A nitric oxide synthase–like protein from *Synechococcus* produces NO/NO_3^- from L-arginine and NAPDH in a tetrahydrobiopterin- and Ca^{2+}-dependent manner

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Running title: *A novel nitric oxide synthase from blue-green algae*

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ABSTRACT

Nitric oxide synthases (NOSs) are heme-based monooxygenases that convert L-arginine (L-arg) to L-citrulline and nitric oxide (NO), a key signaling molecule and cytotoxic agent in mammals. Bacteria also contain NOS proteins, but the role of NO production within these organisms, where understood, differs considerably from that of mammals. For example, a NOS protein in the marine cyanobacterium Synechococcus sp. PCC 7335 (syNOS) has recently been proposed to function in nitrogen assimilation from L-Arg. SyNOS retains the oxygenase (NOS_{ox}) and reductase (NOS_{red}) domains present in mammalian NOS enzymes (mNOSs), but also contains an N-terminal globin domain (NOS_g) homologous to bacterial flavohemoglobin proteins. Herein, we show that syNOS functions as a dimer and produces NO from L-arg and NADPH in a tetrahydrobiopterin (H_4B)-dependent manner at levels similar to those produced by other NOSs, but does not require Ca^{2+}-calmodulin, which regulates NOS_{red}-mediated NOS_{ox} reduction in mNOSs. Unlike other bacterial NOSs, syNOS cannot function with tetrahydrofolate and requires high Ca^{2+} levels (> 200 μM) for its activation. NOS_g converts NO to NO_3^- in the presence of O_2 and NADPH; however, NOS_g did not protect *Escherichia coli* strains against nitrosative stress, even in a mutant devoid of NO-protective flavohemoglobin. We also found that syNOS does not have NOS activity in *E. coli* (which lacks H_4B) and that the recombinant protein does not confer growth advantages on L-arg as a nitrogen source. Our findings indicate that syNOS has both NOS and NO oxygenase activities, requires H_4B and may play a role in Ca^{2+}-mediated signaling.

Introduction

Nitric oxide (NO) is a gaseous free radical involved in numerous biological processes; it is an intermediate in the denitrification pathway (1), a precursor to protein post-translational modification via s-nitrosylation (2), and is the activator of soluble guanylate cyclase in animals or H-NOX proteins in bacteria (3, 4). In mammals, NO is the product of arginine oxidation by nitric oxide synthases (NOS) (5, 6). The three mammalian isoforms, endothelial (eNOS), neuronal (nNOS), and inducible (iNOS) (6–8), share a heme-containing oxygenase domain (NOS_{ox}) and a C-terminal reductase domain (NOS_{red}). NOS_{red}, which functions to reduce NOS_{ox} using NADPH, is composed of an FMN binding domain and a ferredoxin-$NADP^+$-reductase (FNR)-like domain. NOSs function as N-terminal homodimers, whereby the NOS_{red} of one subunit reduces the NOS_{ox} of the opposite subunit (9). Electron transfer is activated by Ca^{2+}-loaded calmodulin (CaM) (10) that binds at a conserved sequence between NOS_{ox} and NOS_{red}, and is also facilitated by the essential cofactor tetrahydrobiopterin (H_4B) that acts to supply electrons to the NOS heme for

oxygen activation (11). Each of the mammalian NOS isoforms play key roles in many biological processes, such as vasoconstriction, immune response, and neuronal plasticity (12–14), and are also involved in several pathologies, including tumorigenesis, septic shock, and cerebral ischaemia (15–18).

Although NOS is ubiquitous in the animal kingdom, it is infrequently found in bacteria. The occurrence and purpose of bacterial NOS is highly species-dependent, ranging from recovery from UV damage (drNOS) (19), signaling biofilm formation (siliNOS) (20), protection from oxidative stress (bsNOS) (21), aiding pathogen virulence (baNOS) (22), and controlling oxygen-based respiration (saNOS) (23, 24). Although their heme domain structure and catalytic mechanisms are similar to that of mammalian NOS, most bacterial NOSs lack a dedicated reductase domain, instead relying on promiscuous cellular reductases (25, 26). One NOS found in *Sorangium cellulosum* has an N-terminal reductase domain containing a 2Fe-2S cluster and ferredoxin-like FAD and NADPH domain, dissimilar to mammalian NOS_{red} (27). No bacterial NOS with a covalently attached. FMN/FNR reductase domain has been biochemically characterized thus far.

NOSs are also found in photosynthetic organisms. A mammalian NOS homolog was characterized from the algae *Ostreococcus tauri* (otNOS) (28), which is intriguing because NOS has not yet been identified in higher plants, despite NO having an undisputed role in plant signaling (29). Recently, a mammalian-like NOS with a C-terminal P-450 reductase domain was identified in the photosynthetic diazotroph *Synechococcus* sp. PCC 7335 (syNOS) (30). SyNOS is the first prokaryotic NOS to contain a mammalian NOS_{red} homolog; in addition, syNOS contains a somewhat unusual globin domain (NOS_g) N-terminal to NOS_{ox}, as well as a 342 residue N-terminal region of unknown properties (Fig. S1). The syNOS-harboring *Synechococcus* strain was shown to produce NO in an arginine (L-arg) dependent manner and this activity was inhibited by known NOS inhibitors (30). Based on genetic experiments in *Synechococcus* and heterologous expression experiments in *E. coli*, syNOS was proposed to function in nitrogen utilization from L-arg (30). Specifically, this model asserts that syNOS first converts L-arg to NO with NOS_{ox}, and then from NO to NO_3^- with NOS_g. Nitrate would then be assimilated back into reduced forms of nitrogen. Herein we report the first recombinant expression, purification, and biochemical characterization of syNOS. The enzyme indeed acts as a bona fide NO synthase and also has strong NO dioxygenase (NOD) activity; however, it cannot utilize the general folate cofactor tetrahydrofolate as do other bacterial NOSs and instead requires tetrahydrobiopterin, like mammalian NOS. Although activation does not depend on CaM, it does strongly rely on Ca^{2+}. Importantly, syNOS does not appear to aid in nitrogen utilization from L-arg when recombinantly expressed in *E. coli* and also has minimal impact on NO detoxification.

Results

Expression, Purification and Oligomeric State of syNOS

Full-length syNOS (residues 1-1468) was co-expressed with the chaperonin GroEL/ES in *E. coli* BL21 DE3 cells; excess chaperonin was necessary to produce consistently well-folded and active enzyme. The yield (approximately 3 mg per liter of culture) and activity were very similar when the protein was expressed from two different vectors (pET28a or pCW-LIC). Affinity chromatography with ADP-sepharose targeting the reductase domain was more effective as a first purification step than with Ni-NTA resin targeting the His_6-tag. On size exclusion chromatography (SEC) syNOS eluted in two major peaks presumably corresponding to monomer and dimer (and a minor amount of aggregate) (Fig. 2A). Non-reducing SDS-PAGE of the trailing peak produced one band corresponding to the syNOS monomer at approximately 166 kDa whereas the second leading peak produced two bands, representing the monomer and the syNOS dimer (Fig. 2A inset). SEC coupled with multiangle light scattering (SEC-MALS) confirmed formation of a syNOS dimer and its sensitivity to factors known to influence NOS dimerization (Fig. 2B and C). The measured molecular weight of the first peak in the elution trace, 333 ± 4 kDa, equates to that of a syNOS dimer and the second peak, 191 ± 6 kDa, corresponds to the monomer. A small peak was also observed at intermediate mass between those of the dimer and monomer. The sample does not appear to suffer from contamination or

degradation, and thus this third peak may represent a third syNOS species in rapid oligomeric exchange. The addition of substrate or calcium did not significantly affect the population of dimer, however, H_4B modestly decreased the amount of dimer.

In order to isolate contributions from the two independent heme domains, variant proteins that removed key heme binding ligands were also expressed and purified in the same manner as the wild-type enzyme. The NOS_{ox} proximal cysteine (Cys539) was identified by alignment to NOS sequences (Fig. S1) and was substituted for alanine (C539A). The NOS_g ligating histidine was identified as His422 with sequence alignments to globins of known structure (Fig. S2) and was also substituted for alanine (H422A) in a separate variant. Heme content of the WT and each variant, measured with the pyridine hemochrome assay, indicated that the mutations substantially reduced heme binding in the targeted domains: syNOS 1.00 ± 0.10 μM heme per μM protein, H422A 0.39 ± 0.08, and C539A 0.72 ± 0.07 (Table S2). A syNOS variant with both heme ligand substitutions (H422A, C539A), bound very little heme (Table S2, Fig. S4). The sum of the heme content in the H422A and C539A variants approximately equaled that of the wild-type, therefore 39% of the syNOS Soret was attributed to the NOS_{ox} heme. The concentration of NOS_{ox} bound heme and the Soret intensity at 415 nm were used to calculate an extinction coefficient for quantifying active protein in subsequent assays.

Spectroscopic Properties

Purified syNOS has a Soret band at 415 nm, which is red-shifted compared to the ferric heme absorption of typical globins (~405 nm) and the high-spin thiol-ligated ferric heme of NOS_{ox} (~397 nm) (Fig. 3A). The Soret for the globin heme (the C539A variant) is observed at 413 nm (Fig. 3C), similar to a flavohemoglobin from *M. tuberculosis* (414 nm) (31, 32), and the NOS_{ox} heme Soret at 417 nm (Fig. 3B) is more similar that of the NOS protein from *S. cellulosum* (416 nm) (27). Broad □-bands characteristic of ferric globin-hemes are observed around 540 nm and 580 nm in all three proteins. A single band at ~550 nm, expected for a NOS-type heme, is not prominent in H422A, perhaps due to remaining globin heme and protonation or dissociation of the NOS_{ox} proximal cysteine to form an inactive P420 state (33, 34). After reduction with dithionite the Soret shifts to 425 nm and peaks at 530 and 560 nm are observed for syNOS and C539A; this is similar to spectra of hexacoordinate neuroglobin, known to oxidize NO to nitrate (35, 36). These peaks are not observed for H422A, indicating there is little globin heme bound in this variant. NOSs are thiolate-ligated P450-type heme proteins with a characteristic ferrous-CO Soret band at ~450 nm (37). For wild-type syNOS, this species was observed as a shoulder at 444 nm corresponding to the NOS_{ox} heme and another intense absorbance at 420 nm corresponding to the ferrous-CO NOS_g heme; however, the NOS_{ox} heme in the P420 state may also contribute to the intensity at 420 nm. As expected, H422A exhibits greater P450 Soret intensity at 444 nm compared to WT-syNOS, however there is still significant absorbance at 420 nm, most likely caused by the inactive P420 species. The ferrous CO-complex of C539A has no Soret peak at 444 nm and only a band from NOS_g is observed. These spectral features are evident in the Fe(II)CO - Fe(III) difference spectra (Fig. 3D).

Mammalian and bacterial NOSs primarily contain five-coordinate low-spin hemes that exhibit a shift to high-spin (Soret band at ~390 nm) upon binding L-Arg; such a Soret shift was difficult to observe in wild-type syNOS. However, H422A undergoes a blue shift to ~391 nm upon addition of excess L-arg (Fig. 3E). A large amount of L-arg (500 mM) is required for complete conversion. This far exceeds the observed Michaelis constant for L-arg (101 ± 12 μM, Fig. S3A) but may reflect the fact that without the globin domain the protein is destabilized (the activity drops by a factor of 8, see Table 1) and the NOS heme at least partially converts to the P420 state. Large amounts of L-arg may stabilize the protein fold and heme center in a non-specific manner so that a substrate-induced transition to a high-spin state can be observed. No Soret shift is observed when L-arg is added to the NOS_{ox} heme-deficient C539A variant.

Recombinant syNOS produces nitric oxide from L-arginine.

NO production by full-length syNOS was first measured through the detection of its oxidized products, nitrate and nitrite, with the Griess assay.

The specific activity of syNOS was 35.7 ± 5 nmol/min/mg (Table 1), approximately half that of the nNOS control 64.0 ± 2 nmol/min/mg, which is low compared to literature values (100 to 400 nmol/min/mg (37)). The syNOS C539A variant had very little measurable activity, and the activity of syNOS H422A was attenuated by about a factor of eight compared to wild-type, in keeping with the results above (Table 1). The loss of NOS activity due to the globin substitution H422A likely reflects a general destabilization of the full-length protein when the globin domain is disrupted.

syNOS activity requires L-arginine, H_4B, calcium, and NADPH (Table 1). Unlike analogous mammalian NOS, syNOS activity was independent of Ca^{2+}-calmodulin (bovine), perhaps not surprisingly given that the calmodulin binding site of mNOS is not conserved in syNOS (Fig. S1) and *Synechococcus* does not contain an obvious homolog of calmodulin. Remarkably, syNOS is substantially activated by calcium (>10-fold); in fact, activity was reduced in the presence of calmodulin, presumably due to competition for calcium. However, the apparent Michaelis constant for Ca^{2+} activation is 228 ± 9 μM (Fig. S3), which may indicate that Ca^{2+} serves as a proxy for another physiological factor that activates the enzyme at lower concentration. syNOS cofactor utilization also differs from other bacterial NOSs in that syNOS cannot substitute tetrahydrofolate (THF) for H_4B. The NOS inhibitors L-NNA and L-NAA, which mimic the substrate L-arg, completely inhibited syNOS. This is in keeping with previous observations that L-NAME inhibits syNOS *in vivo* (30) as L-NAME requires hydrolysis to L-NNA (typically by cellular esterases) for inhibition of NOS (38).

L-citrulline, the byproduct of L-arg based NO production, was detected as the product of the syNOS reaction with analytical HPLC (Fig. 4). After derivatization with the fluorophore ortho-phthaldialdehyde (OPA), samples were applied to a reverse-phase column, and citrulline (8.58 min) was resolved from substrate L-arg (13.34 min). The amount of citrulline detected by HPLC was roughly equivalent to the amount of NO_2^- + NO_3^- measured by Griess, 0.95: 1.

To directly detect NO production from syNOS, NO was chelated by the spin-trap Fe^{2+}-MGD and detected by continuous-wave ESR spectroscopy (Fig. 5). The NO releasing small molecule NOC-7 was used as a positive control. syNOS produced an NO signal identical to that of NOC-7. Moreover, addition of the spin trap reacted with nearly all of the product NO and prevented conversion to NO_2^- or NO_3^- (Table S1).

NOS_{ox} and NOS_g are both directly reduced by NOS_{red}

In mammalian NOS, NOS_{ox} is reduced by NOS_{red} and NADPH. To evaluate whether $syNOS_{red}$ can reduce $syNOS_{ox}$ and $syNOS_g$ independent of each other, the $syNOS_{ox}$ and $syNOS_g$ domains (residues 475-795 and residues 337-469, respectively) were cloned and expressed in isolation and then tested for their ability to accept electrons from NOS_{red} (residues 856–1468). In the case of NOS_{ox}, the reduction experiment was carried out in the presence of CO to trap the reduced heme as a characteristic thiolate-ligated Fe(II)-CO (Soret band at 444 nm). In the presence of NADPH, NOS_{red} produced some reduction of NOS_{ox} as indicated by a small Soret shift to 444 nm (Fig. 6A). However, Ca^{2+} addition substantially increased the reduced form relative to the inactive P420 form. Thus, either Ca^{2+} facilitates NOS_{ox} reduction by NOS_{red}, or Ca^{2+} attenuates the formation of the inactive P420 species through some means of NOS_{ox} stabilization.

Likewise, $syNOS_{red}$ and NADPH directly reduce $syNOS_g$, as indicated by the Soret shift to 426 nm and □-bands at 530 and 560 nm (Fig. 6B). The reductase domains of flavoHbs usually contain binding sites for FAD and NADH, but not FMN (39). Thus, either the FAD-containing FNR domain, or the flavodoxin-like FMN module of $syNOS_{red}$ could directly reduce NOS_g.

syNOS globin oxidizes NO to Nitrate

Upon assay of syNOS with the Griess reaction it was found that the enzyme produces primarily nitrate with little to no nitrite formed, despite nitrite being the initial product of NO oxidation by air. Because related flavohemoglobins detoxify NO to nitrate, $syNOS_g$ may function as a NO dioxygenase (NOD). Thus, we investigated the ability of NO generated by NOC-7 to be oxidized by syNOS (Table 2). NO was oxidized primarily to nitrate (74%) by syNOS in an NADPH dependent manner during the time

course of the experiment (NOS activity was stopped after 30 min, which equates to approximately three NOC-7 half-lives). Removal of the ligating cysteine from NOS_{ox} (C539A) did not decrease nitrate production, confirming NO dioxygenation by the globin heme. In contrast, removal of the proximal histidine from NOS_g did reduce NO_3^- production, but not completely. The H422A variant produced more nitrate than nonenzymatic oxidation by air, suggesting that the NOS_{ox} domain also oxidizes NO to nitrate, as has been found for mNOS (40).

The rate constants for dioxygenation by synNOS and variants were measured with an NO-specific electrode (Table 2). NOC-7 derived NO produced a measurable current on the order of microamperes. Upon addition of synNOS, the NO signal decayed rapidly under first order kinetics. Consistent with results from the Griess assay, the rate constant for NO oxidation by the C539A variant (0.6 ± 0.4 s^{-1} nanomole $heme^{-1}$) is approximately equal to that of WT-synNOS (0.6 ± 0.3 s^{-1} $nmole^{-1}$), and the rate constant of the H422A variant is far less than either (0.10 ± 0.06 s^{-1} $nmole^{-1}$). These results reveal that not only is NOS_g an efficient NOD, but confirm that NOS_{red} directly reduces both the NOS_{ox} and NOS_g heme cofactors.

Activity of synNOS in E. coli cells.

It was previously reported that synNOS enabled *E. coli* to use L-arg as its sole nitrogen source, and that expression of synNOS increased cell density when growing on L-arg, compared to an empty vector (EV) control (30). Under our conditions this benefit of synNOS was not observed; instead we found that synNOS expression conferred no significant advantage for growth on L-arg compared to the EV control (Fig. 7A). Given that synNOS requires H_4B for NO production from L-arg, and *E. coli* does not make H_4B (41), it is unclear how expression of synNOS would increase conversion of L-arg to more oxidized forms of nitrogen, such as nitrate.

Although synNOS should not be active as a NOS when recombinantly expressed in *E. coli*, it should retain NOD activity, which may mitigate the effects of nitrosative stress. To test the ability of recombinant synNOS to protect *E. coli* against NO, synNOS and the NOD deficient variant H422A were expressed from the tac promoter (pCW-LIC) in a WT *E. coli* strain BW25113, as well as the flavohemoglobin deficient strain JW2536. The absence of the flavohemoglobin gene (Δ*hmp*) renders *E. coli* more sensitive to NO (42), and the addition of a NOD should, in theory, allow growth at higher NO concentrations. However, this was not observed (Fig 6B and C). The Δ*hmp* strain is more sensitive to nitrosative stress induced by addition of DETA-NONOate than the WT, but the added expression of synNOS actually increased sensitivity to NO. Additionally, the growth of cells containing the NOD deficient H422A construct was indistinguishable from those containing wild-type synNOS. Thus, synNOS cannot complement a *hmp* mutant of *E. coli*, indicating that its NOD activity in this context is low.

Discussion

Full length synNOS proved to be a challenging protein to express recombinantly in *E. coli*. Although soluble protein with heme and flavin cofactors bound could be produced under several conditions, many attempts at purification produced protein with little or no synthase activity. Furthermore, active and inactive synNOS share the same spectroscopic characteristics and elute similarly on SEC. Co-expression with the chaperonin GroEL/ES was essential to consistently produce active protein. *E. coli* encodes GroEL/ES and several other chaperones in its genome; however, their basal level of expression was insufficient to reliably correct synNOS misfolding.

Biochemical and spectroscopic results confirm synNOS is a genuine NOS and NOD. The NOS_{ox} ferrous-carbonmonoxy species is observed at 444 nm, as expected of a P450 type heme. In the absence of the NOS_{ox} heme, nitric oxide is not produced and in the absence of the NOS_g heme the amount of NO dioxygenation is attenuated. synNOS shares the same substrate, products, and activating cofactors expected of a mammalian NOS, however, there are several unusual facets of synNOS enzymology.

A feature that distinguishes synNOS from animal NOSs is the absence of the calmodulin-binding sequence and auto-inhibitory loop. All three mammalian NOS isoforms require Ca^{2+}-CaM, and in eNOS and nNOS the calcium concentration dependence is dictated by the presence of an auto-inhibitory loop in the FMN

domain (43, 44). Although syNOS does not bind mammalian calmodulin (and no protein in its genome has significant similarity to calmodulin), the addition of calcium increases NO turnover tenfold. Moreover, NOS_{ox} reduction by NOS_{red} is substantially enhanced by Ca^{2+} and thus Ca^{2+} alone may be playing a similar role in syNOS as Ca^{2+}-CaM does in mNOS. No other NOS has been reported to be activated by calcium independent of calmodulin. The Swiss Institute for Bioinformatics ScanProsite tool was used to search for possible EF-hand calcium binding motifs (Prosite accession numbers PS50222, PS00018) in syNOS, but no such sites were identified. It is possible that calcium may have a structural role, perhaps at the dimer interface, similar to zinc in mammalian NOS (45, 46), or at inter-domain contacts to facilitate electron transfer to the NOS_{ox} heme. However, the measured activation constant for calcium was high, 228 ± 9 μM, far exceeding biological concentration ranges (hundreds of nanomolar to 10 micromolar (47, 48)). The mechanism of calcium binding and activation of syNOS is currently unknown; additional cofactors or proteins may be required for efficient calcium use, or Ca^{2+} may serve as a proxy for another factor *in vivo*.

Cofactor utilization also differentiates syNOS from other bacterial NOSs. All bacteria produce THF, but few produce H_4B, which differs from THF in its dihydroxypropyl side chain. All bacterial NOSs characterized to date can utilize both cofactors, and thus the preference of syNOS for H_4B over THF confers with its mammalian-like NOS domain architecture. Genome analysis suggests that *Synechococcus* sp. PCC 7335 can produce H_4B. The H_4B biosynthetic pathway requires GTP cyclohydrolase I (GTPCH I), 6-pyruvoyl tetrahydropterin synthase (PTS), and sepiapterin reductase (SR) (49, 50). Both GTPCH and PTS are found in the genome of *Synechococcus* sp. PCC 7335 and are highly homologous to the mammalian enzymes (>50% identity), however no gene in *Synechococcus* is annotated as a SR. SR belongs to the short-chain dehydrogenase/reductase (SDR) family of oxidoreductases, a large family of proteins found in all kingdoms of life (51). *Synechococcus* encodes many genes belonging to the SDR family. Although none share high sequence similarity (greater than 30% identity) with mammalian SR, one gene annotated as an SDR (CDS YP_002711555.1) is immediately adjacent to a gene encoding GTPCH I. Additionally, of the fifteen photosynthetic prokaryotes containing gene sequences highly similar to syNOS (greater than 60% identity) fourteen also encode an SDR adjacent to a GTPCH I. Thus, it is highly likely that *Synechococcus* has the enzymatic machinery to produce H_4B.

Mammalian NOSs cannot use THF because an N-terminal β-extension, known as the N-terminal hook, occludes the long THF p-aminobenzoyl-glutamate side chain (52). In syNOS, this region is replaced by a short linker (18 residues) to the globin domain. This raises questions concerning not only the manner of selective H_4B binding, but also the manner of $syNOS_{ox}$ dimer formation and coupling to NOS_g. The NOS_{ox} motifs located at the dimer interface in other NOS, the helical lariat and helical T (52), are conserved in syNOS however, the close proximity of NOS_g suggests it could also play a role in stabilizing the NOS_{ox} subunit, as well as the NOS_{ox} dimer. In support of a tight coupling between NOS_{ox} and NOS_g, the H422A substitution in NOS_g appears to also affect the stability of NOS_{ox} and/or its affinity for L-arg.

In addition to structural implications, the NOS_g domain adds a layer of complexity to syNOS chemistry and physiology. Sequence alignments assign this domain to the globin superfamily of proteins. In particular, flavoHbs catalyze reduction of nitrite to nitric oxide and reduction of nitric oxide to nitrous oxide (53), but most commonly carry out the oxidation of NO to nitrate (39, 54). syNOS catalyzes the oxidation of NO to nitrate and this activity depends on a functional globin domain. Removal of the NOS_{ox} heme (the C539A variant) did not hinder NO oxidation, however, the NOS_{ox} domain was also capable of NO dioxygenation because nitrate production was still observed in the absence of the NOS_g heme (H422A). NO dioxygenase activity by NOS enzymes has precedent; mammalian NOSs are also capable of NO dioxygenation, and chimeras composed of $iNOS_{ox}$ and $nNOS_{red}$ exhibit increased NOD activity (40). By producing chimeras that coupled the fast heme reduction (k_r) of nNOS with the slow NO dissociation (k_d) of iNOS, as well as the addition of a V346I substitution that further slowed the NO release

(55), NO dioxygenation by mNOS was substantially accelerated (40). Note that in syNOS the equivalent position of V346 in the distal heme pocket contains Ile natively, typical of bacterial NOS. The NO dioxygenase activity of syNOS has two implications; i) syNOS is the first NOS whose final product can be nitrate and not NO, and ii) the reductase domain of syNOS can reduce both the NOS_{ox} and NOS_g directly. It is also worth noting that the spin trap compound intercepted nearly all NO from syNOS before it could be oxidized to NO_3^- by NOS_g. Thus, NOD activity in syNOS is independent from NOS activity, with any NO produced by NOS_{ox} released to the solution before reaction with NOS_g.

Our biochemical results confirm that syNOS oxidizes L-arg to nitrate (30); however, we are unable to replicate the finding that syNOS allows *E. coli* to use L-arg as the sole nitrogen source. The growth of *E. coli* transformed with empty vector is indistinguishable from that transformed with syNOS. Both strains are capable of growth on L-arg which is not surprising given that *E. coli* already contains the arginine succinyl transferase pathway (AST) to derive reduced nitrogen from arginine (56, 57). Although *Synechococcus* does not contain the AST pathway, it does contain alternate L-arg salvage pathways, that rely on enzymes such as arginase and deaminating L-amino acid oxidases (58, 59)). Furthermore, syNOS is not expected to be active in *E. coli* as the third enzyme in the H_4B biosynthesis pathway, sepiapterin reductase, is absent from its genome (41) and syNOS cannot substitute H_4B with THF. The proposed role of syNOS in nitrogen assimilation is somewhat questionable given the environmental conditions in which the cyanobacteria are found. *Synechococcus* sp. PCC 7335 is a marine organism, where the concentrations of dissolved nitrates (tens of micromolar (60–62)) far exceeds that of arginine in (tens of nanomolar (63–65)). Additionally, this organism is capable of nitrogen fixation (66–68). It is unclear what biochemical merits result from expending reducing power (NADPH) to oxidize L-arg to nitrate, only to then reductively assimilate nitrate back to ammonia.

Owing to the lack of H_4B, $syNOS_{ox}$ should be inactive in *E. coli*. However, $syNOS_g$ and $syNOS_{red}$ do not depend on specialized cofactors and thus syNOS may function as an NO dioxygenase in *E. coli.* However, the flavohemoglobin deficient strain (JW2536) containing syNOS is actually more susceptible to damage by NO than compared to the untransformed control. If syNOS was functioning as a flavoHb we would expect the opposite. Thus, either the protein does not exhibit NOD activity in *E. coli* because of interfering cellular factors, or it has other additional activities that are detrimental to growth that overcome any benefit of NO oxidation to nitrate.

The dual functionality of syNOS as both a NOS and a NOD is mysterious. As syNOS is actively expressed in growing cyanobacteria (30) some regulatory mechanism or "on/off switch" may be necessary to control NO production. NOS_g may participate in such a function. Globin-based regulation of NOS has precedent in animals; eNOS binds to and stabilizes α-globin at the myoendothelial junction so that α-globin can regulate NO signaling by oxidizing NO to nitrate (69). Additionally, *in vitro* experiments found full-length eNOS was able to reduce α-globin to the active ferrous state at a faster rate than the methemoglobin reductase cytochrome B5 reductase (69).

In *S. aureus*, NOS is proposed to play a role in the transition from aerobic respiration to nitrate respiration under microaerobic conditions (23). This control is mediated by the combined action of NOS and flavoHb; at high oxygen concentrations NOS-derived NO is detoxified by flavoHb, whereas under microaerobic conditions flavoHb cannot bind oxygen as substrate and NO is free to inhibit cytochrome oxidase, thus inhibiting oxygen reduction and favoring nitrate respiration. Although syNOS would genetically link NOS and NOD activity for such a purpose, the NOS-containing *Synechococcus* species does not respire nitrate (as it lacks ccNIR and associated *nrf* genes). Finally, a feature of syNOS activity that may provide clues as to its biological function is its reliance on calcium, which is well-known to be a tightly regulated signaling molecule in cyanobacteria (47, 70). Interestingly, Ca^{2+} is used in cyanobacteria as a signal to convey changes in nitrogen utilization. Increased levels of calcium in *Synechoccocus elongatus* accompany acclimation to nitrogen starvation (71), and in *Anabaena* sp. PCC 7120 elevated calcium levels are necessary for heterocyst differentiation (72).

Thus, syNOS may be poised to respond to these signals. The high Ca^{2+} threshold that we observe in our assays is not without note but may be a consequence of the *ex vivo* conditions.

In conclusion, we demonstrate that syNOS has both NOS and NOD activities. The protein represents a bacterial NOS enzyme with properties closely related to its mNOS counterparts, especially with respect to reductase coupling and cofactor utilization. However, the NOS function is not activated by Ca^{2+}-CaM and instead appears to require only Ca^{2+} for activity. The enzyme's reliance on H_4B calls into question any NOS activity when recombinantly expressed in *E. coli*, and likewise the protein is unable to aid a flavoHb null strain in tolerating nitrosative stress. The properties of syNOS in the context of *Synechococcus* metabolism suggest that it is unlikely to be solely involved in nitrogen utilization from arginine and may serve a more typical NOS function in signal transduction. That said, the coupling of NOS and NOD activity in a single protein indicates a genetic link between these respective activities that is beneficial to cyanobacteria.

Experimental Methods

Materials

Synechococcus PCC 7335 (ATCC 29403) was purchased from the American Type Culture Collection. *E. coli* strain JW2536 was purchased from Dharmacon and BW25113 was from the Coli Genetic Stock Center at Yale University. NOC-7 and N-(dithiocarbamoyl)-N-methyl-D-glucamine (MGD) were purchased from Santa Cruz Biotechnology. Nitrate reductase was purchase from Roche. L-NNA, L-NAA, L-citrulline, N-hydroxy arginine, and ortho-phthaldialdehyde (OPA) were purchased from Sigma-Aldrich. Tetrahydrobiopterin (H_4B) was purchased from Cayman Chemical. 2',5' ADP Sepharose 4B and Superdex 200 resins was purchased from GE Healthcare Life Sciences. Ni-NTA was purchased from Thermo Scientific.

Genomic DNA extraction, cloning

Genomic DNA extraction was performed following the method of Singh et al (73). *Synechococcus* (50 mL) was grown for one week and then harvested by centrifugation at 2000 G. Cells were resuspended in 400 µL of lysis buffer (4 M urea, 0.2 M TRIS, pH 7.4, 20 mM NaCl, 0.2 M EDTA) supplemented with 50 µL of 20 mg/mL proteinase K. The sample was incubated for one hour at 55 °C and mixed by gentle inversion every 15 min. One mL of the extraction buffer (3% CTAB, 1.4 M NaCl, 20 mM EDTA, 0.1 M TRIS, pH 8.0, 1% sarkosyl) heated to 55 °C was added to the sample. The resulting sample was subsequently incubated at 55 °C for one hour with gentle inversion every ten min. Once the sample cooled to room temperature, two volumes of chloroform/isoamyl alcohol (24:1) solution were added and the sample was mixed by inversion. The sample was centrifuged for five min at 10,000 G and the upper aqueous phase was removed. Two volumes of ethanol + 0.1 volumes 3 M sodium acetate (pH 5.2) were added to the aqueous phase. This was incubated at -20 °C for one hour, then centrifuged for three min at 10,000 G. The pellet was washed with 500 µL cold 70% ethanol. After evaporating the ethanol, the DNA was dissolved in 50 µL water, and the purity was assessed by the absorbance ratio 260 nm/280 nm.

Full-length syNOS (residues 1 - 1468, NCBI Protein database accession number WP_006458277) was cloned from base pair 486069 to 490475 (NCBI Nucleotide database accession number NZ_DS989905) and inserted into the following vectors: 1) pET28 (Novagen) using the restriction sites NdeI and EcoRI, and 2) pCW-LIC (a gift from Cheryl Arrowsmith, Addgene plasmid # 26098) using BamHI and KpnI. Point mutations were constructed by primer overlap extension PCR.

Each domain of syNOS was subcloned into expression vectors by PCR. NOS_g (residues 337-469), NOS_{ox} (residues 475-795), and NOS_{red} (residues 856-1468) were inserted into the vector pET28 using the restriction sites NdeI and XhoI.

Protein expression and purification

E. coli BL21 DE3 cells were cotransformed with syNOS (in either pCW-LIC or pET28) or its heme domain truncations, plus the chaperonins GroEL/ES in pACYCDuet. The reductase domain truncation was transformed into BL21 DE3 without GroEL/ES. Lysogeny broth Miller was inoculated with an overnight culture

and incubated at 37 °C until the $OD_{600\ nm}$ reached ~0.6. Protein expression was induced by the addition of 25 μg/mL isopropyl β-D-1-thiogalactopyranoside (IPTG), 80 μg/mL δ-aminolevulinic acid, 4 μg/mL hemin, 2 μg/mL flavin adenine dinucleotide (FAD), 2 μg/mL flavin mononucleotide (FMN), and incubated at 17 °C overnight. Hemin and δ-aminolevulinic acid were excluded from NOS_{red} expression, and flavins were excluded from the expression of either heme domain. Cells were harvested 18 hours after induction by centrifugation at 5,000 G, then frozen at -20 °C.

The cell pellet from a 2 L growth was resuspended in 50 mL lysis buffer (200 mM NaCl, 50 mM TRIS, pH 7.5, 10% glycerol) with 174 μg/mL phenylmethylsulfonyl fluoride (PMSF), 1.5 μg/mL pepstatin A, and 1 μg/mL leupeptin. Cells were lysed on ice by sonication using a Fisher Scientific Sonic Dismembrator 550 (amplitude of 7, pulsed 2 sec on, 2 sec off) for a total sonication time of five min. Lysate was centrifuged for one hour at 48,000 G at 4 °C. For the full-length constructs the soluble portion was applied in batch to a 2',5' ADP Sepharose resin pre-equilibrated with lysis buffer and then incubated at 4 °C for two hours with gentle rocking. The resin was collected and washed with five column volumes of lysis buffer, then eluted with 5 mM NADPH. Domain truncations were lysed in the same manner, with 5 mM imidazole in the lysis buffer. After centrifugation, the soluble portion was applied to Ni-NTA and the resin was washed with five column volumes of lysis buffer with 20 mM imidazole, then eluted with lysis buffer plus 200 mM imidazole.

The eluent was concentrated, then further purified on a Superdex 200 (full-length constructs) or 75 (truncations) 26/60 size exclusion column by isocratic elution using gel filtration buffer (25 mM TRIS pH 7.5, 150 mM NaCl, 10% glycerol). Protein was concentrated using a 50 kDa (full-length constructs) or 10 kDa (truncations) cutoff Amicon Ultra centrifugal filter.

Multiangle Light Scattering

MALS was performed using a Phenomenex BioSep SEC-s3000 column (5 μm, 290 Å, 300 mm × 7.8 mm) with a Phenomenex SecurityGuard guard column, connected to an Agilent 1200 series HPLC with G1314D variable wavelength detector. Light scattering was detected using a Wyatt DAWN HELEOS-II and dRI measured by a Wyatt Optilab T-rEX refractometer. The mobile phase contained 100 mM TRIS, pH 7.5, 200 mM NaCl with either 5 mM arginine, 5 mM $CaCl_2$, or 250 μM H_4B with 1.5 mM DTT. A solution of bovine serum albumin (BSA) monomer (5 mg/mL) was used as the standard to control for peak alignment and molecular weight calculations. Data were collected for 30 min at a flow rate of 1 mL/min at 25 °C. ASTRA V software was used to analyze the molecular weight and polydispersity of each peak.

UV-vis analysis of purified syNOS

Heme content was measured using the pyridine hemochrome method. Twenty microliters of protein at 1 mg/mL were diluted to 100 μL in 20% pyridine 0.2 M NaOH. An Agilent 8453 UV-vis spectrophotometer was blanked with this solution, then ~ 0.5 mg solid dithionite was added and the absorbance difference at 557 - 573 nm was recorded (extinction coefficient 32.4 $mM^{-1}\ cm^{-1}$). Protein concentration was measured using the Bradford assay (Bio-Rad protein assay dye) and the calculated extinction coefficient of the denatured protein ($\varepsilon_{280\ nm}$ = 0.24053 $\mu M^{-1}\ cm^{-1}$). The protein was denatured in 4 M urea, then unbound cofactors were removed by concentrating in a spin column and diluting in 4 M urea, which was repeated three times. The protein concentration calculated from the absorbance at 280 nm agreed with that of the Bradford assay.

As syNOS does not appear to be fully loaded with heme, the concentration of active protein was estimated based on the amount of NOS_{oxy} heme bound in the H422A variant. The heme concentration of a syNOS sample was measured as stated previously, and the Soret intensity at 415 nm was recorded. Thirty-nine percent of the measured heme concentration was presumed to originate from the NOS_{oxy} heme, and thus represents the concentration of active protein.

This concentration and the Soret intensity were used to calculate an extinction coefficient that was used to quantify active protein in subsequent assays.

The spectra for the ferrous and ferrous-carbonmonoxy syNOS were taken after the ferric enzyme was sparged with argon and reduced with ~ 0.5 mg solid dithionite, then carbon monoxide gas was gently bubbled into the solution. Difference spectra were constructed by subtracting the spectrum of the ferric species from that of the ferrous-carbonmonoxy species.

NOS enzymatic reaction

NOS activity was assayed following the method of Moreau et al (74), using 250 µM H_4B, 5 mM arginine, 5 mM $CaCl_2$, 1.5 mM DTT, and 1 mM NADPH in 100 mM TRIS, pH 7.5, 200 mM NaCl. Where specified, THF was used at 250 µM, and CaM at 10 µg/mL. The reaction proceeded for 30 min at room temperature and was stopped by rapid heating to 60−70 °C for five min. Samples were centrifuged at 16,000 G for five min to remove any insoluble debris.

Nitrate and nitrite measurement by Griess assay

Nitrate was measured by adding 75 µL 0.2 U/mL nitrate reductase, 1 mM NADPH, and 0.1 mM FAD to 150 µL of sample, then incubated for two hours at 37 °C. Nitrite was quantified similarly but in the absence of nitrate reductase. NADPH was removed by zinc acetate precipitation (75, 76). To each sample 100 µL 0.5 M zinc acetate in 50% ethanol was added and the samples were vortexed. Subsequently, 100 µL 0.5 M sodium carbonate was added, followed by vortexing. After five min of centrifugation at 16,000 G, 150 µL of each sample were plated in duplicate and 25 µL 2% sulfanilamide 1 M HCl were added, followed by 25 µL 0.2% naphthyl-ethylenediamine. The absorbance at 540 nm was recorded immediately afterwards using a Biotek Synergy HT plate reader. A standard curve was prepared from nitrate and nitrite standards under the same conditions as the experimental samples. The standard curve was used to convert the absorbance at 540 nm to concentration.

HPLC product detection

The NOS reaction was performed as stated above, with the substitution of 50 mM HEPES (pH 7.5) for TRIS. HPLC detection of derivatized citrulline was performed using the method of Davydov et al (77) with the following modifications. Using an Agilent 1100 series HPLC equipped with an Agilent 1260 fluorescence detector, an Agilent Eclipse Plus reverse phase column (150 mm × 4.6 mm; equipped with a Supelguard LC-18-DB guard column) was equilibrated with 50 mM trichloroacetic acid (pH 4.0) and 15% acetonitrile at 1 mL/min. The derivatization agent ortho-phthaldialdehyde (OPA) was dissolved in methanol (8 mg/mL), then 100 µL of the OPA reagent was added to 900 µL of 100 mM sodium borate (pH 10.0) and 6 µL β-mercapto ethanol. Then, 20 µL OPA was added to 10 µL filtered sample. Following three min of incubation at room temperature, the mixture was injected onto the column. After injection, the concentration of acetonitrile was increased to 25% over 20 min and fluorescence was detected at $\lambda_{excitation}$= 360 nm and $\lambda_{emission}$= 455 nm. Derivatized citrulline eluted at 8.58 min, followed by NOHA at 12.01 min, and L-arg 13.34 min. A standard curve was prepared from citrulline standards under the same conditions as the experimental samples. The standard curve was used to convert the peak area to concentration.

Fe-MGD spin trap and ESR detection

The NOS reaction was performed as stated above, with the addition of 0.7 mM iron (II) sulfate and 2.7 mM MGD (78). After reacting for 30 min at room temperature glycerol was added to the sample to 15% w/v. The sample was immediately transferred to an X-band electron spin resonance (ESR) tube, and flash frozen in liquid nitrogen. Continuous-wave ESR spectra were acquired using a Bruker Elexsys E500 CW ESR spectrometer with an ER4131VT variable temperature unit at 150 K and 9.4 GHz, with a modulation amplitude of 1.5 G and modulation frequency of 100 kHz.

NO detection by electrochemistry

NO oxidation was measured using an Innovated Instruments amiNO-2000 electrode and a CH Instruments Electrochemical Analyzer CH1630B potentiostat. The electrode was submerged in buffer (100 mM TRIS, pH 7.5, 200 mM NaCl, 1 mM NADPH) while stirring, and a 0.85 V potential was applied for about five min to prime the electrode. Data collection was initiated, and the current was measured at a sampling interval of two per sec. The baseline current was recorded for about five min. Upon baseline stabilization, 10 μM NOC-7 was added and the current was allowed to plateau (about five min). syNOS was then added to initiate NO oxidation and data collection continued for approximately ten min. Signal decay was fit to a mono exponential equation using Matlab and the rate constants were extracted.

Reduction of NOS_g and NOS_{ox} by NOS_{red}

All solutions were sparged with argon then degassed in an anaerobic COY chamber for six hours. NOS_{ox} was added to two molar equivalents of NOS_{red} and 1 mM NADPH, with or without 5 mM $CaCl_2$. NOS_g was added to two molar equivalents of NOS_{red} with 1 mM NADPH. Samples were transferred to an anaerobic cuvette and the absorbance spectra were recorded before and after sparging with carbon monoxide.

Minimal media growth assay

The growth assay described by Lamattina et al (30) was carried out with the following modifications. *E. coli* BL21 (DE3) pLysS cells were transformed with either pET-28a containing syNOS or the empty vector. Ten milliliters of LB broth were inoculated with 100 μL of an overnight culture, with 50 μg/mL kanamycin and 30 μ/mL chloramphenicol, and the culture was incubated at 37 °C until the $OD_{600\ nm}$ was approximately 0.3-0.4. Protein expression was induced with 0.1 mM IPTG, 500 μM δ-aminolevulinic acid, and 1 mM arginine, and incubated at 37 °C for 1.5 hours. Cells were pelleted by centrifugation at 2000 G for ten min then washed three times with five milliliters of minimal media (5.44 g KH_2PO_4, 2 g glucose, and 6 ml salt solution dissolved in one liter of distilled water, pH 7.4; The salt solution contained 10 g $MgSO_4 \cdot 7H_2O$, 1.0 g $MnCl_2 \cdot 4H_2O$, 0.4 g $FeSO_4 \cdot 7H_2O$ and 0.1 g $CaCl_2 \cdot 2H_2O$ dissolved in one liter of distilled water). The cells were resuspended in minimal media and supplemented with 0.1 mM IPTG, 500 μM δ-aminolevulinic acid, and 1 mM arginine in an effort to maintain the conditions specified by Lamattina et al (30). The culture was diluted 1/100 in minimal media containing either 0.2% w/v arginine, 0.3% NH_4Cl, or 0.018% NH_4Cl and incubated at 37 °C. (Washing with minimal media was strictly required; the 1/100 dilution in minimal media contained enough nitrogen to allow for significant growth.) $OD_{600\ nm}$ was recorded using an Agilent 8453 UV-vis spectrophotometer to monitor cell density.

NO minimum inhibitory concentration

The vector pCW-LIC containing syNOS was transformed into cells of the flavohemoglobin deficient *E. coli* strain JW2536 or of the wild-type strain BW25113. LB containing 100 μg/mL ampicillin (and 50 μg/mL kanamycin for strain JW2536) was inoculated with an overnight culture (1:200 dilution) and incubated at 37 °C until the $OD_{600\ nm}$ was approximately 0.6. Cells were diluted to 10^6 CFU/mL ($OD_{600\ nm}$ 1 = 10^8 colony forming units/mL) in LB supplemented with antibiotics and 0, 6.25, 12.5, or 25 μg/mL IPTG. DETA nonoate was diluted in 10 mM NaOH, and 20 uL of each dilution was added to 180 uL of each solution of cells in a 96 well plate. Final concentrations of DETA NONOate were 2.7, 1.35, 0.675, 0.338, 0.169, 0.084, 0.042, and 0 mM. Microplates were wrapped with parafilm to prevent excess evaporation and incubated at 37 °C for 18 hours. The $OD_{600\ nm}$ was recorded using a Biotek Synergy HT plate reader.

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FOOTNOTES

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Abbreviations: AST, arginine succinyl transferase pathway; baNOS, *Bacillus anthracis* nitric oxide synthase; bsNOS, *Bacillus subtilis* nitric oxide synthase; CaM, calmodulin; CO, carbon monoxide; drNOS, *Deinococcus radiodurans* nitric oxide synthase; FAD, flavin adenine dinucleotide; FMN, flavin mononucleotide; FNR, ferredoxin-$NADP^+$ reductase; GTPCH I, guanosine triphosphate cyclohydrolase I; H_4B, (6R,1'R,2'S)-5,6,7,8-tetrahydrobiopterin; iNOS, inducible nitric oxide synthase; L-arg, L-arginine; L-Cit, L-citrulline; L-NAA, N^G-amino-L-arginine; L-NAME, N^G-nitro-L-arginine methyl ester; L-NNA

N^G-nitro-L-arginine; mNOS, mammalian NOS; NADPH, nicotinamide adenine dinucleotide phosphate; NOD, nitric oxide dioxygenase; NOHA, N-hydroxy-L-arginine; nNOS, neuronal NOS; NO, nitric oxide; NOS, nitric oxide synthase; NOS_g, nitric oxide synthase globin domain; $NOS_{g/ox}$, nitric oxide synthase globin and oxygenase domains; NOS_{ox}, nitric oxide synthase oxygenase domain; $NOS_{ox/red}$, nitric oxide synthase oxygenase and reductase domains; NOS_{red}, nitric oxide synthase reductase domain; OPA, *o*-phthaldialdehyde; PTS, 6-pyruvoyl tetrahydrobiopterin synthase; saNOS, *Staphylococcus aureus* nitric oxide synthase; siliNOS, *Silicibacter* nitric oxide synthase; scNOS, *Sorangium cellulosum* nitric oxide synthase; SDR, short-chain dehydrogenase/reductase; SR, sepiapterin reductase; syNOS, *Synechococcus* sp. PCC 7335 nitric oxide synthase; THF, tetrahydrofolate

	Ca^{2+}, H_4B	Ca^{2+}, H_4B, CaM	H_4B	Ca^{2+}, THF	Ca^{2+}, H_4B, L-NNA	Ca^{2+}, H_4B, L-NAA
syNOS	36 ± 5, 34 ± 9*	14.8 ± 1.0	ND	ND	ND	ND
H422A	4.6 ± 0.8					
C539A	0.5 ± 0.2					
nNOS	1.0 ± 0.2	64 ± 2				

Table 1: Specific activity of syNOS, performed using the Griess assay to measure NO_2^- + NO_3^-. Citrulline was quantified with HPLC when indicated with an asterisk (*). ND, no product detected.

	Griess Method		NO oxidation rate constant
	% NO_2^-	% NO_3^-	(s^{-1} nanomole $heme^{-1}$)
syNOS	25.6 ± 0.6	74 ± 2	0.6 ± 0.3
H422A	44.6 ± 1.6	55 ± 3	0.10 ± 0.06
C539A	29.0 ± 1.6	71 ± 7	0.6 ± 0.4
no NADPH	76 ± 3	23 ± 3	ND

Table 2: NO dioxygenation by syNOS (0.5 μM), H422A (1 μM), and C539A (0.5 μM). Samples were incubated for 30 min in the presence of the NO donor NOC-7 before heat denaturing. Percent NO oxidized to NO_2^- + NO_3^- was measured by the Griess assay. The rate constants for NOD activity were measured with an NO electrode. The rate constants were averages of at least nine measurements and a Q test was used to remove outliers. Student's t-test indicated a significant difference between the rate constants of syNOS and H422A ($p < 0.001$) and between H422A and C539A ($p < 0.001$), but no significant difference between syNOS and C539A ($p > 0.7$). ND, not determined.

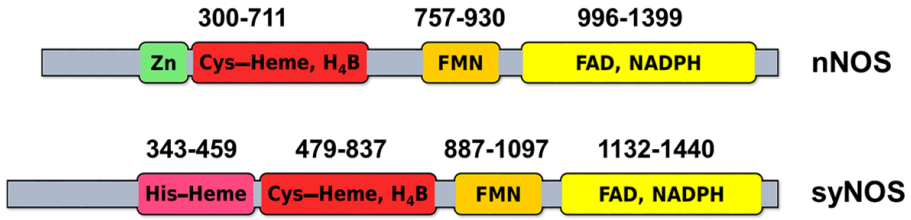


Figure 1: Domain map of nNOS and syNOS. The flavin and heme domains typical of nNOS are also present in syNOS, however the zinc ligating cysteines (Cys327 and Cys332 in nNOS) are absent from syNOS. Instead syNOS also contains a globin domain not found in typical NOSs.

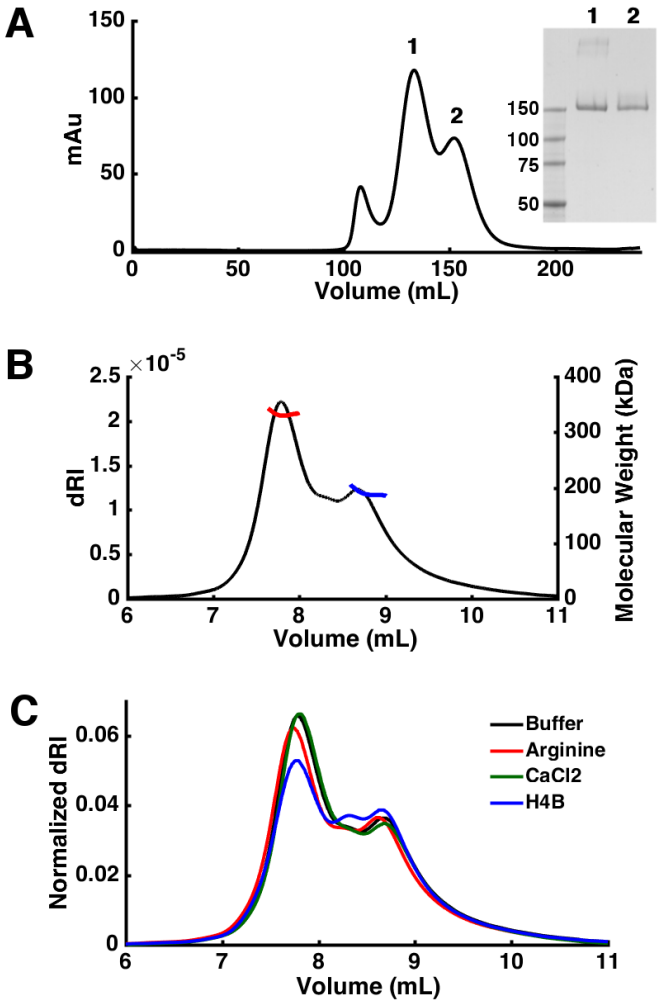


Figure 2: Hydrodynamic properties of syNOS. (A) Elution profiles syNOS on SEC. Inset is SDS-page of peaks 1 and 2. (B) SEC-MALS of syNOS; dimer (red line) 333 ± 4 kDa, and monomer (blue line) 191 ± 6 kDa. (C) SEC-MALS of syNOS in the presence of arginine (red line) Ca^{2+} (green line) or H_4B (blue line).

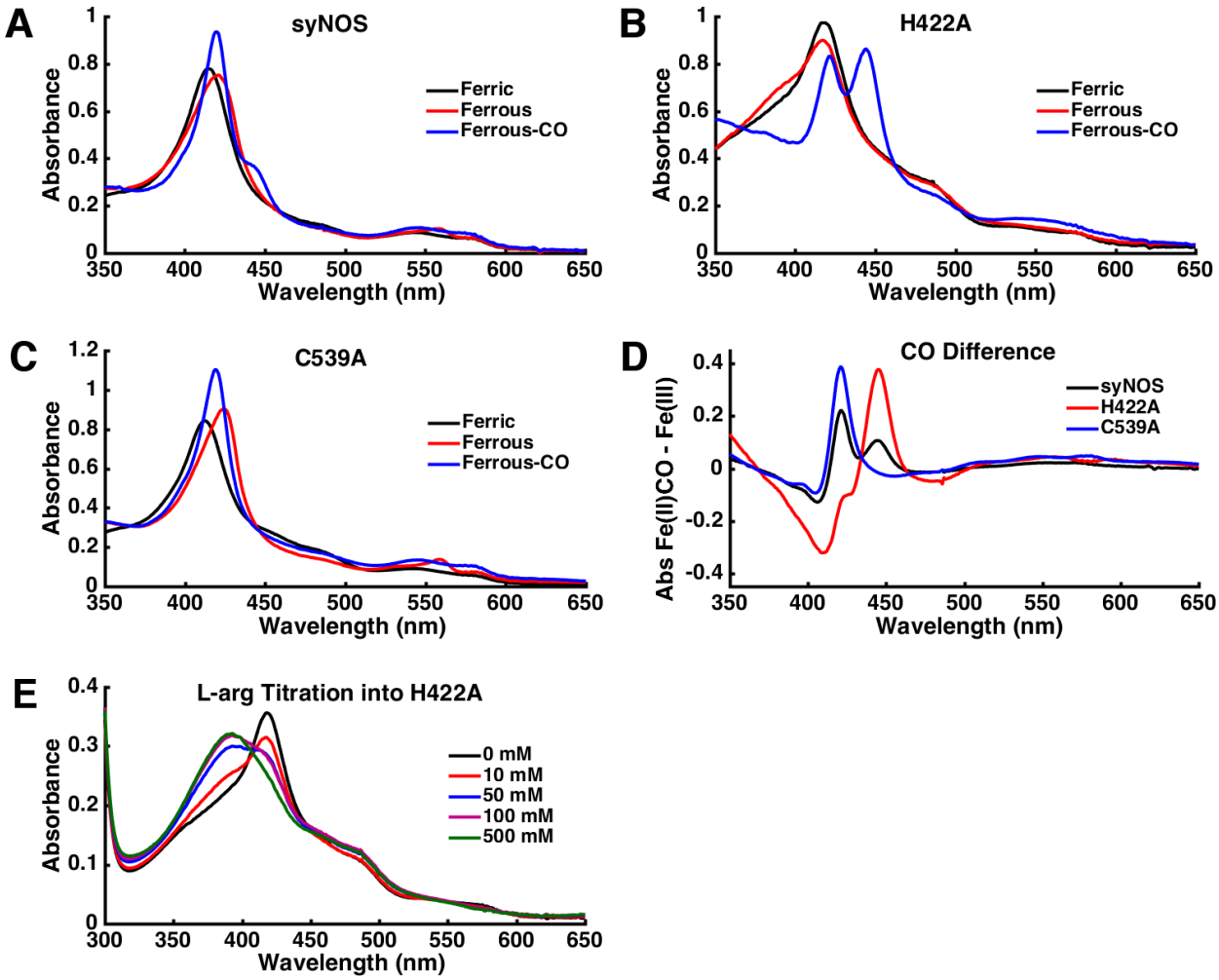


Figure 3: UV-vis spectra of (A) WT syNOS, (B) H422A, and (C) C539A in the ferric (black), ferrous (red), or ferrous-CO (blue) state. Samples were purged with argon before reduction with dithionite. (D) Difference spectrum of the ferrous-CO minus the ferric form of syNOS (black), H422A (red), and C539A (blue). (E) Arginine titration into H422A.

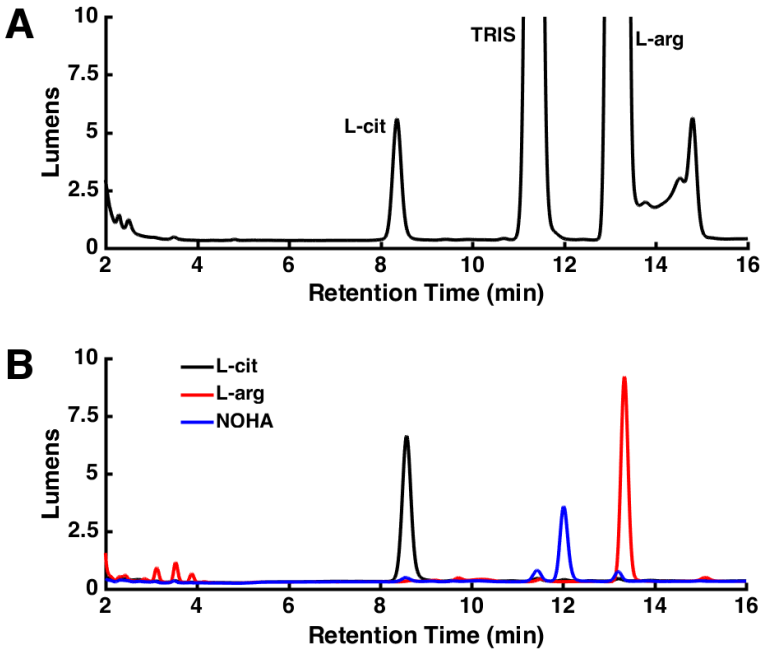


Figure 4: syNOS produces NOHA and citrulline. (A) HPLC trace of syNOS products. (B) HPLC trace of L-citrulline (black line), L-arginine (red line), and N-hydroxy-L-arginine (blue line) standards.

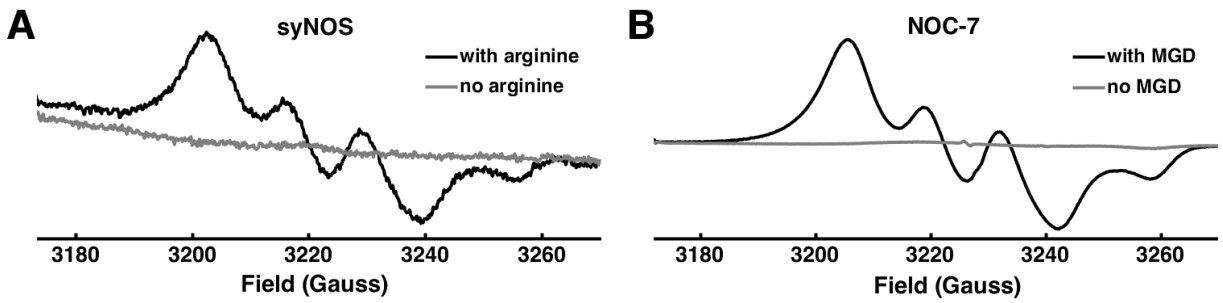


Figure 5: NO production by syNOS. Continuous-wave ESR of the NO complex of spin-trap Fe-MGD for (A) syNOS with (black line) and without (grey line) arginine. (B) NO donor NOC-7 with (black line) and without (grey line)

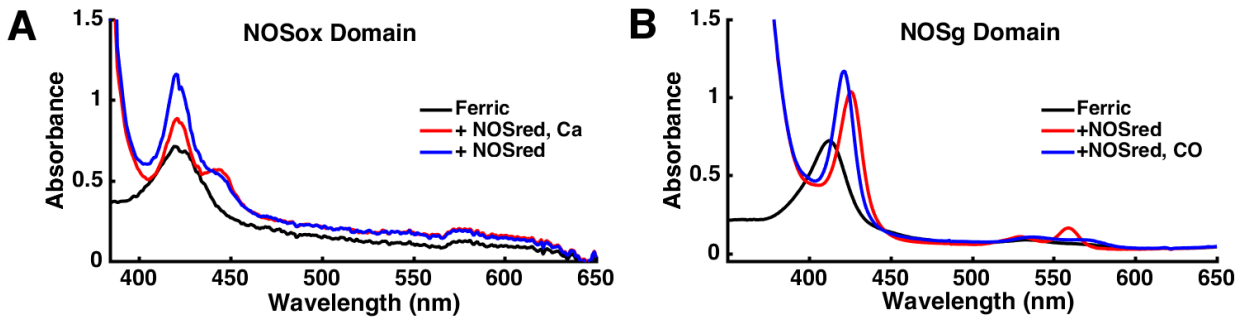


Figure 6. UV-vis spectrum of (A) NOS_{ox} in the presence of NOS_{red}, NADPH, and CO with or without calcium ion (Ca^{2+}), (B) NOS_g in the presence NOS_{red} and NADPH with or without CO. Samples with NADPH were measured under anaerobic conditions.

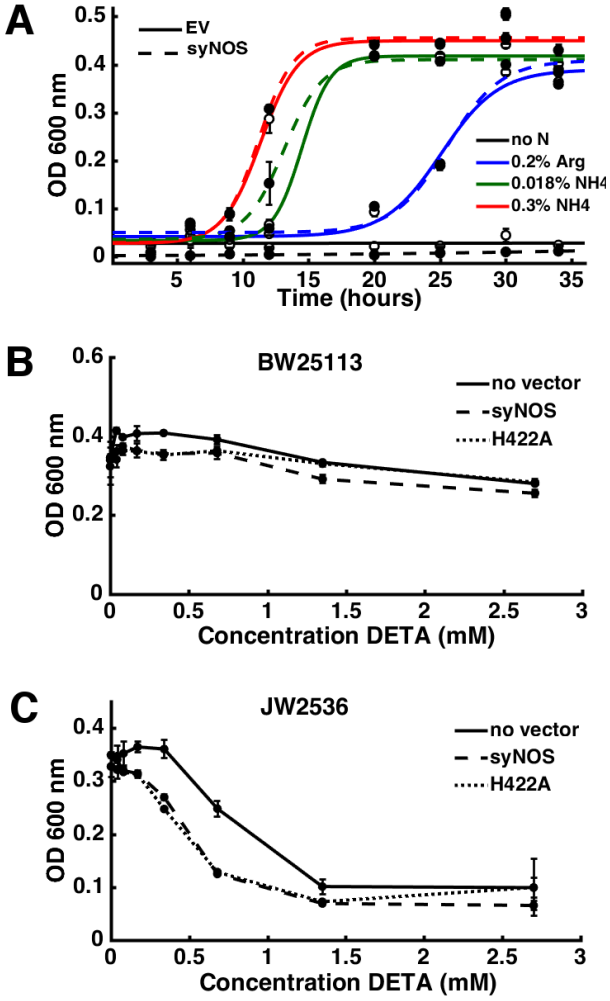


Figure 7: SyNOS expression does not aid growth of *E. coli* on L-arg nor protect against nitrosative stress. (A) Growth of *E. coli* in nitrogen-limited media. Empty vector (EV), solid lines and empty circles; syNOS, dashed lines and filled circles. (B) Growth of *E. coli* in the presence of DETA-NONOate and 26 µM IPTG. (C) Growth of *hmp* deficient *E. coli* in the presence of DETA-NONOate and 26 µM IPTG.

A nitric oxide synthase-like protein from *Synechococcus* produces NO/NO_3^- from L-arginine and NAPDH in a tetrahydrobiopterin- and Ca^{2+}-dependent manner

Angela L. Picciano[1] and Brian R. Crane[1]*

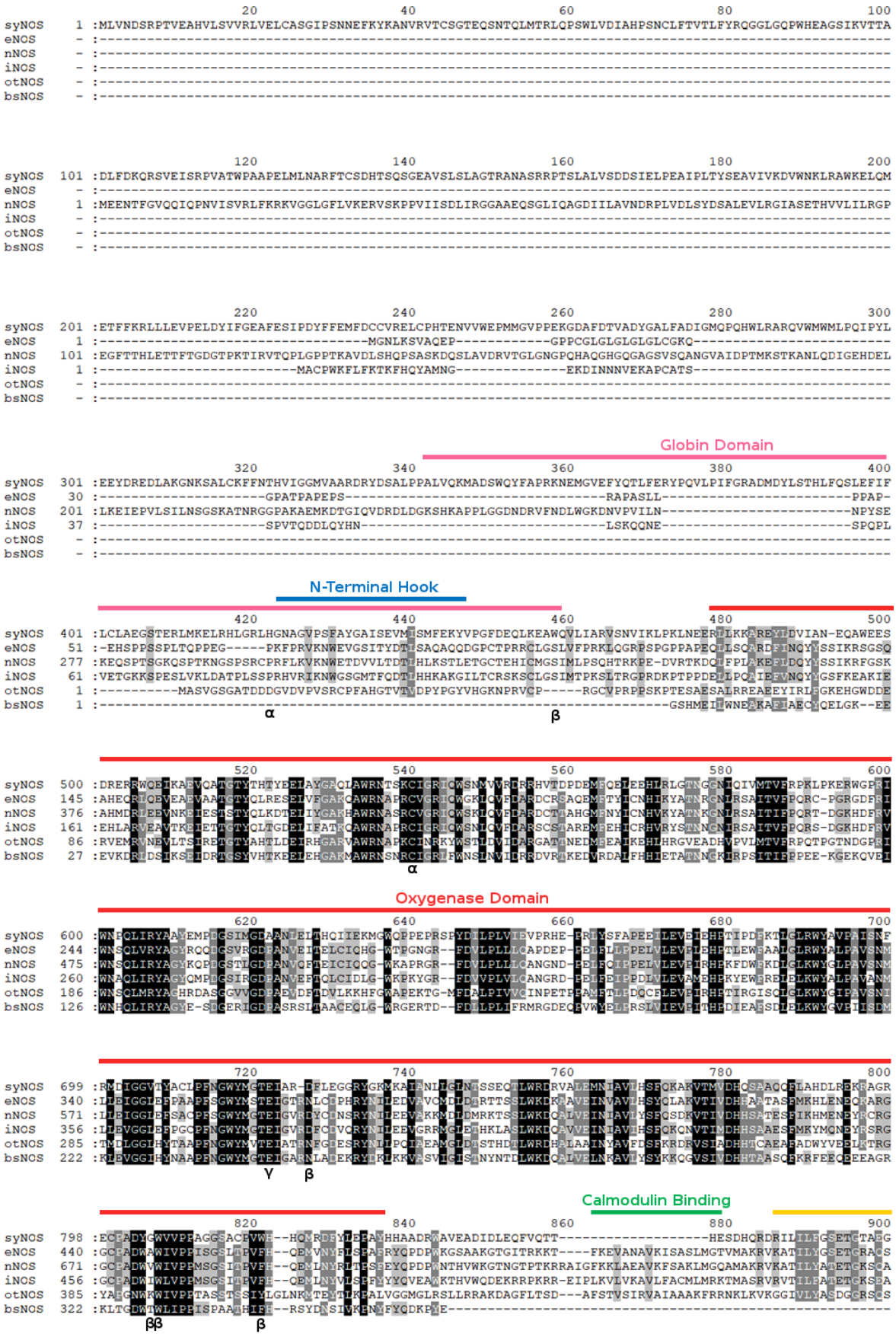
S-2 Table S1: Measurement of NO_2^- + NO_3^- in the presence of Fe-MGD
S-3 Table S2: Heme content of syNOS constructs
S-4 Figure S1: Alignment of syNOS to sequences of NOS proteins
S-5 Figure S2: Alignment of $syNOS_g$ to sequences of globin proteins
S-6 Figure S3: Michaelis Menten plots for Ca^{2+} and L-arg
S-7 Figure S4: Uv-vis spectra of double heme mutant H422A/C539A

	nmol NO_2^- + NO_3^-
syNOS	
+ Fe-MGD	1.0 ± 1.0
- Fe-MGD	35 ± 4
NOC – 7	78 ± 2

Table S1: NO_2^- + NO_3^- production from syNOS measured by the Griess assay, in the presence or absence of the spin-trap Fe-MGD.

	Hemin & δ-ala	δ-ala
syNOS	1.00 ± 0.10	0.77 ± 0.10
C539A	0.72 ± 0.07	0.42 ± 0.02
H422A	0.39 ± 0.08	0.20 ± 0.03
H422A/C539A	0.10 ± 0.02	0.036 ± 0.009

Table S2: Heme incorporation (μM heme per μM protein) of syNOS constructs expressed in the presence of excess hemin and δ-ala, or just δ-ala.


Globin Domain
N-Terminal Hook
α
β
Oxygenase Domain
α
γ
β
Calmodulin Binding
ββ
β

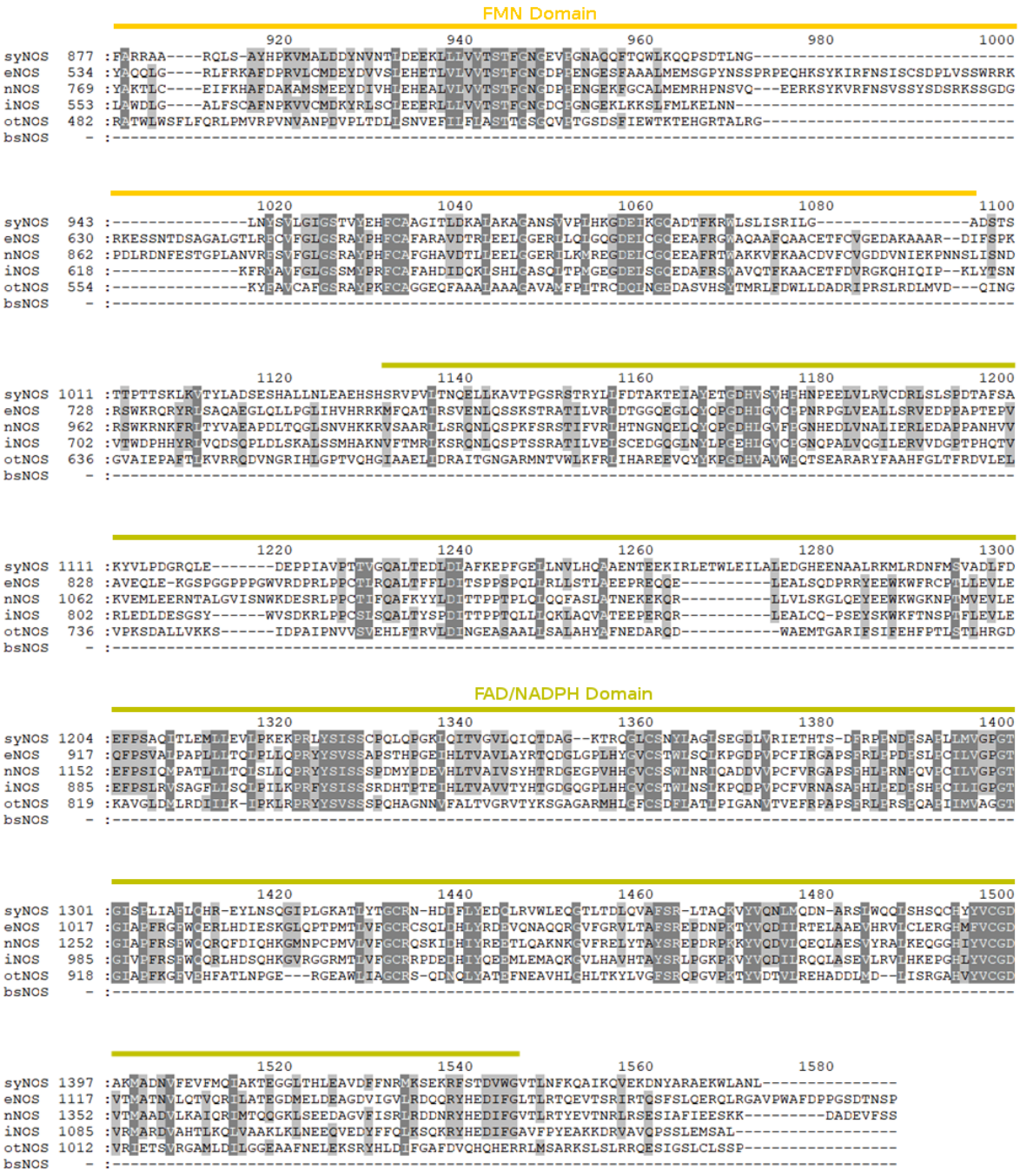


Figure S1: Protein sequence alignment of syNOS to other NOS proteins. The alignment was performed using ClustalX2 and visualized with GeneDoc; proximal heme binding residues (α), pterin binding residues (β), arginine coordinating glutamate (γ), *Homo sapien* endothelial NOS (eNOS), *Rattus norvegicus* neuronal NOS (nNOS), *Homo sapien* inducible NOS (iNOS), *Ostreococcus tauri* NOS (otNOS), *Bacillus subtilis* (bsNOS).

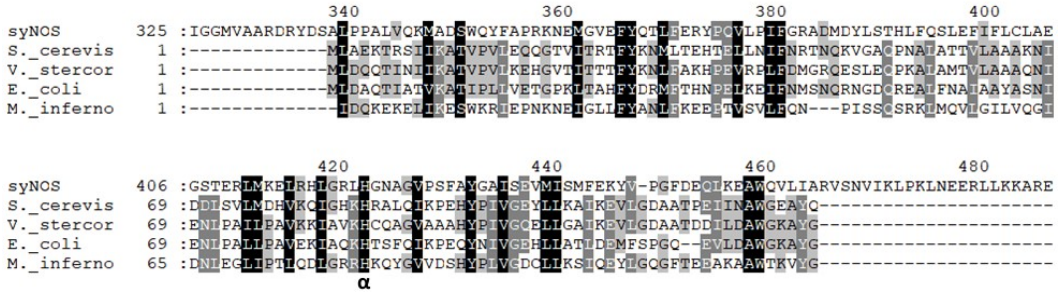


Figure S2: Protein sequence alignment of $syNOS_g$ to other globins and flavohemoglobins of known structures (*Saccharomyces cerevisiae* 4G1V, *Vitreoscilla stercoraria* 1VHB, *Escherichia coli* 1GVH, *Methylokorus infernorum* 3UBC). The alignment was performed using ClustalX2 and visualized with GeneDoc; proximal heme binding residue (α).

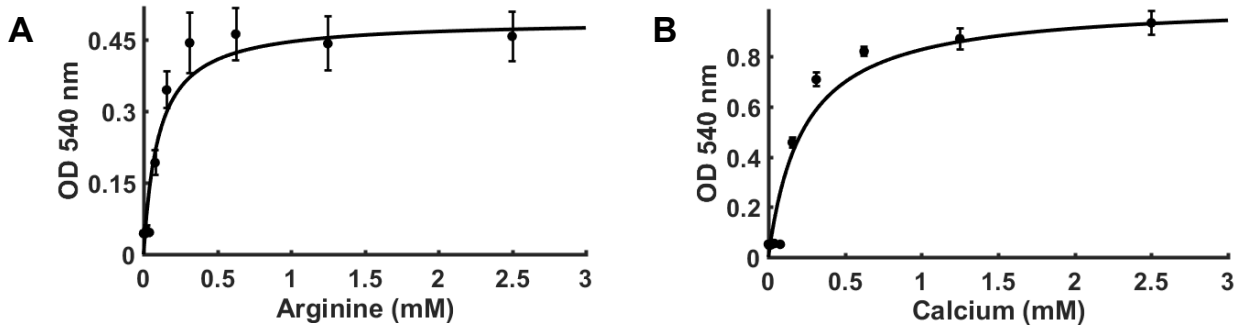


Figure S3: Michaelis-Menten plots for syNOS activity as a function of L-arg concentration (A) and calcium concentration (B). K_M values for arginine and calcium were calculated to be 101 ± 12 μM and 228 ± 9 μM, respectively.

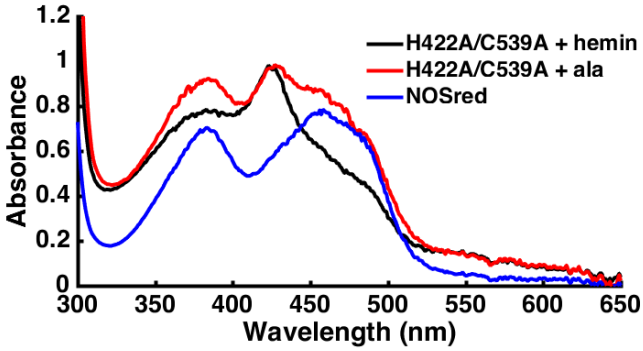


Figure S4: UV-vis spectra of the heme double mutant H422A/C539A compared to the syNOS reductase domain reveals minimal heme is bound when the proximal heme ligands are mutated.