

# Protein stability promotes evolvability

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**The biophysical properties that enable proteins to so readily evolve to perform diverse biochemical tasks are largely unknown. Here, we show that a protein's capacity to evolve is enhanced by the mutational robustness conferred by extra stability. We use simulations with model lattice proteins to demonstrate how extra stability increases evolvability by allowing a protein to accept a wider range of beneficial mutations while still folding to its native structure. We confirm this view experimentally by mutating marginally stable and thermostable variants of cytochrome P450 BM3. Mutants of the stabilized parent were more likely to exhibit new or improved functions. Only the stabilized P450 parent could tolerate the highly destabilizing mutations needed to confer novel activities such as hydroxylating the antiinflammatory drug naproxen. Our work establishes a crucial link between protein stability and evolution. We show that we can exploit this link to discover protein functions, and we suggest how natural evolution might do the same.**

CYP102A1 | cytochrome P450 | directed evolution | lattice protein | mutational robustness

**B**iological systems are evolvable in the sense that mutation and selection are able to create new or improved phenotypes. A major biological question is how a system's physical properties influence its capacity to evolve (1, 2). In recent years, understanding the determinants of evolvability has also become an important practical concern as researchers increasingly use evolution to engineer everything from proteins (3) to designs for civil engineering structures (4).

Proteins are one of the simplest and best examples of evolvable biological systems, because they possess biochemical functions that can be altered with just a few mutations (5). One property that has been broadly hypothesized to contribute to evolvability is robustness to mutations (6), and proteins are often quite mutationally robust, with more than half of the single mutants of many proteins retaining their native functions (7–10). Because proteins usually must fold to function, and because mutated proteins generally adopt the original native structure if they fold at all (11, 12), retention of the basic native structure is normally a prerequisite for the acquisition of new functions. Extra thermodynamic stability makes a protein's native structure and function more robust to random mutations by increasing the fraction of mutants that continue to possess the minimal stability required to fold (10, 13).

Here, we investigate how stability affects a protein's evolvability by using controlled experiments to measure the fraction of a protein's mutants that exhibit new or improved function. We first use a simple computational model to establish a framework for understanding the relationships among protein stability, mutational robustness, and evolvability. We then validate this framework with experiments on members of the biochemically important cytochrome P450 enzyme family and describe specific examples that illustrate the biophysical basis of the connection between protein stability and evolvability. Finally, we discuss the implications of our work for understanding natural protein evolution and designing better protein engineering strategies.

## Results

**Simulations with Model Lattice Proteins.** We used a simple conceptual framework (10) for understanding the relationship between

protein stability and evolution. The premise is that evolution selects for a protein's biochemical function rather than its stability. However, because a protein's function typically depends on its ability to fold to a thermodynamically stable native structure (14), stability is still constrained during evolution. Specifically, we imagine that a protein must fold to its native structure with some minimal stability to remain folded at physiological conditions. If a protein fails to meet this minimal stability threshold, then it will neither fold nor function. If a protein does fold with at least the minimal required stability, then evolution selects for a protein's function and is indifferent to the amount of extra stability it possesses. Most proteins, however, will still be marginally stable, because highly stable sequences are rare (15).

This conceptual framework formed the basis for simulations with lattice proteins. Lattice proteins are highly simplified protein models that are useful tools for studying protein folding and evolution (16, 17). Our lattice proteins were chains of 20 amino acids that fold on a two-dimensional lattice, with the energy of each conformation equal to the sum of the pairwise interactions between nonbonded amino acids (18). Each lattice protein can occupy any of 41,889,578 possible conformations, and, by summing over all of these conformations, we could exactly determine the partition function and free energy of folding ( $\Delta G_f$ ). We set a minimal stability threshold for our lattice proteins by requiring them to fold to the original native structure with a stability of  $\Delta G_f \leq 0$  (in no case did we observe a protein that stably folded to a new structure), which is equivalent to requiring the native structure to have a lower free energy than the ensemble of all nonnative conformations. For those proteins that stably folded, we measured function as the binding energy of the folded protein to a small rigid ligand (19), as shown in Fig. 1A. Our model, therefore, recapitulated the essential requirements imposed on real proteins of simultaneously folding and performing a biochemical task.

We first evolved a model protein to stably fold and strongly bind a ligand (Fig. 1A). This evolved protein had a stability of  $\Delta G_f = -0.5$ , meaning that it was only marginally stable, as is typical for real proteins (20). We then simulated the process of directed evolution with two rounds of random mutagenesis by error-prone PCR and screening to identify a stabilized variant of our model protein ( $\Delta G_f = -1.5$ ) that contained three amino acid substitutions and exhibited the same ligand-binding energy as the original protein. To examine the evolvabilities of the original and stabilized model proteins, we computationally simulated screening libraries of 1,500 randomly mutated sequences for mutants that bound to new ligands with at least twice the affinity of the parent proteins. For all four new ligands we examined, the parent proteins bound the new ligand with equal affinity, yet, each time, the mutant library from the stabilized parent produced more than twice as many unique improved mutants (Fig. 1B).

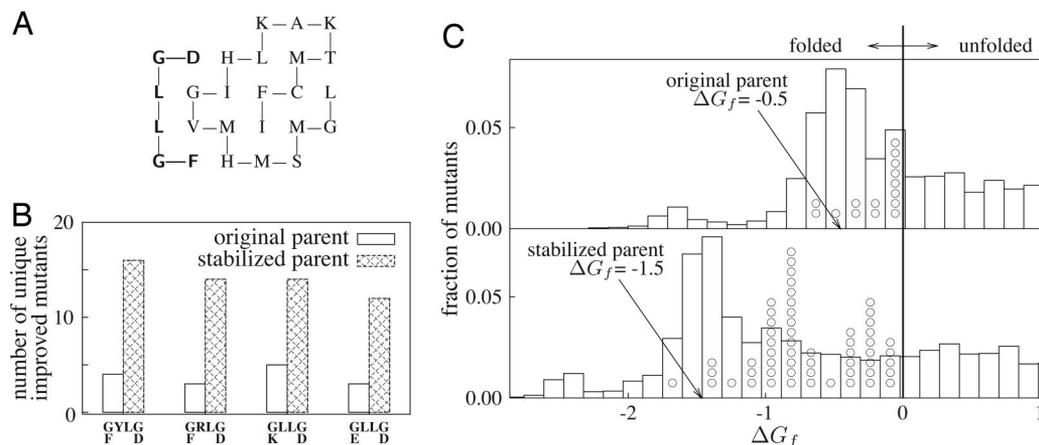
Fig. 1C shows why the stabilized model protein was more

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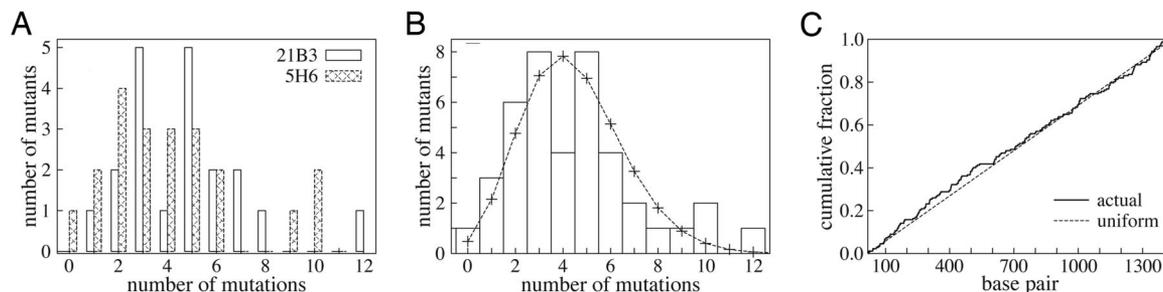
**Fig. 1.** Increased stability enhances evolvability of a model lattice protein. (A) The original model protein (right side) that had been evolved to bind to a rigid ligand (left side, in bold). (B) Mutants of a stabilized model protein were more likely than mutants of the original model protein to show improved binding to the four new ligands shown below the bars. The bars show the number of mutants of 1,500 screened that bound the new ligand with at least twice the affinity of the parent. (C) The stabilized model protein was more evolvable because more of its destabilized but improved mutants satisfied the minimal stability cutoff. The bars show the distribution of stabilities among all mutants in the libraries, and the circles show the stabilities of the improved mutants.

evolvable. The mutants in both libraries exhibited similar changes in stability ( $\Delta\Delta G$  values), but the extra stability of the stabilized protein meant that a larger fraction of its mutants continued to fold (46% versus 35% among all mutants with at least one mutation), confirming previous findings that more stable lattice proteins are more robust to mutations (10, 21).

The improved mutants tended to be destabilized and so were more frequent in the library from the stabilized parent. Although the more stable parent had a <50% increase in the fraction of mutants that folded, it had nearly four times more improved mutants (56 versus 15). The fact that extra stability increases the number of improved mutants much more than it increases the number of mutants that retain parental function indicates that improved mutants tended to be more destabilized than the typical folded mutant.

**Experiments on Cytochrome P450 BM3 Variants.** To experimentally test the effect of stability on the evolvability of real proteins, we randomly mutated two variants of a cytochrome P450 BM3 (also known as CYP102A1) heme domain peroxxygenase (22) and screened for mutants with new or improved activity on five substrates. The cytochrome P450 superfamily contains members involved in important biochemical processes such as drug metabolism and steroid biosynthesis (23, 24). P450 BM3 catalyzes subterminal hydroxylation of medium- and long-chain fatty acids

(25). The 21B3 variant is a laboratory-evolved version of the P450 BM3 heme domain that efficiently hydroxylates 12-*p*-nitrophenoxycarboxylic acid (12-*p*NCA, structure shown in Fig. 2), using hydrogen peroxide in place of the NADPH cofactor and oxygen (22). The 5H6 variant was created by laboratory evolution of 21B3, selecting for mutants that were more thermostable while retaining activity on 12-*p*NCA (26). We quantified the stabilities of the enzymes by the temperature ( $T_{50}$ ) at which half of the protein irreversibly denatured after a 10-min incubation. Because denaturation is irreversible, these  $T_{50}$  values are not equilibrium thermodynamic measurements and so cannot be directly related to  $\Delta G_f$ . However, the  $T_{50}$  values were highly correlated with the stability to irreversible denaturation by urea, supporting the notion that they reflect universal aspects of protein stability rather than unique characteristics of the process of irreversible thermal denaturation (see *Supporting Materials and Methods* and Fig. 5, which are published as supporting information on the PNAS web site). As measured by the  $T_{50}$  values, the 21B3 enzyme is only marginally stable ( $T_{50} = 47^\circ\text{C}$ ), whereas 5H6 is much more stable ( $T_{50} = 62^\circ\text{C}$ ) (melting curves are shown in Fig. 6, which is published as supporting information on the PNAS web site). The 5H6 enzyme differs from 21B3 at 8 residues (of 464 total). Both variants displayed nearly the same activity (measured as total turnovers) on 12-*p*NCA and all other substrates examined in this work.



**Fig. 2.** Distribution of mutations in the two P450 error-prone PCR libraries. (A) The distribution of mutations among 20 randomly chosen 21B3 mutants and 21 randomly chosen 5H6 mutants. The distributions are statistically indistinguishable ( $P = 0.84$ ). (B) The distribution of mutations among all 41 sequenced mutants is consistent with the theoretical prediction for an error-prone PCR library (lines) (49, 50) ( $P = 0.11$ ). (C) The mutations are uniformly distributed along the gene ( $P = 0.66$ ). The lines show the cumulative fraction of mutations that occur at or before that position in the gene. All  $P$  values are from Kolmogorov-Smirnov tests (53) and represent the probability that the samples or theoretical curves would differ by at least this much if they were generated by the same underlying distribution.

**Table 1. Mutation frequencies in error-prone PCR libraries**

Base pairs sequenced	58,719
Total mutations	182
Mutation frequency, %	0.31 ± 0.02
Avg. mutations per gene	4.5 ± 0.3
Synonymous mutations, %	28
Nonsynonymous mutations, %	63
Frameshift/nonsense mutations, %	9
Mutation types, %	
A → T, T → A	25
A → C, T → G	6
A → G, T → C	53
G → A, C → T	10
G → C, C → G	0
G → T, C → A	3
Frameshift	3

Statistics are for all 41 randomly chosen mutants. Standard errors are calculated assuming Poisson counting statistics.

We created mutant libraries of both 21B3 and 5H6 using error-prone PCR. The libraries were generated under identical conditions and had the same distributions of mutations (Fig. 2). The overall mutation rate was  $4.5 \pm 0.3$  nucleotide mutations per gene (Table 1). We examined 522 mutants from each library for retention of folding, as assayed by the characteristic Soret band at 450 nm in the carbon monoxide-binding difference spectrum (27). As expected, mutants of the stabilized 5H6 protein were more likely than those of the 21B3 protein to fold (61% of 5H6

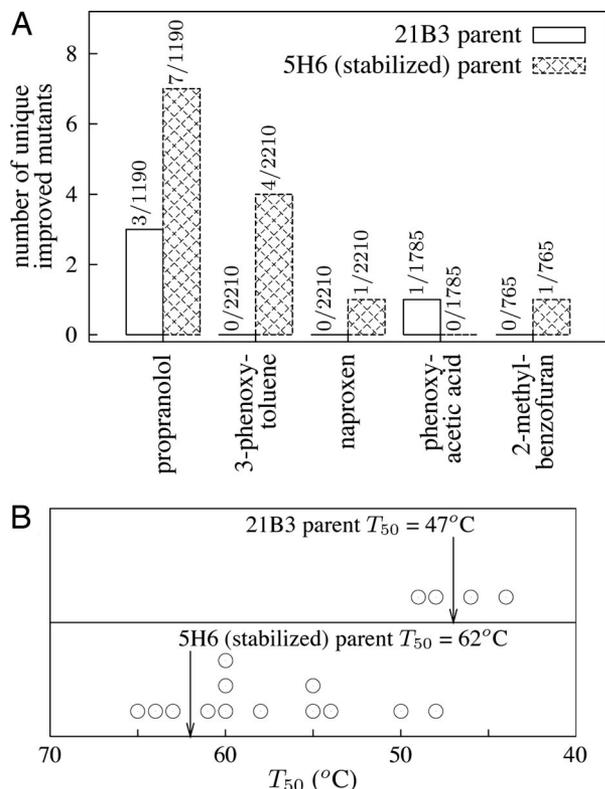
mutants contained at least half the folded protein of the parent versus 33% for 21B3, raw data are shown in Fig. 7 and Table 3, which are published as supporting information on the PNAS web site). Most of these folded mutants retained at least half the parental activity on 12-pNCA (94% and 96% for 5H6 and 21B3), indicating that mutations that disrupted parental function generally did so by preventing the formation of properly folded protein, confirming the experimental findings of ref. 10 that more stable proteins are more robust to mutations.

We examined the evolvability of the 21B3 and 5H6 enzymes by screening for mutants that hydroxylated any of five new substrates: the antiinflammatory drug naproxen, 3-phenoxytoluene, phenoxyacetic acid, the  $\beta$ -adrenergic receptor blocking agent propranolol, and 2-methylbenzofuran (structures shown in Fig. 9, which is published as supporting information on the PNAS web site). We screened for hydroxylation activity using the 4-aminoantipyrene (4-AAP) assay to measure the total amount of product after completion of the reaction (28) and determined that neither 21B3 nor 5H6 had detectable activity on the first three substrates, both had equal weak activity on propranolol, and 21B3 had trace activity on 2-methylbenzofuran (Table 2). We used consistent quantitative criteria to identify mutants that had either acquired new activity or improved by >50% over the parental level in the 4-AAP assay. We screened 8,160 mutant–substrate pairs for each parent. From these pairs, we identified 13 improved mutants of 5H6 and 4 improved mutants of 21B3 (Fig. 3A and Table 2). All of the improved mutants had unique protein sequences (given in Table 4, which is published as supporting information on the PNAS web site). Thus, we found

**Table 2. Summary of improved P450 mutants**

Substrate	21B3				5H6			
	Protein	Activity	$m_{aa}$	$T_{50}$ , °C	Protein	Activity	$m_{aa}$	$T_{50}$ , °C
Propranolol (1,190 screened)	Parent	0.07 ± 0.02	0	47	Parent	0.08 ± 0.02	0	62
	14C10	0.29 ± 0.05	3	44	27G8	0.15 ± 0.01	1	65
	27B2	0.15 ± 0.03	3	49	27G12	0.25 ± 0.03	7	55
	31B12	0.14 ± 0.02	2	48	30B10	0.19 ± 0.02	6	58
					32F7	0.15 ± 0.02	4	55
					36G11	0.22 ± 0.02	3	64
3-Phenoxytoluene (2,210 screened)	Parent	None	0	47	Parent	None	0	62
					20D1	0.05 ± 0.02	1	60
					23E4	0.30 ± 0.03	5	48
					28B5	0.05 ± 0.03	3	60
					29G8	0.05 ± 0.02	2	50
					38F11	0.16 ± 0.02	3	60
Naproxen (2,210 screened)	Parent	None	0	47	Parent	None	0	62
					13C9	0.16 ± 0.02	1	54
Phenoxyacetic acid (1,785 screened)	Parent	None	0	47	Parent	None	0	62
	38F7	0.30 ± 0.04	3	46				
2-Methylbenzofuran (765 screened)	Parent	0.07 ± 0.02	0	47	Parent	None	0	62
					32H1	0.11 ± 0.02	1	61

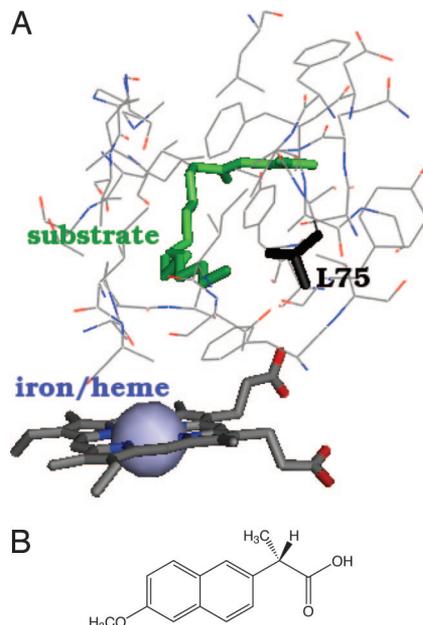
The leftmost column gives the total number of mutants of each parent screened on that substrate. Subsequent columns give the activity, number of amino acid substitutions ( $m_{aa}$ ), and stabilities as measured by the  $T_{50}$  values. Mutants are named according to the plate and well in which they were found, and sequences are given in Table 5. Activities represent the median ± SD of the total product formed per well of 80  $\mu$ l of 5  $\mu$ M protein, as measured by the  $A_{500}$  in the 4-AAP assay (raw data are in Fig. 8, which is published as supporting information on the PNAS web site.) and are indicated as “none” when indistinguishable from the background. With an extinction coefficient of 4,800  $M^{-1} cm^{-1}$  for the 4-AAP/phenol complex (52), each unit of  $A_{500}$  corresponds to  $\approx$ 80 nmol of product from the  $\approx$ 0.4 nmol of protein per well.



**Fig. 3.** Increased stability enhances evolvability of the P450 BM3 heme domain. (A) The stable 5H6 protein yielded more mutants with new or improved activity than the marginally stable 21B3 protein. The counts above the bars give the number of improved mutants of the total number of mutants screened. (B) Some of the improved 5H6 mutants were greatly destabilized relative to the parent protein, whereas the stabilities of the improved 21B3 mutants clustered around those of the parent protein (circles show  $T_{50}$  values for improved mutants).

more than three times more improved mutants in the 5H6 library than in the 21B3 library.

To assess the importance of stability in conferring enhanced evolvability on the 5H6 protein, we measured the stabilities of all improved mutants (melting curves are in Fig. 6). Fig. 3B shows that none of the improved 21B3 mutants was destabilized by  $>3^{\circ}\text{C}$  but that the most stable 5H6 parent produced improved mutants that were destabilized by as much as  $14^{\circ}\text{C}$ . We identified specific beneficial but destabilizing substitutions that could be made only in the stabilized parent. For example, neither 21B3 nor 5H6 exhibited activity on naproxen, presumably because the negatively charged naproxen molecule does not enter the hydrophobic P450 BM3 substrate-binding pocket. Mutating leucine 75 in the substrate-binding pocket to arginine allowed 5H6 to hydroxylate naproxen by providing a compensating positive charge for the naproxen molecule (Fig. 4). However, burial of this arginine residue in the hydrophobic binding pocket substantially destabilized the 5H6 mutant ( $\Delta T_{50} = -8^{\circ}\text{C}$ ). When we made the same substitution to 21B3, we could recover only inactive and improperly folded protein (as indicated by a carbon monoxide difference spectrum peak at 420 nm (29), as shown in Fig. 10, which is published as supporting information on the PNAS web site). The F275S substitution (located 12 Å from the substrate) (30) is another example of a beneficial substitution that could be made only in the stabilized parent. This substitution conferred 3-phenoxytoluene activity on the 5H6 parent, but decreased the  $T_{50}$  by  $7^{\circ}\text{C}$ . When we made this substitution in 21B3, we again could not recover any folded protein (see Fig. 11,



**Fig. 4.** The functionally innovative but destabilizing L75R mutation can only be tolerated by the stabilized parent. (A) Leucine 75 is positioned close to the substrate in the hydrophobic P450 BM3 substrate-binding pocket (30). Mutating L75 to a positively charged arginine conferred naproxen activity on the stabilized 5H6 parent but disrupted the proper folding of the marginally stable 21B3 parent. (B) The antiinflammatory drug naproxen, which contains a negatively charged carboxylic acid group.

which is published as supporting information on the PNAS web site). In contrast, the F205L substitution (located near the substrate-binding pocket) (30) found in a 21B3 mutant with improved activity on propranolol did not have a substantial effect on stability, and slightly improved the activity of both 21B3 and 5H6 when introduced into those sequences (see Fig. 12, which is published as supporting information on the PNAS web site).

## Discussion

We have shown that more stable proteins are more evolvable because they are better able to tolerate functionally beneficial but destabilizing mutations. Our work touches on the relationship between protein stability and function, which has historically been a subject of considerable confusion. Despite repeated speculation to the contrary (31–33), high stability and function are not inherently incompatible, because a wealth of experiments have shown that proteins can be dramatically stabilized without sacrificing their biological functions (34–37). But protein stability and function often appear to trade off at the level of individual mutations. This apparent tradeoff is, at least partly, because of the simple fact that most randomly chosen mutations (functionally beneficial or not) are destabilizing (38–41). In addition, residues in a protein's active site often must satisfy functional constraints (such as maintaining buried charges or cavities in a protein's interior) that make them poorly optimized for stability (42–44). Therefore, mutating active-site residues often enhances stability at the cost of function (42–44), and, likewise, acquiring new functions can require destabilizing mutations (as is the case for our L75R mutation in P450, which confers activity on naproxen by burying a positive charge). However, it remains unclear whether active-site constraints intensify the tradeoff between stability and functional evolution, because a seemingly opposite argument can be made that mutations to an active site that is already poorly optimized for

stability should be less destabilizing than typical mutations (they could even enhance stability if, for example, they confer function on smaller substrates by reducing the size of a cavity in a protein's interior). If functionally innovative mutations tend to be more destabilizing than random mutations, then extra protein stability should enhance the rate of functional innovation more than it enhances the mutational robustness of the native function. In our lattice protein simulations, extra stability increased the rate of functional innovation by nearly 300%, whereas it increased mutational robustness by only 50%; however, we feel that our lattice model is too crude to confidently extrapolate conclusions involving residue-level properties to real proteins. In our P450 experiments, extra stability also increased the number of functionally improved mutants (from 4 to 13) more than it increased mutational robustness (by a factor of 1.8); however, here, the statistics are too poor to conclude that functional innovation is improved significantly more than mutational robustness. Therefore, in our minds, it remains unclear whether extra protein stability promotes evolvability simply by improving the tolerance to all mutations (some of which happen to be functionally beneficial) or whether the effect is further amplified by a tendency for functionally innovative mutations to be especially destabilizing.

In either case, our work argues, quite generally, that extra stability will enhance evolvability. Although it is clearly possible to stabilize proteins without interfering with their functions (34–37), proteins tend to be only marginally more stable than is required by their environment (20). This marginal stability is probably because of the fact that natural selection does not directly favor extra stability in the face of predominantly destabilizing mutations, causing stability to drift toward the minimum evolutionary requirement (15, 45). Naturally evolving proteins must, therefore, wait for functionally neutral mutations to stabilize the structure to counterbalance the effects of other destabilizing but functionally beneficial mutations (46). In this sense, a protein's stability represents a hidden dimension in evolution: Extra stability is neutral with respect to selection for protein function, but it can be crucial in allowing a protein to tolerate mutations that confer beneficial phenotypes. We have shown that protein engineering by directed evolution is more effective if direct selection for extra stability is used to increase a protein's evolvability. The extent to which natural evolution might also select for evolvability has been the subject of much recent theoretical speculation (2, 6, 47). We suggest that one possible mechanism by which natural evolution could increase evolvability would be to stabilize proteins undergoing adaptive evolution or provide systems to buffer the effects of destabilizing protein mutations.

## Methods

**P450 Mutant Libraries.** We used error-prone PCR to create mutant libraries of the marginally stable 21B3 (22) and the thermostable 5H6 (26) variants of the cytochrome P450 BM3 heme domain. The template DNA was the appropriate gene cloned into the pCWori (48) plasmid as described in refs. 22 and 26. We confirmed the sequences of the 21B3 and 5H6 genes by sequencing them with the primers *pCWori\_for* (5'-GAAACAGGATCCATCGATGCTTAGGAGGTCAT-3', *pCWori\_rev* (5'-GCGTATCACGAGGCCCTTTCGTCTCAAGC-3'), and *pCWori\_mid\_rev* (5'-CCAGCTTGTTGGC-CAACCCGAC-3'). The sequences matched those that were reported (22, 26), with 21B3 containing 10 amino acid substitutions relative to the wild-type P450 BM3 heme domain (I58V, F87A, H100R, F107L, A135S, M145V, N239H, S274T, K434E, and V446I in the numbering scheme, where residue 1 is the threonine after the cleaved N-terminal methionine) and 5H6 containing 8 amino acid substitutions relative to 21B3 (L52I, S106R, V145M, A184V, L324I, V340M, I366V, and

E442K) as well as the removal of one histidine from the C-terminal His tag.

The error-prone PCRs for the two parents were carried out in parallel by using identical conditions to ensure the same mutation rate for both. The reactions were 100  $\mu$ l and contained 13 ng of template plasmid (corresponding to 3 ng of gene), 0.5  $\mu$ M of the oligonucleotide primers (*pCWori\_for* and *pCWori\_rev.clone*, 5'-GCTCATGTTTGGACAGCTTATCATCG-3'), 200  $\mu$ M dATP and dGTP, 500  $\mu$ M dTTP and dCTP, 7 mM MgCl<sub>2</sub>, 200  $\mu$ M MnCl<sub>2</sub>, 1 $\times$  Applied Biosystems PCR Buffer, and 5 units of *Taq*. PCR conditions were 95°C for 5 min, followed by 16 cycles of 30 s at 95°C, 30 s at 51°C, and 60 s at 72°C. Gel electrophoresis versus a known standard indicated that this yielded PCR product at a concentration of  $\approx$ 12 ng/ $\mu$ l, for a PCR efficiency of  $\lambda = 0.45$ . The PCR products were cloned into pCWori with BamHI and EcoRI, electroporated into a catalase-free strain of *Escherichia coli* (48) and plated on LB plates containing 100  $\mu$ g/ml ampicillin. Transformation of a control ligation with no insert indicated that the background rate of plasmid self-ligation was <1%.

To measure the mutation rates, we randomly selected 20 21B3 clones and 21 5H6 clones for sequencing with primers *pCWori\_for* and *pCWori\_rev*, allowing us to read each gene from bp 18 to bp 1,436. The 21B3 clones contained a total of 95 nucleotide mutations in the 28,380 sequenced base pairs, with 28 synonymous mutations, 60 nonsynonymous mutations, and 7 mutations leading to premature truncation of the gene (frameshift or nonsense mutations). The 5H6 clones contained a total of 87 mutations in the 29,799 sequenced base pairs, with 23 synonymous mutations, 55 nonsynonymous mutations, and 9 mutations leading to premature truncation of the gene. The distributions of mutations in the two libraries were statistically indistinguishable (Fig. 2A). After confirming that the mutation rates in the two libraries were indistinguishable, we combined the sequencing results for further analysis (Table 1). Fig. 2B shows that the distribution of mutations is consistent with the theoretical distribution for error-prone PCR (49, 50), which gives the probability that a mutant in a library with an average of  $\langle m_{nt} \rangle$  mutations per gene has  $m_{nt}$  nucleotide mutations as

$$\Pr(m_{nt}) = (1 + \lambda)^{-n} \sum_{k=0}^n \binom{n}{k} \lambda^k \frac{(kx)^{m_{nt}} e^{-kx}}{m_{nt}!}, \quad [1]$$

where  $n$  is the number of PCR cycles,  $\lambda$  is the PCR efficiency, and  $\langle m_{nt} \rangle(1 + \lambda)/n\lambda$ . We also confirmed that the mutations were distributed uniformly along the gene sequence (Fig. 2C). If each position in the gene is equally likely to be mutated, then among 41 sequenced clones, 156.3 positions should be mutated once, 9.7 positions should be mutated twice, and 0.4 positions should be mutated three times, in good agreement with the observed values of 148, 13, and 1.

**Screening for Improved Mutants.** Single mutants were grown in 96-well deep-well plates in Luria broth (LB) supplemented with 100  $\mu$ g/ml ampicillin for 20–24 h at 30°C, 215 rpm, and 80% relative humidity. One-hundred  $\mu$ l of these LB cultures were used to inoculate deep-well plates containing 400  $\mu$ l per well of terrific broth (TB) supplemented with 100  $\mu$ g/ml ampicillin, 0.5 mM  $\delta$ -aminolevulinic acid, and 0.2 mM isopropyl  $\beta$ -D-thiogalactoside (IPTG) and grown as before. The cells were pelleted and frozen overnight and then lysed by resuspending each well with 600  $\mu$ l of 100 mM [4-(2-hydroxyethyl)-1-piperazinepropanesulfonic acid] (EPPS) (pH 8.2) containing 0.5 mg/ml lysozyme and 2 units/ml DNase and incubating for 1 hour at 37°C. The lysis debris was pelleted by centrifugation, and 80  $\mu$ l of clarified lysate was added to wells of microtiter plates and then combined with 20  $\mu$ l of 6 $\times$  substrate stock (1.5 mM 12-pNCA in 36% DMSO or a 6 $\times$  stock containing 6% DMSO

and 6% acetone with substrate so that concentrations in the stocks were 60 mM 3-phenoxytoluene, 60 mM naproxen, 150 mM phenoxyacetic acid, 30 mM 2-methylbenzofuran, or 30 mM propranolol). Reactions were initiated by adding 20  $\mu$ l of 24 mM hydrogen peroxide. Endpoints for the 12-pNCA assay were read after 20–30 min at 398 nm (22), whereas endpoints for all other substrate were taken after 1.5–2 h with the 4-amino antipyrene (4-AAP) assay as described in ref. 28. More details are in *Supporting Materials and Methods*.

The 21B3 and 5H6 mutant libraries were screened in parallel by using consistent quantitative criteria for identifying improved mutants. Briefly, all mutants with readings that were at least 50% greater than the larger of the parental or null vector internal standards on the 96-well plate were selected for rescreening. Rescreening was performed by growing and assaying a full row of a 96-well plate for each candidate mutant. Mutants that still appeared at least 50% improved were then expressed in flasks containing 200 ml of TB supplemented with 100  $\mu$ g/ml ampicillin, 0.5 mM  $\delta$ -aminolevulinic acid, and 0.4 mM IPTG. The protein concentrations were normalized to 5  $\mu$ M, and verification assays were performed in microtiter plates. All mutants

identified as improved were required to be at least 50% improved over the parental activity or at least 50% improved over the background reading if there was no parental activity. Summary statistics for this process are shown in Table 4, the final readings in the verification assay are shown in Fig. 8, and a comprehensive description of the methods is in the *Supporting Materials and Methods*.

The  $T_{50}$  values were measured as described in ref. 26, except that we measured retention of the peak in the carbon monoxide difference spectrum (27) rather than retention of activity (*Supporting Materials and Methods*). Site-directed mutants with the L75R, F275S, and F205L substitutions were constructed by using PCR overlap extension mutagenesis (51) and assayed for function as in the verification assays.

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