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## A DISTAL TYROSINE RESIDUE IS REQUIRED FOR LIGAND DISCRIMINATION IN DEVS FROM *Mycobacterium tuberculosis*<sup>†</sup>

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### Abstract

DevS is a heme-based sensor kinase required for sensing environmental conditions leading to non-replicating persistence in *M. tuberculosis*. Kinase activity is observed when the heme is ferrous 5-coordinate high-spin or 6-coordinate low-spin CO or NO complex, but is strongly inhibited in the oxy complex. Discrimination between these exogenous ligands has been proposed to depend on a specific hydrogen bond network with bound oxygen. Here we report resonance Raman data and autophosphorylation assays of wild-type and Y171F DevS in various heme complexes. The Y171F mutation eliminates ligand discrimination for CO, NO and O<sub>2</sub>, resulting in equally inactive complexes. In contrast, the ferrous-deoxy Y171F variant exhibits equivalent autokinase activity as the wild-type. Raman spectra of the oxy complex of Y171F indicate that the environment of the oxy group is significantly altered from that in the wild-type. They also suggest that a solvent molecule in the distal pocket substitutes for the Tyr hydroxyl group to act as a poorer hydrogen bond donor to the oxy group. The wild-type CO and NO complexes exist as a major population in which the CO or NO groups are free of hydrogen bonds while the Y171F mutation results in a mild increase in the distal pocket polarity. The Y171F mutation has no impact on the proximal environment of the heme, and the activity observed with the 5-coordinate ferrous-deoxy wild-type is conserved in the Y171F variant. Thus, while the absence of an exogenous ligand in the ferrous-deoxy proteins leads to a moderate kinase activity, interactions between Tyr171 and distal diatomic ligands turn the kinase activity ON and OFF. The Y171F mutation disrupts the ON/OFF switch and renders all states with a distal ligand inactive. This mechanistic model is consistent with Tyr171 being required for distal ligand discrimination, but non-essential for autophosphorylation activity.

*Mycobacterium tuberculosis* (MTB)<sup>1</sup> is believed to have latently infected as many as 2 billion people worldwide (1). The success of this pathogen relies in part on its ability to exist within the host in a dormant state known as “nonreplicating persistence” (NRP) for extended periods, with subpopulations phenotypically resistant to current chemotherapies (2). Thus, a detailed understanding of NRP and its initiation process are critical for improving the treatment of TB.

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<sup>1</sup>Abbreviations: MTB, *Mycobacterium tuberculosis*; NRP, nonreplicating persistence; GAF domain, protein domain conserved in cyclic GMP-specific and stimulated phosphodiesterases, adenylate cyclases, and *E. coli* formate hydrogenlyase transcriptional activator (Pfam accession number PF01590); GAF A and GAF B, first and second N-terminal GAF domains of DevS and DosT; wt, wild-type; Y171F, Tyrosine 171 to Phenylalanine mutation; IPTG, isopropyl-D-D-thiogalactopyranoside; RR, resonance Raman.

NRP is characterized by the induction of a set of 48 genes, the so-called “dormancy regulon”. Included in this set is  $\alpha$ -crystallin, a heat-shock protein likely involved in the stabilization of essential proteins and cell structures during extended quiescence (3). Hypoxia and NO are likely environmental cues prompting entrance into NRP as expression of the dormancy regulon was found to be induced in response to both hypoxia and exposure to nontoxic concentrations of NO (4). Furthermore, O<sub>2</sub> was shown to competitively inhibit NO-mediated induction of the dormancy regulon (4). These observations strongly suggest that one sensor is responsible for detecting both signals and initiating the expression profile responsible for NRP.

Mutagenesis studies identified the DevR/DevS/DosT system as being required for induction of the dormancy regulon in response to hypoxia and NO (4,5). This is a classical two-component regulatory system where DevR is a response regulator of the LuxR family (6) and DevS, and its closely related (60% identity, 76% similarity) paralog DosT, are histidine protein kinases (HPK) (5) responsible for phosphorylation and activation of DevR.

Both DevS and DosT are modular in nature with an N-terminal sensing core composed of two tandem GAF domains and a C-terminal kinase core with a HisKA (histidine kinase phosphor-acceptor) domain where autophosphorylation occurs and an HATPase (histidine kinase-like ATPase) domain responsible for binding ATP (7). The first GAF domain (GAF A) binds heme and acts as a diatomic gas sensor (7–10). DevS and DosT show autokinase activity when the heme is in the deoxy state, signaling hypoxia, and when NO or CO are bound to the Fe(II) ion (9). In contrast, the kinase activity is strongly inhibited by the binding of O<sub>2</sub> (9). The ferric state (met) of DevS was also reported to lack autophosphorylation activity (10).

Previously, we reported the resonance Raman (RR) characterization of truncated and full-length wt DevS (11). The results suggested that a specific hydrogen bond exists between a distal residue and the proximal oxygen atom of bound O<sub>2</sub>. This hydrogen bond was absent from CO and NO adducts as well as the ferrous unligated state. Based on this evidence and the apparent function of DevS *in vivo*, we proposed that this hydrogen bond was responsible for differentiating exogenous ligands, and that, when engaged, would inhibit kinase activity. Thus, only the kinase activity of the oxy complex would be inhibited whereas the Fe(II), NO and CO bound states should be active. These conclusions were confirmed by autophosphorylation experiments (9,10). Moreover, CO-sensing during macrophage infection has been shown to result in activation of the dormancy regulon (12,13). The X-ray structure of the GAF A domain of DosT shows that the hydroxyl group of Tyr169 (Tyr171 in DevS) acts as a hydrogen bond donor to oxygen (14). As our experiments indicated stability issues with Y169F-DosT, we report on the RR characterization and autokinase activity of the Y171F mutant of DevS in the Fe(III), Fe(II), Fe-CO, Fe-NO, and Fe-O<sub>2</sub> states and compare the results to wt DevS. Because the wt Fe-O<sub>2</sub> complex is inactive, and Tyr171 interacts with the bound O<sub>2</sub>, the Y171F mutation might have been expected to release inhibitory constraints to produce a Y171F variant equally active in the O<sub>2</sub>, NO, and CO complexes. However, our results show that the Y171F variant lacks autokinase activity in all three states where the distal pocket is occupied by an exogenous ligand and retains activity only in the deoxy form. These activity measurements are discussed in conjunction with the RR analysis to propose mechanistic models of regulation in DevS.

## Materials and Methods

### Expression and Purification of Y171F DevS

**Full length DevS Mutagenesis**—The full length DevS gene previously cloned into pET23a+ was mutated using Pfu turbo and the following mutagenic primers: CGTTCGGCACTCTGTTC CTGACTGACAAGACC (forward primer) and GGTCTTGTCAGTCAGGAACAGAGTGCCGAACG (reverse primer). DNA sequencing was used to verify the mutated gene sequence.

**Y171F DevS Expression**—The mutant protein was expressed following the same protocol as in the case of DevS642 (8). Briefly, BL21gold DE3 cells were co-transformed with pET23a + Y171F DevS and pT-GroE and the cells were grown on LB plates containing both ampicillin (50 µg/mL) and chloramphenicol (34 µg/mL). Starter cultures were grown at 37 °C and then used to inoculate flasks containing 1.5 L of LB medium and the antibiotics ampicillin (100 µg/mL) and chloramphenicol (34 µg/mL). The cells were grown to an optical density of OD<sub>600</sub> 0.8–1 at 37 °C and 230 rpm. Hemin was added before induction (45 mg/ 1.5 L culture) and protein expression was induced with IPTG at a final concentration of 1 mM. The cultures were kept at 18 °C for 20 h and then the cells were harvested by centrifugation at 5000 rpm for 25 min.

**Protein Purification**—The cells were lysed in phosphate buffer, pH 7.6 (50 mM NaH<sub>2</sub>PO<sub>4</sub>, 10% glycerol, 200 mM NaCl, 1% Triton X-100, 0.5 mg/mL lysozyme, 5 mM MgCl<sub>2</sub>, 5 mM ATP and protease inhibitors antipain, 1 µg/mL, leupeptin, 1 µM, pepstatin, 1 µM, and PMSF, 0.1 mM). Then the mixture was incubated with shaking at 37 °C for 30 min. The cell membranes were disrupted by repeated sonication cycles at 50% using a Branson sonifier 450 from VWR Scientific, while cooling on ice. The insoluble fraction was isolated by centrifugation at 35000 rpm for 1 h at 4 °C. The cell lysate was applied to a 5 mL His trap column. The column was washed with 20 and 50 mM imidazole buffer. The recombinant protein was then eluted with 250 mM imidazole. The protein sample was applied to a DEAE column. The purified protein was obtained after gradient elution from 0 to 0.5 M NaCl in 50 mM Tris buffer containing 5% glycerol and 1 mM EDTA at pH 8.

**Electronic Absorption and Resonance Raman Spectroscopy**—The RR experiments were performed with ~100 µM protein solutions for the Fe(III) and deoxy Fe(II) forms, and ~300 µM protein solutions for the CO, NO, and O<sub>2</sub> complexes. Ultrafree-0.5 ultrafiltration devices (Millipore) were used for concentrating the protein. A 50 mM potassium phosphate buffer at pH 7.5 with 100 mM NaCl was used for most protein samples. 100 mM MES pH 6.0, 100 mM potassium phosphate pH 7.0, 50 mM HEPES pH 8.0, 200 mM CHES pH 9.5, and 200 mM CAPS pH 11.0 were used in pH dependence experiments. Reduction to the ferrous state was achieved by adding a few µL aliquots of concentrated sodium dithionite solution (35–50 mM) to an argon-purged sample. <sup>12</sup>CO (Airgas) and <sup>13</sup>CO (99% <sup>13</sup>C; ICON Stable Isotopes) adducts were obtained by injecting CO through a septum-sealed capillary containing argon-purged, reduced protein (~20 µL). O<sub>2</sub> (Airgas), <sup>18</sup>O<sub>2</sub> (99% <sup>18</sup>O; ICON Stable Isotopes), NO (Aldrich), and <sup>15</sup>N<sup>18</sup>O (98% <sup>15</sup>N and 95% <sup>18</sup>O; Aldrich) adducts were generated using the same procedure after excess dithionite was removed from the reduced sample with desalting spin columns (Zeba™ 0.5 mL; Pierce). These procedures were performed in a glove box with a controlled atmosphere of less than 1 ppm O<sub>2</sub> (Omni-Lab System; Vacuum Atmospheres Co.). All samples were monitored by UV-vis spectroscopy directly in the capillary using a Cary 50 spectrophotometer (Varian). RR spectra were obtained using a custom McPherson 2061/207 spectrograph (0.67 m with variable gratings) equipped with a Princeton Instruments liquid N<sub>2</sub>-cooled CCD detector (LN-1100PB). Kaiser Optical supernotch filters or long-wave pass filters (RazorEdge Raman filters, Semrock) were used to attenuate Raleigh scattering. A krypton laser (Innova 302, Coherent) and a He/Cd laser (Liconix 4240NB) were used for 413 and 442 nm excitations, respectively. Spectra were collected in a 90° scattering geometry on samples at room temperature. Frequencies were calibrated relative to indene and CCl<sub>4</sub> and are accurate to ±1 cm<sup>-1</sup>. CCl<sub>4</sub> was also used to check the polarization conditions. The integrity of the RR samples, before and after laser illumination, was confirmed by direct monitoring of their UV-vis spectra in the Raman capillaries.

**Autophosphorylation Assays**—Wt or Y171F DevS protein solutions in 50 mM potassium phosphate buffer at pH 7.5 with 100 mM NaCl were purged with Ar and reduced with sodium

dithionite. Excess dithionite was removed using desalting columns and CO, NO, or O<sub>2</sub> gas was added to appropriate samples. The Fe(III) proteins were incubated in 2 mM potassium ferricyanide and desalted using spin columns. These operations were performed in the anaerobic glove box. All samples, except the oxy and Fe(III) proteins, were loaded into septum-sealed microcentrifuge tubes. All 50  $\mu$ L assay samples contained final concentrations of 5.0  $\mu$ M DevS, 100 mM Tris-HCl pH 7.5, 50 mM KCl, 5 mM MgCl<sub>2</sub>, and, with the exception of oxy and Fe(III) samples, 500  $\mu$ M sodium dithionite, after ATP addition. Reactions were initiated by syringe addition of a few  $\mu$ L of a solution containing  $\gamma$ -<sup>32</sup>P ATP (4500 Ci/mmol) (Pharmacia Biotech) and Ar-purged, unlabeled ATP (Sigma) to a final concentration of 200  $\mu$ M and 10  $\mu$ Ci. 10  $\mu$ L aliquots were removed at various time points and combined with 3.0  $\mu$ L stop buffer (208 mM Tris-HCl pH 6.8, 8.3% SDS, 42% glycerol, 167 mM DTT, and 0.08% bromophenol blue). These samples were run through a 12% polyacrylamide gel, which was vacuum-dried at 80 °C for 1.5 hr, and exposed in a PhosphorImager cassette (Molecular Dynamics) for approximately 24 to 48 hr. Levels of phosphorylated protein were imaged on a Typhoon Trio+ PhosphorImager (Amersham Biosciences) and quantified according to Nakamura et al. (15) except that the 1.65 correction factor was eliminated since gels were completely dried. After exposure, dried gels were rehydrated in 20% methanol 5% acetic acid solution and Coomassie stained to confirm consistency in amount of protein loaded and integrity of full length proteins.

## Results

### Autokinase Activity of WT and Y171F DevS

Autophosphorylation assays were performed by monitoring  $\gamma$ -<sup>32</sup>P-labeling of DevS for 10 min at room temperature (Fig. 1). Different states of wt DevS showed autokinase activities consistent with a previous report by Gilles-Gonzalez and coworkers (9). However, in our hands, the ferrous protein is systematically less active than the nitrosyl complex while equivalent activities are reported for these two states in Sousa et al. (9). Indeed, multiple experiments with two different wt DevS constructs yielded the same pattern of activity for the various states of DevS (Fig. S1). Mutation of Tyr171 to Phe has no apparent impact on the autophosphorylation level observed in the Fe(II) state, but the mutation disrupts the discriminatory power of DevS toward exogenous ligands with the CO, NO, and O<sub>2</sub>-bound states all lacking activity (Fig. 1). As reported earlier for wt DevS (10), the met Fe(III) state of Y171F is inactive (Fig. S2). These data are consistent with a determining role for the hydroxyl group of Tyr171 in distinguishing between distal exogenous ligands in DevS. The maintenance of autophosphorylation activity in the deoxy form of Y171F DevS demonstrates that the point mutation does not result in a major protein conformational change. In the deoxy form, the heme is pentacoordinate (see below) and the lack of a distal ligand results in a lack of sensitivity to the Tyr171 to Phe mutation.

### Spectroscopic Analysis of WT and Y171F DevS

UV-vis spectroscopic data for wt and Y171F DevS at pH 7.5 are summarized in Table 1. Distinctive absorption features were obtained for the Fe(II), Fe-CO, and Fe-NO forms, with both proteins displaying nearly identical spectra. The Fe(III) form of Y171F shows significant red shifts in the  $\alpha/\beta$  region, a decrease in intensity of the charge transfer band near 630 nm, as well as a red shift and significant decrease in the extinction coefficient of the Soret band (Table 1, Fig. S3). These observations suggest an increase in the proportion of low-spin Fe(III) heme in the mutant relative to wt protein (16). This interpretation of the UV-vis changes is consistent with the high-frequency RR spectra obtained with Soret excitation (Fig. 2) in which the frequencies of the porphyrin skeletal mode  $\nu_4$  correlate with the oxidation state of the iron, and the  $\nu_3$ ,  $\nu_2$ , and  $\nu_{10}$  modes report the coordination and spin state of the iron (17). Specifically, in the wt, the  $\nu_3$ ,  $\nu_2$ , and  $\nu_{10}$  observed at 1479, 1557, and 1609 cm<sup>-1</sup>, respectively, are indicative



of a 6-coordinate high-spin (6cHS) heme while those at 1506, 1579, and 1639  $\text{cm}^{-1}$  correspond to a 6-coordinate low-spin (6cLS) population (Fig. 2A). Equivalent sets of frequencies are also observed in the RR spectrum of the Y171F variant (Fig. 2B and Table 2), but the relative intensities of these bands suggest a shift of the 6cHS/6cLS distribution, from predominantly 6cHS in the wt protein to predominantly 6cLS in the variant protein.

RR spectra of ferric wt and Y171F DevS at different pH show that conversion from high-spin to low-spin ferric heme occurs at a much lower pH in Y171F (pH  $\sim$  7) than it does in wt DevS (pH  $\sim$  10) (Fig. S4). These observations suggest that the removal of the hydroxyl group of Tyr171 alters the ligand-field strength of the distal ligand. At pH 10, the Tyr171 side chain may coordinate the wt heme Fe(III) as a phenolate ligand. Alternatively, a solvent molecule coordinates the heme Fe(III) with a bond strength that is governed by its interaction with Tyr171. In the Y171F DevS variant, the sixth ligation to the Fe(III) is most likely occupied by a solvent molecule with a  $pK_a$  near 7. Attempts to gather direct evidence identifying the sixth ligand in ferric wt and Y171F DevS were unsuccessful. Specifically, low-frequency RR spectra in  $^{18}\text{OH}_2$  and  $\text{D}_2\text{O}$  did not reveal isotope-sensitive modes that could be assigned to a  $\nu(\text{Fe-OH})$  mode, as previously observed with hydroxy-complexes in heme oxygenases and hemoglobin at high pH (18–21), nor a  $\nu(\text{Fe-O}_{\text{Tyr}})$  as previously observed in the 6cLS alkaline ferric *Chlamydomonas* hemoglobin (22) (Fig. S5).

The high-frequency RR spectra of Fe(II) wt and Y171F DevS are both indicative of a pure 5-coordinate high-spin (5cHS) heme (Fig. 3 and Table 2). Two  $\nu(\text{C}=\text{C})$  vinyl stretches are observed in wt DevS at 1620 and 1625  $\text{cm}^{-1}$ , but a single broad  $\nu(\text{C}=\text{C})$  is observed at 1622  $\text{cm}^{-1}$  in Y171F DevS. A similar perturbation is seen in the Fe(III) state, where two well-resolved  $\nu(\text{C}=\text{C})$  vibrations are observed at 1620 and 1629  $\text{cm}^{-1}$  in the wt protein, while the Y171F variant shows a dominant  $\nu(\text{C}=\text{C})$  at 1628  $\text{cm}^{-1}$  and a shoulder at 1620  $\text{cm}^{-1}$  (Fig. 2). Although these data indicate a slight difference in the vinyl groups in the wt and variant proteins, the equivalent activity of the Fe(II) state in these two proteins suggests that the vinyl perturbations have little impact on function. Low-frequency RR spectra obtained with 442-nm excitation (Fig. 4) exhibit a strong band at 214  $\text{cm}^{-1}$  for the wt protein previously assigned to the  $\nu(\text{Fe-N}_{\text{His}})$  mode (8). This mode shifts  $-1 \text{ cm}^{-1}$  in the RR spectrum of Y171F DevS, while other low-frequency heme peripheral deformation modes are nearly identical in both proteins (Fig. 4). These results indicate that the effect of the Y171F mutation is limited to the distal environment and does not significantly perturb the proximal heme pocket of DevS.

RR spectra of wt and Y171F DevS- $^{12}\text{CO}$  and  $^{13}\text{CO}$  complexes are shown in Figure 5. The RR spectrum of wt DevS shows a major CO conformer with  $\nu(\text{C-O})$  at 1971  $\text{cm}^{-1}$  and  $\nu(\text{Fe-CO})$  at 490  $\text{cm}^{-1}$ , respectively (11). These  $\nu(\text{C-O})$  and  $\nu(\text{Fe-CO})$  frequencies are characteristic of a heme-CO complex with a neutral proximal histidine and a carbonyl group free of hydrogen bond interactions in a hydrophobic environment (11,23). Our previous work with truncated DevS proteins consisting of the single GAF A and the two GAF domains (11) suggested the presence, in full-length DevS, of a second very minor CO conformer with  $\nu(\text{C-O})$  and  $\nu(\text{Fe-CO})$  bands at 1936 and 524  $\text{cm}^{-1}$ , respectively, that is engaged in electrostatic and/or hydrogen bond interactions within the distal pocket. The RR spectra of the CO complex of the Y171F exhibit a  $\nu(\text{C-O})$  at 1965  $\text{cm}^{-1}$  and a  $\nu(\text{Fe-CO})$  at 497  $\text{cm}^{-1}$ , respectively (Fig. 5). The variations in  $\nu(\text{C-O})$  and  $\nu(\text{Fe-CO})$  frequencies in the two proteins suggest only a modest change in the degree of back-bonding from the filled Fe  $d$  orbital to the empty  $\pi^*$  orbital of the bound CO in the variant compared to the wt protein. A  $\delta(\text{Fe-C-O})$  near 568  $\text{cm}^{-1}$  is observed with equivalent intensity and  $^{13}\text{C}$ -shift ( $-12 \text{ cm}^{-1}$ ) in both proteins (Fig. 5). Finally, the Y171F mutation does not appear to affect interactions engaged by the heme propionate groups since the 350 to 450  $\text{cm}^{-1}$  regions of the RR spectra are equivalent in wt and Y171F DevS (Fig. 5). The  $\delta(\text{C}_\beta\text{C}_\gamma\text{C}_\delta)$  propionate deformation modes are sensitive to electrostatic interactions at the

heme propionate groups (24), and are tentatively assigned to bands at 379 and 387  $\text{cm}^{-1}$  (Table 2).

Comparison of the high frequency  $^{14}\text{N}^{16}\text{O} - ^{15}\text{N}^{18}\text{O}$  difference spectra of wt and Y171F DevS lead to an analysis similar to that for the CO data (Fig. 6). As discussed previously (11), vibrational mixing between  $\nu(^{15}\text{N}^{18}\text{O})$  and vinyl  $\nu(\text{C}=\text{C})$  and  $\nu_2$  modes (25) increases the number of differential signals contributing to these traces. Despite these perturbations, the strongest positive band in the  $^{14}\text{N}^{16}\text{O} - ^{15}\text{N}^{18}\text{O}$  difference spectra is readily assigned to the  $\nu(^{14}\text{N}^{16}\text{O})$ , and it is observed at 1638 and 1635  $\text{cm}^{-1}$  in wt and Y171F DevS, respectively (Fig. 6). Moreover, the values for the major  $\nu(\text{N-O})$  and  $\nu(\text{C-O})$  bands in wt and Y171F DevS closely follow the linear correlation observed for other heme proteins sharing proximal histidine ligation (26) (Fig. 6). The minor conformer evidenced by a  $\nu(\text{N-O})$  at 1604  $\text{cm}^{-1}$  in the wt protein (11), is not observed in the Y171F variant. Overall, both NO and CO complexes show a modest increase in back-bonding in Y171F DevS relative to the major conformer of the wt protein. As with the carbonyl complex, the low frequency RR spectra of the nitrosyl adduct show very little difference between wt and Y171F (see  $\nu(\text{Fe-NO})$  and  $\delta(\text{C}_\beta\text{C}_\epsilon\text{C}_\delta)$  frequencies in Table 2).

As was anticipated on the basis of the crystal structure of DosT, the oxy complexes of wt and Y171F DevS show greater divergence than do any other states of these proteins, illustrating that Tyr169 (DosT numbering) directly interacts with the heme-bound oxygen group (14). The Soret absorbance of the variant is red-shifted 6 nm relative to the wt protein (Fig. S6). Porphyrin skeletal modes  $\nu_4$  and  $\nu_3$  in the RR spectra show 1 and 3  $\text{cm}^{-1}$  downshifts, respectively, in the variant protein relative to the wt protein (Fig. S7 and Table 2). The  $\nu(\text{Fe-O}_2)$  mode is isolated from porphyrin modes in the low-frequency RR spectra using  $^{16}\text{O}_2 - ^{18}\text{O}_2$  difference spectra (Fig. 7), and was previously observed in wt DevS at 563  $\text{cm}^{-1}$  with a 22- $\text{cm}^{-1}$   $^{18}\text{O}$ -downshift (11). In Y171F, the  $\nu(\text{Fe-O}_2)$  mode is observed at 567  $\text{cm}^{-1}$ , i.e., 4- $\text{cm}^{-1}$  higher than in the wt oxy complex. We have previously shown that H/D exchange affects the  $\nu(\text{Fe-O}_2)$  mode of wt DevS with a  $\sim 4$   $\text{cm}^{-1}$  upshift of the  $^{16}\text{O}_2 - ^{18}\text{O}_2$  differential signal in  $\text{D}_2\text{O}$  (Fig. 7) (11). No such effect is observed in Y171F (Fig. 7), reflecting a perturbation of hydrogen bonding to the proximal oxygen atom of bound  $\text{O}_2$  in this mutant (27). As seen with the carbonyl and nitrosyl complexes, mutation of Tyr171 had no significant impact on the frequency of the  $\delta(\text{C}_\beta\text{C}_\epsilon\text{C}_\delta)$  propionate deformation modes in the oxy complexes (Fig. 7, Table 2).

## Discussion

The crystal structure of GAF A DosT identifies Tyr169 as the sole polar side chain in the distal pocket and as the hydrogen bond partner to the metal-bound  $\text{O}_2$  in the oxy form of the protein (14). A sequence alignment comparison of DosT and DevS predicts that, in DevS, the Tyr171 hydroxyl group is a hydrogen bond donor to the oxy group in the  $\text{O}_2$ -adduct, as well as in the minor population of hydrogen bonded CO and NO conformers identified in the RR spectra of the wt protein. The RR spectra of Y171F DevS reported here support this hypothesis since these hydrogen-bonded CO and NO conformers are not observed. In addition, the Y171F mutation significantly lowers the pH at which the ferric heme is converted from high-spin to low-spin. Earlier RR characterization of the ferric wt and His149Ala proximal variant suggested weak coordination of a distal residue as a sixth ligand to the heme Fe(III) (8). In view of the crystal structure of GAF A DosT (8), it is tempting to propose that in ferric DevS, the Tyr171 OH group interacts with the ferric heme distal ligation site via the intermediate of a solvent molecule, and that the ionization of Tyr171 at pH  $\sim 10$  converts the ferric heme to a 6-coordinate low-spin species. The absence of the hydroxyl group in the Y171F variant would allow for stabilization of a solvent molecule as a sixth ligand with a  $pK_a$  value similar to those observed in globin ferric-aqua complexes such as myoglobins ( $pK_a \sim 9.0$ ) and heme oxygenases ( $pK_a \sim 8.0$ ) (19,21,28–30). We could not confirm this hypothesis with the observation of a  $\nu$

(Fe-OH) in the RR spectra of the ferric Y171F variant at alkaline pH, presumably because of conformational disorder. However, coordination of the heme Fe(III) in Y171F by a solvent molecule is consistent with the overall data, including those obtained on the reduced protein. Indeed, stretching modes from the CO and NO adducts in Y171F DevS are only marginally changed from their dominant counterparts in the wt protein and rule out a purely hydrophobic distal environment in the Y171F variant. Electrostatic effects from a solvent molecule on the CO and NO groups would account for the slightly lower  $\nu(\text{C-O})$  and  $\nu(\text{N-O})$  frequencies observed in Y171F relative to the wt major conformers. In the oxy complex, the variant protein shows a  $\nu(\text{Fe-O})$  at  $567\text{ cm}^{-1}$ , which suggests a polar environment and a hydrogen bond interaction with a solvent molecule rather than the stronger Tyr171 hydrogen bond donor present in the wt protein (27).

Autophosphorylation assays of wt and Y171F variant DevS in different heme states demonstrate the crucial role of Tyr171 in ligand discrimination. Mutagenesis of Tyr171 to a non-polar residue leads to the inability of DevS to distinguish between the exogenous ligands CO or NO and  $\text{O}_2$ , and leaves all Fe(II)XO (where X = O, N, or C) complexes inactive. In contrast, the Y171F mutation has no significant impact on the activity of the deoxy-ferrous protein. Because the ferrous hemes of wt and variant DevS are 5-coordinate species with a vacant Fe(II) distal ligation site, a conserved level of autophosphorylation activity in the distal variant ferrous protein is not unexpected. Our data also indicate that the autokinase activity in ferrous wt DevS is lower than that of the CO and NO complexes. From these observations, we propose that interactions between Tyr171 and distal diatomic ligands turn the kinase activity ON or OFF, and that the absence of an exogenous distal ligand interacting with Tyr171 leads to a lower level of kinase activity. Mutation of Tyr171 to Phe disrupts the ON/OFF switch leading to an inactive kinase in all states with distal coordination, while the variant retains the lower level kinase activity associated with the empty distal pocket. Many molecular models can be envisioned within this context but we can delineate several important features:

1. The OFF state is dependent on a hydrogen bond interaction observed between the coordinating O-atom of the oxy group and the hydroxyl group of Tyr171. This specific hydrogen bond may lock the phenol side chain in an inhibitory conformation which cannot be achieved with NO or CO. In the ferric protein, which is also inhibited (10), the Fe(III) sixth coordination site is occupied by a water molecule, and based on the crystal structure of GAF A domain of DosT (14), it is hydrogen bonded by Tyr171. Thus, Tyr171 adopts an equivalent conformation in the ferric and the oxy forms of wt DevS.
2. The ON state in the CO and NO complexes requires a hydrogen bond network that involves Tyr171 and that is distinct from that in the oxy form. Although minor populations of NO and CO conformers interact with Tyr171 via a hydrogen bond, the majority of the CO and NO complexes do not (11), and as such, this larger population may release constraints on Tyr171 to allow its hydroxyl group to engage other hydrogen-bond partners in forming the ON state. Alternatively, the hydrogen-bonded NO and CO conformers may be the species responsible for the ON state, but the hydrogen bond acceptor is the non-coordinating oxygen atom of the XO group rather than the coordinating atom as in the oxy complex. In either case, the Y171F mutation prevents the formation of the hydrogen bond network necessary for stabilization of the ON state.
3. The intermediate-level kinase activity observed with the deoxy form of wt DevS is unaffected by the Tyr171 to Phe mutation. The lack of a distal ligand is expected to reduce steric constraints in the distal pocket and, whether the Tyr171 hydroxyl group is present or not, both ON and OFF states may be populated to produce an intermediate level autokinase activity.



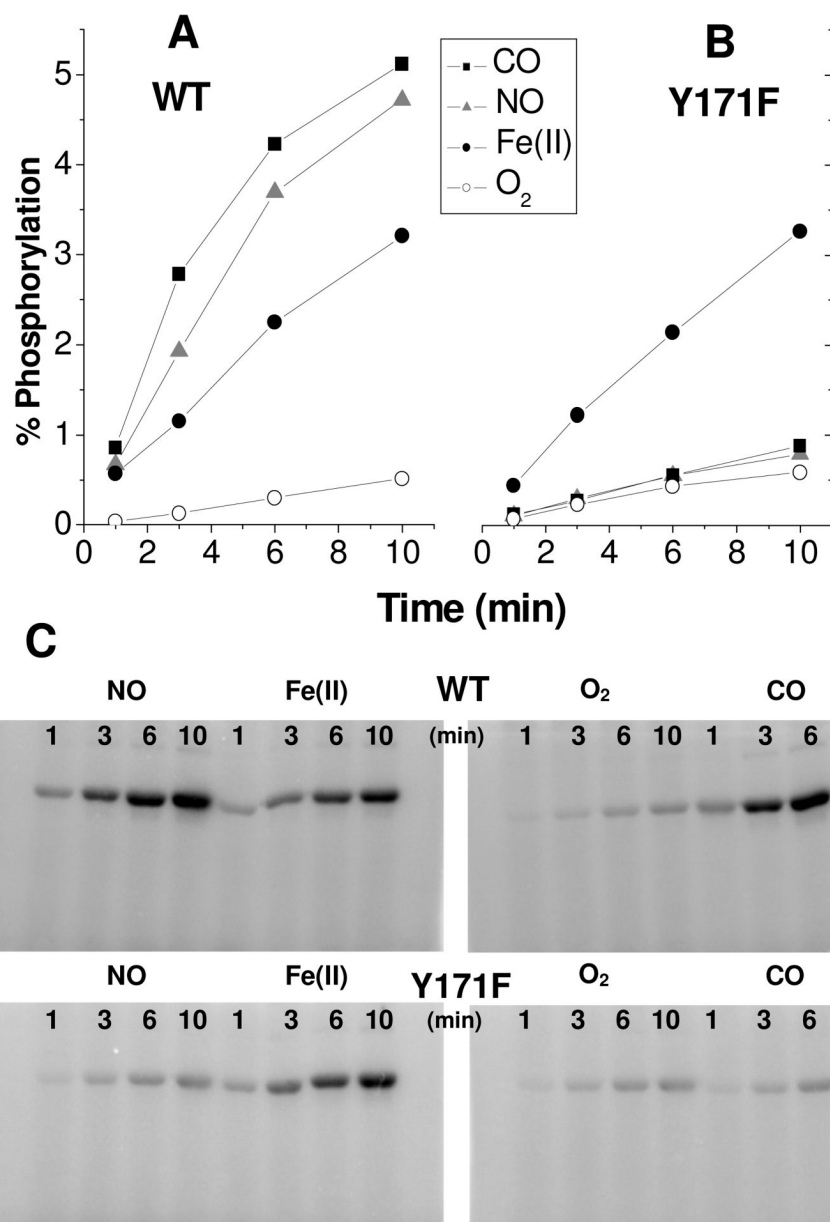
## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

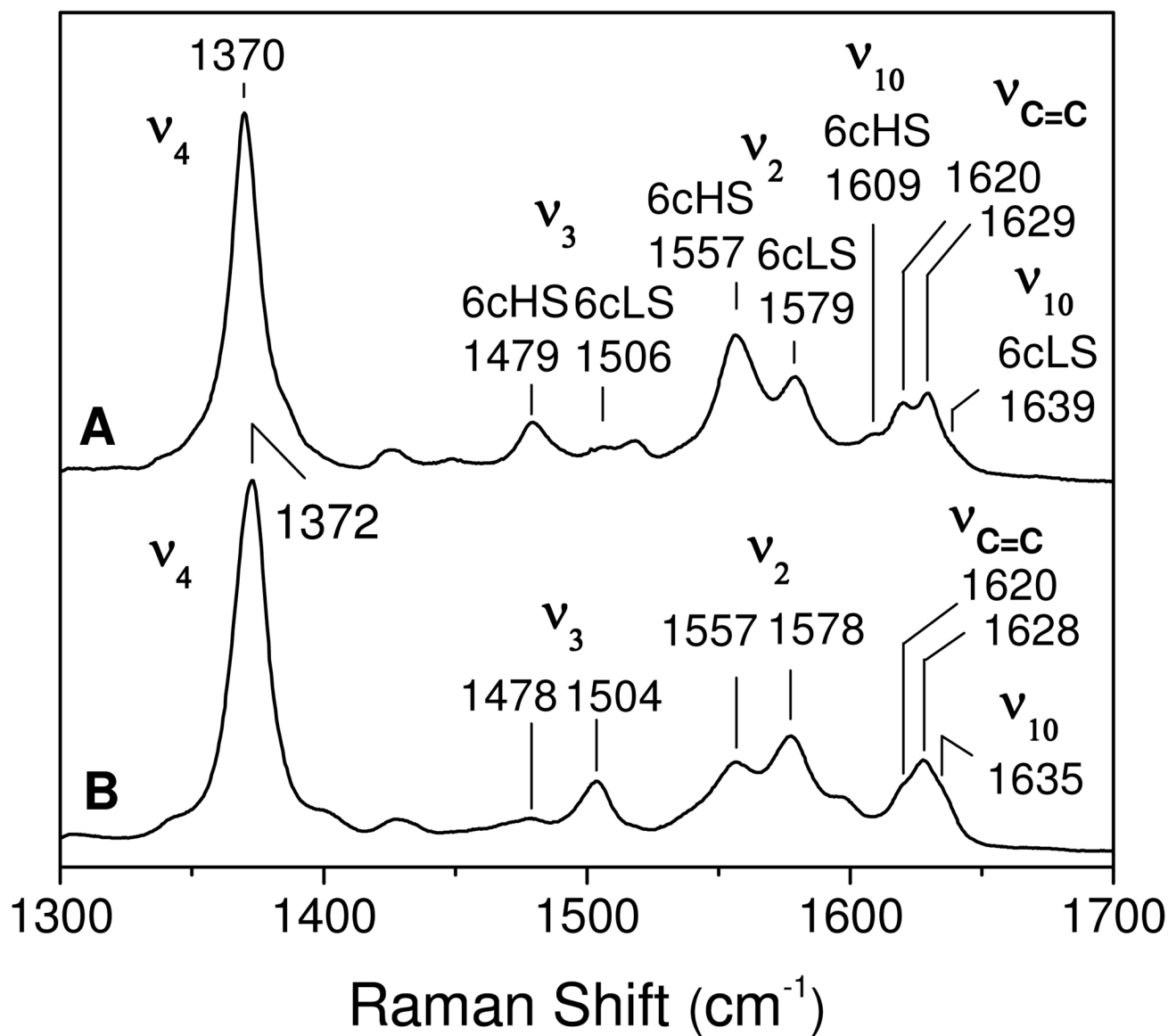
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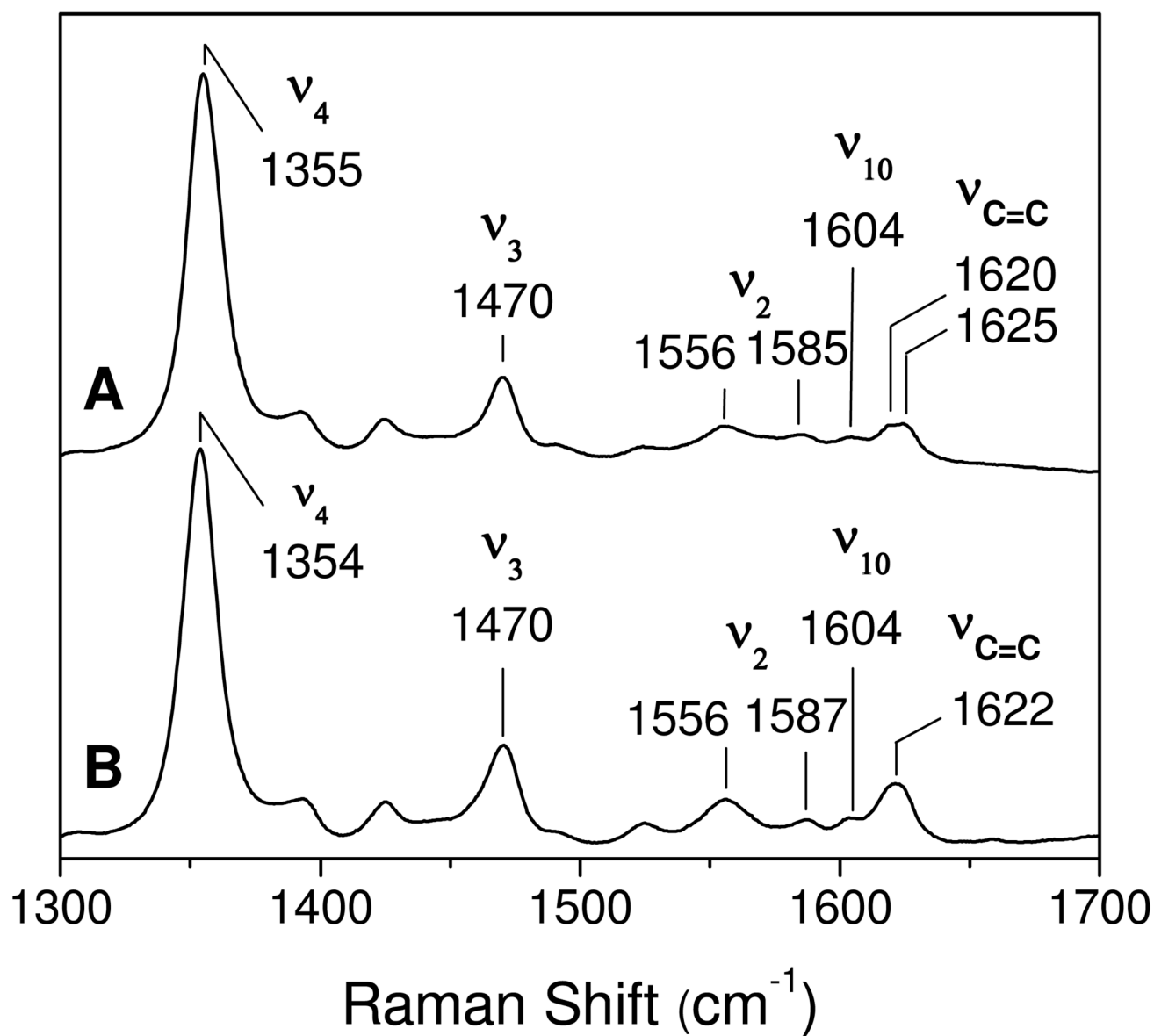
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**Figure 1.**

Top panel: Time courses for the autophosphorylation of wt (A) and Y171F (B) DevS in the Fe (II) (filled circles), Fe(II)-CO (filled squares), Fe(II)-NO (grey triangles) and Fe(II)-O<sub>2</sub> (open circles) forms. Lower panel: Autoradiographs of the dried gels for wt DevS (top) and Y171F DevS (bottom) (C).

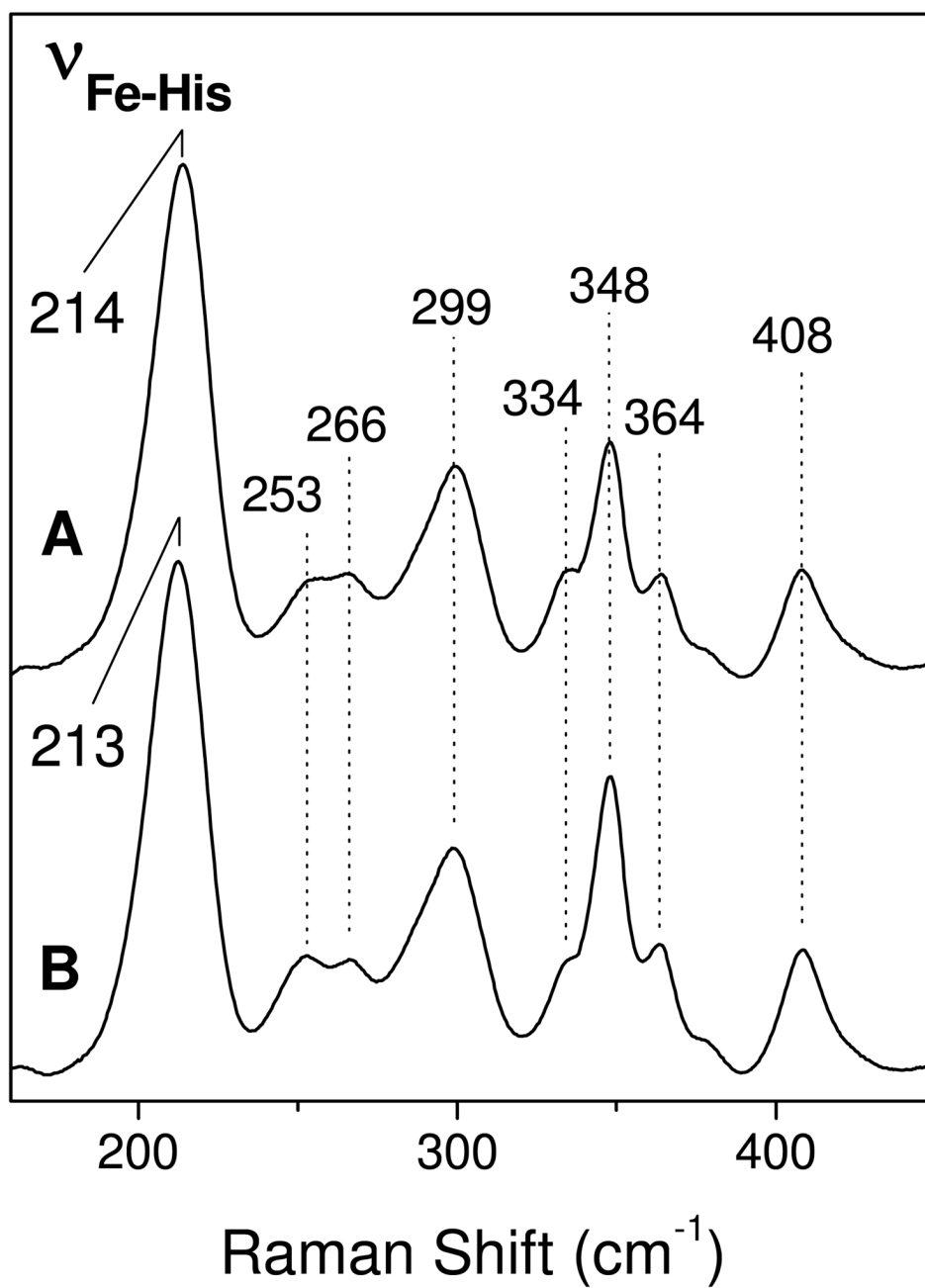


**Figure 2.**  
High-frequency RR spectra of ferric wt DevS (A) and Y171F DevS (B) at room temperature ( $\lambda_{exc} = 413$  nm; 5 mW).

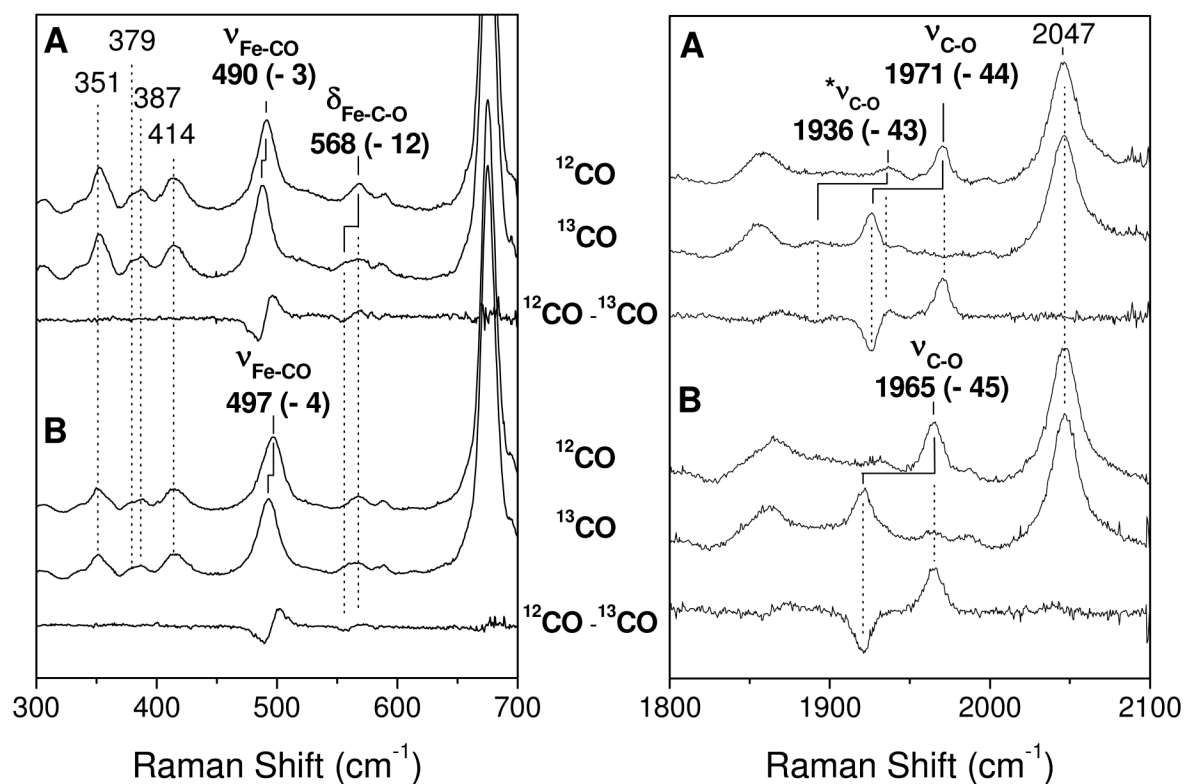


**Figure 3.** High-frequency RR spectra of ferrous deoxy wt DevS (A) and Y171F DevS (B) at room temperature ( $\lambda_{\text{exc}} = 413 \text{ nm}$ ; 5 mW).



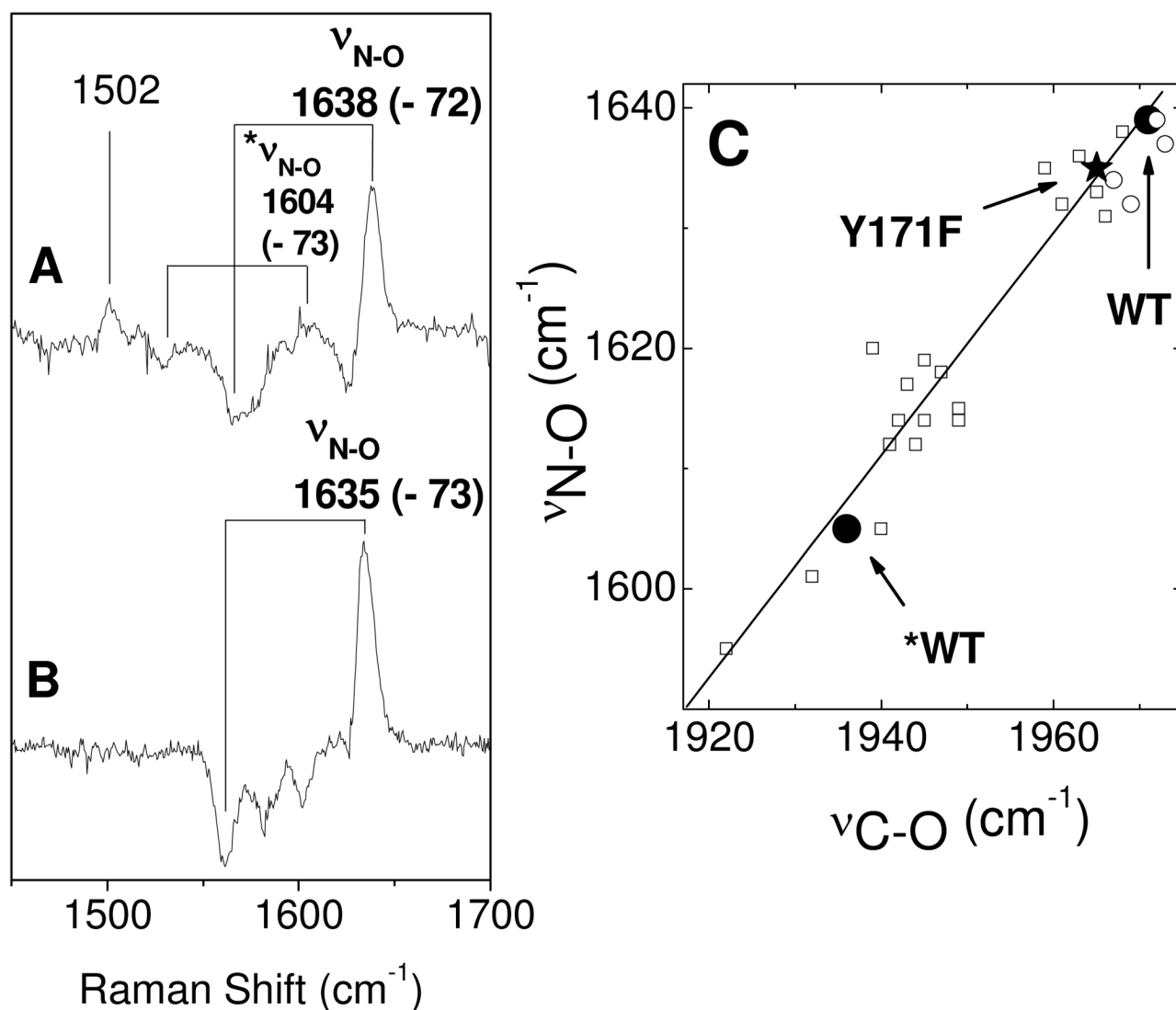


**Figure 4.** Low-frequency RR spectra of ferrous deoxy wt DevS (A) and Y171F DevS (B) at room temperature ( $\lambda_{\text{exc}} = 442 \text{ nm}$ ; 10 mW).



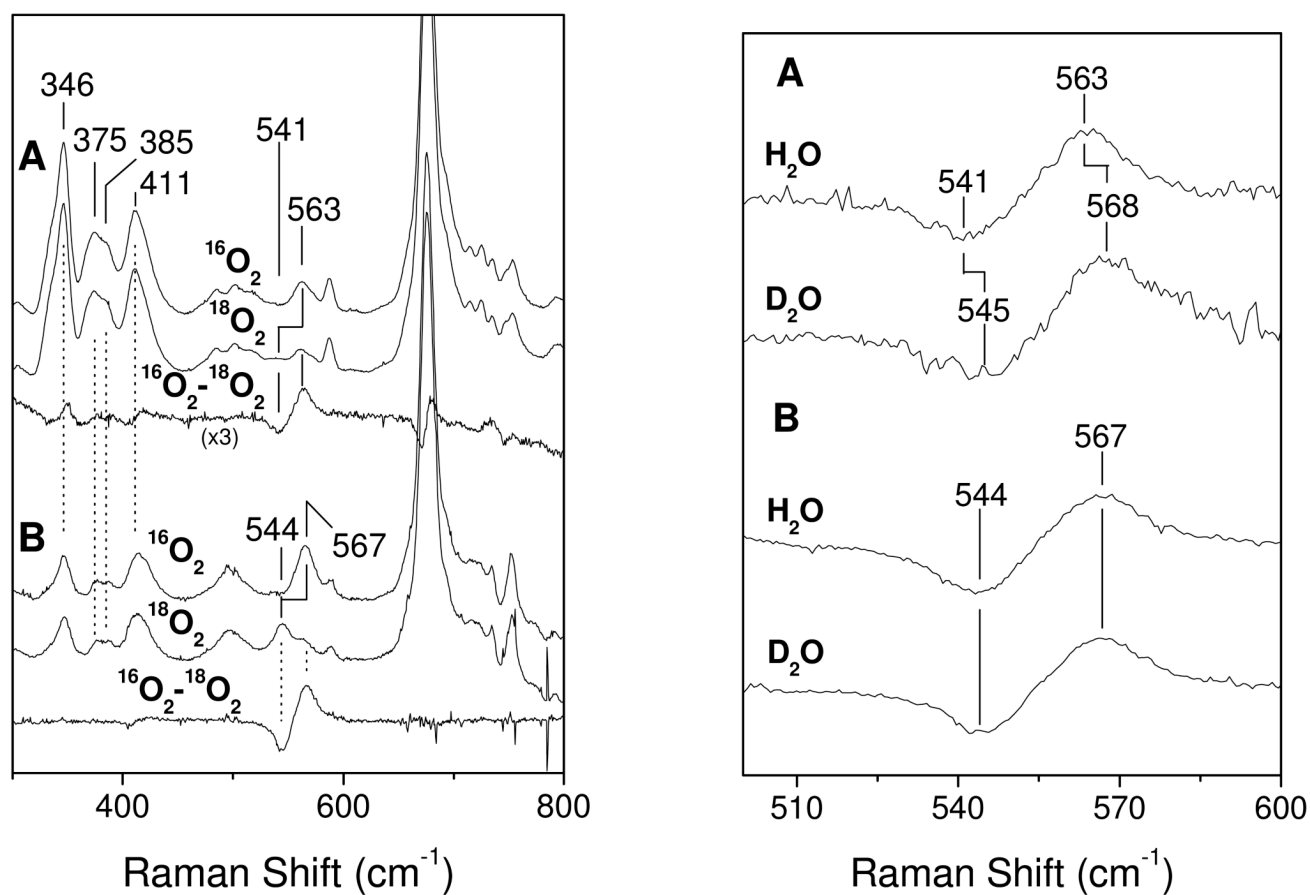
**Figure 5.**

Low- and high-frequency RR spectra of the <sup>12</sup>CO and <sup>13</sup>CO complex of wt DevS (A), and Y171F DevS (B) at room temperature ( $\lambda_{\text{exc}} = 413 \text{ nm}$ ,  $<0.5 \text{ mW}$ ). <sup>12</sup>CO – <sup>13</sup>CO difference spectra are also shown; the asterisk indicates contributions from a minor CO conformer (11).



**Figure 6.**

Left panel: High-frequency RR difference spectra of  $^{14}\text{N}^{16}\text{O} - ^{15}\text{N}^{18}\text{O}$  wt DevS (A) and Y171F (B) ( $\lambda_{\text{exc}} = 413 \text{ nm}$ ; 0.5 mW). The asterisk indicates contributions from a minor NO conformer (11). Right panel:  $\nu(\text{N-O})$  versus  $\nu(\text{C-O})$  plot of heme nitrosyl and carbonyl complexes with proximal His ligation for wt DevS (filled circles, and with asterisk for the minor conformers), Y171F DevS (filled star), wt and distal variants of myoglobin (open squares), and other heme sensor proteins (open circles) (see (11,31) and references therein).



**Figure 7.**

Left panel: Low-frequency RR spectra of wt (A) and Y171F (B) DevS- $^{16}\text{O}_2$ , DevS- $^{18}\text{O}_2$ , and  $^{16}\text{O}_2 - ^{18}\text{O}_2$  difference spectra. Right panel: Low-frequency  $^{16}\text{O}_2 - ^{18}\text{O}_2$  difference spectra<sup>2</sup> of wt DevS in  $\text{H}_2\text{O}$  and  $\text{D}_2\text{O}$  (A), and of Y171F DevS in  $\text{H}_2\text{O}$  and  $\text{D}_2\text{O}$  (B) at room temperature ( $\lambda_{\text{exc}} = 413 \text{ nm}$ ;  $0.5 \text{ mW}$ ).

<sup>2</sup>For both proteins, the solvent H/D exchange was performed by dilution re-concentration cycles in  $\text{D}_2\text{O}$  (99.9% D, Aldrich) to reach enrichment  $>80\%$ . The  $^{16}\text{O}_2 - ^{18}\text{O}_2$  difference spectra were obtained after normalizing the RR spectra on the intense porphyrin  $\nu_7$  at  $676 \text{ cm}^{-1}$ , and the trace for wt DevS was multiplied by a factor 3 to facilitate comparison with that of Y171F DevS. This difference in  $I_{\nu_7}/I_{\nu(\text{Fe-O}_2)}$  is likely to reflect a greater resonance enhancement of the  $\nu(\text{Fe-O}_2)$  mode in Y171F than in wt DevS.

**Table 1**  
UV-Vis Spectroscopic Data for wt and Y171F DevS

DevS Proteins		Soret and visible $\lambda_{\text{max}}$ (nm)		
Fe(III)	wt	406,	500,	630
	Y171F	409,	540,	633
Fe(II)	wt	428,	562	
	Y171F	429,	561	
Fe(II)-CO	wt	422,	570,	540
	Y171F	421,	569,	540
Fe(II)-NO	wt	419,	577,	547
	Y171F	419,	573,	544
Fe(II)-O <sub>2</sub>	wt	414,	578,	543
	Y171F	420,	573,	542



**Table 2**

Resonance Raman frequencies ( $\text{cm}^{-1}$ ) for wt and Y171F DevS in various heme (minor spectral components are in parentheses)

DevS protein	heme state	$\nu_4, \nu_3, \nu_2, \nu_{10}$	$\nu_{C-C}$	$\delta_{CCC}$	$\nu_{Fe-L}$	$\nu_{(X-O)}$
Fe(III)	wt	1370, 1479, 1557, 1609 (1372, 1506, 1579, 1639)	1620, 1629	370, 385		
	Y171F	(n.d., 1478, 1557, n.d.) 1372, 1504, 1578, 1635	1628, 1620sh.	375, 388		
Fe(II)	wt	1355, 1470, 1556, 1604	1620, 1625	348, 364	214 $\nu_{Fe-His}$	
	Y171F	1354, 1470, 1556, 1604	1622broad	348, 364	213 $\nu_{Fe-His}$	
Fe(II)-CO	wt	1372, 1495, 1580, n.d.	1625	379, 387	490 (524)	1971 (1936)
	Y171F	1372, 1496, 1582, n.d.	1626	379, 387	497	1965
Fe(II)-O <sub>2</sub>	wt	1374, 1503, 1578, 1636	1629	375, 385	563	n.o.
	Y171F	1373, 1500, 1578, 1633	1627	375, 385	567	n.o.
Fe(II)-NO	wt	1374, 1498, 1576, n.d.	1626	378, 385	561	1638 (1604)
	Y171F	1375, 1499, 1579, n.d.	1627	378, 385	564	1635