

The Genomics of Disulfide Bonding and Protein Stabilization in Thermophiles

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Thermophilic organisms flourish in varied high-temperature environmental niches that are deadly to other organisms. Recently, genomic evidence has implicated a critical role for disulfide bonds in the structural stabilization of intracellular proteins from certain of these organisms, contrary to the conventional view that structural disulfide bonds are exclusively extracellular. Here both computational and structural data are presented to explore the occurrence of disulfide bonds as a protein-stabilization method across many thermophilic prokaryotes. Based on computational studies, disulfide-bond richness is found to be widespread, with thermophiles containing the highest levels. Interestingly, only a distinct subset of thermophiles exhibit this property. A computational search for proteins matching this target phylogenetic profile singles out a specific protein, known as protein disulfide oxidoreductase, as a potential key player in thermophilic intracellular disulfide-bond formation. Finally, biochemical support in the form of a new crystal structure of a thermophilic protein with three disulfide bonds is presented together with a survey of known structures from the literature. Together, the results provide insight into biochemical specialization and the diversity of methods employed by organisms to stabilize their proteins in exotic environments. The findings also motivate continued efforts to sequence genomes from divergent organisms.

Citation: Beeby M, O'Connor BD, Ryttersgaard C, Boutz DR, Perry J, et al. (2005) The genomics of disulfide bonding and protein stabilization in thermophiles. PLoS Biol 3(9): e309.

Introduction

Structural disulfide bonds are a covalent tertiary interaction in proteins, acting to stabilize a folded protein structure. Until recently, the classical view in biochemistry held that structural disulfide bonds are present almost exclusively in extracellular and compartmentalized proteins, as the reducing environment of the cytosol renders disulfide bonds only marginally stable [1,2]. In cellular compartments where disulfide bonding is abundant, such as the prokaryotic periplasm, disulfide-bond biochemistry is tightly regulated [3,4]. In the case of *Escherichia coli*, the DsbA–DsbB pathway in the periplasm, together with the thioredoxin and glutathione reductases in the cytoplasm, forms a cellular system that regulates disulfide-bond breakdown in the cytoplasm and formation in the periplasm. Interestingly, recent work has shown that alterations in these control mechanisms can make possible the formation of cytoplasmic disulfide bonds [5]. Indeed, it has been shown that certain mutants of *E. coli* can form protein disulfide bonds within the cytoplasm by utilizing thioredoxin as a disulfide exchange protein [6]. These studies illustrate how relatively small genetic changes can lead to cellular conditions that support intracellular protein disulfide formation in organisms with otherwise reducing cytosolic environments. The facility with which the cytosol of an ordinary bacterium can be manipulated to allow disulfide bonding relates to emerging revelations on disulfide bonding in unusual prokaryotes, particularly those of the thermophilic type.

Previous genomic studies by our laboratory provided computational and biochemical evidence for the idea that disulfide bonds in intracellular proteins are present in certain thermophiles (organisms of optimal growth temperature,

T_{opt} , above 50 °C) and hyperthermophiles ($T_{\text{opt}} \geq 80$ °C) [7]. For the remainder of this paper, the term “thermophile” is used to refer to both thermophiles and hyperthermophiles. Here, multiple lines of computational and experimental evidence are presented that illustrate a widespread, yet nuanced, pattern of disulfide-bond utilization in intracellular proteins across 199 prokaryotes. The specific distribution of disulfides observed across these genomes suggests specialization in strategies used by organisms to stabilize their proteins. A comparative phylogenetic analysis is also described that provides compelling support for a specific protein, which has been named protein disulfide oxidoreductase (PDO) [8,9], in forming and maintaining intracellular disulfide bonds in thermophiles. A new crystal structure of another hyperthermophilic protein with three disulfide bonds is also presented along with a survey of disulfide bonding in known three-dimensional structures from thermophiles. We interpret these results as implying a widespread

Received March 13, 2005; Accepted July 1, 2005; Published August 23, 2005
DOI: 10.1371/journal.pbio.0030309

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Abbreviations: CPM, 7-diethylamino-3-(4'-maleimidylphenyl)-4-methylcoumarin; PaPDO, *Pyrobaculum aerophilum* PDO; PDI, protein disulfide isomerase; PDO, protein disulfide oxidoreductase; redox, oxidation–reduction; TCEP, tris(2-carboxyethyl)phosphine hydrochloride

Academic Editor: Greg Petsko, Brandeis University, United States of America

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stabilizing role for these intracellular disulfide bonds in certain organisms.

These findings and other recent results call into question the long-held view that disulfide bonds must be rare in cytosolic proteins in all organisms. Some organisms have evidently modulated their internal biochemistry to enable disulfide bonding as a key mechanism for stabilizing their proteins at high temperatures.

Results

Computational Analysis of Disulfide Richness across Genomes

A method for predicting from genomic data which organisms are rich in disulfide bonds has been described [7,10]. In the present study, a similar strategy was utilized in which genomic sequences are mapped onto the known three-dimensional structures of homologous proteins. Here, our analysis benefits from a vastly greater number of completely sequenced genomes. To begin, intracellular proteins were identified from the National Center for Biotechnology Information prokaryotic genome dataset (<http://www.ncbi.nlm.nih.gov>). If possible, each protein sequence was then matched to a known three-dimensional protein structure using either the BLAST or PSI-BLAST programs. The alignment of a query sequence to a homologous structure infers a likely three-dimensional mapping of the protein sequence in question, yielding homology-based structural predictions for many proteins. Considering all such protein sequences from a given genome as a group, the tendency of each amino acid type to appear in spatial proximity to every other type was then analyzed, taking into account the overall abundances of the 20 amino acid types. Enrichment in cysteine–cysteine proximity above the expected value was taken to indicate an enrichment of disulfide bonding. Since cysteine–cysteine proximity can also indicate metal-binding motifs, proteins were first filtered to remove proteins with metal-binding sites that would otherwise produce false-positive results. In addition, extracellular proteins in which structural disulfide bonds are expected to be observed were removed. These proximity criteria were also used to examine biases in pairwise amino acid proximity across all amino acid types beyond just cysteine–cysteine proximities (Figure 1).

Trends in pairwise amino acid proximities were measured for proteins from 199 distinct prokaryotic genomes, and close cysteine–cysteine pairings were interpreted as likely specific disulfide bonds in these organisms. While all possible pairings of amino acids were examined, close cysteine–cysteine proximity was, by far, the dominant trend in this investigation. With a few exceptions, thermophiles exhibited a pronounced bias in the spatial proximity of cysteine–cysteine residues, supporting a role for disulfide bonds in these organisms. Figure 1 illustrates this trend by showing the tendency of cysteine residues to be near all 20 types of amino acid in three dimensions for several organisms. Of all other possible pairwise combinations, tryptophan–tryptophan was the only other pairing observed to be significant according to our distance criteria, but in a smaller subset of organisms (data not shown). Previous work has established a role for aromatic clustering in thermophilic proteins, and our results may be an indication of this more subtle trend [11].

The predicted disulfide abundance (expressed as a prox-

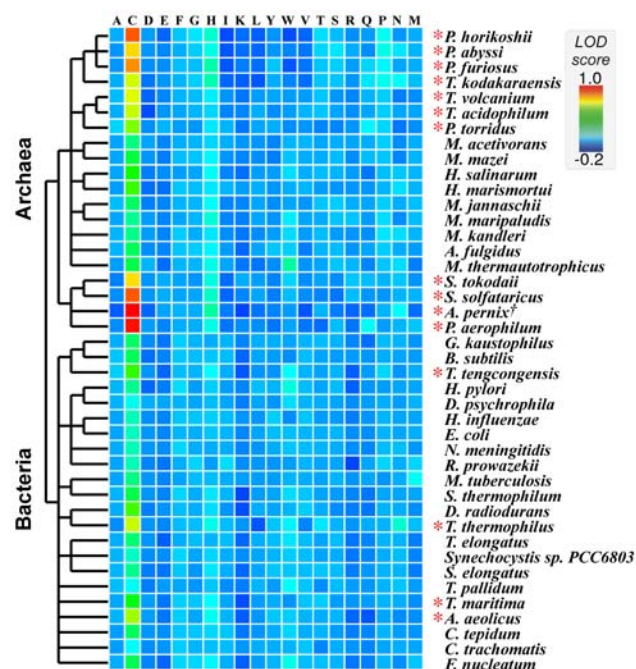


Figure 1. Predicted Protein Disulfide Abundance Across Thermophilic and Mesophilic Microorganisms

For each genome, a colored row illustrates the tendency for cysteine residues in the proteins of that organism to occur close in three-dimensional space to each of the 20 amino acids. The amino acid types are given by their one-letter codes. The values reported are log (base 10) odds ratios, i.e., log ratio of observed over expected occurrences of proximal amino acids, with larger numbers implying a more frequent occurrence of amino acids in proximity. The figure illustrates only a subset of the sequenced organisms analyzed, but includes all the archaeal and bacterial thermophiles. The archaeal and bacterial major branches are noted and species names are provided. Some notable genomes with significant cysteine–cysteine proximity predictions include *P. aerophilum*, *A. pernix*, and *Py. furiosus*. Notably, cysteine–cysteine proximity stands out in thermophiles, particularly in the archaea, when compared with mesophiles such as *E. coli*. Furthermore, a red asterisk next to an organism name refers to the presence of the PDO protein (see text). Note that branch lengths are based on the National Center for Biotechnology Information taxonomy scheme and are not representative of phylogenetic distance, being used as a helpful visualization tool alone. An extended version featuring all genomes analyzed is available in the supporting online material (Figure S1). A dagger indicates that the value for *A. pernix* (1.236) exceeds the upper limit (1.0) of the coloring scheme used here.

DOI: 10.1371/journal.pbio.0030309.g001

imity score for cysteine–cysteine pairs) is shown in Figure 2 as a function of the maximum growth temperature of each organism. Disulfide richness is identified in thermophiles, both archaeal and bacterial. As expected, *Pyrobaculum aerophilum*, an organism singled out in earlier studies [7,12], exhibits a high propensity for cysteines to be in close proximity, with pairs of cysteine residues appearing in proximity nearly ten times more often than expected by chance. For *Aeropyrum pernix*, which shows the greatest enrichment in cysteine–cysteine proximity among all the organisms examined to date, cysteine proximity is higher by a factor of more than 17 times that which was expected on the basis of the total cysteine abundance in that organism. It is interesting to note that many of the organisms that appear to favor disulfide bonds have a reduced total cysteine abundance compared to other thermophiles and mesophiles [13]. This

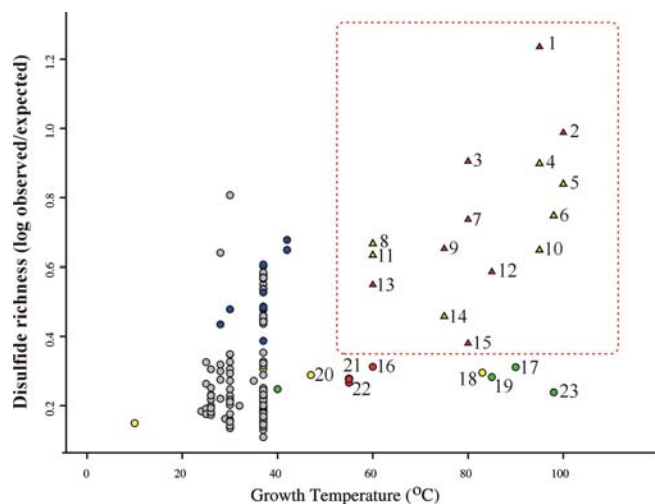


Figure 2. Correspondence of Growth Temperature and Disulfide Richness

A plot of log ratios of cysteine–cysteine proximity versus optimal growth temperature for 99 sequenced genomes is presented. Optimal growth temperatures were taken from the German Collection of Microorganisms and Cell Cultures (DSMZ) and from genome sequence literature. Organisms are classified by color and symbol shape according to the following scheme: mesophiles that include annotations in the literature suggesting some extremophilic property other than thermophilicity (blue); mesophiles that do not include literature annotations suggesting extremophilic qualities (grey); sulfur-reducing bacteria and archaea (yellow); methanogenic bacteria and archaea (green); non-methanogenic/non-sulfur-reducing thermophiles (red); genomes that contain a PDO protein (triangle) (see text); and genomes that do not contain a PDO protein (circle). The genomes containing the PDO protein fit perfectly into the top right segment of the plot, as illustrated by the box drawn in dotted red lines.

Numbers indicate the following organisms: 1, *A. pernix*; 2, *P. aerophilum*; 3, *S. solfataricus*; 4, *Py. horikoshii*; 5, *Py. furiosus*; 6, *Py. abyssi*; 7, *S. tokodaii*; 8, *Thermoplasma volcanium*; 9, *Thermus thermophilus* (both HB8 and HB27); 10, *Thermococcus kodakaraensis*; 11, *T. acidophilum*; 12, *Aquifex aeolicus*; 13, *Picrophilus torridus*; 14, *Thermoanaerobacter tengcongensis*; 15, *Thermotoga maritima*; 16, *Symbiobacterium thermophilum*; 17, *Methanothermobacter thermoautotrophicus*; 18, *Archaeoglobus fulgidus*; 19, *Methanococcus jannaschii*; 20, *Synechococcus elongatus*; 21, *Geobacillus kaustophilus*; 22, *Thermosynechococcus elongatus*; and 23, *Methanopyrus kandleri*.

DOI: 10.1371/journal.pbio.0030309.g002

suggests the possibility of a significant evolutionary pressure against free (thiol) cysteines, and a concomitant elimination of cysteine residues lacking a structural (i.e., disulfide-bonded) or functional (i.e., metal-binding or catalytic) role in such organisms. Whether the placement of cysteines in the proteins of disulfide-rich organisms differs from the placement of cysteines in other organisms remains to be seen.

Interestingly, not all thermophilic organisms appear to contain an abundance of disulfides. Specifically, thermophiles with low disulfide richness include the methanogenic organisms and many of the sulfur-reducing organisms examined here, together with the few thermophilic cyanobacteria. Many of the thermophiles with low cysteine–cysteine pairwise proximity scores are strict anaerobes, growing at very low oxidation–reduction (redox) potentials (i.e., strongly reducing conditions). It may be that the environmental niche or the intrinsic biochemistry of these organisms precludes the significant use of cytosolic disulfide bonds.

In addition to thermophilic prokaryotes, certain other organisms appear to have measurably elevated degrees of

disulfide bonding. These include some halophiles, alkalophiles, acidophiles, and radiation-tolerant organisms. This trend suggests that disulfide bonds might serve generally to stabilize proteins in a variety of extreme environments.

Identification of a Candidate Protein Involved in Disulfide-Bond Formation in Thermophiles

The property of disulfide richness is distributed in a distinctive pattern across the phylogenetic tree, covering select thermophiles belonging to both the archaeal and bacterial domains of life. This suggests a phylogenetic approach for investigating the biochemical mechanisms related to disulfide maintenance. To investigate the hypothesis that proteins present exclusively in the most disulfide-rich thermophiles are involved in establishing or maintaining disulfide bonds, orthologous proteins that were present exclusively in these organisms were identified using techniques similar to ones developed previously [14]. Other studies aimed at identifying proteins involved in thermophilic adaptation [15,16] have been performed, but our study differs in certain respects. Earlier studies have operated under the implicit assumption that all thermophiles would use the same complement of proteins to survive at high temperatures. Here, we operate with the understanding that different organisms appear to use different mechanisms. In particular, the above analysis permits a focus on the disulfide-bonding mechanism. Thus we seek to identify protein(s) exclusive to the subset of organisms predicted here as having high levels of intracellular disulfide bonds.

A small subset of proteins was identified as unique to these organisms (Figure 3). However, only one protein matched a template profile perfectly—a protein from a family previously described as containing possible PDOs [9]. This protein family was previously identified as exclusive to thermophiles, and its potential involvement in a subset of disulfide-rich organisms was noted [8]. Interestingly, proteins from this family were not detected in certain key organisms, notably *P. aerophilum*. Here, a more complete list of PDO proteins was found, and a strikingly precise correlation of the exclusive occurrence of PDO in thermophiles with high disulfide occurrence was discovered (see Figures 1 and 2). Intriguingly, the PDO family is not isolated to a single branch of the organismal tree (see Figure 1) and, as such, its precise co-occurrence with disulfide richness is particularly compelling evidence for a significant relationship to this special cellular property. Our findings therefore strongly reinforce the ideas of Pedone et al. [8] who have performed biochemical and structural characterization of the PDO protein from *Pyrococcus furiosus*.

The Structure and Role of PDO in Disulfide-Rich Microbes

The PDO family, unique to disulfide-rich thermophiles, includes 16 known members from our set of fully sequenced genomes (Figure 4). The PDO protein from *Py. furiosus* has previously been structurally characterized [9] (Figure 5A). Its involvement in disulfide redox chemistry has already been established, where it has been shown to be capable of acting as a disulfide oxidase, reductase, or isomerase in vitro [8,17]. The crystal structure of *Py. furiosus* PDO shows two tandem domains of the thioredoxin/glutaredoxin-fold family. The C-terminal domain has clearly recognizable sequence similarity to glutaredoxins [9], explaining why PDO has not previously

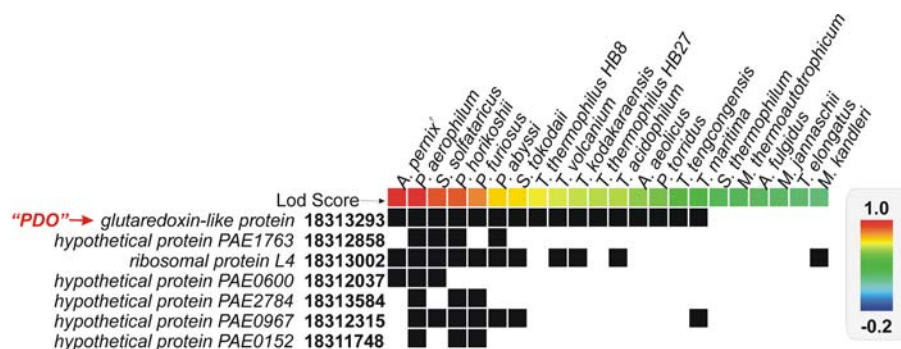


Figure 3. Identification of a Protein Exclusive to Disulfide-Rich Thermophiles

Proteins were searched to find those exclusively present in organisms with high predicted abundance of protein disulfide bonds. Phylogenetic profiles are shown for the seven best protein matches according to our search criteria (see text). All thermophilic genomes are shown across the top, colored according to their predicted disulfide richness (see Figure 1). For each protein row (identified by its GI number), a black box indicates that the homologous protein is present in the genome represented in that column. A single protein, PDO (first profile, GI 18313293, previously annotated as a “glutaredoxin-like protein”, labeled here additionally as “PDO”), is singled out as being most closely correlated with disulfide richness and thermophilicity. Annotation here is taken directly from the annotation provided with the genome. PDO was previously annotated as a “glutaredoxin-like protein” based on its C-terminal similarity to glutaredoxin. A dagger indicates that the value for *A. pernix* (1.236) exceeds the upper limit (1.0) of the coloring scheme used here.

DOI: 10.1371/journal.pbio.0030309.g003

been detected in studies of thermophilic genome complements due to its homology-based classification as a member of the widely distributed glutaredoxin family. The observation of two thioredoxin folds in the PDO protein is provocative in view of the role that thioredoxin superfamily domains are known to play in disulfide-bond biochemistry, including reduction (e.g., thioredoxin), oxidation (e.g., DsbA), and isomerization (e.g., protein disulfide isomerase [PDI]) (reviewed in [18]).

Each of the two domains in PDO contains one CxxC sequence motif, with the exception of the *P. aerophilum* protein whose N-terminal CxxC motif is disrupted by an insert of five amino acids between the cysteines (see Figure 4). It was unclear from the sequence whether the *P. aerophilum* insert might disrupt the N-terminal redox site by preventing the cysteines from forming a disulfide bond. To determine whether this insertion affected the structure of the active site, the quantity of free thiols present in the protein was assayed. Purified recombinant PDO from *P. aerophilum* (PaPDO) was reacted with the fluorescent thiol-reactive label 7-diethylamino-3-(4'-maleimidylphenyl)-4-methylcoumarin (CPM) under denaturing conditions in the presence or absence of the reductant tris(2-carboxyethyl)phosphine hydrochloride (TCEP). The denaturing conditions ensure that all cysteines are accessible to the modifying reagent. If the redox site was disrupted, the cysteines would not be able to form a disulfide bond in the native protein, and thus would exist as reactive free thiols. In fact, the native protein showed minimal labeling (~8%) compared to the reduced and fully labeled control sample (Figure 5B), indicating that both redox sites exist predominantly in their oxidized, disulfide form in the native protein. These results suggest a potential functional relevance of this N-terminal segment, despite the insert observed in the *P. aerophilum* sequence.

Although the specific role the PDO protein might serve in the cell has not been elucidated fully [19], the results presented here suggest that it is involved in the formation or maintenance of intracellular protein disulfide bonds in disulfide-rich organisms, possibly by functioning as a cyto-

plasmic PDI. Based on its apparent cellular function as well as its tandem domain structure, a parallel can be drawn between PDO and the eukaryotic enzyme PDI, which also contains multiple tandem thioredoxin domains as noted by Freedman, et al. [19]. PDI resides in the endoplasmic reticulum where it catalyzes the isomerization of protein disulfide bonds in an oxidizing environment. It is possible to speculate that the enzyme used by eukaryotes to form protein disulfide bonds in the endoplasmic reticulum could have arisen from a similar enzyme in a disulfide-rich thermophile. Further studies will be required to test the predicted function of PDO, and to investigate its potential relationship to eukaryotic PDI, although the lack of a good genetic model organism in the thermophiles limits what can be done in vivo at the present time.

Three Disulfide Bonds Revealed in the Structure of a Cysteine-Rich Protein from *P. aerophilum*

Considering the apparent abundance of disulfide bonding in *P. aerophilum*, proteins containing multiple cysteines in their amino acid sequences would be expected to have a high likelihood of containing disulfide bonds. To test this, a 98-residue protein containing six cysteine residues was selected from the *P. aerophilum* genome [20] for structural characterization. The protein (GI 18312142) could not be assigned a function or three-dimensional fold in advance [20], as it had no recognizable sequence similarity to proteins of known function or structure. The crystal structure of the protein was determined to a resolution of 1.6 Å (Figure 6) with an R-factor of 18.4% (Table S1). The first 70 amino acid residues constitute an N-terminal domain whose three-dimensional fold has been observed previously in the copper chaperone Atx1 [21], but which does not contain the active-site residues of Atx1. The remaining 18 residues form a small C-terminal domain of novel fold that interacts with the N-terminal domain exclusively through hydrophobic contacts. The three-dimensional structure reveals that the six cysteine residues in the primary sequence are paired to form three disulfide bonds in the native fold (C22–C34, C24–C54, and



Figure 4. The PDO Family of Proteins

A multiple sequence alignment of 16 members of the PDO family is shown. The two CxxC motifs are indicated by pairs of red arrows. Each protein is labeled with its organism of origin and GI number. Note the disrupted N-terminal CxxC motif in the *P. aerophilum* PDO sequence.

DOI: 10.1371/journal.pbio.0030309.g004

C80–C83, Figure 6B). Although one disulfide bond (C80–C83) fits the sequence of a potential metal-binding/active-site CxxC motif [18], the C22–C34 and C24–C54 disulfide bonds do not fit any known metal-binding or active-site motifs and appear to serve structural roles within the protein fold. Of the 16 *P. aerophilum* proteins whose structures have been determined to date, a total of 29 cysteine residues have been visualized, and 23 of these have been found to form disulfide bonds. Despite the still relatively small sample size, these numbers provide important three-dimensional structural support for the claim of abundant disulfide bonds in this organism, meriting a further survey of thermophilic protein structures.

Support of the Abundance of Cytosolic Disulfide Bonds in Thermophilic Organisms by Known Structures

Given the number of organisms predicted to have an abundance of cytosolic disulfide bonds, it would be expected that support for this would be evident in the structures of currently known proteins. Although the number of protein structures from thermophilic organisms is still low, trends are emerging that correspond to our predictions. A survey of the Protein Data Bank (<http://www.rcsb.org/pdb>) showed that 79 cytosolic proteins from thermophilic organisms exhibit at least one structural disulfide bond. Interestingly, organisms (with fully sequenced genomes) that are disulfide rich and encode PDO account for 71% of these disulfide-bonded

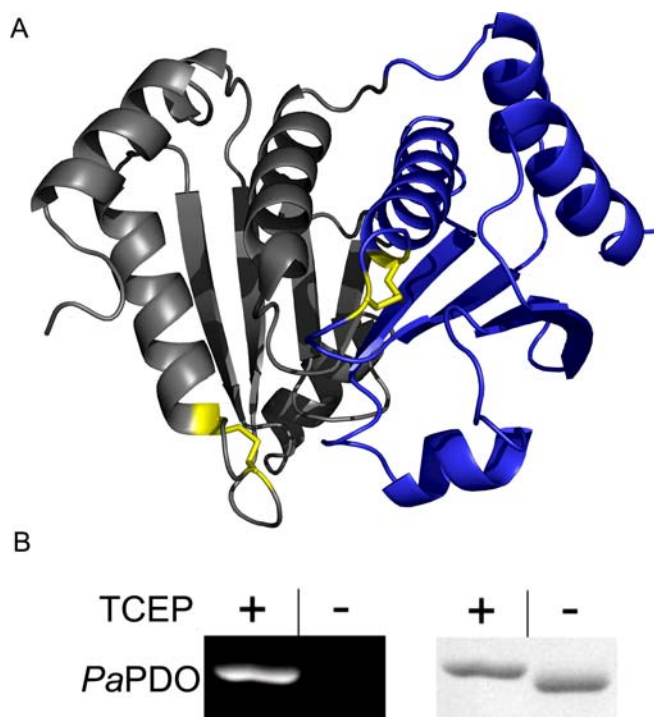


Figure 5. The Previously Determined PDO Structure and Evidence that the *P. aerophilum* Protein Has Similar Disulfide Bonding

(A) The crystal structure of the PDO protein from *Py. furiosus* [12], PDB accession code 1A8L, showed that it contains two fused thioredoxin-like domains (colored grey and blue), with a single contiguous beta-sheet through both thioredoxin domains such that they effectively form one large domain. Each thioredoxin sub-domain bears a CxxC sequence motif with each pair of cysteines forming a disulfide bond (yellow), consistent with the prediction from the profile analysis that it could play a key role in intracellular protein disulfide-bond formation. Figure 5A was generated using PyMOL [54].

(B) Cysteines in purified recombinant *Pa*PDO exist predominantly in disulfide-bonded form. (Left gel) Denatured *Pa*PDO protein was reacted with the thiol-reactive reagent CPM to fluorescently label cysteines in the presence (+) or absence (–) of the strong reducing agent TCEP. Samples separated by sodium dodecyl sulfate–polyacrylamide gel electrophoresis clearly show a minimal labeling of the native protein (in the absence of reductant). (Right gel) Following fluorescence analysis, protein bands were stained with Coomassie Brilliant Blue to determine total protein present. The gel shows that reduced (+) and non-reduced (–) samples contained similar amounts of protein. The slightly lower position of the non-reduced *Pa*PDO compared to reduced *Pa*PDO is attributed to the presence of disulfide bonds in the non-reduced sample, which place constraints on the denatured state of the polypeptide and thus lead to a faster migration rate through the gel.

DOI: 10.1371/journal.pbio.0030309.g005

structures. A survey of the structures available from the top four disulfide-rich organisms in our analysis (Table 1) revealed that 35.6% of the cysteines observed in these structures existed in the disulfide-bonded form. This stands in contrast to the case in *Bacillus subtilis* as a representative example, in which just 2.4% of the total number of cysteines in known structures formed disulfides. In every case where more than one cysteine is present within a *P. aerophilum* protein of known structure, a disulfide bond is found. Furthermore, *P. aerophilum* now accounts for three of the five known structures of thermophilic proteins containing three disulfide bonds (the most yet observed in a single cytosolic protein)—PDB IDs 1WY6, 1V4N, 1XQO, 1F1O, and 1RKI. Although the number of available structures is relatively low

in this case, the prevalence of protein disulfide bonds in *P. aerophilum* proteins, as well as certain other organisms, stands in agreement with our predictions of disulfide abundance.

Disulfide bonds are a common occurrence in extracellular and compartmentalized proteins, where they are utilized to stabilize the folded proteins against the harsh conditions encountered there. The prevalence of disulfides in thermophilic proteins suggests that these bonds may serve a similar role to help stabilize proteins against thermal denaturation. Several stability studies of thermophilic proteins have provided evidence to support this role. Cacciapuoti et al. have shown that the 5'-methylthioadenosine phosphorylase from *Sulfolobus solfataricus* [22], as well as from *Py. furiosus* [23], contains stabilizing disulfide bonds. The 5'-methylthioadenosine phosphorylase from *Sulfolobus solfataricus* forms a homo-hexamer with three intermolecular disulfide bonds per complex, as confirmed by the crystal structure [24], while the homologous protein from *Py. furiosus* contains two intramolecular disulfide bonds [25]. Despite different disulfide patterns, both proteins exhibited a remarkable loss of activity upon exposure to the reducing agent dithiothreitol at optimal temperatures. A similar loss of activity occurred with the glycosyltrehalose trehalohydrolase from *S. solfataricus* upon mutational disruption of the intermolecular disulfide bond [26]. A decrease in melting temperature following disulfide disruption has been observed for *A. permix* isocitrate dehydrogenase ($\Delta T_m = -9.6$ °C) [27], *P. aerophilum* adenylosuccinate lyase ($\Delta T_m = -18.5$ °C) [12], and *Py. woesei* TATA-binding protein ($\Delta T_m = -4$ °C) [28]. Taken together, these results are indicative of a stabilizing role for certain disulfides in cytosolic proteins comparable to their well established structural role in extracellular and compartmentalized proteins. We are in the process of initiating a comprehensive proteomics study to identify proteins in *P. aerophilum* that contain inter- or intra-molecular disulfide bonds.

Discussion

In this work, we describe a variety of computational and biochemical techniques used to imply the use of disulfide bonds as structural stabilization factors in some, but not all, thermophilic organisms. We also demonstrate the correlated presence of a specific protein, PDO, in those organisms thought to employ this mechanism. The discovery and analysis of disulfide-rich organisms provides an important illustration of how much remains to be learned about the diversity of life, as well as a clear example of the continued value of genomic data in exploring new biochemistry and cell biology. A role for disulfide bonds in the stabilization of intracellular thermophilic proteins has not been widely recognized, since—despite the concept's intuitive appeal—it seems to violate contemporary views of redox biochemistry. This study, together with a number of illustrative structures accumulated in recent years, means that the idea of structural disulfide bonds in cytoplasmic proteins in certain organisms must now be considered more routinely.

Numerous factors have previously been implicated in the stabilization of proteins in thermophiles. These include increased atomic packing, as suggested by the first hyperthermophilic enzyme structure determined by Chan et al. [29]; loop shortening, as shown on a genomic level by Thompson and Eisenberg [30]; and increased numbers of

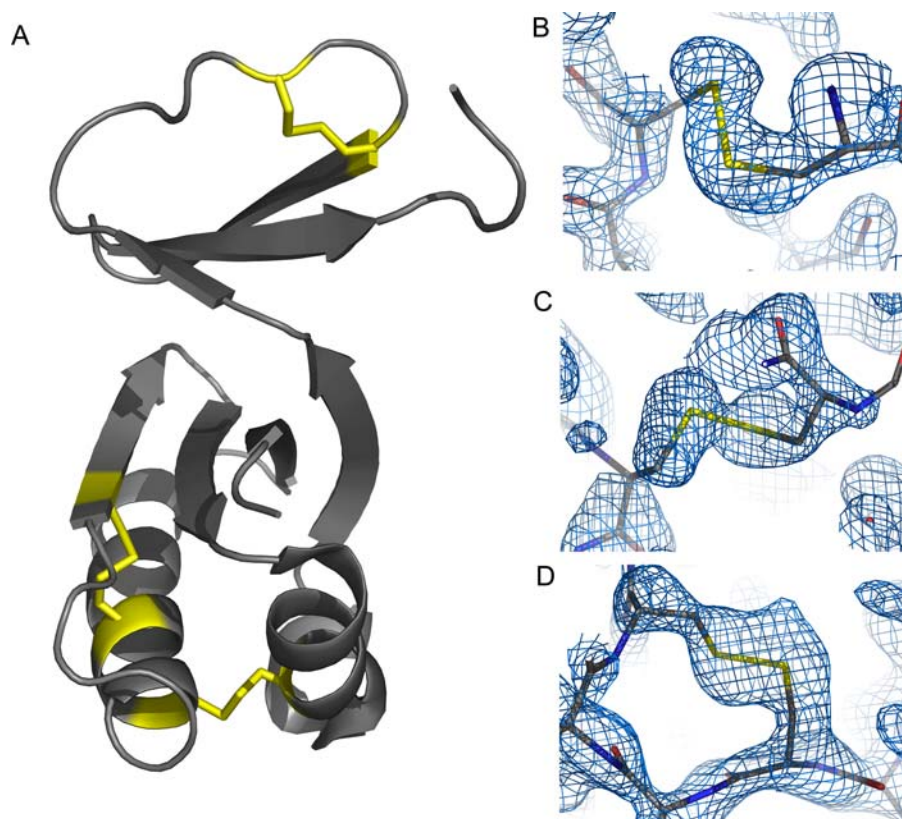


Figure 6. A Novel *P. aerophilum* Protein

(A) A ribbon representation of the crystal structure of a novel *P. aerophilum* protein (GI 18312142) is presented. The six cysteine residues form three disulfide bonds (shown as stick models in yellow).

(B–D) Simulated annealing electron density (“omit”) maps in the regions of the disulfide bonds between (B) Cys22 and Cys34, (C) Cys24 and Cys54, and (D) Cys80 and Cys83 are shown. All densities are contoured at 1 standard deviation. Images were generated using PyMOL [54].

DOI: 10.1371/journal.pbio.0030309.g006

salt bridges as described by Karshikoff and Ladenstein [31]. The view that different proteins use disparate techniques for protein stabilization has been widely noted [32–37], and this study furthers the argument that there are multiple paths to protein stabilization.

The specific distribution of disulfide richness in a characteristic pattern across organisms is intriguing, present-

ing the possibility that different organisms may have evolved different solutions to the problem of protein stabilization. The disulfide-bond solution is particularly noteworthy in that it likely requires the presence of a specific protein, PDO. Disulfide bonding perhaps provides the most clearly delineated stabilization strategy thus far described, as a single covalent disulfide bond is able to effect a stabilization equivalent to that expected for numerous non-covalent stabilizing interactions acting together. It should be noted that not every protein in the organisms highlighted utilizes disulfide bonds for stability. Thus, we suggest that the methods employed in the stabilization of proteins, even from these thermophilic organisms, are a mosaic of all those mentioned above, with each organism employing different methods to varying degrees.

The discoveries presented here raise questions for further experimental studies. For example, what thermodynamic and kinetic considerations explain how certain organisms are able to use disulfide bonds for stability in the cytosol? Do these organisms have oxidizing cellular environments? Why have most mesophiles forgone the use of disulfide bonds for protein stabilization? We are currently in the process of identifying disulfide-bonded proteins in the lysate of certain thermophiles in order to shed light on questions like these. However, the lack of knowledge concerning the basic biology of many thermophiles, particularly the archaea, has limited the ability to investigate important aspects of this phenom-

Table 1. Summary of Disulfide-Bond Content in Protein Structures from Select Organisms

Organism ^a	Proteins	Cysteines	Cysteines in Disulfide Bonds ^b	Percentage of Total Cysteines in Disulfide Bonds
<i>P. aerophilum</i>	16	29	23	79
<i>A. pernix</i>	11	18	12	67
<i>S. solfataricus</i>	28	33	8	24
<i>P. horikoshii</i>	56	66	9	14
Total	111	146	52	36
<i>B. subtilis</i>	148	245	6	2

^aThe first four organisms highlighted were chosen on the basis of having a high predicted disulfide content over their whole genome by the sequence-to-structure mapping method (see text). *B. subtilis* represents a control with low predicted disulfide content.

^bOdd numbers of cysteines involved in disulfide bonds come from the presence of disulfide bonds between two polypeptide chains in homodimers.

DOI: 10.1371/journal.pbio.0030309.t001

enon. Research into the identification of the small-molecule thiols acting as redox buffer systems, as well as development of a genetic system for recombinant protein expression in these organisms, as is currently under way in the genus *Sulfolobus* (for review, see Ciaramella et al. [38]), will greatly enhance our ability to further investigate disulfide abundance.

With regard to the question of whether organisms rich in protein disulfide bonds must have oxidizing cellular environments, we hypothesize that regulation of disulfide-bond formation could be achieved through an interplay of thermodynamic and kinetic effects. The concept of a “reduction potential” for the entire cytoplasm is a synthesis of the reduction potentials of various molecular components of the cell. If thermodynamically favorable redox reactions are not kinetically aided by the presence of appropriate enzymes, the rates of those reactions could be so slow as to be effectively absent. Thus we argue that it may be possible to form deoxyribonucleotides (by reduction of ribonucleotides) for DNA synthesis using ribonucleotide reductase, while simultaneously allowing the formation of structural protein disulfide bonds in the cytoplasm, if these two pathways are kinetically separated. The non-equilibrium nature of cellular systems—enabled by enzymatic recognition and catalysis—makes it possible for two such seemingly opposing redox processes to coexist. We anticipate that the PDO protein may be only one facet of a complex disulfide-bond maintenance system.

The knowledge of disulfide richness in certain organisms suggests practical applications, including engineering enhanced protein stability and facilitating protein-fold recognition. Disulfide-rich organisms should allow the development of novel tools and approaches for attacking such problems of current interest. This work depends upon the availability of sequenced genomes, and the availability of additional thermophilic genomes has enabled the identification of an enigmatic protein family as a potential player in the biochemistry of cytoplasmic disulfide bonds. We hope this study will promote continued interest in sequencing more genomes from diverse organisms so as to further enhance the scope and resolution of comparative genomics techniques. As more genomes become available, we anticipate that the ease of discovery of specific genomic adaptations to the environment will improve and yield further insights into molecular evolution and cell biology.

Materials and Methods

Genomes. Predicted protein sequences from the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov>) for all genomes predicted to encode 700 or more proteins (199 prokaryotic genomes as of March 2005) were used for disulfide-bond predictions. Smaller genomes were discarded to safeguard against low signal-to-noise results. Pairwise amino acid proximity matrices (below) were calculated for each of these genomes.

Filtering. Extracellular proteins were removed using predictions from SignalP 2.0 (<http://www.abcc.ncicrf.gov/app/htdocs/appdb/index.php?info=protein>) to detect signal peptides at the N-termini (first 70 residues), thus ensuring that the preponderance of proteins examined were intracellular [39]. A protein was considered to contain an export signal if at least one SignalP test was positive. Transmembrane proteins were identified and eliminated using TMPred (European Molecular Biology Laboratory, Heidelberg, Germany) [40] (version dated October 30, 1998) with a threshold value of 1,000 to remove proteins with potential extracellular or periplasmic domains. Proteins with known metal-binding motifs were also discarded to

ensure that cysteines involved with metal binding were not included in the disulfide predictions. Motifs were identified from the Prosite database (Swiss-Prot Group, Swiss Institute of Bioinformatics, Geneva, Switzerland), and the ScanProsite 1.3 program (Swiss-Prot Group) [41] was used to exclude any proteins containing the motifs. Similarly, residues separated by fewer than four positions in the primary sequence were excluded as well as proteins with dual CxxC motifs. The end result was a dataset enriched for intracellular proteins, with cysteines not involved in metal-binding sites.

Pairwise amino acid proximity analysis. The process of mapping genomic protein sequences of unknown structure onto known structures was adapted from Mallick et al. [7]. Initially, 371,215 proteins from 199 prokaryotic organisms were queried against the Protein Data Bank (<http://www.rcsb.org/pdb>) [42] using BLAST (<http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/information3.html>) [43] (version dated April 23, 2002). If a hit was not identified with an E-value of <0.0001 , the process was repeated with PSI-BLAST [44] (version dated April 23, 2002). When a homologous protein could be identified in the Protein Data Bank, the amino acid sequence of the query protein and the known structure were aligned with *mlocals*, an implementation of the Smith and Waterman local alignment algorithm from the Seqaln package (<http://www-hto.usc.edu/software/seqaln>) [45] (version 2.0). Based on this correspondence, three-dimensional coordinates were extracted for each amino acid position in the alignment. Those amino acids whose α -carbons were less than 8 Å apart and were separated by more than four positions in the primary sequence were tabulated by amino acid types. Predictions for disulfide bonds were made for specific proteins using these criteria. This criterion has previously been shown to predict disulfide bond state with $\sim 80\%$ accuracy [7].

In addition, every pairing of amino acid types that met these criteria was examined. The number of times that particular pair was found in proximity was divided by the number expected by random chance, taking amino acid abundances into account. For display, these values were converted to the base 10 logarithm of the calculated odds ratios (LOD score). The resulting pairwise proximity score was used to measure biases in three-dimensional placement of all possible amino acid pairs. In the case of cysteine–cysteine pairs, the resulting pairwise proximity score was used as a general measure of disulfide richness for that organism. Specific disulfide predictions for proteins, and pairwise proximity matrices for all genomes examined, are available at <http://www.doe-mbi.ucla.edu/Services/GDAP>.

Identification of proteins exclusive to disulfide-rich organisms. The phylogenetic profile method [14] was used with some modification to search for proteins exclusively present in those genomes predicted to be disulfide rich. Orthologous protein families were defined using the BLAST program [43], where each *P. aerophilum* protein was used as a probe against the other 198 genomes. The process was then reversed with each protein from every genome queried with BLAST against the *P. aerophilum* genome to obtain a list of reciprocal best hits. These reciprocal best hits were further filtered such that probe–subject proteins were of roughly equivalent length. In this case, only those reciprocal best hits such that $0.9L_p \leq L_s \leq 1.1L_p$ were selected, where L_p is the length of the probe protein and L_s is the length of the subject protein. This resulted in a phylogenetic profile for each template protein in *P. aerophilum*, denoting patterns of presence and absence of orthologous proteins in the other organisms. This list was filtered for proteins exclusive to those thermophiles with high predicted levels of intracellular disulfide bonds by constructing a series of idealized template profiles by selecting the top n organisms as ranked by LOD score, for $6 \leq n \leq 23$. Each of these templates was used to extract proteins with profiles that matched a template within a bit-distance of three. Multiple alignment of the PDO family was performed using ClustalW 1.82 (<http://www.cbi.pku.edu.cn/Doc/tools/practices/evolution/>) [46] using the PAM alignment matrix with otherwise default parameters. Visualization was performed using SecSeq 1.0 [47] with secondary structure assignment based on the *Py. furiosus* PDO structure.

Experimental procedures. For the purposes of purification, crystallization, and structure determination, the protein (GI 18312142) was cloned into a pET-22b(+) expression vector, and expressed in *E. coli* BL21-Gold(DE3) (Novagen, Madison, Wisconsin, United States) as a histidine-tag fusion protein. Purification was carried out on a nickel column followed by removal of the histidine tag by thrombin cleavage and concentration to 36 mg/ml in 20 mM Tris–HCl (pH 8.0), 500 mM NaCl. Crystals were grown at 293 K by hanging-drop vapor diffusion, adding 1 μ l of protein solution to 1 μ l of well solution (0.1 M acetate [pH 4.6], 0.2 M Li_2SO_4 , and 26% polyethylene glycol 8000). The crystals were transferred into a well solution containing an additional 20% (w/v) glycerol and then flash-

frozen in liquid nitrogen. An in-house RU200 generator/R-Axis-IV detector (Rigaku, Tokyo, Japan) was used to collect X-ray diffraction data on a native crystal and two crystals soaked with potassium iodide and cesium chloride, respectively. The in-house native dataset was merged with a 1.6-Å native dataset collected at beamline 8.2.2. at Advanced Light Source (Berkeley, California, United States). All data were processed using Denzo and Scalepack (HKL Research, Charlottesville, Virginia, United States). The structure was solved by multiple isomorphous replacement using iodide and cesium sites located by SHELXD (<http://shelx.uni-ac.gwdg.de/SHELX>) [48]. The heavy-atom coordinates were refined with MLPHARE followed by solvent flattening using DM, both in the CCP4 [49] suite of programs (Collaborative Computational Project; <http://www.ccp4.ac.uk>). A traceable electron-density map was subsequently produced and a model was built using the program O [50] (http://xray.bmc.uu.se/~alwyn/Distribution/distrib__frameset.html). Initial rounds of refinement were performed using simulated annealing as implemented in CNS (<http://cns.csb.yale.edu/v1.1>) [51], and later steps of the refinement were carried out with REFMAC5 in CCP4. The model contains two chains with residues 1–101 and 1–97, respectively, as well as two fragments of polyethylene glycol–hexaethylene glycol and tetraethylene glycol, together with two sulfate ions and one chloride ion. The quality of the model was evaluated with the ERRAT (<http://www.doe-mbi.ucla.edu/Services/ERRAT>) [52] and PROCHECK (<http://www.biochem.ucl.ac.uk/bsm/biocomp>) [53] programs. Details of the data collections and refinement are shown in Table S1.

To enable the determination of the redox state of PaPDO cysteines, the protein (GI 18313293) was cloned into a pET-16b expression vector and expressed in *E. coli* as a histidine-tag fusion protein. Cells were lysed by sonication in lysis buffer (50 mM Tris [pH 8.0], 0.2% NP40, 300 mM NaCl, and 10% glycerol) and centrifuged. The supernatant was collected and an initial heat-purification step was performed by heating at 80–85 °C in a water bath, denaturing the majority of the *E. coli* proteins. The supernatant was then passed over a nickel column and the protein eluted using an imidazole gradient. Finally, the eluant was run on a gel filtration column and the fractions corresponding to PDO pooled. Purified recombinant PaPDO was diluted to 0.1 mg/ml in denaturation buffer (1% SDS, 10 mM Tris [pH 8.0], and 10 mM EDTA) and divided into non-reduced and reduced samples. Both samples were heated to 95 °C for 3 min to denature them. For the non-reduced sample, a 5-fold excess of CPM (Molecular Probes, Eugene, Oregon, United States) was added prior to heating to ensure immediate labeling of exposed thiols. Following heat denaturation, the reduced sample was reacted with 10 mM TCEP (Sigma, St. Louis, Missouri, United States) for 20 min at room temperature to reduce disulfide-bonded cysteines. Following the reduction reaction, both non-reduced and reduced samples were reacted with a 10-fold excess of CPM in the dark at room temperature for 20 min. Samples were mixed with 2× SDS-PAGE sample loading buffer and run on a 12% acrylamide gel. Gels were imaged on AlphaImager 2200 (Alpha Innotech, San Leandro, California, United States). In-gel fluorescence was quantified using AlphaEase 5.5 (Alpha Innotech). Fluorescence of the non-reduced sample was below reasonable detection at the point of signal saturation for the reduced sample, so a series of 2-fold dilutions of the reduced sample was

carried out to compare more accurately the amount of labeling of non-reduced relative to reduced sample. Following fluorescence analysis, gels were stained with Coomassie Brilliant Blue (Sigma) and imaged on AlphaImager 2200 (Alpha Innotech).

Supporting Information

Figure S1. Trends in Apparent Disulfide Abundance across Thermophilic and Mesophilic Microorganisms

For each genome, a colored row illustrates the tendency for cysteine residues in the encoded proteins to occur in spatial proximity to each of the 20 types of amino acids, including cysteine itself. The amino acid types are given by their one-letter codes (C = cysteine). The values reported are log (base 10) odds ratios. The archaeal and bacterial major branches are noted and organism names are provided. Some notable genomes include *P. aerophilum*, *A. pernix*, and *E. coli*. Cysteine–cysteine proximity stands out in thermophiles, particularly in the archaea, when compared with mesophiles such as *E. coli*. An asterisk indicates that the value for *A. pernix* (1.236) exceeds the upper limit (1.0) of the coloring scheme used here.

Found at DOI: 10.1371/journal.pbio.0030309.sg001 (26.6 MB TIF).

Table S1. Statistics of Data Reduction and Refinement

Found at DOI: 10.1371/journal.pbio.0030309.st001 (22 KB DOC).

Accession Numbers

The GenBank (<http://www.ncbi.nlm.nih.gov/Genbank>) accession number for *Py. furiosus* is 18976466, and the Protein Data Bank (<http://www.rcsb.org/pdb>) accession number for the *Py. furiosus* PDO structure is 1A8L. The GenBank accession number for the 98-residue protein containing six cysteine residues selected from the *P. aerophilum* genome is 18312142. Atomic coordinates for protein GI 18312142 have been deposited in the Protein Data Bank under accession code 1RKL.

Acknowledgments

We thank Duilio Cascio and Michael Sawaya for crystallographic work, Laurence Lavelle for helpful discussions, and Wendy Liu for protein purification. This work was supported by the Biological and Environmental Research Program (Office of Science, US Department of Energy), by a US Public Health Service National Research Service Award (GM07185) to BDO, and by National Institutes of Health grant GM31299.

Competing interests. The authors have declared that no competing interests exist.

Author contributions. MB and BDO performed the computational analyses. DRB performed the structural database survey and the PDO disulfide experiments. CR determined the crystal structure of GI 18312142. LJP and TOY conceived and designed the studies described.

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