAAGLAVVT SSIEDADMAAEMSEMTKYKILTQTSISMLSQANQTPQMLTQLINS
P. lumi. MAQVINTNSLSLLTQNNLNRSQGTLGSAIERLSSGLRINSAKDDAAGQAIAN SRIEDADYATEVSNMSRGQILQQAGTAVLAQANQVPQNVMSLLR-
P. aer. MALTVNTNIASLNTQRNLNASSNDLNTSLQRLTTGYRINSAKDDAAGLQISN SRIKDTDFAAETAALSKNQVLQQAGTAILAQANQLPQAVLSLLR-
Y. ent. -MAVINTNSLSLLTQNNLNKSQSSLGTAIERLSSGLRINSAKDDAAGQAIAN SRIQDADYSTEVSNMSRAQILQQAGTSVLAQANQVPQTVLSLLR-
1
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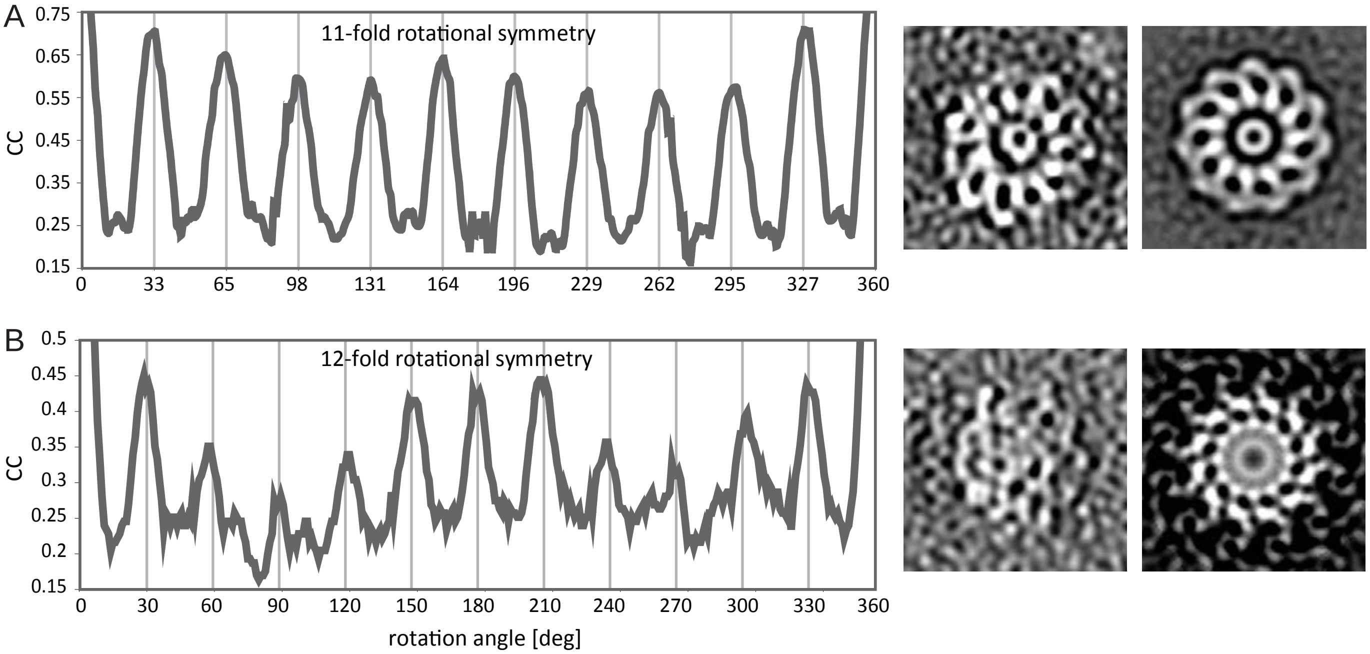
30
40
50 52
452
460
470
480
490
496

Figure S3


A
11-fold rotational symmetry
CC
0.75
0.65
0.55
0.45
0.35
0.25
0.15
0
33
65
98
131
164
196
229
262
295
327
360
B
12-fold rotational symmetry
CC
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0
30
60
90
120
150
180
210
240
270
300
330
360
rotation angle [deg]