

# Structural basis of Gabija anti-phage defence and viral immune evasion

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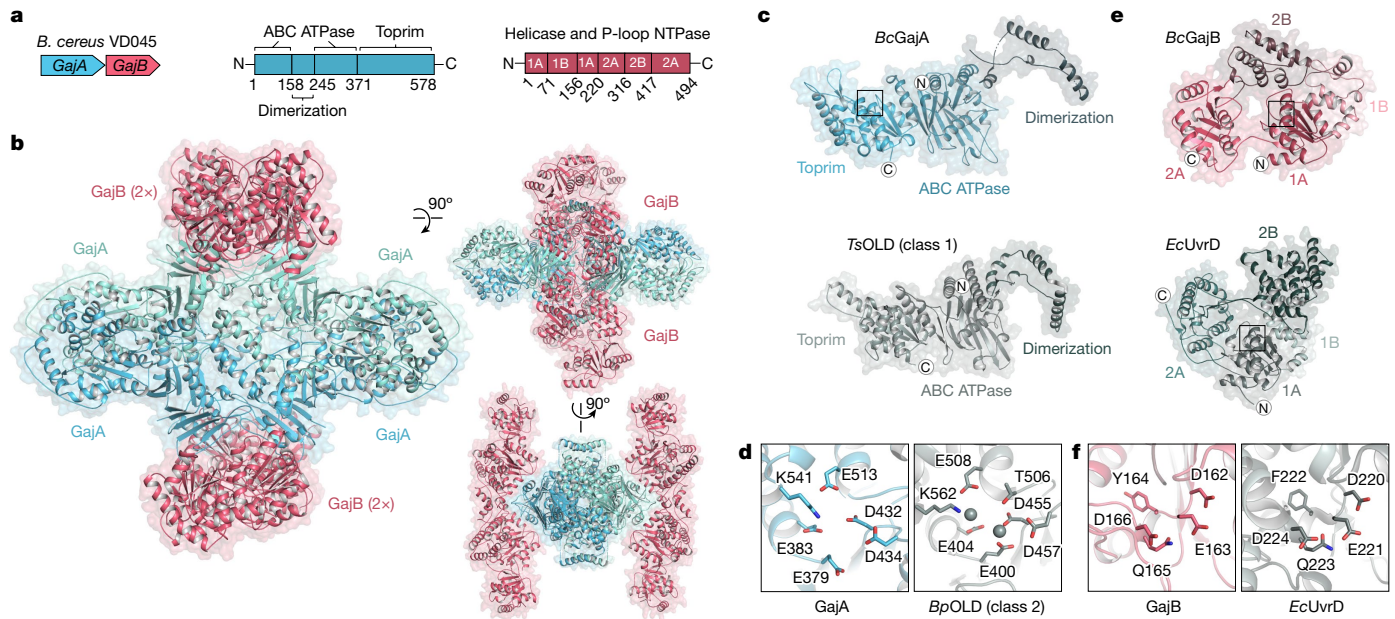
Bacteria encode hundreds of diverse defence systems that protect them from viral infection and inhibit phage propagation<sup>1–5</sup>. Gabija is one of the most prevalent anti-phage defence systems, occurring in more than 15% of all sequenced bacterial and archaeal genomes<sup>1,6,7</sup>, but the molecular basis of how Gabija defends cells from viral infection remains poorly understood. Here we use X-ray crystallography and cryo-electron microscopy (cryo-EM) to define how Gabija proteins assemble into a supramolecular complex of around 500 kDa that degrades phage DNA. Gabija protein A (GajA) is a DNA endonuclease that tetramerizes to form the core of the anti-phage defence complex. Two sets of Gabija protein B (GajB) dimers dock at opposite sides of the complex and create a 4:4 GajA–GajB assembly (hereafter, GajAB) that is essential for phage resistance in vivo. We show that a phage-encoded protein, Gabija anti-defence 1 (Gad1), directly binds to the Gabija GajAB complex and inactivates defence. A cryo-EM structure of the virally inhibited state shows that Gad1 forms an octameric web that encases the GajAB complex and inhibits DNA recognition and cleavage. Our results reveal the structural basis of assembly of the Gabija anti-phage defence complex and define a unique mechanism of viral immune evasion.

Bacterial Gabija defence operons encode the proteins GajA and GajB, which together protect cells against diverse phages<sup>1</sup>. To define the structural basis of Gabija anti-phage defence, we co-expressed *Bacillus cereus* VD045 GajA and GajB and determined a 3.0 Å X-ray crystal structure of the protein complex (Fig. 1a,b, Extended Data Fig. 1a,b and Extended Data Table 1). The structure of the GajAB complex reveals an intricate 4:4 assembly with a tetrameric core of GajA subunits braced on either end by dimers of GajB (Fig. 1b). We focused our analysis first on individual Gabija protein subunits. GajA contains an N-terminal ATPase domain that is divided into two halves by the insertion of a protein dimerization interface (discussed further below) (Fig. 1c). The GajA ATPase domain consists of an eleven-stranded  $\beta$ -sheet ( $\beta 1^{ABC}$ ,  $\beta 2^{ABC}$ ,  $\beta 4-6^{ABC}$  and  $\beta 3^{ABC}$ ,  $\beta 7-11^{ABC}$ ) that folds around the central  $\alpha 1^{ABC}$  helix (Fig. 1c and Extended Data Fig. 2a). Sequence analysis of diverse GajA homologues shows that the GajA ATPase domain contains a highly conserved ATP-binding site that is shared with canonical ABC ATPase proteins<sup>8</sup> (Extended Data Fig. 2a). The GajA C terminus contains a four-stranded parallel  $\beta$ -sheet  $\beta 1-\beta 4^T$  surrounded by three  $\alpha$ -helices  $\alpha 3^T$ ,  $\alpha 4^T$  and  $\alpha 12^T$  that form a Toprim (topoisomerase-primase) domain associated with proteins that catalyse double-stranded DNA (dsDNA) breaks<sup>9,10</sup> (Fig. 1c and Extended Data Fig. 2a). Consistent with a role in dsDNA cleavage, the structure of GajA confirms previous predictions of overall shared homology between GajA and a class of DNA endonucleases named OLD (overcoming lysogenization defect) nucleases<sup>11,12</sup>. Discovered at first as an *Escherichia coli* phage P2 protein responsible for cell toxicity in

*recB* and *recC* mutant cells<sup>13–15</sup>, OLD nucleases occur in diverse bacterial genomes, either as single proteins (class 1) or associated with partner UvrD/PcrA/Rep-like helicase proteins (class 2), but the specific function of most OLD nuclease proteins is unknown<sup>11,12</sup>. GajA is a class 2 OLD nuclease, with the Toprim domain containing a complete active site composed of DxD after  $\beta 3^T$  (D432 and D434), an invariant glutamate after  $\beta 2^T$  (E379) and an invariant glycine between  $\alpha 1^T$  and  $\beta 1^T$  (G409). This is similar to the active site of *Burkholderia pseudomallei* (BpOLD), which was previously shown to be essential for a two-metal-dependent mechanism of DNA cleavage<sup>11</sup> (Fig. 1d and Extended Data Fig. 2a).

The structure of GajB reveals a superfamily 1A DNA helicase domain. Bacterial DNA helicases belonging to this superfamily typically have a role in DNA repair<sup>16</sup> (Fig. 1e). Superfamily 1A helicase proteins such as UvrD, Rep and PcrA translocate along single-stranded DNA in the 3' to 5' direction, and are architecturally divided into four subdomains—1A, 1B, 2A and 2B—that reposition relative to each other during helicase function<sup>16</sup>. GajB contains all of the conserved helicase motifs that are required for ATP hydrolysis and nucleic acid unwinding, including a Walker A motif Gx(4)GK-[TT] and a UvrD-like DEXQD-box Walker B motif that is responsible for the hydrolysis of nucleoside triphosphate<sup>16–18</sup> (Fig. 1f and Extended Data Fig. 3a). Activation of superfamily 1A DNA helicase proteins such as UvrD and Rep is known to require protein dimerization and the rotation of the 2B subdomain<sup>19–21</sup>. Comparisons with UvrD and Rep show that GajB protomers in the GajAB complex exhibit a partial rotation of the 2B domain relative to 2A–1A–1B,

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**Fig. 1 | Structure of the Gabija anti-phage defence complex.** **a**, Schematic of *B. cereus* (*Bc*) Gabija defence operon and domain organization of GajA and GajB. **b**, Overview of the GajAB X-ray crystal structure shown in three orientations. GajA protomers are depicted in two shades of blue and GajB protomers are in red. **c**, Isolated GajA monomer (top) and comparison with a TsOLD nuclease monomer (bottom) (Protein Data Bank (PDB) ID:6P74)<sup>12</sup>. **d**, Magnified views

of Toprim catalytic residues in GajA (left) and *Bp*OLD (right) (PDB ID: 6NKS)<sup>11</sup>. The location of the GajA cut-away image is indicated with a box in **c** and magnesium ions are depicted as grey spheres. **e**, Isolated GajB monomer (top) and comparison with *E. coli* (*Ec*) UvrD (bottom) (PDB ID: 2IS2)<sup>20</sup>. **f**, Magnified views of the DEXQD-box motif in GajB (left) and *Ec*UvrD (right). The locations of the GajB and UvrD cut-away images are indicated with boxes in **e**.

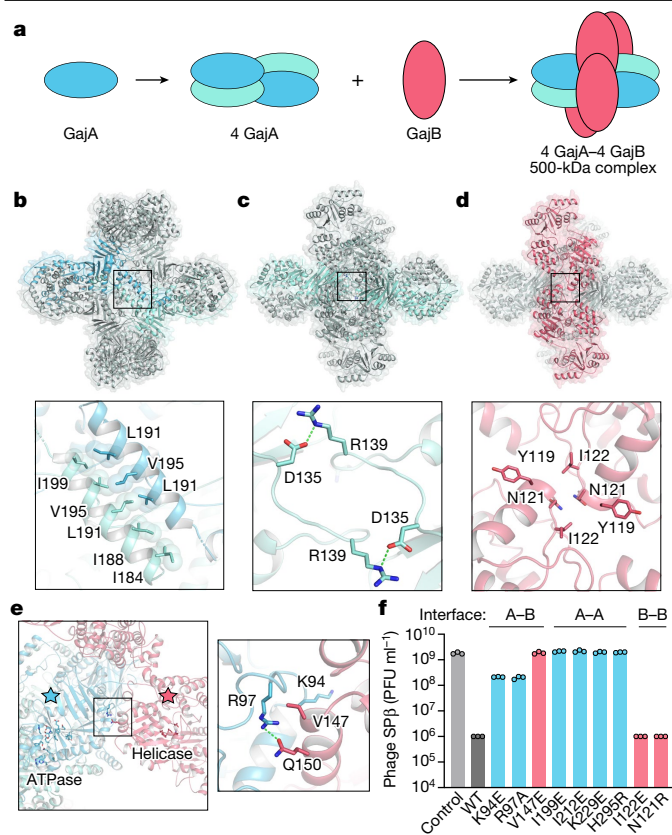
consistent with a partially active conformation that is poised to interact with phage DNA (Extended Data Fig. 1e).

### Gabija forms a supramolecular complex

To define the mechanism by which the Gabija complex assembles, we analysed oligomerization interfaces within the GajAB structure. Purification of individual Gabija proteins shows that GajA alone is sufficient to oligomerize into a homo-tetrameric assembly (Extended Data Fig. 1a). GajB migrates as a monomer on size-exclusion chromatography, supporting a stepwise model of GajAB assembly (Fig. 2a and Extended Data Fig. 1a). GajA tetramers form through two highly conserved oligomerization interfaces (Fig. 2b,c and Extended Data Fig. 2). First, the GajA N-terminal ATPase domain contains an insertion between  $\beta 7^{ABC}$  and  $\beta 8^{ABC}$  that consists of four  $\alpha$ -helices ( $\alpha 1$ – $\alpha 4^D$ ) that zip up against a partnering GajA protomer to form a hydrophobic interface along the  $\alpha 2^D$  helix (Fig. 2b). A similar  $\alpha 1$ – $\alpha 4^D$  dimerization interface exists in the structure of the *Thermus scotoductus* class 1 OLD (TsOLD) protein, which shows that this interface is conserved within divergent OLD nucleases<sup>12</sup> (Figs. 1c and 2c). The GajA ATPase domain contains a second oligomerization interface in a loop between  $\beta 6^{ABC}$  and  $\alpha 6^{ABC}$ , in which hydrogen-bond contacts between D135 and R139 interlock two GajA dimers to form the tetrameric core assembly (Fig. 2c). Compared to GajA, the GajB–GajB dimerization interface is minimal and consists of a hydrophobic surface in the GajB helicase 1B domain centred at Y119 and I122 (Fig. 2d). Major GajA–GajB contacts also occur in the GajB helicase 1B domain, in which GajA R97 in a loop between  $\alpha 4^{ABC}$  and  $\beta 5^{ABC}$  forms hydrogen-bond contacts with Q150 in GajB  $\alpha 7$  along with hydrophobic packing interactions centred at GajB V147 (Fig. 2e and Extended Data Fig. 3a). Notably, the GajAB structure shows that the GajB helicase 1A subdomain, which includes the DEXQD-box active site, is positioned adjacent to the GajA ATPase domain, suggesting that GajB ATP hydrolysis and DNA-unwinding activity might regulate the activation of the GajA ATPase domain (Fig. 2e).

In addition to the major GajAB interface contacts, Gabija supramolecular complex assembly is driven by extensive protomer interactions that result in around 31,000 Å<sup>2</sup> of surface area buried for the GajA tetramer and around 1,800 Å<sup>2</sup> of surface area buried for each GajB subunit.

We reconstituted Gabija activity *in vitro* and observed that the GajAB complex binds to and rapidly cleaves a previously characterized 56-bp dsDNA substrate that contains a sequence-specific motif derived from phage lambda DNA<sup>22</sup> (Extended Data Fig. 1c). The GajAB complex can interact with a scrambled DNA sequence but is unable to cleave this target DNA (Extended Data Fig. 1c,d). GajA and GajB proteins are each essential for phage defence *in vivo*<sup>1,22</sup>, but we observed, in agreement with previous results, that GajA is alone sufficient to cleave target DNA and does not require GajB *in vitro*<sup>22,23</sup> (Extended Data Fig. 1c). These results suggest that GajAB complex formation could have a specific role in controlling substrate recognition or nuclease activation during phage infection. To confirm these findings, we analysed protein interaction interfaces in the GajAB complex structure and tested the effects of a panel of mutations on the assembly of the Gabija complex *in vitro* and the ability of Gabija to defend *Bacillus subtilis* cells from phage SP $\beta$  infection *in vivo*. Mutations to the GajA–GajB hetero-oligomerization interface, including GajA K94E and R97A and GajB V147E and Q150R, disrupted complex formation, indicating that these regions are crucial for Gabija complex assembly (Extended Data Fig. 1f). Likewise, these substitutions to the GajA–GajB interface markedly reduced the ability of Gabija to inhibit phage replication in *B. subtilis*. Substitutions to the GajA–GajA dimerization interface including I199E, I212E and K229E also resulted in the complete loss of phage resistance (Fig. 2f). By contrast, phage resistance was tolerant to mutations in the GajB–GajB interface, which suggests that this minimal interaction surface is not strictly essential for anti-phage defence. Together, these results define the structural basis of GajA and GajB interaction and show that the formation of the GajAB supramolecular complex is crucial for Gabija anti-phage defence.



**Fig. 2 | Mechanism of Gabjia supramolecular complex assembly.** **a**, Schematic model of GajAB complex formation by GajA tetramerization and GajB docking. **b**, Overview of the GajA  $\alpha 2^D$ - $\alpha 2^D$  dimerization interface and detailed view of interacting residues. For clarity, each GajA monomer is depicted in two shades of blue. **c**, Overview of the GajA-GajA ATPase interaction and detailed view of the inter-subunit D135-R139 interaction. **d**, Overview of the minimal GajB-GajB dimer interface and detailed view of GajB-GajB hydrophobic interactions centred around Y119, N121 and I122. **e**, Left, overview of the GajA-GajB interface, highlighting the proximity of GajA ABC ATPase and GajB helicase active-site residues. Right, the box indicates the location of GajA R97 and GajB V147 and Q150 interaction. **f**, Analysis of mutations in the GajA-GajB (A-B), GajA-GajA (A-A), and GajB-GajB (B-B) multimerization interfaces. GajA and GajB mutations were selected by identifying central residues with well-defined protein-protein contacts within each multimerization interface, and were tested to determine their effects on the ability of the *B. cereus* Gabjia operon to defend cells against phage infection. Data represent the phage SP $\beta$  average plaque-forming units (PFU) ml<sup>-1</sup> of three biological replicates, with individual data points shown. WT, wild type.

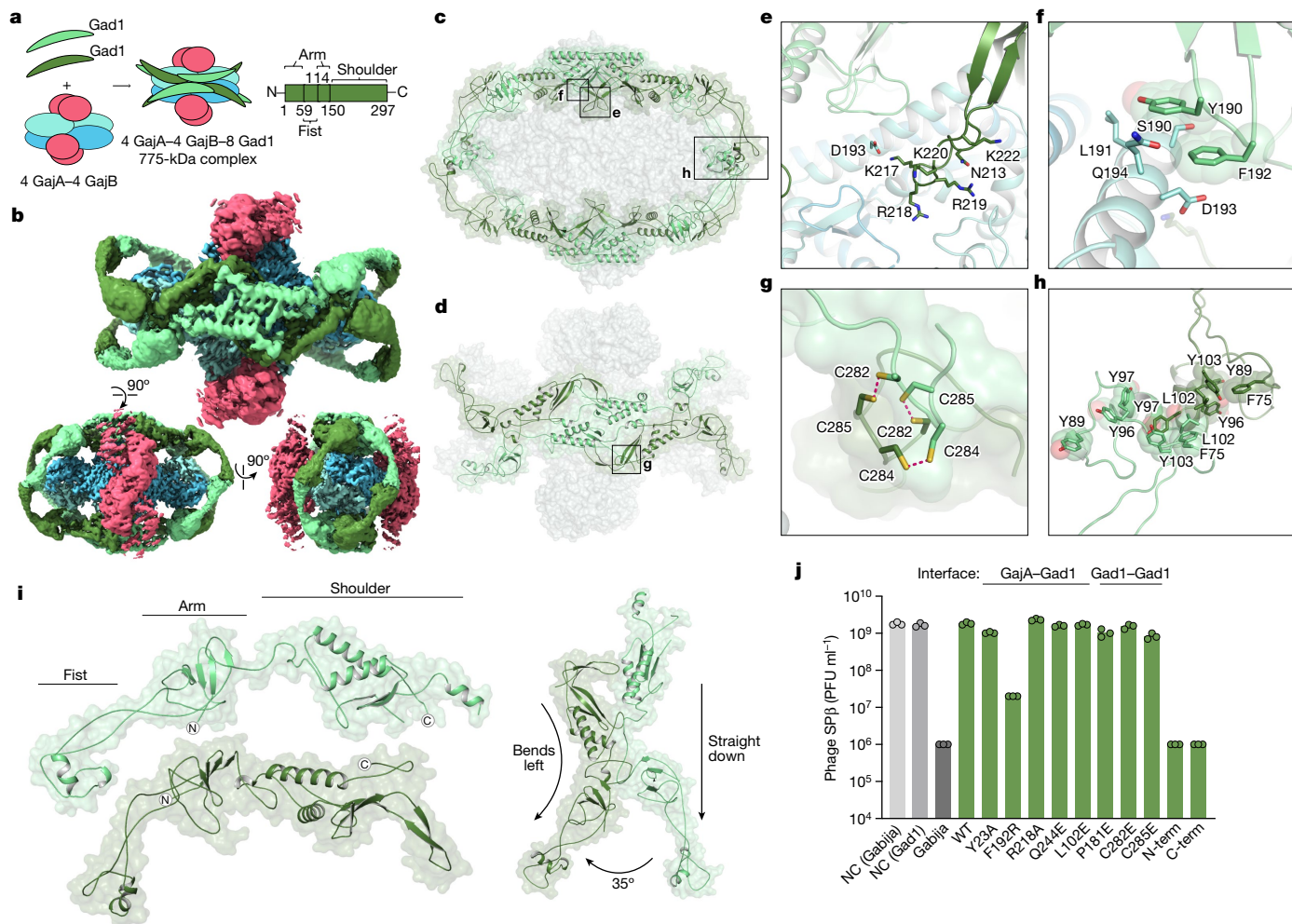
### Structural basis of Gabjia viral evasion

To overcome host immunity, phages encode evasion proteins that specifically inactivate anti-phage defence<sup>24-29</sup>. In a companion study, Yirmiya et al. report the discovery of a viral inhibitor of Gabjia anti-phage defence<sup>30</sup>, and we reasoned that defining the mechanism of immune evasion would provide further insight into the function of the Gabjia complex. Gad1 is a *Bacillus* phage Phi3T protein that is atypically large (35 kDa) compared to other characterized phage immune-evasion proteins (Extended Data Fig. 4a). Protein interaction analysis showed that Gad1 binds directly to GajAB (Extended Data Fig. 4b,c), and we used cryo-EM to determine a 2.6 Å structure of the GajAB-Gad1 co-complex assembly (Fig. 3a,b, Extended Data Figs. 5 and 6a-g and Extended Data Table 2). The GajAB-Gad1 co-complex structure reveals a mechanism of inhibition in which Gad1 proteins form an oligomeric web that wraps 360° around the host defence complex. Eight copies of phage Gad1 encircle the GajAB assembly, forming a 4:4:8 GajAB-Gad1 complex

that is around 775 kDa in size (Fig. 3b,c). Gad1 mainly recognizes the GajA nuclease core, forming extensive contacts along the surface of the GajA dimerization domain (Fig. 3c,d). Key GajAB-Gad1 contacts include hydrogen-bond interactions from a Gad1 positively charged loop located between  $\beta 5$  and  $\beta 6$  with GajA  $\alpha 2^D$  (Fig. 3e and Extended Data Fig. 7a-c), and hydrophobic packing interactions between Gad1 Y190 and F192 with GajA  $\alpha 2^D$  (Fig. 3f and Extended Data Fig. 7a). Although the contacts between Gad1 and GajB are limited, both GajA and GajB are necessary for Gad1 interaction, indicating that Gad1 specifically targets the fully assembled GajAB complex to inactivate host anti-phage defence (Extended Data Fig. 4d).

Gad1 wraps around the GajAB complex using a network of homooligomeric interactions and notable conformational flexibility. On either side of the GajAB complex, four copies of Gad1 interlock into a tetrameric interface along the primary GajA-binding site (Fig. 3d). The Gad1 tetrameric interface is formed by hydrogen-bond interactions between the C-terminal ‘shoulder’ domain of each Gad1 monomer and a highly conserved set of three cysteine residues, C282, C284 and C285, which form disulfide interactions at an inter-subunit interface (Fig. 3d,g and Extended Data Fig. 7a,d). The N terminus of each Gad1 monomer forms an ‘arm’ domain that extends out from the shoulder and reaches around the GajA nuclease active site to connect to a partnering Gad1 protomer from the opposite side of the complex. At the end of the Gad1 arm is an N-terminal ‘fist’ domain that allows two partnering Gad1 protomers to interact and complete the octameric web assembly (Fig. 3c,h). Structural flexibility limits resolution in this portion of the cryo-EM map, but AlphaFold2 modelling<sup>31,32</sup> and rigid-body placement of the Gad1 N-terminal fist domain suggests that conserved hydrophobic residues around the Gad1  $\alpha 1$  helix mediate the fist-fist interactions (Fig. 3h and Extended Data Fig. 7a). To fully encircle GajAB, Gad1 adopts two distinct structural conformations. Each pair of Gad1 proteins that wrap around and connect at the edge of the GajAB complex are formed by one Gad1 protomer reaching out from the shoulder with an arm domain extended straight down and one Gad1 protomer reaching out with an arm domain bent around 35° to the left (Fig. 3i and Extended Data Fig. 6h). Sequence analysis of Gad1 proteins from phylogenetically diverse phages shows that the Gad1 N-terminal arm domain is highly variable in length (Extended Data Fig. 7a), providing further evidence that conformational flexibility in this region is crucial to inhibit host Gabjia defence.

To test the importance of individual GajAB-Gad1 interfaces, we next analysed a series of Gad1 substitution and truncation mutants for their ability to interact with GajAB and inhibit Gabjia anti-phage defence. The Gad1 residue F192 is located between  $\beta 4$  and  $\beta 5$  and is part of a highly conserved region that forms the centre of the primary GajA-Gad1 interface (Extended Data Fig. 7a). The Gad1 substitution F192R blocked the ability of Gad1 to interact with GajAB in vitro and inhibit Gabjia anti-phage defence in vivo (Fig. 3j and Extended Data Fig. 7a,e). However, individual mutations throughout the periphery were insufficient to disrupt Gad1 inhibition of Gabjia anti-phage defence. This shows that the large footprint of Gad1 is tolerant to small perturbations that might enable host resistance. Similarly, mutations to the conserved Gad1 cysteine residues in the tetrameric shoulder interface greatly reduced the stability of GajAB-Gad1 complex formation in vitro but only exhibited a threefold decrease and mostly still permitted Gad1 to block phage defence in *B. subtilis* cells (Fig. 3j and Extended Data Fig. 7e). The formation of the GajAB-Gad1 complex was also disrupted in vitro by a Y103R mutation in the Gad1 fist-fist interface (Fig. 3h and Extended Data Fig. 7f). Finally, in contrast to wild-type Gad1, expression of the Gad1 N-terminal fist-arm or C-terminal shoulder domains alone was unable to inhibit Gabjia, providing evidence that full wrapping of Gad1 around the GajAB complex is necessary to enable phage evasion of anti-phage defence (Fig. 3j and Extended Data Fig. 7e).



**Fig. 3 | Structural basis of viral evasion of Gabija defence.** **a**, Schematic model of GajAB–Gad1 co-complex formation and domain organization of phage Phi3T Gad1. **b**, Cryo-EM density map of *BcGajAB* in complex with Phi3T Gad1, shown in three different orientations. The map is coloured by the model, with Gad1 monomers depicted in two shades of green. **c,d**, Side view of the complete Gad1 octameric complex (**c**) and top-down view of the Gad1 tetrameric interface (**d**), with boxes highlighting views that are magnified in **e–h**. **e,f**, Magnified views of major Gad1–GajA interface contacts including a Gad1 positively charged loop (**e**) and hydrophobic interactions with GajA  $\alpha 2^D$  (**f**). **g,h**, Magnified views of major Gad1–Gad1 oligomerization interactions including disulfide bonds in the C-terminal shoulder domain (**g**) and fist–fist domain contacts modelled by rigid-body placement of an AlphaFold2 fist-domain structure prediction into

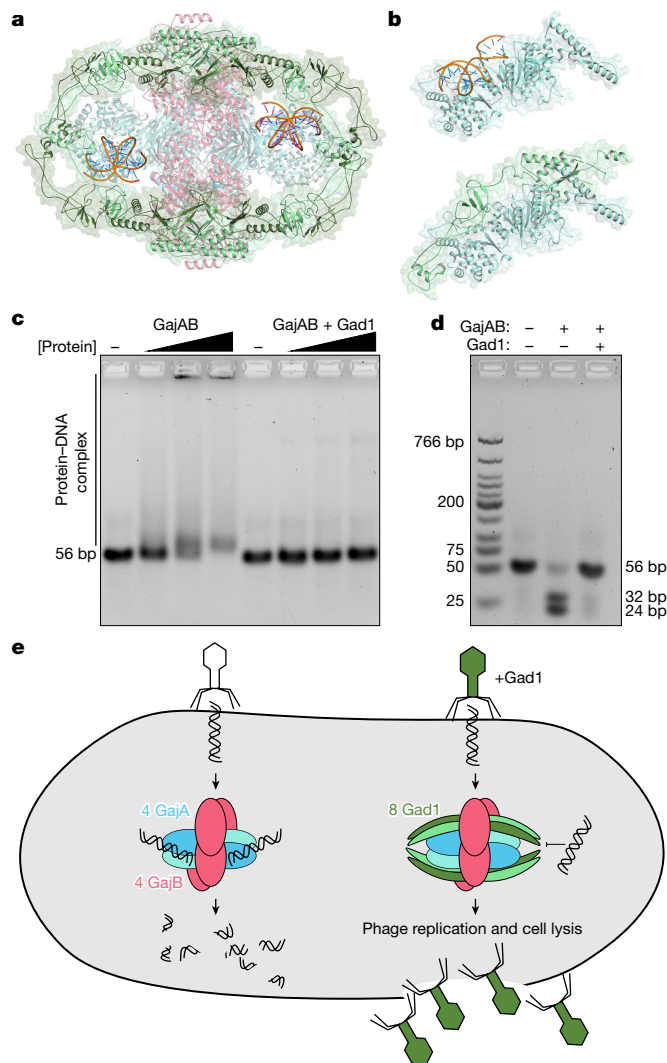
the cryo-EM map (**h**). **i**, Two distinct conformations of Gad1 observed in the GajAB–Gad1 co-complex structure. Differences in the rotation of the Gad1 arm domain are highlighted on the right. **j**, Analysis of the effect of Gad1 mutations in the GajA–Gad1 and Gad1–Gad1 multimerization interfaces on the ability of Gad1 to enable evasion of Gabija defence. Data represent PFU ml<sup>-1</sup> of phage SP $\beta$  infecting cells expressing *BcGabija* and *Shewanella* sp. phage 1/4 Gad1, or negative control (NC) cells expressing empty vector for either plasmid. *Shewanella* sp. phage 1/4 Gad1 residues are numbered according to the Phi3T Gad1 structure. *Shewanella* sp. phage 1/4 Gad1 N-terminal and C-terminal truncations (N-term and C-term, respectively) are MI–L152 and V153–E348, respectively. Data are the average of three biological replicates, with individual data points shown.

### Gad1 blocks Gabija DNA cleavage

Superposition of the GajAB–Gad1 and GajAB complexes shows that Gad1 binding does not induce a notable conformational change in GajAB, and suggests that Gad1 instead functions through steric hindrance of Gabija anti-phage defence (Extended Data Fig. 7h). To define the mechanism of Gad1 inhibition of Gabija anti-phage defence, we modelled interactions between GajAB and target DNA. The GajA Toprim domain is structurally homologous to the *E. coli* protein MutS, which is involved in DNA repair<sup>33</sup>. Superimposing the MutS–DNA structure revealed positively charged patches lining a groove in the GajA Toprim domain that dips into the nuclease active site (Extended Data Fig. 8). Notably, the Gad1 arm domain directly occupies this putative DNA-binding surface, supporting a model in which the phage protein directly clashes with the path of target dsDNA (Fig. 4a,b). To determine the effect of viral inhibition on GajAB catalytic function, we tested the

role of Gad1 in individual steps of DNA binding and target DNA cleavage. Gad1 prevented GajAB from binding to target DNA and abolished all nuclease activity in vitro (Fig. 4c,d and Supplementary Fig. 1). Gad1 proteins with F192R or C282E mutations were no longer able to inhibit DNA cleavage, in agreement with the inability of F192R-mutant proteins and the reduced ability of C282E-mutant proteins to block Gabija defence in vivo and form stable GajAB–Gad1 complexes in vitro (Extended Data Fig. 7g). Together, these results show that phage Gad1 binds to and wraps around the GajAB complex to block target DNA degradation. Our findings reveal a complete mechanism by which phages evade the Gabija defence system of the host (Fig. 4e).

Our study defines the structural basis of the formation of the Gabija supramolecular complex, and explains how phages block DNA cleavage to overcome this type of host immunity. The approximately 500-kDa GajAB complex expands an emerging theme in anti-phage defence, whereby protein subunits assemble into large machines to resist phage



**Fig. 4 | Inhibition of Gabija DNA binding and cleavage enables viral evasion.** **a**, Cartoon representation of the GajAB–Gad1 co-complex structure with modelled DNA (orange), based on structural homology with *E. coli* MutS (PDB ID 3K0S)<sup>33</sup>. **b**, Top, isolated GajA protomer with modelled DNA (orange) bound to the Toprim domain. Bottom, the same GajA promoter with Gad1, showing substantial steric clashes between Gad1 and the path of the DNA. **c,d**, Biochemical analysis of GajAB 56-bp target DNA binding (**c**) and target cleavage (**d**) shows that Gad1 potentially inhibits the activity of GajAB. Data are representative of three independent experiments. **e**, Model of Gabija anti-phage defence and mechanism of Gad1 immune evasion.

infection—similarly to the supramolecular complexes in CRISPR<sup>34</sup>, CBASS<sup>35,36</sup> and RADAR<sup>37,38</sup> immunity. These results parallel human innate immunity, in which key effectors in inflammasome, Toll-like receptor, RIG-I-like receptor and cGAS–STING signalling pathways also oligomerize into large assemblies to block viral replication<sup>39,40</sup>. In contrast to the exceptionally large defence complexes of the host, phage evasion proteins are typically small, 5–20-kDa proteins that sterically occlude key protein binding and active-site motifs<sup>25,26</sup>. Breaking this rule, the 35-kDa anti-Gabija protein Gad1 is one of the largest described viral protein–protein inhibitors of host immune signalling (Extended Data Fig. 4). Whereas most viral evasion proteins that are larger than 20 kDa are enzymatic domains that catalytically modify target host factors or signalling molecules, the large size of Gad1 is necessary to bind to, oligomerize and encircle the entire host GajAB complex. Resistance to small phage proteins that simply block the GajA active site could explain why Gabija is a highly prevalent defence system in diverse bacterial

phyla. A key question opened by our structures of the Gabija complex is how GajB helicase activity is linked to the activation of the GajA nuclease domain to control the cleavage of target DNA. Gad1 encasing the GajAB complex to trap it in an inactive state is a new mechanism by which phages evade host defences, and this finding provides a template to understand how viruses disrupt the complex mechanisms of activation of diverse anti-phage defence systems in bacteria.

**Online content**

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-023-06855-2>.

- Doron, S. et al. Systematic discovery of antiphage defense systems in the microbial pangenome. *Science* **359**, eaar4120 (2018).
- Gao, L. et al. Diverse enzymatic activities mediate antiviral immunity in prokaryotes. *Science* **369**, 1077–1084 (2020).
- Millman, A. et al. An expanded arsenal of immune systems that protect bacteria from phages. *Cell Host Microbe* **30**, 1556–1569 (2022).
- Rousset, F. et al. Phages and their satellites encode hotspots of antiviral systems. *Cell Host Microbe* **30**, 740–753 (2022).
- Vassallo, C. N., Doering, C. R., Littlehale, M. L., Teodoro, G. I. C. & Laub, M. T. A functional selection reveals previously undetected anti-phage defence systems in the *E. coli* pangenome. *Nat. Microbiol.* **7**, 1568–1579 (2022).
- Tesson, F. et al. Systematic and quantitative view of the antiviral arsenal of prokaryotes. *Nat. Commun.* **13**, 2561 (2022).
- Payne, L. J. et al. PADLOC: a web server for the identification of antiviral defence systems in microbial genomes. *Nucleic Acids Res.* **50**, W541–W550 (2022).
- Hopfner, K.-P. Invited review: architectures and mechanisms of ATP binding cassette proteins. *Biopolymers* **105**, 492–504 (2016).
- Aravind, L., Leipe, D. D. & Koonin, E. V. Toprim—a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecF proteins. *Nucleic Acids Res.* **26**, 4205–4213 (1998).
- Berger, J. M., Gamblin, S. J., Harrison, S. C. & Wang, J. C. Structure and mechanism of DNA topoisomerase II. *Nature* **379**, 225–232 (1996).
- Schiltz, C. J., Lee, A., Partlow, E. A., Hofsdorf, C. J. & Chappie, J. S. Structural characterization of Class 2 OLD family nucleases supports a two-metal catalysis mechanism for cleavage. *Nucleic Acids Res.* **47**, 9448–9463 (2019).
- Schiltz, C. J., Adams, M. C. & Chappie, J. S. The full-length structure of *Thermus scotoductus* OLD defines the ATP hydrolysis properties and catalytic mechanism of Class 1 OLD family nucleases. *Nucleic Acids Res.* **48**, 2762–2776 (2020).
- Sironi, G. Mutants of *Escherichia coli* unable to be lysogenized by the temperate bacteriophage P2. *Virology* **37**, 163–176 (1969).
- Sironi, G., Bialy, H., Lozeron, H. A. & Calendar, R. Bacteriophage P2: Interaction with phage lambda and with recombination-deficient bacteria. *Virology* **46**, 387–396 (1971).
- Lindahl, G. On the control of transcription in bacteriophage P2. *Virology* **46**, 620–633 (1971).
- Raney, K. D., Byrd, A. K. & Aarattuthodiyil, S. Structure and mechanisms of SF1 DNA helicases. *Adv. Exp. Med. Biol.* **767**, 17–46 (2013).
- Gorbalenya, A. E. & Koonin, E. V. Helicases: amino acid sequence comparisons and structure–function relationships. *Curr. Opin. Struct. Biol.* **3**, 419–429 (1993).
- Tanner, N. K. & Linder, P. DEXD/H Box RNA helicases: from generic motors to specific dissociation functions. *Mol. Cell* **8**, 251–262 (2001).
- Korolev, S., Hsieh, J., Gauss, G. H., Lohman, T. M. & Waksman, G. Major domain swiveling revealed by the crystal structures of complexes of *E. coli* Rep helicase bound to single-stranded DNA and ADP. *Cell* **90**, 635–647 (1997).
- Lee, J. Y. & Yang, W. UvrD Helicase unwinds DNA one base pair at a time by a two-part power stroke. *Cell* **127**, 1349–1360 (2006).
- Ordbayev, Y. A., Nguyen, B., Kozlov, A. G., Jia, H. & Lohman, T. M. UvrD helicase activation by MutL involves rotation of its 2B subdomain. *Proc. Natl Acad. Sci. USA* **116**, 16320–16325 (2019).
- Cheng, R. et al. A nucleotide-sensing endonuclease from the Gabija bacterial defense system. *Nucleic Acids Res.* **49**, 5216–5229 (2021).
- Cheng, R. et al. Prokaryotic Gabija complex senses and executes nucleotide depletion and DNA cleavage for antiviral defense. *Cell Host Microbe* **31**, 1331–1344 (2023).
- Bondy-Denomy, J., Pawluk, A., Maxwell, K. L. & Davidson, A. R. Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. *Nature* **493**, 429–432 (2013).
- Stanley, S. Y. & Maxwell, K. L. Phage-encoded anti-CRISPR defenses. *Annu. Rev. Genet.* **52**, 445–464 (2018).
- Hampton, H. G., Watson, B. N. J. & Fineran, P. C. The arms race between bacteria and their phage foes. *Nature* **577**, 327–336 (2020).
- Hobbs, S. J. et al. Phage anti-CBASS and anti-Pycsar nucleases subvert bacterial immunity. *Nature* **605**, 522–526 (2022).
- Huiting, E. et al. Bacteriophages inhibit and evade cGAS-like immune function in bacteria. *Cell* **186**, 864–876 (2023).
- Jenson, J. M., Li, T., Du, F., Ea, C.-K. & Chen, Z. J. Ubiquitin-like conjugation by bacterial cGAS enhances anti-phage defence. *Nature* **616**, 326–331 (2023).

30. Yirmiya, E. et al. Phages overcome bacterial immunity via diverse anti-defence proteins. *Nature*, <https://doi.org/10.1038/s41586-023-06869-w> (2023).
31. Jumper, J. et al. Highly accurate protein structure prediction with AlphaFold. *Nature* **596**, 583–589 (2021).
32. Mirdita, M. et al. ColabFold: making protein folding accessible to all. *Nat. Methods* **19**, 679–682 (2022).
33. Lebbink, J. H. G. et al. Magnesium coordination controls the molecular switch function of DNA mismatch repair protein MutS. *J. Biol. Chem.* **285**, 13131–13141 (2010).
34. Wang, J. Y., Pausch, P. & Doudna, J. A. Structural biology of CRISPR–Cas immunity and genome editing enzymes. *Nat. Rev. Microbiol.* **20**, 641–656 (2022).
35. Morehouse, B. R. et al. Cryo-EM structure of an active bacterial TIR–STING filament complex. *Nature* **608**, 803–807 (2022).
36. Hogrel, G. et al. Cyclic nucleotide-induced helical structure activates a TIR immune effector. *Nature* **608**, 808–812 (2022).
37. Duncan-Lowey, B. et al. Cryo-EM structure of the RADAR supramolecular anti-phage defense complex. *Cell* **186**, 987–998 (2023).
38. Gao, Y. et al. Molecular basis of RADAR anti-phage supramolecular assemblies. *Cell* **186**, 999–1012 (2023).
39. Kagan, J. C., Magupalli, V. G. & Wu, H. SMOCs: supramolecular organizing centres that control innate immunity. *Nat. Rev. Immunol.* **14**, 821–826 (2014).
40. Ablasser, A. & Chen, Z. J. cGAS in action: expanding roles in immunity and inflammation. *Science* **363**, eaat8657 (2019).

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**Bacterial strains and phages**

*B. subtilis* BEST7003 was grown in MMB (LB supplemented with 0.1 mM MnCl<sub>2</sub> and 5 mM MgCl<sub>2</sub>) with or without 0.5% agar at 37 °C or 30 °C respectively. Whenever applicable, media were supplemented with ampicillin (100 µg ml<sup>-1</sup>), chloramphenicol (34 µg ml<sup>-1</sup>) or kanamycin (50 µg ml<sup>-1</sup>) to ensure the maintenance of plasmids. *B. subtilis* phages phi3T (BGSCID 1L1) and SPβ (BGSCID 1L5) were obtained from the Bacillus Genetic Stock Center (BGSC). Prophages were induced using Mitomycin C (Sigma, M0503).

Phage titre was determined using the small-drop plaque assay method<sup>41</sup>. Four hundred microlitres of overnight culture of bacteria was mixed with 0.5% agar and 30 ml MMB and poured into a 10-cm<sup>2</sup> plate followed by incubation for 1 h at room temperature. In cases of bacteria expressing Gad1 homologue and Gad1 mutations, 0.1–1 mM IPTG was added to the medium. Tenfold serial dilutions in MMB were performed for each of the tested phages and 10-µl drops were put on the bacterial layer. After the drops had dried up, the plates were inverted and incubated at room temperature overnight. Plaque-forming units (PFUs) were determined by counting the derived plaques after overnight incubation, and lysate titre was determined by calculating PFU ml<sup>-1</sup>. When no individual plaques could be identified, a faint lysis zone across the drop area was considered to be ten plaques. Efficiency of plating was measured by comparing plaque assay results on control bacteria and bacteria containing the defence system and/or a candidate anti-defence gene.

**Plasmid construction**

For protein purification and biochemistry, *B. cereus* VDO45 *GajA* (IMG ID 2519684552) and *GajB* (IMG ID 2519684553) genes were codon-optimized for expression in *E. coli*, synthesized as gBlocks (Integrated DNA Technologies) and cloned into custom pET vectors with an N-terminal 6×His-SUMO2 fusion tag (*GajB* alone) or a C-terminal 6×His tag (*GajA* alone). *GajA* and *GajB* proteins were co-expressed using a custom pET vector with an N-terminal 6×His-SUMO2 or N-terminal 6×His-SUMO2-5×GS tag on *GajA* and a ribosome-binding site between *GajA* and *GajB*. Phi3T and *Shewanella* sp. phage 1/4 Gad1 (IMG ID 2708680195) gBlocks were cloned into a custom pBAD vector containing a chloramphenicol resistance gene and an IPTG-inducible promoter. For Gad1 pull-down assays, *Shewanella* sp. phage 1/4 Gad1 was cloned with a ribosome-binding site after the *GajB* gene in the N-terminal 6×His-SUMO2-5×GS *GajAB* plasmid.

For plaque assays, the DNA of Gad1 was amplified from the phage phi3T genome using KAPA HiFi HotStart ReadyMix (Roche, KK2601). Because Gad1 was toxic in *B. subtilis* cells containing Gabija, *Shewanella* sp. phage 1/4 Gad1 was used and synthesized by GenScript. Gad1 and related homologues were cloned into the pSG-thrC-Phspank vector<sup>42</sup> and transformed to DH5α competent cells. The cloned vector and the vector containing Gad1 substitution and truncation mutants were subsequently transformed into *B. subtilis* BEST7003 cells containing Gabija integrated into the *amyE* locus<sup>1</sup>, resulting in cultures expressing both Gabija and a Gad1 homologue. As a negative control, a transformant with an identical plasmid containing GFP instead of the anti-defence gene was used. Transformation in *B. subtilis* was performed using MC medium as previously described<sup>1</sup>. Sanger sequencing was then applied to verify the integrity of the inserts and the mutations. The pSG1 plasmids containing point mutations in Gabija were constructed by subcloning the Gabija sequence into pGEM9Z using restriction enzymes, site-directed mutagenesis as previously described<sup>43</sup> and Gibson assembly back into pSG1, and the plasmids were transformed into *B. subtilis* BEST7003 cells. Sanger sequencing of the mutations regions was applied to verify the mutations in Gabija.

**Protein expression and purification**

Recombinant GajAB and GajAB–Gad1 complexes were purified from *E. coli* as previously described<sup>44</sup>. In brief, the expression plasmids described above were transformed into BL21(DE3), BL21(DE3)-RIL (Agilent) or LOBSTR-BL21(DE3)-RIL cells (Kerastar), plated on MDG medium plates (1.5% Bacto agar, 0.5% glucose, 25 mM Na<sub>2</sub>HPO<sub>4</sub>, 25 mM KH<sub>2</sub>PO<sub>4</sub>, 50 mM NH<sub>4</sub>Cl, 5 mM Na<sub>2</sub>SO<sub>4</sub>, 0.25% aspartic acid, 2–50 µM trace metals, 100 µg ml<sup>-1</sup> ampicillin and 34 µg ml<sup>-1</sup> chloramphenicol) and grown overnight at 37 °C. Five colonies were used to inoculate 30 ml of MDG starter overnight cultures (37 °C, 230 rpm). Ten millilitres of MDG starter cultures were then inoculated in 1 l M9ZB expression cultures (47.8 mM Na<sub>2</sub>HPO<sub>4</sub>, 22 mM KH<sub>2</sub>PO<sub>4</sub>, 18.7 mM NH<sub>4</sub>Cl, 85.6 mM NaCl, 1% Cas-Amino acids, 0.5% glycerol, 2 mM MgSO<sub>4</sub>, 2–50 µM trace metals, 100 µg ml<sup>-1</sup> ampicillin and 34 µg ml<sup>-1</sup> chloramphenicol) and induced with 0.5 mM IPTG after reaching an optical density at 600 nm (OD<sub>600nm</sub>) of 1.5 or higher (overnight, 16 °C, 230 rpm).

After overnight induction, cells were pelleted by centrifugation, resuspended and lysed by sonication in 60 ml lysis buffer (20 mM HEPES pH 7.5, 400 mM NaCl, 10% glycerol, 20 mM imidazole and 1 mM DTT). Lysate was clarified by centrifugation, and supernatant was poured over Ni-NTA resin (Qiagen). Resin was then washed with lysis buffer, lysis buffer supplemented with 1 M NaCl and lysis buffer again, and was finally eluted with lysis buffer supplemented with 300 mM imidazole. Samples were then dialysed overnight in 14-kDa MWCO dialysis tubing (Ward's Science) with SUMO2 cleavage by hSEN2 as previously described<sup>29,30</sup>. hSEN2 did not efficiently cleave N-terminal 6×His-SUMO2-GajAB and the complex was therefore purified with an additional 5×GS linker. Proteins for crystallography and cryo-EM were dialysed in dialysis buffer (20 mM HEPES-KOH pH 7.5, 250 mM KCl and 1 mM DTT), purified by size-exclusion chromatography using a 16/600 Superdex 200 column (Cytiva) and stored in gel filtration buffer (20 mM HEPES-KOH pH 7.5, 20 mM KCl and 1 mM TCEP-KOH). Proteins for biochemical assays were dialysed in dialysis buffer, purified by size-exclusion chromatography using a 16/600 Superdex 200 column (Cytiva) or 16/600 Sephacryl 300 column (Cytiva) and stored in gel filtration buffer with 10% glycerol. Purified proteins were concentrated to more than 10 mg ml<sup>-1</sup> using a 30-kDa MWCO centrifugal filter (Millipore Sigma), aliquoted, flash-frozen in liquid nitrogen and stored at –80 °C.

Co-expression of Gabija with Phi3T Gad1 results in mild toxicity in *E. coli* grown on MDG medium plates. No toxicity was observed using a closely related Gad1 homologue from the *Shewanella* phage 1/4. Biochemical analysis of Gabija–Gad1 interactions was therefore conducted with *Shewanella* phage 1/4 Gad1. Notably, all Gad1 residues analysed are 100% conserved between Phi3T Gad1 and *Shewanella* phage 1/4 Gad1. For *Shewanella* phage 1/4 Gad1 pull-down assays, SUMO2-5×GS-GajA-GajB-Gad1 point-mutant plasmids were transformed and expressed in BL21(DE3)-RIL or LOBSTR-BL21(DE3)-RIL cells, and subjected to Ni-NTA column chromatography and SUMO2 cleavage with SEN2. Gad1 pull-down was analysed by SDS–PAGE and Coomassie Blue staining.

**Crystallization and X-ray structure determination**

Crystals were grown in hanging drop format using EasyXtal 15-well trays (NeXtal). Native GajAB crystals were grown at 18 °C in 2-µl drops mixed 1:1 with purified protein (10 mg ml<sup>-1</sup>, 20 mM HEPES, 250 mM KCl and 1 mM TCEP-KOH) and reservoir solution (100 mM HEPES-NaOH pH 7.5, 2.4% PEG-400 and 2.2 M ammonium sulfate). Crystals were grown for seven days before cryo-protection with reservoir solution supplemented with 25% glycerol, and were collected by plunging in liquid nitrogen. X-ray diffraction data were collected at the Advanced Photon Source (beamlines 24-ID-C and 24-ID-E). Data were processed using the SSRL autoxds script (A. Gonzalez, Stanford SSRL). Experimental phase information was determined by molecular replacement

using monomeric GajA and GajB AlphaFold2-predicted structures<sup>31,32</sup> in PHENIX<sup>45</sup>. Model building was completed in Coot<sup>22</sup> and then refined in PHENIX. The final structure was refined to stereochemistry statistics as reported in Extended Data Table 1. Structure images and figures were prepared in PyMOL.

### Electrophoretic mobility shift assay

56-bp sequence-specific motif target dsDNA (5' TTTTTTTTTTTTTT TTTTAATAACCCGGTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3') (ref. 22) or scrambled dsDNA (5' TTTTTTTTTTTTTTTTGACAT TACATTCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3') was incubated with a final concentration of 2  $\mu$ M, 5  $\mu$ M or 10  $\mu$ M purified GajAB, GajA[E379A]–GajB or GajAB–Gad1 complexes in 20  $\mu$ l gel shift reactions containing 1  $\mu$ M dsDNA, 5 mM CaCl<sub>2</sub> and 20 mM Tris-HCl pH 8.0 for 30 min at 4 °C. Ten microlitres was then mixed with 2  $\mu$ l of 50% glycerol and separated on a 2% TB (Tris-borate) agarose gel. The gel was then run at 250 V for 45 min, post-stained with TB containing 10  $\mu$ g ml<sup>-1</sup> ethidium bromide while rocking at room temperature, de-stained in TB buffer for 40 min and imaged on a ChemiDoc MP Imaging System.

### DNA cleavage assay

The same 56-bp dsDNA substrates as above were incubated with GajAB, GajA[E379A]–GajB or GajAB–Gad1 complexes in a 20- $\mu$ l DNA cleavage reaction buffer containing 1  $\mu$ M dsDNA, 1  $\mu$ M GajAB, GajA[E379A]–GajB or GajAB–Gad1, 1 mM MgCl<sub>2</sub> and 20 mM Tris-HCl pH 9.0 for 20 min at 37 °C. After incubation, reactions were stopped with DNA loading buffer containing 60 mM EDTA, and 10  $\mu$ l was analysed on a 2% TB agarose gel, which was run at 250 V for 45 min. The gel was then post-stained while rocking at room temperature with TB buffer containing 10  $\mu$ g ml<sup>-1</sup> ethidium bromide, de-stained in TB buffer alone for 40 min and imaged on a ChemiDoc MP Imaging System.

### Cryo-EM sample preparation and data collection

For the SUMO2–GajAB–Gad1 co-complex sample, 3  $\mu$ l of 1 mg ml<sup>-1</sup> was vitrified using a Mark IV Vitrobot (Thermo Fisher Scientific). Before sample vitrification, 2/1 Carbon Quantifoil grids were glow-discharged using an easiGlow (Pelco). Grids were then double-sided blotted for 9 s, with a constant force of 0, 100% relative humidity chamber at 4 °C and a 10-s wait time before plunging into liquid ethane and storing in liquid nitrogen.

GajAB–Gad1 co-complex cryo-EM grids were screened using a Talos Arctica microscope (Thermo Fisher Scientific) operating at 200 kV, and the final map was collected on a Titan Krios microscope (Thermo Fisher Scientific) operating at 300 kV. Both microscopes operated with a K3 direct electron detector (Gatan). SerialEM software v.3.8.6 was used for all data collection. For final data collection, a total of 9,243 movies were taken at a pixel size of 0.3115 Å, a total dose of 41.1 e<sup>-</sup> per Å<sup>2</sup> and a dose per frame of 0.63 e<sup>-</sup> per Å<sup>2</sup> at a defocus range of –0.8 to –1.9  $\mu$ m.

### Cryo-EM data processing

SBGrid Consortium provided data-processing software<sup>46</sup>. Movies were imported into cryoSPARC<sup>47</sup> for patch-based motion correction, patch-based CTF estimation, two-dimensional and three-dimensional particle classification and non-uniform refinement. The cryoSPARC data-processing procedure is outlined in Extended Data Fig. 6. In brief, after patch-based CTF estimation, 500 micrographs were selected and autopicked using Blob Picker, which resulted in 625,295 particles after extracting from micrographs. Two-dimensional classifications were then used to generate five templates for Template Picker, from which 110,654 particles were picked from 500 micrographs. After three more rounds of 2D classification, 648,298 particles from all 9,243 micrographs were used in ab initio ( $K = 3$ ), followed by heterogenous refinement. The best class with 573,410 particles was then used to go back and extract from all micrographs, which resulted in 570,485 particles used in a final 2D classification and ab initio. A total of 351,193 particles from

one ab-initio class were used in non-uniform refinement along with defocus and global CTF refinement, resulting in a 2.84 Å C<sub>1</sub> symmetry and 2.57 Å D<sub>2</sub> symmetry map, which was then used for model building.

### Cryo-EM model building

Model building was performed in Coot<sup>48</sup> by manually docking AlphaFold2-predicted structures<sup>31,32</sup> as starting models and then manually completing refinement and model correction. To model the Gad1 fist domain, an AlphaFold2 model of the Gad1 arm–fist region was superimposed on the cryo-EM density of the manually built shoulder–arm region and then fit into density in Coot<sup>48</sup>. To complete the model for the sparse GajB density, the X-ray GajB structure was superimposed on the cryo-EM density. GajAB–Gad1 model was refined in PHENIX<sup>45</sup>, and the structure stereochemistry statistics are reported in Extended Data Table 2. Figures were prepared in PyMOL and UCSF ChimeraX<sup>49</sup>.

### Statistics and reproducibility

Experimental details about replicates are found in the figure legends.

### Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

### Data availability

Coordinates and structure factors of the Gabija GajAB complex have been deposited in the PDB under the accession code 8SM3. Coordinates and density maps of the GajAB–Gad1 co-complex are deposited with the PDB and the Electron Microscopy Data Bank (EMDB) under the accession codes 8U71 and EMD-41983. All other data are available in the manuscript or Supplementary Fig. 1. Source data are provided with this paper.

- Mazzocco, A., Waddell, T. E., Lingohr, E. & Johnson, R. P. Enumeration of bacteriophages using the small drop plaque assay system. *Methods Mol. Biol.* **501**, 81–85 (2009).
- Leavitt, A. et al. Viruses inhibit TIR cGADPR signalling to overcome bacterial defence. *Nature* **611**, 326–331 (2022).
- Liu, H. & Naismith, J. H. An efficient one-step site-directed deletion, insertion, single and multiple-site plasmid mutagenesis protocol. *BMC Biotechnol.* **8**, 91 (2008).
- Zhou, W. et al. Structure of the human cGAS-DNA complex reveals enhanced control of immune surveillance. *Cell* **174**, 300–311 (2018).
- Liebschner, D. et al. Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. *Acta Crystallogr. D* **75**, 861–877 (2019).
- Morin, A. et al. Collaboration gets the most out of software. *eLife* **2**, e01456 (2013).
- Punjani, A., Rubinstein, J. L., Fleet, D. J. & Brubaker, M. A. cryoSPARC: algorithms for rapid unsupervised cryo-EM structure determination. *Nat. Methods* **14**, 290–296 (2017).
- Emsley, P. & Cowtan, K. Coot: model-building tools for molecular graphics. *Acta Crystallogr. D* **60**, 2126–2132 (2004).
- Pettersen, E. F. et al. UCSF ChimeraX: structure visualization for researchers, educators, and developers. *Protein Sci.* **30**, 70–82 (2021).
- Yin, P., Zhang, Y., Yang, L. & Feng, Y. Non-canonical inhibition strategies and structural basis of anti-CRISPR proteins targeting type I CRISPR-Cas systems. *J. Mol. Biol.* **435**, 167996 (2023).
- Tock, M. R. & Dryden, D. T. The biology of restriction and anti-restriction. *Curr. Opin. Microbiol.* **8**, 466–472 (2005).
- Wilkinson, M. et al. Structures of RecBCD in complex with phage-encoded inhibitor proteins reveal distinctive strategies for evasion of a bacterial immunity hub. *eLife* **11**, e83409 (2022).
- Athukoralage, J. S. et al. An anti-CRISPR viral ring nuclease subverts type III CRISPR immunity. *Nature* **577**, 572–575 (2020).

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**Author contributions** The study was designed and conceived by S.P.A. and P.J.K. All protein purification and biochemical assays were performed by S.P.A. and S.E.M. Crystallography structural analysis was performed by S.P.A. Cryo-EM structural analysis was performed by S.P.A., A.G.J. and M.L.M. Model building and analysis were performed by S.P.A. and P.J.K. Bioinformatics and protein sequence analysis were performed by E.Y., A.L., G.A. and R.S.

Phage challenge assays were performed by A.L. and R.S. Figures were prepared by S.P.A. with assistance from S.E.M. The manuscript was written by S.P.A. and P.J.K. All authors contributed to editing the manuscript, and support its conclusions.

**Competing interests** R.S. is a scientific cofounder and advisor of BiomX and EcoPhage. The remaining authors declare no competing interests.

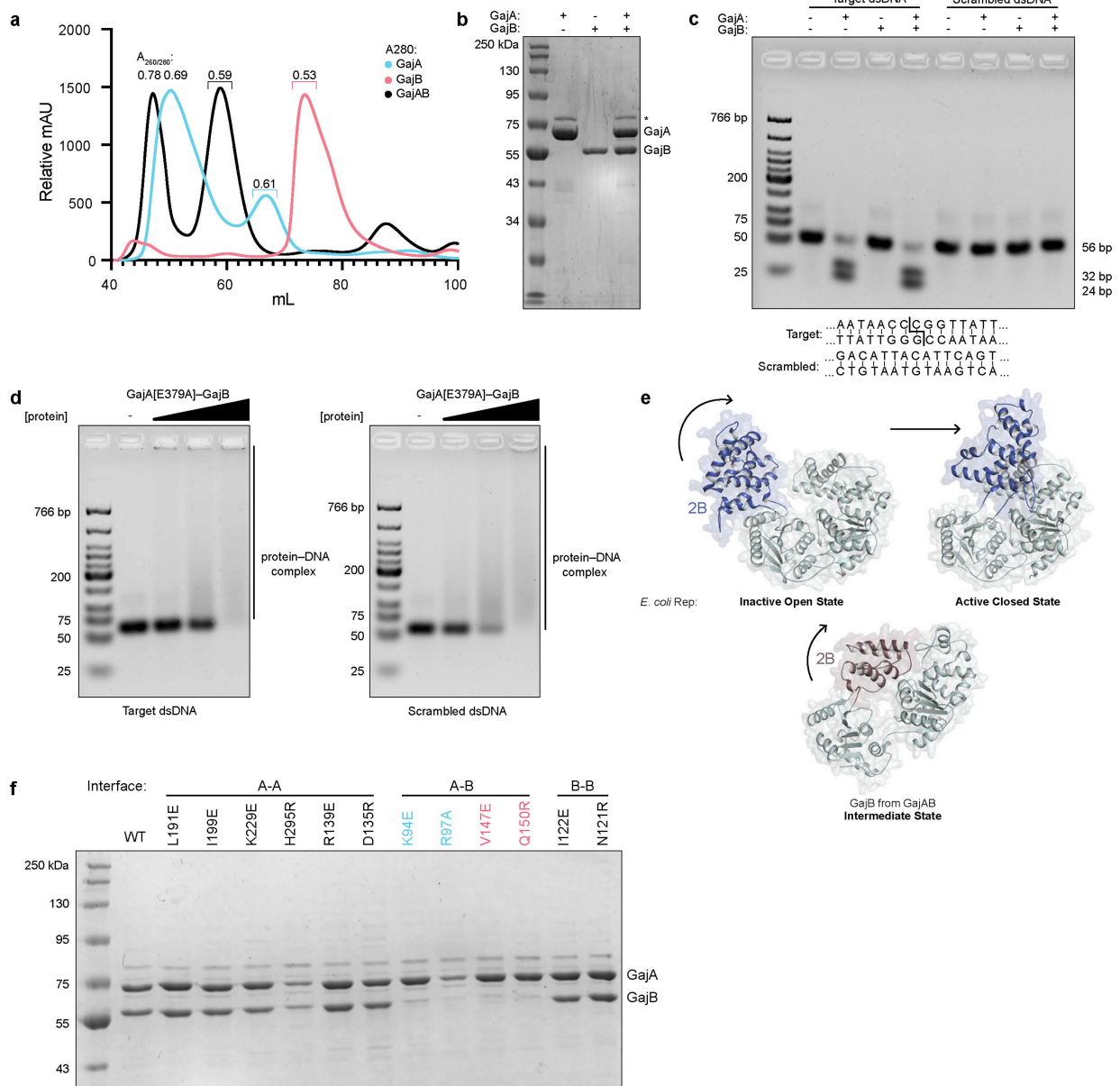
## Additional information

**Supplementary information** The online version contains supplementary material available at <https://doi.org/10.1038/s41586-023-06855-2>.

**Correspondence and requests for materials** should be addressed to Philip J. Kranzusch.

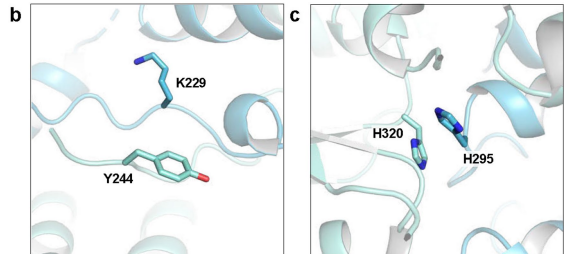
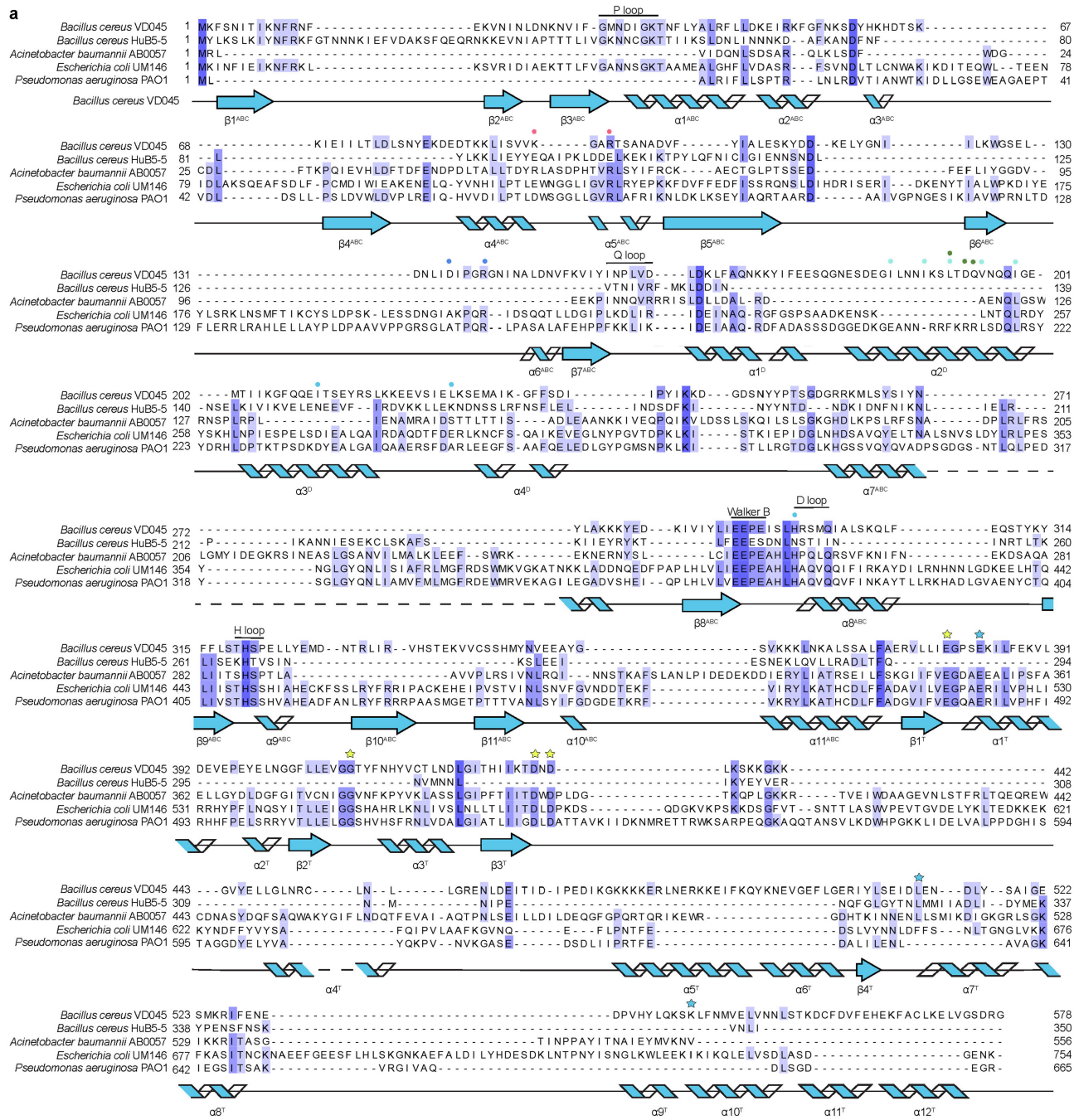
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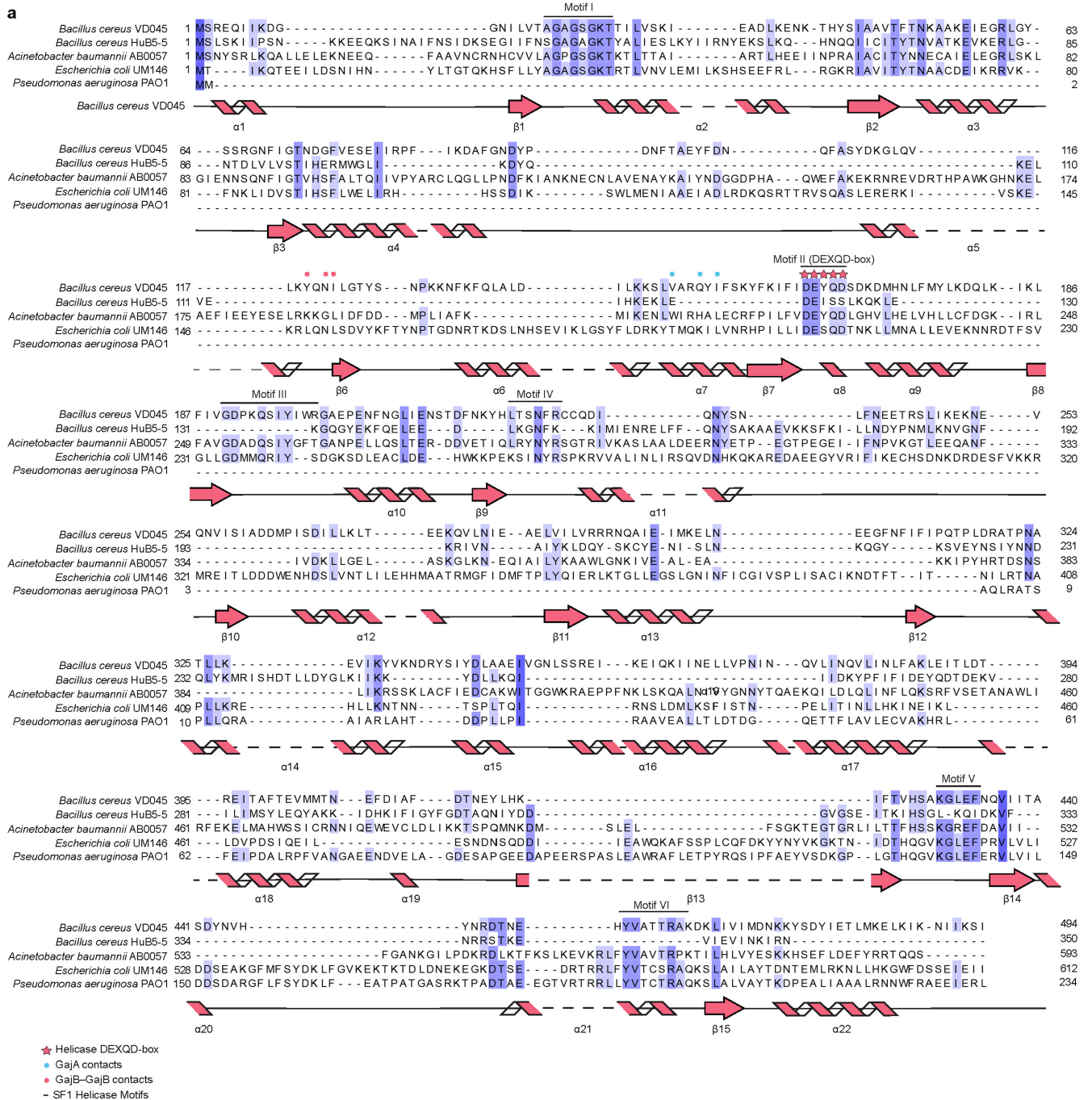
**Extended Data Fig. 1 | GajA and GajB form a supramolecular complex that cleaves phage lambda DNA in vitro.** **a**, Size-exclusion chromatography (16/600 S200) analysis of recombinant *Bc*GajA and *Bc*GajB proteins, and the co-expressed *Bc*GajAB complex. Brackets indicate fractions collected for biochemical and structural analysis with A<sub>260/280</sub> of the final purified proteins listed above. **b**, SDS-PAGE analysis of purified GajA, GajB, and GajAB. Asterisk indicates minor contamination with the *E. coli* protein ArnA. Data are representative of at least 3 independent experiments. **c**, Agarose gel analysis of the ability of GajA, GajB, and GajAB to cleave a 56-bp target and scrambled dsDNA demonstrates that GajA alone and the GajAB complex can cleave target DNA only. The sequence-specific GajA target dsDNA with cleavage site

described in Cheng et al.<sup>22</sup> and the scrambled 15-bp sequence are shown below. **d**, Catalytic dead GajA[E379A]-GajB complex binding to target dsDNA (left) and scrambled dsDNA (right). **e**, Structural comparison of GajB and *Ec*Rep (PDB ID 1UAA)<sup>19</sup> demonstrates the GajB 2B domain is rotated in a partially active intermediate position in the GajAB complex structure. **f**, SDS-PAGE analysis of *Bc*GajAB mutant protein complex formation after co-expression and Ni-NTA pull-down demonstrates that mutations to the GajA-GajB interface disrupt complex formation. The GajA and GajB homo-oligomerization interfaces are not required for GajA-GajB interaction, but it is not known if these mutants remain competent at forming the wild-type 4:4 complex. Data in **c,d,f** are representative of 3 independent experiments.



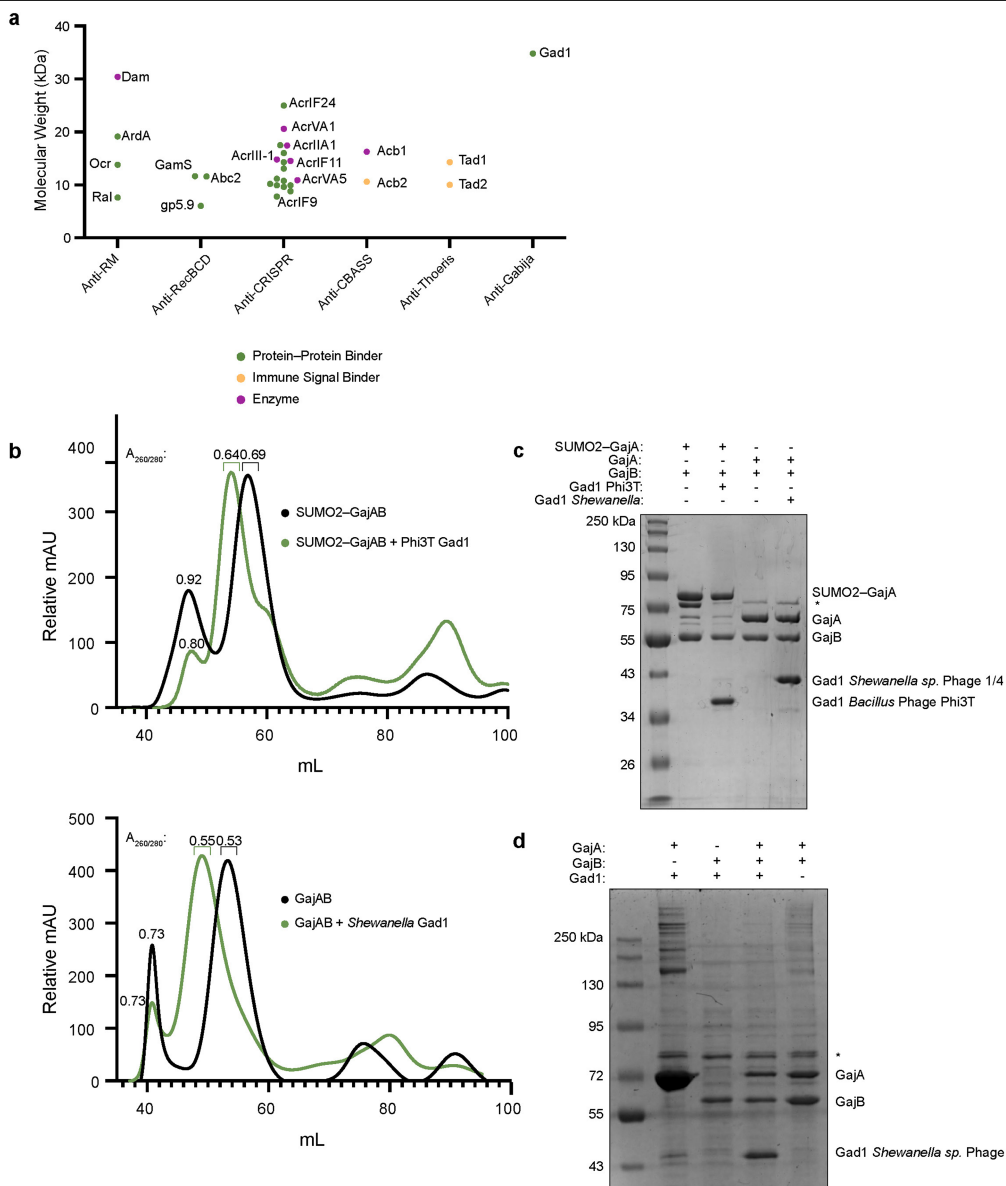
**Extended Data Fig. 2 | Structural characterization of GajA. a**, Structure-guided alignment of GajA proteins from indicated bacteria coloured according to amino acid conservation. The determined *Bacillus cereus* VD045 GajA secondary structure is displayed, and active-site and oligomerization interface residues are annotated according to the key below. Secondary structure

abbreviations include ABC ATPase domain (ABC), dimerization domain (D), and Toprim domain (T). **b, c**, Zoomed-in views of GajA-GajA oligomerization interactions including dimerization domain interactions (**b**) and ABC ATPase domain interactions (**c**).



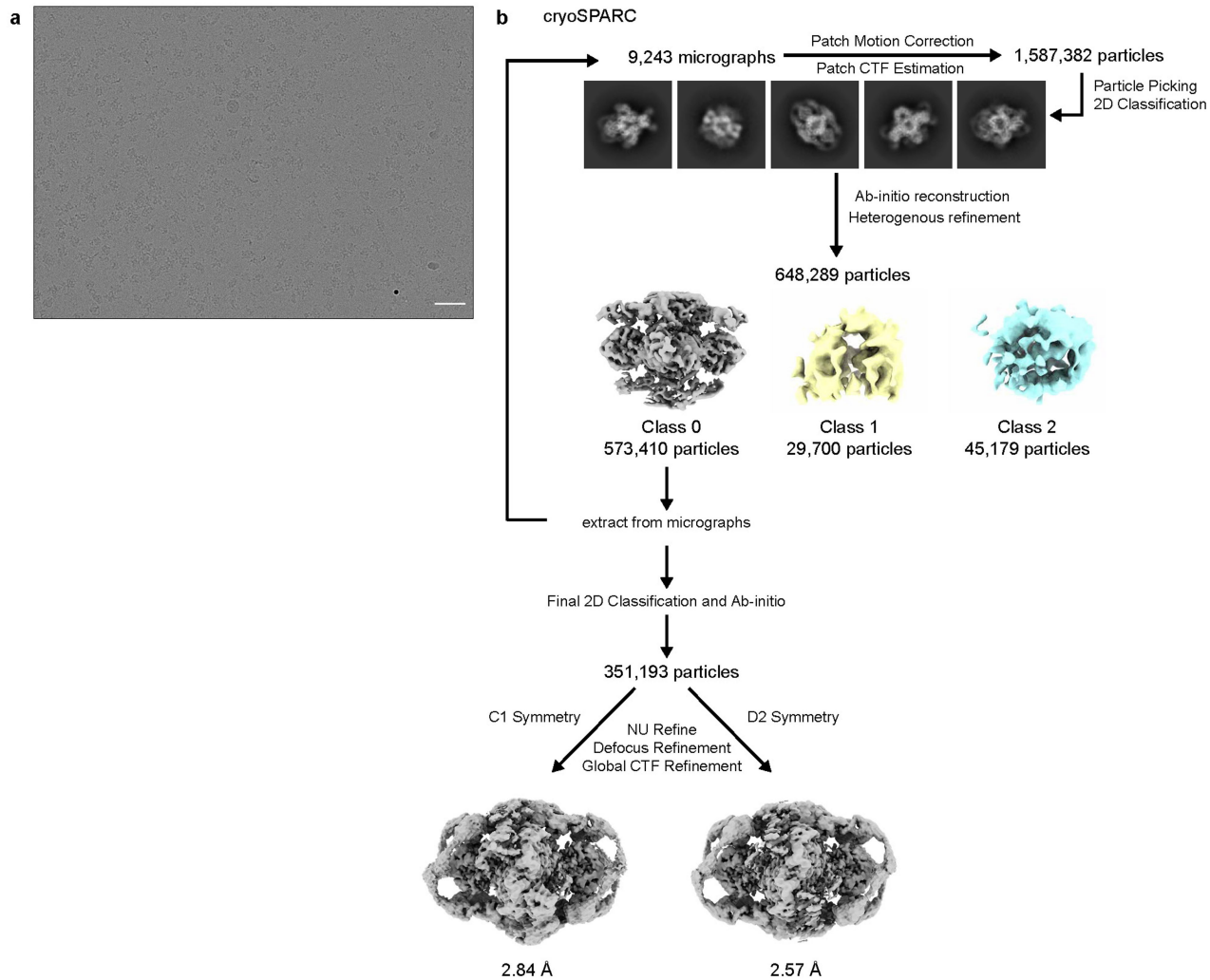
**Extended Data Fig. 3 | Structural characterization of GajB. a.** Structure-guided alignment of GajB proteins from indicated bacteria coloured according to amino acid conservation. The determined *Bacillus cereus* VDO45 GajB secondary

structure is displayed, and active-site and oligomerization interface residues are annotated according to the key below.

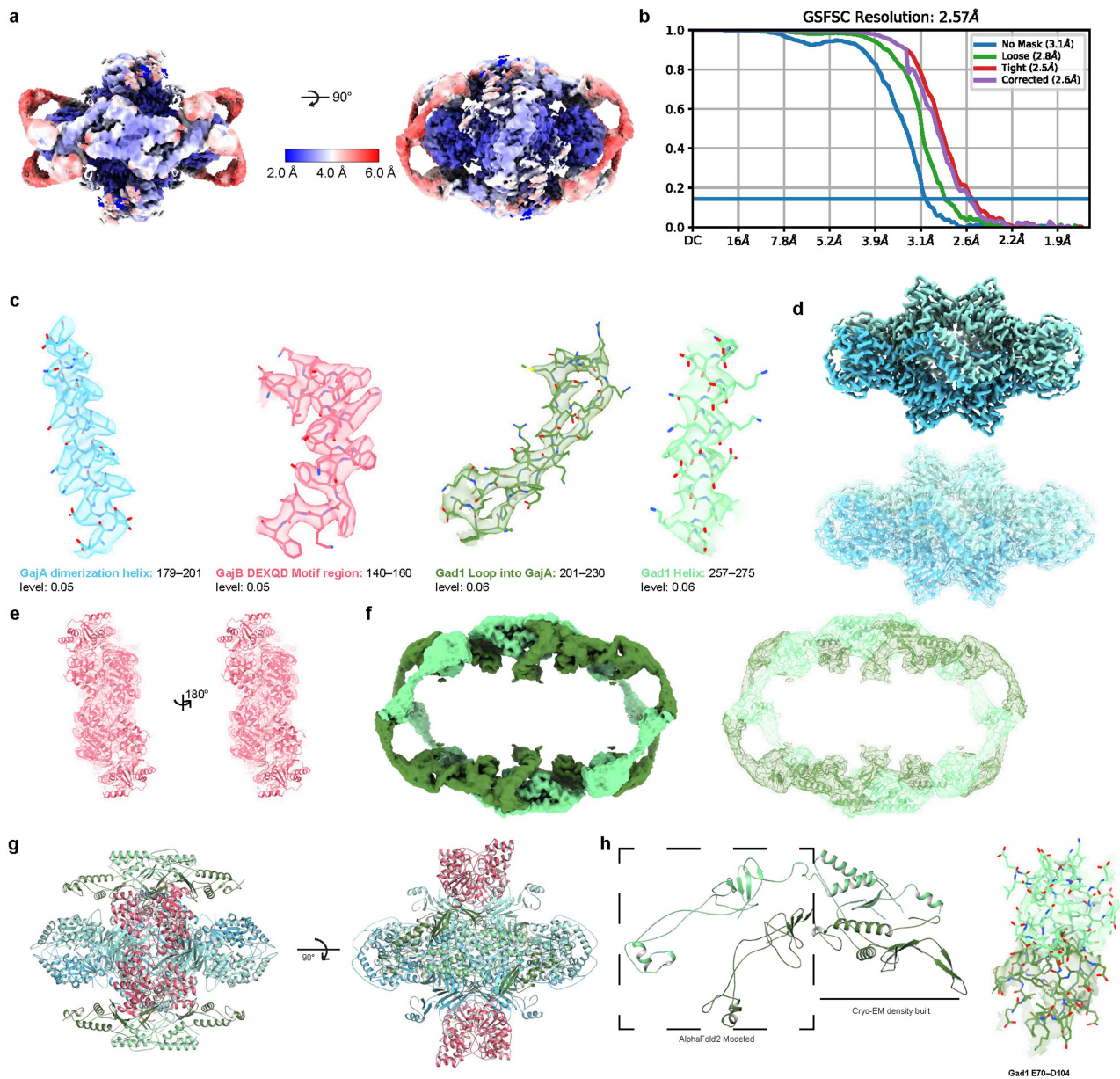


**Extended Data Fig. 4 | Size comparison of Gad1 with known phage immune-evasion proteins and biochemical characterization of Gad1 for binding to the GajAB complex.** **a**, Analysis of known phage immune-evasion proteins according to function and molecular weight demonstrates that Gad1 is atypically large for an evasion protein that functions through protein-protein interactions with a host anti-phage defence system. Phage immune-evasion proteins are categorized and exhibited as coloured dots coloured according to the key below. Notable evasion proteins are indicated with text labels<sup>24-28,42,50-53</sup>. **b**, Top, size-exclusion chromatography analysis (16/600 S200) of SUMO2-tagged *BcGajAB* with or without phage Phi3T Gad1 used for cryo-EM structural studies. Bottom, size-exclusion chromatography analysis (16/600 S300) of *BcGajAB*

with or without *Shewanella* phage 1/4 Gad1 used for biochemical studies. Brackets indicate fractions collected and the  $A_{260/280}$  of the final purified proteins is indicated above. *Shewanella* phage 1/4 Gad1 was used preferentially for biochemical studies due to less toxicity during *E. coli* expression. **c**, SDS-PAGE analysis of purified SUMO2-tagged GajAB, SUMO2-tagged GajAB in complex with phage Phi3T Gad1, untagged GajAB, and untagged GajB in complex with *Shewanella* phage 1/4 Gad1. **d**, SDS-PAGE analysis of Ni-NTA co-purified GajA, GajB, and GajAB with *Shewanella* phage 1/4 Gad1 indicates that Gad1 only binds the fully assembled GajAB complex. Asterisk indicates minor contamination with the *E. coli* protein ArnA. Data in **b-d** are representative of 3 independent experiments.

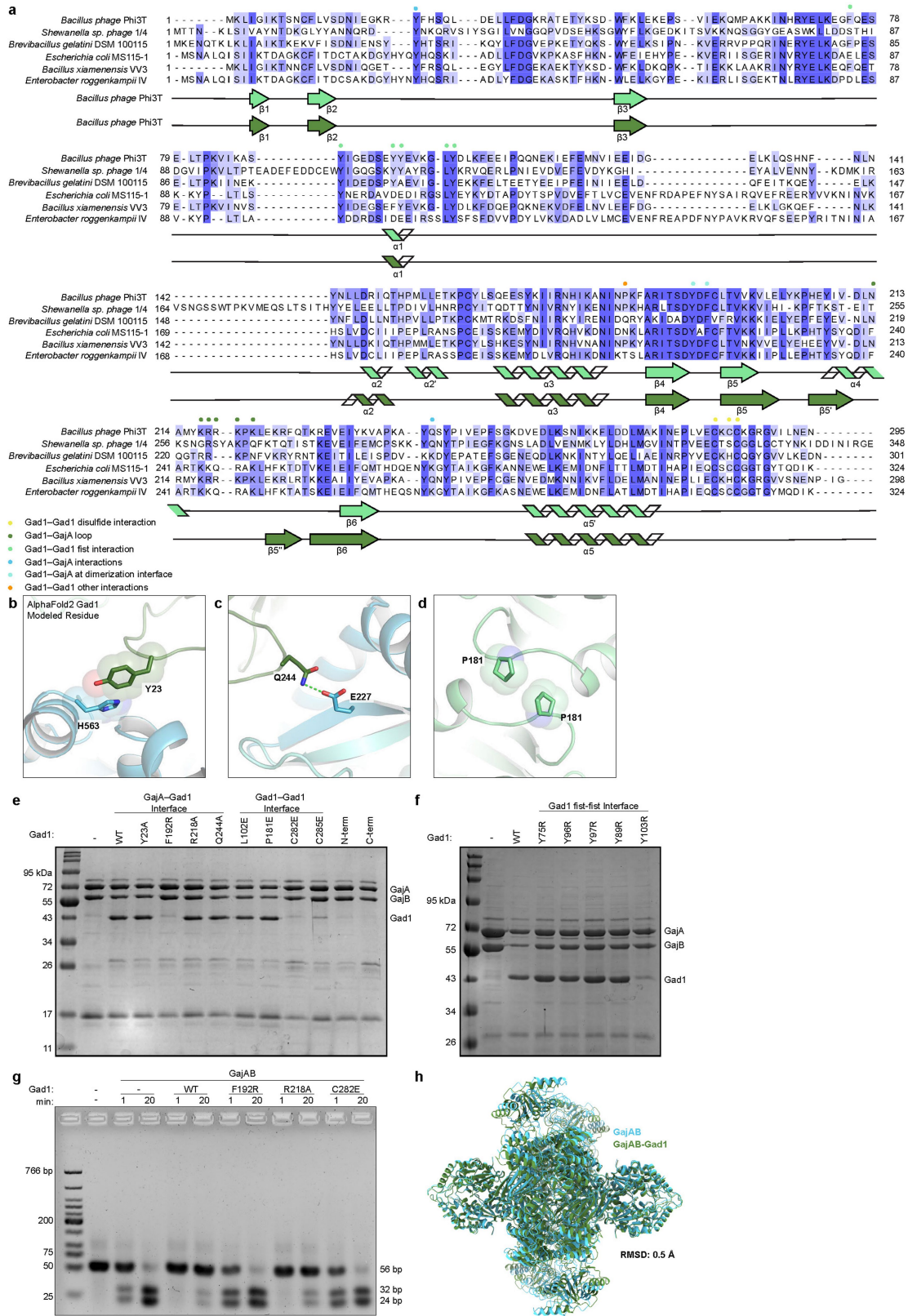


**Extended Data Fig. 5 | Cryo-EM data processing for the GajAB–Gad1 co-complex. a**, Section of a representative electron micrograph ( $n=9,243$ ) of SUMO2–GajAB in complex with phage Phi3T Gad1. Scale bar, 50 nm. **b**, Data-processing scheme used to generate the final 2.57-Å map.



**Extended Data Fig. 6 | Cryo-EM map quality of the GajAB-Gad1 co-complex and model to map fitting.** **a**, Reconstruction of the GajAB-Gad1 co-complex coloured by local resolution. **b**, Fourier shell correlation (FSC) of the EM map. **c**, GajA, GajB, and Gad1 map to model fit for designated regions. **d-f**, Isolated GajA (**d**), GajB (**e**) and Gad1 (**f**) density maps with model fitting. **g**, GajAB-Gad1

model that was used for refining the cryo-EM map for Extended Data Table 2. **h**, Left, sections of Gad1 chains that were built de novo from the cryo-EM density and built using rigid-body placement of AlphaFold2 modelled residues. Right, cryo-EM density used to fit placement of Gad1 fist-fist domain contacts that complete protomer interactions.



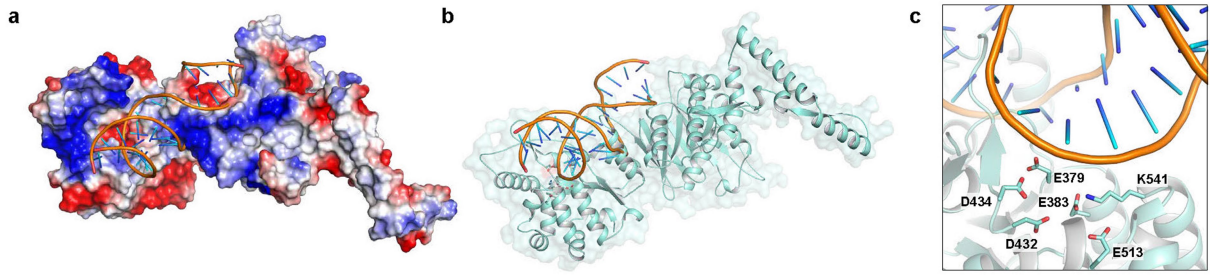
Extended Data Fig. 7 | See next page for caption.



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**Extended Data Fig. 7 | Biochemical and structural characterization of the GajAB–Gad1 co-complex.** **a**, Structure-guided alignment of Gad1 proteins from indicated phage or prophage genomes coloured according to amino acid conservation. The *Bacillus* phage Phi3T Gad1 secondary structure is displayed according to the two different conformations observed in the GajAB–Gad1 co-complex structure. Oligomerization interface residues are annotated according to the key below. **b, c**, Magnified views of Gad1–GajA interface contacts including hydrophobic interactions in AlphaFold2 arm domain structure of Gad1 and the Toprim domain of GajA (**b**) and Gad1 shoulder domain residue Q244 interaction with GajA dimerization domain residue E277 (**c**). **d**, Magnified view of Gad1–Gad1 oligomerization interactions between shoulder domains of Gad1 protomers. **e**, SDS–PAGE analysis of the ability of *Shewanella* phage 1/4 Gad1 mutant proteins to interact with the GajAB complex. *Shewanella* phage 1/4 Gad1 mutant proteins were co-expressed with SUMO2-tagged GajAB (GajA-tagged) and co-purified by Ni-NTA pull-down. *Shewanella* sp. phage 1/4 Gad1 residues are numbered according to the Phi3T Gad1 structure. To measure

high stringency of GajAB–Gad1 interactions, complexes were washed with a 1 M NaCl buffer prior to elution and co-purification. Notably, the Gad1 mutant C282E is no longer able to interact with GajAB in vitro under these stringent conditions, but retains the ability to disrupt Gabija defence in vivo, suggesting that lower-affinity interactions still occur. **f**, SDS–PAGE analysis of the ability of *Shewanella* phage 1/4 Gad1 fist–fist interface mutant proteins to interact with the GajAB complex. *Shewanella* phage 1/4 Gad1 mutant proteins were co-expressed with SUMO2-tagged GajAB (GajA-tagged), co-purified by Ni-NTA pull-down, and treated with SENP2 to cleave the SUMO2 tag prior to SDS–PAGE gel loading. *Shewanella* sp. phage 1/4 Gad1 residues are numbered according to the Phi3T Gad1 structure. **g**, Agarose gel analysis of the ability of GajAB–Gad1 mutant complexes to cleave target 56-bp dsDNA after a 1 min or 20 min incubation. **h**, Superposition of the GajAB crystal structure and GajAB from the GajAB–Gad1 cryo-EM structure demonstrates no significant conformational change after Gad1 binding. Data in **e–g** are representative of 3 independent experiments.



**Extended Data Fig. 8 | Modelling DNA-bound GajA.** **a, b.** Isolated GajA protomer modelled with DNA bound to the Toprim domain shown with surface electrostatic potential (**a**) and in cartoon format (**b**). DNA modelling was

performed using structural homology with the *E. coli* MutS–DNA complex (PDB ID 3K0S)<sup>33</sup>. **c.** Magnified view of the GajA Toprim active site with modelled DNA.

# Article

## Extended Data Table 1 | Summary of X-ray data collection, phasing and refinement statistics

Gabija GajA–GajB (8SM3)	
<b>Data collection</b>	
Space group	P 6 <sub>2</sub> 2 2
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	215.79 215.79 173.81
$\alpha$ , $\beta$ , $\gamma$ (°)	90.0, 90.0, 120.0
Resolution (Å)	49.24–3.00 (3.10–3.00)
<i>R</i> <sub>pim</sub>	4.0 (80.5)
<i>I</i> / $\sigma$ ( <i>I</i> )	15.4 (1.4)
Completeness (%)	100.0 (100.0)
Redundancy	18.1 (16.1)
<b>Refinement</b>	
Resolution (Å)	49.24–3.00
No. reflections	
Total	872109
Unique	48144
Free	2000
<i>R</i> <sub>work</sub> / <i>R</i> <sub>free</sub>	23.69 / 26.60
No. atoms	
Protein	8501
Ligand / ion	5
Water	–
<i>B</i> -factors	
Protein	130.19
Ligand / ion	174.06
Water	–
R.m.s. deviations	
Bond lengths (Å)	0.002
Bond angles (°)	0.442

Dataset was collected from an individual crystal. Values in parentheses are for the highest resolution shell.

**Extended Data Table 2 | Cryo-EM data collection, refinement and validation statistics**

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	GajAB-Gad1 co-complex (EMD-41983) (PDB 8U7I)
<b>Data collection and processing</b>	
Magnification	37,000
Voltage (kV)	300
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	41.1
Defocus range (μm)	-0.8 to -1.9
Pixel size (Å)	0.3115
Symmetry imposed	D2
Initial particle images (no.)	1,587,382
Final particle images (no.)	351,193
Map resolution (Å)	2.6
FSC threshold	0.143
Map resolution range (Å)	2.56–2.95
<b>Refinement</b>	
Initial model used (PDB code)	
Model resolution (Å)	2.57
FSC threshold	0.143
Model resolution range (Å)	2.56–2.58
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-99.0
Model composition	
Non-hydrogen atoms	38,864
Protein residues	4,760
Ligands	0
<i>B</i> factors (Å <sup>2</sup> )	
Proteins	162.67
R.m.s. deviations	
Bond lengths (Å)	0.004
Bond angles (°)	0.622
Validation	
MolProbity score	2.06
Clashscore	10.01
Poor rotamers (%)	3.07
Ramachandran plot	
Favored (%)	97.06
Allowed (%)	2.86
Disallowed (%)	0.09

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| <input checked="" type="checkbox"/> | <input type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons   |
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| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings  |
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Coordinates and structure factors of the Gabija GajAB complex have been deposited in PDB under the accession code 8SM3. Coordinates and density maps of the GajAB–Gad1 co-complex are being deposited with PDB and EMDB under accession codes 8U71 and EMDB-41983. All other data are available in the manuscript or the supplementary materials. Source Data are available for Figures 2 and 3.

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Sample size	No sample size calculations were performed as this is not relevant to biochemical, structural or phage challenge .
Data exclusions	No data were excluded from the analyses.
Replication	All data were performed with replicates as described. Biochemical or phage challenge experiments were performed with 3 technical replicates and at least 3 independent biological replicates. Figures show one example of a biologically independent replicate and other replicates not shown showed similar results within expected variation.
Randomization	Randomization is not relevant to the structural, biochemical, or phage challenge assays described in this study as it would not influence the interpretation of the results.
Blinding	Data was not blinded as the data were collected using quantitative measures that were not subjective.

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