University of Reading

The di-iron RIC protein (YtfE) of Escherichia coli interacts with the DNA-binding protein from starved cells (Dps) to diminish RIC-protein-mediated redox stress

Article

Accepted Version

Silva, L. S. O., Baptista, J. M., Batley, C., Andrews, S. C. and Saraiva, L. M. (2018) The di-iron RIC protein (YtfE) of Escherichia coli interacts with the DNA-binding protein from starved cells (Dps) to diminish RIC-protein-mediated redox stress. Journal of Bacteriology, 200 (24). e00527-18. ISSN 1098-5530 doi: https://doi.org/10.1128/JB.00527-18 Available at https://centaur.reading.ac.uk/79288/

It is advisable to refer to the publisher's version if you intend to cite from the work. See Guidance on citing.

To link to this article DOI: http://dx.doi.org/10.1128/JB.00527-18

Publisher: American Society for Microbiology

All outputs in CentAUR are protected by Intellectual Property Rights law, including copyright law. Copyright and IPR is retained by the creators or other copyright holders. Terms and conditions for use of this material are defined in the End User Agreement.

University of Reading

www.reading.ac.uk/centaur

CentAUR

Central Archive at the University of Reading

Reading's research outputs online

1 **The di-iron RIC (YtfE) protein of *Escherichia coli* interacts with the DNA-binding**
2 **protein from starved cells (Dps) to diminish RIC-protein-mediated redox stress**

3

4 Liliana S. O. Silva[1], Joana M. Baptista[1], Charlotte Bately[2], Simon C. Andrews[2], and Lígia M
5 Saraiva[1,*]

6 [1]Instituto de Tecnologia Química e Biológica NOVA, Av. da República, 2780-157 Oeiras,
7 Portugal

8 [2] School of Biological Sciences, Knight Building, University of Reading, Reading RG6 6AJ,
9 UK

10

11 *Corresponding author:

12 Lígia M. Saraiva

13 Av. da República, 2780-157 Oeiras, Portugal

14 Phone: +351-214469328; Fax: +351-214411277

15 E-mail: lst@itqb.unl.pt

16

17

18

19 **Abstract**

20

21 The RIC (Repair of Iron Clusters) protein of *Escherichia coli* is a di-iron hemerythrin-like
22 protein that has a proposed function in repairing stress-damaged iron-sulphur clusters. In this
23 work, we performed a Bacterial Two Hybrid screening to search for RIC-protein interaction
24 partners in *E. coli*. As a result, the DNA-binding protein from starved cells (Dps) was
25 identified and its potential interaction with RIC was tested by BACTH, Bimolecular-
26 Fluorescence-Complementation and pull-down assays. Using the activity of two Fe-S-
27 containing enzyme as indicators of cellular Fe-S cluster damage, we observed that strains
28 with single deletions of *ric* or *dps* have significantly lower aconitase and fumarase activities.
29 In contrast, the double *ric dps* mutant strain displayed no loss of aconitase and fumarase
30 activity with respect to the wild type. Additionally, while complementation of the *ric dps*
31 double mutant with *ric* led to a severe loss of aconitase activity, this effect was no longer
32 observed when a gene encoding a di-iron site variant of the RIC protein was employed. The
33 *dps* mutant exhibited a large increase in ROS levels, but this increase was eliminated when
34 *ric* was also inactivated. Absence of other iron-storage proteins, or of peroxidase and
35 catalases, had no impact on RIC-mediated redox stress induction. Hence, we show that RIC
36 interacts with Dps in a manner that serves to protect *E. coli* from RIC-protein-induced ROS.

37

38

39

40

41 **Importance**

42 The mammalian immune system produces reactive oxygen and nitrogen species that kill
43 bacterial pathogens by damaging key cellular components such as lipids, DNA and proteins.
44 However, bacteria possess detoxifying and repair systems that mitigate these deleterious
45 effects. The *E. coli* RIC (Repair of Iron Clusters) protein is a di-iron hemerythrin-like protein
46 that repairs stress-damaged iron-sulphur clusters. *E. coli* Dps is an iron-storage protein of the
47 ferritin superfamily with DNA-binding capacity that protects cells from oxidative stress. This
48 work shows that the *E. coli* RIC and Dps proteins interact in a fashion that counters RIC-
49 protein-induced ROS. Altogether, we provide evidence for the formation of a new bacterial
50 protein complex and reveal a novel contribution for Dps in bacterial redox-stress protection.

51

52

53 **Keywords**

54 *E. coli*, di-iron RIC protein, YtfE, Dps, oxidative stress, nitrosative stress

55

56

57 **Running Title**

58 Di-iron RIC protein interacts with Dps

59

60

61 **Introduction**

62 During the infection process, bacterial pathogens are able to survive aggressive environments
63 through the activation of specific stress-resistance genes. One such example of a stress-
64 induced gene is *ric*. This gene encodes the 'Repair of Iron Centre' (RIC) protein that contains
65 a di-iron centre and contributes to the protection of bacterial pathogens such as *Escherichia*
66 *coli*, *Haemophilus influenzae*, *Salmonella* spp., *Yersinia* spp. and *Clostridium* spp. during
67 exposure to nitrosative and/or oxidative stress (1). The *ric* gene is induced upon exposure to
68 either oxidative or nitrosative stress, and in *E. coli, Staphylococcus aureus, Neisseria*
69 *gonorrhoeae, H. influenza* and *Cryptococcus neoformans* the RIC protein is thought to confer
70 stress resistance through maintenance of the activity of various Fe-S containing enzymes (1–
71 3). Such an effect is well demonstrated for *E. coli* and *S. aureus* where RIC proteins restore
72 the activity of oxidatively and nitrosatively-damaged Fe-S clusters in the TCA cycle
73 enzymes, aconitase and fumarase (1, 4, paper Jeff cole). In *E. coli*, the RIC protein also acts
74 under non-stress conditions to maintain aconitase and fumarase activities (5). Further, the *E.*
75 *coli* RIC protein delivers iron (most likely in the ferrous state) for the assembly of Fe-S
76 clusters in spinach apo-ferredoxin and in the *E. coli* Fe-S cluster-assembly scaffold protein,
77 IscU (6). The RIC protein also contributes to the survival of *S. aureus* and *H. influenzae* in
78 activated macrophages, and is required for full virulence in *S. aureus* when infecting the wax
79 moth larva infection-model, *Galleria mellonella* (3, 7). Thus, the RIC protein has an apparent
80 role in bacterial pathogenicity through mediation of Fe-S cluster stability during exposure to
81 redox- and/or nitrosative-stress.

82 The RIC proteins of *E. coli* and *S. aureus* contain di-iron centres of the histidine/carboxylate
83 type within a four-helix-bundle fold (8). The UV-visible spectrum of oxidized RIC protein

84 exhibits a broad band at *ca.* 350 nm and Electron Paramagnetic Resonance (EPR)
85 spectroscopy indicates that the principal g-values are below 2 (g=1.96, 1.92 and 1.88), which
86 is indicative of a S=½ spin state in a mixed valence and anti-ferromagnetically coupled
87 Fe(III)-Fe(II) binuclear iron centre. Mössbauer spectroscopy showed that the mixed-valence
88 Fe(III)–Fe(II) di-iron centre of the RIC protein is more labile than that of the μ(oxo)-diferric
89 form (6).

90 RIC proteins possess several highly-conserved amino acid residues of which some have been
91 shown to influence the properties of the di-iron centre and/or function of the protein. In
92 particular, substitution of residues His129, Glu133 or Glu208 of the *E. coli* RIC protein
93 abrogated its ability to protect the Fe-S cluster of aconitase. Moreover, two μ-carboxylate
94 bridges contributed by Glu133 and Glu208, linking the two di-iron site atoms, were shown
95 to be required for the assembly of a stable di-iron centre (9). These studies also demonstrated
96 the important contribution of the conserved His84, His129, His160, His204, Glu133 and
97 Glu208 residues in ligating the di-iron centre within the four-helix bundle fold, and these di-
98 iron coordination roles were recently confirmed by X-ray crystallographic structural studies
99 (10).

100 In the work reported here, we sought to identify proteins that interact with, and support the
101 function of, the RIC protein of *E. coli*. For this purpose, an *E. coli* library was screened for
102 RIC protein interaction partners using the Bacterial Adenylate Cyclase Two Hybrid system
103 (BACTH). Potential interacting gene products were further tested by BACTH, Bimolecular
104 Fluorescence Complementation (BiFC) and pull-down assays. Our protein-protein
105 interaction studies revealed that the RIC protein interacts with the DNA-binding protein from

starved cells (Dps). Dps is a symmetrical dodecameric iron-storage protein of the ferritin superfamily that contains a di-iron ferroxidation centre located at the interface between subunits (11–13). Dps sequesters ferrous iron, which is oxidized preferentially by hydrogen peroxide at its di-iron centre and then deposited for storage as Fe(III) oxyhydroxide in the central cavity as an iron core; the sequestered iron can subsequently be released by reduction (13, 14). The ferroxidase activity, DNA-binding and iron-sequestration properties of Dps confer cells with protection from oxidative stress and nutrient deprivation, as judged by the reduced survival of *dps* mutants under stress conditions including starvation, oxidative stress, metal toxicity, and thermal stress (15). The physiological relevance of the interaction between the RIC protein and Dps was examined and the results revealed that Dps modulates the function of RIC.

Results

126

127 **Identification of novel potential RIC-protein-interaction partners by screening a**
128 **bacterial two-hybrid *E. coli* library**

129

130 We used a genetic approach to further assess the physiological role of RIC in *E. coli,* by
131 employing the bacterial two-hybrid (BACTH) system (16) to screen the *E. coli* genome for
132 gene products that could interact with RIC. For this purpose, RIC was fused to the C-terminus
133 of the *B. pertussis* adenylate cyclase T25 fragment and used as 'bait' to screen previously
134 constructed partial-*Sau*3A-digested *E. coli* DNA random libraries that express fusions to the
135 N-terminus of the *B. pertussis* adenylate cyclase T18 fragment (17). We isolated 22 positive
136 recombinant Lac^{+} colonies, from which plasmids were purified and then transformed into *E.*
137 *coli* DHM1 harbouring pKT25-RIC, or the empty vector pKT25 (negative control), or
138 pKT25-TorD (false positive control), followed by the determination of the β-galactosidase
139 specific activities (Figure 1). Seven pKT25-RIC transformants, harbouring plasmids A to G,
140 exhibited significant β-galactosidase activity indicative of a specific interaction (Figure 1).
141 Nucleotide sequencing followed by BLAST analysis was used to identify the genes within
142 the inserts of these plasmids. Sequencing data revealed that plasmids A to C contain an ~2
143 kb *E. coli* DNA fragment upstream of the T18 Cya domain, and that all cases included the
144 complete *efp* and *ecnA* genes, and part of the *ecnB* gene. The *efp* gene encodes the elongation
145 factor EF-P, a translation factor that facilitates the *in vitro* the formation of the first peptide
146 bond during translation (18, 19). The gene cluster *ecnAB* expresses two small cell-membrane
147 associated entericidin lipoproteins, forming EcnAB a toxin-antitoxin module that regulates a
148 programmed bacterial cell death under high osmolarity conditions, with EcnA acting as the
149 antidote for the bacteriolytic entericidin, EcnB (20).

150 The other four plasmids D to G also contained a ~2 kb insert located upstream of the T18
151 Cya domain, but in these cases the inserts carried the entire *rhtA* gene, encoding an inner-
152 membrane transporter involved in resistance to homoserine/threonine (21), and the *dps* gene,
153 encoding the DNA-binding and iron-storage protein from *s*tarved cells (11). Like RIC, *E. coli*
154 Dps has been implicated in oxidative-stress protection, which raises the possibility of a
155 functional association between these two proteins that might be dependent on their direct
156 interaction. For this reason, the potential interaction between the two proteins was
157 investigated further in order to establish its validity and determine its physiological purpose.
158
159 ***E. coli* RIC protein interacts with Dps**
160
161 To determine whether the interaction between the RIC protein and Dps, as identified through
162 the screening of the pUT18 library, is indeed genuine, further BACTH experiments were
163 performed. To enable such experiments, the gene encoding the RIC protein was cloned into
164 pUT18C and pUT18 vectors (to create T18-RIC and RIC-T18 fusions), and the *dps*-coding
165 region was introduced into the pKNT25 vector (to give Dps-T25 fusions), following which
166 the β-galactosidase activities of the corresponding co-transformants were measured. High β-
167 galactosidase activities were recorded for both sets of the RIC-Dps BATCH combinations
168 tested, with activities 4-6 times greater than those of the controls (Figure 2A), indicative of
169 interaction between the RIC protein and Dps within the cytosol of *E. coli*.
170 A second approach was used to test the proposed RIC-Dps interaction, which involved a
171 Bimolecular Fluorescence Complementation (BiFC) assay. In this method, one of the two
172 proteins of interest is fused to the N-terminal half of the green fluorescent protein (GFP), and
173 the other protein of interest is fused to the C-terminal half; the assay depends upon an

174 interaction between the two proteins that promotes the reassembly of the two halves of GFP
175 such that emission of fluorescence is restored (22). Thus, GFP fusions (both the N- and C-
176 terminal domains) were generated for both the RIC protein and Dps, and the fluorescence
177 intensity of the corresponding *E. coli* cells containing plasmids co-expressing the RIC and
178 Dps fusions was measured (Figure 2BC). The data showed that cells expressing $RIC^{C\text{-}GFP}$
179 and $Dps^{N\text{-}GFP}$ exhibit an approximately six-fold higher fluorescence relative to the control,
180 although transformants expressing $RIC^{N\text{-}GFP}$ and $Dps^{C\text{-}GFP}$ presented fluorescence levels
181 similar to that of the control samples.

182 The RIC protein consists of two domains: a short N-terminal 'ScdA_N' domain of ~60
183 residues of unclear function with a highly-conserved pair of Cys residues (10); and a larger
184 C-terminal 'hemerythrin' domain of ~140 residues that forms a di-iron centre. We tested the
185 BiFC interaction between Dps and a truncated form of RIC that lacks the so-called first
186 Scd_N domain to determine which of the two RIC protein domains is responsible for the
187 observed interaction with Dps. The results showed that the degree of interaction between the
188 truncated RIC protein and Dps is similar to that observed when using the full-length protein
189 (Figure 2C). Thus, the interaction observed here between the RIC protein and Dps appears
190 to be mediated through the C-terminal hemerythrin domain of the RIC protein.

191 The interaction between RIC and Dps was also investigated by a pull-down assay. To this
192 end, cells containing plasmids that express non-labelled Dps and N-terminally His-tagged-
193 RIC were treated with formaldehyde, as described in Methods, to promote *in vivo* cross-
194 linking. The cell extract was loaded into a Ni-chelating column and the His-Tag RIC was
195 eluted at 100 mM of imidazole buffer. The fraction was analysed by SDS-PAGE, and
196 Western blotting in which the *E. coli* Dps antibody was used. Also, cells expressing only the

197 non-labelled Dps were treated and analysed similarly to serve as control. The results depicted
198 in Figure 2D show that elution of His-Tag RIC occurred together with a band that has a
199 molecular mass correspondent to that of Dps. This band was proved by Western-blotting to
200 be the *E. coli* Dps (Figure 2D). Therefore, the pull-down assays support the interaction
201 between RIC and Dps.

202

203 **Dps modulates the function of the RIC protein in maintaining Fe-S cluster status**

204 The RIC protein has been linked to the resistance of *E. coli* to oxidative and nitrosative
205 stresses as its inactivation decreases the survival of *E. coli* upon exposure to hydrogen
206 peroxide or nitric oxide donors (4). Due to the interaction of the RIC and Dps proteins shown
207 above, we questioned whether Dps could contribute to the stress protection afforded by the
208 RIC protein. To test this possibility, a Δ*dps* Δ*ric* double mutant was constructed and the
209 growth of *E. coli* wild type, Δ*ric*, Δ*dps*, Δ*dps* Δ*ric* mutants under oxidative and nitrosative
210 stress conditions was tested (Figure 3). The growth experiments showed that inactivation of
211 *ric* resulted in impaired growth under stress conditions imposed by 4 mM H_2O_2 or 250 µM
212 spermine NONOate (Figure 3), which is consistent with previous reports (4). However, the
213 *dps* mutation had little impact on growth under these conditions. Combining the Δ*dps*
214 mutation with the Δ*ric* mutation did not result in any further growth reduction under the same
215 stress conditions, i.e. the Δ*dps* Δ*ric* strain grew similarly to the Δ*ric* strain under the oxidative
216 and nitrosative stress conditions employed (Figure 3). Thus, Dps does not notably
217 compensate for the lack of the RIC protein under peroxide or NO-induced stress.

218 Another characteristic of the *E. coli ric* mutant is the reduced endogenous activity of Fe-S
219 cluster-containing proteins, such as aconitase and fumarase, that contain solvent-exposed Fe-
220 S clusters with a marked sensitivity to redox and nitrosative stress (4). Therefore, the possible
221 contribution of Dps to this phenotype was explored by comparing the aconitase activity of
222 the Δ*dps* and Δ*dps* Δ*ric* strains to that of the wild type and Δ*ric* mutant. The results showed
223 that the Δ*dps* mutation caused a 50% reduction in aconitase activity in log phase (Figure 4A),
224 consistent with a role for Dps in maintaining Fe-S cluster status. As expected, a similar effect
225 was observed for the Δ*ric* mutant, although the reduction in activity (30%) was only
226 approximately half as great as that observed for the Δ*dps* mutant (Figure 4A). Surprisingly,
227 the Δ*dps*Δ*ric* mutant exhibited aconitase activity that was higher than that of the
228 corresponding single mutants and similar to that of the wild type (Figure 4A). These
229 aconitase-activity effects were apparent in both the early-log and the post-exponential phase
230 (OD_{600} 0.6 and 2, respectively; Figure 4A and B), suggesting that the phenotype is
231 independent of growth stage (note that *dps* is stationary-phase induced).

232 Similar effects were observed when testing the activity of another Fe-S enzyme, namely
233 fumarase. The data showed a reduction of 70% in fumarase activity in the Δ*dps* mutant when
234 compared to wild type during the early-log phase (OD_{600}=0.6). Accordingly, in the Δ*ric*
235 mutant there was a reduction in fumarase activity of about 40% while the double mutant
236 Δ*dps*Δ*ric* displayed a fumarase activity similar to that of the wild type (Figure 4C).

237 The restoration of aconitase and fumarase activity to wildtype levels in the double *dps ric*
238 mutant (with respect to the corresponding single mutants) suggests that the negative impact
239 of the lack of the RIC protein on such activity is dependent on the presence of Dps (and vice-

240 versa), and this in turn indicates a hitherto unrecognised functional interdependence for these
241 two proteins.

242 The association of the above aconitase-activity effects with the RIC protein was confirmed
243 by complementation using a multicopy plasmid bearing the wild type *ric* gene under control
244 of its natural promoter. Complementation of the single Δ*ric* mutant led to the recovery of
245 aconitase activity to levels similar to those of the wild type (Figure 4D). More importantly,
246 provision of a wild type version of *ric* (in multicopy) caused a large (60%) and significant
247 reduction in the aconitase activity of the Δ*dps*Δ*ric* double mutant (Figure 4D). Thus, as
248 anticipated, the *ric*-complemented double mutant exhibited the same phenotype as the *dps*
249 mutant. This confirms that the RIC protein is responsible for decreasing aconitase activity in
250 a *dps*$^{-}$ background.

251 To investigate whether the role of the RIC protein in lowering aconitase activity in the *dps*
252 mutant is dependent on a biochemically-functional version of the RIC protein, the ability of
253 a RIC protein variant (lacking a complete di-iron site due to an E133L substitution; (9)), was
254 used in the complementation experiments (Figure 4D). The resulting activity data clearly
255 show that he non-functional E133L-RIC variant does not enable a notable decrease in
256 aconitase activity when expressed in the Δ*dps*Δ*ric* strain (Figure 4D).

257 In summary, the above data suggest that in the absence of Dps, the RIC protein has a
258 deleterious effect on aconitase and fumarase activities, but that such an effect is not exhibited
259 when Dps is present. This would imply that the interaction between Dps and the RIC protein,
260 as revealed here, acts to ensure that neither of these two proteins can participate in processes
261 that negatively impact the activity of these Fe-S enzymes.

262

263 **RIC does not interact with other *E. coli* iron-storage proteins**

264 *Escherichia coli* Dps is an iron-sequestering protein composed of 12 identical subunits
265 forming a shell surrounding a central cavity where up to ~500 ferric iron atoms can be
266 sequestered. As *E. coli* encodes two other iron-storage proteins, namely bacterioferritin (Bfr)
267 and ferritin (FtnA), the possibility that the RIC protein might interact with these other iron-
268 storage proteins was also investigated. Thus, corresponding BiFC experiments were
269 performed in cells carrying recombinant plasmids that express the RIC protein with either
270 Bfr or FtnA, as N- or C-terminal fusions to GFP domains. The resulting fluorescence
271 intensity data failed to support any protein-protein interaction between the RIC protein and
272 Bfr or FtnA (Figure 5A).

273 In a second set of experiments, the aconitase activity of wild type, Δ*ric,* Δ*bfr,* Δ*ftnA,* Δ*bfr*Δ*ric*
274 and Δ*ftnA*Δ*ric* strains, grown to the exponential phase (OD_{600} of 0.6), was determined.
275 Similarly to the Δ*dps* strain, the Δ*bfr* and Δ*ftnA* strains both displayed ~50% lower aconitase
276 activity levels (Figure 5B). But contrary to the effect of combining the Δ*dps* and Δ*ric*
277 mutations, the combined absence of the RIC protein and the Bfr or FtnA proteins resulted in
278 aconitase activities similar to those present in the correspondent single mutant strains (Figure
279 5B). Thus, the lower aconitase activity caused by the Δ*ric* mutation is not additive with
280 respect to lower activity of resulting from the Δ*bfr* or Δ*ftnA* mutations. Further, it can be
281 concluded that (unlike Dps) Bfr and FtnA do not interact with the RIC protein, and that their
282 absence does not result in a RIC-protein dependent decrease in aconitase activity.

283

284 **The RIC protein increases intracellular ROS levels when Dps is absent**

285 Dps protects cells from oxidative stress due to its ability to couple the reduction of hydrogen
286 peroxide to water with the oxidation of free-ferrous iron to sequestered-ferric iron. In
287 addition, its association with DNA helps to prevent ROS-induced DNA damage (27). This
288 suggests that the role of Dps in preventing RIC-protein induced inhibition of aconitase
289 activity may arise from the ability of Dps to detoxify ROS that might be produced by the di-
290 iron centre of the RIC protein (e.g. through binding and reduction of oxygen). Therefore, the
291 ROS content of Δ*ric*, Δ*dps* and Δ*dps* Δ*ric* strains were compared with those found in the wild
292 type to determine whether the presence of the RIC protein, in the absence of Dps, results in
293 raised levels of ROS (Figure 6A). Data show that the wild type and Δ*ric* mutant contain
294 similar amounts of ROS while the Δ*dps* strain had significantly higher (~2-fold) levels
295 (Figure 6A). This is as expected given the known role of Dps in redox-stress resistance (27).
296 However, introduction of the *ric* mutation into the *dps* mutant eliminated the increased
297 intracellular ROS levels of the single Δ*dps* mutant (Figure 6A). This suggests that the raised
298 ROS levels of the *dps* single mutant are a consequence of an increase in RIC-protein-
299 dependent ROS production which thus supports a role for Dps in interacting with the RIC
300 protein to restrict its release of ROS species.

301 To discover whether other elements of the redox-stress resistance response might also act to
302 lessen RIC-protein induced ROS production, the Δ*ric* mutation was introduced into a strain
303 (Δ*hpx*) lacking capacity to degrade hydrogen peroxide due to inactivation of both catalase
304 genes as well as the alkyl-hydroperoxide reductase genes (Table 1; (28, 29)). Assay of the
305 resulting aconitase activity levels showed that the Δ*hpx*Δ*ric* quadruple mutant has activity
306 levels similar to those determined for the Δ*ric* and Δ*hpx* mutants (Figure 6B). Therefore, we

307 concluded that the three major peroxidases (KatE, KatG, AhpCF) of *E. coli* are not involved
308 in countering any RIC-protein mediated ROS production, at least under conditions where
309 Dps is active.

310

311 **Discussion**

312 Aconitase and fumarase are enzymes of the TCA cycle that are prone to oxidative stress
313 damage. We previously showed that the di-iron RIC protein repairs these enzymes and is
314 able to transfer iron to Fe-S containing proteins (4–6). In the work described here, we
315 screened an *E. coli* BACTH library in order to identify proteins that interact with the RIC
316 protein and thus might be required to assist its function. As a consequence of our screening,
317 Dps emerged as a RIC protein interaction candidate. This suggested interaction was
318 supported by generation and analysis of additional Dps and RIC protein BACTH constructs
319 and by GFP complementation and pull-down assays. Dps belongs to the ferritin superfamily
320 which led us to investigate the possible interaction of RIC with the two other ferritins present
321 in *E. coli*, namely ferritin and bacterioferritin. However, neither of these proteins were found
322 to interact with the RIC protein or to influence its activity *in vivo*.

323 We also observed that inactivation of the RIC protein resulted in lower aconitase and
324 fumarase activity, which is consistent with previous findings indicating that this protein
325 contributes to the protection of solvent accessible Fe-S clusters from ROS damage under
326 aerobic growth conditions (5). Similar results were herein obtained for the single mutant
327 strains of *dps*, *ftnA* and *bfr*, indicating that lack of any of these gene products results in lower
328 endogenous aconitase activity. The role of FtnA and Bfr in aconitase protection was

329 previously demonstrated as the two ferritins promote the reactivation of aconitase activity
330 following stress damage in *Salmonella enterica* serovar Typhimurium (30). In contrast with
331 our findings with *E. coli*, no loss of aconitase activity was observed for *S. enterica ftnA* or
332 *bfr* single mutants in the absence of stress; this discrepancy may be related to different
333 physiological roles and expression control of ferritins in *Salmonella* and *E. coli* species (30,
334 31).
335 A surprising result was the finding that the defective aconitase activity of the Δ*dps* and Δ*ric*
336 single mutant strains was reversed when these two mutations were combined in the Δ*dps*Δ*ric*
337 double mutant, such that activity was restored to that measured in the wild type. This result,
338 together with the lower amounts of ROS observed in the Δ*dps*Δ*ric* mutant compared to the
339 Δ*dps* mutant, suggests that the RIC protein is responsible for the generation of ROS, but only
340 in the absence of Dps and, thus, that the interaction of Dps and the RIC protein serves to
341 enable Dps to restrict ROS release (which is presumed to damage the Fe-S cluster of
342 aconitase and fumarase, and hence lower the observed activity of these enzymes in a *dps*
343 mutant) by the RIC protein. Interestingly, other redox-stress resistance components (KatE,
344 KatG and AhpCF) failed to impact the RIC-protein-mediated inhibition of aconitase activity
345 (at least in the presence of Dps). These results suggest that the effect of Dps on the ROS-
346 generation activity of the RIC protein is one that is highly specific and not replicated by the
347 other peroxide-consuming cytosolic factors examined. Indeed, the findings relayed here
348 indicate that a direct interaction is required to enable Dps to quench the ROS-generating
349 activity of the RIC protein. The exact mechanism involved in the apparent quenching of RIC-
350 protein-mediated ROS production by Dps is unclear; such understanding will require *in vitro*
351 reaction studies combining the Dps and RIC proteins. However, two possible processes by
352 which Dps could exert a ROS-quenching action upon the RIC protein can be considered: Dps

might sequester iron released from the di-iron site of the RIC protein and thus restrict Fe-driven Fenton chemistry; or Dps could consume hydrogen peroxide (or hydroxyl radicals; (14, 32)) generated by the RIC protein through reaction at its di-iron site with molecular oxygen.

Although the absence of the RIC protein in the presence of Dps resulted in reduced aconitase and fumarase activity, lack of RIC protein had no impact on ROS levels when Dps was present. The reason for this effect is unclear but may indicate a role for the RIC protein in supply of iron from Dps for Fe-S cluster repair and/or synthesis.

The proposed role of the RIC protein (4) is to repair damaged Fe-S clusters of [Fe-S]-proteins, such as aconitase and fumarase, by donating iron from its di-iron centre leading to the formation of an intermediate mononuclear iron centre that is prone to react with oxygen to generate ROS such as hydrogen peroxide. In this process, the interaction with Dps would fulfil two roles, namely by trapping ROS released by the RIC protein and providing a sink for iron liberated from the di-iron centre of RIC.

In conclusion, we report an interaction between the Dps and RIC proteins of *E. coli* which represents the first example of a protein that interacts with the ferritin-like Dps protein. In addition, our results indicate that the Dps-RIC protein interaction contributes to the function of RIC, which is one of the few known bacterial proteins involved in repair.

374 **Materials and Methods**

375 *Bacterial strains and growth conditions*

376 *Escherichia coli* strains used in this work are listed in Table 1, and were grown at 37 ^{o}C. *E.*
377 *coli* XL2Blue and *E. coli* reporter strain DHM1 non-reverting adenylate cyclase deficient
378 (*cya*) were used as host strain and for detection of protein-protein interactions, respectively.

379 Construction of the *E. coli* double mutant strains was performed by bacteriophage P1-
380 mediated transduction (33), and the corrected mutations were confirmed by PCR using
381 primers listed in Table 2.

382 *E. coli* cells were grown in LB medium under aerobic conditions in flasks containing a 1/5
383 volume of culture or under anaerobic conditions in rubber seal-capped flasks filled with
384 medium and extensively bubbled with nitrogen prior to growth. For the stress assays, cells
385 were grown, at 37 °C and 150 rpm, in M9B minimal medium (60 mM K_2HPO_4, 33 mM
386 KH_2PO_4, 7.6 mM $(NH_4)_2SO_4$, 1.7 mM sodium citrate, 1 mM $MgSO_4$ and 10 µM $MnCl_2$, pH
387 7) supplemented with 10 µg/mL thiamine and 40 µg/mL L-arginine, L-leucine, L-proline, L-
388 threonine and 40 mM glucose. Cultures at an OD_{600} of 0.3 were either left untreated or
389 exposed to 4 mM H_2O_2 for 6 h or to 250 µM spermine-NONOate for 9 h.

390

391 *BACTH experiments*

392 The Bacterial Adenylate Cyclase-based Two-Hybrid (BACTH) system assay (16) was used
393 to identify RIC-interacting proteins. *E. coli* RIC protein was fused to the C-terminal of

394 *Bordetella pertussis* Cya (adenylate cyclase) T25 domain (pKT25-RIC) and used to screen
395 an *E. coli* MC4100 gene library containing chromosomal fragments fused to the N-terminal
396 of *B. pertussis* Cya T18 domain. The DNA fragments were obtained by partial digestion with
397 *Sau*3AI and cloning into the *Bam*HI site of pUT18 plasmids (17). About 1 µg of
398 pUT18*Bam*HI DNA library was transformed together with pKT25-RIC into *E. coli* DHM1
399 cells by electroporation. Blue colonies present in Amp^R Cm^R selective plates (L-agar with 5-
400 bromo-4-chloro-3-indolyl β-D-galactopyranoside (X-Gal)) were identified after incubation
401 at 30 °C for 36 h, and cells with the highest β-galactosidade were considered to contain
402 recombinant plasmids harbouring genes encoding polypeptides that interact with the *E. coli*
403 RIC protein. Twenty two colonies were obtained and the corresponding plasmids were
404 isolated, co-transformed with pKT25-RIC plasmid in *E. coli* DHM1, and the strength of the
405 protein-protein interactions observed was again estimated by quantification of the β-
406 galactosidase activity. Seven isolates considered positive were named 'A' to 'G' (Figure 1),
407 and subject to nucleotide sequencing using primer $T18_{Fw}$ (Table 2). To identify the encoded
408 genes, the sequences were screened against the *E. coli* K-12MG1655 genome using BLAST.
409 Genes coding for the RIC protein and Dps were PCR amplified from *E. coli* K-12 genomic
410 DNA using the oligonucleotides described in Table 2, and cloned into pKT25 (fused to Cya
411 C-terminal T25 domain), pKNT25 (fused to Cya N-terminal T25 domain), pUT18 (fused to
412 Cya N-terminal T18 domain) and pUT18C (fused to Cya C-terminal T18 domain) plasmids,
413 and the enzyme *Pfu* DNA polymerase (Thermo Scientific). The resulting recombinant
414 plasmids encoded Dps or RIC with either a C- or N-terminally linked T25 or T18 domain
415 from the *B. pertussis* Cya protein. Two complementary plasmids, one carrying a T25
416 fragment and the other a T18 fragment, were co-transformed into the *E. coli* DHM1 strain

417 (cya^-). *E. coli* DHM1 cells containing the *ric*-encoding pUT18 or pUT18C plasmids were co-
418 transformed with complementary pKTN25 empty plasmid that served as negative controls.

419 In all cases, false positives were tested by co-transformation of *E. coli* DHM1 with plasmids
420 containing each gene and pKT25-TorD, which expresses *E. coli* TorD that binds non-
421 specifically to a wide variety of polypeptides (34).

422 For β-galactosidase activity determination (35), at least 3 representative colonies of each
423 transformation plate were inoculated, in duplicate, in LB medium, and following an overnight
424 growth at 37 ºC, transformant cultures were re-inoculated (at a 0.01 dilution) into LB with
425 ampicillin (100 µg/mL), kanamycin (50 µg/mL) and IPTG (0.5 mM). When cultures reached
426 an OD_{600}=0.5 (approximately after 16 h of growth, at 30 ºC), 1 mL of each culture was
427 collected by centrifugation (5000 *g*, 5 min at 4 ºC). The pellets were lysed by incubation with
428 100 µL BugBuster HT 1x (Novagen) at 37 ºC, for 30 min. Cellular debris was then removed
429 by centrifugation and the β-galactosidase activities were assayed in 20 µL suspensions in a
430 microplate reader. The assays were initiated by addition of a reaction mixture comprising:
431 0.27% β-mercaptoethanol (v/v) and 0.9 mg/mL ONPG (o-nitrophenyl-β-D-
432 galactopyranoside) in buffer A (60 mM $Na_2HPO_4.7H_2O$, 40 mM $NaH_2PO_4.H_2O$, 1 mM
433 $MgSO_4.7H_2O$, 10 mM KCl). Reactions were incubated at 28 ºC, and the absorbance was
434 recorded at 420 nm at 2 min intervals, for 90 min. The β-galactosidase specific activity was
435 defined as ONP/min/milligram of protein. Interactions were considered positive for those
436 reactions where β-galactosidase activity was at least four times higher than the negative
437 control.

438 *Bimolecular fluorescence complementation (BiFC) assays*

439 BiFC assay was performed essentially as described previously (36). For this purpose, the
440 genes encoding RIC protein, a truncated version of the RIC protein (lacking the first 57 amino
441 acid residues in N-terminal (9)), Dps, Bfr and FtnA were PCR amplified from genomic DNA
442 of *E. coli* K-12 using the oligonucleotides described in Table 2. Tthe DNA fragments were
443 cloned into vectors (pET11a-link-N-GFP and pMRBAD-link-C-GFP (36)) that express the
444 green fluorescence protein, GFP, to allow formation of corresponding N- or C-terminal GFP
445 fusions, respectively. Cloning was achieved using *Xho*I and *Bam*HI sites (for cloning into
446 pET11a-link-N-GFP) or *Nco*I and *Aat*II sites (for cloning into pMRBAD-link-C-GFP) sites,
447 except for Dps for which *Sph*I replaced *Nco*I. All recombinant plasmids were sequenced
448 confirming the integrity of the genes and the absence of undesired mismatches. Cells
449 harboring pET11a-link-N-GFP and pMRBAD-link-C-GFP served as negative control.

450 *E. coli* BL21(DE3)Gold (Agilent) was co-transformed with the resulting recombinant
451 pET11a-link-N-GFP and pMRBAD-link-C-GFP vectors, in various combinations (RIC/Dps,
452 truncated-RIC/Dps, RIC/Bfr and RIC/FtnA), and plated on selective LB-agar. Colonies were
453 inoculated in LB medium, grown overnight, at 37 ^{o}C and 150 rpm, and plated onto inducing
454 LB agar medium containing 20 µM IPTG and 0.2% of arabinose. After an overnight
455 incubation at 30 ˚C followed by two days incubation at room temperature, colonies were
456 suspended in PBS and spread onto 1.7% agarose slides. Cells were examined for green
457 fluorescence in a Leica DM6000 B upright microscope coupled to an Andor iXon+ camera,
458 using a 1000x amplification and a FITC filter. The images were analysed using the
459 MetaMorph Microscopy Automation and Image Analysis Software.

460 *Pull-down and Western Blot assays*

461 The genes encoding RIC and Dps were amplified from *E. coli* K-12 genomic DNA by PCR,
462 using the oligonucleotides listed in Table 2, cloned into pET28a and pACYCDuet-1 vectors,
463 respectively, and sequenced which confirmed their integrity and the absence of undesired
464 mutations. *E. coli* BL21(DE3)Gold was transformed with the following pair of plasmids : i)
465 pET28a-RIC (expressing the RIC protein fused to a N-terminal His-Tag-RIC) and
466 pACYCDuet-1-Dps (expressing a non-labelled Dps); and ii) pET28a (empty vector) together
467 with pACYCDuet-1-Dps. Cells harboring the later pair of recombinant plasmids served as
468 control samples. Cells were grown in LB medium, supplemented with 10 μM of Fe and the
469 appropriate antibiotics, at 30 ˚C to an OD_{600} of 0.3. At this time, 0.3 mM IPTG was added
470 to induce the expression of the His-tagged-RIC and Dps proteins, and after 4 h the cross-
471 linking agent formaldehyde (1% final concentration) was added to the cells. The cross-
472 linking reaction (25) was carried at 37 ˚C for 20 min, and the reaction was stopped by
473 incubation with glycine (final concentration of 0.5 M) at room temperature for 5 min.
474 Bacterial cells were harvested by centrifugation, washed twice with PBS and resuspended in
475 PBS. Cells were disrupted in a French Press (Thermo) and cell debris were removed by
476 centrifugation. The total protein concentration of the supernatants was determined by the
477 Pierce BCA Protein Assay Kit (Thermo Scientific). For the pull-down experiments, these
478 supernatants were loaded into Ni-Chelating Sepharose Fast Flow columns (GE Healthcare),
479 which were first washed with 10 mM Tris-HCl (pH 7.5), and the proteins were eluted with
480 imidazole containing buffers. The protein fractions were analysed by 12.5% SDS-PAGE and
481 Western blotting
482 For Western Blot analysis, samples that were first resolved by SDS-PAGE were transferred
483 to a nitrocellulose blotting membrane (GE Healthcare) in a Trans-blot semi-dry cell apparatus
484 (Bio-Rad). The membrane was blocked by addition of TBS (20 mM Tris-HCl pH 7.5, 500

485 mM NaCl) containing 5% of dried skimmed milk and incubation at room temperature for 1
486 h. Then, the membrane was incubated with the primary antibody against *E. coli* K-12 Dps
487 (1:1000 dilution in TBS-T (TBS + 0.05% Tween-20) plus 5% of dried skimmed milk).
488 Following an overnight incubation at 4 ˚C, the membrane was washed with TBS-T and
489 incubated with the secondary antibody (anti-rabbit IgG-alkaline phosphatase from Sigma)
490 diluted 1:10000 in TBS-T + 5% of dried skimmed milk). The reaction proceeded for 1 h at
491 room temperature, and the color was developed by addition of 10 μL of NBT-BCIP (Sigma)
492 in 10 mL buffer (100 mM Tris-HCl pH 9.5, 100 mM NaCl, 5 mM $MgCl_2$)..

493 *Enzyme activity assays and determination of endogenous ROS*

494 *E. coli* wild type, Δ*ric*, Δ*dps* and Δ*dps* Δ*ric* strains that were transformed with either pUC18,
495 pUC18-RIC or pUC18-RIC-E133L (prepared described in (9)) were tested for endogenous
496 aconitase and fumarase activities. To this end, the *E. coli* cells strains were grown in LB
497 medium at 37 ^{o}C, under aerobic conditions, to an OD_{600} of 0.6 and 2, as indicated in each
498 case.

499 For the aconitase assays, cells grown to the desired cell density were centrifuged, washed in
500 reaction buffer (50 mM Tris-HCl, 0.6 mM $MnCl_2$, pH 8), and the pellets were frozen in liquid
501 nitrogen. The following experiments were performed under anaerobic conditions. Prior to
502 the activity assay, the cell pellets were resuspended in reaction buffer containing 0.5 mg/mL
503 lysozyme and 0.2 mg/mL DNAse and incubated on ice for 10 min, and then centrifuged at
504 9600 *g* for 10 min, at 4 ^{o}C. The aconitase activity was determined in these supernatants (falta
505 qtds usadas) in reaction mixtures that also contained 200 μM $NADP^+$, 1 U isocitrate
506 dehydrogenase and 30 mM sodium citrate (9). and by recording the formation of NADPH at
507 340 nm.

508 For the fumarase activity assays (37), once the cells reached the desired cell density they
509 were centrifuged, washed with 50 mM sodium phosphate pH 7.3 buffer, and frozen in liquid
510 nitrogen. Cell pellets were resuspended in 2 mL of the same phosphate buffer, lysed by five
511 freeze-thaw cycles that used liquid nitrogen and a water bath at room temperature. The
512 resulting cell extracts were cleared by addition of sodium deoxycholate, to a final
513 concentration of 0.5%. Fumarase activity was determined under anaerobic conditions in
514 reaction mixtures that contained the cell lysates falta qtds usadas , 50 mM L-malate, and xxx
515 of fumarate, and by following the consumption of fumarate at 240 nm.
516

517 Endogenous reactive oxygen species content was determined in *E. coli* wild type, Δ*ric*, Δ*dps,*
518 Δ*dps* Δ*ric*, Δ*bfr,* Δ*bfr* Δ*ric,* Δ*ftnA*, Δ*ftnA* Δ*ric* strains (Table 1). Cells were grown aerobically
519 to an OD_{600} of 0.6, collected by centrifugation, resuspended in PBS, and distributed in 96-
520 well microtitre plates. Following the addition of dichloro-dihydro-fluorescein diacetate (10
521 μM DCFH-DA), the fluorescence was measured in a spectrofluorimeter Varian Cary
522 (Agilent) at λ_{ex} = 485 nm and λ_{em} = 538 nm,, and for 2 h. The Fluorescence Intensity (FI)
523 was normalized in relation to the optical density of each culture at 600 nm.

524

525 **Acknowledgments**

526 We thank Professor Hirotada Mori (Graduate School of Biological Sciences, Nara Institute
527 of Science and Technology, Ikoma, Nara, Japan) for provision of the mutants from the Keio
528 collection, and Professor James Imlay (Department of Microbiology, B103 CLSL, 601 S
529 Goodwin Ave, Urbana, IL 61801, USA) for the Hpx mutant. We also grateful to Professors

530 Tracy Palmer and Frank Sargent (Centre for Bacterial Cell Biology, Newcastle University)
531 for providing the BACTH *E. coli* library.
532 This work was financially supported by: Project LISBOA-01-0145-FEDER-007660
533 (Microbiologia Molecular, Estrutural e Celular) funded by FEDER funds through
534 COMPETE2020 - Programa Operacional Competitividade e Internacionalização (POCI) and
535 by national funds through FCT - Fundação para a Ciência e a Tecnologia" for grants
536 PTDC/BBB-BQB/5069/2014, and SFRH/BD/118545/2016 (LSOS). This project has also
537 received funding from the European Union's Horizon 2020 research and innovation
538 programme under grant agreement number 810856.

539

540

541

542 **Reformatar referencias**

543 **References**

544

545 1. Overton TW, Justino MC, Li Y, Baptista JM, Melo AMP, Cole J a, Saraiva LM. 2008.
546 Widespread distribution in pathogenic bacteria of di-iron proteins that repair oxidative
547 and nitrosative damage to iron-sulfur centers. J Bacteriol 190:2004–13.

548 2. Chow ED, Liu OW, O'Brien S, Madhani HD. 2007. Exploration of whole-genome
549 responses of the human AIDS-associated yeast pathogen *Cryptococcus neoformans*
550 var grubii: nitric oxide stress and body temperature. Curr Genet 52:137–148.

551 3. Harrington JC, Wong SMS, Rosadini C V., Garifulin O, Boyartchuk V, Akerley BJ.
552 2009. Resistance of *Haemophilus influenzae* to reactive nitrogen donors and gamma

553 interferon-stimulated macrophages requires the formate-dependent nitrite reductase
554 regulator-activated ytfE gene. Infect Immun 77:1945–1958.

555 4. Justino MC, Almeida CC, Teixeira M, Saraiva LM. 2007. *Escherichia coli* di-iron
556 YtfE protein is necessary for the repair of stress-damaged iron-sulfur clusters. J Biol
557 Chem 282:10352–9.

558 5. Justino MC, Almeida CC, Gonçalves VL, Teixeira M, Saraiva LM. 2006. *Escherichia*
559 *coli* YtfE is a di-iron protein with an important function in assembly of iron-sulphur
560 clusters. FEMS Microbiol Lett 257:278–84.

561 6. Nobre LS, Garcia-Serres R, Todorovic S, Hildebrandt P, Teixeira M, Latour J-M,
562 Saraiva LM. 2014. *Escherichia coli* RIC is able to donate iron to iron-sulfur clusters.
563 PLoS One 9:e95222.

564 7. Silva LO, Nobre LS, Mil-Homens D, Fialho A, Saraiva LM. 2018. Repair of Iron
565 Centers RIC protein contributes to the virulence of *Staphylococcus aureus.* Virulence
566 9:312–317.

567 8. Todorovic S, Justino MC, Wellenreuther G, Hildebrandt P, Murgida DH, Meyer-
568 Klaucke W, Saraiva LM. 2008. Iron-sulfur repair YtfE protein from *Escherichia coli*:
569 Structural characterization of the di-iron center. J Biol Inorg Chem 13:765–770.

570 9. Nobre LS, Lousa D, Pacheco I, Soares CM, Teixeira M, Saraiva LM. 2015. Insights
571 into the structure of the diiron site of RIC from *Escherichia coli*. FEBS Lett 589:426–
572 431.

573 10. Lo F-C, Hsieh C-C, Maestre-Reyna M, Chen C-Y, Ko T-P, Horng Y-C, Lai Y-C,
574 Chiang Y-W, Chou C-M, Chiang C-H, Huang W-N, Lin Y-H, Bohle DS, Liaw W-F.

575 2016. Crystal Structure Analysis of the Repair of Iron Centers Protein YtfE and Its
576 Interaction with NO. Chem - A Eur J 1–10.

577 11. Almiron M, Link a J, Furlong D, Kolter R. 1992. A novel DNA-binding protein with
578 regulatory and protective roles in starved *Escherichia coli*. Genes Dev 6:2646–2654.

579 12. Grant R a, Filman DJ, Finkel SE, Kolter R, Hogle JM. 1998. The crystal structure of
580 Dps, a ferritin homolog that binds and protects DNA. Nat Struct Biol 5:294–303.

581 13. Calhoun LN, Kwon YM. 2011. Structure, function and regulation of the DNA-binding
582 protein Dps and its role in acid and oxidative stress resistance in *Escherichia coli*: a
583 review. J Appl Microbiol 110:375–86.

584 14. Zhao G, Ceci P, Ilari A, Giangiacomo L, Laue TM, Chiancone E, Chasteen ND. 2002.
585 Iron and hydrogen peroxide detoxification properties of DNA-binding protein from
586 starved cells. A ferritin-like DNA-binding protein of *Escherichia coli*. J Biol Chem
587 277:27689–96.

588 15. Karas VO, Westerlaken I, Meyer AS. 2015. The DNA-Binding Protein from Starved
589 Cells (Dps) Utilizes Dual Functions To Defend Cells against Multiple Stresses. J
590 Bacteriol 197:3206–15.

591 16. Karimova G, Pidoux J, Ullmann A, Ladant D. 1998. A bacterial two-hybrid system
592 based on a reconstituted signal transduction pathway. Proc Natl Acad Sci U S A
593 95:5752–5756.

594 17. Jack RL, Buchanan G, Dubini A, Hatzixanthis K, Palmer T, Sargent F. 2004.
595 Coordinating assembly and export of complex bacterial proteins. EMBO J 23:3962–
596 72.

597 18. Blaha G, Stanley RE, Steitz TA. 2009. Formation of the first peptide bond: The
598 structure of EF-P bound to the 70S ribosome. Science (80-) 325:966–970.

599 19. Ganoza MC, Aoki H. 2000. Peptide bond synthesis: function of the efp gene product.
600 Biol Chem 381:553–559.

601 20. Bishop RE, Leskiw BK, Hodges RS, Kay CM, Weiner JH. 1998. The entericidin locus
602 of *Escherichia coli* and its implications for programmed bacterial cell death. J Mol
603 Biol 280:583–596.

604 21. Livshits VA, Zakataeva NP, Aleshin V V., Vitushkina M V. 2003. Identification and
605 characterization of the new gene rhtA involved in threonine and homoserine efflux in
606 *Escherichia coli*. Res Microbiol 154:123–135.

607 22. Magliery TJ, Wilson CGM, Pan W, Mishler D, Ghosh I, Hamilton AD, Regan L. 2005.
608 Detecting protein-protein interactions with a green fluorescent protein fragment
609 reassembly trap: Scope and mechanism. J Am Chem Soc 127:146–157.

610 23. Vasilescu J, Guo X, Kast J. 2004. Identification of protein-protein interactions using
611 in vivo cross-linking and mass spectrometry. Proteomics 4:3845–3854.

612 24. Herzberg C, Weidinger LAF, Dörrbecker B, Hübner S, Stülke J, Commichau FM.
613 2007. SPINE: A method for the rapid detection and analysis of protein-protein
614 interactions in vivo. Proteomics 7:4032–4035.

615 25. Ferreira E, Giménez R, Aguilera L, Guzmán K, Aguilar J, Badia J, Baldomà L. 2013.
616 Protein interaction studies point to new functions for *Escherichia coli* glyceraldehyde-
617 3-phosphate dehydrogenase. Res Microbiol 164:145–154.

618 26. Yang B, Tang S, Ma C, Li ST, Shao GC, Dang B, DeGrado WF, Dong MQ, Wang

619 PG, Ding S, Wang L. 2017. Spontaneous and specific chemical cross-linking in live
620 cells to capture and identify protein interactions. Nat Commun 8.

621 27. Chiancone E, Ceci P. 2010. The multifaceted capacity of Dps proteins to combat
622 bacterial stress conditions: Detoxification of iron and hydrogen peroxide and DNA
623 binding. Biochim Biophys Acta 1800:798–805.

624 28. Park S, You X, Imlay J a. 2005. Substantial DNA damage from submicromolar
625 intracellular hydrogen peroxide detected in Hpx- mutants of *Escherichia coli*. Proc
626 Natl Acad Sci U S A 102:9317–9322.

627 29. Seaver LC, Imlay JA. 2004. Are respiratory enzymes the primary sources of
628 intracellular hydrogen peroxide? J Biol Chem 279:48742–50.

629 30. Velayudhan J, Castor M, Richardson A, Main-Hester KL, Fang FC. 2007. The role of
630 ferritins in the physiology of *Salmonella enterica* sv. Typhimurium: A unique role for
631 ferritin B in iron-sulphur cluster repair and virulence. Mol Microbiol 63:1495–1507.

632 31. Abdul-Tehrani H, Hudson AJ, Chang YS, Timms AR, Hawkins C, Williams JM,
633 Harrison PM, Guest JR, Andrews SC. 1999. Ferritin mutants of *Escherichia coli* are
634 iron deficient and growth impaired, and fur mutants are iron deficient. J Bacteriol
635 181:1415–1428.

636 32. Bellapadrona G, Ardini M, Ceci P, Stefanini S, Chiancone E. 2010. Dps proteins
637 prevent Fenton-mediated oxidative damage by trapping hydroxyl radicals within the
638 protein shell. Free Radic Biol Med 48:292–297.

639 33. Lennox ES. 1955. Transduction of linked genetic characters of the host by
640 bacteriophage P1. Virology 1:190–206.

641 34. Pommier J, Mejean V, Giordano G, Iobbi-Nivol C. 1998. TorD, a cytoplasmic
642 chaperone that interats with the unfolded trimethylamine N-oxide reductase enzyme
643 (TorA) in *Escherichia coli*. J Biol Chem 273:16615–16620.

644 35. Thibodeau SA, Fang R, Joung JK. 2004. High-throughput B-galactosidase assay for
645 bacterial cell-based reporter systems. Biotechniques 36:410–415.

646 36. Wilson CGM, Magliery TJ, Regan L. 2004. Detecting protein-protein interactions
647 with GFP-fragment reassembly. Nat Methods 1:255–262.

648 37. Puchegger S, Redl B, Stoffler G. 1990. Purification and properties of a thermostable
649 fumarate hydratase from the archaeobacterium *Sulfolobus solfataricus*. J Gen
650 Microbiol 136:1537–1541.

651 38. Vine CE, Justino MC, Saraiva LM, Cole J. 2010. Detection by whole genome
652 microarrays of a spontaneous 126-gene deletion during construction of a ytfE mutant:
653 confirmation that a ytfE mutation results in loss of repair of iron-sulfur centres in
654 proteins damaged by oxidative or nitrosative stress. J Microbiol Methods 81:77–79.

655 39. Baba T, Ara T, Hasegawa M, Takai Y, Okumura Y, Baba M, Datsenko KA, Tomita
656 M, Wanner BL, Mori H. 2006. Construction of *Escherichia coli* K-12 in-frame, single-
657 gene knockout mutants: The Keio collection. Mol Syst Biol 2.

658 40. Seaver LC, Imlay JA. 2001. Alkyl hydroperoxide reductase is the primary scavenger
659 of endogenous hydrogen peroxide in *Escherichia coli*. J Bacteriol 183:7173–81.

660 41. Jang S, Imlay J a. 2010. Hydrogen peroxide inactivates the *Escherichia coli* Isc iron-
661 sulphur assembly system, and OxyR induces the Suf system to compensate. Mol
662 Microbiol 78:1448–1467.

663

664

665 **Table 1 –Strains and plasmids used in this study**

E.coli	Description	Source
Strains		
DHM1	F′, *cya-854, recA1, endA1, gyrA96* (Nal^R), *thi1, hsdR17, spoT1, rfbD1, glnV44(AS)*	Euromedex
Wild type	K-12 ATCC 23716	ATCC
Δ*ric*	K-12 Δ*ric*::*cat*	(38)
Δ*dps*	JS091 Δ*dps*::*kan*	(39)
Δ*bfr*	JW3298 Δ*bfr*::*kan*	(39)
Δ*ftnA*	MC4100 Δ*ftnA*::*spc*	(31)
Δ*dps*Δ*ric*	K-12 Δ*dps*::*kan*, Δ*ric*::*cat*	This study
Δ*bfr*Δ*ric*	K-12 Δ*bfr*::*kan*, Δ*ric*::*cat*	This study
Δ*ftnA*Δ*ric*	K-12 Δ*ftnA*::*spc*, Δ*ric*::*cat*	This study
MG1655	F^- WT	(40)
SJ90	BW25113 Δ*ric*::*cat*	(41)
LC106 (*hpx*)	Δ*ahpCF'kan::'ahpḞ,* Δ(*katG17*::Tn*10*)1, Δ(*katE12*::Tn*10*)1	(29)
Δ*hpx*Δ*ric*	LC106 Δ*ric1*::cat	This study
XL2 Blue	*recA1*, *endA1*, *gyrA96*, *thi-1*, *hsdR17*, *supE44*, *relA1*, *lac* [F' *proAB*$^+$, *lacIqZ*ΔM15 Tn*10* (Tet^r)]	Agilent
BL21Gold(DE3)	*E. coli* B, F^-, *ompT*, *hsdS* (r_B^- m_B^-), *dcm*$^+$, Tet^r, *gal*, λ(DE3), *endA*, Hte	Agilent

Plasmids		
pUT18/pUT18C	Vector that allows construction of in-frame fusions at the N-terminus/C-terminus of T18 fragment (amino acids 225-399 of CyaA)	(16)
pKT25/pKNT25	Vector that allows construction of in-frame fusions at the N-terminus/C-terminus of T25 fragment (amino acids 1-224 of CyaA)	(16)
pUT18/pUT18C-RIC	RIC fused to T18 fragment in N/C-terminal	This study
pKT25/pKNT25-RIC	RIC fused to T25 fragment in N/C-terminal	This study
pUT18/pUT18C-Dps	Dps fused to T18 fragment in N/C-terminal	This study
pKT25/pKNT25-Dps	Dps fused to T25 fragment in N/C-terminal	This study
pUT18-Zip	Leucine zipper fused to T18 fragment in the N-terminal	(16)
pKT25-Zip	Leucine zipper fused to T25 fragment in the C-terminal	(16)
pUT18-TorD	TorD fused to T18 fragment in N-terminal	(17)
pKT25-TorD	TorD fused to T25 fragment in C-terminal	(17)
*Bam*HI	pUT18 plasmid that contains chromosomal fragments obtained by partial digest of the MC4100 chromosomal DNA with Sau3A1 and cloned into de *Bam*HI site	(17)
pUC18	Expression vector	ATCC

pUC18-RIC	Vector for expression of RIC	(4)
pUC18-RIC-Glu133Leu	Vector for expression of RIC-Glu133Leu	(9)
pET11a-link-GFP	Vector for expression of fusions with N- terminal fragment of GFP	(36)
pMRBAD-link-GFP	Vector for expression of fusions with C- terminal fragment of GFP	(36)
pET11a-RIC-GFP	RIC fused to N-terminal GFP fragment	This study
pMRBAD-RIC-GFP	RIC fused to C-terminal GFP fragment	This study
pET11a-Dps-GFP	Dps fused to N-terminal GFP fragment	This study
pMRBAD-Dps-GFP	Dps fused to C-terminal GFP fragment	This study
pET11a-Bfr-GFP	Bfr fused to N-terminal GFP fragment	This study
pMRBAD-Bfr-GFP	Bfr fused to C-terminal GFP fragment	This study
pET11a-FtnA-GFP	FtnA fused to N-terminal GFP fragment	This study
pMRBAD-FtnA-GFP	FtnA fused to C-terminal GFP fragment	This study
pET11a-RICTrunc-GFP	Truncated RIC fused to N-terminal GFP fragment	This study
pMRBAD-RICTrunc-GFP	Truncated RIC fused to C-terminal GFP fragment	This study
pET-28a	Expression vector	Novagen
pET-28a-RIC(HisTag)	Vector for expression of N-terminal Poly-HisTag-RIC	This study
pACYCDuet-1-Dps	Vector for expression of Dps	This study

666

667

668 **Table 2 – Oligonucleotides used in this study**

Primer Name	Sequence
Construction of plasmids used in BACTH	
ric_Fw	GAGGTGTCGACTATGGCTTATC
ric_Rv	CTTTTAGGATCCTCACCCGCC
dps_Fw	GTTAATTACTGGGATCCAACATCAAGAGG
dps_Rv	TCCTGTCAGGTACCCGCTTTTATC
T18_Fw	CATTAGGCACCCCAGGCTTTAC
T18_Rv	GAGCGATTTTCCACAACAAGTC
T18C_Fw	CATACGGCGTGGCGGGGAAAAG
T18C_Rv	AGCGGGTGTTGGCGGGTGTCG
T25_Fw	ATGCCGCCGGTATTCCACTG
T25_Rv	CGGGCCTCTTCGCTATTACG
NT25_Fw	CACCCCAGGCTTTACACTTTATGC
NT25_Rv	CAATGTGGCGTTTTTTTCCTTCG
Construction of plasmids used in BiFC	
ric_xhoFw	GAATGAGGTCTCGAGTATGGCTTATC
ric_bamRv	GCGCAATGGGATCCAGCTTTTAGA
ric_ncoFw	GAGGTATCAGCCATGGCTTATCG
ric_aatRv	CCAGCTTTTAGACGTCTCACCC
dps_xhoFw	CGTTAATTACTCGAGCATAACATCAAG
dps_bamRv	GTACTAAGGATCCGCACCATCAGC
dps_sphFw	CAAGAGGATATGCATGCATGAGTACCGCTA
dps_aatRv	CATCAGCGATGGGACGTCTCGATGTTAG

bfr_xhoFw	GAGTGGAAGCGCTCGAGTCAAAAAATG
bfr_bamRv	GGAGGGTTCTGGATCCCGACACG
bfr_ncoFw	GAAGGAGTCAAACCATGGAAGGTGATAC
bfr_aatRv	CGGACGTCCCTTCTTCGCGGATC
truncric_xhoFw	CTTTAAGAAGGCTCGAGACATATGGCTG
truncric_ncoFw	GGAGATATACCCATGGCTGAACAAC
ftna_xhoFw	CAAATATAACCTTTCTCGAGCACTATC
ftna_bamRv	TGAAACGGATCCAGTAAACCTGC
ftna_ncoFw	GAGCACTACCATGGTGAAACCAGAAAT
ftna_aatRv	CGGAGAGGACGTCTTTTGTGTGTC
Construction of plasmids used for protein expression	
pric_ndeFw	AAGAATGAGGTATCACATATGGCTTATCGC
pric_ecoriRv	GGCTGTTTATTGGTAAGAATTCGGCTGCTG
pdps_ndeFw	GAGGATATGAACATATGAGTACCGC
pdps_kpnRV	GTACTAAAGTTCGGTACCATCAGCG
Double mutant construction confirmation	
Conf_dps_Fw	CAGAATAGCGGAACACATAGC
Conf_dps_Rv	GATGCACTAAATAAGTGCGTTG
Conf_bfr_Fw	CTCTTCAAAGAGTGGAAGCG
Cof_bfr_Rv	GATCTCTTATTAACCGGGAGG
Conf_ftnA_Fw	CAAATTATAGTGACGCCACAG
Conf_ftnA_Rv	ACCGATCAGAGTAAGATTTGC
Conf_ric_Fw	AAGAATGAGGTATCACATATGGCTTATCGC

Conf_ric_Rv	GGCTGTTTATTGGTAAGAATTCGGCTGCTG

669