TRANSAMINASE REACTIONS

1. TECHNICAL FIELD

[0001] The present disclosure relates to transaminase biocatalysts and methods of using the biocatalysts.

2. REFERENCE TO SEQUENCE LISTING, TABLE OR COMPUTER PROGRAM

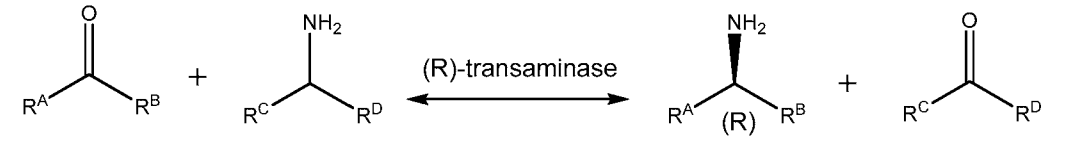
[0002] The official copy of the Sequence Listing is submitted concurrently with the specification as a 359 kbyte ASCII formatted file, "CX2-019WO1_ST25.txt," created June 21, 2010. The Sequence Listing is filed via EFS-Web as part of the specification and is hereby incorporated in its entirety by reference herein. The Sequence Listing file is identical except for minor formatting changes to the 367 kbyte ASCII formatted Sequence Listing file "376247-042USP1.txt" created on February 26, 2010 which was incorporated by reference in the priority US provisional application 61/308,873.

3. BACKGROUND

[0003] Aminotransferases, also known as transaminases (E.C. 2.6.1) catalyze the transfer of an amino group, a pair of electrons, and a proton from a primary amine of an amino donor substrate to the carbonyl group of an amino acceptor molecule.

[0004] A general transaminase reaction is shown in Reaction I, below. In this reaction, an amino acceptor (keto, or ketone) which is the precursor of the desired amino acid product, is reacted with an amino donor. The transaminase enzyme exchanges the amino group of the amino donor with the keto group of the amino acceptor. The reaction therefore results in the desired chiral amine product and a new amino acceptor (keto) compound, which is a by-product.

Reaction I



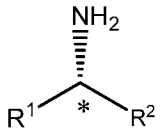
Amino acceptor | Amino donor | Chiral Amine Product | Amino acceptor byproduct

[0005] An exemplary stereoselective transamination by a transaminase is demonstrated by the activity of transaminase from *Arthrobacter sp.* KNK168 on 3,4-dimethoxyphenylacetone (see e.g., Iwasaki et al., 2006, Appl. Microbiol. Biotechnol. 69: 499-505; and US Patent 7,169,592, each of which is hereby incorporated by reference herein). Thus, transaminase enzymes have potential industrial use for stereoselective synthesis of optically pure chiral amines and the enantiomeric enrichment of chiral amines and amino acids (Shin et al., 2001, Biosci. Biotechnol. Biochem. 65:1782-1788; Iwasaki et al., 2003, Biotech. Lett. 25:1843-1846; Iwasaki et al., 2004, Appl. Microb.

Biotech. 69:499-505, Yun et al., 2004, Appl. Environ. Microbiol. 70:2529-2534; and Hwang et al., 2004, Enzyme Microbiol. Technol. 34: 429-426). Chiral amines play an important role in the pharmaceutical, agrochemical and chemical industries. Chiral amines are frequently used as intermediates or synthons for the preparation of various pharmaceuticals, such as cephalosporin or pyrrolidine derivatives. Examples of the use of aminotransferases to generate useful chemical compounds include: preparation of intermediates and precursors of pregabalin (e.g., WO 2008/127646); the stereospecific synthesis and enantiomeric enrichment of β-amino acids (e.g., WO 2005/005633); the enantiomeric enrichment of amines (e.g., US Patent No. 4,950,606, US Patent No. 5,300,437, and US Patent No. 5,169,780); and the production of amino acids and derivatives (e.g., US Patent No. 5,316,943, US Patent No. 4,518,692, US Patent No. 4,826,766, US Patent No. 6,197,558, and US Patent No. 4,600,692). Hence, transaminases are useful for the enantiomeric enrichment and stereoselective synthesis of chiral amines.

4. SUMMARY

[0006] The present disclosure provides processes for the biocatalytic conversion of prochiral keto substrates to chiral amines in presence of an amino group donor, and transaminase biocatalysts and corresponding polynucleotides for use in the processes. In one aspect, the present invention comprise a process for preparing an amine product of structural formula (I):



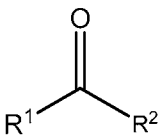
(I)

having the indicated stereochemical configuration at the stereogenic center marked with an *; in enantiomeric excess over the opposite enantiomer, wherein

R^1 is optionally substituted aryl or heteroaryl; and

R^2 is an optionally substituted C_1-C_6 alkyl, $-R^3C(O)R^4$, or $-R^3OC(O)R^5$;

wherein R^3 is an optionally substituted C_1-C_4 alkyl; and R^4 is H, an optionally substituted C_1-C_4 alkyl, NR^6R^7, or OR^8, where R^5, R^6, R^7, and R^8 are independently H or C_1-C_4 alkyl, which process comprises contacting a ketone substrate of structural formula (II):



(II)

with a transaminase polypeptide in presence of an amino donor under reaction conditions suitable for converting the ketone substrate to the amine product. In some embodiments, the transaminase polypeptide has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO:4 and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to the transaminase of SEQ ID NO:2.

[0007] In some embodiments, the transaminase polypeptide has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102 and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to the transaminase of SEQ ID NO:2. Specific embodiments of the engineered transaminases for use in the processes are further provided in the detailed description.

[0008] In some embodiments, the engineered transaminase has at least 5%, 10%, 20%, 30%, 40%, 50% or more activity of SEQ ID NO:74.

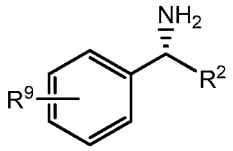
[0009] In any of the embodiments of the processes disclosed herein, the process can be carried out wherein the transaminase polypeptide is capable of converting the sitagliptin ketoamide substrate to sitagliptin at a rate that is improved as compared to the transaminase of SEQ ID NO:2, and has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO:4.

[0010] In some embodiments, the amine product is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments of the processes described above, the amine product is produced in at least 99% enantiomeric excess.

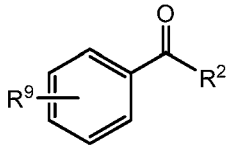
[0011] In some embodiments of the process, R^1 is an optionally substituted phenyl. In some embodiments, R^1 is an optionally substituted pyridinyl. In some embodiments, the substitutions on the aryl or heteroaryl are selected from C_1-C_4 alkyl, -OR', -SR', -NR'R', -NO_2, -NO, -CN, -CF_3, halogen (e.g., -F, -Cl, -Br and –I), -C(O)R', -C(O)OR', -C(O)NR', -$S(O)_2$R', -$S(O)_2$NR'R'', where each R' and R'' are independently selected from the group consisting of hydrogen and (C_1-C_4) alkyl. In some embodiments R^2 is methyl or halo substituted methyl. In some embodiments, R^2 is CF_2H or CF_3.

[0012] In some embodiments, the substitution on C_1-C_6 alkyl and R^3 of group R^2 are selected from halogen, NR^5R^6 or -OR^8, where R^5 and R^6 are defined above and R^8 is H or C_1-C_4 alkyl. In some embodiments, the compounds of formula (I) produced in the process described above are substantially chirally pure compounds. In certain embodiments, the compounds of formula (I) produced in the process described above are chirally pure.

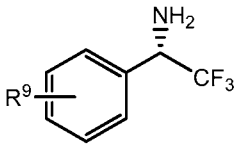
[0013] In some embodiments of the process, the amine product of formula (I) is:



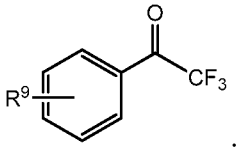
wherein R^9 is H, Cl, Br, F, CH_3, CF_3, NH_2, NO_2, CN, SCN, or OCH_3, and R^2 is an optionally substituted C_1-C_6 alkyl, and the ketone substrate of formula (II) is:



[0014] In some embodiments of the process, the amine product of formula (I) is:

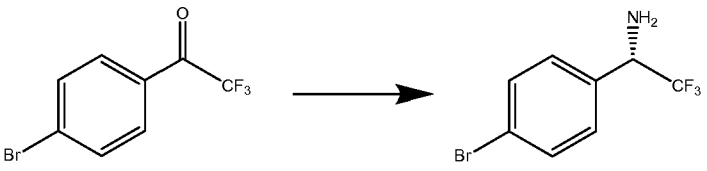


wherein R^9 is H, Cl, Br, F, CH_3, CF_3, NH_2, NO_2, CN, SCN, or OCH_3, and the ketone substrate of formula (II) is:

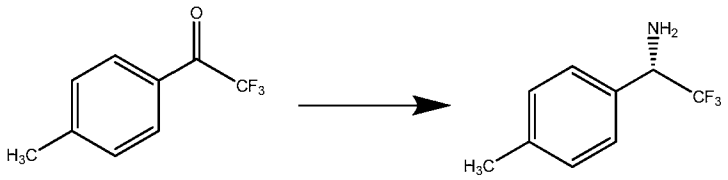


[0015] In some embodiments R^9 is Br, CH_3, or CF_3. In some embodiments, R^9 is in the para position on the phenyl ring.

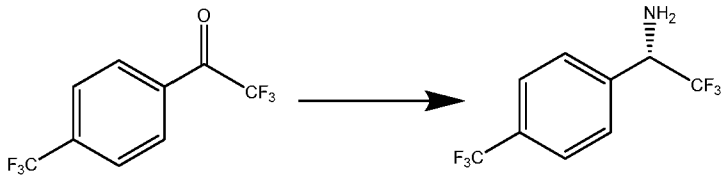
[0016] In some embodiments of the process, the amine product (*S*)-1-(4-bromophenyl)-2,2,2-trifluoroethanamin is prepared in enantiomeric excess from 1-(4-bromophenyl)-2,2,2-trifluoroethanone:



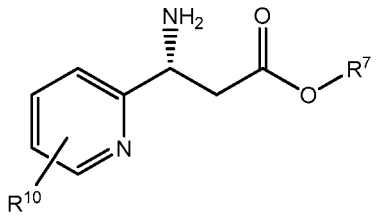
[0017] In some embodiments of the process, the amine product (*S*)-2,2,2-trifluoro-1-p-tolylethanamine is prepared in enantiomeric excess from 2,2,2-trifluoro-1-p-tolylethanone:



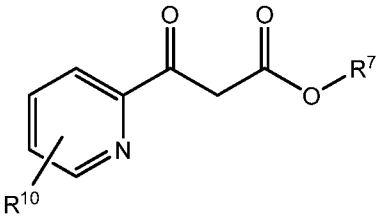
[0018] In some embodiments of the process, the amine product (S)-2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanamine is prepared in enantiomeric excess from 2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanone:



[0019] In some embodiments of the process, the amine product of formula (I) is:

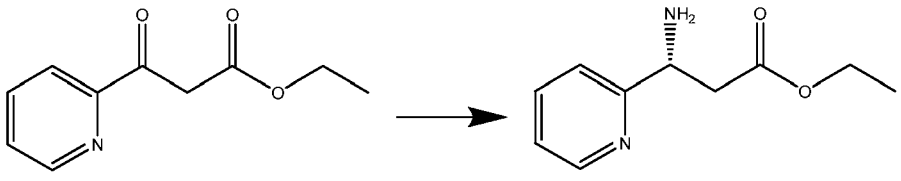


and the ketone substrate of formula (II) is:

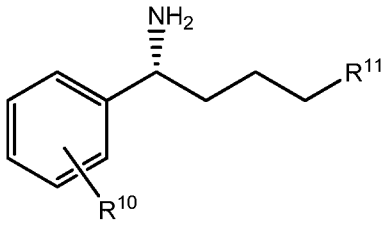


wherein R^7 is optionally substituted C_1-C_4 alkyl, and R^{10} is R^9 defined above. In some embodiments, R^{10} is H or F. In some embodiments, R^7 is C_1-C_4 alkyl.

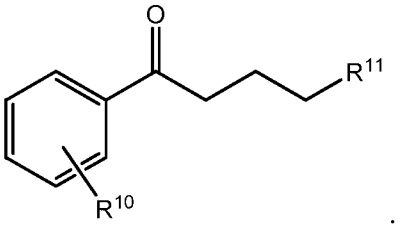
[0020] In some embodiments of the process, the amine product (*R*)-ethyl-3-amino-3-(pyridin-2-yl)propanoate is prepared in enantiomeric excess from ethyl 3-oxo-3-(pyrindin-2-yl)propanoate:



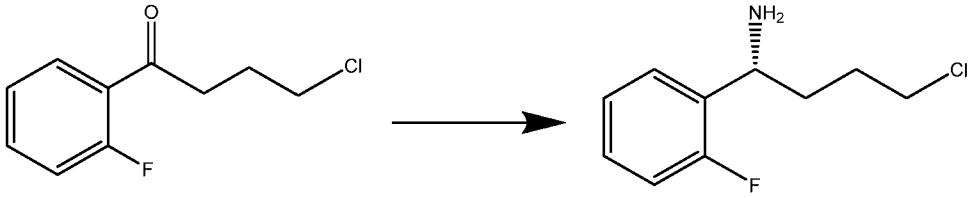
[0021] In some embodiments of the process, the amine product of formula (I) is:



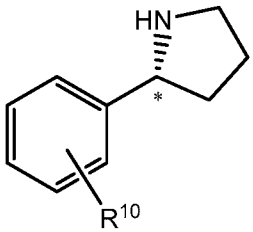
wherein R^{11} is halogen, OH, -C(O)R^4, -OC(O)R^5, or NR^6R^7, wherein R^4, R^5, R^6, R^7, and R^{10} are defined above, and the ketone substrate of formula (II) is:



[0022] In some embodiments of the process, the amine product (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine is prepared in enantiomeric excess from 4-chloro-1-(2-fluorophenyl)butan-1-one:



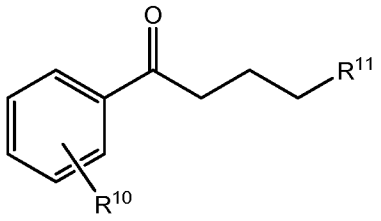
[0023] In some embodiments, the disclosure provides a process for preparing the compound of formula (III) :



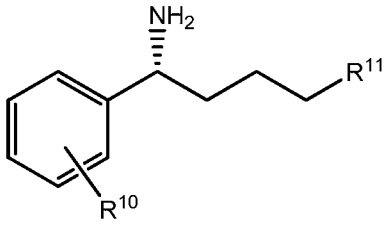
(III)

having the indicated stereochemical configuration at the stereogenic center marked with an *, in enantiomeric excess over the opposite enantiomer, wherein R^{10} is as defined above, which process comprises:

(a) contacting a ketone substrate of formula:



wherein R^{11} and R^{10} are as defined above, with a transaminase polypeptide described herein in presence of an amino donor under reaction conditions suitable for converting the ketone substrate to an amine product of formula:

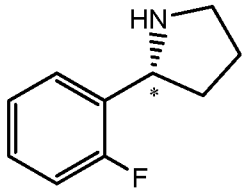


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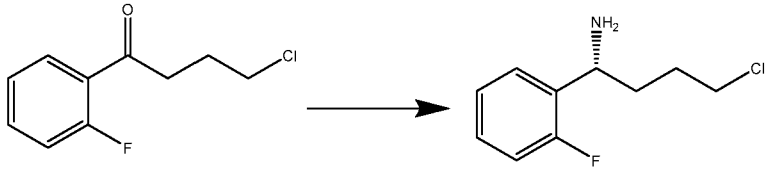
and

(b) cyclizing the amine product under suitable conditions to form the compound of formula (III).

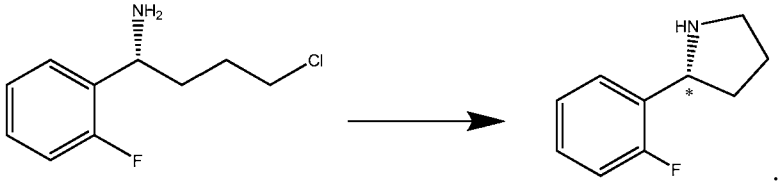
[0024] In some embodiments, the disclosure provides a process for preparing (*R*)-2-(2-fluorophenyl)pyrrolidine:



which process comprises converting ketone substrate 4-chloro-1-(2-fluorophenyl)butan-1-one to the amine product (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine in enantiomeric excess:



and cyclizing the (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine to form (R)-2-(2-fluorophenyl)pyrrolidine:



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in enantiomeric excess.

[0025] Various engineered transaminases can be used for carrying out the processes are described in the detailed description. In some embodiments, the process can use the engineered transaminases represented by SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102.

[0026] Any suitable amino donor can be used for the transamination reaction. In some embodiments, the amino group donor is selected from isopropylamine, alanine, 3-aminobutyric acid, or methylbenzylamine. A preferred amino group donor is isopropylamine.

[0027] As noted herein, the processes described herein are carried out in reaction conditions suitable for converting the ketone substrate to the corresponding chiral amine product in enantiomeric excess. In some embodiments, the reaction condition comprises a temperature of 20°C to 65°C. In some embodiments, the reaction condition comprises a temperature of 40°C to 65°C. In some embodiments, the reaction condition comprises a temperature of 50°C to 65°C.

[0028] In some embodiments, the reaction condition under which the processes are carried out comprises a pH of about 7.0 to about 11.0. In some embodiments, the reaction condition comprises a pH of about 7.0 to about 9.0. In some embodiments, the reaction condition for the process is a pH of about 8.5.

[0029] Various organic solvents can be used in the process to facilitate the enzyme reaction and to place the substrate and/or product in solution. In some embodiments of the process, the organic solvent comprises a polar solvent, such as methanol or dimethylsulfoxide (DMSO). In some embodiments, the organic solvent is DMSO, which can be present from about 10% to about 40% volume/volume (v/v). In some embodiments, the DMSO is present at about 40% v/v.

5. DETAILED DESCRIPTION

[0030] The present disclosure provides processes for converting certain prochiral keto substrates to chiral amine products using stereoselective engineered transaminase polypeptide biocatalysts. Embodiments of various processes and the transaminases are described herein.

[0031] As used in this specification and the appended claims, the singular forms "a", "an" and "the" include plural referents unless the context clearly indicates otherwise. Thus, for example, reference to "a protein" includes more than one protein, and reference to "a compound" refers to more than one compound.

[0032] Moreover, the use of "or" means "and/or" unless stated otherwise. Similarly, "comprise," "comprises," "comprising" "include," "includes," and "including" are interchangeable and not intended to be limiting.

[0033] It is to be further understood that where descriptions of various embodiments use the term "comprising," those skilled in the art would understand that in some specific instances, an

embodiment can be alternatively described using language "consisting essentially of" or "consisting of".

5.1 Abbreviations and Definitions

[0034] For the purposes of the descriptions herein, the abbreviations used for the genetically encoded amino acids are conventional and are as follows:

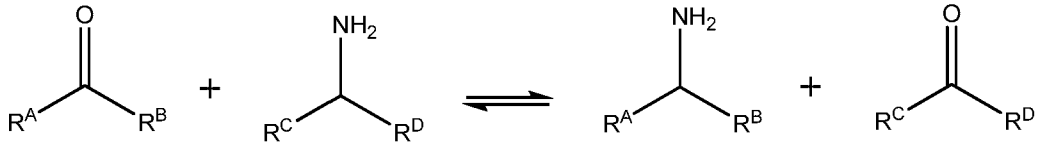
Amino Acid	Three-Letter Abbreviation	One-Letter Abbreviation
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartate	Asp	D
Cysteine	Cys	C
Glutamate	Glu	E
Glutamine	Gln	Q
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

[0035] When the three-letter abbreviations are used, unless specifically preceded by an "L" or a "D" or clear from the context in which the abbreviation is used, the amino acid may be in either the L- or D-configuration about α-carbon (Cα). For example, whereas "Ala" designates alanine without specifying the configuration about the α carbon, "D-Ala" and "L-Ala" designate D-alanine and L-alanine, respectively. When the one-letter abbreviations are used, upper case letters designate amino acids in the L-configuration about the α-carbon and lower case letters designate amino acids in the D-configuration about the α-carbon. For example, "A" designates L-alanine and "a" designates D-alanine. When peptide sequences are presented as a string of one-letter or three-letter abbreviations (or mixtures thereof), the sequences are presented in the N→C direction in accordance with common convention.

5.2 Definitions

[0036] The technical and scientific terms used in the descriptions herein will have the meanings commonly understood by one of ordinary skill in the art, unless specifically defined otherwise. Accordingly, the following terms are intended to have the following meanings.

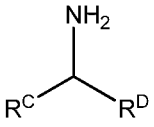
[0037] "Aminotransferase" and "transaminase" are used interchangeably herein to refer to a polypeptide having an enzymatic capability of transferring an amino group (NH_2) and a hydrogen atom from a primary amine (2) to an acceptor carbonyl (keto) compound (1), converting the amine donor into its corresponding carbonyl (keto) compound (4) and converting the acceptor into its corresponding primary amine (3) .



(1) (2) (3) (4)

[0038] "Protein", "polypeptide," and "peptide" are used interchangeably herein to denote a polymer of at least two amino acids covalently linked by an amide bond, regardless of length or post-translational modification (e.g., glycosylation, phosphorylation, lipidation, myristilation, ubiquitination, etc.). Included within this definition are D- and L-amino acids, and mixtures of D- and L-amino acids.

[0039] "Amino group donor" refers to an amino compound which is capable of donating an amino group to an acceptor carbonyl compound (i.e., an amino group acceptor), thereby becoming a carbonyl by-product. Amino group donors are molecules of general formula:



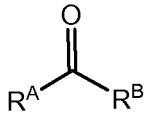
in which each of R^C, R^D, when taken independently, is an alkyl, an alkylaryl group, or aryl group which is unsubstituted or substituted with one or more enzymatically acceptable groups. R^C can be the same or different from R^D in structure or chirality. The groups R^C and R^D, taken together, may form a ring that is unsubstituted, substituted, or fused to other rings. Typical amino group donors that can be used with the invention include chiral and achiral amino acids, and chiral and achiral amines.

[0040] "Chiral amine" refers to amines of general formula R^X-$CH(NH_2)$-R^Y wherein R^X and R^Y are nonidentical and is employed herein in its broadest sense, including a wide variety of aliphatic and alicyclic compounds of different, and mixed, functional types, characterized by the presence of a primary amino group bound to a secondary carbon atom which, in addition to a hydrogen atom,

carries either (i) a divalent group forming a chiral cyclic structure, or (ii) two substituents (other than hydrogen) differing from each other in structure or chirality.

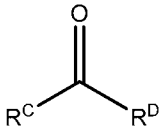
[0041] "Substrate" as used herein refers to an amino group acceptor, such as a ketone, that accepts the amino group from an amino group donor in a reaction mediated by a transaminase. In the context of the present disclosure, substrate for the transaminase includes, among others, the compound of formula (II), as further described herein.

[0042] "Amino acceptor" and "amine acceptor", "keto substrate", "keto" and "ketone" are used interchangeably herein to refer to a carbonyl (keto, or ketone) compound which accepts an amino group from a donor amine. Amino acceptors are molecules of general formula,



in which each of R^A and R^B in some embodiments, when taken independently, can be an alkyl, an alkylaryl group, or aryl group which is unsubstituted or substituted with one or more enzymatically acceptable groups. R^A may be the same or different from R^B in structure or chirality. R^A and R^B, taken together, may form a ring that is unsubstituted, substituted, or fused to other rings. Specific amino acceptor compounds are further described in the detailed description.

[0043] "Carbonyl by-product" and "keto by-product" refer to the carbonyl compound formed from the amino group donor when the amino group on the amino group donor is transferred to the amino group acceptor in a transamination reaction. The carbonyl by-product has the general structure of formula:



wherein R^C and R^D are defined above for the amino group donor.

[0044] "Pyridoxal-phosphate", "PLP", "pyridoxal-5'-phosphate", "PYP", and "P5P" are used interchangeably herein to refer to the compound that acts as a coenzyme in transaminase reactions. In some embodiments, pyridoxal phosphate is defined by the structure 1-(4'-formyl-3'-hydroxy-2'-methyl-5'-pyridyl)methoxyphosphonic acid, CAS number [54-47-7]. Pyridoxal-5'-phosphate is produced *in vivo* by phosphorylation and oxidation of pyridoxal (also known as pyridoxine or Vitamin B6). In transamination reactions using transaminase enzymes, the amino group of the amino group donor is transferred to the coenzyme to produce a keto byproduct, while pyridoxal-5'-phosphate is converted to pyridoxamine phosphate. Pyridoxal-5'-phosphate is regenerated by reaction with a different keto compound (the amino group acceptor). The transfer of the amino group from

pyridoxamine phosphate to the amino acceptor produces a chiral amine and regenerates the coenzyme. The pyridoxal-5'-phosphate of the current invention can be replaced by other members of the vitamin B_6 family, including, among others, pyridoxal (PL), pyridoxamine (PM), and their phosphorylated counterparts; pyridoxine phosphate (PNP), and pyridoxamine phosphate (PMP).

[0045] "Coding sequence" refers to that portion of a nucleic acid (e.g., a gene) that encodes an amino acid sequence of a protein.

[0046] "Naturally occurring" or "wild-type" refers to the form found in nature. For example, a naturally occurring or wild-type polypeptide or polynucleotide sequence is a sequence present in an organism that can be isolated from a source in nature and which has not been intentionally modified by human manipulation.

[0047] "Recombinant" when used with reference to, e.g., a cell, nucleic acid, or polypeptide, refers to a material, or a material corresponding to the natural or native form of the material, that has been modified in a manner that would not otherwise exist in nature, or is identical thereto but produced or derived from synthetic materials and/or by manipulation using recombinant techniques. Non-limiting examples include, among others, recombinant cells expressing genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise expressed at a different level.

[0048] "Percentage of sequence identity," "percent identity," and "percent identical" are used herein to refer to comparisons between polynucleotide sequences or polypeptide sequences, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which either the identical nucleic acid base or amino acid residue occurs in both sequences or a nucleic acid base or amino acid residue is aligned with a gap to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Determination of optimal alignment and percent sequence identity is performed using the BLAST and BLAST 2.0 algorithms (see e.g., Altschul et al., 1990, J. Mol. Biol. 215: 403-410 and Altschul et al., 1977, Nucleic Acids Res. 3389-3402). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information website.

[0049] Briefly, the BLAST analyses involve first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as, the neighborhood word score threshold (Altschul et al, supra). These

initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, 1989, Proc Natl Acad Sci USA 89:10915).

[0050] Numerous other algorithms are available that function similarly to BLAST in providing percent identity for two sequences. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman, 1981, Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch, 1970, J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman, 1988, Proc. Natl. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the GCG Wisconsin Software Package), or by visual inspection (see generally, Current Protocols in Molecular Biology, F. M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1995 Supplement) (Ausubel)). Additionally, determination of sequence alignment and percent sequence identity can employ the BESTFIT or GAP programs in the GCG Wisconsin Software package (Accelrys, Madison WI), using default parameters provided.

[0051] "Reference sequence" refers to a defined sequence to which an altered sequence is compared. A reference sequence may be a subset of a larger sequence, for example, a segment of a full-length gene or polypeptide sequence. Generally, a reference sequence is at least 20 nucleotide or amino acid residues in length, at least 25 residues in length, at least 50 residues in length, or the full length of the nucleic acid or polypeptide. Since two polynucleotides or polypeptides may each (1) comprise a sequence (i.e., a portion of the complete sequence) that is similar between the two sequences, and (2) may further comprise a sequence that is divergent between the two sequences, sequence comparisons between two (or more) polynucleotides or polypeptide are typically performed by comparing sequences of the two polynucleotides over a comparison window to identify and compare local regions of sequence similarity.

[0052] The term "reference sequence" is not intended to be limited to wild-type sequences, and can include engineered or altered sequences. For example, in some embodiments, a "reference sequence" can be a previously engineered or altered amino acid sequence. For instance, a "reference sequence based on SEQ ID NO:2 having a glycine residue at position X284" refers to a reference sequence corresponding to SEQ ID NO:2 with a glycine residue at X284 (the un-altered version of SEQ ID NO:2 has alanine at X284).

[0053] "Comparison window" refers to a conceptual segment of at least about 20 contiguous nucleotide positions or amino acids residues wherein a sequence may be compared to a reference sequence of at least 20 contiguous nucleotides or amino acids and wherein the portion of the sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The comparison window can be longer than 20 contiguous residues, and includes, optionally 30, 40, 50, 100, or longer windows.

[0054] "Substantial identity" refers to a polynucleotide or polypeptide sequence that has at least 80 percent sequence identity, at least 85 percent sequence identity, at least 89 percent sequence identity, at least 95 percent sequence identity, and even at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 residue positions, frequently over a window of at least 30-50 residues, wherein the percentage of sequence identity is calculated by comparing the reference sequence to a sequence that includes deletions or additions which total 20 percent or less of the reference sequence over the window of comparison. In specific embodiments applied to polypeptides, the term "substantial identity" means that two polypeptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80 percent sequence identity, preferably at least 89 percent sequence identity, at least 95 percent sequence identity or more (e.g., 99 percent sequence identity). Preferably, residue positions which are not identical differ by conservative amino acid substitutions.

[0055] "Corresponding to", "reference to" or "relative to" when used in the context of the numbering of a given amino acid or polynucleotide sequence refers to the numbering of the residues of a specified reference sequence when the given amino acid or polynucleotide sequence is compared to the reference sequence. In other words, the residue number or residue position of a given polymer is designated with respect to the reference sequence rather than by the actual numerical position of the residue within the given amino acid or polynucleotide sequence. For example, a given amino acid sequence, such as that of an engineered transaminase, can be aligned to a reference sequence by introducing gaps to optimize residue matches between the two sequences. In these cases, although the gaps are present, the numbering of the residue in the given amino acid or polynucleotide sequence is made with respect to the reference sequence to which it has been aligned.

[0056] "Stereoselectivity" refers to the preferential formation in a chemical or enzymatic reaction of one stereoisomer over another. Stereoselectivity can be partial, where the formation of one stereoisomer is favored over the other, or it may be complete where only one stereoisomer is formed. When the stereoisomers are enantiomers, the stereoselectivity is referred to as enantioselectivity, the fraction (typically reported as a percentage) of one enantiomer in the sum of both. It is commonly alternatively reported in the art (typically as a percentage) as the enantiomeric excess (e.e.) calculated therefrom according to the formula [major enantiomer − minor enantiomer]/[major enantiomer + minor enantiomer]. Where the stereoisomers are diastereoisomers, the stereoselectivity is referred to as diastereoselectivity, the fraction (typically reported as a percentage) of one diastereomer in a mixture of two diastereomers, commonly alternatively reported as the diastereomeric excess (d.e.). Enantiomeric excess and diastereomeric excess are types of stereomeric excess.

[0057] "Highly stereoselective" refers to a chemical or enzymatic reaction that is capable of converting a substrate (e.g., formula (II)) to its corresponding product (e.g., formula (I)) with at least about 85% stereoisomeric excess.

[0058] "Improved enzyme property" refers to any enzyme property made better or more desirable for a particular purpose as compared to that property found in a reference enzyme. For the engineered transaminase polypeptides described herein, the comparison is generally made to the wild-type transaminase enzyme, although in some embodiments, the reference transaminase can be another improved engineered transaminase. Enzyme properties for which improvement can be made include, but are not limited to, enzymatic activity (which can be expressed in terms of percent conversion of the substrate in a period of time), thermal stability, solvent stability, pH activity profile, coenzyme requirements, refractoriness to inhibitors (e.g., product inhibition), stereospecificity, and stereoselectivity (including enantioselectivity).

[0059] "Increased enzymatic activity" or "increased activity" refers to an improved property of an engineered enzyme, which can be represented by an increase in specific activity (e.g., product produced/time/weight protein) or an increase in percent conversion of the substrate to the product (e.g., percent conversion of starting amount of substrate to product in a specified time period using a specified amount of transaminase) as compared to a reference enzyme. Exemplary methods to determine enzyme activity are provided in the Examples. Any property relating to enzyme activity may be affected, including the classical enzyme properties of K_m, V_{max} or k_{cat}, changes of which can lead to increased enzymatic activity. Improvements in enzyme activity can be from about 1.5 times the enzymatic activity of the corresponding wild-type or engineered enzyme, to as much as 2 times, 5 times, 10 times, 20 times, 25 times, 50 times, 75 times, 100 times, or more enzymatic activity than the naturally occurring enzyme (e.g., a transaminase) or another engineered enzyme from which the enzymes exhibiting increased activity were derived. In specific embodiments, the engineered transaminase enzymes of the present disclosure exhibit improved enzymatic activity in the range of

1.5 to 50 times, 1.5 to 100 times or greater than that of the parent transaminase enzyme (i.e., the wild-type or engineered transaminase from which they were derived). It is understood by the skilled artisan that the activity of any enzyme is diffusion limited such that the catalytic turnover rate cannot exceed the diffusion rate of the substrate, including any required coenzymes. The theoretical maximum of the diffusion limit is generally about 10^8 to 10^9 (M^{-1} s^{-1}). Hence, any improvements in the enzyme activity of the transaminase will have an upper limit related to the diffusion rate of the substrates acted on by the transaminase enzyme. Transaminase activity can be measured by any one of standard assays used for measuring transaminases, such as change in substrate or product concentration, or change in concentration of the amino group donor. Comparisons of enzyme activities are made using a defined preparation of enzyme, a defined assay under a set condition, and one or more defined substrates, as further described in detail herein. Generally, when enzymes in cell lysates are compared, the numbers of cells and the amount of protein assayed are determined as well as use of identical expression systems and identical host cells to minimize variations in amount of enzyme produced by the host cells and present in the lysates.

[0060] "Conversion" refers to the enzymatic transformation of a substrate to the corresponding product. "Percent conversion" refers to the percent of the substrate that is converted to the product within a period of time under specified conditions. Thus, for example, the "enzymatic activity" or "activity" of a transaminase polypeptide can be expressed as "percent conversion" of the substrate to the product.

[0061] "Thermostable" or "thermal stable" are used interchangeably to refer to a polypeptide that is resistant to inactivation when exposed to a set of temperature conditions (e.g., 40-80°C) for a period of time (e.g., 0.5-24 hrs) compared to the untreated enzyme, thus retaining a certain level of residual activity (more than 60% to 80% for example) after exposure to elevated temperatures.

[0062] "Solvent stable" refers to a polypeptide that maintains similar activity (more than e.g., 60% to 80%) after exposure to varying concentrations (e.g., 5-99%) of solvent , (e.g., isopropyl alcohol, dimethylsulfoxide, tetrahydrofuran, 2-methyltetrahydrofuran, acetone, toluene, butylacetate, methyl tert-butylether, acetonitrile, etc.) for a period of time (e.g., 0.5-24 hrs) compared to the untreated enzyme.

[0063] "pH stable" refers to a polypeptide that maintains similar activity (more than e.g., 60% to 80%) after exposure to low or high pH (e.g., 4.5-6 or 8 to 12) for a period of time (e.g., 0.5-24 hrs) compared to the untreated enzyme.

[0064] "Thermo- and solvent stable" refers to a polypeptide that is both thermostable and solvent stable.

[0065] "Derived from" as used herein in the context of engineered enzymes identifies the originating enzyme, and/or the gene encoding such enzyme, upon which the engineering was based. For

example, the engineered transaminase enzyme of SEQ ID NO: 4 was obtained by mutating the transaminase of SEQ ID NO:2. Thus, this engineered transaminase enzyme of SEQ ID NO:4 is "derived from" the type polypeptide of SEQ ID NO:2.

[0066] "Amino acid" or "residue" as used in context of the polypeptides disclosed herein refers to the specific monomer at a sequence position (e.g., P8 indicates that the "amino acid" or "residue" at position 8 of SEQ ID NO: 2 is a proline.)

[0067] "Hydrophilic amino acid or residue" refers to an amino acid or residue having a side chain exhibiting a hydrophobicity of less than zero according to the normalized consensus hydrophobicity scale of Eisenberg *et al.,* 1984, J. Mol. Biol. 179:125-142. Genetically encoded hydrophilic amino acids include L-Thr (T), L-Ser (S), L-His (H), L-Glu (E), L-Asn (N), L-Gln (Q), L-Asp (D), L-Lys (K) and L-Arg (R).

[0068] "Acidic amino acid or residue" refers to a hydrophilic amino acid or residue having a side chain exhibiting a pK value of less than about 6 when the amino acid is included in a peptide or polypeptide. Acidic amino acids typically have negatively charged side chains at physiological pH due to loss of a hydrogen ion. Genetically encoded acidic amino acids include L-Glu (E) and L-Asp (D).

[0069] "Basic amino acid or residue" refers to a hydrophilic amino acid or residue having a side chain exhibiting a pKa value of greater than about 6 when the amino acid is included in a peptide or polypeptide. Basic amino acids typically have positively charged side chains at physiological pH due to association with hydronium ion. Genetically encoded basic amino acids include L-Arg (R) and L-Lys (K).

[0070] "Polar amino acid or residue" refers to a hydrophilic amino acid or residue having a side chain that is uncharged at physiological pH, but which has at least one bond in which the pair of electrons shared in common by two atoms is held more closely by one of the atoms. Genetically encoded polar amino acids include L-Asn (N), L-Gln (Q), L-Ser (S) and L-Thr (T).

[0071] "Hydrophobic amino acid or residue" refers to an amino acid or residue having a side chain exhibiting a hydrophobicity of greater than zero according to the normalized consensus hydrophobicity scale of Eisenberg *et al.*, 1984, J. Mol. Biol. 179:125-142. Genetically encoded hydrophobic amino acids include L-Pro (P), L-Ile (I), L-Phe (F), L-Val (V), L-Leu (L), L-Trp (W), L-Met (M), L-Ala (A) and L-Tyr (Y).

[0072] "Aromatic amino acid or residue" refers to a hydrophilic or hydrophobic amino acid or residue having a side chain that includes at least one aromatic or heteroaromatic ring. Genetically encoded aromatic amino acids include L-Phe (F), L-Tyr (Y) and L-Trp (W). Although owing to the pKa of its heteroaromatic nitrogen atom L-His (H) it is sometimes classified as a basic residue, or as

an aromatic residue as its side chain includes a heteroaromatic ring, herein histidine is classified as a hydrophilic residue or as a "constrained residue" (see below).

[0073] "Constrained amino acid or residue" refers to an amino acid or residue that has a constrained geometry. Herein, constrained residues include L-Pro (P) and L-His (H). Histidine has a constrained geometry because it has a relatively small imidazole ring. Proline has a constrained geometry because it also has a five membered ring.

[0074] "Non-polar amino acid or residue" refers to a hydrophobic amino acid or residue having a side chain that is uncharged at physiological pH and which has bonds in which the pair of electrons shared in common by two atoms is generally held equally by each of the two atoms (i.e., the side chain is not polar). Genetically encoded non-polar amino acids include L-Gly (G), L-Leu (L), L-Val (V), L-Ile (I), L-Met (M) and L-Ala (A).

[0075] "Aliphatic amino acid or residue" refers to a hydrophobic amino acid or residue having an aliphatic hydrocarbon side chain. Genetically encoded aliphatic amino acids include L-Ala (A), L-Val (V), L-Leu (L) and L-Ile (I).

[0076] "Cysteine" or L-Cys (C) is unusual in that it can form disulfide bridges with other L-Cys (C) amino acids or other sulfanyl- or sulfhydryl-containing amino acids. The "cysteine-like residues" include cysteine and other amino acids that contain sulfhydryl moieties that are available for formation of disulfide bridges. The ability of L-Cys (C) (and other amino acids with -SH containing side chains) to exist in a peptide in either the reduced free -SH or oxidized disulfide-bridged form affects whether L-Cys (C) contributes net hydrophobic or hydrophilic character to a peptide. While L-Cys (C) exhibits a hydrophobicity of 0.29 according to the normalized consensus scale of Eisenberg (Eisenberg *et al.*, 1984, *supra*), it is to be understood that for purposes of the present disclosure L-Cys (C) is categorized into its own unique group.

[0077] "Small amino acid or residue" refers to an amino acid or residue having a side chain that is composed of a total of three or fewer carbon and/or heteroatoms (excluding the α-carbon and hydrogens). The small amino acids or residues may be further categorized as aliphatic, non-polar, polar or acidic small amino acids or residues, in accordance with the above definitions. Genetically-encoded small amino acids include L-Ala (A), L-Val (V), L-Cys (C), L-Asn (N), L-Ser (S), L-Thr (T) and L-Asp (D).

[0078] "Hydroxyl-containing amino acid or residue" refers to an amino acid containing a hydroxyl (-OH) moiety. Genetically-encoded hydroxyl-containing amino acids include L-Ser (S) L-Thr (T) and L-Tyr (Y).

[0079] "Amino acid difference" or "residue difference" refers to a change in the residue at a specified position of a polypeptide sequence when compared to a reference sequence. For example, a

residue difference at position X8, where the reference sequence has a serine, refers to a change of the residue at position X8 to any residue other than serine. As disclosed herein, an enzyme can include one or more residue differences relative to a reference sequence, where multiple residue differences typically are indicated by a list of the specified positions where changes are made relative to the reference sequence (e.g., "one or more residue differences as compared to SEQ ID NO:2 at the following residue positions: X4; X5; X8; X18; X25; X26; X27; X28; X30; X41; X42; X48; X49; X50; X54; X55; X60; X61; X62; X65; X81; X94; X96; X102; X117; X120; X124; X126; X136; X137; X138; X146; X148; X150; X152; X155; X156; X160; X163; X164; X169; X174; X178; X195; X199; X204; X208; X209; X211; X215; X217; X225; X230; X252; X269; X273; X282; X292; X297; X302; X306; X321; and X329.").

[0080] "Conservative" amino acid substitutions or mutations refer to the interchangeability of residues having similar side chains, and thus typically involves substitution of the amino acid in the polypeptide with amino acids within the same or similar defined class of amino acids. However, as used herein, in some embodiments, conservative mutations do not include substitutions from a hydrophilic to hydrophilic, hydrophobic to hydrophobic, hydroxyl-containing to hydroxyl-containing, or small to small residue, if the conservative mutation can instead be a substitution from an aliphatic to an aliphatic, non-polar to non-polar, polar to polar, acidic to acidic, basic to basic, aromatic to aromatic, or constrained to constrained residue. Further, as used herein, A, V, L, or I can be conservatively mutated to either another aliphatic residue or to another non-polar residue. The table below shows exemplary conservative substitutions.

[0081] Table 1

Residue	**Possible Conservative Mutations**
A, L, V, I	Other aliphatic (A, L, V, I) Other non-polar (A, L, V, I, G, M)
G, M	Other non-polar (A, L, V, I, G, M)
D, E	Other acidic (D, E)
K, R	Other basic (K, R)
P, H	Other constrained (P, H)
N, Q, S, T	Other polar
Y, W, F	Other aromatic (Y, W, F)
C	None

[0082] "Non-conservative substitution" refers to substitution or mutation of an amino acid in the polypeptide with an amino acid with significantly differing side chain properties. Non-conservative substitutions may use amino acids between, rather than within, the defined groups listed above. In one embodiment, a non-conservative mutation affects (a) the structure of the peptide backbone in the

area of the substitution (e.g., proline for glycine) (b) the charge or hydrophobicity, or (c) the bulk of the side chain.

[0083] "Deletion" refers to modification of the polypeptide by removal of one or more amino acids from the reference polypeptide. Deletions can comprise removal of 1 or more amino acids, 2 or more amino acids, 5 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, up to 20% of the total number of amino acids, or up to 30% of the total number of amino acids making up the polypeptide while retaining enzymatic activity and/or retaining the improved properties of an engineered transaminase enzyme. Deletions can be directed to the internal portions and/or terminal portions of the polypeptide. In various embodiments, the deletion can comprise a continuous segment or can be discontinuous.

[0084] "Insertion" refers to modification of the polypeptide by addition of one or more amino acids to the reference polypeptide. In some embodiments, the improved engineered transaminase enzymes comprise insertions of one or more amino acids to the naturally occurring transaminase polypeptide as well as insertions of one or more amino acids to other improved transaminase polypeptides. Insertions can be in the internal portions of the polypeptide, or to the carboxy or amino terminus. Insertions as used herein include fusion proteins as is known in the art. The insertion can be a contiguous segment of amino acids or separated by one or more of the amino acids in the naturally occurring polypeptide.

[0085] "Fragment" as used herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion, but where the remaining amino acid sequence is identical to the corresponding positions in the sequence. Fragments can be at least 14 amino acids long, at least 20 amino acids long, at least 50 amino acids long or longer, and up to 70%, 80%, 90%, 95%, 98%, and 99% of the full-length transaminase polypeptide, for example the polypeptide of SEQ ID NO:4.

[0086] "Isolated polypeptide" refers to a polypeptide which is substantially separated from other contaminants that naturally accompany it, e.g., protein, lipids, and polynucleotides. The term embraces polypeptides which have been removed or purified from their naturally-occurring environment or expression system (e.g., host cell or *in vitro* synthesis). The improved transaminase enzymes may be present within a cell, present in the cellular medium, or prepared in various forms, such as lysates or isolated preparations. As such, in some embodiments, the improved transaminase enzyme can be an isolated polypeptide.

[0087] "Substantially pure polypeptide" refers to a composition in which the polypeptide species is the predominant species present (i.e., on a molar or weight basis it is more abundant than any other individual macromolecular species in the composition), and is generally a substantially purified composition when the object species comprises at least about 50 percent of the macromolecular species present by mole or % weight. Generally, a substantially pure transaminase composition will

comprise about 60 % or more, about 70% or more, about 80% or more, about 90% or more, about 95% or more, and about 98% or more of all macromolecular species by mole or % weight present in the composition. In some embodiments, the object species is purified to essential homogeneity (i.e., contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species. Solvent species, small molecules (<500 Daltons), and elemental ion species are not considered macromolecular species. In some embodiments, the isolated improved transaminases polypeptide is a substantially pure polypeptide composition.

[0088] "Stringent hybridization" is used herein to refer to conditions under which nucleic acid hybrids are stable. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_m) of the hybrids. In general, the stability of a hybrid is a function of ion strength, temperature, G/C content, and the presence of chaotropic agents. The T_m values for polynucleotides can be calculated using known methods for predicting melting temperatures (see, e.g., Baldino et al., Methods Enzymology 168:761-777; Bolton et al., 1962, Proc. Natl. Acad. Sci. USA 48:1390; Bresslauer et al., 1986, Proc. Natl. Acad. Sci USA 83:8893-8897; Freier et al., 1986, Proc. Natl. Acad. Sci USA 83:9373-9377; Kierzek et al., Biochemistry 25:7840-7846; Rychlik et al., 1990, Nucleic Acids Res 18:6409-6412 (erratum, 1991, Nucleic Acids Res 19:698); Sambrook et al., supra); Suggs et al., 1981, In Developmental Biology Using Purified Genes (Brown et al., eds.), pp. 683-693, Academic Press; and Wetmur, 1991, Crit Rev Biochem Mol Biol 26:227-259. All publications incorporate herein by reference). In some embodiments, the polynucleotide encodes the polypeptide disclosed herein and hybridizes under defined conditions, such as moderately stringent or highly stringent conditions, to the complement of a sequence encoding an engineered transaminase enzyme of the present disclosure.

[0089] "Hybridization stringency" relates to hybridization conditions, such as washing conditions, in the hybridization of nucleic acids. Generally, hybridization reactions are performed under conditions of lower stringency, followed by washes of varying but higher stringency. The term "moderately stringent hybridization" refers to conditions that permit target-DNA to bind a complementary nucleic acid that has about 60% identity, preferably about 75% identity, about 85% identity to the target DNA; with greater than about 90% identity to target-polynucleotide. Exemplary moderately stringent conditions are conditions equivalent to hybridization in 50% formamide, 5× Denhart's solution, 5×SSPE, 0.2% SDS at 42°C., followed by washing in 0.2×SSPE, 0.2% SDS, at 42°C. "High stringency hybridization" refers generally to conditions that are about 10°C or less from the thermal melting temperature T_m as determined under the solution condition for a defined polynucleotide sequence. In some embodiments, a high stringency condition refers to conditions that permit hybridization of only those nucleic acid sequences that form stable hybrids in 0.018M NaCl at 65°C. (i.e., if a hybrid is not stable in 0.018M NaCl at 65°C, it will not be stable under high stringency

conditions, as contemplated herein). High stringency conditions can be provided, for example, by hybridization in conditions equivalent to 50% formamide, 5× Denhart's solution, 5×SSPE, 0.2% SDS at 42°C, followed by washing in 0.1×SSPE, and 0.1% SDS at 65°C. Another high stringency condition is hybridizing in conditions equivalent to hybridizing in 5X SSC containing 0.1% (w:v) SDS at 65°C and washing in 0.1x SSC containing 0.1% SDS at 65°C. Other high stringency hybridization conditions, as well as moderately stringent conditions, are described in the references cited above.

[0090] "Heterologous" polynucleotide refers to any polynucleotide that is introduced into a host cell by laboratory techniques, and includes polynucleotides that are removed from a host cell, subjected to laboratory manipulation, and then reintroduced into a host cell.

[0091] "Codon optimized" refers to changes in the codons of the polynucleotide encoding a protein to those preferentially used in a particular organism such that the encoded protein is efficiently expressed in the organism of interest. Although the genetic code is degenerate in that most amino acids are represented by several codons, called "synonyms" or "synonymous" codons, it is well known that codon usage by particular organisms is nonrandom and biased towards particular codon triplets. This codon usage bias may be higher in reference to a given gene, genes of common function or ancestral origin, highly expressed proteins versus low copy number proteins, and the aggregate protein coding regions of an organism's genome. In some embodiments, the polynucleotides encoding the transaminases enzymes may be codon optimized for optimal production from the host organism selected for expression.

[0092] "Preferred, optimal, high codon usage bias codons" refers interchangeably to codons that are used at higher frequency in the protein coding regions than other codons that code for the same amino acid. The preferred codons may be determined in relation to codon usage in a single gene, a set of genes of common function or origin, highly expressed genes, the codon frequency in the aggregate protein coding regions of the whole organism, codon frequency in the aggregate protein coding regions of related organisms, or combinations thereof. Codons whose frequency increases with the level of gene expression are typically optimal codons for expression. A variety of methods are known for determining the codon frequency (e.g., codon usage, relative synonymous codon usage) and codon preference in specific organisms, including multivariate analysis, for example, using cluster analysis or correspondence analysis, and the effective number of codons used in a gene (see GCG CodonPreference, Genetics Computer Group Wisconsin Package; CodonW, John Peden, University of Nottingham; McInerney, J. O, 1998, Bioinformatics 14:372-73; Stenico et al., 1994, Nucleic Acids Res. 222437-46; Wright, F., 1990, Gene 87:23-29). Codon usage tables are available for a growing list of organisms (see for example, Wada et al., 1992, Nucleic Acids Res. 20:2111-2118; Nakamura et al., 2000, Nucl. Acids Res. 28:292; Duret, et al., supra; Henaut and Danchin, "Escherichia coli and Salmonella," 1996, Neidhardt, et al. Eds., ASM Press, Washington D.C., p. 2047-2066. The data

source for obtaining codon usage may rely on any available nucleotide sequence capable of coding for a protein. These data sets include nucleic acid sequences actually known to encode expressed proteins (e.g., complete protein coding sequences-CDS), expressed sequence tags (EST), or predicted coding regions of genomic sequences (see for example, Mount, D., Bioinformatics: Sequence and Genome Analysis, Chapter 8, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001; Uberbacher, E. C., 1996, Methods Enzymol. 266:259-281; Tiwari et al., 1997, Comput. Appl. Biosci. 13:263-270).

[0093] "Control sequence" is defined herein to include all components, which are necessary or advantageous for the expression of a polynucleotide and/or polypeptide of the present disclosure. Each control sequence may be native or foreign to the polynucleotide of interest. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator.

[0094] "Operably linked" is defined herein as a configuration in which a control sequence is appropriately placed (i.e., in a functional relationship) at a position relative to a polynucleotide of interest such that the control sequence directs or regulates the expression of the polynucleotide and/or polypeptide of interest.

[0095] "Promoter sequence" is a nucleic acid sequence that is recognized by a host cell for expression of a polynucleotide of interest, such as a coding sequence. The control sequence may comprise an appropriate promoter sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of a polynucleotide of interest. The promoter may be any nucleic acid sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

[0096] "Alkyl" refers to straight or branched chain hydrocarbon groups. When numbers appear in subscript after the symbol "C", the subscript defines with more specificity the number of carbon atoms that a particular group can contain. For example, "C_1-C_6 alkyl" refers to straight and branched chain alkyl groups with one to six carbon atoms, such as methyl, ethyl, n-propyl, isopropyl, n-butyl, t-butyl, n-pentyl, and so forth. Alkyl groups may be optionally substituted with one or more substituent groups. As used herein, alkyl includes alkanyl and alkylene, as further described below.

[0097] "Alkanyl" by itself or as part of another substituent refers to a saturated branched, straight-chain or cyclic alkyl derived by the removal of one hydrogen atom from a single carbon atom of a parent alkane. Alkanyl groups include, but are not limited to methanyl; ethanyl; propanyls such as propan-1-yl, propan-2-yl (isopropyl), cyclopropan-1-yl, etc.; butanyls such as butan-1-yl, butan-2-yl (*sec*-butyl), 2-methyl-propan-1-yl (isobutyl), 2-methyl-propan-2-yl (*t*-butyl), cyclobutan-1-yl, etc.; and the like. In some embodiments, the alkanyl groups are (C_1-C_6) alkanyl.

[0098] "Alkylene" by itself or as part of another substituent refers to a saturated or unsaturated, branched, straight-chain or cyclic divalent hydrocarbon radical derived by the removal of two hydrogen atoms from a single carbon atom or two different carbon atoms of a parent alkane, alkene or alkyne. For example, $-CH_2CH_3$ is an ethyl, while $-CH_2CH_2-$ is an ethylene. The term "alkylene" includes "cycloalkylene". The term "alkylene" is specifically intended to include groups having any degree or level of saturation, i.e., groups having exclusively single carbon-carbon bonds, groups having one or more double carbon-carbon bonds, groups having one or more triple carbon-carbon bonds and groups having mixtures of single, double and triple carbon-carbon bonds.

[0099] "Alkenyl" and "alkene" refer to straight or branched chain hydrocarbon groups having at least one double bond. When numbers appear in subscript after the symbol "C", the subscript defines with more specificity the number of carbon atoms that a particular group can contain. For example, "C_1-C_6 alkenyl" refers to straight and branched chain alkyl groups with one to six carbon atoms that include at least one double bond. Typical alkenyl groups include are well known in the art, and include, but are not limited to: ethenyl, 1-methyl-ethenyl, 1- or 2-propenyl, 1-methyl-l-propenyl, 1-methyl-2-propenyl, 1,1-dimethyl-2-propenyl, 2-methyl-2-propenyl, 1-, 2- or 3-butenyl, 1-methyl-l-butenyl, 2-methyl-l-butenyl, 3-methyl-1-butenyl, 3,3-dimethyl-l-butenyl, 2,3-dimethyl-l-butenyl, 1-methyl-2-butenyl, 1,1-dimethyl-2-butenyl, 2-methyl-2-butenyl, 3-methyl-2-butenyl, 1,3-butadienyl, 1,3-dimethyl-1,3-butadienyl, 1-, 2-, 3- or 4-pentenyl, and so forth. Alkenyl groups may be optionally substituted with one or more substituent groups.

[0100] "Alkynyl" and "alkyne" refer to straight or branched chain hydrocarbon groups having at least one triple bond. When numbers appear in subscript after the symbol "C", the subscript defines with more specificity the number of carbon atoms that a particular group can contain. For example, "C_1-C_6 alkynyl" refers to straight and branched chain alkyl groups with one to six carbon atoms that include at least one triple bond. Typical alkynyl groups include are well known in the art, and include, but are not limited to: ethynyl, 1- or 2-propynyl, 1-methyl-2-propynyl, 1,1-dimethyl-2-propynyl, 1-, 2- or 3-butynyl, 3-methyl-l-butynyl, 3,3-dimethyl-l-butynyl, 1-methyl-2butynyl, 1,1-dimethyl-2-butynyl, 1-, 2-, 3-, or 4-pentynyl, and so forth. Alkynyl groups may be optionally substituted with one or more substituent groups.

[0101] "Aryl" refers to a monovalent aromatic hydrocarbon radical of 6 to about 20 carbon atoms derived by the removal of one hydrogen atom from a single carbon atom of a parent aromatic ring system. Aryl groups include, but are not limited to, groups derived from aceanthrylene, acenaphthylene, acephenanthrylene, anthracene, azulene, benzene, chrysene, coronene, fluoranthene, fluorene, hexacene, hexaphene, hexalene, as indacene, s-indacene, indane, indene, naphthalene, octacene, octaphene, octalene, ovalene, penta-2,4-diene, pentacene, pentalene, pentaphene, perylene, phenalene, phenanthrene, picene, pleiadene, pyrene, pyranthrene, rubicene, triphenylene, trinaphthalene, and the like, as well as the various hydro isomers thereof. In some embodiments, the

aryl group is (C_5-C_{15}) aryl, with (C_5-C_{10}) being preferred. In some embodiments, the aryls are cyclopentadienyl, phenyl and naphthyl. Aryl groups may be optionally substituted with one or more substituent groups.

[0102] "Heteroaryl" and "heteroaromatic" refer to an aryl group in which one or more of the carbon atoms of the parent aromatic ring system are replaced by a heteroatom (O, N, or S). Typical heteroaryl groups include, but are not limited to, groups derived from acridine, benzimidazole, benzisoxazole, benzodioxan, benzodiaxole, benzofuran, benzopyrone, benzothiadiazole, benzothiazole, benzotriazole, benzoxazine, benzoxazole, benzoxazoline, carbazole, β-carboline, chromane, chromene, cinnoline, furan, imidazole, indazole, indole, indoline, indolizine, isobenzofuran, isochromene, isoindole, isoindoline, isoquinoline, isothiazole, isoxazole, naphthyridine, oxadiazole, oxazole, perimidine, phenanthridine, phenanthroline, phenazine, phthalazine, pteridine, purine, pyran, pyrazine, pyrazole, pyridazine, pyridine, pyrimidine, pyrrole, pyrrolizine, quinazoline, quinoline, quinolizine, quinoxaline, tetrazole, thiadiazole, thiazole, thiophene, triazole, xanthene, and the like, as well as the various hydro isomers thereof. In some embodiments, the heteroaryl group is a 5-14 membered heteroaryl. In some embodiments, the heteroaryl group is a 5-10 membered heteroaryl.

[0103] "Acyl" by itself or as part of another substituent refers to -C(O)R^a, where R^a is hydrogen, or substituted or unsubstituted alkyl, cylcoalkyl, cycloheteroalkyl, aryl, arylalkyl, heteroalkyl, heteroaryl, or heteroarylalkyl as defined herein. Typical acyl groups include, but are not limited to, formyl, acetyl, cyclohexylcarbonyl, cyclohexylmethylcarbonyl, benzoyl, benzylcarbonyl, and the like.

[0104] "Acyloxy" by itself or as part of another substituent refers to -OC(O)R^b, where R^b represents a hydrogen, or substituted or unsubstituted alkyl, heteroalkyl, cycloalkyl, heterocycloalkyl, aryl, arylalkyl, and heteroaryl groups as defined herein. Alkylacyloxy refers an acyloxy where R^b is (C_1-C_{12}) alkyl, (C_1-C_8) alkyl, or (C_1-C_4) alkyl. Arylacyloxy refers to an acyloxy where R^b is an aryl optionally substituted with selected substituents, including, but not limited to, hydroxyl, alkyl, halogen, (C_1-C_4) alkyl, (C_1-C_4) alkoxy, and carboxyl.

[0105] "Alkoxy" by itself or as part of another substituent refers to –OR^c, where R^c represents an alkyl or cycloalkyl group as defined herein. Typical alkoxy groups include, but are not limited to, methoxy, ethoxy, propoxy, butoxy, cyclohexyloxy, and the like.

[0106] "Alkylcarbonyl" by itself or as part of another substituent refers to –C(O)-$R^{d'}$, where $R^{d'}$ is an alkyl, as defined above. Typical alkoxycarbonyl include, but are not limited to, acetyl, ethylcarbonyl, n-propylcarbonyl, and the like.

[0107] "Alkylthio" by itself or as part of another substituent, refers to –S-R^e. where R^e is an alkyl. Typical alkylthio include, but are not limited to, methylthio, ethylthio, n-propylthio, and the like.

[0108] "Alkoxycarbonyl" by itself or as part of another substituent, refers to C(O)OR^f where R^f represents an alkyl or cycloalkyl group as defined herein. Typical alkoxycarbonyl groups include, but are not limited to, methoxycarbonyl, ethoxycarbonyl, proproxycarbonyl, butoxycarbonyl, cyclohexyloxycarbonyl, and the like.

[0109] "Alkoxycarbonylalkyl" by itself or as part of another substituent refers to –R^g -C(O)OR^h, where each R^g and R^h is independently an alkyl. Typical alkoxycarbonylalkyl include, but are not limited to, methoxycarbonylmethyl, (1,1-dimethylethoxy)carbonylmethyl, 2-(methoxycarbonyl)ethyl, and the like.

[0110] "Amino" by itself or as part of another substituent refers to the group -NH_2. Substituted amino refers to the group –NHR^i', NR^iR^j', and $NR^iR^jR^k$, where each R^i, R^j, and R^k are independently selected from substituted or unsubstituted alkyl, cycloalkyl, cycloheteroalkyl, alkoxy, aryl, heteroaryl, heteroarylalkyl, acyl, alkoxycarbonyl, sulfanyl, sulfinyl, sulfonyl, and the like. Typical amino groups include, but are limited to, dimethylamino, diethylamino, trimethylamino, triethylamino, methylysulfonylamino, furanyl-oxy-sulfamino, and the like.

[0111] "Carbonyl" refers to -C(=O).

[0112] "Halogen" or "Halo" by themselves or as part of another substituent, unless otherwise stated, refer to fluoro, chloro, bromo and iodo.

[0113] "Haloalkyl" by itself or as part of another substituent refers to an alkyl group in which one or more of the hydrogen atoms is replaced with a halogen. Thus, the term "haloalkyl" is meant to include monohaloalkyls, dihaloalkyls, trihaloalkyls, etc. up to perhaloalkyls. For example, the expression "(C_1-C_2) haloalkyl" includes 1-fluoromethyl, difluoromethyl, trifluoromethyl, 1-fluoroethyl, 1,1-difluoroethyl, 1,2-difluoroethyl, 1,1,1-trifluoroethyl, perfluoroethyl, etc.

[0114] "Substituted" when used to modify a specified group or radical, means that one or more hydrogen atoms of the specified group or radical are each, independently of one another, replaced with the same or different substituent(s). Typical substituents (also referred to herein as "substituents", "substituent groups," "functional groups," or "groups") are well known in the art and include, but are not limited to heteroatoms or halo groups (e.g., -F, -Cl, -Br, -I), straight-chain, branched, or cyclic alkyls, straight-chain, branched, or cyclic alkenyls, heteroatom substituted alkyls or alkenyls (e.g., -O-alkyl, -S-alkyl), aryl or heteroaryl, and other functional groups with or without heteroatoms (e.g., -OH, -NH_2, -CF_3, -CN, -OCN, -SCN, -NO, and -NO_2). When a first substituent group is "substituted with one or more" second groups, one or more hydrogen atoms of the first group

are replaced with a corresponding number of second groups. When the number of second groups is two or greater, each second group can be the same or different.

[0115] "Substituted alkyl, aryl, or heteroaryl" refers to an alkyl, aryl, or heteroaryl group in which one or more hydrogen atoms is replaced with another substituent group. Exemplary substituent groups include, but are not limited to, $-OR^l$, $-SR^l$, $-NR^lR^m$, $-NO_2$, -NO, -CN, $-CF_3$, halogen (e.g., -F, -Cl, -Br and –I), $-C(O)R^l$, $-C(O)OR^l$, $-C(O)NR^l$, $-S(O)_2R^l$, $-S(O)_2NR^lR^m$, where each R^l and R^m are independently selected from the group consisting of hydrogen and (C_1-C_4) alkyl.

[0116] "Optional" or "optionally" refers to a described event or circumstance may or may not occur, and that the description includes instances where the event or circumstance occurs and instances where the event or circumstance does not. For example, "optionally substituted aryl" refers to an aryl group that may or may not be substituted and that the description encompasses both substituted aryl group and unsubstituted aryl group.

[0117] "Stereoisomer," "stereoisomeric form," and the like are used interchangeably herein to refer to all isomers of individual molecules that differ only in the orientation of their atoms in space. In includes enantiomers and isomers of compounds with more than one chiral center that are not mirror images of one another ("diastereomers").

[0118] "Chiral center" refers to a carbon atom to which four different groups are attached.

[0119] "Enantiomer" or "enantiomeric" refers to a molecule that is nonsuperimposable on its mirror image and hence optically active where the enantiomer rotates the plane of polarized light in one direction and its mirror image rotates the plane of polarized light in the opposite direction.

[0120] "Enriched" in reference to component in a composition, such as a particular chiral compound, enantiomer, or diastereomer refers to a composition where the component comprises greater than 50% and typically comprises at least about 60%, 70%, 80%, 90%, or even more of that particular chiral compound, enantiomer, or diastereomer. The amount of enrichment can be determined using conventional analytical methods routinely used by those of ordinary skill in the art, including but not limited to, NMR spectroscopy in the presence of chiral shift reagents, gas chromatographic analysis using chiral columns, and high pressure liquid chromatographic analysis using chiral columns. In some embodiments a single chiral compound, enantiomer, or diastereomer will be substantially free of other corresponding chiral compound, enantiomer, or diastereomers. Chirally enantiomerically, or diastereomerically enriched compositions that contain at least about 95% of a specified chiral compound, enantiomer, or diastereomer are referred to herein as "substantially chirally pure," "substantially enantiomerically pure" and "substantially diastereomerically pure," respectively. Compositions that contain at least about 99% of a specified chiral compound, enantiomer, or

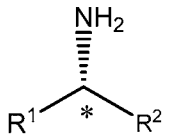
diastereomer are referred to herein as "chirally pure," "enantiomerically pure," and "diastereomerically pure," respectively.

[0121] "Compound" as used herein refers to any compounds encompassed by the identified structural formula and/or chemical name associated with the compound as disclosed herein. Compounds may be identified either by their chemical structure and/or chemical name. When the chemical structure and chemical name conflict, the chemical structure is determinative of the identity of the compound. Each compound identified by structural formulae and/or chemical name disclosed herein may contain one or more chiral centers and/or double bonds, and therefore, may exist as more than one stereoisomer, such as double-bond isomers (i.e., geometric isomers), enantiomer, or diastereomer. Accordingly, unless specifically depicted or noted otherwise, the chemical structures depicted herein encompass all possible enantiomers and stereoisomers of the illustrated compounds including the stereoisomerically pure form (e.g., geometrically pure, enantiomerically pure or diastereomerically pure) and enantiomeric and stereoisomeric mixtures. Enantiomeric and stereoisomeric mixtures can be resolved into their component enantiomers or stereoisomers using separation techniques or chiral synthesis techniques well known to the skilled artisan. The compounds may also exist in several tautomeric forms including the enol form, the keto form and mixtures thereof. Accordingly, the chemical structures depicted herein encompass all possible tautomeric forms of the illustrated compounds. Similarly, the compounds described also include all isotopically labeled versions of the compounds where one or more atoms have an atomic mass different from the atomic mass conventionally found in nature. Examples of isotopes that may be incorporated into the compounds of the disclosure include, but are not limited to, ^{2}H, ^{3}H, ^{13}C, ^{14}C, ^{15}N, ^{18}O, ^{17}O, etc. Compounds may exist in unsolvated forms as well as solvated forms, including hydrated forms and as N-oxides. In general, compounds may be hydrated, solvated or N-oxides. Certain compounds may exist in multiple crystalline or amorphous forms. In general, all physical forms are equivalent for the uses contemplated herein and are intended to be within the scope of the present disclosure. Further, it should be understood, when partial structures of the compounds are illustrated, that brackets indicate the point of attachment of the partial structure to the rest of the molecule.

5.3 Biocatalytic Transamination Processes

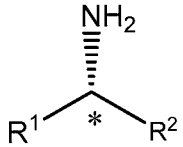
[0122] The biocatalytic transamination processes described herein are based on engineered transaminase polypeptides that were prepared for their ability to carry out the transamination of the ketoamide substrate, 4-oxo-4-[3-(trifluoromethyl)-5,6-dihydro[1,2,4]triazolo[4,3-a]pyrazin-7(8*H*)-yl]-1-(2,4,5-trifluorophenyl)butan-2-one to the chiral amine product, (2*R*)-4-oxo-4-[3-(trifluoromethyl)-5,6-dihydro[1,2,4]triazolo[4,3-a]pyrazin-7(8*H*)-yl]-1-(2,4,5-trifluorophenyl)butan-2-amine, in the

presence of an amino group donor. This chiral amine product, known as sitagliptin, is the active ingredient in JANUVIA® used for the treatment of Type 2 diabetes. The corresponding naturally occurring transaminase or the transaminase of SEQ ID NO:2 does not measurably exhibit activity on the sitagliptin ketoamide substrate. The present disclosure shows that these engineered transaminases are also capable of carrying out transamination of other keto substrates to produce chiral amines in enantiomeric excess. The chiral amine products have the general structure



wherein R^1 is optionally substituted aryl or heteroaryl and R^2 is an optionally substituted alkyl, or an acyl, acyloxy, or alkoxy groups attached to the chiral carbon by a substituted or unsubstituted alkylene. The corresponding prochiral ketone substrates are contacted with a transaminase under suitable reaction conditions to produce the amine product in enantiomeric excess. The resulting amine compounds can be used in the synthesis of various drug products and isomers thereof, as further described below.

[0123] In some embodiments, the disclosure provides for a process for preparing an amine product of structural formula (I):



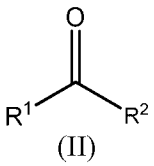
(I)

having the indicated stereochemical configuration at the stereogenic center marked with an *; in an enantiomeric excess over the opposite enantiomer, wherein

R^1 is optionally substituted aryl or heteroaryl; and

R^2 is an optionally substituted C_1-C_6 alkyl, $-R^3C(O)R^4$, or $-R^3OC(O)R^5$

wherein R^3 is an optionally substituted C_1-C_4 alkyl, and R^4 is H, an optionally substituted C_1-C_4 alkyl, NR^6R^7, or OR^8, where R^5, R^6, R^7, and R^8 are independently H or C_1-C_4 alkyl, and which process comprises contacting a ketone substrate of structural formula (II):



(II)

with a transaminase polypeptide in presence of an amino donor under reaction conditions suitable for converting the ketone substrate to the amine product, wherein the transaminase polypeptide is an

engineered transaminase described herein. In some embodiments, the transaminase polypeptide has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO:4 and is capable of converting the ketone substrate of formula (II) to the amine product of formula (I) at a rate that is improved as compared to the transaminase of SEQ ID NO:2.

[0124] In some embodiments, the transaminase polypeptide has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102, and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to the transaminase of SEQ ID NO:2. Specific embodiments of the engineered transaminases for use in the processes are further described below.

[0125] In some embodiments, the engineered transaminase has at least 5%, 10%, 20%, 30%, 40%, 50% or more activity of SEQ ID NO:74.

[0126] In some embodiments, the amine product is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments of the processes described above, the amine product is produced in at least 99% enantiomeric excess.

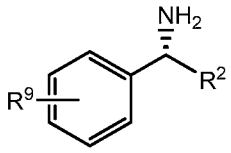
[0127] As mentioned above, the transaminase polypeptides useful in the processes of the present disclosure can be characterized in terms of the ability to convert the sitagliptin ketoamide substrate to the sitagliptin. Accordingly, in any of the embodiments of the processes disclosed herein, the process can be carried out wherein the transaminase polypeptide is capable of converting the sitagliptin ketoamide substrate to the sitagliptin at a rate that is improved as compared to the transaminase of SEQ ID NO:2, and has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO:4.

[0128] In some embodiments of the process above, R^1 is an optionally substituted phenyl. In some embodiments R^1 is an optionally substituted pyridinyl. In some embodiments, R^1 is a substituted aryl or heteroaryl. In some embodiments, the substitutions on the aryl or heteroaryl are selected from C_1-C_4 alkyl, -OR', -SR', -NR'R', $-NO_2$, -NO, -CN, $-CF_3$, halogen (e.g., -F, -Cl, -Br and –I), -C(O)R', -C(O)OR', -C(O)NR', $-S(O)_2R'$, $-S(O)_2NR'R''$, where each R' and R'' are independently selected from the group consisting of hydrogen and (C_1-C_4) alkyl. In some embodiments, the (C_1-C_4) alkyl is a halo substituted alkyl.

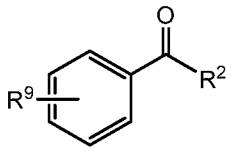
[0129] In some embodiments, R^2 is a C_1-C_4 alkyl or halo substituted C_1-C_4 alkyl, particularly methyl, halo substituted methyl, propyl or halo substituted propyl. In some embodiments R^2 is CF_2H or CF_3.

[0130] In some embodiments of R^2, the substitution on the C_1-C_6 alkyl and R^3 groups are selected from halogen, OH, NR^5R^6, or OR^8, where R^5, R^6 and R^8 are defined above. In some embodiments, the compounds of formula (I) produced in the process described above are substantially chirally pure compounds. In certain embodiments, the compounds of formula (I) produced in the process described above are chirally pure.

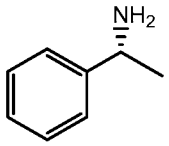
[0131] In some embodiments of the process, the amine product of formula (I) is:



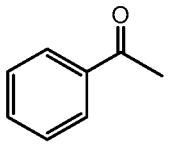
wherein R^9 is H, Cl, Br, F, CH_3, CF_3, NH_2, NO_2, CN, SCN, OCF_3, or OCH_3, and R^2 is an optionally substituted C_1-C_6 alkyl, and the ketone substrate of formula (II) is:



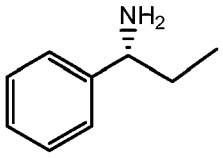
[0132] In some embodiments of the process, the amine product of formula (I) is:



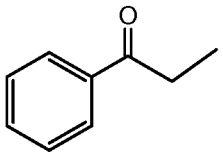
and the ketone substrate of formula (II) is:



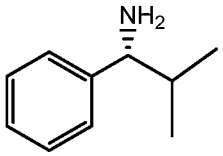
[0133] In some embodiments of the process, the amine product of formula (I) is:



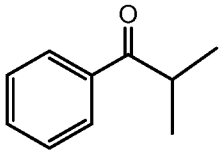
and the ketone substrate of formula (II) is:



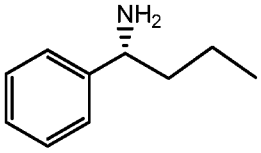
[0134] In some embodiments of the process, the amine product of formula (I) is:



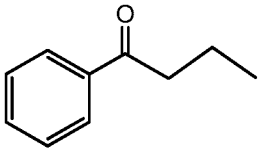
and the ketone substrate of formula (II) is:



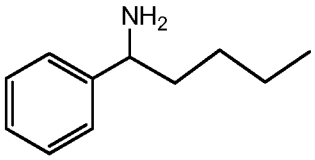
[0135] In some embodiments of the process, the amine product of formula (I) is:



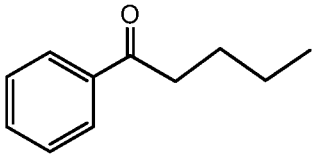
and the ketone substrate of formula (II) is:



[0136] In some embodiments of the process, the amine product of formula (I) is:

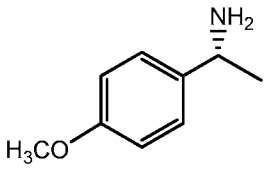


and the ketone substrate of formula (II) is:

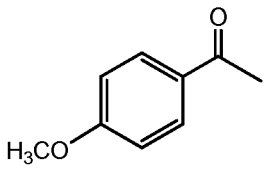


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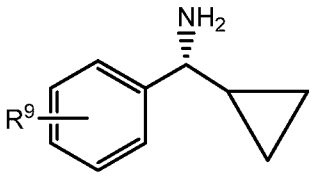
[0137] In some embodiments of the process, the amine product of formula (I) is:



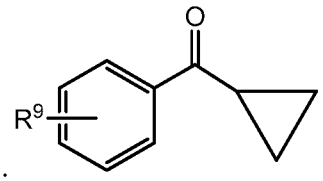
and the ketone substrate of formula (II) is:



[0138] In some embodiments of the process, the amine product of formula (I) is:

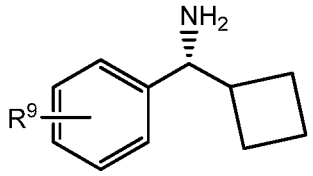


wherein R^9 as defined above, and the ketone substrate of formula (II) is

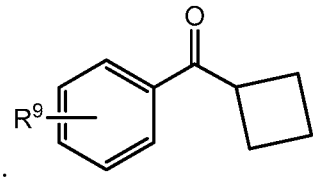


[0139] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

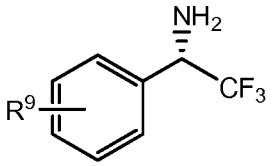
[0140] In some embodiments of the process, the amine product of formula (I) is:



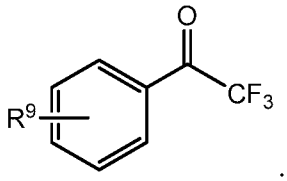
wherein R^9 as defined above, and the ketone substrate of formula (II) is



[0141] In some embodiments of the process, the amine product of formula (I) is:

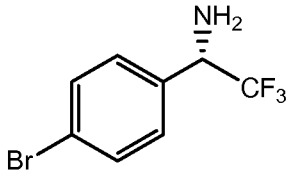


wherein R^9 is H, Cl, Br, F, CH_3, CF_3, NH_2, NO_2, CN, SCN, OCF_3, or OCH_3, and the ketone substrate of formula (II) is:

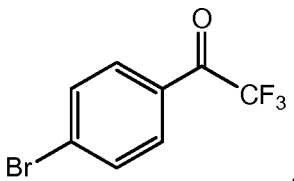


[0142] In some embodiments R^9 is H, Br, CH_3, or CF_3. In some embodiments R^9 is in the para position on the phenyl ring. In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0143] In some embodiments of the process, the amine product of formula (I) is (*S*)-1-(4-bromophenyl)-2,2,2-trifluoroethanamine:

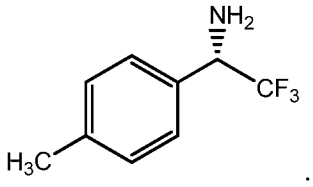


and the ketone substrate of formula (II) is 1-(4-bromophenyl)-2,2,2-trifluoroethanone:

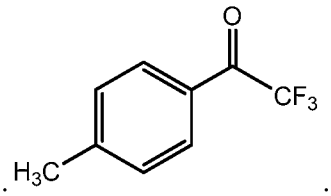


[0144] In some embodiments of the process, the (*S*)-1-(4-bromophenyl)-2,2,2-trifluoroethanamine is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the (*S*)-1-(4-bromophenyl)-2,2,2-trifluoroethanamine produced is substantially chirally pure compounds. In certain embodiments, the (*S*)-1-(4-bromophenyl)-2,2,2-trifluoroethanamine produced in the process is chirally pure.

[0145] In some embodiments of the process, the amine product of formula (I) is (*S*)-2,2,2-trifluoro-1-p-tolylethanamine:

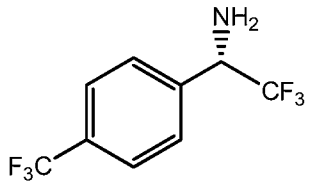


and the ketone substrate of formula (II) is 2,2,2-trifluoro-1-p-tolylethanone

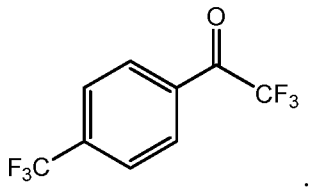


[0146] In some embodiments, the (*S*)-2,2,2-trifluoro-1-p-tolylethanamine is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the (*S*)-2,2,2-trifluoro-1-p-tolylethanamine produced is substantially chirally pure. In certain embodiments, the (*S*)-2,2,2-trifluoro-1-p-tolylethanamine produced in the process is chirally pure.

[0147] In some embodiments of the process, the product amine of formula (I) is (*S*)-2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanamine:

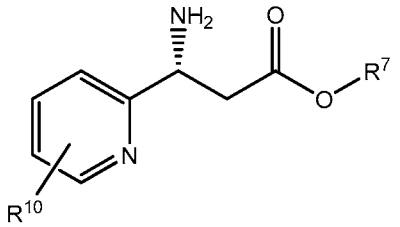


and the ketone substrate of formula (II) is 2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanone:

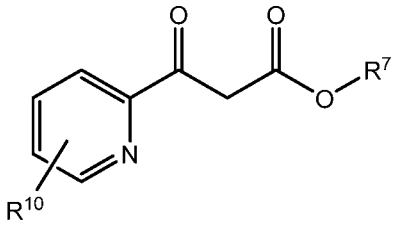


[0148] In some embodiments, the (*S*)-2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanamine is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the (*S*)-2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanamine produced is substantially chirally pure. In certain embodiments, the (*S*)-2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanamine produced in the process is chirally pure.

[0149] In some embodiments of the process, the product amine of formula (I) is:



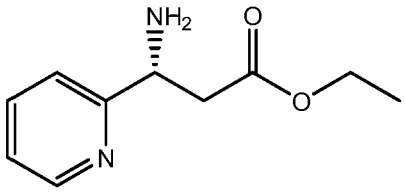
and the ketone substrate of formula (II) is:



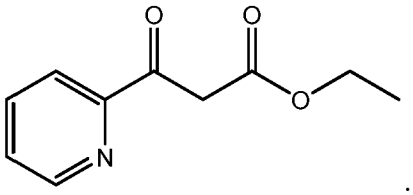
wherein R^7 is an optionally substituted C_1-C_4 alkyl and R^{10} is hydrogen, halogen, amino or substituted amino, C_1-C_4 alkyl, halo substituted C_1-C_4 alkyl, nitro, cyano, thiocyano, or alkoxy. In some embodiments, R^{10} is R^9 described above. In some embodiments, R^{10} is H or F. In some embodiments, R^7 is C_1-C_4 alkyl.

[0150] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0151] In some embodiments of the process, the amine product of formula (I) is (*R*)-ethyl-3-amino-3-(pyridin-2-yl)propanoate:

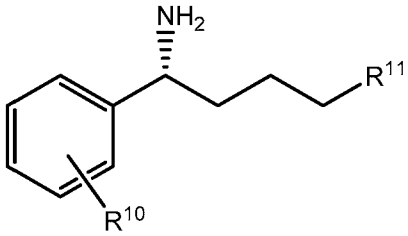


and the ketone substrate of formula (II) is ethyl 3-oxo-3-(pyrindin-2-yl)propanoate:

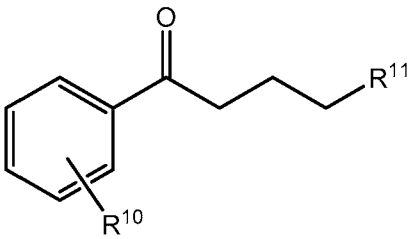


[0152] In some embodiments, the (*R*)-ethyl-3-amino-3-(pyridin-2-yl)propanoate is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the (*R*)-ethyl-3-amino-3-(pyridin-2-yl)propanoate produced is substantially chirally pure. In certain embodiments, the (*R*)-ethyl-3-amino-3-(pyridin-2-yl)propanoate produced in the process is chirally pure.

[0153] In some embodiments of the process, the amine product of formula (I) is:

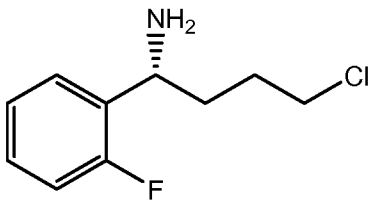


wherein R^{11} is halogen, OH, -C(O)R^4, -OC(O)R^5, or NR^6R^7, where R^4, R^5, R^6, R^7, and R^{10} are defined above, and the ketone substrate of formula (II) is:

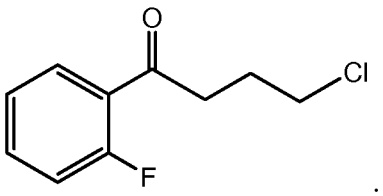


[0154] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0155] In some embodiments the amine product of formula (I) is (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine:

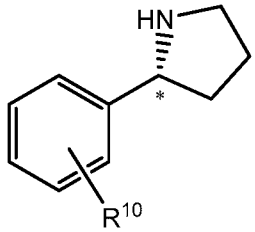


and the ketone substrate of formula (II) is 4-chloro-1-(2-fluorophenyl)butan-1-one:



[0156] In some embodiments, the (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine produced is substantially chirally pure. In certain embodiments, the (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine produced in the process is chirally pure.

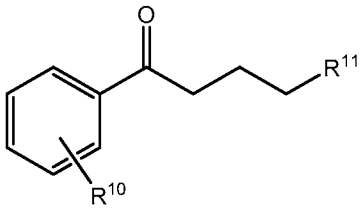
[0157] In some embodiments, the process using the transaminase biocatalysts can be used for preparing the compound of formula (III):



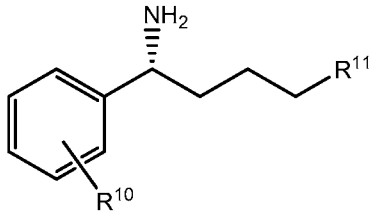
(III)

having the indicated stereochemical configuration at the stereogenic center marked with an *, in an enantiomeric excess over the opposite enantiomer, wherein R^{10} is as defined above. The process for preparing the amine product of compound (III) can comprise:

(a) contacting a ketone substrate of formula



wherein R^{10} and R^{11} are as defined above, with a transaminase polypeptide described herein in presence of an amino donor under reaction conditions suitable for converting the ketone substrate to an amine product of formula:

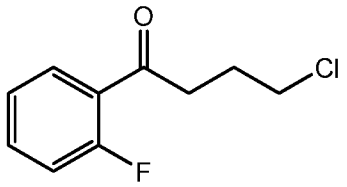


and

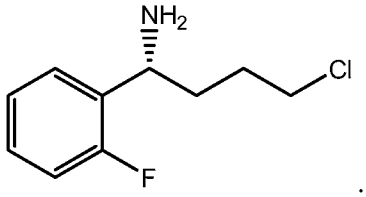
(b) cyclizing the amine product under suitable conditions to form the compound of formula (III).

[0158] In some embodiments, the cyclized amine product for formula (III) in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

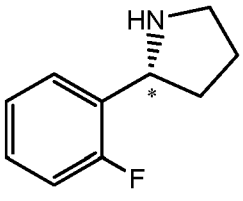
[0159] In some embodiments the ketone substrate is 4-chloro-1-(2-fluorophenyl)butan-1-one:



and the amine product is (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine:



thereby forming (*R*)-2-(2-fluorophenyl)pyrrolidine:

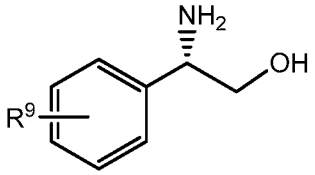


in enantiomeric excess.

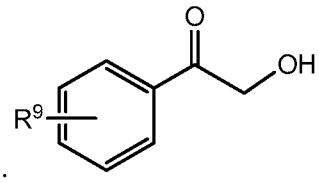
[0160] In some embodiments, the (*R*)-2-(2-fluorophenyl)pyrrolidine is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments,

the (*R*)-2-(2-fluorophenyl)pyrrolidine produced is substantially chirally pure. In certain embodiments, the (*R*)-2-(2-fluorophenyl)pyrrolidine produced in the process is chirally pure.

[0161] In some embodiments of the process, the amine product of formula (I) is:



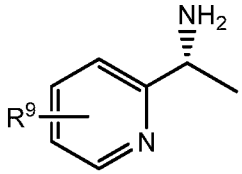
wherein R^9 as defined above, and the ketone substrate of formula (II) is



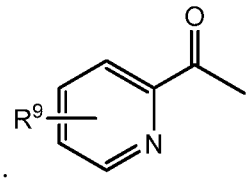
.

[0162] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0163] In some embodiments of the process, the amine product of formula (I) is:



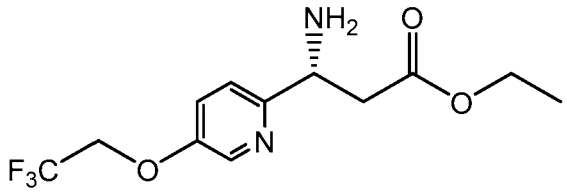
wherein R^9 as defined above, and the ketone substrate of formula (II) is



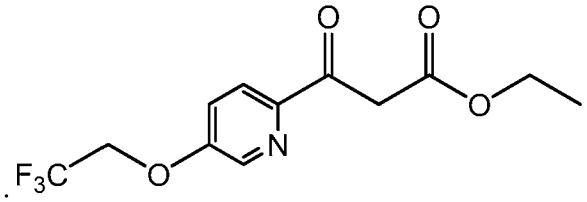
.

[0164] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0165] In some embodiments of the process, the amine product of formula (I) is:

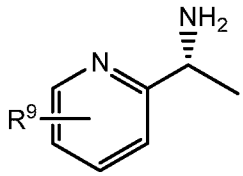


wherein R^9 as defined above, and the ketone substrate of formula (II) is

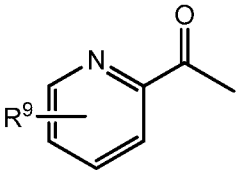


[0166] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0167] In some embodiments of the process, the amine product of formula (I) is:



wherein R^9 as defined above, and the ketone substrate of formula (II) is

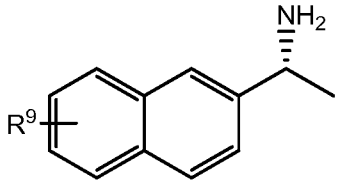


[0168] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

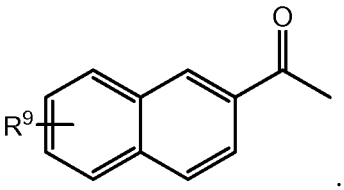
[0169] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments,

the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

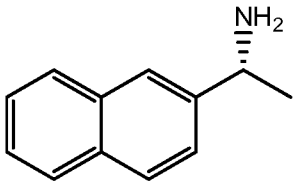
[0170] In some embodiments of the process, the amine product of formula (I) is:



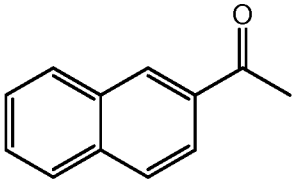
wherein R^9 is defined above, and the ketone substrate of formula (II) is:



[0171] In some embodiments of the process, the amine product of formula (I) is:



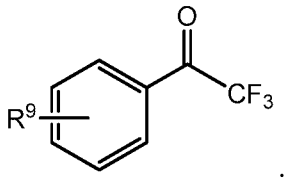
wherein R^9 as defined above, and the ketone substrate of formula (II) is:



[0172] In some embodiments, the amine product in the foregoing process is produced in at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 96%, or 99% or more enantiomeric excess. In some embodiments, the compounds produced in the foregoing process are substantially chirally pure compounds. In some embodiments, the compounds produced in the foregoing process are chirally pure compounds.

[0173] As noted above, the processes described above are carried out in reaction conditions suitable for converting the ketone substrate to the corresponding chiral amine product in enantiomeric excess. In some embodiments, the reaction condition comprises a temperature of about 20°C to about 65°C. In some embodiments the reaction condition comprises a temperature of about 40°C to about 65°C. In

some embodiments the reaction condition comprises a temperature of about 50°C to about 65°C. For instance, for the process using the following ketone substrate:



the reaction condition comprises a temperature of 40°C to 65°C. An exemplary temperature is 60°C.

[0174] In some embodiments the reaction condition under which the processes described above are done comprises a pH of about 7.0 to about 11.0. In some embodiments the reaction condition comprises a pH of about 7.0 to about 9.0. In some embodiments, the reaction condition for the process is a pH of about 8.5. While the pH can be adjusted during the process using any base and/or acid, in some embodiments, the pH can be maintained by adding isopropylamine, which also provides a source of amino donor to push the reaction equilibrium toward amine product formation.

[0175] Various organic solvents can be used in the process to facilitate the enzyme reaction and to place the substrate and/or product in solution. In some embodiments of the process, the organic solvent comprises a polar solvent, such as methanol or dimethylsulfoxide (DMSO). In some embodiments, the organic solvent is DMSO, which can be present from about 10% to about 40% volume/volume (v/v). In some embodiments, the organic solvent is DMSO, which can be present from about 10% to about 50% volume/volume (v/v). In some embodiments, the DMSO is present at about 40% v/v.

[0176] As discussed above, the amino group donor used in the process can be a chiral amine or an achiral amine. An achiral amino group donor has the advantage of not being limited in its reaction to a specific stereoisomer, thus requiring less of the amino group donor. Various suitable amino group donors can be used, including, by way of example and not limitation, isopropylamine (also referred to as 2-aminopropane), L, D or DL alanine, phenylalanine, glutamate, glutamine, leucine (or any other suitable α-amino acids), 3-aminobutyric acid (or any other suitable β-amino acids), and methylbenzylamine. In some embodiments, the amino group donor is isopropylamine. In some embodiments, other amino group donors may be used, including, among others, α-phenethylamine (also termed 1-phenylethanamine), and its enantiomers (S)-1-phenylethanamine and (R)-1-phenylethanamine, 2-amino-4-phenylbutane, glycine, L-glutamic acid, L-glutamate, monosodium glutamate, L-aspartic acid, L-lysine, L-ornithine, β-alanine, taurine, n-octylamine, cyclohexylamine, 1,4-butanediamine, 1,6-hexanediamine, 6-aminohexanoic acid, 4-aminobutyric acid, tyramine, and benzyl amine, 2-aminobutane, 2-amino-1-butanol, 1-amino-1-phenylethane, l-amino-1-(2-methoxy-5-fluorophenyl)ethane, 1-amino-1-phenylpropane, 1-amino-1-(4-hydroxyphenyl)propane, 1-amino-1-(4-bromophenyl)propane, 1-amino-1-(4-nitrophenyl)propane, l-phenyl-2-aminopropane, 1-(3-

trifluoromethylphenyl)-2-aminopropane, 2-aminopropanol, l-amino-l-phenylbutane, l-phenyl-2-aminobutane, 1-(2,5-dimethoxy-4-methylphenyl)-2-aminobutane, l-phenyl-3-aminobutane, 1-(4-hydroxyphenyl)-3-aminobutane, 1-amino-2-methylcyclopentane, l-amino-3-methylcyclopentane, l-amino-2-methylcyclohexane, l-amino-1-(2-naphthyl)ethane, 3-methylcyclopentylamine, 2-methylcyclopentylamine, 2-ethylcyclopentylamine, 2-methylcyclohexylamine, 3-methylcyclohexylamine, 1-aminotetralin, 2-aminotetralin, 2-amino-5-methoxytetralin, and 1-aminoindan, including both (R) and (S) single isomers where possible and including all possible salts of the amines.

[0177] In some embodiments of the processes above, the step in the process can further comprise removal of the carbonyl by-product formed from the amino group donor when the amino group is transferred to the amino group acceptor. Such removal *in situ* can reduce the rate of the reverse reaction such that the forward reaction dominates and more substrate is then converted to product.

[0178] Removal of the carbonyl by-product can be carried in a number of ways. Where the amino group donor is an amino acid, such as alanine, the carbonyl by product, a keto acid, can be removed by reaction with a peroxide (see, e.g., US 2008/0213845, incorporated herein by reference). Peroxides which can be used include, among others, hydrogen peroxide; peroxyacids (peracids) such as peracetic acid (CH_3CO_3H), trifluoroperacetic acid and metachloroperoxybenzoic acid; organic peroxides such as t-butyl peroxide ($(CH_3)_3COOH$), or other selective oxidants such as tetrapropylammonium perruthenate, MnO_2, $KMnO_4$, ruthenium tetroxide and related compounds. Alternatively, pyruvate removal can be achieved via its reduction to lactate by employing lactate dehydrogenase to shift equilibrium to the product amine (see, e.g., Koszelewski et al.,, 2008, *Adv. Syn. Catal.* 350: 2761-2766). Pyruvate removal can also be achieved via its decarboxylation to carbon dioxide acetaldehyde by employing pyruvate decarboxylase (see e.g., Höhne et al., 2008, *ChemBioChem* 9: 363-365).

[0179] In some embodiments, where the choice of the amino group donor results in a carbonyl by-product that has a vapor pressure higher than water (e.g., a low boiling co-product such as a volatile organic carbonyl compound), the carbonyl by-product can be removed by sparging the reaction solution with a non-reactive gas or by applying a vacuum to lower the reaction pressure and removing the carbonyl by-product present in the gas phase. A non-reactive gas is any gas that does not react with the reaction components. Various non-reactive gases include nitrogen and noble gases (e.g., inert gases). In some embodiments, the non-reactive gas is nitrogen gas.

[0180] In some embodiments, the amino acid donor used in the process is isopropylamine, which forms the carbonyl by-product acetone upon transfer of the amino group to the amino group acceptor. The acetone can be removed by sparging with nitrogen gas or applying a vacuum to the reaction solution and removing the acetone from the gas phase by an acetone trap, such as a condenser or other

cold trap. Alternatively, the acetone can be removed by reduction to isopropanol using a ketoreductase.

[0181] In some embodiments of the processes above where the carbonyl by-product is removed, the corresponding amino group donor can be added during the transamination reaction to replenish the amino group donor and/or maintain the pH of the reaction. Replenishing the amino group donor also shifts the equilibrium towards product formation, thereby increasing the conversion of substrate to product. Thus, in some embodiments wherein the amino group donor is isopropylamine and the acetone product is removed *in situ*, isopropylamine can be added to the solution to replenish the amino group donor lost during the acetone removal and to maintain the pH of the reaction (e.g., at about 8.5). Alternatively, in embodiments where an amino acid is used as amino group donor, the keto acid carbonyl by-product can be recycled back to the amino acid by reaction with ammonia and NADH using an appropriate amino acid dehydrogenase enzyme, thereby replenishing the amino group donor.

[0182] The ketone substrate can be present in appropriate amounts, depending on factors, among others, such as the nature of solvent, the stability of the transaminase to reaction temperature, the amount and activity of the enzyme. In some embodiments, the substrate is present at 5 to 50 g/L. In some embodiments, the substrate is present at 5-25 g/L.

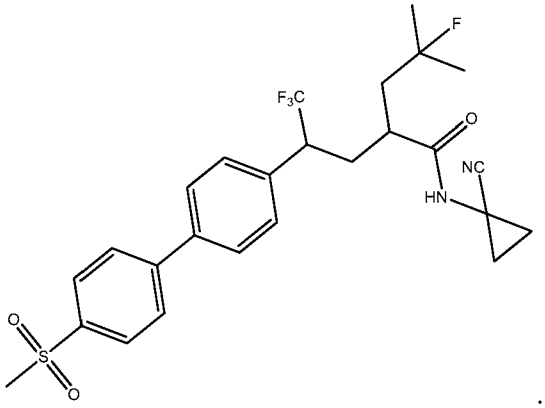
[0183] In some embodiments, the process described above comprises contacting the keto substrate at about 10 to 50 g/L with about 1 to 20 g/L of a transaminase described herein under reaction conditions of pH 7.5 to 9.0 and a temperature of 40 to 60°C in presence of isopropylamine of from about 1 M to about 2 M, wherein at least 80%, 85%, 90%, 92%, 94%, 96%, or 98% or more of the substrate is converted to product in 24 hrs. In some embodiments, the transaminase polypeptide capable of carrying out the foregoing reaction comprises an amino acid sequence corresponding to SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, 102, 110 or 166.

[0184] In some embodiments, the processes above can further comprise the step of isolating the amine products, such as the amine products of structural formulas (I), (III), or (V), from the reaction mixture.

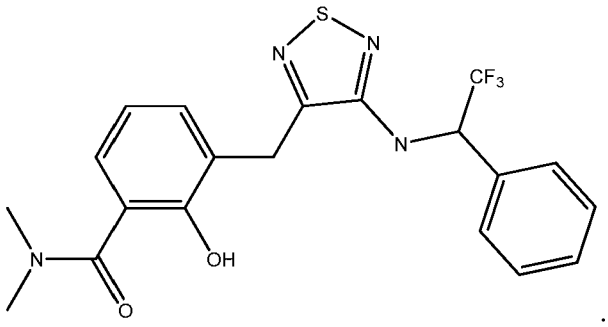
[0185] Also provided herein are compositions of the transaminases and substrates/products. In some embodiments, the compositions can comprise the amine products of structural formulas (I), (III), or (V) and a transaminase of the disclosure. Any one or more of the engineered transaminases can be part of the composition.

[0186] In some embodiments, the compositions can further comprise an amino group donor. In some embodiments of the compositions, the amino group donor can comprise isopropylamine, alanine, 3-aminobutyric acid, or methylbenzylamine. In some embodiments of the compositions, the amino group donor is an isopropylamine.

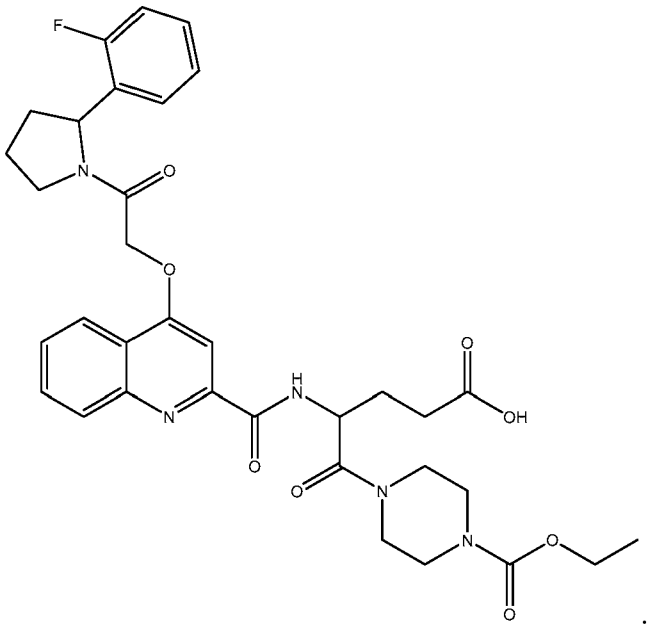
[0187] The processes of the disclosure are useful for producing various intermediates for the synthesis of isomers and derivatives of pharmaceutical molecules. For example, the processes of the disclosure that produce compounds of formula (I), can be used in the synthesis of molecules such as Odanacatib or related derivatives, an investigational selective cathepsin K inhibitor for the prevention of bone turnover in cancer patients. Odanacatib has the following structure:



[0188] The processes that produce compounds of formula (I) can be used to make intermediates for synthesis of certain thiadaizoles such as the molecule below. The thiadaizoles are CXC- and CC-chemokine receptor ligands, purported to have anti-inflammatory and anti-tumor properties (WO 2005/066147).



[0189] The processes of the disclosure that produce compounds of formula (V) can be used to synthesize compounds such as:



WO 2008/128647 discloses similar quinoline-carboxamide derivatives as P2Y12 antagonists which are potentially useful in the treatment of cardiovascular disorders.

5.4 Transaminase Polypeptides and Polynucleotides

[0190] As noted above, the transaminase polypeptides used in the above-described methods were initially identified based on their ability to convert the ketoamide substrate 4-oxo-4-[3-(trifluoromethyl)-5,6-dihydro[1,2,4]triazolo[4,3-*a*]pyrazin-7(8*H*)-yl]-1-(2,4,5-trifluorophenyl)butan-2-one ("the sitagliptin ketoamide substrate") to the product (2*R*)-4-oxo-4-[3-(trifluoromethyl)-5,6-dihydro[1,2,4]triazolo[4,3-*a*]pyrazin-7(8*H*)-yl]-1-(2,4,5-trifluorophenyl)butan-2-amine for the synthesis of sitagliptin. The transaminase polypeptide of SEQ ID NO; 2 does not efficiently carry out the transamination reaction. These transaminases polypeptides can be described in relation to their activity toward the sitagliptin ketoamide substrate, or to the substrates described herein.

[0191] Transaminases, including those described herein, typically contain a coenzyme, pyridoxal phosphate (PLP), which participates in the transamination reaction. PLP can be provided by the host cell in which the polypeptide is synthesized, or provided by adding PLP to a solution of the polypeptide. While the transaminase is described with respect to the amino acid sequence, it will be understood by those skilled in the art that the active polypeptide contains PLP or a suitable analog as a coenzyme.

[0192] As noted above, in some embodiments, the transaminase polypeptide has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO:4 and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to the transaminase of SEQ ID NO:2.

[0193] In some embodiments, the transaminase polypeptide has at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more amino acid sequence identity to SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102, and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to the transaminase of SEQ ID NO:2.

[0194] In some embodiments, the engineered transaminase polypeptides comprise an amino acid sequence that has one or more residue differences as compared to a transaminase reference sequence. The residue differences can be non-conservative substitutions, conservative substitutions, or a combination of non-conservative and conservative substitutions. With respect to the residue differences and the descriptions of residue positions, the transaminases provided herein can be described in reference to the amino acid sequence of the naturally occurring transaminase of *Arthrobacter sp* KNK168, or the transaminase of SEQ ID NO:2, or another engineered transaminase, such as the polypeptide of SEQ ID NO:4. For the descriptions herein, the amino acid residue position in the reference sequence is determined in the transaminase beginning from the initiating methionine (M) residue (i.e., M represents residue position 1), although it will be understood by the skilled artisan that this initiating methionine residue may be removed by biological processing machinery, such as in a host cell or in vitro translation system, to generate a mature protein lacking the initiating methionine residue.

[0195] The polypeptide sequence position at which a particular amino acid or amino acid change ("residue difference") is present is sometimes described herein as "Xn", or "position n", where n refers to the residue position with respect to the reference sequence.

[0196] A specific substitution mutation, which is a replacement of the specific residue in a reference sequence with a different specified residue may be denoted by the conventional notation "X(number)Y", where X is the single letter identifier of the residue in the reference sequence, "number" is the residue position in the reference sequence, and Y is the single letter identifier of the residue substitution in the engineered sequence.

[0197] In some embodiments, the residue differences can occur at one or more of the following residue positions: X4; X5; X8; X18; X25; X26; X27; X28; X30; X41; X42; X48; X49; X50; X54; X55; X60; X61; X62; X65; X69; X81; X94; X96; X102; X117; X120; X122; X124; X126; X136; X137; X138; X146; X148; X150; X152; X155; X156; X160; X163; X164; X169; X174; X178; X195; X199; X204; X208; X209; X211; X215; X217; X223; X225; X230; X252; X269; X273; X282, X284; X292; X297; X302; X306; X321; and X329. In some embodiments, the residue differences or combinations thereof, are associated with the improved enzyme properties. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60

residue differences at residue positions other than those specific positions denoted by "Xn" listed above. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other amino acid residue positions. In some embodiments, the residue differences at other residue positions comprise substitutions with conservative amino acid residues.

[0198] In the embodiments herein, the residue differences as compared to SEQ ID NO:2 at residue positions affecting substrate binding on the transaminase allows accommodation of various ketoamide substrates. Without being bound by theory, at least two regions, a first substrate binding region and a second substrate binding region, interact with different structural elements of ketoamide substrates. The first binding region comprises residue positions X62, X136, X137, X195, X199, X208, X209, X223, X225, and X282, while the second binding region comprises residue positions X69, X122, and X284. Accordingly, the transaminase polypeptides herein have one or more residue differences at residue positions comprising X62, X69, X122, X136, X137, X195, X199, X208, X209, X223, X225, X282, and X284. In some embodiments, the transaminase polypeptides herein have at least two or more, three or more, four or more, five or more, or six or more residue differences at the specified residue positions associated with substrate binding.

[0199] In some embodiments, the residue differences as compared to SEQ ID NO:2 are at one or more of residue positions forming a first substrate binding region comprised of residue positions X62, X136, X137, X195, X199, X208, X209, X223, X225, and X282. Accordingly, in some embodiments, the engineered transaminase comprises an amino acid sequence that includes at least one residue difference as compared to SEQ ID NO:2 at residue positions X62, X136, X137, X195, X199, X208, X209, X223, X225, and X282.

[0200] In some embodiments, the residue differences as compared to SEQ ID NO:2 are at one or more of residue positions forming a second substrate binding region comprised of residue positions X69, X122, and X284. Accordingly, in some embodiments, the engineered transaminase comprises an amino acid sequence that includes at least one residue difference as compared to SEQ ID NO:2 at residue positions X69, X122, and X284.

[0201] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes residue differences at the first binding region in combination with residue differences at the second binding region. Accordingly, in some embodiments, the engineered transaminase comprises an amino acid sequence that includes one or more residue difference as compared to SEQ ID NO:2 at residue positions X62, X136, X137, X195, X199, X208, X209, X223, X225, and X282 in combination with one or more residue difference as compared to SEQ ID NO:2 at residue positions X69, X122, and X284.

[0202] In some embodiments of the engineered transaminases of the disclosure, the amino acid residues at a residue position can be can be defined in terms of the amino acid "features" (e.g., type or property of amino acids) that can appear at that position. Thus, in some embodiments the amino acid residues at the positions specified above can be selected from the following features: X4 is an aromatic residue; X5 is a basic residue; X8 is a constrained residue; X18 is a cysteine (C) or an aliphatic residue; X25 is a polar residue; X26 is an aromatic or constrained residue; X27 is a polar residue; X28 is a constrained residue; X30 is a polar or non-polar residue; X41 is a constrained or polar residue; X42 is a non-polar residue; X48 is a polar, acidic, aliphatic or non-polar residue; X49 is a polar residue; X50 is an aliphatic residue; X54 is a constrained residue; X55 is an aliphatic residue; X60 is an aromatic residue; X61 is an aromatic residue; X62 is an aromatic or polar residue; X65 is an aliphatic residue; X69 is a cysteine (C) or non-polar, polar, or aliphatic residue; X81 is a non-polar residue; X94 is an aliphatic residue; X96 is an aliphatic residue; X102 is an aliphatic or basic residue; X117 is a non-polar residue; X120 is an aromatic residue; X122 is a constrained, non-polar or aliphatic residue; X124 is a polar or constrained residue; X126 is a polar residue; X136 is an aromatic residue; X137 is a polar or aliphatic residue; X138 is a basic or constrained residue; X146 is a basic residue; X148 is an aliphatic or aromatic residue; X150 is aromatic, constrained or polar residue; X152 is a cysteine (C), non-polar, aliphatic, or polar residue; X155 is a non-polar or polar residue; X156 is a polar residue; X160 is an aliphatic residue; X163 is an aliphatic or constrained residue; X164 is an aliphatic or constrained residue; X169 is an aliphatic residue; X174 is an aliphatic residue; X178 is a polar residue; X195 is an aromatic or polar residue; X199 is an aliphatic or aromatic residue; X204 is an aliphatic residue; X208 is a cysteine (C) or a constrained, non-polar, aromatic, polar, or basic residue; X209 is an aliphatic residue; X211 is an aliphatic residue; X215 is a cysteine (C); X217 is a polar residue; X223 is a constrained residue; X225 is an aromatic residue; X230 is an aliphatic residue; X252 is an aromatic or aliphatic residue; X269 is a constrained residue; X273 is an aromatic residue; X282 is a polar residue; X284 is a non-polar residue; X292 is a polar residue; X297 is a polar residue; X302 is an aliphatic residue; X306 is an aliphatic residue; X321 is a constrained residue, and X329 is a constrained or aromatic residue. In some embodiments, where the amino acid residue at the corresponding residue position of the reference sequence are encompassed within the category of amino acids described for the specified position, a different amino acid within that amino acid category can be used in light of the guidance provided herein.

[0203] In some embodiments, the amino acid residue at the residue positions specified above can be selected from the following features: X4 is Y, F, or W, particularly Y; X5 is K or R, particularly K; X8 is H or P, particularly P; X18 is C, A, V, or I, particularly C or I; X25 is N, Q, S, or T, particularly Q; X26 is F, W, H or P, particularly H; X27 is N, Q, S, or T, particularly T; X28 is P or H, particularly P; X30 is N, Q, S, T, G, M, A, V, L or I, particularly Q or M; X41 is P, H, N, Q, S, or T, particularly H or S; X42 is G, M, A, V, L or I, particularly G; X48 is N, Q, S, T, D, E, G, M, A, V, L,

or I, particularly Q, D, V, G, or A; X49 is N, Q, or T, particularly T; X50 is A, V, L or I, particularly L; X54 is P or H; X55 is A, V, or L, particularly V; X60 is F or W, particularly F; X61 is Y, F, or W, particularly Y; X62 is S, T, N, Q, Y, F, or W, particularly T, Y or F; X65 is A, L or I, particularly A; X69 is C, G, M, A, L I, S, T, N or Q, particularly G, C, T, A, or S; X81 is G, M, A, V, L, I, particularly G; X94 is A, V, L or I, particularly I or L; X96 is A, V or L, particularly L; X102 is A, V, L, I, K or R, particularly L or K; X117 is G, M, A, V, L or I, particularly G; X120 is Y, W, or F, particularly Y; X122 is G, M, A, V, I, L, P or H, particularly M, I, L, V, or H; X124 is T, N, Q, P, or H, particularly T, H or N; X 126 is N, Q, or T, particularly T; X136 is Y, F or W, particularly Y or F; X137 is S, T, N, Q, A, V, L or I, particularly T or I; X138 is K, P or H, particularly K or P; X146 is K or R, particularly R; X148 is A, V, L I, W, or F, particularly A or F; X150 is F, W, H, P, S, T, N, or Q, particularly F, H, or S; X152 is C, G, M, A, L, I, S, T, N, or Q, particularly I, L, S or C; X155 is N, S, T, G, M, A, V, L or I, particularly M, V or T; X156 is N, Q, S, or T, particularly Q; X160 is A, V, L or I, particularly L; X163 is P, H, A, V, or L, particularly H or V; X164 is A, V, L, I, P or H, particularly V or P; X169 is V, L or I, particularly L; X174 is A, V, L or I, particularly A; X178 is S, N, or Q, particularly S; X195 is F, Y, W, S, T, N or Q, particularly F or Q; X199 is A, L, I, Y, F, W, particularly W or I; X204 is A, V, L, or I, particularly A; X208 is H, C, G, K, N, Y, D or S; X209 is V, L or I, particularly L; X211 is A, V, or I, particularly I; X215 is C; X217 is S, T, N or Q, particularly N; X223 is H or P, particularly P; X225 is W or Y, particularly Y; X230 is A, V, or L, particularly V; X252 is A, V, I, Y, F, or W, particularly F; X269 is H or P, particularly P; X273 is Y, F or W, particularly Y; X282 is S, N or Q, particularly S; X284 is G, M, V, L or I, particularly G; X292 is T, N, or Q, particularly T; X297 is S, T, N or Q, particularly S; X302 is A, L, or I, particularly A; X306 is A, L or I, particularly L; X321 is H or P, particularly P; and X329 is H, P, Y, F, or W, particularly H.

[0204] In some embodiments, the amino acid residue at the residue positions specified above can be selected from the following features: X4 is Y; X5 is K; X8 is P; X18 is C or I; X25 is Q; X26 is H; X27 is T; X28 is P; X30 is Q or M; X41 is H or S; X42 is G; X48 is Q, D, V, G, or A; X49 is T; X50 is L; X54 is P or H; X55 is V; X60 is F; X61 is Y; X62 is T , Y or F; X65 is A; X69 is G, C, T, A, or S; X81 is G; X94 is I or L; X96 is L; X102 is L or K; X117 is G; X120 is Y; X122 is M, I, L, V, or H; X124 T, H or N; X 126 is T; X136 is Y or F; X137 is T or I; X138 is K or P; X146 is R; X148 is A or F; X150 is F, H, or S; X152 is I, L, S or C; X155 is M, V or T; X156 is Q; X160 is L; X163 is H or V; X164 is V or P; X169 is L; X174 is A; X178 is S; X195 is F or Q; X199 is W or I; X204 is A, V, L, or I, particularly A; X208 is H, C, G, K, N, Y, D or S; X209 is L; X211 is I; X215 is C; X217 is N; X223 is P; X225 is Y; X230 is V; X252 is F; X269 is P; X273 is Y; X282 is S; X284 is G; X292 is T; X297 is S; X302 is A; X306 is L; X321 is P; and X329 is H.

[0205] In some embodiments, the amino acid residue at the residue positions specified above can be selected from the following features: X8 is P; X60 is F; X61 is Y; X62 is T , Y or F; X65 is A; X69 is

G, C, T, A, or S; X81 is G; X94 is I or L; X96 is L; X122 is M, I, L, V, or H; X124 T, H or N; X136 is Y or F; X169 is L; X178 is S; X199 is W or I; X209 is L; X215 is C; X217 is N; X223 is P; X269 is P; X273 is Y; X282 is S; X284 is G; X297 is S; X321 is P and X329 is H.

[0206] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes one or more of the following features: residue corresponding to X69 is cysteine (C) or a non-polar, polar, or aliphatic residue; residue corresponding to X122 is a constrained, non-polar or aliphatic residue; residue corresponding to X223 is a constrained residue; and residue corresponding to X284 is a non-polar residue.

[0207] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: (1) residue corresponding to X69 is C or a non-polar, aliphatic or polar residue, and/or residue corresponding to X284 is a non-polar residue; (2) residue corresponding to X122 is a constrained, non-polar or aliphatic residue; and (3) residue corresponding to X223 is a constrained residue.

[0208] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X69 is C or a non-polar, aliphatic or polar residue; X122 is a constrained, non-polar or aliphatic residue; and X223 is a constrained residue.

[0209] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X69 is C, G, M, A, L, I, S, T, N or Q, particularly G, C, T, A, or S; X122 is G, M, A, V, L, I, P or H, particularly M, I, V, L, or H; and X223 is H or P, particularly P.

[0210] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X122 is a constrained, non-polar or aliphatic residue; X223 is a constrained residue; and X284 is a non-polar residue.

[0211] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X122 is G, M, A, V, L, I, P or H, particularly M, I, V, L or H; X223 is H or P particularly P; and X284 is G, M, V, L or I, particularly G.

[0212] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X69 is C or a non-polar, polar or aliphatic residue; X122 is a constrained, non-polar or aliphatic residue; X223 is a constrained residue; and X284 is a non-polar residue.

[0213] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X69 is C, G, M, A, L, I, S, T, N or Q,

particularly G, C, T, A, or S; X122 is G, M, A, V, L, I, P or H, , particularly M, I, V, L, or H; X223 is H or P, particularly P; and X284 is G, M, A, V, L or I, particularly G.

[0214] In some embodiments, the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the following features: X69 is C or T; X122 is M or I; X223 is P; and X284 is G.

[0215] In some embodiments, the engineered transaminase polypeptides with one or more of the specified features or combinations of features at residue positions X69, X122, X223, and X284, can additionally have one or more residue differences as compared to SEQ ID NO:2 at the following residue positions: X4; X5; X8; X18; X25; X26; X27; X28; X30; X41; X42; X48; X49; X50; X54; X55; X60; X61; X62; X65; X81; X94; X96; X102; X117; X120; X124; X126; X136; X137; X138; X146; X148; X150; X152; X155; X156; X160; X163; X164; X169; X174; X178; X195; X199; X204; X208; X209; X211; X215; X217; X225; X230; X252; X269; X273; X282; X292; X297; X306; X321; and X329. In addition to residue positions X69, X122, X223, and X284, these other residue positions are associated with effects on various properties of the transaminase polypeptide, and thus can have residue differences as compared to SEQ ID NO:2 to effect desirable changes in enzyme properties.

[0216] As noted above, residue positions X62, X136, X137, X195, X199, X208, X209, X225, and X282 along with residue positions X69, X122, X223, and X284, are associated with binding of the substrate to the enzyme, and thus the transaminase polypeptide can have residue differences at these recited positions as compared to SEQ ID NO:2 to effect desirable changes in enzyme activity.

[0217] Residue positions X4, X5, X8, X26, X48, X60, X65, X81, X96, X102, X124, X160, X163, X169, X174, X178, X211, X217, X225, X230, X252, X269, X273, X292, X297, X306, X321, X329 are also associated with additional increases in enzyme activity, and thus the transaminase polypeptide can have residue differences at these recited positions as compared to SEQ ID NO:2 to effect additional desirable changes in enzyme activity, for example increase in efficiency of conversion at high substrate loading conditions.

[0218] Residue positions X18, X25, X27, X28, X30, X41, X42, X49, X50, X54, X55, X117, X120, X126, X138, X146, X148, X150, X152, X155, X156, X164, X204, X302 are associated also with increases in thermostability and/or solvent stability, such as DMSO, and thus the transaminase polypeptide can have residue differences at these recited positions as compared to SEQ ID NO:2 to effect desirable changes in thermostability and/or solvent stability.

[0219] Residue positions X61, X94, X215 are associated also with the ability to carry out the reaction at high concentrations of amino donor isopropylamine, and thus the transaminase polypeptide can have residue differences at these recited positions as compared to SEQ ID NO:2 to effect increase in efficiency of conversion at high (e.g., 1 – 2 M) concentrations of isopropylamine.

[0220] It is to be understood that the residue differences from SEQ ID NO:2 at residue positions associated with the various properties of the enzymes can be used in various combinations to form transaminase polypeptides having desirable enzymatic characteristics, for example combination of increases in enzyme activity, solvent and temperate stability, and utilization of amino donor. Exemplary combinations are described herein.

[0221] In some embodiments, the amino acid residues for the specified residue positions can be selected according to the descriptions above. For example, the amino acid residues can be selected based on the following features: X4 is an aromatic residue; X5 is a basic residue; X8 is a constrained residue; X18 is a cysteine (C) or an aliphatic residue; X25 is a polar residue; X26 is an aromatic or constrained residue; X27 is a polar residue; X28 is a constrained residue; X30 is polar or non-polar residue; X41 is a constrained or polar residue; X42 is non-polar residue; X48 is a polar, acidic, aliphatic or non-polar residue; X49 is a polar residue; X50 is an aliphatic residue; X54 is a constrained residue; X55 is an aliphatic residue; X60 is an aromatic residue; X61 is an aromatic residue; X62 is an aromatic or polar residue; X65 is an aliphatic residue; X81 is a non-polar residue; X94 is an aliphatic residue; X96 is an aliphatic residue; X102 is an aliphatic or basic residue; X117 is a non-polar residue; X120 is an aromatic residue; X124 is a polar or constrained residue; X126 is a polar residue; X136 is an aromatic residue; X137 is a polar or aliphatic residue; X138 is a basic or constrained residue; X146 is a basic residue; X148 is an aliphatic or aromatic residue; X150 is aromatic, constrained or polar residue; X152 is C, non-polar, aliphatic, or polar residue; X155 is non-polar or polar residue; X156 is a polar residue; X160 is an aliphatic residue; X163 is an aliphatic or constrained residue; X164 is an aliphatic or constrained residue; X169 is an aliphatic residue; X174 is an aliphatic residue; X178 is a polar residue; X195 is an aromatic or polar residue; X199 is an aliphatic or aromatic residue; X204 is an aliphatic residue; X208 is cysteine (C) or a constrained, non-polar, aromatic, polar, or basic residue; X209 is an aliphatic residue; X211 is an aliphatic residue; X215 is C; X217 is a polar residue; X225 is an aromatic residue; X230 is an aliphatic residue; X252 is an aromatic or aliphatic residue; X269 is a constrained residue; X273 is an aromatic residue; X282 is a polar residue; X292 is a polar residue; X297 is a polar residue; X302 is an aliphatic residue; X306 is an aliphatic residue; X321 is a constrained residue; and X329 is a constrained or aromatic residue. Specific amino acid residues that can be used at these residue positions are described above.

[0222] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, can have additionally one or more of the following features: X26 is an aromatic or constrained residue; X61 is an aromatic residue; X62 is an aromatic or polar residue; X65 is an aliphatic residue; X94 is an aliphatic residue; X136 is an aromatic residue; X137 is a polar or aliphatic residue; X199 is an aliphatic or aromatic residue; X209 is an aliphatic residue; X215 is C; and X282 is a polar residue.

[0223] In some embodiments, in addition to the preceding features, the transaminase amino acid sequence can include additionally one or more of the following features: X8 is a constrained residue; X60 is an aromatic residue; X81 is a non-polar or small residue; X96 is an aliphatic residue; X124 is a polar or constrained residue; X169 is an aliphatic residue; X217 is a polar residue; X269 is a constrained residue; X273 is an aromatic residue; X297 is a polar residue; and X321 is a constrained residue.

[0224] In some embodiments, in addition to the preceding features, the transaminase amino acid sequence can include additionally one or more of the following features: X4 is an aromatic residue; X48 is a polar, acidic, aliphatic or non-polar residue; X102 is an aliphatic or basic residue; X150 is aromatic, constrained or polar residue; X152 is C or a non-polar, aliphatic or polar residue; X160 is an aliphatic residue; X163 is an aliphatic or constrained residue; X174 is an aliphatic residue; X178 is a polar residue; X195 is an aromatic or polar residue; X208 is C or a constrained, non-polar, aromatic, polar, or basic residue; X211 is an aliphatic residue; X225 is an aromatic residue; X230 is an aliphatic residue; X252 is an aromatic or aliphatic residue; X292 is a polar residue; X306 is an aliphatic residue; and X329 is a constrained or aromatic residue.

[0225] In some embodiments, the engineered transaminase having the features at one or more or combinations of features at residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X26 is an aromatic or constrained residue, and/or X62 is an aromatic or polar residue; X65 is an aliphatic residue; X136 is an aromatic residue; X199 is an aliphatic or aromatic residue; and X209 is an aliphatic residue.

[0226] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X61 is an aromatic residue; X62 is an aromatic or polar residue; X65 is an aliphatic residue; X94 is an aliphatic residue; X136 is an aromatic residue; X199 is an aliphatic or aromatic residue; X209 is an aliphatic residue; X215 is C, and X282 is a polar residue.

[0227] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X8 is a constrained residue; X61 is an aromatic residue; X62 is an aromatic or polar residue; X65 is an aliphatic residue; X81 is a non-polar or small residue; X94 is an aliphatic residue; X136 is an aromatic residue; X199 is an aliphatic or aromatic residue; X209 is an aliphatic residue; X215 is a C; X217 is a polar residue; X269 is a constrained residue; X282 is a polar residue; X297 is a polar residue; and X321 is a constrained residue.

[0228] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X8 is a constrained residue; X60 is an aromatic residue; X61 is an aromatic residue; X62 is

an aromatic or polar residue; X65 is an aliphatic residue; X81 is a non-polar residue; X94 is an aliphatic residue; X96 is an aliphatic residue; X124 is a polar or constrained residue; X136 is an aromatic residue; X169 is an aliphatic residue; X199 is an aliphatic or aromatic residue; X209 is an aliphatic residue; X215 is C; X217 is a polar residue; X269 is a constrained residue; X273 is an aromatic residue. X282 is a polar residue; X297 is a polar residue; and X321 is a constrained residue.

[0229] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X8 is a constrained residue; X60 is an aromatic residue; X61 is an aromatic residue; X62 is an aromatic or polar residue; X65 is an aliphatic residue; X81 is a non-polar residue; X94 is an aliphatic residue; X96 is an aliphatic residue; X124 is a polar or constrained residue; X126 is a polar residue; X136 is an aromatic residue; X150 is an aromatic, constrained or polar residue; X152 is a cysteine (C), non-polar, aliphatic, or polar residue; X169 is an aliphatic residue; X199 is an aliphatic or aromatic residue; X209 is an aliphatic residue; X215 is C; X217 is a polar residue; X269 is a constrained residue; X273 is an aromatic residue. X282 is a polar residue; X297 is a polar residue; and X321 is a constrained residue.

[0230] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X26 is P, H, F, or W, particularly H, and/or X62 is S, T, N, Q, Y, F, or W, particularly T or F; X65 is A, L or I, particularly A; X136 is Y, F or W, particularly Y or F; X199 is A, L, I, Y, F, or W, particularly W or I; and X209 is V, L or I, particularly L.

[0231] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X61 is Y, F, or W, particularly Y; X62 is S, T, N, Q, Y, F, or W, particularly T or F; X65 is A, L or I, particularly A; X94 is A, V, L or I, particularly I or L; X136 is Y, F, or W, particularly Y or F; X199 is A, L, I, Y, F, or W, particularly W or I; X209 is V, L or I, particularly L; X215 is C; and X282 is S, N or Q, particularly S.

[0232] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X8 is H or P, particularly P; X61 is Y, F, or W, particularly Y; X62 is S, T, N Q, Y, F, or W, particularly T or F; X65 is A, L or I, particularly A; X81 is G, M, A, V, L or I, particularly G; X94 is A, V, L or I, particularly I or L; X136 is Y, F, or W, particularly Y or F; X199 is A, L, I, Y, F, or W, particularly W or I; X209 is V, L or I, particularly L; X215 is C; X217 is S, T, N, or Q, particularly N; X269 is H or P, particularly P; X282 is S, N or Q, particularly S. X297 is S, T, N or Q, particularly S; and X321 is H or P, particularly P.

[0233] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X8 is H or P, particularly P; X60 is F or W, particularly F; X61 is Y, F, or W, particularly Y; X62 is Y, F, W, S, T, N or Q, particularly T or F; X65 is A, L or I, particularly A; X81 is G, M, A, V, L or I, particularly G; X94 is A, V, L or I, particularly I or L; X96 is A, V or L, particularly L; X124 is P, H, T, N, or Q, particularly T, H or N; X136 is Y, F or W, particularly Y or F; X169 is V, L, or I, particularly L; X199 is Y, F, W, A, L or I, particularly W or I; X209 is V, L or I, particularly L; X215 is C; X217 is S, T, N or Q, particularly N; X269 is H or P, particularly P; X273 is Y, F, or W, particularly Y; X282 is S, N or Q, particularly S; X297 is S, T, N or Q, particularly S; and X321 is H or P, particularly P.

[0234] In some embodiments, the engineered transaminase having the features at one or more residue positions X69, X122, X223, and X284 as described above, includes at least the following additional features: X8 is H or P, particularly P; X60 is F or W, particularly F; X61 is Y, F, or W, particularly Y; X62 is Y, F, W, S, T, N or Q, particularly T or F; X65 is A, L or I, particularly A; X81 is G, M, A, V, L or I, particularly G; X94 is A, V, L or I, particularly I or L; X96 is A, V or L, particularly L; X124 is P, H, T, N, or Q, particularly T, H or N; X 126 is N, Q, or T, particularly T; X136 is Y, F or W, particularly Y or F; X150 is F, W, H, P, S, T, N, or Q, particularly F, H, or S; X152 is C, G, M, A, L, I, S, T, N, or Q, particularly G, I, L, S or C; X169 is V, L, or I, particularly L; X199 is Y, F, W, A, L or I, particularly W or I; X209 is V, L or I, particularly L; X215 is C; X217 is S, T, N or Q, particularly N; X269 is H or P, particularly P; X273 is Y, F, or W, particularly Y; X282 is S, N or Q, particularly S; X297 is S, T, N or Q, particularly S; and X321 is H or P, particularly P.

[0235] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X223 is a constrained residue, particularly P; X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference amino acid sequence based on SEQ ID NO:2 having the features described for the preceding specified residue positions (i.e. X122; X223; and X284) (e.g., SEQ ID NO:8 or 10), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residues.

[0236] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X223 is a constrained residue, particularly P; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (i.e., X69; X122; X223; and X284)(e.g., SEQ ID NO:4), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence having at least the features described for the specified residues.

[0237] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; and X223 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for the preceding specified residue positions (e.g., SEQ ID NO:6), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residues. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:6.

[0238] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X174 is an aliphatic residue, particularly A; X223 is a constrained residue, particularly P; and X284 is a non-polar residue, particularly G. In some embodiments, the

transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:12), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:12.

[0239] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X223 is a constrained residue, particularly P; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:14), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:14.

[0240] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a

constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X178 is a polar residue, particularly S; X199 is an aliphatic or aromatic residue, particularly W or I, particularly X223 is a constrained residue, particularly P; X225 is an aromatic residue, particularly Y, X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:16), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:16.

[0241] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X223 is a constrained residue, particularly P; X225 is an aromatic residue, particularly Y, X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:18), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide

can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:18.

[0242] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:20, 22, 28, 30, 32, 34, 38 or 40), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:20, 22, 28, 30, 32, 34, 38 or 40.

[0243] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X223 is a constrained residue, particularly P; X225 is an aromatic residue, particularly Y, X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue

differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:24), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:24.

[0244] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X174 is an aliphatic residue, particularly A; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X223 is a constrained residue, particularly P; X230 is an aliphatic residue, particularly V; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:26), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:26.

[0245] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X26 is an aromatic or constrained residue, particularly H; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65

is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:36), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:36.

[0246] In some embodiments, the engineered transaminases comprise an amino acid sequence that includes at least the following features: X4 is an aromatic residue, particularly Y; X26 is an aromatic or constrained residue, particularly H; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue

positions (e.g., SEQ ID NO:42), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:42.

[0247] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO: 44, 46, or 48), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:44, 46, or 48.

[0248] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly P; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a cysteine (C); X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S;

and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO: 50), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:50.

[0249] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X152 is C, non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO: 52), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%,

87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:52.

[0250] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO: 54 or 56), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:54 or 56.

[0251] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50,

55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO: 58 or 60), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:58 or 60.

[0252] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X160 is an aliphatic residue, particularly L; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:62), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:62.

[0253] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-

polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X137 is a polar or aliphatic residue, particularly T or I; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; X284 is a non-polar residue, particularly G; and X306 is an aliphatic residue, particularly L. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:64), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:64.

[0254] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X102 is an aliphatic or basic residue, particularly L or K; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X150 is aromatic, constrained or polar residue, particularly F, H, or S; X152 is C, non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%,

87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:66), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:66.

[0255] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X48 is a polar, acidic aliphatic or non-polar residue, particularly D, V, G, Q or A; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X102 is an aliphatic or basic residue, particularly L or K; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X163 is an aliphatic or constrained residue, particularly H or V; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X211 is an aliphatic residue, particularly I; X215 is a C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X252 is an aromatic or aliphatic residue, particularly F; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:68), with the proviso that the engineered transaminase polypeptide comprises polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:68.

[0256] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X48 is a polar, acidic, aliphatic or non-polar residue, particularly A; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X282 is a polar residue, particularly S; X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:70), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:70.

[0257] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X223 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions.

In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:72), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:72.

[0258] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X178 is a polar residue, particularly S; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X282 is a polar residue, particularly S; X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:74), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:74.

[0259] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X152 is C or a non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X178 is a polar residue, particularly S; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X252 is an aromatic or aliphatic residue, particularly F; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:76), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:76.

[0260] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X169 is an aliphatic residue, particularly L; X178 is a polar residue, particularly S; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is

C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X292 is a polar residue, particularly T; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:78), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:78.

[0261] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:80), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:80.

[0262] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X169 is an aliphatic residue, particularly L; X178 is a polar residue, particularly S; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:82), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:82

[0263] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue,

particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X124 is a polar or constrained residue, particularly T, H or N; X136 is an aromatic residue, particularly Y or F; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:84, 86, 88, 96, 98, or 100), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:84, 86, 88, 96, 98, or 100.

[0264] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X136 is an aromatic residue, particularly Y or F; X150 is aromatic, constrained or polar residue, particularly F, H, or S; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue,

particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:90), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:90.

[0265] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X124 is a polar or constrained residue, particularly T, H or N; X136 is an aromatic residue, particularly Y or F; X150 is aromatic, constrained or polar residue, particularly F, H, or S; X152 is C or a non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue

positions (e.g., SEQ ID NO:92), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:92.

[0266] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X124 is a polar or constrained residue, particularly T, H or N; X136 is an aromatic residue, particularly Y or F; X150 is aromatic, constrained or polar residue, particularly F, H, or S; X152 is C or a non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is a C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:94), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:94.

[0267] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue,

particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X124 is a polar or constrained residue, particularly T, H or N; X136 is an aromatic residue, particularly Y or F; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; and X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; X321 is a constrained residue, particularly P; and X329 is a constrained or aromatic residue, particularly H. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:102), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:102.

[0268] In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X124 is a polar or constrained residue, particularly T, H or N; X136 is an aromatic residue, particularly Y or F; X150 is aromatic, constrained or polar residue, particularly S; X152 is cysteine (C), non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained

residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:110), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:110.

In some embodiments, the engineered transaminase comprises an amino acid sequence that includes the following features: X8 is a constrained residue, particularly is P; X49 is a polar residue, particularly T; X60 is an aromatic residue, particularly F; X61 is an aromatic residue, particularly Y; X62 is an aromatic or polar residue, particularly T, Y or F; X65 is an aliphatic residue, particularly A; X69 is C or a non-polar, aliphatic or polar residue, particularly G, C, T, A, or S; X81 is a non-polar residue, particularly G; X94 is an aliphatic residue, particularly I or L; X96 is an aliphatic residue, particularly L; X117 is a non-polar residue, particularly G; X122 is a constrained, non-polar or aliphatic residue, particularly M, I, L, V, or H; X124 is a polar or constrained residue, particularly T, H or N; X126 is a polar residue, particularly T; X136 is an aromatic residue, particularly Y or F; X150 is aromatic, constrained or polar residue, particularly S; X152 is cysteine (C), non-polar, aliphatic, or polar residue, particularly G, I, L, S or C; X169 is an aliphatic residue, particularly L; X199 is an aliphatic or aromatic residue, particularly W or I; X209 is an aliphatic residue, particularly L; X215 is C; X217 is a polar residue, particularly N; X223 is a constrained residue, particularly P; X269 is a constrained residue, particularly P; X273 is an aromatic residue, particularly Y; X282 is a polar residue, particularly S; X284 is a non-polar residue, particularly G; X297 is a polar residue, particularly S; X302 is an aliphatic residue, particularly A; and X321 is a constrained residue, particularly P. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other residue positions. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20,

22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at the other residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence based on SEQ ID NO:2 having the features described for preceding specified residue positions (e.g., SEQ ID NO:166), with the proviso that the engineered transaminase polypeptide comprises an amino acid sequence that includes at least the features described for the specified residue positions. In some embodiments, the engineered transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to a reference sequence of SEQ ID NO:166.

[0269] Table 2 below provides exemplary engineered transaminase polypeptides, with each row listing two SEQ ID NOs, the odd number referring to the nucleotide sequence encoding the amino acid sequence provided by the even number. The residue differences are based on comparison to reference sequence of SEQ ID NO:2, a transaminase derived from *Arthrobacter sp* KNK168 and differs from the naturally occurring enzyme in having a substitution of isoleucine (I) at residue position X306 with valine (V). In the Activity column, the levels of increasing activity (i.e., "+" "++" "+++" etc.) were defined as follows: "+" indicates at least equal to but not greater than 2 times the activity of SEQ ID NO:4 (assay conditions: 2 g/L ketoamide substrate, 0.5 M isopropylamine, 22°C, pH 7.5, 5% DMSO, 100 μM PLP); "++" indicates about 50-to-100 times greater than the activity of SEQ ID NO:4 (assay conditions: 2 g/L ketoamide substrate, 0.5 M isopropylamine, 22°C, pH 7.5, 5% MeOH, 100 μM PLP); "+++" indicates about 1.1 to about 5 times greater than the activity of SEQ ID NO:22 (assay conditions: 5-10 g/L ketoamide substrate, 0.5-1 M isopropylamine, 22-30°C, pH 7.5, 5% MeOH, 100 μM PLP); "++++" indicates about 1.1 to 5 times greater than the activity of SEQ ID NO:48 (assay conditions: 10-40 g/L ketoamide substrate, 1 M isopropylamine, 30-45°C, pH 8.5, 10% MeOH, 100 μM PLP); "+++++" indicates about 1.1 to 5 times or greater than the activity of SEQ ID NO:58 (assay conditions: 40-100 g/L ketoamide substrate, 1 M isopropylamine, 45°C, pH 8.5, 10% MeOH-25% DMSO, 250 μM PLP); "++++++" indicates about 1.1 to 5 times or greater than the activity of SEQ ID NO:104 (assay conditions: 40-100 g/L ketoamide substrate, 1 M isopropylamine, 45°C, pH 8.5, 50% DMSO, 1000 μM PLP). Exemplary assay conditions for measuring activity using methanol and DMSO are described in Examples 6-11.

[0270] Table 2

SEQ ID NO	Residue differences relative to SEQ ID NO:2	No. Residue Differ-ences	Activity
1/2	-	-	--
3/4	V69G; F122V; S223P; A284G	4	+

SEQ ID NO	Residue differences relative to SEQ ID NO:2	No. Residue Differ-ences	Activity
5/6	V65A; V69G; F122I; S223P	4	+
7/8	F122L; S223P; A284G	3	+
9/10	F122I; S223P; A284G	3	+
11/12	F122L; S174A; S223P; A284G	4	+
13/14	Y26H; V65A; V69G; F122I; S223P; A284G	6	+
15/16	Y26H; H62T; V65A; V69G; F122I; T178S; V199W; S223P; F225Y; T282S; A284G	11	++
17/18	Y26H; H62F; V65A; V69G; F122V; G136Y; V199I; A209L; S223P; F225Y; T282S; A284G	12	++
19/20	Y26H; H62T; V65A; V69G; F122V; G136Y; E137T; V199I; A209L; S223P; T282S; A284G	12	++
21/22	Y26H; H62T; V65A; V69G; F122I; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	12	++
23/24	Y26H; H62T; V65A; V69G; F122I; G136Y; E137T; V199I; A209L; S223P; F225Y; T282S; A284G	13	++
25/26	Y26H; V65A; V69G; F122V; G136Y; E137I; S174A; V199I; A209L; S223P; I230V; A284G	12	++
27/28	Y26H; H62T; V65A; V69G; F122H; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	12	+++
29/30	Y26H; H62T; V65A; V69T; F122I; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	12	+++
31/32	Y26H; H62T; V65A; V69C; F122I; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	12	+++
33/34	Y26H; H62T; V65A; V69A; F122I; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	12	+++
35/36	Y26H; L61Y; H62T; V65A; V69G; F122I; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	13	+++
37/38	Y26H; H62Y; V65A; V69G; F122I; G136Y; E137I; V199I; A209L; S223P; T282S; A284G	12	+++
39/40	Y26H; H62T; V65A; V69G; F122I; G136F; E137I; V199I; A209L; S223P; T282S; A284G	12	+++
41/42	S4Y; Y26H; H62T; V65A; V69G; M94I; F122I; G136Y; E137T; V199I; A209L; G215C; S223P; T282S; A284G	15	+++
43/44	H62T; V65A; V69G; M94I; F122I; G136Y; E137I; V199I; A209L; G215C; S223P; T282S; A284G	13	+++
45/46	H62T; V65A; V69G; M94I; F122I; G136Y; E137T; V199I; A209L; G215C; S223P; T282S; A284G	13	+++
47/48	H62T; V65A; V69C; M94I; F122I; G136Y; E137T; V199I; A209L; G215C; S223P; T282S; A284G	13	+++
49/50	S8P; H62T; V65A; V69C; M94I; F122I; G136Y; E137T; V199I; A209L; G215C; S223P; T282S; A284G	14	++++
51/52	L61Y; H62T; V65A; V69S; M94I; F122I; G136F; E137T; V152I; V199I; A209L; G215C; S223P; T282S; A284G	15	++++
53/54	L61Y; H62T; V65A; V69C; M94I; F122V; G136F; E137T; V199I; A209L; G215C; S223P; T282S; A284G	14	++++
55/56	L61Y; H62T; V65A; V69T; M94I; F122V; G136F; E137T; V199I; A209L; G215C; S223P; T282S; A284G	14	++++
57/58	L61Y; H62T; V65A; V69T; M94I; F122I; G136F; V199I; A209L; G215C; S223P; T282S; A284G	13	++++

SEQ ID NO	Residue differences relative to SEQ ID NO:2	No. Residue Differ-ences	Activity
59/60	L61Y; H62T; V65A; V69T; M94I; F122H; G136F; V199I; A209L; G215C; S223P; T282S; A284G	13	++++
61/62	L61Y; H62T; V65A; V69C; M94I; F122I; G136Y; E137T; F160L; A169L; V199I; A209L; G215C; S223P; L269P; T282S; A284G	17	++++
63/64	L61Y; H62T; V65A; V69C; M94L; F122I; G136Y; E137T; A169L; V199I; A209L; G215C; S223P; T282S; A284G; V306L	16	++++
65/66	L61Y; H62T; V65A; V69C; M94I; Q102L; F122I; G136F; Y150F; V152I; V199I; A209L; G215C; S223P; T282S; A284G	16	++++
67/68	S8P; P48A; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; Q102K; F122I; G136F; I163V; V199I; A209L; L211I; G215C; G217N; S223P; L252F; L273Y; T282S; A284G; S321P	24	+++++
69/70	S8P; P48A; L61Y; H62T; V65A; V69T; D81G; M94I; F122I; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; T282S; A284G; P297S; S321P	21	+++++
71/72	S8P; L61Y; H62T; V65A; V69T; M94I; F122I; G136F; V199I; A209L; G215C; S223P; T282S; A284G	14	+++++
73/74	S8P; L61Y; H62T; V65A; V69T; D81G; M94L; I96L; F122I; G136F; T178S; V199I; A209L; G215C; S223P; L269P; T282S; A284G; P297S; S321P	20	+++++
75/76	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; G136F; V152L; T178S; V199I; A209L; G215C; G217N; S223P; L252F; L269P; L273Y; T282S; A284G; P297S; S321P	25	+++++
77/78	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94L; I96L; F122I; G136F; A169L; T178S; V199I; A209L; G215C; G217N; S223P; L269P; T282S; A284G; S292T; P297S; S321P	24	+++++
79/80	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	23	+++++
81/82	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94L; I96L; F122I; G136F; A169L; T178S; V199I; A209L; G215C; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	23	+++++
83/84	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; S124T; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
85/86	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; S124H; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
87/88	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; S124N; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
89/90	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; G136F; Y150H; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
91/92	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124H; G136F; Y150H; V152S; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	26	+++++
93/94	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	26	+++++

SEQ ID NO	Residue differences relative to SEQ ID NO:2	No. Residue Differ-ences	Activity
95/96	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124N; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
97/98	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122I; S124H; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
99/100	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124N; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	24	+++++
101/102	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124N; G136F; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P; Q329H	25	+++++
103/104	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	26	+++++
105/106	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; S126T; G136F; R138K; Y150S; V152G; Q155M; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	29	+++++
107/108	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; R138P; Q146R; Y150S; V152S; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	28	+++++
109/110	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; S126T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
111/112	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; I163H; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
113/114	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y148A; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
115/116	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; W156Q; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
117/118	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; R164V; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
119/120	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y148F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
121/122	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; E120Y; F122M; S124T; G136F; Y150S; V152C; A169L; V199I;	27	++++++

SEQ ID NO	Residue differences relative to SEQ ID NO:2	No. Residue Differ-ences	Activity
	A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P		
123/124	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; Q155V; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
125/126	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; R164P; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
127/128	S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; Q155T; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
129/130	S8P; E50L; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
131/132	S8P; L18I; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
133/134	S8P; D25Q; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
135/136	S8P; E42G; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
137/138	S8P; P48D; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
139/140	S8P; P30Q; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N ;S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
141/142	S8P; L28P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
143/144	S8P; I41H; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
145/146	S8P; P30M; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++

SEQ ID NO	Residue differences relative to SEQ ID NO:2	No. Residue Differ-ences	Activity
147/148	S8P; S54H; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
149/150	S8P; L18C; I55V; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	28	++++++
151/152	S8P; P48G; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
153/154	S8P; P48V; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
155/156	S8P; I41S; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
157/158	S8P; E27T; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
159/160	S8P; S54P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
161/162	S8P; P48Q; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	27	++++++
163/164	A5K; S8P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; S126T; G136F; Y150S; V152C; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	28	++++++
165/166	S8P; S49T; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; E117G; F122M; S124T; S126T G136F; Y150S; V152S; A169L; V199I; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; V302A; S321P	30	++++++
167/168	S8P; S54P; Y60F; L61Y; H62T; V65A; V69T; D81G; M94I; I96L; F122M; S124T; S126T; G136F; Y150S; V152S; A169L; V199I; D204A; A209L; G215C; G217N; S223P; L269P; L273Y; T282S; A284G; P297S; S321P	29	++++++

[0271] As noted above, in some embodiments, the transaminase polypeptide can comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence of SEQ ID NO: 6, 8, 10, 12, 14,

16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 or 168. In some embodiments, the transaminase polypeptides can have 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences as compared to the naturally occurring transaminase represented by SEQ ID NO:2. In some embodiments, the number of residue differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 differences as compared to SEQ ID NO:2.

[0272] In some embodiments, the transaminase polypeptide comprises an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence of SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102. In some embodiments, the transaminase polypeptides can have 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences as compared to the naturally occurring transaminase represented by SEQ ID NO:2. In some embodiments, the number of residue differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 differences as compared to SEQ ID NO:2.

[0273] In some embodiments, the transaminase polypeptide comprises an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 or 168, with the proviso that the transaminase amino acid sequence comprises any one of the set of residue differences contained in any one of the polypeptide sequences listed in Table 2 as compared to SEQ ID NO:2. In some embodiments, the transaminase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 residue differences at other amino acid residue positions as compared to the reference sequence. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 residue differences at other residue positions. In some embodiments, the residue differences at other residue positions comprise substitutions with conservative amino acid residues.

[0274] As noted above, in some embodiments, the transaminase polypeptide is also capable of converting keto substrates to amino products with at least 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% enantiomeric excess. Exemplary transaminase polypeptides with

the specified levels of enantioselectivity can comprise an amino acid sequence corresponding to SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 or 168.

[0275] In some embodiments, the engineered transaminase polypeptides can comprise deletions of the engineered transaminase polypeptides described herein. Thus, for each and every embodiment of the transaminase polypeptides of the disclosure, the deletions can comprise one or more amino acids, 2 or more amino acids, 3 or more amino acids, 4 or more amino acids, 5 or more amino acids, 6 or more amino acids, 8 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, up to 10% of the total number of amino acids, up to 20% of the total number of amino acids, or up to 30% of the total number of amino acids of the transaminase polypeptides, as long as the functional activity of the transaminase activity is maintained. In some embodiments, the deletions can comprise, 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, 1-50, 1-55, or 1-60 amino acid residues. In some embodiments, the number of deletions can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, 50, 55, or 60 amino acids. In some embodiments, the deletions can comprise deletions of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, 20, 22, 24, 26, 28, or 30 amino acid residues.

[0276] As described herein, the transaminase polypeptides of the disclosure can be in the form of fusion polypeptides in which the transaminase polypeptides are fused to other polypeptides, such as, by way of example and not limitation, antibody tags (e.g., myc epitope), purifications sequences (e.g., His tags for binding to metals), and cell localization signals (e.g., secretion signals). Thus, the transaminase polypeptides can be used with or without fusions to other polypeptides.

[0277] The polypeptides described herein are not restricted to the genetically encoded amino acids. In addition to the genetically encoded amino acids, the polypeptides described herein may be comprised, either in whole or in part, of naturally-occurring and/or synthetic non-encoded amino acids. Certain commonly encountered non-encoded amino acids of which the polypeptides described herein may be comprised include, but are not limited to: the D-stereoisomers of the genetically-encoded amino acids; 2,3-diaminopropionic acid (Dpr); α-aminoisobutyric acid (Aib); ε-aminohexanoic acid (Aha); δ-aminovaleric acid (Ava); N-methylglycine or sarcosine (MeGly or Sar); ornithine (Orn); citrulline (Cit); t-butylalanine (Bua); t-butylglycine (Bug); N-methylisoleucine (MeIle); phenylglycine (Phg); cyclohexylalanine (Cha); norleucine (Nle); naphthylalanine (Nal); 2-chlorophenylalanine (Ocf); 3-chlorophenylalanine (Mcf); 4-chlorophenylalanine (Pcf); 2-fluorophenylalanine (Off); 3-fluorophenylalanine (Mff); 4-fluorophenylalanine (Pff); 2-bromophenylalanine (Obf); 3-bromophenylalanine (Mbf); 4-bromophenylalanine (Pbf); 2-methylphenylalanine (Omf); 3-methylphenylalanine (Mmf); 4-methylphenylalanine (Pmf); 2-

nitrophenylalanine (Onf); 3-nitrophenylalanine (Mnf); 4-nitrophenylalanine (Pnf); 2-cyanophenylalanine (Ocf); 3-cyanophenylalanine (Mcf); 4-cyanophenylalanine (Pcf); 2-trifluoromethylphenylalanine (Otf); 3-trifluoromethylphenylalanine (Mtf); 4-trifluoromethylphenylalanine (Ptf); 4-aminophenylalanine (Paf); 4-iodophenylalanine (Pif); 4-aminomethylphenylalanine (Pamf); 2,4-dichlorophenylalanine (Opef); 3,4-dichlorophenylalanine (Mpcf); 2,4-difluorophenylalanine (Opff); 3,4-difluorophenylalanine (Mpff); pyrid-2-ylalanine (2pAla); pyrid-3-ylalanine (3pAla); pyrid-4-ylalanine (4pAla); naphth-1-ylalanine (1nAla); naphth-2-ylalanine (2nAla); thiazolylalanine (taAla); benzothienylalanine (bAla); thienylalanine (tAla); furylalanine (fAla); homophenylalanine (hPhe); homotyrosine (hTyr); homotryptophan (hTrp); pentafluorophenylalanine (5ff); styrylkalanine (sAla); authrylalanine (aAla); 3,3-diphenylalanine (Dfa); 3-amino-5-phenypentanoic acid (Afp); penicillamine (Pen); 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid (Tic); β-2-thienylalanine (Thi); methionine sulfoxide (Mso); N(w)-nitroarginine (nArg); homolysine (hLys); phosphonomethylphenylalanine (pmPhe); phosphoserine (pSer); phosphothreonine (pThr); homoaspartic acid (hAsp); homoglutamic acid (hGlu); 1-aminocyclopent-(2 or 3)-ene-4 carboxylic acid; pipecolic acid (PA), azetidine-3-carboxylic acid (ACA); 1-aminocyclopentane-3-carboxylic acid; allylglycine (aOly); propargylglycine (pgGly); homoalanine (hAla); norvaline (nVal); homoleucine (hLeu), homovaline (hVal); homoisoleucine (hIle); homoarginine (hArg); N-acetyl lysine (AcLys); 2,4-diaminobutyric acid (Dbu); 2,3-diaminobutyric acid (Dab); N-methylvaline (MeVal); homocysteine (hCys); homoserine (hSer); hydroxyproline (Hyp) and homoproline (hPro). Additional non-encoded amino acids of which the polypeptides described herein may be comprised will be apparent to those of skill in the art (see, *e.g.*, the various amino acids provided in Fasman, 1989, *CRC Practical Handbook of Biochemistry and Molecular Biology*, CRC Press, Boca Raton, FL, at pp. 3-70 and the references cited therein, all of which are incorporated by reference). These amino acids may be in either the L- or D-configuration.

[0278] Those of skill in the art will recognize that amino acids or residues bearing side chain protecting groups may also comprise the polypeptides described herein. Non-limiting examples of such protected amino acids, which in this case belong to the aromatic category, include (protecting groups listed in parentheses), but are not limited to: Arg(tos), Cys(methylbenzyl), Cys (nitropyridinesulfenyl), Glu(δ-benzylester), Gln(xanthyl), Asn(N-δ-xanthyl), His(bom), His(benzyl), His(tos), Lys(fmoc), Lys(tos), Ser(O-benzyl), Thr (O-benzyl) and Tyr(O-benzyl).

[0279] Non-encoding amino acids that are conformationally constrained of which the polypeptides described herein may be composed include, but are not limited to, N-methyl amino acids (L-configuration); 1-aminocyclopent-(2 or 3)-ene-4-carboxylic acid; pipecolic acid; azetidine-3-carboxylic acid; homoproline (hPro); and 1-aminocyclopentane-3-carboxylic acid.

[0280] As described above the various modifications introduced into the naturally occurring polypeptide to generate an engineered transaminase enzyme can be targeted to a specific property of the enzyme.

[0281] In another aspect, the present disclosure provides polynucleotides encoding the improved transaminase polypeptides. The polynucleotides may be operatively linked to one or more heterologous regulatory sequences that control gene expression to create a recombinant polynucleotide capable of expressing the transaminase polypeptide. Expression constructs containing a heterologous polynucleotide encoding the engineered transaminase can be introduced into appropriate host cells to express the corresponding transaminase polypeptide.

[0282] Because of the knowledge of the codons corresponding to the various amino acids, availability of a protein sequence provides a description of all the polynucleotides capable of encoding the subject. The degeneracy of the genetic code, where the same amino acids are encoded by alternative or synonymous codons allows an extremely large number of nucleic acids to be made, all of which encode the improved transaminase polypeptides disclosed herein. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the protein. In this regard, the present disclosure specifically contemplates each and every possible variation of polynucleotides that could be made by selecting combinations based on the possible codon choices, and all such variations are to be considered specifically disclosed for any polypeptide disclosed herein, including the amino acid sequences presented in Table 2.

[0283] In some embodiments, the polynucleotides can be selected and/or engineered to comprise codons that are preferably selected to fit the host cell in which the protein is being produced. For example, preferred codons used in bacteria are used to express the gene in bacteria; preferred codons used in yeast are used for expression in yeast; and preferred codons used in mammals are used for expression in mammalian cells. Since not all codons need to be replaced to optimize the codon usage of the transaminases (e.g., because the natural sequence can have preferred codons and because use of preferred codons may not be required for all amino acid residues), codon optimized polynucleotides encoding the transaminase polypeptides may contain preferred codons at about 40%, 50%, 60%, 70%, 80%, or greater than 90% of codon positions of the full length coding region.

[0284] In some embodiments, the polynucleotide encodes a transaminase polypeptide comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to the reference sequence of SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102, wherein the polypeptide is capable of converting the ketone substrate to

the amine product with an activity that is improved as compared to the activity of the naturally occurring transaminase of *Arthrobacter sp* KNK168 or the transaminase of SEQ ID NO:2.

[0285] In some embodiments, the polynucleotide encodes a transaminase polypeptide comprising an amino acid sequence that has at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more sequence identity to the polypeptide comprising an amino acid sequence corresponding to SEQ ID NO: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 or 168. wherein the polypeptide has one or more improved properties in converting the ketone substrate to the amine product in the presence of an amino group donor. In some embodiments, the encoded transaminase polypeptide has an activity that is equal to or greater than the activity of the polypeptide of SEQ ID NO:2.

[0286] In some embodiments, the polynucleotide encodes a transaminase polypeptide comprising an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence of SEQ ID NO: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 or 168.

[0287] In some embodiments, the polynucleotide encodes a transaminase polypeptide comprising an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 or 168, with the proviso that the improved transaminase amino acid sequence comprises any one of the set of residue differences contained in any one of the polypeptide sequences listed in Table 2 as compared to SEQ ID NO:2.

[0288] In some embodiments, the polynucleotides encoding the improved transaminase polypeptides are selected from SEQ ID NO: 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, or 167.

[0289] In some embodiments, the polynucleotides are capable of hybridizing under highly stringent conditions to a polynucleotide comprising SEQ ID NO: 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, or 167, or a complement thereof, where the highly stringently hybridizing polynucleotides encode a transaminase polypeptide capable of converting the compounds of formula (II) to the amine products of formula (I) in presence of an amino group donor with an activity that is improved as compared to the polypeptide of SEQ ID NO:2.

[0290] In some embodiments, the polynucleotides encode the polypeptides described herein but have about 80% or more sequence identity, about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more sequence identity at the nucleotide level to a reference polynucleotide encoding the engineered transaminase described herein. In some embodiments, the reference polynucleotide is selected from SEQ ID NO:3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, or 167.

[0291] An isolated polynucleotide encoding an improved transaminase polypeptide may be manipulated in a variety of ways to provide for expression of the polypeptide. In some embodiments, the polynucleotides encoding the engineered transaminase polypeptides can be provided as expression vectors where one or more control sequences is present to regulate the expression of the polynucleotides. Manipulation of the isolated polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides and nucleic acid sequences utilizing recombinant DNA methods are well known in the art. Guidance is provided in Sambrook et al., 2001, Molecular Cloning: A Laboratory Manual, 3rd Ed., Cold Spring Harbor Laboratory Press; and Current Protocols in Molecular Biology, Ausubel. F. ed., Greene Pub. Associates, 1998, updates to 2006.

[0292] In some embodiments, the control sequences include among others, promoters, leader sequence, polyadenylation sequence, propeptide sequence, signal peptide sequence, and transcription terminator. For bacterial host cells, suitable promoters for directing transcription of the nucleic acid constructs of the present disclosure, include the promoters obtained from the E. coli lac operon, E. coli trp operon, bacteriophage λ, Streptomyces coelicolor agarase gene (dagA), Bacillus subtilis levansucrase gene (sacB), Bacillus licheniformis alpha-amylase gene (amyL), Bacillus stearothermophilus maltogenic amylase gene (amyM), Bacillus amyloliquefaciens alpha-amylase gene (amyQ), Bacillus licheniformis penicillinase gene (penP), Bacillus subtilis xylA and xylB genes,

and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, Proc. Natl Acad. Sci. USA 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, Proc. Natl Acad. Sci. USA 80: 21-25).

[0293] For filamentous fungal host cells, suitable promoters for directing the transcription of the nucleic acid constructs of the present disclosure include promoters obtained from the genes for Aspergillus oryzae TAKA amylase, Rhizomucor miehei aspartic proteinase, Aspergillus niger neutral alpha-amylase, Aspergillus niger acid stable alpha-amylase, Aspergillus niger or Aspergillus awamori glucoamylase (glaA), Rhizomucor miehei lipase, Aspergillus oryzae alkaline protease, Aspergillus oryzae triose phosphate isomerase, Aspergillus nidulans acetamidase, and Fusarium oxysporum trypsin-like protease (see e.g., WO 96/00787, which is hereby incorporated by reference herein), as well as the NA2-tpi promoter (a hybrid of the promoters from the genes for Aspergillus niger neutral alpha-amylase and Aspergillus oryzae triose phosphate isomerase), and mutant, truncated, and hybrid promoters thereof.

[0294] In a yeast host, useful promoters can be from the genes for Saccharomyces cerevisiae enolase (ENO-1), Saccharomyces cerevisiae galactokinase (GAL1), Saccharomyces cerevisiae alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP), and Saccharomyces cerevisiae 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos et al., 1992, Yeast 8:423-488.

[0295] The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleic acid sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

[0296] For example, exemplary transcription terminators for filamentous fungal host cells can be obtained from the genes for Aspergillus oryzae TAKA amylase, Aspergillus niger glucoamylase, Aspergillus nidulans anthranilate synthase, Aspergillus niger alpha-glucosidase, and Fusarium oxysporum trypsin-like protease.

[0297] Exemplary terminators for yeast host cells can be obtained from the genes for Saccharomyces cerevisiae enolase, Saccharomyces cerevisiae cytochrome C (CYC1), and Saccharomyces cerevisiae glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos et al., 1992, supra.

[0298] The control sequence may also be a suitable leader sequence, a non-translated region of an mRNA that is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used. Exemplary leaders for filamentous fungal host cells are obtained from the genes for Aspergillus oryzae TAKA amylase and Aspergillus nidulans triose phosphate isomerase. Suitable leaders for yeast host cells are obtained from the genes for

Saccharomyces cerevisiae enolase (ENO-1), Saccharomyces cerevisiae 3-phosphoglycerate kinase, Saccharomyces cerevisiae alpha-factor, and Saccharomyces cerevisiae alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

[0299] The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleic acid sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention. Exemplary polyadenylation sequences for filamentous fungal host cells can be from the genes for Aspergillus oryzae TAKA amylase, Aspergillus niger glucoamylase, Aspergillus nidulans anthranilate synthase, Fusarium oxysporum trypsin-like protease, and Aspergillus niger alpha-glucosidase. Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, Mol Cell Bio 15:5983-5990.

[0300] The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleic acid sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region that encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region that is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region.

[0301] Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for Bacillus NClB 11837 maltogenic amylase, Bacillus stearothermophilus alpha-amylase, Bacillus licheniformis subtilisin, Bacillus licheniformis beta-lactamase, Bacillus stearothermophilus neutral proteases (nprT, nprS, nprM), and Bacillus subtilis prsA. Further signal peptides are described by Simonen and Palva, 1993, Microbiol Rev 57: 109-137.

[0302] Effective signal peptide coding regions for filamentous fungal host cells can be the signal peptide coding regions obtained from the genes for Aspergillus oryzae TAKA amylase, Aspergillus niger neutral amylase, Aspergillus niger glucoamylase, Rhizomucor miehei aspartic proteinase, Humicola insolens cellulase, and Humicola lanuginosa lipase.

[0303] Useful signal peptides for yeast host cells can be from the genes for Saccharomyces cerevisiae alpha-factor and Saccharomyces cerevisiae invertase. Other useful signal peptide coding regions are described by Romanos et al., 1992, supra.

[0304] The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive

and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for Bacillus subtilis alkaline protease (aprE), Bacillus subtilis neutral protease (nprT), Saccharomyces cerevisiae alpha-factor, Rhizomucor miehei aspartic proteinase, and Myceliophthora thermophila lactase (see e.g., WO 95/33836, which is hereby incorporated by reference herein).

[0305] Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

[0306] It may also be desirable to add regulatory sequences, which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. In prokaryotic host cells, suitable regulatory sequences include the lac, tac, and trp operator systems. In yeast host cells, suitable regulatory systems include, as examples, the ADH2 system or GAL1 system. In filamentous fungi, suitable regulatory sequences include the TAKA alpha-amylase promoter, Aspergillus niger glucoamylase promoter, and Aspergillus oryzae glucoamylase promoter.

[0307] Other examples of regulatory sequences are those which allow for gene amplification. In eukaryotic systems, these include the dihydrofolate reductase gene, which is amplified in the presence of methotrexate, and the metallothionein genes, which are amplified with heavy metals. In these cases, the nucleic acid sequence encoding the transaminase polypeptide of the present invention would be operably linked with the regulatory sequence.

[0308] Thus, in another embodiment, the present disclosure is also directed to a recombinant expression vector comprising a polynucleotide encoding an engineered transaminase polypeptide or a variant thereof, and one or more expression regulating regions such as a promoter and a terminator, a replication origin, etc., depending on the type of hosts into which they are to be introduced. The various nucleic acid and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleic acid sequence encoding the polypeptide at such sites. Alternatively, the nucleic acid sequence of the present disclosure may be expressed by inserting the nucleic acid sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

[0309] The recombinant expression vector may be any vector (e.g., a plasmid or virus), which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the polynucleotide sequence. The choice of the vector will typically depend on the compatibility of the

vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

[0310] The expression vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

[0311] The expression vector of the present invention preferably contains one or more selectable markers, which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like. Examples of bacterial selectable markers are the dal genes from Bacillus subtilis or Bacillus licheniformis, or markers, which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol, or tetracycline resistance. Suitable markers for yeast host cells are ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3.

[0312] Selectable markers for use in a filamentous fungal host cell include, but are not limited to, amdS (acetamidase), argB (ornithine carbamoyltransferase), bar (phosphinothricin acetyltransferase), hph (hygromycin phosphotransferase), niaD (nitrate reductase), pyrG (orotidine-5'-phosphate decarboxylase), sC (sulfate adenyltransferase), and trpC (anthranilate synthase), as well as equivalents thereof. Embodiments for use in an Aspergillus cell include the amdS and pyrG genes of Aspergillus nidulans or Aspergillus oryzae and the bar gene of Streptomyces hygroscopicus.

[0313] The expression vectors for expressing the transaminases can contain an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome. For integration into the host cell genome, the vector may rely on the nucleic acid sequence encoding the polypeptide or any other element of the vector for integration of the vector into the genome by homologous or nonhomologous recombination.

[0314] Alternatively, the expression vector may contain additional nucleic acid sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, preferably 400 to 10,000 base pairs, and most preferably 800 to 10,000 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of

homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleic acid sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

[0315] For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are P15A ori or the origins of replication of plasmids pBR322, pUC19, pACYCl77 (which plasmid has the P15A ori), or pACYC184 permitting replication in E. coli, and pUB110, pE194, pTA1060, or pAMβ1 permitting replication in Bacillus. Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6. The origin of replication may be one having a mutation which makes it's functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proc Natl Acad Sci. USA 75:1433).

[0316] More than one copy of a nucleic acid sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleic acid sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleic acid sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleic acid sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

[0317] Many of the expression vectors for use in the present invention are commercially available. Suitable commercial expression vectors include p3xFLAGTMTM expression vectors from Sigma-Aldrich Chemicals, St. Louis MO., which includes a CMV promoter and hGH polyadenylation site for expression in mammalian host cells and a pBR322 origin of replication and ampicillin resistance markers for amplification in E. coli. Other suitable expression vectors are pBluescriptII SK(-) and pBK-CMV, which are commercially available from Stratagene, LaJolla CA, and plasmids which are derived from pBR322 (Gibco BRL), pUC (Gibco BRL), pREP4, pCEP4 (Invitrogen) or pPoly (Lathe et al., 1987, Gene 57:193-201).

[0318] In another aspect, the present disclosure provides a host cell comprising a polynucleotide encoding an improved transaminase polypeptide of the present disclosure, the polynucleotide being operatively linked to one or more control sequences for expression of the transaminase enzyme in the host cell. Host cells for use in expressing the transaminase polypeptides encoded by the expression vectors of the present invention are well known in the art and include but are not limited to, bacterial cells, such as E. coli, Lactobacillus, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178));

insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, BHK, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and growth conditions for the above-described host cells are well known in the art.

[0319] Polynucleotides for expression of the transaminase may be introduced into cells by various methods known in the art. Techniques include among others, electroporation, biolistic particle bombardment, liposome mediated transfection, calcium chloride transfection, and protoplast fusion. Various methods for introducing polynucleotides into cells will be apparent to the skilled artisan.

[0320] An exemplary host cell is Escherichia coli W3110. The expression vector was created by operatively linking a polynucleotide encoding an improved transaminase into the plasmid pCK110900 operatively linked to the lac promoter under control of the lacI repressor. The expression vector also contained the P15a origin of replication and the chloramphenicol resistance gene. Cells containing the subject polynucleotide in Escherichia coli W3110 were isolated by subjecting the cells to chloramphenicol selection.

[0321] The improved transaminases and polynucleotides encoding such polypeptides can be prepared using methods commonly used by those skilled in the art. As noted above, the naturally-occurring amino acid sequence and corresponding polynucleotide encoding the transaminase enzyme of *Arthrobacter* sp KNK168, from which the parent sequence SEQ ID NO:2 was derived, represented herein as SEQ ID NO:2) is available in US Patent No. 7,169,592, which is hereby incorporated by reference herein. In some embodiments, the parent polynucleotide sequence is codon optimized to enhance expression of the transaminase in a specified host cell. The polynucleotide sequence designated SEQ ID NO: 1 was the parent sequence utilized as the starting point for most experiments and library construction of engineered transaminases.

[0322] The engineered transaminases can be obtained by subjecting the polynucleotide encoding the naturally occurring transaminase to mutagenesis and/or directed evolution methods. An exemplary directed evolution technique is mutagenesis and/or DNA shuffling as described in Stemmer, 1994, Proc Natl Acad Sci USA 91:10747-10751; WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; WO 01/75767 and U.S. Pat. 6,537,746 (each of which is hereby incorporated by reference herein).

[0323] Other directed evolution procedures that can be used include, among others, staggered extension process (StEP), in vitro recombination (Zhao et al., 1998, Nat. Biotechnol. 16:258–261), mutagenic PCR (Caldwell et al., 1994, PCR Methods Appl. 3:S136-S140), and cassette mutagenesis (Black et al., 1996, Proc Natl Acad Sci USA 93:3525-3529). Mutagenesis and directed evolution techniques useful for the purposes herein are also described in the following references: Ling, et al., 1997, "Approaches to DNA mutagenesis: an overview," Anal. Biochem. 254(2):157-78; Dale et al., 1996, "Oligonucleotide-directed random mutagenesis using the phosphorothioate method," Methods

Mol. Biol. 57:369-74; Smith, 1985, "In vitro mutagenesis," Ann. Rev. Genet. 19:423-462; Botstein et al., 1985, "Strategies and applications of in vitro mutagenesis," Science 229:1193-1201; Carter, 1986, "Site-directed mutagenesis," Biochem. J. 237:1-7; Kramer et al., 1984, "Point Mismatch Repair," Cell 38:879-887; Wells et al., 1985, "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites," Gene 34:315-323; Minshull et al., 1999, "Protein evolution by molecular breeding," Curr Opin Chem Biol 3:284-290; Christians et al., 1999, "Directed evolution of thymidine kinase for AZT phosphorylation using DNA family shuffling," Nature Biotech 17:259-264; Crameri et al., 1998, "DNA shuffling of a family of genes from diverse species accelerates directed evolution," Nature 391:288-291; Crameri et al., 1997, "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," Nature Biotech 15:436-438; Zhang et al., 1997, "Directed evolution of an effective fructosidase from a galactosidase by DNA shuffling and screening," Proc Natl Acad Sci USA 94:45-4-4509; Crameri et al., 1996, "Improved green fluorescent protein by molecular evolution using DNA shuffling,' Nature Biotech 14:315-319; and Stemmer, 1994, "Rapid evolution of a protein in vitro by DNA shuffling," Nature 370:389-391. All publications are incorporated herein by reference.

[0324] In some embodiments, the clones obtained following mutagenesis treatment are screened for transaminases having a desired improved enzyme property. Measuring transaminase enzyme activity from the expression libraries can be performed using the standard techniques, such as separation of the product (e.g., by HPLC) and detection of the product by measuring UV absorbance of the separated substrate and products and/or by detection using tandem mass spectroscopy (e.g., MS/MS). Exemplary assays are described in Example 4 below. The rate of increase in desired product per unit time indicates the relative (enzymatic) activity of the transaminase polypeptide in a fixed amount of the lysate (or a lyophilized powder made therefrom). Where the improved enzyme property desired is thermal stability, enzyme activity may be measured after subjecting the enzyme preparations to a defined temperature and measuring the amount of enzyme activity remaining after heat treatments. Clones containing a polynucleotide encoding the desired transaminases are then isolated, sequenced to identify the nucleotide sequence changes (if any), and used to express the enzyme in a host cell.

[0325] Where the sequence of the engineered polypeptide is known, the polynucleotides encoding the enzyme can be prepared by standard solid-phase methods, according to known synthetic methods. In some embodiments, fragments of up to about 100 bases can be individually synthesized, then joined (e.g., by enzymatic or chemical litigation methods, or polymerase mediated methods) to form any desired continuous sequence. For example, polynucleotides and oligonucleotides of the invention can be prepared by chemical synthesis using, e.g., the classical phosphoramidite method described by Beaucage et al., 1981, Tet Lett 22:1859-69, or the method described by Matthes et al., 1984, EMBO J. 3:801-05, e.g., as it is typically practiced in automated synthetic methods. According to the phosphoramidite method, oligonucleotides are synthesized, e.g., in an automatic DNA synthesizer,

purified, annealed, ligated and cloned in appropriate vectors. In addition, essentially any nucleic acid can be obtained from any of a variety of commercial sources, The Great American Gene Company, Ramona, CA, ExpressGen Inc. Chicago, IL, Operon Technologies Inc., Alameda, CA, and many others.

[0326] The engineered transaminase enzymes expressed in a host cell can be recovered from the cells and or the culture medium using any one or more of the well known techniques for protein purification, including, among others, lysozyme treatment, sonication, filtration, salting-out, ultra-centrifugation, and chromatography. Suitable solutions for lysing and the high efficiency extraction of proteins from bacteria, such as E. coli., are commercially available under the trade name CelLytic BTM from Sigma-Aldrich of St. Louis MO.

[0327] Chromatographic techniques for isolation of the transaminase polypeptide include, among others, reverse phase chromatography high performance liquid chromatography, ion exchange chromatography, gel electrophoresis, and affinity chromatography. Conditions for purifying a particular enzyme will depend, in part, on factors such as net charge, hydrophobicity, hydrophilicity, molecular weight, molecular shape, etc., and will be apparent to those having skill in the art. In some embodiments, the engineered transaminases can be expressed as fusion proteins with purification tags, such as His-tags having affinity for metals, or antibody tags for binding to antibodies, e.g., myc epitope tag.

[0328] In some embodiments, affinity techniques may be used to isolate the improved transaminase enzymes. For affinity chromatography purification, any antibody which specifically binds the transaminase polypeptide may be used. For the production of antibodies, various host animals, including but not limited to rabbits, mice, rats, etc., may be immunized by injection with an engineered polypeptide. The polypeptide may be attached to a suitable carrier, such as BSA, by means of a side chain functional group or linkers attached to a side chain functional group. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacilli Calmette Guerin) and Corynebacterium parvum.

6. EXAMPLES

[0329] Various features and embodiments of the disclosure are illustrated in the following representative examples, which are intended to be illustrative, and not limiting.

Example 1: Wild-type transaminase gene acquisition and construction of expression vectors.

[0330] Transaminase (TA) encoding genes were designed for expression in *E. coli.* based on the reported amino acid sequence of the transaminase, and a codon optimization algorithm as described in Example 1 of US application publication 20080248539, which is hereby incorporated by reference herein. Genes were synthesized using oligonucleotides, generally composed of 42 nucleotides, and the gene cloned into the expression vector pCK110700 (depicted as FIG. 1 in US application publication 20050153417, which is hereby incorporated by reference herein) or pCK110900 (depicted as FIG. 3 in US application publication 20060195947, which is hereby incorporated by reference herein) under the control of a lac promoter. This expression vector also contains the P15a origin of replication and the chloramphenicol resistance gene. Resulting plasmids were transformed into *E. coli.* W3110 using standard methods. Codon optimized genes and the encoding polypeptides are listed in Table 2, and their sequences provided as SEQ ID NOs:1 and 2.

[0331] Likewise, the genes encoding the engineered transaminases of the present disclosure listed in Table 2 (SEQ ID NOs: 3-168) were cloned into vector pCK110700 or pCK110900 for expression in *E. coli* W3110.

Example 2: Production of transaminase powders - shake flask procedure.

[0332] A single microbial colony of *E. coli* containing a plasmid encoding a transaminase of interest was inoculated into 50 mL Luria Bertani broth containing 30 μg/mL chloramphenicol and 1% glucose. Cells were grown overnight (at least 16 hrs) in an incubator at 30°C with shaking at 250 rpm. The culture was diluted into 250 mL M9YE (1.0 g/L ammonium chloride, 0.5 g/L of sodium chloride, 6.0 g/L of disodium monohydrogen phosphate, 3.0 g/L of potassium dihydrogen phosphate, 2.0 g/L of Tastone-154 yeast extract, 1 L/L de-ionized water) containing 30 μg/mL chloramphenicol and 100 μM pyridoxine, in a 1 liter flask to an optical density at 600 nm (OD600) of 0.2 and allowed to grow at 30°C. Expression of the transaminase gene was induced by addition of isopropyl β D-thiogalactoside (IPTG) to a final concentration of 1 mM when the OD600 of the culture is 0.6 to 0.8 and incubation was then continued overnight (at least 16 hrs). Cells were harvested by centrifugation (5000 rpm, 15 min, 4°C) and the supernatant discarded. The cell pellet was resuspended with an equal volume of cold (4°C) 100 mM triethanolamine (chloride) buffer, pH 7.5 containing 100 μM pyridoxal 5'-phosphate (PLP), and harvested by centrifugation as above. The washed cells were resuspended in two volumes of the cold triethanolamine (chloride) buffer containing PLP and passed through a French Press twice at 12,000 psi while maintained at 4°C. Cell debris was removed by centrifugation (9000 rpm, 45 min., 4°C). The clear lysate supernatant was collected and stored at -20°C. Lyophilization of frozen clear lysate provides a dry powder of crude transaminase enzyme. Alternatively, the cell pellet (before or after washing) may be stored at 4°C or 80°C.

Example 3: Production of transaminase - fermentation procedure.

[0333] A single microbial colony of *E. coli.* containing a plasmid with the transaminase gene of interest was inoculated into 2 mL M9YE broth (1.0 g/L ammonium chloride, 0.5 g/L of sodium

chloride, 6.0 g/L of disodium monohydrogen phosphate, 3.0 g/L of potassium dihydrogen phosphate, 2.0 g/L of Tastone-154 yeast extract, 1 L/L de-ionized water) containing 30 μg/ml chloramphenicol and 1% glucose. Cells were grown overnight (at least 12 hrs) in an incubator at 37°C with shaking at 250 rpm. After overnight growth, 0.5 mL of this culture was diluted into 250 ml M9YE Broth, containing 30 μg/ml chloramphenicol and 1% glucose in 1 liter flask and allowed to grow at 37°C with shaking at 250 rpm. When the OD600 of the culture is 0.5 to 1.0, the cells were removed from the incubator and either used immediately, or stored at 4°C.

[0334] Bench-scale fermentations were carried out at 30°C in an aerated, agitated 15 L fermentor using 6.0 L of growth medium (0.88 g/L ammonium sulfate, 0.98 g/L of sodium citrate; 12.5 g/L of dipotassium hydrogen phosphate trihydrate, 6.25g/L of potassium dihydrogen phosphate, 3.3g/L of Tastone-154 yeast extract, 0.083 g/L ferric ammonium citrate, and 8.3 ml/L of a trace element solution containing 2 g/L of calcium chloride dihydrate, 2.2 g/L of zinc sulfate heptahydrate, 0.5 g/L manganese sulfate monohydrate, 1 g/L cuprous sulfate heptahydrate, 0.1 g/L ammonium molybdate tetrahydrate and 0.02 g/L sodium tetraborate. The vessel was sterilized at 121°C and 15 PSI for 30 minutes, and 100 μM pyridoxine was added post sterilization. The fermentor was inoculated with a late exponential culture of *E. coli* W3110 containing a plasmid encoding the transaminase gene of interest (grown in a shake flask as described above to a starting OD_{600} of 0.5 to 1.0. The fermentor was agitated at 250-1250 rpm and air was supplied to the fermentation vessel at 0.6-25 L/min to maintain a dissolved oxygen level of 50% saturation or greater. The pH of the culture was maintained at 7.0 by addition of 20% v/v ammonium hydroxide. Growth of the culture was maintained by addition of a feed solution containing 500 g/L Cerelose dextrose, 12 g/L ammonium chloride and 5.1 g/L magnesium sulfate heptahydrate. After the culture reached an OD_{600} of 70 +-10, expression of transaminase was induced by addition of isopropyl-β-D-thiogalactoside (IPTG) to a final concentration of 1 mM and fermentation is continued for another 18 hours. The culture was then chilled to 4°C and maintained at that temperature until harvested. Cells were collected by centrifugation at 5000 G for 40 minutes in a Sorval RC12BP centrifuge at 4°C. Harvested cells were used directly in the following downstream recovery process or they may be stored at 4°C or frozen at -80°C until such use.

[0335] The cell pellet was resuspended in 2 volumes of 100 mM triethanolamine (chloride) buffer, pH 7.5 containing 100 μM pyridoxal 5'-phosphate (PLP), at 4°C to each volume of wet cell paste. The intracellular transaminase was released from the cells by passing the suspension through a homogenizer fitted with a two-stage homogenizing valve assembly using a pressure of 12000 psig. The cell homogenate was cooled to -20°C immediately after disruption. A solution of 11% w/v polyethyleneimine pH 7.2 was added to the lysate to a final concentration of 0.5% w/v. A solution of 1M Na_2SO_4 was added to the lysate to a final concentration of 100mm. The lysate was then stirred for 30 minutes. The resulting suspension was clarified by centrifugation at 5000G in a Sorval RC12BP

centrifuge at 4°C for 30 minutes. The clear supernatant was decanted and concentrated ten-fold using a cellulose ultrafiltration membrane with a molecular weight cut off of 30 kD. The final concentrate was dispensed into shallow containers, frozen at -20°C and lyophilized to powder. The transaminase powder was stored at –80°C.

Example 4: High-throughput screening for identification of variants of the *Arthrobacter sp.* KNK168 transaminase capable of stereoselectively converting the sitagliptin ketoamide substrate to sitagliptin.

[0336] Achiral HPLC method to determine conversion of the sitagliptin ketoamide substrate to sitagliptin: Enzymatic conversion of sitagliptin ketoamide substrate (prepared as described in United States Patent No. 7,326,708) to sitagliptin was determined using an Agilent 1200 HPLC equipped with an Agilent Eclipse XDB-C8 column (4.6 x 150 mm, 5 μm), using 45:55 10 mM NH_4Ac/MeCN as eluent at a flow rate of 1.5 ml/min and a column temperature 40°C. Retention times: sitagliptin ketoamide substrate: 1.4 min; sitagliptin: 1.7 min. The sitagliptin ketoamide substrate and product in the eluant were determined as the peak area at 210 nm or 286 nm, with a path length of 1 cm. Using these conditions, the limit of detection for sitagliptin was 5 μg/mL. Generally, an incident wavelength of 210 nm was used for activity measurements for transaminases with activity similar or equal to SEQ ID NO:4.

[0337] Chiral HPLC method to determine stereopurity of sitagliptin: Stereoisomeric purity of sitagliptin was determined using an Agilent 1200 HPLC equipped with a Daicel Chiralpak AD-H column (4.6 x 150 mm, 5 μm) using 60:40:0.1:0.1 EtOH/Heptane/diethylamine/water as the eluent at a flow rate of 0.8 ml/min and a column temperature of 35°C. Retention times: sitagliptin ketoamide substrate: 6.3 min; (*S*)-enantiomer: 8.4 min; sitagliptin: 10.8 min. The sitagliptin ketoamide substrate and product were determined as the peak area at 210 nm or 268 nm with a path length of 1 cm.

[0338] Liquid chromatography-mass spectroscopy (LC/MS) method for detecting low-level conversion of the sitagliptin ketoamide substrate to sitagliptin: Low-level enzymatic conversion of sitagliptin ketoamide substrate to sitagliptin was determined using an LC/MS/MS method. Five microliters of sample was loaded into an Eclipse XDB-C8 HPLC column (4.6 x 150 mm) and eluted isocratically with a 40:60 mobile phase of 0.2% ammonium formate and methanol at 1.0 mL/min. The retention time of sitagliptin was 1.5 minutes at 35°C. Mass spectrometry was used for detection on a Waters Quattro triple quadruple. Q1 was set to pass the M+H ion at 408.1 AMU and Q3 was set to pass the 235.1 daughter ion. The collision cell (Q2) had a collision energy of 17.0 and Argon gas flow of 0.3 mL/min. Ionization was by APCI with a corona discharge of 5 μA, source temperature of 130°C and probe temperature of 600°C. Desolvation gas flow was 100 L/minute and the cone gas was set to 50 L/minute. Using these conditions the limit of detection for sitagliptin was 71 pg/mL.

Example 5: High-throughput screening for identification of variants of the *Arthrobacter sp.* KNK168 transaminase capable of stereoselectively converting sitagliptin ketoamide substrate to sitagliptin.

[0339] The gene encoding transaminase, constructed as described in Example 1, was mutagenized using methods described above and the population of altered DNA molecules was used to transform a suitable *E. coli* host strain. Antibiotic resistant transformants were selected and processed to identify those expressing a transaminase with an improved ability to transaminate the sitagliptin ketoamide substrate stereoselectively to sitagliptin in the presence of a suitable amino group donor (i.e., isopropylamine). Cell selection, growth, induced expression of transaminase variant enzymes and collection of cell pellets were as described below.

[0340] Recombinant *E. coli* colonies carrying a gene encoding transaminase were picked using a Q-Bot® robotic colony picker (Genetix USA, Inc., Boston, MA) into 96-well shallow well microtiter plates containing in each well 180 μL LB Broth, 1% glucose and 30 μg/mL chloramphenicol (CAM). Cells were grown overnight at 30°C with shaking at 200 rpm. A 10 μL aliquot of this culture was then transferred into 96-deep well plates containing 390 μL M9YE broth, 100 μM pyridoxine and 30 μg/mL CAM. After incubation of the deep-well plates at 30°C with shaking at 250 rpm for 2-3 hrs, recombinant gene expression within the cultured cells was induced by addition of IPTG to a final concentration of 1 mM. The plates were then incubated at 30°C with shaking at 250 rpm for 18 hrs.

[0341] Cells were pelleted by centrifugation (4000 RPM, 10 min, 4°C), resuspended in 200 μL lysis buffer and lysed by shaking at room temperature for 2 hours. The lysis buffer contained 100 mM triethanolamine (chloride) buffer, pH 7.5 or 8.5, 1 mg/mL lysozyme, 500 μg/mL polymixin B sulfate (PMBS) and 250 μM PLP. After sealing the plates with aluminum/polypropylene laminate heat seal tape (Velocity 11, Menlo Park, CA, Cat# 06643-001), they were shaken vigorously for 2 hours at room temperature. Cell debris was pelleted by centrifugation (4000 RPM, 10 min., 4°C) and the clear supernatant assayed directly or stored at 4°C until use.

[0342] For screening in methanol or DMSO at pH 7.5, with early-stage engineered transaminases (i.e., early-stage "evolvants"), a 10 μL aliquot of a solution of sitagliptin ketoamide substrate (40 mg/mL) in methanol or DMSO was added to each well of a Costar® deep well plate, followed by addition of 90 μL of 1.1 M isopropylamine hydrochloride using a Biomek NXp robotic instrument (Beckman Coulter, Fullerton, CA). This was then followed by addition of 100 μL of the recovered lysate supernatant, also performed using the Biomek NXp, to provide a reaction comprising of 2 mg/ml sitagliptin ketoamide substrate, 500 mM isopropyl amine hydrochloride, 50 mM triethanolamine pH 7.5, and 5% methanol or DMSO (v/v). The plates were heat-sealed with aluminum/polypropylene laminate heat seal tape (Velocity 11, Menlo Park, CA, Cat# 06643-001) at 175°C for 2.5 seconds and then shaken overnight (at least 16 hours) at 30°C. Reactions were quenched by the addition of 1 ml acetonitrile using a Phoenix Liquid Handling System (Art Robbins

Instruments, Sunnyvale, CA). Plates were resealed, shaken for 5 min, and then centrifuged at 4000 rpm for 10 min. A 200 μL aliquot of the cleared reaction mixture was transferred to a new shallow well polypropylene plate (Costar #3365), sealed and analyzed as described in Example 4.

[0343] For screening in DMSO at pH 8.5 with late-stage engineered transaminases (i.e., late-stage "evolvants"), a 50 μL aliquot of a solution of sitagliptin ketoamide substrate (400 mg/mL) in dimethyl sulfoxide (DMSO) was added to each well of a Costar® deep well plate, followed by addition of 50 μL of 4 M isopropylamine hydrochloride using a Biomek NX robotic instrument (Beckman Coulter, Fullerton, CA). This was then followed by addition of 100 μL of the recovered lysate supernatant, also performed using the Biomek NX, to provide a reaction comprising of 100 mg/ml sitagliptin ketoamide substrate, 1 M isopropyl amine hydrochloride, 50 mM triethanolamine pH 8.5, and 25% DMSO (v/v). The plates were heat-sealed with aluminum/polypropylene laminate heat seal tape (Velocity 11, Menlo Park, CA, Cat# 06643-001) at 175°C for 2.5 seconds and then shaken overnight (at least 16 hours) at 45°C. Reactions were quenched by the addition of 1 ml acetonitrile using a Phoenix Liquid Handling System (Art Robbins Instruments, Sunnyvale, CA). Plates were resealed, shaken for 5 min, and then centrifuged at 4000 rpm for 10 min. A 10 μL aliquot of the cleared reaction mixture was transferred to a new shallow well polypropylene plate (Costar #3365) containing 190 μL acetonitrile, sealed and analyzed as described in Example 4.

[0344] The transaminase of SEQ ID NO:2 expressed as in Examples 1 and 2 exhibited no detectable activity on the sitagliptin ketoamide substrate using the detection methods of Example 4. Variants of the *Arthrobacter sp.* KNK168 transaminase capable of converting sitagliptin ketoamide substrate to sitagliptin were identified using the approaches and procedures disclosed above. Multiple iterations of these processes, in which one or more improved isolates from one round were used as the starting material for subsequent rounds of mutagenesis and screening, were used to develop or "evolve" *Arthrobacter sp.* KNK168 transaminase variants with an improved ability to reduce the sitagliptin ketoamide substrate stereoselectively to sitagliptin.

Example 6: Stereoselective transamination in methanol of the sitagliptin ketoamide substrate by engineered transaminases in Table 2 derived from *Arthrobacter sp.* KNK168 transaminase.

[0345] Improved transaminases designated "+" in Table 2 derived from *Arthrobacter sp.* KNK168 transaminase were evaluated at preparative scale in DMSO as follows. A 500 μL solution of transaminase variant (20 mg/mL) in 100 mM triethanolamine-chloride buffer pH 7.5 with 250 μM pyridoxal 5'-phosphate was added to 5 mL reaction vial equipped with a magnetic stir bar. Subsequently, 450 μL of 1.1 M isopropylamine hydrochloride, followed by 50 μL of a solution of sitagliptin ketoamide substrate (40 mg/mL) in DMSO was added to the transaminase solution. The reaction was stirred at 22°C and monitored by HPLC analysis of samples taken periodically from the reaction mixture (*see* Example 4 for analytical conditions). Table 2 provides the SEQ ID NO.

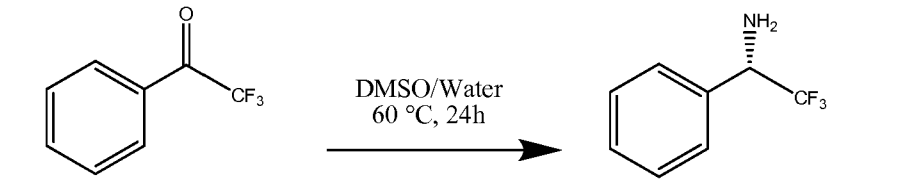
corresponding to transaminase variants designated "+", the number of amino acid residue differences from the wild-type transaminase, and activity of each toward sitagliptin ketoamide substrate relative to that of the enzyme having the amino acid sequence of SEQ ID NO: 4.

[0346] The improved transaminases designated "++", "+++", "++++", and "+++++" in Table 2 were assayed with conditions adjusted as follows: "++": 2 g/L sitagliptin ketoamide substrate, 0.5 M isopropylamine, 22°C, pH 7.5, 5% MeOH; "+++": 5-10 g/L sitagliptin ketoamide substrate, 0.5-1 M isopropylamine, 22-30°C, pH 7.5, 5% MeOH; "++++": 10-40 g/L sitagliptin ketoamide substrate, 1 M isopropylamine, 30-45°C, pH 8.5, 10% MeOH; "+++++": 40-100 g/L sitagliptin ketoamide substrate, 1 M isopropylamine, 45°C, pH 8.5, 10% MeOH-25% DMSO; and "++++++": 40-100 g/L ketoamide substrate, 1 M isopropylamine, 45°C, pH 8.5, 50% DMSO, 1000 μM PLP. Relative activities of the improved transaminases designated "+++", "++++", "+++++", "++++++" were determined relative to the activities of SEQ ID NO: 22, SEQ ID NO: 48, SEQ ID NO: 58, and SEQ ID NO:104, respectively.

[0347] For many engineered transaminases, conversion of sitagliptin ketoamide substrate to sitagliptin can also be achieved using amino group donors such as D-alanine, 3-aminobutyric acid, or α-methylbenzylamine at a suitable concentration.

Example 7: Preparation of (*S*)-2,2,2-trifluoro-1-phenylethanamine from 2,2,2-trifluoro-1-phenylethanone.

[0348] Preparation of (*S*)-2,2,2-trifluoro-1-phenylethanamine is illustrated as follows:



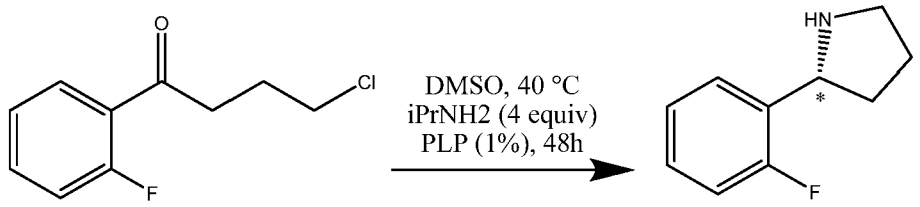
2,2,2-trifluoro-1-phenylethanone (*S*)-2,2,2-trifluoro-1-phenylethanamine

[0349] Process. 1.4 g of isopropyl amine hydrochloride was added to 14 mL of 0.1M triethanolamine buffer at pH 8.5. After dissolving the isopropylamine hydrochloride, 20 mg of PLP and 100 mg of a transaminase of SEQ ID NO:74 were added and dissolved with gentle agitation at 400 rpm. The reactor was heated to 60 °C and the pH of the solution was adjusted to pH 8.5 with 5N NaOH. About 400 mg of 2,2,2-trifluoro-1-phenylethanone ketone substrate was dissolved in 6 mL of DMSO and added dropwise to the solution over 2 hours. The reactor was then stirred at 500 RPM, 60 °C, and pH set at 8.5 for 24 h. After 24 h, the reaction had reached 99% conversion to the (*S*)-2,2,2-trifluoro-1-phenylethanamine product. During workup, the temperature of the reaction was decreased to 45°C and 2 N HCl was added dropwise to decrease the pH of the reaction to pH 2. The reaction was allowed to stir for 1 hour and the precipitate was filtered through a glass fritted funnel equipped with cotton towel. The precipitate was washed three times with 10 mL of 0.1 N HCl. The aqueous

filtrates were combined and the pH was increased to pH 11 with 5 N NaOH, followed by extraction with 2 x 100 mL of IPAC. IPAC layers were washed with 25 mL brine, dried with $MgSO_4$, filtered, and concentrated to an oil of the (*S*)-2,2,2-trifluoro-1-phenylethanamine product.

Example 8: Preparation of (*R*)-2-(2-fluorophenyl)pyrrolidine from 4-chloro-1-(2-fluorophenyl)butan-1-one.

[0350] Preparation of (*R*)-2-(2-fluorophenyl)pyrrolidine is illustrated as follows:

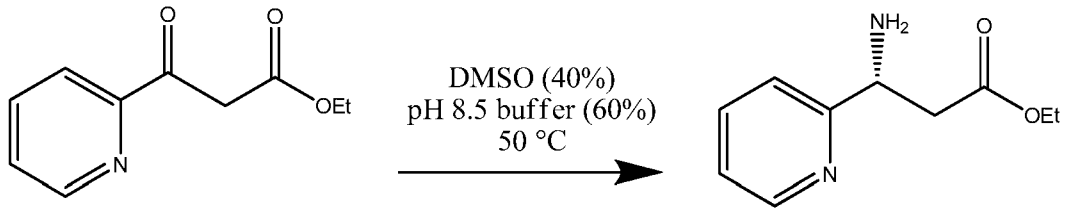


4-chloro-1-(2-fluorophenyl)butan-1-one (*R*)-2-(2-fluorophenyl)pyrrolidine

[0351] Process. To a HPLC vial added charged 10 μL of ketone and 200 μL DMSO. To a 50 mL Falcon tube was added 3.75 g Isopropylamine-HCl and 30 mL of 0.1M TEA buffer. About 37.5 mg PLP is added and the reaction mixture vortexed to mix. To 15 mL Falcon tubes was added 25 mg of a transaminase of SEQ ID NO:80. A 5 mL solution of PLP/buffer was added to the enzyme containing tube and vortexed to dissolve the enzyme. 1.0 mL of the enzyme solution was added to the LC vial containing the 4-chloro-1-(2-fluorophenyl)butan-1-one ketone substrate and DMSO and the vial placed at 45°C and mixed at 1000 rpm on a thermomixer. After several days, the LCMS analysis showed a 53 LCAP conversion to product with an M+1 mass of 166. Coinjection with an authentic standard of the desired (*R*)-2-(2-fluorophenyl)pyrrolidine product confirmed identity of this peak. The reaction mixture was extracted with 1.0 mL EtOAC. The sample was concentrated and then diluted with methanol. Assay by SFC using ChiralPak AD-H column as stationary phase showed (*R*)-2-(2-fluorophenyl)pyrrolidine in an enantiomeric excess of 95%.

Example 9: Preparation of (*R*)-ethyl 3-amino-3-(pyridin-2-yl)propanoate from ethyl 3-oxo-3-(pyridin-2-yl)propanoate

[0352] Preparation of (*R*)-ethyl 3-amino-3-(pyridin-2-yl)propanoate is illustrated as follows:



ethyl 3-oxo-3-(pyridin-2-yl)propanoate (*R*)-ethyl 3-amino-3-(pyridin-2-yl)propanoate

[0353] Methods/Materials: The reaction was carried out in a 3L round bottom flask with pH monitor, overhead stirring, heating mantle, and thermocouple. About 100 g of the ethyl 3-oxo-3-

(pyridin-2-yl)propanoate ketoester substrate was dissolved in 800 mL DMSO which resulted in a solution that is green. About 4 g of vitamin-B6 ("PLP") was prepared in 1.2 L of 0.5M triethanolamine buffer, pH 8.4 with 100g/L isopropylamine-HCl. After addition, the pH was 8.3. The pH was adjusted pH to 8.8 by addition of 3mL 20 wt% KOH. The transaminase polypeptide of SEQ ID NO:86 (2g) was prepared in buffer and mixed until fully dissolved. The pH of the solution is 8.77 and the solution kept at 21.7°C. The ketoester substrate prepared in DMSO stock was added directly into batch in one portion.

[0354] Reaction: The reaction is exothermic and heats the batch temp to 38.1°C while the pH of solution is 8.45 and appears as a greenish slurry. The solution is heated to 50°C. At a temperature of 47°C, the pH of solution is 8.31, and the pH was then adjusted to 8.6 by adding 2 mL 20 wt% KOH. After 2 hr from substrate charge, the pH was 8.07, and the pH was adjusted to 9.02 by adding 4 mL of 4M isopropylamine solution. 6 hr after the substrate charge, the pH was 8.05, and the pH was adjusted to 8.9 by adding 4 mL of 4 M isopropylamine solution. The reaction was allowed to incubate overnight. After 15 hr from substrate charge, the pH was 7.4, and 47.6 mL of water added and the stirring increased (volume was reduced ~ 25%). About 8 mL of 4M isopropylamine was added to adjust the pH to 8.85. After 17.25 hr, the pH was 8.5, and the reaction was allowed to proceed without further adjustment of pH. At 18.33 hr, the pH was 8.27 and the reaction was complete as determined by assay on RP-HPLC.

[0355] Reaction Workup: 2 g Solka Floc® was added to the solution at room temperature. The pH of the solution increased to 9.2 upon cooling as there was a temperature dependent pH shift with the buffer. The pH of the solution was adjusted to 1.8 with addition of 4.5 mL concentrated H_2SO_4 and aged 1hr. The solution was then vacuum filtered through a 5 μm filter cloth with a filtering flask and fritted filter (60 mL-40M). The filtration took 1.5 hr. The cake was washed with 50.6 g of dilute H_2SO_4 (pH 1.6) by physically mixing with wash solution. The filtration took about 20 min. The cake was washed again with 50 g of dilute acidic solution followed by rapid filtration in < 5 min. The first wash and first acidic aqueous solutions were combined and 67 mL heptane and 3.3 mL toluene added in one portion. The solution was mixed thoroughly and the layers separated in a separation funnel. The first acidic aqueous 1 results in about 63% recovery of the theoretical yield of combined (*R*)-ethyl 3-amino-3-(pyridin-2-yl)propanoate amino acid/aminoester products. Acidic wash 1 results in about 27% recovery while the second acidic wash results in about 10% recovery.

[0356] About 99.4 g of 20 wt% KOH was added to the solution to adjust the pH to 13 and the solution was incubated at 50°C. After 20 min, an additional 11.8 g of 20 wt% KOH was added to adjust the pH from 12.1 to 13. After an additional 20 min, the pH stabilized at 12.8 and hydrolysis was complete as determined by HPLC. Solids were observed precipitating out of solution. The basic solution was filtered on a fritted funnel (solids were dissolved in water and appeared to be inorganic

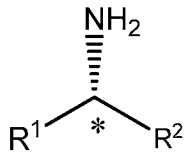
as only small amount of product was observed, the solids did not go into MeCN). The basic solution was concentrated on roto-evaporator to yield a crude potassium-salt solution of (*R*)-ethyl 3-amino-3-(pyridin-2-yl)propanoate in 75 % yield.

[0357] All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entireties for all purposes to the same extent as if each individual publication, patent, patent application or other document were individually indicated to be incorporated by reference for all purposes.

[0358] While various specific embodiments have been illustrated and described, it will be appreciated that various changes can be made without departing from the spirit and scope of the invention(s).

What is claimed is:

1. A process for preparing an amine product of structural formula (I):



(I)

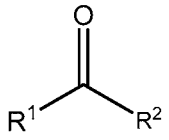
having the indicated stereochemical configuration at the stereogenic center marked with an *; in an enantiomeric excess over the opposite enantiomer, wherein

R^1 is optionally substituted aryl or heteroaryl;

R^2 is an optionally substituted C_1-C_6 alkyl, $-R^3C(O)R^4$, or $-R^3OC(O)R^5$

R^3 is an optionally substituted C_1-C_4 alkyl, and R^4 is H, an optionally substituted C_1-C_4 alkyl, NR^6R^7, or OR^8, where R^5, R^6, R^7, and R^8 are independently H or C_1-C_4 alkyl;

the process comprising contacting a ketone substrate of structural formula (II):



(II)

with a transaminase polypeptide in presence of an amino donor under reaction conditions suitable for converting the ketone substrate to the amine product, wherein the transaminase polypeptide has at least 80% sequence identity to SEQ ID NO:74 and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to SEQ ID NO:2.

2. The process of claim 1, wherein R^1 is an optionally substituted phenyl.

3. The process of claim 1, wherein R^1 is an optionally substituted pyridinyl.

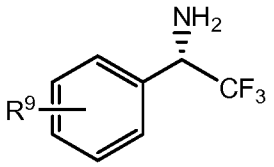
4. The process of claim 1, wherein R^1 is a substituted aryl or heteroaryl.

5. The process of claim 1, wherein the substitution on the C_1-C_6 alkyl and R^3 are selected from halogen, NR^5R^6, or OR^8, where R^5 and R^6 are defined above and R^8 is H or C_1-C_4 alkyl.

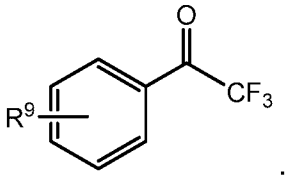
6. The process of claim 1, wherein R^2 is methyl or halo substituted methyl.

7. The process of claim 6, wherein the halo substituted methyl is CF_2H or CF_3.

8. The process of claim 1, wherein the amine product of formula (I) is:

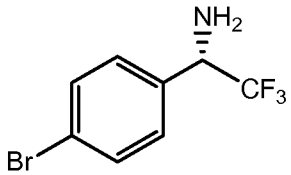


wherein R^9 is H, Cl, Br, F, CH_3, CF_3, CN, SO_2, -OCH_3, -$C(O)CH_3$, or NO_2, and the ketone substrate of formula (II) is:

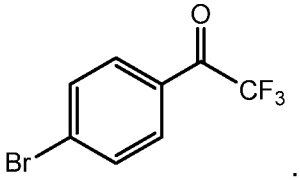


9. The process of claim 9 wherein R^9 is in the para position on the phenyl ring.

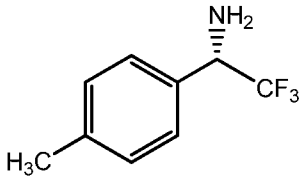
10. The process of claim 1 wherein the amine product of formula (I) is (*S*)-1-(4-bromophenyl)-2,2,2-trifluoroethanamine:



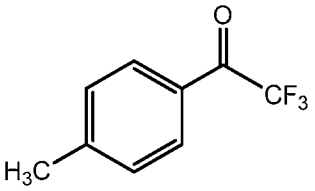
and the ketone substrate of formula (II) is 1-(4-bromophenyl)-2,2,2-trifluoroethanone:



11. The process of claim 1 wherein the amine product of formula (I) is (*S*)-2,2,2-trifluoro-1-p-tolylethanamine:

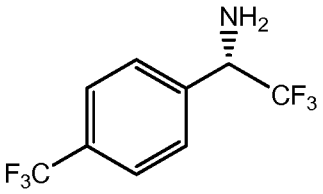


and the ketone substrate of formula (II) is 2,2,2-trifluoro-1-p-tolylethanone

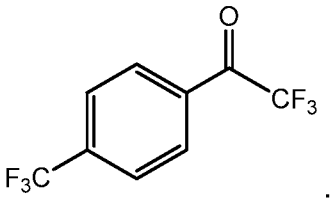


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12. The process of claim 1 wherein the product amine of formula (I) is (*S*)-2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanamine:

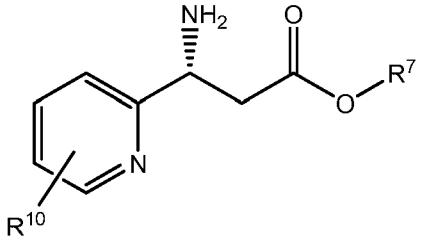


and the ketone substrate of formula (II) is 2,2,2-trifluoro-1-(4-(trifluoromethyl)phenyl)ethanone:

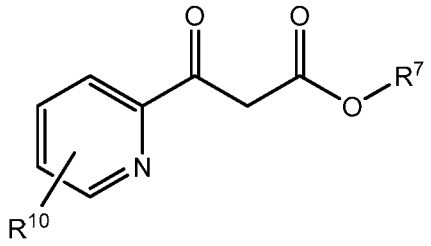


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13. The process of claim 1, wherein the amine product of formula (I) is:

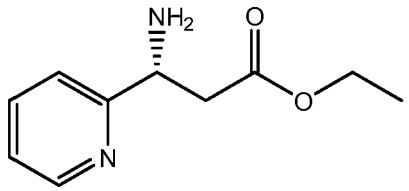


and the ketone substrate of formula (II) is:

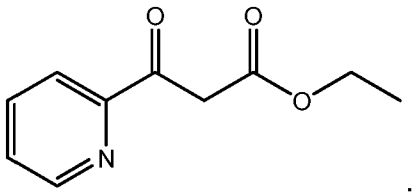


wherein R^7 is optionally substituted C_1-C_4 alkyl, and R^{10} is R^9 defined above.

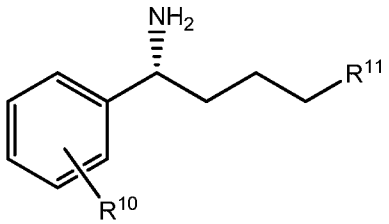
14. The process of claim 1, wherein the amine product of formula (I) is (*R*)-ethyl-3-amino-3-(pyridin-2-yl)propanoate:



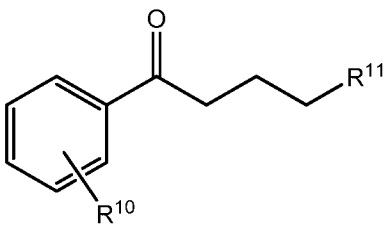
and the ketone substrate of formula (II) is ethyl 3-oxo-3-(pyrindin-2-yl)propanoate:



15. The process of claim 1, wherein the amine product of formula (I) is:

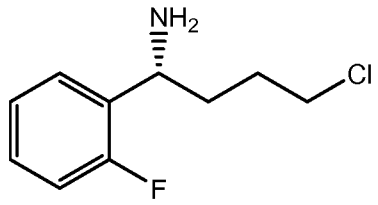


and the ketone substrate of formula (II) is:

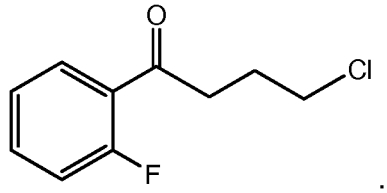


wherein R^{11} is halogen, OH, $-C(O)R^4$, $-OC(O)R^5$, or NR^6R^7, wherein R^4, R^5, R^6, R^7, R^7 and R^{10} are defined above.

16. The process of claim 1, wherein the amine product of formula (I) is (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine:

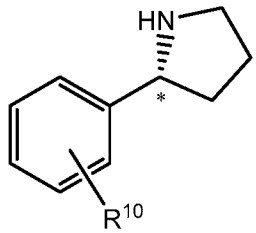


and the ketone substrate of formula (II) is 4-chloro-1-(2-fluorophenyl)butan-1-one:



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17. A process for preparing the compound of formula (III) :



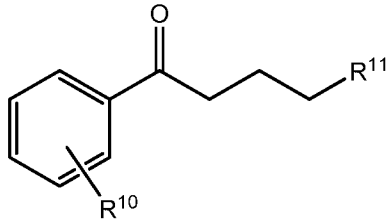
(III)

having the indicated stereochemical configuration at the stereogenic center marked with an * in an enantiomeric excess over the opposite enantiomer,

wherein, R^{10} is Cl, Br, F, CH_3, CF_3, CN, SO_2, $-OCH_3$, or NO_2,

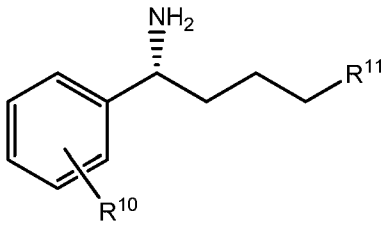
the process comprising:

(a) contacting a ketone substrate of formula:



wherein R^a is halogen, OH, -C(O)R^4, -OC(O)R^5, or NR^6R^7, wherein R^4, R^5, R^6, and R^7 is H or C_1-C_4 alkyl, and R^{10} is as defined above,

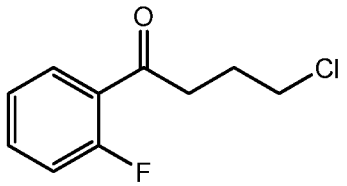
with a transaminase polypeptide in presence of an amino donor under reaction conditions suitable for converting the ketone substrate to an amine product of formula:



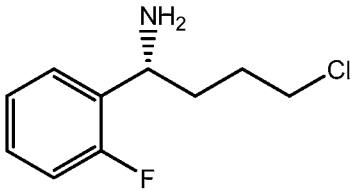
wherein the transaminase polypeptide has at least 80% sequence identity to SEQ ID NO:74 and is capable of converting the ketone substrate to the amine product at a rate that is improved as compared to SEQ ID NO:2.; and

(b) cyclizing the amine product under suitable conditions to form the compound of formula (III).

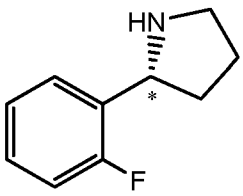
18. The process of claim 17, wherein the ketone substrate is 4-chloro-1-(2-fluorophenyl)butan-1-one:



and the amine product is (*S*)-4-chloro-1-(2-fluorophenyl)butan-1-amine:



thereby forming (*R*)-2-(2-fluorophenyl)pyrrolidine:



in enantiomeric excess.

19. The process of any one of claims 1 to 18, wherein the reaction condition comprises a temperature of 20 °C to 65 °C.

20. The process of claim 19, wherein the reaction condition comprises a temperature of 40°C to 65°C.

21. The process of any one of claims 6 to 12, wherein the reaction condition comprises a temperature of about 50°C to 65°C.

22. The process of any one of claims 1 to 18, wherein the amine product is produced in at least 90% enantiomeric excess.

23. The process of any one of claims 1 to 18, wherein the amine product is produced in at least 99% enantiomeric excess.

24. The process of any one of claims 1 to 18, wherein the amino donor is selected from isopropylamine, alanine, 3-aminobutyric acid, or methylbenzylamine.

25. The process of claim 24, wherein the amino donor is isopropylamine.

26. The process of any one of claims 1 to 18, further comprising the step of removing a carbonyl by-product of the reaction.

27. The process of claim 26, wherein the amino donor is an amino acid and the carbonyl by-product is a keto acid.

28. The process of claim 27, wherein the carbonyl by-product has a vapor pressure higher than water, and removal of the carbonyl byproduct is by sparging with a non-reactive gas or by applying a vacuum.

29. The process of claim 28, wherein the non-reactive gas is nitrogen gas.

30. The process of claim 28, wherein the amino group donor is isopropylamine and the carbonyl by-product is acetone.

31. The process of any one of claims 1 to 18, wherein the reaction condition is from a pH of about 7.0 to a pH of about 11.0.

32. The process of claim 31, wherein the pH is maintained by adding isopropylamine.

33. The process of any one of claims 1 to 18, wherein the reaction condition comprises a solvent of dimethylsulfoxide (DMSO).

34. The process of claim 33, wherein the DMSO is between about 10% to about 40% (v/v).

35. The process of any one of claims 1 to 18, wherein the substrate is present at 5 to 25 g/L.

36. The process of any one of claims 1 to 18, wherein the transaminase comprises an amino acid sequence having a residue difference as compared to SEQ ID NO:2 at one or more residue positions selected from: X4; X5; X8; X18; X25; X26; X27; X28; X30; X41; X42; X48; X49; X50; X54; X55; X60; X61; X62; X65; X81; X94; X96; X102; X117; X120; X124; X126; X136; X137; X138; X146; X148; X150; X152; X155; X156; X160; X163; X164; X169; X174; X178; X195; X199; X204; X208; X209; X211; X215; X217; X225; X230; X252; X269; X273; X282, X292; X297; X306; X321; and X329.

37. The process of claim 36, wherein the residue difference with a transaminase polypeptide of SEQ ID NO:2 occurs at one or more residue positions selected from: X62, X69, X122, X136, X137, X195, X199, X208, X209, X223, X225, X282, and X284.

38. The process of claim 36, wherein the type of amino acid residue at the position of the residue difference is selected from:

X4 is an aromatic residue,
X8 is a constrained residue;
X26 is an aromatic or constrained residue;
X48 is a polar, acidic, aliphatic or non-polar residue;
X60 is an aromatic residue;
X61 is an aromatic residue;
X62 is an aromatic or polar residue;
X65 is an aliphatic residue;
X69 is a cysteine (C) or non-polar, polar, or aliphatic residue
X81 is a non-polar residue;
X94 is an aliphatic residue;
X96 is an aliphatic residue;
X102 is an aliphatic or basic residue;
X122 is a constrained, non-polar or aliphatic residue;
X124 is a polar or constrained residue;
X136 is an aromatic residue;
X137 is a polar or aliphatic residue;
X150 is aromatic, constrained or polar residue;
X152 is cysteine (C), non-polar, aliphatic, or polar residue;
X160 is an aliphatic residue;

X163 is an aliphatic or constrained residue;

X169 is an aliphatic residue;

X174 is an aliphatic residue;

X178 is a polar residue;

X195 is an aromatic or polar residue;

X199 is an aliphatic or aromatic residue;

X208 is cysteine (C) or constrained, non-polar, aromatic, polar, or basic residue;

X209 is an aliphatic residue;

X211 is an aliphatic residue;

X215 is a cysteine (C);

X217 is a polar residue;

X223 is a constrained residue;

X225 is an aromatic residue;

X230 is an aliphatic residue;

X252 is an aromatic or aliphatic residue;

X269 is a constrained residue;

X273 is an aromatic residue;

X282 is a polar residue;

X284 is a non-polar residue

X292 is a polar residue;

X297 is a polar residue;

X306 is an aliphatic residue;

X321 is a constrained residue, and

X329 is a constrained or aromatic residue.

39. The process of claim 36, wherein the amino acid residue at the position of the residue difference is selected from: X4 is Y; X8 is P; X26 is H; X48 is Q, D, V, G, or A; X60 is F; X61 is Y; X62 is T , Y or F; X65 is A; X69 is G, C, T, A, or S; X81 is G; X94 is I or L; X96 is L; X102 is L or K; X122 is M, I, L, V, or H; X124 T, H or N; X136 is Y or F; X137 is T or I; X150 is F, H, or S; X152 is I, L, S or C; X160 is L; X163 is H or V; X169 is L; X174 is A; X178 is S; X195 is F or Q; X199 is W or I; X208 is H, C, G, K, N, Y, D or S; X209 is L; X211 is I; X215 is C; X217 is N; X223 is P; X225 is Y; X230 is V; X252 is F; X269 is P; X273 is Y; X282 is S; X284 is G; X292 is T; X297 is S; X306 is L; X321 is P; and X329 is H.

40. The process of claim 39, wherein the amino acid residue at the position of the residue difference is selected from: X8 is P; X60 is F; X61 is Y; X62 is T , Y or F; X65 is A; X69 is

G, C, T, A, or S; X81 is G; X94 is I or L; X96 is L; X122 is M, I, L, V, or H; X124 T, H or N; X136 is Y or F; X169 is L; X178 is S; X199 is W or I; X209 is L; X215 is C; X217 is N; X223 is P; X269 is P; X273 is Y; X282 is S; X284 is G; X297 is S; X321 is P and X329 is H..

41. The process of claim 36, wherein the transaminase polypeptide has an amino acid sequence that corresponds to the sequence of SEQ ID NO: 58, 72, 74, 80, 86, 96, 98, 100, or 102.