Lignin is a combinatorial polymer comprising monomeric units that are linked via covalent bonds. Although lignin is a potential source of valuable aromatic chemicals, its recalcitrance to chemical or biological digestion presents major obstacles to both the production of second-generation biofuels and the generation of valuable coproducts from lignin’s monoaromatic units. Degradation of lignin has been relatively well characterized in fungi, but it is less well understood in bacteria. A catabolic pathway for the enzymatic breakdown of aromatic oligomers linked via β-aryl ether bonds typically found in lignin has been reported in the bacterium Sphingobium sp. SYK-6. Here, we present x-ray crystal structures and biochemical characterization of the glutathione-dependent β-etherases, LigE and LigF, from this pathway. The crystal structures show that both enzymes belong to the canonical two-domain fold and glutathione binding site architecture of the glutathione S-transferase family. Mutagenesis of the conserved active site serine in both LigE and LigF shows that, whereas the enzymatic activity is reduced, this amino acid side chain is not absolutely essential for catalysis. The results include descriptions of cofactor binding sites, substrate binding sites, and catalytic mechanisms. Because β-aryl ether bonds account for 50–70% of all interunit linkages in lignin, understanding the mechanism of enzymatic β-aryl ether cleavage has significant potential for informing ongoing studies on the valorization of lignin.

The primary obstacle in the production of lignocellulosic biofuels is the release of sugars in high quantities at low cost from recalcitrant biomass feedstocks (1). Lignin is the prime source of this recalcitrance, and there has been renewed interest in the microbial enzymes capable of lignin degradation and catabolism of lignin-derived compounds (2, 3). Generally, white rot fungi secrete lignin peroxidases, versatile peroxidase, manganese peroxidases, and laccases that are involved in the initial degradation of lignin (4, 5), whereas bacteria are thought to play a role in further degradation of lignin-derived lower molecular weight compounds (6).

Sphingobium sp. strain SYK-6, one of the most well studied bacteria implicated in lignin-derived compound degradation, has the ability to grow on a wide variety of dimeric aromatic compounds representing the various units, with their characteristic interunit linkages, present in plant lignins (6, 7). The cleavage of β-aryl ether (termed simply β-ether hereafter) linkages is an essential step in any catabolic process for degradation of lignin-derived aromatic oligomers, because this bond type accounts for 50–70% of all interunit linkages in lignin polymers (8). Using a β-ether-linked phenolic lignin model substrate, guaiacylglycerol-β-guaiacyl ether (GGE; Fig. 1), three enzymatic reactions composing the β-ether degradation pathway were identified in Sphingobium sp. strain SYK-6 (7, 9, 10). Following oxidation of the α-hydroxyl group in GGE by a Cu-dehydrogenase, stereospecific glutathione (GSH)-dependent cleavage of the β-ether linkage in β-(3′-methoxyphenoxo)-γ-hydroxypropiovanillone (MPHPV) is catalyzed by the glutathione S-transferase (GST) enzymes LigE and LigF, forming β-glutathionyl-γ-hydroxypropiovanillone (GS-HPV) and guaiacol. LigE catalyzes stereospecific cleavage of (βR)-MPHPV to (βS)-GS-HPV, whereas LigF catalyzes the cleavage of (βS)-MPHPV to (βR)-GS-HPV. Finally, GSH-dependent and stereospecific elimination of GSH from (βS)-GS-HPV is catalyzed by the GST lyase LigG, generating glutathione disulfide (GSSG) and the

The abbreviations used are: GGE, guaiacylglycerol-β-guaiacyl ether; MPHPV, β-(3′-methoxyphenoxo)-γ-hydroxypropiovanillone; GS-HPV, β-glutathionyl-γ-hydroxypropiovanillone; CPD, cysteine protease domain; FPHPV, β-(1′-formyl-3′-methoxyphenoxo)-γ-hydroxypropioveratrone; F-FPHPV, fluoro-(1′-formyl-3′-methoxyphenoxo)-γ-hydroxypropioveratrone.
achiral derivative γ-hydroxypropiovanillone, which ultimately serves as the growth substrate for strain SYK-6 (6, 10) (Fig. 1). The fate of the corresponding (R)-stereoisomer of GS-HPV is not presently understood. Recently, it has been reported that these GST family member enzymes have the ability to work with lignin-derived materials in vitro (11, 12).

GST superfamily members are multifunctional enzymes often involved in cellular detoxification processes via GSH conjugation (13). However, some bacterial GSTs are implicated in basal metabolism and supply bacterial cells with carbon (14). GSTs with >40% sequence identity are traditionally considered to be in the same class, whereas proteins of different classes have typically <25% protein sequence identity (15). However, these classifications are also based on a number of other considerations, including structure, function, and biochemical properties (15). Although there are seven classes of GSTs in mammals (Alpha, Mu, Pi, Sigma, Theta, Omega, and Zeta), there is an ever-increasing number of non-mammalian classes, including Beta, Chi, Delta, Epsilon, Lambda, Phi, and Tau, as well as a number of more recently defined novel classes (15–17). Previous studies have suggested that the β-etherase enzymes LigE and LigF might be classified in the fungal GST-FuA class of GSTs based on sequence phylogeny (18).

Because plant lignins are racemic polymers, complementary stereospecificities of the multiple enzymes in the β-ether degradation pathway are required by bacteria to oxidize and cleave the various stereoisomers that are present in lignin polymers (19–22). Here, we describe three protein crystal structures and provide the corresponding biochemical data for the LigE and LigF enzymes involved in the β-ether cleavage step of the Sphingobium sp. strain SYK-6 degradation pathway. The modest structural homology of these two enzymes highlights the fitness adaptation afforded in this and probably other microbial catabolic pathways that can degrade lignin-derived materials, required for enzymatic degradation of such racemic products. This work provides new insights into the structure-function relationships and biochemistry of this pathway, expanding our knowledge of the bacterial catabolism of lignin-derived compounds. Because lignin is the most abundant aromatic polymer in nature, this study informs broader lignin valorization efforts that will ultimately enable the development of efficient pathways for the conversion of lignin into renewable aromatics with applications in advanced biofuels and chemicals (23).

**Experimental Procedures**

*Gene Cloning*—LigE was synthesized and cloned into a custom vector (pCPD) assembled by GenScript (Piscataway, NJ). This vector combined the pVP16 backbone (provided by the Center for Eukaryotic Structural Genomics, Madison, WI) with the gene of interest and a C-terminal fusion protein tag containing the Vibrio cholerae MARTX toxin cysteine protease domain (CPD) (24). During protein purification, the CPD tag can be activated by the addition of inositol hexakisphosphate, cleaving at a leucine positioned between the N terminus protein

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**FIGURE 1. The Sphingobium sp. strain SYK-6 β-etherase pathway.** Chiral carbons at which stereospecific reactions occur are highlighted (red). Stereospecific reactions for (αS,βR)-GGE and (αS,βS)-GGE oxidation (by LigL and LigN) and for (αR,βR)-GGE and (αR,βS)-GGE oxidation (by LigD and LigO), the GSH-dependent stereospecific cleavage reactions of (βR)-MPHPV (by LigE) and (βS)-MPHPV (by LigF), and the stereospecific lyase reaction of LigG with (βS)-GS-HPV are shown.
TABLE 1
LigE and LigF statistics

Summary of crystal parameters, data collection, and refinement statistics. Values in parentheses are for the highest resolution shell.

|                      | LigEΔ242-GSH | LigEΔ255 | LigEΔ255-GSH |
|----------------------|--------------|----------|--------------|
| Crystal parameters   |              |          |              |
| Space group          | P632         | C2       | C2           |
| Unit cell parameters | a, b, c (Å)  | 123.71, 123.71, 66.42 | 122.55, 97.15, 131.38 | 121.00, 96.13, 126.16 |
| β                    |              | 106.65   | 81.52        |
| Data collection      |              |          |              |
| Wavelength ( Å)      | 0.9785       | 0.999    | 1.000        |
| Resolution range ( Å) | 50.00–2.07  | 50–1.90 (1.93–1.90) | 50–2.6 (2.65–2.60) |
| No. of reflections (measured/unique) | 336,246/18,884 | 575,459/114,153 | 160,219/42,163 |
| Completeness (%)     | 99.8 (98.5)  | 99.2 (99.9) | 97.7 (93.8)  |
| Rmerge a             | 0.076 (0.637) | 0.137 (0.63) | 0.135 (0.61) |
| Redundancy           | 17.3 (12.9)  | 5.0 (4.9)  | 3.8 (3.6)    |
| Mean I(σ(I))         | 9.1 (3.8)    | 9.0 (1.6)  | 6.1 (2.5)    |
| Refinement and model statistics |              |          |              |
| Resolution range ( Å) | 40.49–2.07  | 48–1.90 (1.95–1.90) | 48–2.6 (2.65–2.60) |
| No. of reflections (work/test) | 17,278/964 | 114,138/1,999 | 42,158/2,000 |
| Rmerge b             | 0.161 (0.182) | 0.227 (0.289) | 0.222 (0.266) |
| Rfree c              | 0.214 (0.263) | 0.271 (0.350) | 0.267 (0.290) |
| Root mean square deviation bonds (Å) | 0.008 | 0.004 | 0.003 |
| Root mean square deviation angles (degrees) | 1.022 | 0.956 | 0.776 |
| B factor (protein/solvent) (Å²) | 39.58/43.93 | 29.13/37.54 | 34.22/27.38 |
| B factor (GSH) (Å²) | 26 | 146, 148, 149, 146 |
| No. of protein atoms | 1,983 | 9,405 | 8,491 |
| No. of waters        | 229 | 1,159 | 165 |
| Auxiliary molecules (real space correlation coefficient (CC)) | 1 glutathione (0.97), 1 Tris (0.95), 1 PEG (0.95) | 4 glutathione (1 per chain), A = 0.71, B = 0.58, C = 0.58, D = 0.61 |
| Ramachandran plot    |              |          |              |
| Favorable region     | 98.4         | 95.8     | 94.4         |
| Additional allowed region | 1.6 | 3.0 | 4.3 |
| Disallowed region    | 0            | 1.2      | 1.3          |
| Protein Data Bank entry | 4XT0         | 4YAM     | 4YAN         |

a Rmerge = Σᵢ|İᵢ(h)–İᵢ(0)|/Σᵢİᵢ(0), where İᵢ(0) is the intensity of an individual measurement of the reflection, and (İ(h)) is the mean intensity of the reflection.

b Rcryst = Σᵢ|Fᵢᵢ(obs)|–|Fᵢᵢ(calc)|/Σᵢ|Fᵢᵢ(obs)|, where Fᵢᵢ(obs) and Fᵢᵢ(calc) are the observed and calculated structure factor amplitudes, respectively.

c Rfree was calculated as Rcryst using 5.0% of randomly selected unique reflections that were omitted from the structure refinement.

of interest and CPD. The pVP80K_LigΔ242 vector was prepared using polymerase incomplete primer extension as described previously using Phusion High-Fidelity PCR master mix with HF buffer (New England Biolabs Inc., Ipswich, MA), and primers from Integrated DNA Technologies (Coralville, IA) (25). The pVP80K vector was provided by the Center for Eukaryotic Structural Genomics (Madison, WI), and the pVP102KSSLigF vector containing full-length wild type LigF was prepared as described previously (9). Insert and vector backbone PCR products were mixed 1:1 and immediately transformed into Escherichia coli One Shot TOP10 cells (Invitrogen). The pVP80K_LigΔ242 vector was purified from E. coli (One Shot® TOP10, 10 ml of LB with kanamycin, 18 h at 37 °C) using the QIAprep® spin miniprep kit (Qiagen, Germantown, MD) and transformed into the laboratory strain E. coli B834(DE3) Z-competent cells (Zymo Research, Orange, CA). The N-terminally His-tagged LigΔ242 fusion protein was purified from the supernatant by immobilized nickel affinity chromatography using a HiTrap Q HP anion exchange column on an ÄKTA FPLC system (GE Healthcare, Piscataway, NJ). Fractions containing LigE, as confirmed by SDS-PAGE, were pooled and concentrated. Final protein cleanup was done using gel filtration on a Superdex 200 10/300 GL column (GE Healthcare).

The N-terminally His-tagged LigΔ242 fusion protein was purified from the supernatant by immobilized nickel affinity chromatography using a HiTrap Q HP anion exchange column on an ÄKTA FPLC system (GE Healthcare, Piscataway, NJ). Fractions containing LigΔ242, as determined by SDS-PAGE, were combined and dialyzed overnight at 4 °C. LigΔ242 was cleaved from the fusion protein using tobacco etch virus protease (1 mg/100 mg of protein) provided by the Center for Eukaryotic Structural Genomics). Following cleavage, LigΔ242 and the polyhistidine tag were separated using a HiTrap Q HP anion exchange column. Pooled fractions containing LigΔ242, as confirmed by SDS-PAGE, were pooled and concentrated to 3
Final size exclusion purification was performed on a HiLoad™ 26/60 Supradex™ 200 preparation grade column. Enzyme Kinetic Assays—In vitro /H9252-etherase assays with LigE, LigF, LigF/H9004 242, and LigF/H9004 242-S13A were conducted in an aqueous assay buffer (25 mM Tris, 2.5% DMSO, 5 mM GSH, pH 7.0–10.0) at 30 °C with an initial substrate concentration of 1.5 mM and enzyme concentrations of either 160 nM (LigE), 170 nM (LigF), 180 nM (LigF/H9004 242), 3.9 M (LigF/H9004 242-S13A), 11.2 M (LigE with (S)-F-FPHPV), or 12.0 M (LigF with (R)-F-FPHPV). Enantiopure preparations of (R)-FPHPV and (S)-FPHPV were obtained from chiral chromatographic separation of the parent racemate as described previously (9). Similarly, chiral chromatography was used for the separation of (S)-F-FPHPV and (R)-F-FPHPV, with (S)-F-FPHPV being used as a substrate in the LigE assays. Synthesis and purification details for enzymatic substrates FPHPV and F-FPHPV are described in the supplemental material.

Michaelis-Menten curves were generated by measuring the enzymatic specific activities over a range of initial substrate concentrations (1.50, 1.25, 1.00, 0.75, 0.50, and 0.25 mM) obtained from serial dilution of a 1.5 mM substrate buffer made immediately prior to conducting the assays. The 1-ml assays were conducted in triplicate and were managed as follows: 1) the substrate was dissolved in DMSO at 60 mM, and 25 µl were added to a 2-ml vial; 2) 875 µl of 25.7 mM Tris, pH X, was added (where X is higher than the intended pH of the assay to account for the acidic effect of GSH (e.g. pH X = 11.5 drops to pH 8.0 after the addition of 5 mM GSH)); 3) 50 µl of 100 mM GSH was added (100 mM GSH stock solution was prepared by adding GSH to 25 mM Tris (pH X)); 4) 50 µl of 20× concentrated enzyme was added; 5) 150-µl samples were collected after 0, 6, 12, 18, 24, and 30 s of incubation, and enzymatic activity was abolished by pipetting each sample into 5 µl of 5 M phosphoric acid; and 6) the remaining reaction volume was used to measure the pH of the mixture with pH paper.

Each sample was then subjected to C18-reversed phase HPLC using a Beckman 125NM solvent delivery module equipped with a Beckman 168 UV detector. Samples and external standards were quantified by UV absorption at 280 nm. The HPLC mobile phase was a mixture of aqueous buffer (5 mM formic acid in 95:5 water/acetonitrile) and methanol at a flow rate of 1.0 ml/min. The ratio of buffers was adjusted as follows: 0–6 min, 30% methanol; 6–15 min, gradient from 30 to 80% methanol; 15–25 min, 80% methanol; 25–26 min, gradient from 80 to 30% methanol; 26–33 min, 30% methanol. Vanillin concentrations were quantified for each time point, and a linear regression was generated over the 30-s assay period in order to calculate the specific activity of each reaction. Averages of the triplicate assays were reported.
**Sphingobium LigE and LigF Crystal Structures**

**FIGURE 3. Theoretical and experimental small angle x-ray scattering scatter curves.** The scattering angle (q) versus the intensity of the scattering plots shows the experimentally observed data and the theoretical scattering determined using CRYSOI from the x-ray structures of the dimers. LigF is shown at the top in blue, and LigE is shown at the bottom in red.

**Crystallization**—LigE was concentrated to 9 mg ml$^{-1}$ and dialyzed against 20 mM HEPES, pH 7.4, and 50 mM NaCl. LigF was dialyzed in 10 mM HEPES buffer, pH 7.5, containing 50 mM sodium chloride, 0.5 mM tris(2-carboxyethyl)phosphine, and 1 mM GSH, and concentrated to 18.5 mg ml$^{-1}$. LigE and LigF proteins were screened using the sparse matrix method (27) with a Phoenix Robot (Art Robbins Instruments, Sunnyvale, CA) and a Mosquito dispenser (TTP LabTech, Melbourne, UK) utilizing the following crystallization screens: Berkeley Screen (Lawrence Berkeley National Laboratory), Crystal Screen, SaltRx, PEG/Ion, Index and PEGRx (Hampton Research, Aliso Viejo, CA), and JSCG-plus HT-96 and PACT premier HT-96 (Molecular Dimensions, Altamonte Springs, FL). The optimum conditions for crystallization of the different pathway proteins were found as follows: LigE, 0.1 M ammonium citrate, 0.1 M MES, pH 5.5, 20% PEG 3,350, and 5% isopropl alcohol; LigF, 25% polyethylene glycol monomethyl ether 2000, 0.25 M trimethylamine N-oxide, and 0.1 M Tris, pH 8.5. LigE crystals were obtained after 2–7 days by the sitting drop vapor diffusion method with the drops consisting of a mixture of 0.2 μl of protein solution and 0.2 μl of reservoir solution. LigF crystals were obtained in <24 h with drops containing a mixture of 1 μl of protein solution, 0.8 μl of reservoir solution, and 0.2 μl of seed crystals (pulverized LigF$\Delta$242 crystals in 0.2 M magnesium formate, 30% polyethylene glycol 3350, and 1 mM GSH).

**X-ray Data Collection and Structure Determination**—The LigE crystals were placed in a reservoir solution containing 10–20% (v/v) glycerol and then flash-cooled in liquid nitrogen. The x-ray data sets for LigE were collected at the Berkeley Center for Structural Biology beamlines 8.2.1 and 8.2.2 of the Advanced Light Source at Lawrence Berkeley National Laboratory. LigF crystals were cryoprotected with a reservoir solution containing 30% polyethylene glycol monomethyl ether 2000 and 1 mM GSH. X-ray diffraction data were collected at Life Sciences Collaborative Access Team Sector 21 with x-ray wavelength 0.9793 at the Advanced Photon Source at Argonne National Laboratory. Data sets were indexed and scaled using HKL2000 (28). The LigF crystal structure was determined by molecular replacement using the program PHASER (29) within the Phenix suite (30) with the coordinates of a LigF homologue (Lig37), whose sequence was identified from a metagenomic analysis of a rice-straw-enriched compost microbial community (Berkeley, CA) (31, 32). The crystal structure of LigE was solved using selenomethionine-labeled protein by the single-wavelength anomalous dispersion method (33) with the phenix.autosol (34) and phenix.autobuild (35) programs. Structure refinement was performed using the phenix.refine program (36). Manual rebuilding using COOT (37) and the addition of water molecules allowed construction of the final models. Root mean square deviation differences from ideal geometries for bond lengths, angles, and dihedrals were calculated with Phenix (30). The overall stereochemical quality of all final models was assessed using the program MOLPROBITY (38), and all figures were generated in PyMOL (39). Structures were observed and analyzed using a stereoscopic television display (40).

**Small Angle X-ray Scattering**—LigE and LigF were dialyzed for 15 h at 4 °C into buffer containing 10 mM HEPES, pH 7.5, 50 mM sodium chloride, 1 mM GSH, and 0.5 mM tris(2-carboxyethyl)phosphine. Prior to data collection, samples were filtered through a 0.2-μm syringe filter and diluted to the working concentrations. After dilution, samples were clarified via centrifugation. The buffer blank was also syringe-filtered and clarified by centrifugation. Small angle scattering data were collected on a Bruker NANOSTAR x-ray generator located at the National Magnetic Resonance Facility at the University of Wisconsin (Madison, WI). Three data collections of 1 h each were taken for each sample and buffer. Data were merged and indexed using the Bruker NANOSTAR small angle x-ray scattering system software (Bruker AXS, Madison, WI). The scattering intensity was obtained by subtracting the scattering of the buffer blank from the sample scattering using the PRIMUS software (41). All SAXS data were processed using GNOM, integrated in the PRIMUS software, to obtain the pair distance distribution function (42). The GNOM output was used with DAMMIF to calculate 10 ab initio dummy atom models (43). Models were averaged using DAMAVER and aligned to x-ray crystal structures using SUPCOMB (44, 45). Theoretical scattering curves for the x-ray crystal structure of LigE and a model of the dimer of LigF were calculated using CRYSOI (46).

**Molecular Docking**—Docking of MPHPV to the LigF$\Delta$242-GSH structure was performed using the SwissDock server (47, 48). Docking was performed using the “Accurate” parameter.
Results

Structural Analysis—Attempts to solve the structure of full-length wild-type LigE (282 residues) and LigF (254 residues) were unsuccessful, but C-terminal truncation constructs of both proteins were generated, successfully crystallized, and used for structural analysis. Truncations of LigE and LigF were designed based on homology models generated by I-TASSER Online and disorder predictions generated using PONDR (52, 53). LigEΔ255 and the LigEΔ255-GSH complex crystallized in the space group C2 with four molecules in the asymmetric unit with electron density for the bound GSH molecule. LigFΔ242-GSH crystallized in the space group P6_22 with one molecule in the asymmetric unit. Well defined electron density corresponding to the GSH molecule is also visible in the structure. Data collection, refinement, and model statistics for LigE and LigF are summarized in Table 1.
Consistent with their classification as GST enzymes, LigE and LigF each adopt the canonical GST domain fold with an N-terminal thioredoxin domain (residues 1–82 and 1–76, respectively) and a C-terminal α-helical domain (residues 93–255 and 93–242, respectively) connected by a short linker (residues 83–92 and 77–92, respectively) (Fig. 2). In both LigE and LigF, the thioredoxin domain comprises four β-strands and three α-helices following the topology β1α1β2α2β3β4α3. The loop between β1 and α1 is longer in LigE than in LigF and occupies the space between the thioredoxin domain and the α-helical domain, whereas in LigF, this loop is moved away from the domain interface toward the surface of the thioredoxin domain. The loop between β2 and α2 is longer in LigF than in LigE, but both interact with the α-helical domain on the protein face opposite the linker (Fig. 2). The C-terminal domains of both LigE and LigF are composed of six and eight α-helices, respectively. The root mean square deviation between the C-α locations of monomers of LigE and LigF is 4.42 Å, indicating that, although they catalyze very similar reactions, the enzymes display significant structural differences.

Biochemical and small angle x-ray scattering data suggest that both LigE and LigF exist as dimers in solution, and these dimers, related by 2-fold symmetry, can be seen in the respective crystal structures. The dimer interface accounts for 1,066 and 1,092 Å² of buried surface area in LigE and LigF, respectively (PISA European Bioinformatics Institute) (54). The overall dimeric shapes of both LigF and LigE were confirmed using small angle x-ray scattering on both the truncated and full-length proteins. The protein envelopes determined by ab initio modeling align well with the crystal structures of both proteins (Fig. 2). The theoretical scattering curves predicted from the x-ray structures match well with the experimentally determined scattering curves with a χ value of 2.4 and 1.4 for LigF and LigE, respectively (Fig. 3).

The LigF dimer forms via interactions between helices α3 and α4, in the thioredoxin and C-terminal domains, respectively, of each monomer, forming a four-helix bundle. The dimer interface is largely polar, lacking the traditional lock-and-key motif or hydrophobic surface common in other GST dimers, specifically the Alpha, Pi, and Mu classes (14, 15). The LigF dimer more closely matches those of the Beta or Theta class, which, like LigF, lack a hydrophobic lock-and-key motif, and there is no open V-shape to the dimer interface (14). Although the arrangement and characterization of the dimer forms in GST structures differ within and between classes, most are canonically anchored through contacts between α3 (or the final helix of the thioredoxin domain) and α4 (the first helix in the C-terminal domain) (13, 15, 55, 56). Variability in the arrangement of secondary structural elements away from the α3/α4 four-helix bundle changes the total buried surface area of the various GST dimers as well as changing the architecture of the enzyme in the vicinity of the active site (57). Representative structures demonstrating the variability of dimer packing in GSTs are shown in Fig. 4. The Alpha (Protein Data Bank entry 1GUH, human GST A1-1), Mu (2GST, rat), Pi (2GSR, pGST P1-1 from pig), Sigma (1GSQ, squid), Theta (1LJR, human hGST T2-2), Beta (2PMT, bacterial GST from Proteus mirabilis), Omega (3FL, human GST Omega-1), and LigG (4G10, Sphingobium sp. SYK-6) dimers show variations on the α3/α4 canonical 4-helix bundle dimer structure (58–65). In the LigE
Sphingobium LigE and LigF Crystal Structures

The enzymatic active sites of these GST family members are often located in a cleft between the thioredoxin domain and the \( \alpha \)-helical domain (15). Both the LigE and LigF enzymes contain the \( \beta \beta \alpha \) motif required for anchoring GSH in the active site (56). In LigF, Glu-65 and Ser-66 located in the turn connecting \( \beta 4 \) and \( \alpha 3 \), recognize the \( \gamma \)-glutamyl moiety of GSH as part of the \( \beta \beta \alpha \) motif (Fig. 5A). Additionally, Gln-52 and the backbone of Val-53 interact with the cysteinyl moiety, whereas Gln-144, His-40, Tyr-148, and Gln-39 anchor the glycine residue of the active site GSH molecule. In LigE, Asp-71 and Ser-72, both located in the turn between \( \beta 4 \) and \( \alpha 3 \), hydrogen-bond with the amino and carboxylate groups, respectively, of the \( \gamma \)-glutamyl residue of the GSH molecule (Fig. 5B). Additionally, the backbone of Val-59 interacts with the cysteinyl moiety, whereas weak hydrogen bonds are formed between the GSH glycine and Arg-138 and Tyr-133.

Due to the occlusion of one face of the GSH binding pocket in LigF, we propose that the substrate binding site is located on the opposite face of the LigF monomer from the dimer interface (Fig. 2B, black circle). In the absence of a substrate-bound structure, SwissDock (47, 48) was used to generate a LigF\( \Delta 242 \)-GSH-(\( \beta 5 \))-MPHPV complex model (Fig. 6A) from the LigF\( \Delta 242 \)-GSH structure and a molecular model of (\( \beta 5 \))-MPHPV. The model supports our assignment of the substrate binding site. However, in LigE, this side of the GSH binding pocket is blocked by a number of loops, whereas the face of the GSH binding site shared with the dimer has been opened, due to the dimer rearrangement (Fig. 2D, black circle). Based on the binding site of GSH in LigE, we propose a potential location for the native substrate-binding site at the highly hydrophobic region consisting of residues Tyr\(^{23} \), Phe\(^{45} \), Trp\(^{107} \), Phe\(^{115} \), Tyr\(^{133} \), and Trp\(^{197} \) (Fig. 6B). The aromatic rings of these hydrophobic residues are probably important in stacking interactions with the aromatic compounds from low molecular weight lignin derivative compounds.

The LigE\( \Delta 255 \)-GSH and LigF\( \Delta 242 \)-GSH structures revealed LigE Ser-21 (Fig. 5B) and LigF Ser-13 (Fig. 5A) as potential catalytic residues, based on their proximities to the thiol of the bound GSH. To further investigate the roles of LigE Ser-21 and LigF Ser-13 in \( \beta \)-etherase catalysis, variants LigE-S21A and LigF\( \Delta 242 \)-S13A, in which serine residues were replaced with alanine, were expressed, purified, and tested for activity in the \( \beta \)-etherase assays.

**Enzymatic Analysis and Mutagenesis**—To analyze the enzymatic activities of the GSH-dependent \( \beta \)-etherase enzymes, FPHPV degradation rates were measured by the accumulation of vanillin, a monoaromatic product of FPHPV cleavage (Figs. 7 and 8). Whereas \( \beta \)-etherase catalysis with MPHPV results in the release of guaiacol (Fig. 1), vanillin is more easily detected by UV absorption, thus improving the sensitivity of the assays. In addition to LigE and LigF, we tested the rates of \( \beta \)-etherase catalysis for LigE variant LigE-S21A and two LigF variants, LigF\( \Delta 242 \) and LigF\( \Delta 242 \)-S13A.

We found that LigE catalysis resulted in stereospecific (\( \beta R \))-FPHPV cleavage, whereas LigF selectively degraded the (\( \beta S \))-FPHPV enantiomer, as is consistent with previous reports (7,
Sphingobium LigE and LigF Crystal Structures

A

\[(\beta R)-FPHPV\]  
\[\text{LigE}\]  
\[\text{GSH}\]  
\[\text{vanillin}\]  
\[\text{GS-HPV}\]  

\[(\beta S)-FPHPV\]

B

\[(\beta S)-FPHPV\]  
\[\text{LigE}\]  
\[\text{GSH}\]  
\[\text{vanillin}\]  
\[\text{GS-HPV}\]  

\[(\beta R)-GS-HPV\]

The effect of pH on β-etherase activities was determined for each enzyme, revealing that LigE (circles), LigF (squares), LigF \(\Delta 242\) (diamonds), and LigF \(\Delta 242\)-S13A (squares) have pH optima at pH 8.0. Plotted as a function of pH (x axis) are the specific enzymatic activities (y axis) of β-etherases with either (\(\beta R\))-FPHPV (LigE) or (\(\beta S\))-FPHPV (LigF, LigFA242, and LigF \(\Delta 242\)-S13A) as the assay substrate (1.5 mM initial concentration). Error bars, S.D. of triplicate measurements.

Because LigF Ser-13 was the only potential acid-base catalyst revealed in the active site of the LigF \(\Delta 242\)-GSH structure (Fig. 5A), we hypothesized that an \(S_{\text{n2}}\)-type nucleophilic attack mechanism is responsible for catalysis in LigF. The LigF \(\Delta 242\)-GSH-(\(\beta S\))-MPHPV complex model, generated using SwissDock (47, 48), revealed that the GSH thiolate is in the appropriate orientation for an \(S_{\text{n2}}\) attack relative to the substrate β-carbon.

The LigE \(\Delta 255\)-GSH structure revealed several potential catalytic residues in the active site, leaving open the possibility that the LigE β-etherase mechanism involves additional acid-base reactions. A substrate analog model compound, (\(\beta S\))-fluoro-(1′-formyl-3′-methoxyphenoxo)-γ-hydroxypropioveratrone [(\(\beta S\))-F-FPHPV] (Fig. 7), was used to test the possibility of a non-\(S_{\text{n2}}\) mechanism that would involve the deprotonation of the β-carbon of the substrate. (\(\beta S\))-F-FPHPV and (\(\beta R\))-FPHPV (despite their Cahn-Ingold-Prelog-derived R/S notations (66)) have the same enantiomeric configuration with respect to the orientation of their β-ether bonds and differ only in replacement of the hydrogen at the β-carbon in (\(\beta R\))-FPHPV with a fluorine in (\(\beta S\))-F-FPHPV, and this fluorine is predicted to inhibit deprotonation. We found that LigE catalyzed conversion of (\(\beta S\))-FPHPV to vanillin and a glutathione-conjugated coproduct, albeit at a much lower velocity compared with cleavage of (\(\beta R\))-FPHPV (Table 2), exactly as predicted based on the hypothesis that an \(S_{\text{n2}}\) catalytic mechanism would not involve deprotonation of the β-proton. Based on NMR analysis of the reaction products, we conclude that the LigE-catalyzed β-ether cleavage of (\(\beta S\))-FPHPV resulted in formation of the expected glutathione-conjugated product, (\(\beta S\))-F-GS-HPV. Although it is unclear why the reaction with (\(\beta S\))-FPHPV was some 3 orders of magnitude slower than LigE-catalyzed cleavage of (\(\beta R\))-FPHPV (Table 2), we hypothesize that the fluorine atom affects the β-ether bond angle and inhibits the approach of the thiolate ion for \(S_{\text{n2}}\) elimination. It is possible that these effects were even more pronounced in the active site of LigF, because LigF showed no detectable activity with the (\(\beta R\))-F-FPHPV enantiomer.
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**TABLE 2**

LigE and LigF kinetic parameters

| Enzyme   | Substrate          | $V_{\text{max}}$ a | % WT activity with (bS)-FPHPV b | $k_{\text{cat}}$ | $K_{\text{m}}$ | $k_{\text{cat}}/K_{\text{m}}$ |
|----------|--------------------|--------------------|-------------------------------|------------------|--------------|--------------------------|
| LigE     | (bR)-FPHPV         | 59.7 ± 1.2         | 100                            | 31.9 ± 0.6       | 554 ± 16     | 57.6 ± 4.8               |
| LigE-S21A| (bR)-MPHPV         | 63.8 ± 0.4         | 13.5 b                         | 31.9 ± 0.1       | 269 ± 1      | 118.4 ± 1.1              |
| LigF     | (bS)-FPHPV         | 69.3 ± 4.9         | 100                            | 269 ± 1          |              |                          |
| LigF242  | (bS)-FPHPV         | 1.5 ± 0.1 a        | 100                            | 269 ± 1          |              |                          |
| LigF242-S13A | (bS)-FPHPV | 0.02 a            | 100                            | 269 ± 1          |              |                          |
| LigF     | (bS)-F-MPHPV       | NDA                |                                |                  |              |                          |

*Where noted (i.e., in the absence of Michaelis-Menten curves), activity is reported as the velocity from assays in which the initial substrate concentration was 1.5 mM.

Where noted, independent assays using substrate (bR)-MPHPV and either LigE or LigE-S21A as catalysts indicated that the LigE $V_{\text{max}}$ was approximately 7-fold greater than that for LigE-S21A.

**Discussion**

The biocatalytic breakdown of lignin-derived compounds represents a potential source of aromatic products that would be valuable for the chemical, food, and pharmaceutical industries (2). In contrast to known fungal systems, the bacterium *Sphingobium* sp. strain SYK-6 possesses an enzymatic route to the breakdown of lignin-derived components that is stereospecific and independent of chemical mediators and requires common cellular cofactors, such as pyridine nucleotides and glutathione. These combined structural and biochemical studies of the $\beta$-aryl ether cleavage pathway enzymes provide insights into the features important for substrate and cofactor binding and catalysis. We propose that both LigE and LigF cleave $\beta$-ether-linked lignin dimer molecules via an $S_N\text{2}$ nucleophilic attack on the $\beta$-carbon of the substrate that is consistent with previous results showing inversion of the chiral center at the $\beta$-carbon (9). Because LigE catalyzed the conversion of (bS)-F-FPHPV to (bS)-F-GS-HVP, we conclude that the LigE mechanism is unlikely to involve formation of an enzyme-substrate adduct and does not involve C$\beta$ deprotonation or substrate enolization.

Although the sequences and x-ray crystal structures show a conserved serine in the active site of both LigE and LigF (serine 21 and 13, respectively) near the thiol of the bound glutathione (4.1 and 5.4 Å, respectively; Fig. 5), the serine is not essential for catalysis. In both LigE and LigF, mutation of the active site serine greatly reduced, but did not abolish, the enzymatic activity and did not shift the pH optimum, indicating that it may play a role other than deprotonation of the GSH thiol or perturbation of the apparent $K_p$ of the bound glutathione. A conserved catalytic serine is a characteristic of the Theta class, Zeta class, and some bacterial GSTs (15), but there is evidence of GSTs from the bacteria *P. mirabilis, Ochrobactrum anthropi*, and *E. coli* in which this active site serine is not critical for catalytic activity (67–69). Based on the data presented here and support from previous studies, it is clear that although the active site serine is not responsible for the direct activation of the thiolate anion by deprotonation or perturbation of the $pK_a$ of the bound glutathione, it may be active in binding GSH in the active site, orienting the thiol group of GSH in the catalytic step, or stabilization of the transition state. Because GSH-dependent cleavage of these molecules does not occur readily in vitro in the absence of enzyme, it may be that the enzyme is able to stabilize the thiolate anion via a network of interactions within the active site or that the binding of the substrates in the optimal orientation and distance for the $S_N\text{2}$ attack is sufficient for catalysis.

The structures of the LigE and LigF enzymes also highlight the nature of stereospecific control that is key to this pathway. These enzymes possess dramatically different structural arrangements within the monomers and different dimer interfaces, reflected in very different dimer shapes. As a result, the substrate binding surfaces of the two enzymes are on opposite faces of the thioredoxin domain and glutathione binding site. This observation means that if a substrate with the wrong stereochemistry were to bind, it would not be in the correct orientation with respect to the glutathione for catalysis, hence introducing stereospecificity. Due to the completely different geometry of the active site, there is no simple set of mutations that would switch substrate specificity or make each individual enzyme more promiscuous.

Based on structural properties, LigE is most similar to the fungal GSTFuA class (13), suggesting that the enzymes in this class are present in both prokaryotes and fungi. Other representatives in this class are from saprotrophic fungi, suggesting a functional connection among the members of the class (18). Although it has been suggested that LigF also belongs in the GSTFuA class (13), the dimer interface present in the structure is inconsistent with other members of the class. Based on our data, LigF is best placed in a new structural class closely related to GSTFuAs or as a fungal Ure2p-like GST based on structural similarities and function in saprotrophic organisms, although it does not strictly fit the class (70). Assignments to different GST family classes, combined with the structural and biochemical information presented here, suggest that LigE and LigF evolved to cleave unique stereoisomers of the aromatic dimers that are predicted to be found in plant lignins.

The detailed structural and biochemical characterization of LigE and LigF in this study and other members of the $\beta$-aryl etherase pathway reveal important new aspects of the enzyme mechanism and the determinants of substrate stereospecificity. Future enzyme engineering studies informed by these results may focus on optimizing the pathway for catalysis of specific lignin-derived compounds, formed as byproducts of industrial biomass processing, into suitable products for use as, or precursors of, advanced biofuels and renewable chemicals.
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Author Contributions—K. E. H. designed experiments, produced protein, solved structure, analyzed LigF structure, performed all small angle x-ray scattering experiments, co-wrote the initial draft of manuscript, designed and compiled figures, and edited the manuscript; J. H. P. designed experiments, produced protein, solved structure, analyzed LigE structures, co-wrote initial draft of manuscript, and edited. D. L. G. designed experiments, synthesized substrates, cloned genes, expressed protein, performed enzymatic assays, co-wrote the initial draft of the manuscript, and edited the manuscript; R. A. H. designed experiments, synthesized substrates, cloned genes, expressed protein, performed enzymatic assays, and edited the manuscript; R. P. M. performed crystallographic data collection; C. B. designed experiments, assisted in construct design and crystallomtics, and coordinated x-ray data collection; K. D. synthesized substrates; K. C. H. produced protein; D. R. N. designed experiments, led enzymology on LigF, provided substrates, and edited the manuscript; B. A. S. provided research direction, contributed lignin-specific and ligninolytic enzyme expertise, and edited the manuscript; K. L. S. provided research direction, contributed lignin-specific and ligninolytic enzyme expertise, and edited the manuscript; J. R. provided research direction, contributed lignin-specific expertise, and edited the manuscript; T. J. D. provided research direction, contributed microbiological specific expertise, and edited the manuscript; P. D. A. provided research direction, contributed crystallographic and structural biology expertise, and edited the manuscript; G. N. P. provided research direction, contributed crystallographic and structural enzymology expertise, and edited the manuscript.

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