

## Research Article

### **Title: Bacterial microcompartment-directed polyphosphate kinase promotes stable polyphosphate accumulation in *E. coli***

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**Abbreviations:** BMC, bacterial microcompartment; enhanced biological phosphorus removal, EBPR; PPK1, polyphosphate kinase; PPX, exopolyphosphatase.

**1 Abstract**

2 Temporary manipulation of bacterial polyphosphate levels by phased environmental  
3 stimuli underlies wastewater biological phosphate removal processes. In *E. coli*  
4 polyphosphate levels are controlled via polyphosphate kinase (PPK1, synthesizing) and  
5 exopolyphosphatases (PPX and GPPA), and are temporarily enhanced by PPK1  
6 overexpression and reduced by PPX overexpression. We hypothesised that partitioning  
7 PPK1 from cytoplasmic exopolyphosphatases would increase and stabilise *E. coli*  
8 polyphosphate levels. Partitioning was achieved by coexpression of *E. coli* PPK1 fused  
9 with a microcompartment-targeting sequence and an artificial operon of *Citrobacter*  
10 *freundii* bacterial microcompartment genes. Encapsulation of targeted PPK1 resulted in  
11 stably increased cellular polyphosphate and persistent net phosphate cellular uptake into  
12 stationary phase, while temporary polyphosphate increase and phosphate uptake was  
13 observed with PPK1 overexpression alone. Targeted PPK1 increased polyphosphate in the  
14 microcompartment fraction 8-fold compared with non-targeted PPK1. Co-expression of  
15 PPX and non-targeted PPK1 abolished any increase in cellular polyphosphate from PPK1  
16 expression alone. Co-expression of PPX with targeted PPK1 however resulted in elevated  
17 polyphosphate levels due to persisting polyphosphate in bacterial microcompartments.  
18 Subcellular polymerising enzyme targeting to bacterial microcompartments sequesters  
19 metabolic products from competing catabolism by preventing catabolic enzyme access.  
20 Specific application of this process to polyphosphate is of potential application for  
21 biological phosphate removal.

22

23

## 1        **1. Introduction**

2 Polyphosphate is a molecule thought to be present in all organisms [1] playing a role in  
3 cellular metabolic processes, stress response processes, virus replication and cell structure  
4 [2]. Bacterial polyphosphate accumulation underlies the enhanced biological phosphorus  
5 removal (EBPR) process, which uses microorganisms to remove inorganic phosphate (Pi)  
6 from wastewater [3]. Phosphate recovery processes are required to reduce eutrophication,  
7 the overgrowth of cyanobacteria and plants in water polluted by excess phosphorus from  
8 human activity [4], and because of the unsustainability of current phosphorus resources  
9 beyond the next century [5]. In EBPR, cycling of wastewater sludge through aerobic and  
10 anaerobic phases of incubation lasting several hours, when continued over a period of  
11 weeks selects a bacterial consortium that has a net effect of removing phosphorus from  
12 wastewater over the cycle by accumulating it in the sludge. Polyphosphate-accumulating  
13 bacteria are key consortium components [6, 7]. Phosphate release from the consortium  
14 occurs in the anaerobic phase in parallel with consumption of volatile fatty acids,  
15 polyhydroxyalkanoate polymer formation and glycogen utilisation. In the aerobic phase  
16 stored polyhydroxyalkanoate is catabolised, glycogen replenished and phosphate taken up  
17 to form polyphosphate granules [7]. EBPR is a complex dynamic process - an uncultured  
18 bacterium *Candidatus Accumulibacter phosphatis* performs a key role in EBPR  
19 polyphosphate accumulation [8], and an established EBPR reactor may fail for unknown  
20 reasons [3, 9].

21

22 Genetic manipulation of aspects of phosphate binding, uptake and storage by a single  
23 model organism such as *E. coli* has been suggested as an alternative or additive approach

1 to biological phosphorus removal [10–13]. One issue with over-expression of a  
2 polyphosphate forming enzyme in *E. coli* has been that most of the consequent increase of  
3 polyphosphate is temporary, probably because of the existence of competing catabolic  
4 enzymes [14, 15] and phosphate release from the cells then occurs as the polyphosphate is  
5 broken down.

6

7 In *E. coli* polyphosphate kinase PPK1 (E.C. 2.7.4.1) is the enzyme responsible for  
8 assembling inorganic polyphosphate polymers in the bacterial cytoplasm by catalysing the  
9 reaction  $n\text{ATP} \rightleftharpoons (\text{polyphosphate})_n + n\text{ADP}$  [16, 17]. Although this is a reversible reaction,  
10 in *E. coli* this enzyme generally favours synthesis of polyphosphate over breakdown ( $V_{\text{max}}$   
11 ratio of 4.1) [17] (Fig. 1A). However, the balance between net accumulation and breakdown  
12 changes dynamically during culture growth and also in response to external stimuli, in part  
13 due to the action of degradative exopolyphosphatases. In this respect *E. coli* contains two  
14 such polyphosphatases that release orthophosphate from the termini of long chain  
15 polyphosphate:  $(\text{polyphosphate})_n \rightarrow (\text{polyphosphate})_{n-1} + \text{P}_i$ . The two polyphosphatases  
16 are called PPX (E.C. 3.6.1.11, sometimes referred to as PPX1) [18, 19], which is encoded  
17 in the same operon as PPK1, and its homologue guanosine pentaphosphate  
18 phosphohydrolase (GPPA or PPX2) [17, 20]. GPPA (E.C. 3.6.1.40) also hydrolyses  
19 guanosine pentaphosphate (pppGpp) to guanosine tetraphosphate (ppGpp) with phosphate  
20 release as part of the control of the stringent response. Both PPX and GPPA are  
21 competitively inhibited by pppGpp [21]. Consequently, amino acid starvation in *E. coli*  
22 leads to the accumulation of large amounts of polyphosphate due to the high levels of  
23 pppGpp produced as part of the stringent response [21]. In *E. coli* *ppk1* and *ppx* are adjacent

1 genes forming an operon and knockout of *ppx* alone has been engineered by combined  
2 knockout of *ppk1* and *ppx* with heterologous plasmid expression of *ppk1* [15, 22, 23].  
3 Elevation of polyphosphate levels in these cells rapidly declines a few hours after *ppk1*  
4 plasmid induction whether *ppx* is active or knocked out [15], showing that PPX is not the  
5 sole cause of instability in polyphosphate levels in *E. coli*. We hypothesized that an  
6 alternative approach to prevent the access of all other cytoplasmic enzymes, (not just PPX)  
7 to polyphosphate formed from recombinant PPK1 would stabilise cellular polyphosphate  
8 levels and create a phosphate-retaining phenotype. The mechanism used to achieve this is  
9 targeting of PPK1 to a recombinant bacterial microcompartment.

10

11 Bacterial microcompartments (BMCs) are proteinaceous vesicles found in certain bacteria  
12 that house specific metabolic pathways encased within a closed polyhedral shell of 100-  
13 150 nm diameter. The shells are made of thin protein sheets [24] containing pores less than  
14 1 nm in diameter [25] which can be positively or negatively charged. There are two broad  
15 groups of BMCs, those associated with the anabolic process of RuBisCO-mediated carbon  
16 fixation (carboxysomes) and those associated with catabolic fermentative processes such  
17 as 1,2-propanediol utilisation (metabolosomes) [26, 27]. Although BMCs were first seen  
18 over fifty years ago in photosynthetic cyanobacteria [28], their presence in the cytoplasm  
19 of heterotrophic bacteria was only confirmed in 1998 [29] after they were detected in thin  
20 sections of *Salmonella enterica* grown on 1,2-propanediol. In fact, around twenty per cent  
21 of bacterial genome sequences contain BMC structural genes [26], in many cases  
22 associated with enzymes of unknown function [30].

23

1 A significant proportion of bacteria therefore make a major investment in retaining and  
2 expressing large (15+ gene) operons encoding these structures and associated enzymes. It  
3 is believed the structures help mediate metabolic efficiency by selective limitation of the  
4 shell pores on the passage of substrates [31], by metabolite channelling, or other  
5 mechanisms achieving retention of reaction intermediates within the structure [32, 33].  
6 *Salmonella enterica* Serovar Typhimurium accrues a competitive metabolic advantage by  
7 BMC-mediated respiration of ethanolamine in a mouse colitis model [34].  
8 Enterohaemorrhagic *E. coli* obtains a similar competitive advantage from BMC-mediated  
9 ethanolamine fermentation in bovine intestinal fluid [35], favouring persistent intestinal  
10 carriage.

11

12 Recombinant BMCs using genes from *Citrobacter freundii* can be expressed  
13 heterologously in *E. coli* [36], both with and without [37] the associated interior enzymes.  
14 Peptide sequences enabling enzyme localisation to the BMC interior have been identified  
15 [37] [38]. For instance, the first 18 amino acids of PduP, P18, or the first 18 or 60 amino  
16 acids of PduD (D18 or D60) can be used as fusions to direct “foreign” proteins into the  
17 BMC [39]. Compartmentalisation of the cellular interior is a functionally transforming  
18 process often thought of as characteristic of eukaryotes [40], but specific localisation of  
19 any enzyme to a re-engineered BMC in bacteria could increase metabolic flexibility of the  
20 bacterial host enabling novel phenotypes [41]. Nanotechnological applications of other  
21 biological compartment systems have included the use of viral capsids for DNA delivery  
22 [42], lumazine synthase enclosure of HIV protease [43], and the engineering of novel  
23 metabolites. We hypothesized that directing PPK to a BMC would enhance polyphosphate

1 formation within a cellular compartment and that segregation from the known degradative  
2 polyphosphatases and other cytoplasmic enzymes should stabilise accumulation of  
3 polyphosphate (Fig.1).

4

## 5 **2. Materials and Methods**

### 6 **Strains, plasmids and culture conditions**

7 *E. coli* was grown in LB or MOPS medium [44] with either 0.5 mM or 1.0 mM K<sub>2</sub>HPO<sub>4</sub>  
8 as indicated. Expression of pET cloned genes was induced by IPTG in *E. coli* BL21 (DE3)  
9 and *E. coli* BL21 Tuner (DE3) (Novagen). Strains and plasmids are listed in Table 1 and  
10 oligonucleotides in Supplementary Data Table S1. Incubation for phosphate uptake  
11 experiments was at 37 °C, otherwise pDuet inductions were incubated at 18 °C.

12

### 13 **Molecular techniques**

14 **Plasmid cloning** was carried out in *E. coli* JM109 or *E. coli* TOP10 (Invitrogen) with  
15 subsequent transfer to *E. coli* BL21 (DE3) and *E. coli* BL21 Tuner (DE3) for expression  
16 using standard transformation techniques [45]. For PCR experiments standard protocols  
17 were applied using an MJ Research PTC-200 Thermal Cycler for reaction cycles. Genomic  
18 DNA was extracted from *E. coli* JM109 using a Wizard® Genomic DNA Purification Kit  
19 (Promega). Plasmid constructs were sequenced commercially (GATC Biotech).

20

### 21 **Targeting of PPK1**

22 The strategy used is summarised in Supplementary Data Fig.S1. The *ppk1* gene coding for  
23 polyphosphate kinase (PPK1) was PCR-amplified with a proofreading DNA polymerase

1 (Bioline High Velocity Polymerase, Bioline UK, London), using genomic DNA from *E.*  
2 *coli* JM109 as template, using the forward primer ppk1-F and a reverse primer ppk1-R  
3 (Table S1). The PCR product was digested with *Sac* I and *Hind* III (Fermentas) followed  
4 by ligation to pET23b-GFP-pduP18 digested with *Sac* I and *Hind* III. The gene encoding  
5 the GFP was thus replaced by *ppk* with retention of the *pdu* localization sequence. The  
6 ligation product was transformed into *E. coli* Top 10 electrocompetent cells (Invitrogen)  
7 by electroporation. The new vector, named pML001 (pET23bpduP18-*ppk1*), was extracted  
8 and the *ppk1* insert was sequenced (GATC-Biotech) to confirm no mutation had occurred.  
9 Two constructs, pML001 and pLysSpduABJKNU (pSF37), expressing an empty *pdu* BMC  
10 [37]), were co-transformed into *E. coli* BL21 (DE3) by heat shock.

11

## 12 **Co-localisation of PPK1 and Microcompartments**

13

### 14 **Peptide fingerprinting of microcompartment cellular fraction**

15 Recombinant BMCs were extracted from *E. coli* by a modification of a published method  
16 [46]. A single colony pick was grown in 200 ml of LB to an OD of 0.4 followed by  
17 induction with 0.4 mM IPTG. Cells at OD1.0-1.2 were harvested and washed twice with  
18 40 ml of buffer A (50 mM Tris-HCl (pH 8.0), 500 mM KCl, 12.5 mM MgCl<sub>2</sub>, 1.5% 1,2-  
19 PD). Cells (1 g wet weight) were resuspended in a mixture of 10 ml of buffer A and 15 ml  
20 of BPER-II supplemented with 5mM mercaptoethanol, Complete Protease Inhibitor  
21 Cocktail (Roche) at the manufacturer's recommended working dilution, 25 mg of  
22 lysozyme, and 2 mg of DNase I. The suspension was incubated for 30 min on a shaking  
23 incubator at room temperature and on ice for 5 min. After initial removal of cell debris by



1 centrifugation at 12,000 *g* for 5 min at 4°C repeated twice, the BMC fraction was  
2 precipitated by spinning at 20,000 *g* for 20 min at 4°C. The pellet was washed once with a  
3 mixture of 4 ml of buffer A and 6 ml of BPER-II and resuspended in 0.5 ml of buffer B  
4 (50mMTris-HCl pH 8.0, 50 mM KCl, 5 mM MgCl<sub>2</sub>, 1% 1,2-PD) containing Complete  
5 Protease Inhibitor Cocktail (Roche) at the manufacturer's recommended working dilution.  
6 Remaining cell debris was removed by centrifugation for 1 min at 12,000 *g* 4°C repeated  
7 three times. Aliquots (50  $\mu$ g) of extracted protein were separated by SDS-PAGE using a  
8 15% polyacrylamide gel under denaturing conditions in a MiniProtean apparatus (Bio-Rad)  
9 and stained with Coomassie Brilliant Blue R250 (Fig.1B). Peptide fingerprinting carried  
10 out as previously described [47]. In microcompartment extraction for ATP regeneration  
11 assays (Fig. 1C,D) and whole cell polyphosphate assays (Fig 2) CellLytic B (Sigma-  
12 Aldrich) was initially substituted for BPER-II because of published efficacy of this reagent  
13 for polyphosphate extraction [48]. In later microcompartment extractions (Fig. 3)  
14 comparisons of BPER-II extractions and CellLytic B extractions had shown little  
15 difference in measured polyphosphate levels and BPER-II was used. Micrococcal nuclease  
16 2 mg (Sigma-Aldrich) prepared with calcium buffer was substituted for DNase 1 for all  
17 microcompartment extractions where polyphosphate was assayed because of the potential  
18 adverse effect of Mg<sup>2+</sup> containing buffers on polyphosphate [49].

### 19 **ATP regeneration assay**

20 A combination of two previously described PPK1 assay methods [48, 50] using luciferase  
21 to detect ATP produced from polyphosphate by PPK1 was used as a biochemical screen  
22 for the presence of PPK1 and polyphosphate in microcompartment fractions. Briefly, to  
23 assay relative PPK1 content 20  $\mu$ L of BMC extract was added to a 100  $\mu$ L reaction mixture

1 containing: ultrapure ADP (ATP-free, Cell Technology Inc, Ca), 30 mM MgCl<sub>2</sub>, 1% (w/v)  
2 Polyphosphate (Sigma), 50 mM Tris-HCl (pH 7.8). The reaction mixture was diluted 1:100  
3 in 100 mM Tris-HCl (pH 8.0)–4 mM EDTA, of which 0.1 mL was added to 0.1 mL of  
4 luciferase reaction mixture from ATP Bioluminescence Assay Kit CLS II (Roche).  
5 Luminescence was measured by using a luminometer (Luminoskan, Thermo Labsystems).  
6 A standard curve for ATP by dilution in 100 mM Tris-HCl (pH 8.0) containing 4 mM  
7 EDTA was used. To assay relative polyphosphate content, the same reaction omitting  
8 added polyphosphate was performed (Figure 1C).

9

#### 10 **Co-expression of targeted and untargeted PPK1 and PPX**

11 The pCOLADuet-1 coexpression vector (Novagen) system encoding two multiple cloning  
12 sites (MCS) each preceded by a T7 promoter, *lac* operator, and ribosome binding site was  
13 used to express targeted and untargeted *E. coli* PPK1 and PPX (*ppx* amplified from *E. coli*  
14 JM109) in combination (pYY005, pYY007, pYY008) and alone (pYY002, pYY010) (see  
15 Table 1).

16 Polyphosphate concentration presented in Fig. 3 was determined following lysis of pelleted  
17 cells from 10 ml of cultures described above. A metachromatic assay was employed using  
18 the 530/630nm absorbance ratio of 10 µL of lysate added to 1 mL of toluidine dye solution  
19 (6 mg/L toluidine blue in 40 mM acetic acid) as described [51]. In later experiments (Fig.  
20 4) polyphosphate was determined by a higher-yielding method using 4'-6-diamidino-2-  
21 phenylindole (DAPI) as described [52] on whole cells or microcompartment cell fractions  
22 obtained with BPER-II extraction. Briefly, cells were harvested by centrifuging at 5000g  
23 for 10 min at 4° C. After washing in 50mM HEPES buffer (pH7.5) the cell pellet or

1 microcompartment fraction was frozen at -20° C followed by defrosting at room  
2 temperature. Cell pellets/microcompartment fractions were resuspended in HEPES buffer  
3 at an appropriate dilution to ensure that the cellular polyP concentration was in the linear  
4 range of the DAPI assay (0-6  $\mu$ g polyP/ml). Total assay volume was 300 $\mu$ l which included  
5 100  $\mu$ L of polyP containing samples and 200  $\mu$ L of DAPI assay buffer containing 150 mM  
6 KCl, 20 mM HEPES-KOH (pH 7.0) and 10  $\mu$ M DAPI solution. After a 10 min incubation  
7 at room temperature DAPI fluorescence was measured with a platereader equipped with  
8 excitation and emission filters of 420 nm and 550 nm respectively.

9

10 A polyphosphate standard curve was prepared using sodium phosphate glass Type 45  
11 (S4379 Aldrich) and sodium hexametaphosphate (SX0583). Protein concentration of cell  
12 extracts was measured using a 10 $\mu$ L sample, with Coomassie Plus Protein Assay Reagent  
13 (Pierce) with bovine serum albumin as the standard resuspended in the same buffer as the  
14 sample.

15

16 **Phosphate uptake** was determined as follows (Fig. 2A). Bacteria was grown to OD<sub>600</sub> 0.4-  
17 0.6 in Luria broth and then induced by 0.5 mM of IPTG for 1 hr before transfer to pH 5.5  
18 MOPS medium [44] containing 0.01 mM iron and 0.5 mM potassium phosphate, at an  
19 OD<sub>600</sub> of 0.2. Incubation was continued at 37°C with intermittent sampling of 0.2 mL up  
20 to 48 hrs. Samples were centrifuged and supernatant used for phosphate assay, and the  
21 pellet used for polyphosphate and protein assays. Phosphate was assayed using a  
22 molybdovanadate colorimetric method [53]. 0.2 mL of molybdovanadate solution  
23 (Reagecon, cat no: 1056700) was added to 5 mL of culture supernatant, mixed and

1 incubated at room temperature for 5 min. Optical density of 1 mL at 430 nm was measured  
2 against a blank of 4% molybdovanadate in distilled water and a calibration curve of  
3 potassium phosphate in MOPS.

4

#### 5 **Light Microscopy**

6 Polyphosphate granules were visualised in fixed films (Fig. 4) by Neisser's stain using  
7 Chrysoidin counterstain [54].

8

#### 9 **Electron Microscopy**

10 *E. coli* BL21(DE3) cells containing targeted/untargeted PPK1 and pLySsPduABJKNU (for  
11 expressing empty microcompartments) were grown in 50 mL of LB broth containing 100  
12 mg/litre ampicillin and 32 mg/L chloramphenicol with shaking at 37 °C. Upon reaching an  
13 OD<sub>600</sub> of 0.5, protein production was induced with 0.5 mM isopropyl-D-thiogalactoside,  
14 and the cultures were incubated by shaking overnight at 18 °C. Harvested cells were  
15 resuspended in 2 mL of fixative consisting of 2.5% glutaraldehyde in 100 mM sodium  
16 cacodylate (CAB) buffer (pH 7.2). The cells were pelleted and washed twice with CAB to  
17 remove traces of the fixing solution. Cells were then stained for 1 hr in 1% osmium  
18 tetroxide (w/v) and washed with CAB before dehydration. Dehydration was carried out by  
19 placing the samples into an ethanol gradient: 50%, 70%, 90% once for 10 minutes, and  
20 100% dried ethanol three times for 15 minutes. Samples were rinsed twice for 15 minutes  
21 in propylene oxide and then incubated in 50/50 propylene oxide/Agar LV resin for 30  
22 minutes. Samples were incubated 2 x 2 hr in fresh Agar LV resin before embedding in  
23 Beem capsules by centrifugation at 11,000 rpm for 5 minutes followed by incubation at 60

1 °C overnight to polymerize. Specimens were thin sectioned with a diamond knife on an  
2 RMC MT-6000-XL ultramicrotome, collected on 400 mesh copper grids, and post-stained  
3 with 4.5% uranyl acetate for 45 min at RT and lead citrate for 7 min at RT. Sections were  
4 then observed and photographed with a JEOL-1230 transmission electron microscope at  
5 an accelerating voltage of 80 kV.

6

### 7 **Electron microscopy for parallel electron energy loss spectroscopy (PEELS) and** 8 **element mapping by electron spectroscopic imaging (ESI)**

9 Unstained cells were fixed in 3% (v/v) glutaraldehyde – 10 mM HEPES, pH 7.3 (Sigma),  
10 dehydrated in an acetone-series and embedded in epoxy resin (Spurr, hard mixture; [55]),  
11 as described [56]. For elemental analysis 30 - 40 nm ultrathin sections (otherwise 90 nm  
12 for general ultrastructure) were sectioned with a Reichelt-Jung ultramicrotome (Leica,  
13 Vienna, Austria), equipped with a diamond knife and were picked up with 300 mesh Cu-  
14 grids. Electron micrographs were recorded in the elastic brightfield mode (slit width: 10  
15 eV) with an EF-TEM (operated in general at 120 kV acceleration voltage), equipped with  
16 an in-column Omega-type energy filter (LIBRA120 plus, Zeiss, Oberkochen Germany), in  
17 a magnification range from x 4000 to x 32000 with a bottom-mount cooled 2048 x 2048  
18 CCD camera (sharp:eye; Tröndle, Moorenweis, Germany).

19

### 20 **Parallel electron energy loss spectroscopy (PEELS)**

21 Spot-PEELS were recorded within electron dense cytoplasmic inclusion bodies. Spot-size  
22 was set to 16 nm and the objective aperture was 60  $\mu\text{m}$  (spectrum magnification: x100;  
23 energy range: 67 – 290 eV; recording time: 10 s ; emission current: 1  $\mu\text{A}$ ) and the spectrum

1 energy resolution was about 1.6 eV at zero-loss (FWHM). Recorded PEELS data were  
2 corrected for background, applying the ‘potence’ underground function of the EsiVision  
3 Pro Software (EsiVision Pro, Vers. 3.2; SIS – Soft Imaging Systems, Munster, Germany)  
4 and were ‘medium’-filtered (settings: 1.5 eV width).

5

### 6 **Element mapping by electron spectroscopic imaging (ESI)**

7 Phosphorus mapping was performed as previously described [56] with unstained 35 nm  
8 ultrathin sections. According to the '3-window method' energy-windows were set to a  
9 dedicated energy loss for the P-L23 edge, as it was given by the corresponding first  
10 intensity maximum from the spot-PEELS, i.e. 138 eV (W1: 125 eV; W2: 115 eV). The  
11 energy selective slit was set to 6 eV width, and images were recorded with an illumination  
12 aperture of 0.63 mrad, an emission current of 1  $\mu$ A, a 60  $\mu$ m objective aperture, and a  
13 nominal magnification of x 6300. Background subtraction for calculating the phosphorus  
14 element map was performed by the ‘multiwindow exponential difference’ method.

15

## 16 **3. Results**

### 17 **BMC localisation of PPK1**

18 The localisation of PPK1 to a recombinant BMC was achieved by engineering the fusion  
19 of the P18 targeting peptide to the N-terminus of the enzyme. The recombinant BMC with  
20 the associated P18-PPK1 was isolated after lysis of the cells using a protein extraction  
21 reagent followed by differential salt precipitation and centrifugation. Analysis of the  
22 purified BMC fraction by SDS-PAGE revealed the presence of P18-PPK1 together with  
23 the BMC-associated shell proteins (Fig. 1B).

1

2 A functional assay designed to maximise PPK1's ATP breakdown function was employed  
3 to determine the activity of PPK1 when it was directed to the BMC. In comparison to BMC  
4 extracts from cells producing only empty BMCs or empty BMCs and non-targeted PPK,  
5 the purified BMC cell fractions from the cells co-producing BMCs and P18-PPK1  
6 generated over twenty-fold more ATP per mg of protein from added polyphosphate  
7 (Fig.1C). There was little activity in the equivalent protein fraction that had been prepared  
8 from cells producing only P18-PPK1 (i.e. P18-PPK1 produced in the absence of BMCs).  
9 This showed that polyphosphate kinase activity had been transferred to the  
10 microcompartments by enzyme targeting.

11

12 The same ATP regeneration assay was run again but this time in the absence of any added  
13 exogenous polyphosphate (Fig.1D). Any ATP generated in this assay would therefore  
14 reflect the amount of endogenous polyphosphate within the fraction. The BMC fraction  
15 from the cells that co-produced both the BMCs and P18-PPK1 generated more than twice  
16 as much ATP as control BMC fractions from cells expressing empty BMCs or BMCs with  
17 non-targeted PPK1 (Fig. 1D). This result indicates that the BMC fraction from cells co-  
18 expressing targeted PPK1 had increased levels of polyphosphate, compatible with  
19 localisation of PPK1 to the microcompartment and formation of polyphosphate in situ.

20

### 21 **PPK1 targeting effect on polyphosphate content and phosphate uptake,**

22 The effect of PPK1 overexpression on cellular polyphosphate was both qualitative and  
23 quantitative, and targeted PPK1 with co-expressed BMCs gave a distinct phenotype. DAPI

1 negative staining of polyphosphate extracts, size-separated on a PAGE gel (Supplementary  
2 Data Figure S2), showed that the polyphosphate detected in strains over-expressing either  
3 *p18ppk1* alone or *p18ppk1* and *pduABJKNU* exceeded the length of the sodium phosphate  
4 glass Type 45 polyphosphate control. This indicates that long chain polyphosphate is  
5 present in these strains. No qualitative difference in chain length was detected between  
6 these two clones but long chain polyphosphate in the *E. coli* strain over expressing *p18ppk1*  
7 and recombinant BMCs persisted to a later phase of growth (Fig. S2) than in cells  
8 expressing *p18ppk1* alone. No long chain polyphosphate was detected in the *E. coli* control.

9

10 A simultaneous assay of the cellular polyphosphate and phosphate content of the culture  
11 supernatant from the cultures used in the polyphosphate chain length assay was also  
12 undertaken. Here, increased phosphate uptake from culture medium was observed in  
13 comparison to the host *E. coli* control (Fig. 2A) by both the *p18ppk1*-expressing strain and  
14 the strain expressing both *p18ppk1* and *pduABJKNU*. A maximal uptake of approximately  
15 0.25 mM at 20 hours was observed for both constructs. However, the *p18ppk1*-expressing  
16 strain returned a third of this phosphate to the supernatant after 48 hours, while the strain  
17 expressing both *p18ppk1* and *pduABJKNU* returned less than 9% of phosphate taken by 48  
18 hours. Correspondingly, the cell associated polyphosphate levels of the *p18ppk1* clone  
19 were maximal at 20 hours and declined thereafter, while the *p18ppk1* and *pduABJKNU*  
20 expressing strain retained approximately the same level of cell associated polyphosphate  
21 at 48 hours as at 20 hours.

22

23 **BMC protects endogenous polyphosphate from exogenous polyphosphatases**



1 The induction of non-targeted PPK1 from the pDuet vector increased whole cell  
2 polyphosphate levels 5-fold in comparison to control cells containing the BMC shell  
3 protein operon and the pDuet vector with no enzyme insert (the enzyme-free control, Fig.  
4 3). It did not increase the polyphosphate content of co-expressed recombinant  
5 microcompartments when compared to the enzyme-free control. However, P18-PPK1,  
6 when co-produced with the BMCs, increased polyphosphate levels in the BMC fraction 8-  
7 fold in comparison to the enzyme-free control, while giving a similar overall 5-fold  
8 increase in whole cell polyphosphate to that seen with expression of non-targeted PPK1.  
9

10 Co-expression of non-targeted polyphosphatase PPX with non-targeted PPK1 reduced  
11 whole cell polyphosphate levels by 50% compared with non-targeted PPK1 expression  
12 alone, with little effect on polyphosphate levels in the microcompartment fraction. Co-  
13 expression of non-targeted PPX and BMC-targeted P18-PPK1 reduced whole cell  
14 polyphosphate levels by 22% and BMC-associated polyphosphate by 18% when compared  
15 with microcompartment targeted PPK1 alone. BMC-associated polyphosphate was still at  
16 least 2.5 times greater than in cells co-expressing non-targeted PPK1 in the presence or  
17 absence of non-targeted PPX. Co-expression of BMC targeted P18-PPK1 with PPX  
18 targeted to the microcompartment using a different tag (D60) reduced the BMC-associated  
19 polyphosphate content by 50% in comparison to the BMC-targeted P18-PPK1 alone, while  
20 reducing whole cell polyphosphate by 22%. These data suggest that the BMC-targeting of  
21 PPK1 results in the synthesis of polyphosphate that is located primarily within the BMC  
22 fraction of the cell and is relatively inaccessible to cytoplasmic co-expressed PPX, but  
23 more accessible to BMC-targeted PPX.

1

**2 Microscopy**

3 Blue-black granules were apparent with Neisser's stain in a proportion of all cells  
4 overexpressing P18-PPK1, but not the *E. coli* BL21 insert-free control or without any  
5 targeted enzyme (Fig. 4). These appearances are consistent with the accumulation of  
6 intracellular polyphosphate in *E. coli* cells with increased PPK1 activity. All cells  
7 overexpressing P18-PPK1 showed a heterogeneous granule phenotype, with a proportion  
8 of non-toluidine blue staining cells in all fields.

9

10 *E. coli* expressing the recombinant microcompartment and P18-PPK1 retained the  
11 polyphosphate staining at 44 hours (Fig. 4) whereas cells expressing P18-PPK1 without  
12 the recombinant microcompartment showed reduced staining after 40 hours (Fig. 3).

13 All *E.coli* expressing the recombinant microcompartment had a proportion of cells which  
14 were greatly elongated. All *E.coli* forming multiple polyphosphate granules tended to be  
15 larger than the non-granulated cells, presumably because of distension by the granules.  
16 However, the largest cells were seen with the combination of recombinant  
17 microcompartment and P18-PPK1.

18

**19 Electron-loss spectroscopic analysis by Energy-filtered Transmission Electron  
20 Microscopy (EFTEM).**

21

22 Increased phosphorus deposition was detected in all cells expressing recombinant *E.coli*  
23 PPK1 (Fig. 5C,D,E,F), verified from PEELS measurement (see below), compared with

1 control *E. coli* strains with no recombinant gene expression (Fig. 5A) or expressing  
2 microcompartment genes (Fig. 5B). In cells expressing PPK1 alone, most phosphate signal  
3 was represented by particles <5 nm, but some large homogeneous masses > 200 nm with  
4 plane edges were visible (Fig. 5C) in a few cells. In cells expressing targeted PPK1 and a  
5 recombinant microcompartment operon, in addition to signals from particles <5 nm,  
6 multiple phosphate signals from particles 50-100 nm were present (Fig.5D,E,F) and in  
7 some cases large circular masses/crescents > 300 nm were present (Fig. 5D,F). These large  
8 masses were not homogeneous and appeared composed of small particles and the cells  
9 containing them were enlarged. These images appeared similar to light microscopy  
10 observations (Fig. 4D,H,L).

11

## 12 **Parallel electron energy loss spectroscopy (PEELS)**

13 Spot-PEELS recorded from dark inclusions apparent as electron dense regions about 100  
14 nm in diameter (Fig 5G), confirmed they contained phosphate, verified from the  
15 characteristic ELNES-fingerprint (Energy-Loss Near-Edge Structure) of reference spectra  
16 that were recorded from sodium polyphosphate (Fig.5G). The largest polyphosphate  
17 inclusion in figure 5E, shown in yellow, is magnified in the inset of the spot-PEELS (Fig.  
18 5G); here the 16 nm beam spot and its position are indicated (white circle).

19

20

21

#### 1        4. Discussion

2 Polyphosphate accumulation is the basis of the enhanced biological phosphorus removal  
3 (EBPR) process, which uses microorganisms to remove inorganic phosphate (Pi) from  
4 wastewater. Accumulation occurs in aerobic conditions as intracellular polyphosphate [8,  
5 12] is released as Pi in anaerobic conditions [57] and supplied with organic carbon or  
6 heated [12]. The best characterized enzyme responsible for polyphosphate synthesis  
7 (PPK1), originally found in *E. coli* [58], can only be detected by bioinformatics in the  
8 genome sequences of a minority of bacterial genera [59]. The enzyme responsible for  
9 polyphosphate synthesis in most bacteria therefore remains to be identified [59].

10

11 In *E. coli*, polyphosphate accumulation in wild-type strains occurs with amino acid  
12 starvation or in the stationary phase [21, 50, 60]. Large amounts of polyphosphate  
13 accumulate only if the copy number of *ppk* is increased, or a heterologous *ppk* gene is  
14 supplied, or *phoU* is mutated [61]. Even in *E. coli* strains overexpressing *ppk*, initial  
15 accumulation of polyphosphate is known to be partially or completely reversed as the cells  
16 reach stationary phase [14, 15]. Because this also occurs in *E. coli* overexpressing *ppk* with  
17 no chromosomal functioning *ppx* gene it has been suggested to be due to either product-  
18 induced reversal of the PPK-catalysed reaction, or the activity of another phosphatase  
19 enzyme present in the cytoplasm [15]. We observed a similar reversal of polyphosphate  
20 accumulation in our overexpressing *ppk* clone, accompanied by increasing Pi in the culture  
21 supernatant (Fig. 2). This did not occur when the *ppk* gene was engineered to encode an N-  
22 terminal BMC localisation sequence and was expressed in trans with an operon encoding  
23 for an empty BMC.

1

2 Cells co-producing P18-PPK1 and the empty BMC had a different phosphorus distribution  
3 by EFTEM (Fig 5D,E,F) to those expressing PPK1 alone (Fig. 5C), containing single or  
4 agglomerated particles in the BMC size range. BMC extractions show the presence of  
5 metabolically active PPK1 (Fig.1C,D) and polyphosphate in the BMC fraction  
6 (Fig.1D, Fig.3) when PPK1 is microcompartment-targeted in this way. Our results suggest  
7 that targeting of PPK1 to a bacterial microcompartment still allows access of the small  
8 molecule substrate ATP to the enzyme (Figure 1A), but effectively stabilises the large  
9 polymer polyphosphate product (Fig. 2B,3).

10

11 We hypothesized that this stabilisation results from reduced access of PPX, GPPA or  
12 other cytoplasmic phosphatases to the polyphosphate produced by BMC-targeted PPK1.  
13 To confirm this we carried out co-expression experiments of PPK1 with PPX (Fig. 3).  
14 Co-production of PPX with PPK1 resulted in lower cellular polyphosphate levels than  
15 expression of *ppk1* alone (Fig. 3), as has been previously reported [62]. This reduction in  
16 total cellular polyphosphate was partially prevented by BMC-association of PPK1, due to  
17 increased levels of polyphosphate in the BMC fraction. BMC-targeting of PPK1 therefore  
18 results in the synthesis of polyphosphate that is located primarily in the BMC fraction of  
19 the cell. Polyphosphate in the BMC fraction is inaccessible to cytoplasmic co-expressed  
20 PPX. Adding BMC targeting to PPX (D60-PPX) co-expressed with targeted PPK1 (P18-  
21 PPK1) partially reverses the increase in polyphosphate levels in the BMC fraction  
22 conferred by targeted PPK1, presumably by increasing access of the PPX to  
23 polyphosphate in the BMC fraction. This suggests that the mechanism of stabilisation of

1 polyphosphate conferred by BMC targeting of PPK1 involves reduced access by  
2 cytoplasmic phosphatases.

3

4 Other examples of such macromolecular association of enzymes exist. A variant of  
5 lumazine synthase was recently employed to encapsidate HIV protease within an *E. coli*  
6 host [43] facilitating recombinant synthesis of this potentially toxic enzyme by separating  
7 it from the remaining cytoplasm. Lumazine synthase compartments are genetically  
8 unrelated to BMCs involved in catabolic metabolism, and form pentameric components  
9 form smaller 30-40 nm icosahedral structures that more closely resemble viral capsids [63].  
10 The enzyme is bound to part of the shell molecule forming the inner surface by an  
11 electrostatic mechanism [43, 64], (N-terminal fusion displays it on the outside [65]).  
12 Enzymically active inclusion bodies can be formed within bacterial cells by C-terminal  
13 attachment of short self-assembling peptide sequences [66], or N-terminal fusion with a  
14 self aggregating protein [67] but these enzymes are not enclosed within a structure  
15 accessed via pores. Subcellular localisation of enzymes catalysing successive reactions in  
16 a metabolic pathway to peroxisomes in fungi [68] or BMCs [39] can promote product  
17 formation.

18

19 Our results demonstrate that P18-PPK1 is targeted to a recombinant BMC. The  
20 observation that polyphosphate accumulates within the BMC suggests that targeted PPK1  
21 is internalised within the structure and remains functional, generating polymeric product.  
22 ATP must be able to enter the recombinant BMC to allow it to act as one of the substrates  
23 for the P18-PPK1 enzyme (Fig. 1A). However, this is not surprising as the native Pdu

1 BMC must allow ATP access as it is required by PduO (located within the  
2 microcompartment) for the regeneration of the coenzyme form of cobalamin needed by  
3 the diol dehydratase complex [69]. The association of PPK1 with the BMC however  
4 leads to sequestration of the enzyme's metabolic product, presumably because its size  
5 does not allow it to leave the BMC by the same route by which the enzyme substrate  
6 ATP arrived. Protection of the polyphosphate product from catabolism from cytosolic  
7 enzymes is therefore achieved, illustrating a general mechanism by which BMC can be  
8 used to re-engineer cellular metabolism. The specific polymer generated, polyphosphate,  
9 is an important intermediary in the enhanced biological phosphate removal (EBPR)  
10 process employing environmental bacteria to remove phosphate from wastewater [3, 12]  
11 and has industrial applications [70]. EBPR requires prolonged cycles of aerobic and  
12 aerobic incubation to operate. The ability to stabilise polyphosphate produced in a single  
13 growth phase so that phosphate is not returned to the cell exterior could lead to a  
14 streamlined process with a single phase of incubation. This would require transfer of the  
15 recombinant microcompartment and targeted enzyme from *E. coli* to a more  
16 environmentally robust organism.

17

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- 15

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22

23

**Table 1**  
**Plasmids and strains used in this study**

Plasmids and strains	Genotype*	Source
<b>Plasmids</b>		
pET23b	pBR322, T7 Ap	Novagen
pCOLADuet-1™	ColA ori lacI T7lac Kan <sup>r</sup>	Novagen
pET23b-GFPPduP18	pET23b with <i>gfp</i> <sup>▲</sup> and <i>pduP18</i> <sup>†</sup> leader sequence	Prof. Martin Warren, University of Kent
pLysSPduABJKNU (pSF37)	Cam <sup>R</sup> , Tet <sup>R</sup> <i>pduABJKNU</i> <sup>†</sup>	[37]
pML001	pET23b with <i>pduP18</i> <sup>†</sup> - <i>ppk1</i> fusion without <i>gfp</i> <sup>▲</sup>	This study
pML002	pET23b- <i>ppk1</i>	This study
pCOLADuetPPK (pYY002)	pCOLADuet-1 with <i>ppk1</i>	This study
pCOLADuetP18PPK (pYY010)	pCOLADuet-1 with <i>pduP18</i> <sup>†</sup> - <i>ppk1</i> fusion	This study
pCOLADuetPPXPPK (pYY005)	pCOLADuet-1 with <i>ppk1</i> and <i>ppx</i>	This study
pCOLADuetP18PPKPPX (pYY007)	pCOLADuet-1 with <i>pduP18</i> <sup>†</sup> - <i>ppk1</i> fusion and <i>ppx</i>	This study
pCOLADuetD60PPXP18PPK (pYY008)	pCOLADuet-1 with <i>ppk1</i> and <i>pduD60</i> <sup>†</sup> - <i>ppx</i> fusion	This study
<b>Strains</b>		
<i>E. coli</i> JM109	<i>endA1 glnV44 thi-1 relA1 gyrA96 recA1 mcrB</i> <sup>+</sup> $\Delta$ ( <i>lac-proAB</i> ) <i>e14- hsdR17</i> ( <i>rK</i> <sup>-</sup> <i>mK</i> <sup>+</sup> )	Promega
<i>E. coli</i> Top 10	F- <i>mcrA</i> $\Delta$ ( <i>mrr-hsdRMS-mcrBC</i> ) $\phi$ 80 <i>lacZ</i> $\Delta$ M15 $\Delta$ <i>lacX74 nupG recA1 araD139 <math>\Delta</math>(<i>ara-leu</i>)7697 <i>galE15 galK16 rpsL</i>(<i>Str</i><sup>R</sup>) <i>endA1</i> <math>\lambda</math><sup>-</sup></i>	Invitrogen
<i>E. coli</i> BL21 (DE3)	F <sup>-</sup> <i>ompT hsdS<sub>B</sub></i> ( <i>r<sub>B</sub></i> <sup>-</sup> <i>m<sub>B</sub></i> ) <i>gal dcm</i> (DE3)	Stratagene
<i>E. coli</i> Tuner (DE3)	F <sup>-</sup> <i>ompT hsdS<sub>B</sub></i> ( <i>r<sub>B</sub></i> <sup>-</sup> <i>m<sub>B</sub></i> ) <i>gal dcm lacY1</i> (DE3)	Stratagene

\*All inserts from *E. coli* JM109 unless specified †From *Citrobacter freundii* ▲From *Aequorea victoria*

## Figure Legends

### Fig. 1. Effect of microcompartment-targeting of polyphosphate kinase (PPK1) in *E. coli*

- A. Proposed mechanism of increasing polyphosphate content of *E. coli* by microcompartment-targeting of polyphosphate kinase (PPK1).
- B. SDS-PAGE gel of *E. coli* BL21 (DE3) microcompartment extracts showing presence of PPK1 band. M: MW marker. NE: no enzyme, microcompartment only, (pLysSPduABJKNU). PPK1 : non-targeted PPK1 plus microcompartment, pML2 (ppk1) pLysSPduABJKNU. P18PPK1(2 lanes): microcompartment-targeted P18PPK1 fusion plus microcompartment, pML1 (p18ppk1) pLysSPduABJKNU.
- C & D. ATP generation assay with microcompartment fraction of *E. coli* BL21 (DE3) as substrate detecting polyphosphate kinase activity and polyphosphate when PPK1 is microcompartment-targeted. NE, PPK1, P18PPK1: as above. NS,P18PPK1: no shell, plasmid-located targeted PPK1 only, pML1 (p18ppk1). C: polyphosphate kinase (PPK1) assay with addition of ADP and polyphosphate. D: polyphosphate assay with addition of ADP alone.

### Fig. 2. Co-expression of targeted PPK1 and recombinant microcompartments in *E. coli* results in stable polyphosphate retention and orthophosphate uptake.

Dashed line with filled circles: NS, *E. coli* BL21 DE3 control. Continuous red line with filled squares : NS,P18PPK1, no shell, plasmid-located targeted PPK1 only, *E. coli* BL21 DE3 pML01 (p18ppk1). Continuous green line with filled triangles : S,P18PPK1, microcompartment-targeted P18PPK1 fusion plus microcompartment shell *E. coli* BL21 DE3 pML1 (p18ppk1) pLysSPduABJKNU

- A. Supernatant orthophosphate levels. B. Whole cell polyphosphate content

### Fig. 3. Co-expression of microcompartment-targeted PPK1 and recombinant microcompartments in *E. coli* increases the polyphosphate content of the microcompartment fraction of lysed cells and protects it from co-expressed cytoplasmic polyphosphatase

DAPI polyphosphate assay from *E. coli* BL21 DE3 pLysSPduABJKNU all expressing recombinant microcompartments with different co-expressed enzymes. Blue bars polyphosphate content of microcompartment extractions, purple bars whole cell polyphosphate content. NE: no enzyme, microcompartment only, (pLysSPduABJKNU). S,PPK1 : non-targeted PPK1 and microcompartment, pML2 (ppk1). PPX,PPK1 : non-targeted PPK1 and non-targeted PPX, pYY005 (ppk1 ppx). D60PPX,P18PPK: targeted PPK1 and targeted PPK, pYY08 (ppk1 pduD60-ppx) . PPX,P18PPK1 : targeted PPK1 and non-targeted PPX, pYY07 (pduP18-ppk1 ppx). P18PPK1: targeted PPK1, pYY010 (pduP18-ppk1)

### Fig. 4. Co-expression of targeted PPK1 and recombinant microcompartments in *E. coli* results in cytoplasmic polyphosphate granule formation persisting into stationary phase.

Light microscopy of Neisser stained fixed cells (toluidine blue and chrysoidine counterstain. A,E,I: control *E. coli* BL21 DE3. B,F,J: *E. coli* BL21 DE3 NE: no enzyme, microcompartment only, (pLysSPduABJKNU). C,G,K *E. coli* BL21 DE3 pML01 (pduP18-ppk1). D,H,L BL21 DE3 pML01 (pduP18-ppk1) pLysSPduABJKNU. Incubation time in MOPS : A,B,C,D 4 hours, E,F,G,H 18 hours, I,J,K,L 44 hours.

**Fig. 5. Phosphorus content of cytoplasmic granules in *E. coli* expressing recombinant polyphosphate kinase is confirmed by ultrastructural and electron-loss spectroscopic analysis using energy-filtered transmission electron microscopy (EFTEM) and is increased and qualitatively altered by recombinant microcompartment co-expression**

A: control *E. coli* Tuner<sup>TM</sup>(DE3). B: *E. coli* Tuner<sup>TM</sup> (DE3) NE: no enzyme, microcompartment only, (pLysSPduABJKNU). C: *E. coli* BL21 DE3 pML01 (*pduP18-ppk1*).

D,E,F,G: *E. coli* Tuner<sup>TM</sup> (DE3) pET23bPduP18ppk1 pLySsPduABJKNU .

A-F: Electron spectroscopic imaging. Phosphorus signals are shown as overlays: green in A,B,C,F: red in D: yellow in E. Scale bar 1  $\mu$ m unless stated. G: Parallel electron energy-loss spectroscopy (PEELS) of the largest granule in E. The red line represents SpotPEELS of the large inclusion from E with the spot (size: 16 nm) placed centrally (electron micrograph inset). The green-boxed area represents the P-L<sub>2,3</sub> energy-loss near-edge structure (ELNES), characterized by the two peaks (asterisks). The blue-coloured dashed spectrum is referenced from sodium polyphosphate.