Biochemical Properties and Crystal Structure of a β-Phenylalanine Aminotransferase from *Variovorax paradoxus*


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By selective enrichment, we isolated a bacterium that can use β-phenylalanine as a sole nitrogen source. It was identified by 16S rRNA gene sequencing as a strain of *Variovorax paradoxus*. Enzyme assays revealed an aminotransferase activity. Partial genome sequencing and screening of a cosmid DNA library resulted in the identification of a 1,302-bp aminotransferase gene, which encodes a 46,416-Da protein. The gene was cloned and overexpressed in *Escherichia coli*. The recombinant enzyme was purified and showed a specific activity of 17.5 U mg⁻¹ at 30°C and 33 U mg⁻¹ at the optimum temperature of 55°C. The β-specific aminotransferase exhibits a broad substrate range, accepting ortho-, meta-, and para-substituted β-phenylalanine derivatives as amino donors and 2-oxoglutarate and pyruvate as amino acceptors. The enzyme is highly enantioselective toward (S)-β-phenylalanine (enantioselectivity [E], > 100) and derivatives thereof with different substituents on the phenyl ring, allowing the kinetic resolution of various racemic β-amino acids to yield (R)-β-amino acids with >95% enantiomeric excess (ee). The crystal structures of the holoenzyme and of the enzyme in complex with the inhibitor 2-aminoxyacetate revealed structural similarity to the β-phenylalanine aminotransferase from *Mesorhizobium* sp. strain LUK. The crystal structure was used to rationalize the stereo- and regioselectivity of *V. paradoxus* aminotransferase and to define a sequence motif with which new aromatic β-amino acid-converting aminotransferases may be identified.

Various nonproteinogenic β-amino acids occur naturally as free metabolites and as components of biosynthetic products (1). The simplest β-amino acid, β-alanine, occurs in carnosine, coenzyme A, and pantothenic acid. Other β-amino acids are present in bioactive peptides, such as the protease inhibitor bestatin, which contains a (2S,3R)-3-amino-2-hydroxy-4-phenylbutanoyl group, and microcystin, a cyclic nonribosomal peptide that acts as a phosphatase inhibitor and contains both an aliphatic and an aromatic β-amino acid moiety (2–4). Further examples are cryptophycins, which are antitumor agents containing an α-methyl-β-alanine group (5), and paclitaxel, an antitumor agent from *Taxus brevifolia* that contains a (2R,3S)-N-benzoyl-3-phenylisoserine group that is derived from (R)-β-phenylalanine (6). Other β-amino acids occur as building blocks in β-lactam antibiotics (4, 7) and in antifungal compounds, such as jaspakinolide (8). In view of the growing importance of pharmaceutical compounds containing β-amino acid groups, there is demand for new tools for their production in enantipure form. Chemical and biochemical reactions yielding enantiopure β-amino acids have recently been reviewed (9). However, the possibilities for biocatalytic processes are scarce, and most existing options rely on kinetic resolution of racemates instead of the more attractive asymmetric conversions (10, 11).

Microorganisms that can synthesize or degrade specific organic compounds are a rich source of enzymes for application in biocatalytic processes. However, the microbial metabolism of β-amino acids has been poorly investigated. Some information is available about the formation of aliphatic β-amino acids, such as β-lysine, β-leucine, or β-glutamate, which can be formed from α-amino acids by catabolic bacterial aminotransferases and which are subject to deamination by aminotransferases (ATs) or ammonia lyases (12–14). The formation of β-alanine in *Escherichia coli* proceeds by decarboxylation of aspartate (15). Aromatic β-amino acids that occur in secondary-metabolite biosynthesis can be formed from proteinogenic α-amino acids by 4-methylideneimidazol-5-one (MIO)-dependent aminotransferases that have a biosynthetic function. The uncommon MIO cofactor also plays a key role in catabolic ammonia lyases that act upon α-histidine, α-phenylalanine, and α-tyrosine (16).

Attractive enzymes for asymmetric synthesis are ATs. These are pyridoxal 5′-phosphate (PLP)-dependent enzymes that transfer amino groups between different metabolites and are ubiquitously present in prokaryotic and eukaryotic cells (17, 18). There is evidence for a role of aminotransferases (also known as transaminases) in the biodegradation of β-amino acids by microorganisms. For example, a study on a β-phenylalanine-utilizing strain of *Mesorhizobium* led to the discovery of a transaminase that converts β-phenylalanine into 3-oxo-3-phenylpropionic acid (19–21).

Based on the latest update of the B6 database, which compiles information on PLP-dependent enzymes, seven fold types can be distinguished (22). The ATs occur in fold types I and IV. Typical
examples of fold type I ATs are aspartate AT, aromatic AT, and ω-ATs (23). According to a broader classification introduced in the 1980s, based on the reaction that is catalyzed, ATs are divided into two subgroups: I, α-ATs, which catalyze transamination of amino groups at the α-carbon, and II, ω-ATs, which perform transamination at a β-amino group, a γ-amino group, or another, more distal amino group of the substrate (24). According to this older, nonphylogenetic classification, all ATs that convert β-amino acids are confusingly considered to be ω-ATs. Enzymes from subgroup II include β-alanine AT, 4-aminobutyrate AT, ornithine AT, acetylornithine AT, and 7,8-diaminopelargonic acid AT (25, 26), as well as a β-transaminase from Mesorhizobium sp. strain LUK (MesAT) (27).

Application of ATs in biocatalysis has mainly been investigated for the production of proteinogenic amino acids, unnatural amino acids, and various other amines and amino alcohols (28–34). The catalytic activities can be quite high (apparent $k_{cat}$ values up to 50 s$^{-1}$) (35), and apart from PLP, which is sometimes added, there is no requirement for an external cofactor. Aminotransferases that catalyze synthesis or conversion of β-amino acids could be attractive for biocatalysis if they are enantioselective (36) and stable and exhibit a wide substrate scope. Here, we describe the gene cloning, the biochemical properties, and the three-dimensional (3D) structure of VpAT, an aromatic β-amino acid aminotransferase discovered in a strain of Variovorax paradoxus isolated from soil. Based on the crystal structure, we offer a rationale for the regio- and stereoselectivity of β-transaminases and identify a signature sequence motif that allows the discovery of new aromatic β-amino acid-converting aminotransferases.

MATERIALS AND METHODS

Chemicals. PLP and rac-3-amino-3-phenylpropionic acid (β-phenylala
nine) were purchased from Acros Organics, and 2-oxoglutarate (α-keto
 glutarate) disodium salt and Brij 35 were purchased from Fluka. Ortho
phthalaldehyde (OPA), dimethyl sulfoxide (DMSO), trans-cinnamic
acid, sodium pyruvate, rac-β-leucine, and 2-aminooxyacetic acid (AOA)
were purchased from Sigma-Aldrich. (S)-β-Phenylalanine and (R)-β-
phenylalanine were purchased from PepTech Corp. Racemic and enan
tomerically pure ortho-, meta-, and para-substituted β-phenylalanines
and α-phenylalanines were either purchased from PepTech Corp. or syn
thesized according to published procedures (37). Other chemicals were
purchased as follows: (R)-3-amino-butyric acid (Chemcube), (R)-3-
amino-5-methyl-hexanoic acid (Fluorochrom), β-asparagine (Bachem),
and rac-3-amino-3-(4-hydroxyphenyl)-propionic acid (β-tyrosine) (In
nochem GmbH).

Enrichment of a β-phenylalanine-degrading microorganism. Sam
ples of grassland soil (1 to 2 g) were used as a source of microorganisms.
Minimal medium, pH 7.0, contained (per liter) 5.3 g Na$_2$HPO$_4$, 12H$_2$O, 1.4 g KH$_2$PO$_4$, 0.2 g MgSO$_4$, 7H$_2$O, 1.0 g (NH$_4$)$_2$SO$_4$, 1 ml vitamin solution (38), and 5 ml trace element solution (39). In nutrient-free minimal medium, (NH$_4$)$_2$SO$_4$ was replaced by Na$_2$SO$_4$, and Ca(NO$_3$)$_2$, 4H$_2$O was omitted from the trace element solution. Stock solutions of a carbon source (cinnamic acid or glucose) and a nitrogen source (rac-β-phenyl-
alanine) were prepared in 50 mM sodium phosphate buffer (pH 7.5).
Inoculated flasks containing 50 ml minimal medium supplemented with 5
mM cinnamic acid and 1 mM rac-β-phenylalanine were incubated in the
dark at 20°C without shaking. After 2 or 3 transfers, pure cultures were
isolated on minimal medium agar plates supplemented with β-phenylal-
anine as a sole nitrogen source and cinnamic acid as a carbon source. A
fast-growing strain, named CBF3, was chosen for further study.

Bacterial strains and plasmids. *E. coli* strains VCS257, DH5α,
MC1061, and C41(DE3) were used as hosts for the construction of
a cosmid library and a sublibrary, for proliferation of cloned genes, and for
overexpression of protein, respectively. Plasmids pLAFR3, pZErO-2 (In
vitrogen), and pET28b+ (Novagen) were used for DNA libraries, sub-
cloning, and overexpression, respectively.

Preparation of cell extracts. To obtain a high yield of cells expressing
aminotransferase, strain CBF3 was grown on glucose (10 mM) with rac-
β-Phe (2 mM) as a nitrogen source. From a 1-liter culture, about 1 g of wet
cells was obtained. The cells were washed with 50 mM Tris-SO$_4$ buffer
(pH 8.0) and then suspended in 3 ml of this buffer containing 0.01% (vol/vol) β-mercaptoethanol. Sonication was performed with a Sonic
Wabra cell, followed by centrifugation at 15.000 rpm and 4°C for 1 h. The
supernatants were used as cell-free extracts (CFEs).

Enzyme assays and amino acid analysis. To test the enzyme activity,
an AT assay cocktail was prepared, consisting of 10 mM rac-β-phenyl-
alanine, 5 mM 2-oxoglutarate (or pyruvate), and 50 μM PLP in 50 mM
MOPS (morpholinopropanesulfonic acid), pH 7.6. Reactions were started
by addition of purified enzyme or CFE and incubated at 30°C. The con-
version was monitored by taking samples at different times. To a 50-μl sample, 50 μl 2 M HCl was added to quench the reaction, and the mixture
was kept on ice for 5 min. Then, 45 μl 2 M NaOH was added to neutralize the
pH and 50 μl of water was added for dilution. Immediately prior to injec-
tion, 1 μl of sample was mixed with 2 μl OPA solution and 5 μl of 0.4
M Na$_2$BO$_4$, pH 10.4, in a high-performance liquid chromatography
(HPLC) autosampler (40). The OPAs were prepared by first dissolving 15 mg OPA in 50 μl absolute ethanol, which then was added to a mixture of 4.42 ml of 0.4 M Na$_2$BO$_4$, pH 10.4, 15 μl of 30% (wt/vol) Brij 35, and 11 μl of β-mercaptoethanol.

Quantification of glutamate, alanine, and β-phenylalanine was per-
formed with a C$_18$ OPA Adsorbosphere column connected to a Jasco
HPLC system after prederivatization with OPA. Elution was done with 20
mM sodium acetate, pH 5.5, containing 5% (vol/vol) tetrahydrofuran
(TFE) as eluent A and acetonitrile as eluent B, with a flow rate of 1 ml/
min. Eluent A and eluent B were used with a gradient program as follows:
0 to 5 min, 100:0; 5 to 12 min, from 100:0 to 80:20; 12 to 16 min, 80:20; 16
to 24 min, from 80:20 to 40:60; 24 to 28 min, 40:60; from 28 to 30 min,
40:60 to 100:0; from 30 to 35 min, reequilibration at 100:0. Detection was
done with a fluorescence detector, using excitation at 350 nm and mea-
suring emission at 450 nm. Retention times for derivatized l-α-glutamate,
l-α-alanine, and β-phenylalanine were 2.3 min, 7.7 min, and 23.2 min, respectively. One unit is defined as the amount of enzyme that catalyzes the formation of 1 μmol of α-amino acid from 1 μmol of α-amino acid at concentrations of 10 mM rac-β-phenylalanine and 5 mM 2-oxoglutarate. Protein concentra-
tions were determined with Coomassie brilliant blue.

To determine the pH optimum of VpAT, Britton-Robinson buffer was
used at a pH range from pH 2 to pH 12. The buffer consists of a mixture of
0.04 M H$_2$BO$_3$, 0.04 M H$_3$PO$_4$, and 0.04 M CH$_3$COOH titrated to the
desired pH with 0.2 M NaOH. A sufficient amount of enzyme was added,
and its activity was assayed using rac-β-phenylalanine (10 mM) as the
amino donor and 2-oxoglutarate (5 mM) as the amino acceptor. The initial
reaction rates were plotted against pH.

The optimum temperature was determined by measuring the specific
activity of VpAT in MOPS buffer (50 mM, pH 7.6) at temperatures be-
tween 20°C and 65°C. Enzyme was added, and activity was assayed with
rac-β-phenylalanine (10 mM) as the amino donor and 2-oxoglutarate (5
mM) as the amino acceptor.

To follow the kinetic resolution of rac-β-phenylalanines with VpAT,
separation of enantiomers was performed using a Crownpak CR (+)
HPLC column connected to a UV detector (210 nm), as described previ-
sely (37). Because of the low solubility of the racemates, they were tested
in 50 mM MOPS (pH 7.6) at a concentration of 3 mM, using 5 mM
2-oxoglutarate and 30 μM PLP at 30°C.

Cloning and sequence analysis. All chemicals used in DNA manipu-
lation procedures were purchased from Roche Diagnostics (Mannheim,
Germany) and Qiagen NV (Venlo, The Netherlands) and used as recom-
ended by the manufacturer.

The 16S rRNA gene of strain CBF3 was sequenced after PCR amplifi-

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cation. For amplification, two universal primers of the 16S rRNA gene were used, namely, 27F as the forward primer (5′-AGAGTTTGATCMTGGCTCAG-3′) and 1492R as the reverse primer (5′-GGTACCTTGTTACGACTT-3′), with genomic DNA as the template (41). The PCR product was sequenced by GATC Biotech, Konstanz, Germany.

Genomic DNA was isolated from bacterial cells as described previously (42) and subjected to paired-end sequencing by Baseclex BLV (Leiden, The Netherlands), using an Illumina GAIIx platform to obtain about 50-bp reads as raw data. The DNA reads were assembled into contigs using CLC Genomics Workbench software (CLC Bio).

For library construction, chromosomal DNA was partially digested with Sau3A, resulting in DNA fragments of 15 kb to 40 kb, which were cloned in BamHI-digested and dephosphorylated cosmid vector pLAFR3 (43, 44). Ligated DNA was packaged in vitro and transfected to E. coli VCS257 according to the recommendations supplied with the kit (Stratagene). Recombinant clones were stored as glycerol stocks at −20°C. Transformants were grown in 96-well microtiter plates (MTPs) containing 1 ml of LB medium and tetracycline (25 µg/ml) at 30°C and 900 rpm. After 24 h, rac-β-phenylalanine was added to a final concentration of 7.5 to 10 mM to each well of the MTP. Screening for AT activity was performed by testing for the formation of acetophenone, which is formed by spontaneous decarboxylation of the expected transaminase product 3-oxo-3-phenylpropionic acid. The assay is based on the reaction of acetophenone with 2,4-dinitrophenylhydrazine (DNPH), forming a hydrazone that appears as an orange-red precipitate (45). For screening, MTPs were covered with a paper filter impregnated with a DNPH solution and incubated for 2 days at 30°C and 900 rpm.

For subcloning, the vector pZero-2 and the pLAFR3-positive clone were digested with EcoRI, and fragments were ligated. DNA was transformed to E. coli DH5α electroMax cells (Invitrogen), and screening was performed as described for the pLAFR3 cosmid library. A 5-kb insert containing the CBF3 VpAT-encoding gene was isolated and sequenced by primer walking (GATC Biotech). Sequence comparisons were performed with Clustal Ω (46) and Genious Pro software version 5.5 (47).

For amplification of the entire VpAT gene, two primers were designed, a forward primer (5′-GGCGGGCATATGACCATGCGCCATAG-3′) (the Ndel site is underlined; the stop codon is in boldface) and a reverse primer (5′-GGCGGGCTCTGATTTGCGGCGGACG-3′) (the XhoI site is underlined; the stop codon is in boldface). The 1.3-kb PCR product was cloned using the Ndel and XhoI sites of the pET28b+ plasmid. The MesAT I56V/A312S/M414F triple mutant was prepared by site-directed mutagenesis (QuikChange; Stratagene). The R41A forward primer (5′-GGAGCCAACAGGCGCTCTGCTGCTT-3′) and R41A reverse primer (5′-GGACA GCACGAGGCGCTTGCTGCTC-3′) (mutated codons are in boldface) were used according to the manufacturer’s recommendations. All constructs were confirmed by sequencing (GATC Biotech AG, Konstantz, Germany). The MesAT I56V/A312S/M414F triple mutant was prepared by site-directed mutagenesis (QuikChange; Stratagene) in three rounds.

Overexpression and purification of VpAT in E. coli. The pET28b+ construct containing the gene for VpAT was used to produce the enzyme with an N-terminal His tag (MGSSHHHHHHHHH) followed by a 10-amino-acid linker (SSGLVPRSGSH) in E. coli C41 (DE3). Cells were grown at 37°C in LB medium with 50 µg/ml kanamycin. Expression of VpAT was induced by adding 0.8 mM isopropyl-β-D-thiogalactopyranoside (IPTG) to the growing cells when the optical density at 600 nm (OD600) reached 0.6. Cultivation was continued for 16 h at 28°C and 170 rpm. Cells were obtained by centrifugation and disrupted by sonication at 4°C, followed by centrifugation for 45 min at 15,000 rpm to obtain CFE. The enzyme was purified in two steps using immobilized metal affinity chromatography (IMAC) (HisTrap HP column; 5 ml; GE Healthcare) and ion-exchange chromatography (IEXC) (Q-Sepharose HP column; 5 ml; GE Healthcare). In the case of IMAC, VpAT was eluted at a flow rate of 1 ml/min with 15 column volumes of a linear gradient of 0 to 0.5 M imidazole in a buffer containing 20 mM Tris-HCl, pH 8.0, 0.5 M NaCl, and 0.01% (vol/vol) β-mercaptoethanol, whereas for IEXC, elution was performed with 15 column volumes of a gradient of 0 to 1 M NaCl in a buffer containing 20 mM Tris-HCl, pH 8.0, and 0.01% (vol/vol) β-mercaptoethanol. For use in crystallization experiments, the fractions containing active enzyme were pooled, concentrated (Ultracel 30K MWCO; Amicon), and applied to a Superdex 200 10/300 GL size exclusion chromatography column (GE Healthcare) equilibrated in 20 mM Tris-HCl, pH 7.5, containing 200 mM NaCl. After elution, the fractions corresponding to the protein peak were pooled, concentrated (Amicon), and dialyzed overnight against a buffer containing 20 mM Tris-HCl, pH 7.5, and 10 µM PLP and concentrated to 20 mg/ml.

Protein crystallization. Crystallization experiments were set up at 20°C, and a single crystal was obtained under 0.02 M sodium/potassium phosphate, 0.1 M 1,3-bis(tris(hydroxymethyl)-methylamino)-propane, pH 6.5, and 20% (wt/vol) polyethylene glycol (PEG) 3350K. Crystals of VpAT grew within a week, after which they were transferred to a cryoprotein solution consisting of the mother liquor with 20% (vol/vol) glycerol. This was achieved in 4 steps of 5 min each, starting with a solution containing 2% (vol/vol) glycerol, followed by solutions with 5, 10, and finally 20% glycerol. Crystals from the last solution were cooled in liquid nitrogen. For the AOA binding study, the same steps were followed, but with the cryoprotection solutions supplemented with 2, 5, and 20 mM AOAT.

Diffraction data collection and processing. Diffraction data were collected at beamline ID14-4 of the European Synchrotron Radiation Facility (ESRF) (Grenoble, France). Indexing and integration of reflections was done using DXT (49), and scaling and merging of the data were achieved using SCALA (50) from the CCP4 software suite (51). For molecular replacement, the Phaser program (52) was used with MesAT (Protein Data Bank [PDB] code 2YKU [48]) as the input model. The resulting model structure was subjected to successive rounds of automatic model building using ARP/wARP (53) at 1.7-Å resolution, followed by manual model building and manipulation in Coot (54). Refmac5 was used for refinement of the atomic coordinates and atomic B factors (55). After refinement, the model quality was validated with MolProbity (56). Heteroatom coordinates were obtained from the HIC-Up server (57), while the PRODRG2 server (58) was used to generate the stereochemical restraints. Structural homologues of VpAT were obtained with the DALI server (39). PISA from the CCP4 software suite was used for protein interface analysis (60), while PyMOL (http://www.pymol.org/) was used to make images of the protein structure. Data collection and refinement statistics are given in Table S2 in the supplemental material.

Substrate docking. Docking of the PLP-(S)-β-phenylalanine intermediate was carried out with Rosetta software, which allows both side chain and backbone flexibility during docking (61, 62). Rosetta’s redesign specification file was obtained (without permitting mutations); the application allowed optimization of the surrounding protein structure to bind the (S)-β-phenylalanine intermediate while preserving the known binding orientation of the PLP (MesAT; PDB code 2YKU). To model the flexibility of the protein, Monte Carlo optimizations of side chain rotamers (collections of thermodynamically accessible conformations) were carried out three times. Each of these optimization rounds was followed by an energy minimization, which also allowed backbone atoms to move. Residues up to 8 Å from the intermediate were allowed to change conformation. Rotamers for the PLP-(S)-α-phenylalanine intermediate were prepared with Yasara (http://www.yasara.org) (64). AM1-BM3 charges of the PLP intermediate were assigned by OEchem (65). A total of 1,040 docking runs were carried out, among which the lowest-energy solution was selected.

Accession numbers. The 16S rRNA gene sequence of V. paraloxidus CBF3 has been deposited at GenBank under accession number JN990697. The sequences of the DNA contig containing the VpAT-encoding gene and of the VpAT enzyme were deposited at EMBL under accession numbers HE608883 and CCE46017, respectively. Atomic coordinates and
structure factors have been deposited in the Protein Data Bank (http://www.pdb.org) under accession codes 4AO9 for the VpAT holoenzyme and 4AOA for VpAT complexed with 2-aminooxyacetic acid.

RESULTS

Isolation of a β-phenylalanine-degrading bacterium. The isolation of a bacterial strain possessing β-phenylalanine transaminase activity was carried out by an enrichment procedure using rac-β-phenylalanine as the sole nitrogen source. After growth was observed, a pure culture was obtained by repeated transfer to fresh medium and streaking onto minimal medium plates supplemented with β-phenylalanine as the sole nitrogen source. The pure culture was obtained by repeated transfer to fresh medium and streaking onto minimal medium plates supplemented with β-phenylalanine as the sole nitrogen source. Light gray shading indicates the boundaries of secondary structure elements. The black squares indicate relevant residues for substrate and cofactor binding. Proteins: VpAT, β-transaminase of V. paradoxus (this study) (CCE46017.1; PDB code 4AO9); PoGSAM, glutamate-1-semialdehyde 2,1-aminomutase of Polaromonas sp. strain JS666 (ABL43415.1); MesAT, β-transaminase of Mesorhizobium sp. strain LUK (ABL43415.1; PDB code 2YKY); SeGSAM, glutamate-1-semialdehyde 2,1-aminomutase from S. elongatus (ABB56677.1; PDB code 2H0Z); AdbpAT, β-alaninepyruvate transaminase of A. denitrificans (AAP92672.1). The numbers 6, 11, 17, 23, 29, 35, 40 and 46 refer to proteins that are listed in Table S3 in the supplemental material.

Activity assays with HPLC analysis showed that strain CBF3 possesses a β-phenylalanine AT activity that converts β-phenylalanine and 2-oxoglutarate (or pyruvate) to 3-oxo-3-phenylpropionic acid and L-α-glutamate (or L-α-alanine). Attempts to purify VpAT using wild-type CBF3 as the source of enzyme failed due to low protein recovery after partial purification.

Isolation of the VpAT gene. A DNA library, consisting of about 4,000 clones, was constructed in cosmid pLABR3. The insert size of the DNA fragments was between 15 and 25 kb. The genome size of V. paradoxus is about 6.7 Mb (67); thus, the number of clones obtained was sufficient for 9-fold coverage of the whole genome. Screening individual clones for AT activity yielded two positive clones, one of which was investigated further. The insert was subcloned into vector pZErO-2, and rescreening for acetophenone formation yielded six positive hits. Restriction analysis identified a shared 5-kb EcoRI fragment that likely contains the AT-encoding gene. DNA sequence analysis showed the presence of a 1,302-bp gene encoding an aminotransferase, which was subsequently transferred to the pET28b+ expression vector. The encoded 434-amino-acid protein has a theoretical pI of 6.06 and a calculated molecular mass of 46.42 kDa (http://web.expasy.org/compute_pi/). The sequence of a 20.6-kb contig found by paired-end genome sequencing indicated that around the VpAT gene there were no regulatory regions or open reading frames related to other enzymes of amino acid metabolism.

Protein sequence analysis. Sequence analysis showed that VpAT has 55% sequence identity to glutamate-1-semialdehyde-2,1-aminomutase from Polaromonas sp. strain JS666 (PoGSAM), which has been reported to have activity with aromatic β-amino acids (ABL43415.1) (Fig. 1). 51% sequence identity to the aromatic β-phenylalanine aminotransferase (MesAT) (ABL74379.1) from Mesorhizobium sp. LUK, and 35% sequence identity to a
glutamate-1-semialdehyde-2,1-aminomutase from *Synechococcus elongatus* (SeGSAM) (ABB56677.1). These data suggest that VpAT, just like MesAT and PoGSAM, is a fold type I aminotransferase, and furthermore, that VpAT belongs to subgroup II transaminases, which is based on an enzyme’s substrate specificity (27, 48, 68). VpAT has 19% sequence identity to a transaminase from *Alcaligenes denitrificans* that has been reported to have activity toward aliphatic ω-aminos (AdbpAT) (AAP92672.1) (21). A sequence comparison between VpAT, MesAT, PoGSAM, and AdbpAT shows that the amino acid residues that are involved in cofactor binding are conserved, in addition to several residues that, based on the structures of VpAT and MesAT, are involved in substrate and cofactor binding (Fig. 1).

**Purification of VpAT expressed in E. coli.** The recombinant protein was overproduced with an N-terminal His<sub>6</sub> tag in *E. coli* strain C41(DE3). VpAT was mainly present as a soluble protein. The enzyme was purified by three chromatography steps. Size exclusion chromatography indicated a molecular mass of approximately 100 kDa, suggesting that VpAT exists as a dimer in solution. The purified protein showed a single band of about 48 kDa in an SDS-PAGE gel (see Fig. S1 in the supplemental material). The overall yield from 1 liter of culture was 40 to 50 mg (see Table S1 in the supplemental material). The specific activity of the purified enzyme was 17.5 U mg<sup>−1</sup> at 30°C, corresponding to a k<sub>cat</sub> of 11.8 s<sup>−1</sup> per monomer. The VpAT R41A mutant was overexpressed and purified under the same conditions as the wild-type enzyme, resulting in similar amounts of purified protein.

**Catalytic properties.** The pH activity profile of VpAT showed that the enzyme has high activity over a broad pH range (4 to 11.2) at 30°C. The optimum temperature of the enzyme was tested by measuring the specific activity at temperatures between 20°C and 65°C. VpAT exhibits a maximum specific activity of 33 U mg<sup>−1</sup> at 55°C, which is about 2-fold higher than the specific activity at 30°C (see Fig. S2 in the supplemental material). These data show that VpAT is more active toward (S)-β-phenylalanine than other ω-transaminases reported previously (21, 27, 68). The activity of VpAT with pyruvate is 85% of that with α-ketoglutarate as the amino acceptor.

The relationship between the reaction rate and the substrate concentration displayed Michaelis-Menten kinetics with a substrate inhibition constant (K<sub>s</sub>) of 14.2 mM (Table 1, entry 1). The enzyme showed no activity for α-phenylalanine or its meta- or para-bromo-, chloro- or hydroxy-substituted derivatives (which have a similar configuration of functional groups around the chiral carbon atom but a change in Cahn-Ingold-Prelog priority). The enzyme showed no activity for α-phenylalanine and other α-aminos (27). However, we could not confirm the activity of MesAT toward α-phenylalanine.

VpAT further preferentially converts the (S)-enantiomers of aromatic β-aminos (Table 1, entries 1 to 3, 9, 10, 12, and 16) and the (R)-enantiomers of aliphatic β-aminos (which have a similar configuration of functional groups around the chiral carbon atom but a change in Cahn-Ingold-Prelog priority). However, the activity of VpAT toward several aliphatic β-aminos was quite low (Table 1, entries 22 to 23). We also investigated the regio- and enantioselectivity of VpAT with several racemic substrates (Table 1, entries 1, 9, 10, 12, and 16). The enzyme appeared highly enantioselective toward the (S)-enantiomers of β-phenylalanine and its meta- and para-ring-substituted derivatives, thereby producing highly pure (R)-enantiomer preparations with high enantioselectivity (ex<sub>e</sub> > 95%).

**3D structure of VpAT.** The crystal structure of the VpAT holoenzyme was solved by molecular replacement, using the structure of MesAT (PDB code 2YKU) (48) as a search model, and subsequently refined at 1.5-Å resolution. VpAT crystallizes in space group P<sub>2</sub>₁<sub>1</sub> with two molecules (chains A and B) per asymmetric unit, which are related by noncrystallographic 2-fold symmetry. Chains A and B are very similar to each other, with root mean square deviation (RMSD) values of C-α atom positions of approximately 0.2 Å. For both monomers, electron density is absent for the first 21 N-terminal residues. This includes the N-terminal His<sub>6</sub> tag, 10 amino acids included as a linker in the expression construct, and the first amino acid (methionine) of the VpAT polypeptide. The interface between the monomers buries an area of about 4,400 Å<sup>2</sup>, which equals a quarter of the total surface area of the monomer pair (Fig. 2). Since the active sites of chains A and B are located at this interface and shaped by residues from both monomers, this suggests that the two monomers in the asymmetric unit form the functional VpAT dimer observed in solution (see above).

**The structure of the VpAT monomer.** The VpAT monomer has a curved shape and consists of a PLP-binding domain and a domain formed by the N and C termini of the polypeptide chain (NC domain; residues 1 to 86 and 320 to 434) (Fig. 2). The two domains line a cleft into which the PLP cofactor protrudes. The monomer consists of 11 α-helices of at least 2 turns and 13 β-strands that form a central 7-stranded mixed β-sheet in the PLP-binding domain and two 3-stranded antiparallel β-sheets in the NC domain. The overall structure of the enzyme is similar to that of aspartate aminotransferase, the archetype of a fold type I aminotransferase (z-score, 22; RMSD, 4.3 Å for 308 C-α atoms; 17% sequence identity; PDB code 1BKG) (70, 71), but is most similar to that of MesAT (z-score, 60; RMSD, 1.1 Å for 429 C-α atoms; 50% sequence identity; PDB code 2YKU) (48).

The PLP cofactor. Each VpAT dimer contains one PLP cofactor per monomer, which is positioned close to the surface (Fig. 3). The PLP cofactor is anchored to the protein via a covalent imine bond, with the ε-amin group of residue K267, which is conserved in the sequence alignment of homologous PLP-dependent enzymes. In addition, the three phosphate oxygen atoms are at hydrogen-bonding distance from the amide protons of residues
TABLE 1 Substrate range of VpAT<sup>a</sup>

<table>
<thead>
<tr>
<th>Type</th>
<th>Entry</th>
<th>Amino donor</th>
<th>Relative activity (%)</th>
<th>Conversion (%)</th>
<th>ee (%), E</th>
</tr>
</thead>
<tbody>
<tr>
<td>I (β-phenylalanine derivatives)</td>
<td>1</td>
<td>rac-β-Phenylalanine</td>
<td>100</td>
<td>49</td>
<td>&gt;99 (R), &gt;200</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>(S)-β-Phenylalanine</td>
<td>100</td>
<td>99&lt;sup&gt;b&lt;/sup&gt;</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>(R)-β-Phenylalanine</td>
<td>NA&lt;sup&gt;b&lt;/sup&gt;</td>
<td>--</td>
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<tr>
<td></td>
<td>4</td>
<td>rac-2-Methyl-β-phenylalanine</td>
<td>5</td>
<td>19</td>
<td>ND&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>rac-2-Fluoro-β-phenylalanine</td>
<td>15</td>
<td>26</td>
<td>ND</td>
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<tr>
<td></td>
<td>6</td>
<td>rac-2-Chloro-β-phenylalanine</td>
<td>4</td>
<td>32</td>
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<tr>
<td></td>
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<td>4</td>
<td>25</td>
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<td></td>
<td>8</td>
<td>rac-3-Methyl-β-phenylalanine</td>
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<td>64</td>
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<tr>
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<td>9</td>
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<td>48</td>
<td>&gt;98 (R), &gt;200</td>
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<td>10</td>
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<td>56</td>
<td>47</td>
<td>&gt;95 (R), &gt;100</td>
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<td>rac-4-Methyl-β-phenylalanine</td>
<td>100</td>
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<td>&gt;95 (R), &gt;200</td>
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<tr>
<td></td>
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<td>(R)-3-Amino-butryic acid</td>
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<td>11</td>
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<td>23</td>
<td>(R)-3-Amino-5-methyl-hexanoic acid</td>
<td>48</td>
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<tr>
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<td>4</td>
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<td>rac-β-Leucine</td>
<td>38</td>
<td>51</td>
<td>ND</td>
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<tr>
<td></td>
<td>26</td>
<td>β-Alanine</td>
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</tr>
<tr>
<td></td>
<td>27</td>
<td>β-Glutamic acid</td>
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<tr>
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<td>29</td>
<td>(S)-α-Phenylalanine</td>
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<tr>
<td></td>
<td>32</td>
<td>(S)-α-Tyrosine</td>
<td>NA</td>
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</tbody>
</table>

<sup>a</sup> Reaction mixtures (0.4-ml volume) contained an amino donor (3 mM) and α-ketoglutarate (5 mM) as the acceptor. Initial rates were measured, and conversion was determined after 16 h at 30°C. The activity for β-phenylalanine, corresponding to 17.5 U mg<sup>−1</sup>, was taken as 100%.

<sup>b</sup> NA, no activity (less than 0.001 U mg<sup>−1</sup>).

<sup>c</sup> Conversion after 0.5 h.

<sup>d</sup> --, no conversion observed after 16 h.

<sup>e</sup> ND, not determined.

G132, T133, and T300* (monomer B). Two of the phosphate oxygen atoms also make a hydrogen bond to a water molecule, which in turn is hydrogen bonded to peptide backbone atoms. The phosphate ester oxygen atom is not involved in hydrogen bond formation. The PLP cofactor is positioned between V242 (at the Si face of the C-4’ of the aldimine) and Y159 (at the Re face of the C-4’ of the aldimine), while the pyridine nitrogen makes a hydrogen bond with the side chain of D240. The interactions of the PLP cofactor

FIG 2 Structures of the monomer and dimer of VpAT. (A) Monomer of VpAT with the PLP cofactor (magenta) positioned in the cleft between the PLP-binding domain (left half of the monomer, containing the 7-stranded mixed β-sheet) and the NC domain (right half of the monomer, containing the two 3-stranded antiparallel β-sheets and the N and C termini of the polypeptide chain, indicated by N and C, respectively). (B) Two monomers of VpAT assemble into a dimer, here viewed along the 2-fold noncrystallographic axis relating the two monomers. The two PLP cofactors are shown in magenta and are linked to the polypeptide backbone via a Schiff base with K267. The β-helices are blue, the β-strands are yellow, and the loops are red. N and C indicate the N and C termini, respectively.
FIG 3 Wall-eyed stereo presentation of VpAT bound with an inhibitor and a docked intermediate. (A) The PLP cofactor (yellow) is shown bound to AOA (yellow). Monomer A of VpAT is shown in light blue, whereas monomer B is shown in orange. (B) AOA bound in VpAT. The holoenzyme without inhibitor is shown in green. The X-ray structure with AOA bound is shown with different colors for monomer A (light blue), monomer B (orange), and the inhibitor (yellow). (C) X-ray structure of holo-VpAT with docked (S)-β-phenylalanine. The X-ray structure of the holoenzyme is shown in green, while the modeled structure with docked (S)-β-phenylalanine is in light blue for monomer A and orange for monomer B. The docked intermediate is shown in yellow. The side chains of residues interacting with the docked intermediate and the backbone atoms of A212 are also shown. R41 (P pocket) is the residue that binds the α-carboxylate of β-phenylalanine. In the O pocket, R398 is the arginine switch residue (compare panels B and C).
with residues K267, V242, Y159, and D240 keep the PLP cofactor fixed in the active site (Fig. 3A).

The binding of 2-aminoxyacetic acid. AOA, a mimic of β-alanine, is a known inhibitor of aminotransferases (72) and also inhibits VpAT. To investigate how AOA binds in VpAT, enzyme crystals were soaked with AOA. The structure of VpAT with AOA (Fig. 3A and B) shows that the amino group of the inhibitor covalently binds to the C-4A atom of the PLP cofactor, as also described for aspartate aminotransferase (73) and recently for MesAT (48). The ether-oxygen atom (Ox1) of AOA is positioned close (3.0 Å) to the ε-amino group of residue K267. The carboxylate group binds via a salt bridge to the Ne- and Nn2-atoms of R41. The binding of AOA in the active site of VpAT is similar to the way in which AOA binds in the active site of MesAT (PDB code 2YKV). AOA inhibits aminotransferase activity because the amine-ether oxygen bond of AOA cannot be weakened by K267, and hence, hydrolysis and formation of the pyridoxamine 5'-phosphate (PMP) intermediate does not occur (Fig. 3B).

Docking of PLP-(S)-β-phenylalanine in the active site of VpAT. To investigate how an aromatic β-amino acid, such as (S)-β-phenylalanine, binds in the active site of VpAT, initially, a structure was determined after a VpAT crystal had been soaked with (S)-β-phenylalanine. However, this structure only revealed the presence of a PMP intermediate in the active site of the enzyme. Since trapping of (S)-β-phenylalanine in the active site of VpAT apparently had not occurred, the external (S)-β-phenyl alanine aldime intermediate was modeled into the active site of VpAT using Rosetta, which allows docking with flexible backbone and side chains. In the docked structure, the aromatic ring of the substrate is bound between V43, Y76, Y159, and A212 (Fig. 3C), similar to the way (S)-β-phenylalanine is bound to MesAT (48).

We previously termed this region the O pocket, because it is positioned on the 3-hydroxyl side of the PLP cofactor (48) (see below). Similar to the conformational changes observed in MesAT upon formation of the external aldime intermediate with (S)-β-phenylalanine (48), in VpAT the arginine switch residue R398 in the O pocket is also displaced during docking, freeing space for the phenyl ring of the substrate. Instead, the R398 side chain Nn2 atom forms a hydrogen bond to the carbonyl oxygen of A212. Also, V43 and Y159 have reoriented to better accommodate the docked external aldime intermediate. In the absence of (S)-β-phenylalanine, the docking procedure resulted in minor shifts (less than 0.5 Å) of the backbone atoms around the active site. While the ortho hydrogen atoms of the phenyl ring of the bound intermediate are buried, the para and meta hydrogen atoms of the phenyl ring are solvent exposed in the docked structure. The carboxylate of the docked (S)-β-phenylalanine is buried in a region we term the P pocket, which is at the phosphate group side of the PLP cofactor. Here, residue R41 is directly involved in binding of (S)-β-phenylalanine by making a salt bridge to the carboxylate group (Fig. 3C).

The importance of R41 for the binding of (S)-β-phenylalanine is underscored by the observation that the R41A mutant was inactive when tested with (S)-β-phenylalanine as amino donor and α-ketoglutarate as amino acceptor.

Identification of aromatic β-amino acid aminotransferases. The VpAT structure with bound AOA, a β-alanine mimic, and the docking results with β-phenylalanine show that R41 is important for binding the α-carboxylate of β-amino acids, as is the corresponding residue R54 in MesAT (48). The side chain of R41 interacts with E75, which may assist the function of R41 by orienting its side chain and shaping the carboxylate-binding P pocket. We therefore hypothesized that the presence of an R41-E75 pair in an aminotransferase protein sequence indicates enzymatic activity with β-amino acids. A comparison of the crystal structures of VpAT and MesAT showed that the R41-E75 salt bridge is conserved in MesAT (R54-E88). In addition, a sequence alignment between VpAT and a glutamate-1-semialdehyde-2,1-aminomutase from Polonaromonas sp. JS666 (PoGSAM), for which no structure is available but which has activity toward aromatic β-amino acids (68), also showed conservation of R41 and E75 (as R51 and E85, respectively) (Fig. 1). In contrast, the crystal structure of S. elongatus glutamate-1-semialdehyde-2,1-aminomutase (SeGSAM) (PDB code 2HOZ) (74), which is structurally very similar to that of VpAT (z-score, 47; RMSD, 1.8 Å for 404 C-α atoms; 35% sequence identity), shows that no Arg and Glu residues equivalent to R41 and E75 of VpAT are present, in agreement with the enzyme’s lack of activity on β-amino acids.

We subsequently tested whether R41 and E75 could be used to define a sequence motif with which aromatic β-amino acid aminotransferases can be distinguished from aminotransferases with a similar fold but with a different substrate specificity. For this, BLAST searches were performed using the VpAT, MesAT, and PoGSAM (ABE43415.1) protein sequences. For each query sequence, 2,000 homologous sequences were retrieved with ≥18% sequence identity. After omitting duplicates, the resulting 2,222 sequences were included in a multiple-sequence alignment and inspected for residues that are important for substrate binding.

We used the P-pocket R41-E75 pair as the starting point to identify a motif with which aminotransferases with activity toward aromatic β-amino acids can be distinguished from aminotransferases with a similar fold but a different activity. The R41-E75 starting pair was subsequently broadened by including the O-pocket residues V43 and Y76, since the equivalent residues in MesAT (I56 and Y89) were shown to be involved in substrate binding. At position 43, Val, Ile, and Ala were allowed, but hydrophobic residues with more bulky side chains, such as Leu, Phe, Tyr, and Trp were excluded, since they were expected to prevent aromatic substrate binding for sterics reasons. At position 75, apart from Glu, we also allowed Asp, Gln, and Asn, since they may still be able to interact with the side chain of R41. At position 76, Phe and Trp were also allowed, since they are frequently found in the same position as Tyr in other fold type I aminotransferases. We next extended the motif with conserved residues at positions that appear structurally important by adding a conserved Pro at position 50, which is in the center of a hydrophobic cluster in the VpAT and MesAT structures, and an Asp at position 65 and a Gly at position 66, which form a β-turn, in which the Asp is hydrogen bonded to A23 and S24, residues that are located in the α-helix that precedes loop 1.

The motif that was finally defined, R-X-[AVI]-X(6)-P-X(14)-D-G-X(8)-[EDNQ]-[YFW] (Fig. 1), retrieved 46 unique sequences (see Table S3 in the supplemental material) that we hypothesize may represent fold type I aminotransferases with activity toward aromatic β-amino acids.

**DISCUSSION**

Catalytic properties and enantioselectivity of Variovorax AT. Isolation of microorganisms that use β-phenylalanine as a sole nitrogen source yielded a Gram-negative bacterium of the species...
V. paradoxus that produces a β-amino acid selective aminotransferase. The gene encoding this enzyme was cloned, sequenced, and overexpressed to a high level in E. coli. Sequence analysis showed that the enzyme is a fold type I AT, just like several other subgroup II ω-ATs. VpAT shows the highest sequence identity with biochemically characterized β-phenylalanine ATs (27, 68), including the Mesorhizobium aminotransferase (MesAT), described by Kim et al. (27), the structure of which was recently solved (48). MesAT and VpAT have similar activities with α-ketoglutarate and pyruvate as amino acceptors (27) but differ from α-transaminases, which generally show a clear preference for either pyruvate, α-ketoglutarate, or oxaloacetate (75–77). Striking differences between MesAT and VpAT are the facts that VpAT has a higher catalytic activity, is active over a very broad range of pH values, and accepts only β-amino acids. On the other hand, VpAT shows the same enantioselectivity for (S)-β-phenylalanine and a very high enantioselectivity (E > 100), just like MesAT (19) and PoGSAM (68). This allows a biotechnologically relevant kinetic resolution of racemic mixtures, from which the remaining (R)-β-phenylalanines can be obtained with very high ee (Table 1, entries 1, 9, 10, 12, and 16).

Although the differences in activity are difficult to explain, a comparison of the residues surrounding the active site of VpAT with those of MesAT shows that V43, S298* (monomer B), and F400, which line the hydrophobic O pocket of the active site of VpAT, differ from the residues found at these positions in MesAT (156, A312*, and M414). A triple mutant of MesAT (I56V/A312S/M414F) was generated and showed a 2-fold increase (3.3 U mg⁻¹) in activity with (S)-β-phenylalanine compared to the MesAT WT (1.6 U mg⁻¹ [27]), indicating an important role of these residues in activity with (S)-β-phenylalanine.

Structure of VpAT and architecture of the active site. The structure of VpAT revealed the overall topology of the enzyme and the position of the cofactor and provided insight into the architecture of the active site of VpAT. Comparison with the structure of MesAT shows that the two enzymes are structurally similar (RMSD, 1.0 Å for 423 Cα atoms; 51% sequence identity) and confirms that they both belong to the fold type I aminotransferase family (70). As in MesAT, both monomers in VpAT contribute to the binding of the PLP cofactor, suggesting that dimerization is essential for catalytic activity (Fig. 3).

Previously, we proposed to use the notation P pocket (pointing in the same direction as the PLP phosphate) and O pocket (at the side of the hydroxyl substituent of the PLP) to define substrate binding sites of amino acid-converting fold type I ATs (48). This notation is more generally applicable than using L (large) and S (small) pocket (78), since the size of a pocket at a topologically conserved position may vary, whereas the O pocket and the P pocket are topologically fixed (Fig. 4).

Computer-aided docking of (S)-β-phenylalanine suggested binding of β-phenylalanine with the carboxylate group in the P pocket, which is opposite to the binding mode of the α-phenylalanine analogue 3-phenylpropionate in the active site of aromatic amino acid aminotransferase from Paracoccus denitrificans (PDB code 1AY8) (79) but similar to the binding mode of β-phenylalanine in MesAT (48). The docking results further indicated that several residues in the O pocket, including R398, must rearrange to enable binding of the phenyl ring of β-phenylalanine (Fig. 3C).

This switch was also observed for MesAT complexed with (S)-β-phenylalanine (PDB code 2KYK) and 2-oxoglutarate (PDB code 2YKX) and appears necessary to allow binding of both the phenyl group of (S)-β-phenylalanine AT and the α-carboxylate of 2-oxoglutarate (48). In class I ATs accepting aromatic α-amino acids, a so-called arginine switch has also been identified (e.g., R292 in ArOAT), but here, the arginine switch and consubstrate α-carboxylate-binding site are located in the P pocket, in agreement with the reverse mode of substrate binding of β-Phe in VpAT and MesAT compared to α-phenylalanine in ArOAT (80). The docking further indicated that the para and meta positions of the phenyl ring are solvent exposed while the ortho position is buried in the O pocket of the protein (Fig. 3C). This is in agreement with the higher catalytic activities observed for substrates substituted at the para and meta positions relative to ortho-substituted substrates (Table 1, entries 4 to 7), for which steric hindrance by S298* (monomer B) and Y76 may prevent productive binding (Fig. 3C).

The importance of steric crowding at the ortho position is confirmed by the relatively high activity with the ortho-fluorine-substituted substrate compared to the compounds with larger substituents, i.e., chlorine and bromine (Table 1, entries 5 to 7). Thus, it appears that the substrate specificity of VpAT with regard to substituted β-phenylalanine derivatives is mainly determined by the residues that line the hydrophobic O pocket.

A sequence motif for aromatic β-amino acid aminotransferases. A combination of sequence analysis, structural data, and information on substrate range may be used to define aminotransferase sequence motifs that can be applied to identify enzymes with certain substrate specificities (81). As observed in the VpAT structure bound with AOA (Fig. 3A and B), as well as in the modeled VpAT–(S)-β-phenylalanine structure (Fig. 3C), residues R41 in loop 1 and E75 in loop 2 of the NC domain contribute to shaping the carboxylate-binding site for β-amino acids in the P pocket. For this reason, and also taking into account that E75 is conserved in MesAT and PoGSAM but not in SoGSAM (Fig. 1), we used the conserved functional P-pocket R41/E75 pair as the starting point to identify a motif that may distinguish aminotransferases with activity toward aromatic β-amino acids from aminotransferases with a similar fold but different activity. Extension of the R41/E75 motif with residues selected on the basis of sequence conservation or position in the structure yielded a motif, R-X-[AV1]-X(6)-P-X(14)-D-G-X(8)-[EDNQ]-[YFW], that comprises...
36 residues in the N-terminal segment of the NC domain. When used to screen a set of over 2,200 (putative) class I aminotransferases, it allowed the selection of 46 sequences (see Table S3 in the supplemental material), among which were the sequences of the conserved β-selective enzymes VpAT, MesAT, and PoGSAM. Although several retrieved sequences have been annotated as glutamate-1-semialdehyde 2,1-aminomutase (see Table S3 in the supplemental material), we propose that the sequences selected by the motif are ATs with activity toward aromatic β-amino acids. Although our motif may be applied to identify aminotransferases in a set of fold type I aminotransferases, it probably cannot predict α-aminotransferase activity in less related sequences or enzymes lacking activity with aromatic substrates. For example, AdbpAT (21), which is inactive with aromatic β-amino acids and has an enantiopreference for aliphatic β-amino acids opposite that of VpAT (Table 1) and MesAT (27), is not covered by the motif. This may suggest that AdbpAT belongs to a different phylogenetic cluster and may have a different mode of substrate binding.

Outlook. Although more experiments or structure and modeling studies are needed, we are confident that the newly discovered β-phenylalanine aminotransferase from V. paradoxus strain CBF3, along with its promising biocatalytic properties and its 3D engineering efforts toward the synthesis of enantiomerically pure β-amino acids, holds promise.

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