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(54) **COMPOSITIONS, SYSTEMS, AND METHODS
FOR EXTRACTION OF METALS FROM
MINERALS**

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(60) Provisional application No. 63/583,201, filed on Sep. 15, 2023.

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ABSTRACT

Provided herein are methods, systems, and compositions for degrading minerals. The methods, systems, and compositions provided herein involve the use of enzymes having silicase activity and an increased ability to degrade minerals such as silicate materials. The methods, systems, and compositions provided herein may be used to release metal from the amorphous silica. The methods, systems, and compositions provided herein may further involve collecting, extracting, and/or purifying the metal released from the minerals.

Specification includes a Sequence Listing.

contact a mineral material with an enzyme having silicase activity

solubilize and release the metal from the mineral material into a solution

collect the solution containing the metal

further process and/or purify the metal from the solution

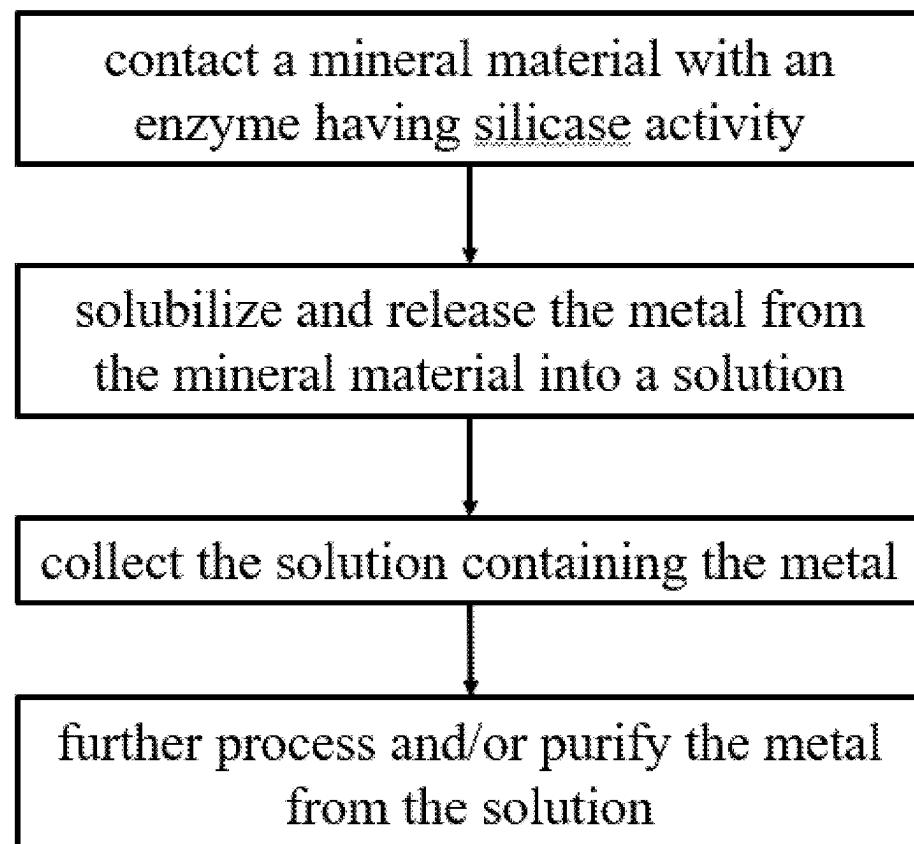
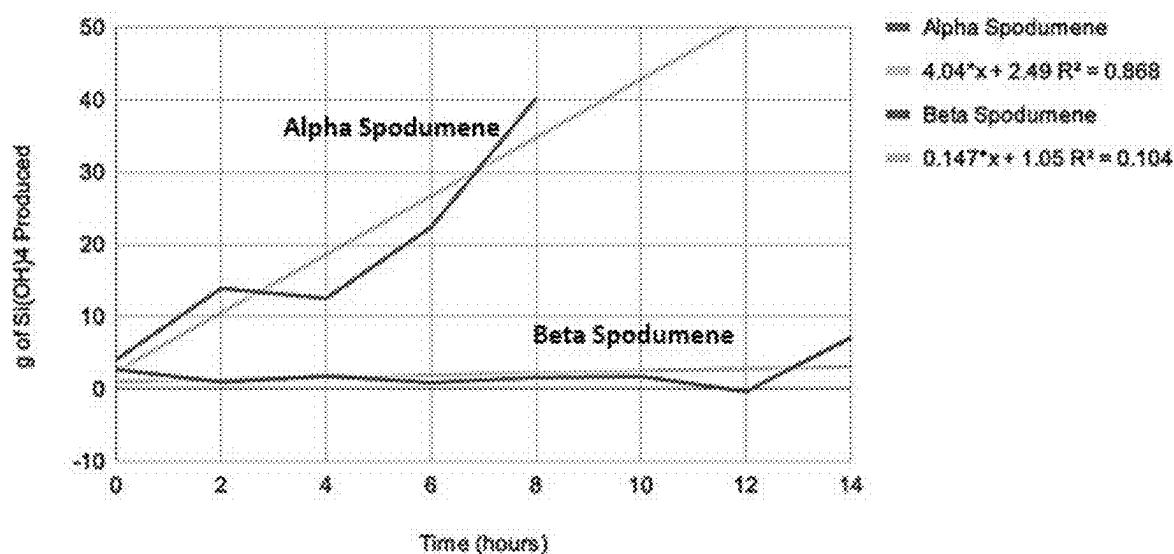


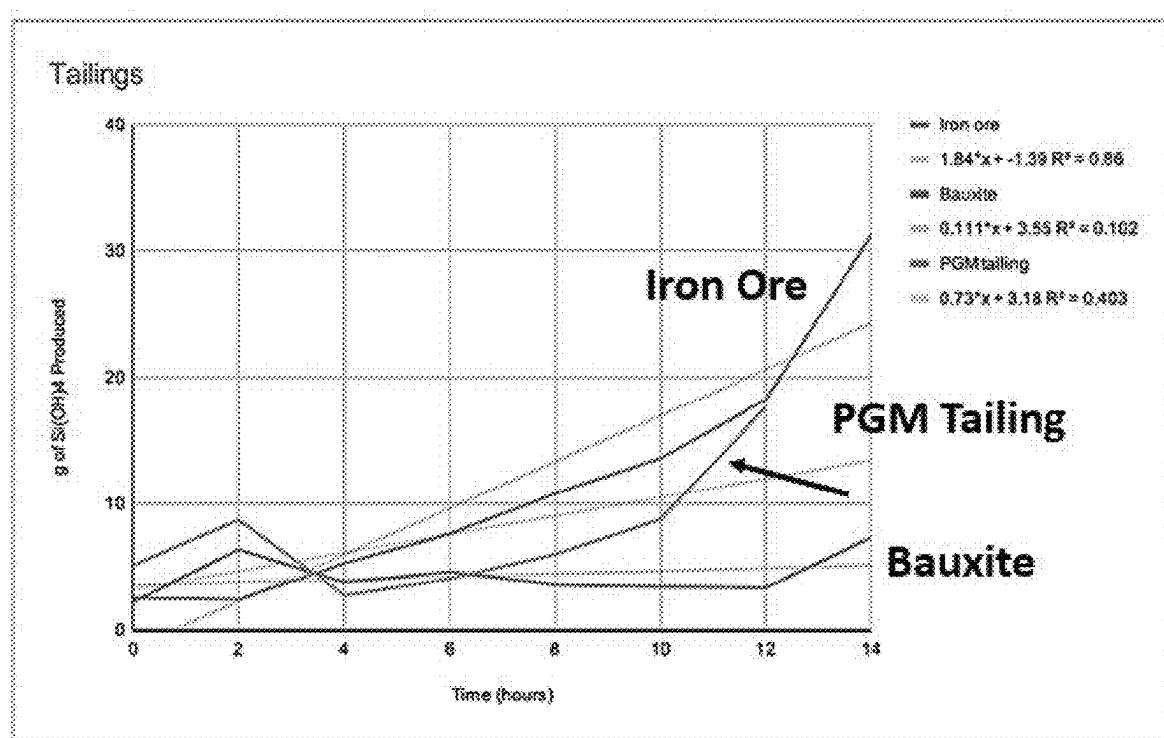
FIG. 1

Alpha and Beta Spodumene



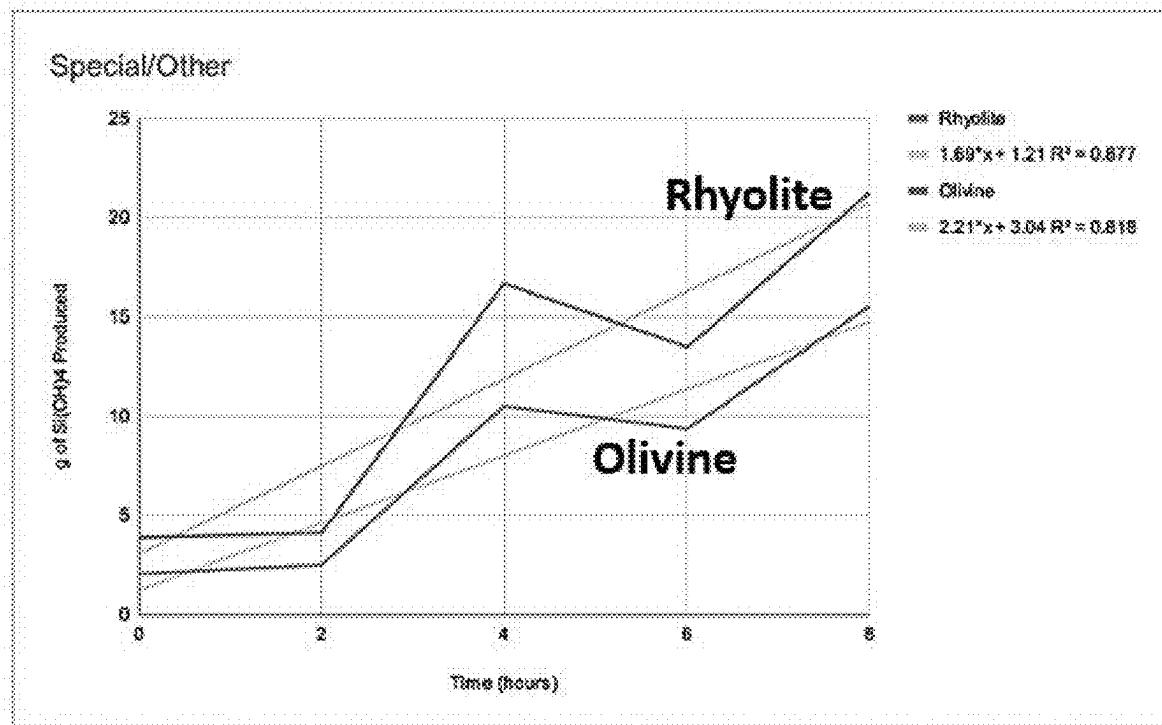
Reaction rates (mg/ml/h)	
Alpha Spodumene	Beta Spodumene
4.04	0.147
Reaction rates (mg/h)	
Alpha Spodumene	Beta Spodumene
28.28	1.029
Reaction rates (g_salicylic_acid_created/g_enzyme/h)	
Alpha Spodumene	Beta Spodumene
336.67	6.431

FIG. 2



Reaction rates (mg/ml/h)		
Iron ore	Bauxite	PGM tailing
1.84	0.639	0.73
Reaction rates (mg/h)		
Iron ore	Bauxite	PGM tailing
12.88	4.473	5.11
Reaction rates (g_salicic_acid_created/g_enzyme/h)		
Iron ore	Bauxite	PGM tailing
80.5	27.956	31.938

FIG. 3



Reaction rates (mg/ml/h)

Rhyolite	Olivine
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1.69	2.21
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Reaction rates (mg/h)

Rhyolite	Olivine
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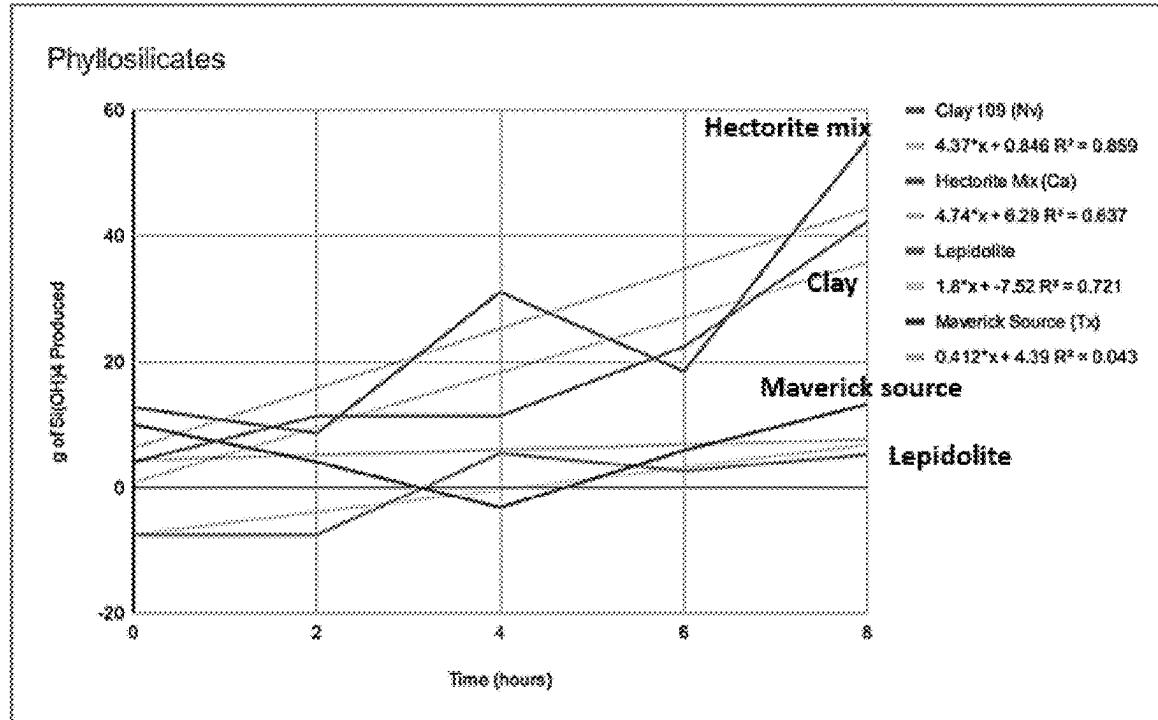
11.83	15.47
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Reaction rates (g_salicic_acid_created/g_enzyme/h)

Rhyolite	Olivine
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140.83	184.17
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FIG. 4



Reaction rates (mg/ml/h)

Clay 109 (Nevada)	Hectonite Mix (Ca)	Lepidolite	Maverick Source (Tx)
-4.37	4.74	1.8	0.466

Reaction rates (mg/h)

Clay 109 (Nevada)	Hectonite Mix (Ca)	Lepidolite	Maverick Source (Tx)
-30.59	33.18	12.8	3.262

Reaction rates (g_salicylic_acid_created/g_enzymes/h)

Clay 109 (Nevada)	Hectonite Mix (Ca)	Lepidolite	Maverick Source (Tx)
-364.17	395	150	20.388

FIG. 5

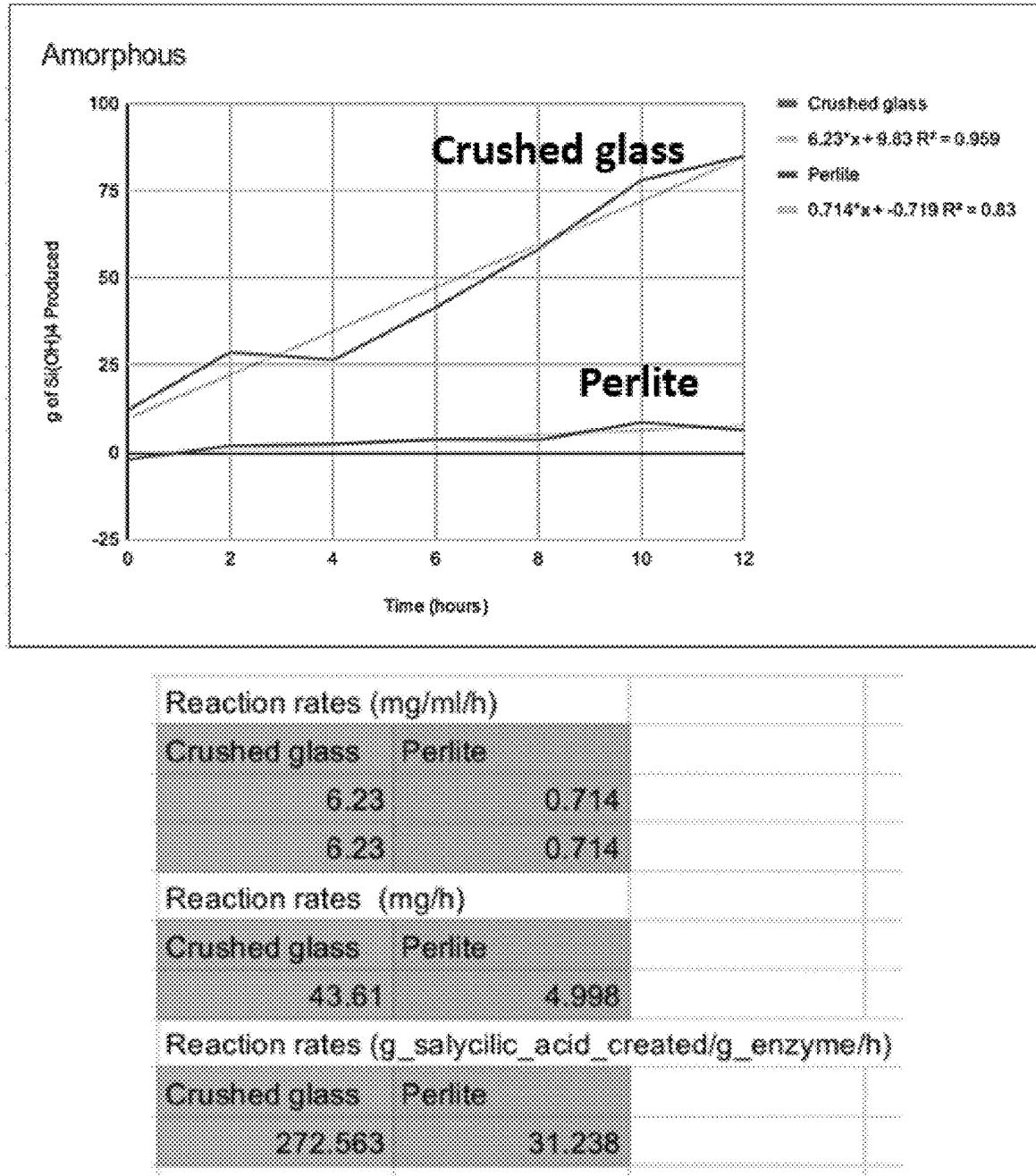
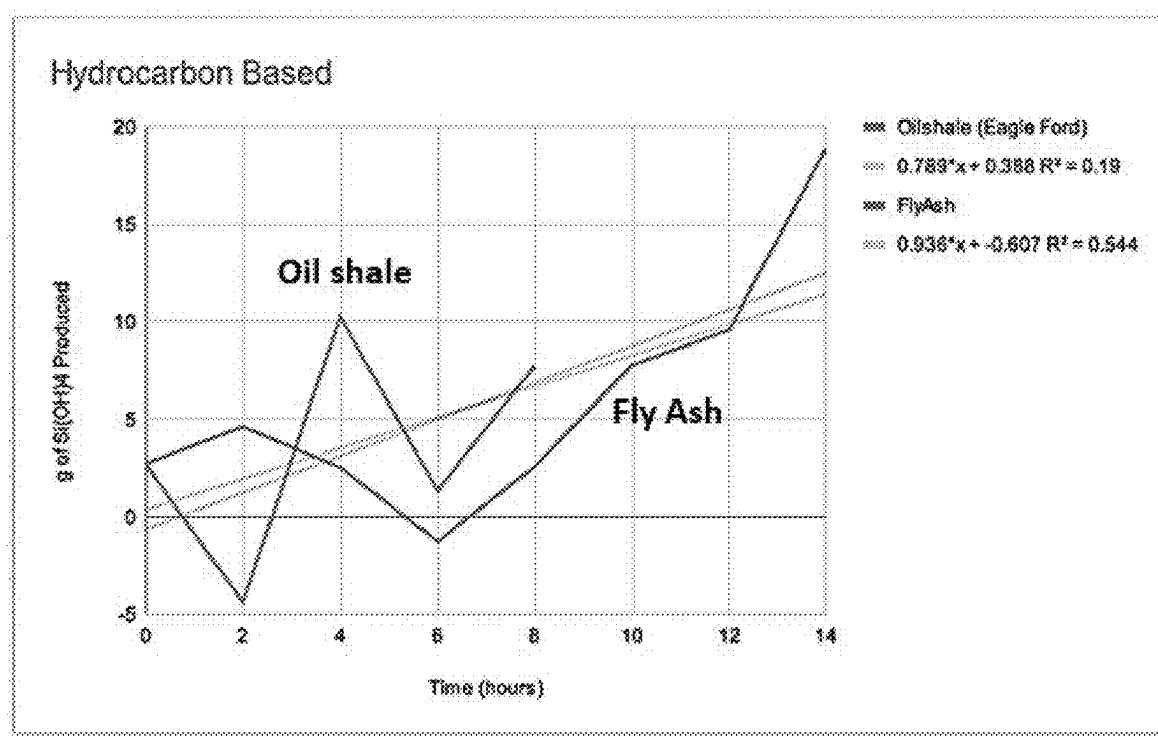


FIG. 6



Reaction rates (mg/ml/h)	
Oil shale	Fly Ash
0.789	0.936
Reaction rates (mg/h)	
Oil shale	Fly Ash
5.523	6.552
Reaction rates (g_salicylic_acid_created/g_enzyme/h)	
Oil shale	Fly Ash
65.75	40.95

FIG. 7

COMPOSITIONS, SYSTEMS, AND METHODS FOR EXTRACTION OF METALS FROM MINERALS

CROSS-REFERENCE

[0001] This application is a continuation of International Application No. PCT/US2024/046780, filed Sep. 13, 2024, which claims the benefit of U.S. Provisional Application No. 63/583,201, filed Sep. 15, 2023, each of which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on Oct. 14, 2024, is named 66122_702_301.xml and is 614,155 bytes in size.

BACKGROUND

[0003] Metals such as lithium, aluminum, iron, nickel, cobalt, strontium, and rare earth elements have vast industrial applications and are in high demand across various industries. For example, lithium is widely used for energy storage, rechargeable batteries, electronic motors, electric vehicles, air mobility, clean energy, energy storage from solar panels, and other applications. Lithium has pharmaceutical applications, such as in lithium-based bipolar disorder treatments. Currently available sources and technologies for obtaining metals for use in industrial applications and products are limited, inefficient, costly, energy-intensive, and harmful to the environment.

SUMMARY

[0004] There is a significant unmet need for compositions, methods, and systems that facilitate access to existing sources of metals, such as to extract and/or collect the metals from their sources, separate them, process them, and make them available for use in various industrial applications and/or products, in a manner that is industrially scalable, efficient, and inexpensive. This is at least in part to meet the demand for such metals in the industrial applications and products in need thereof. Many of the currently available methods and techniques for doing so are limited with respect to efficiency, scalability, and high cost. In many cases, such existing technologies may require performing processes and reactions at high temperatures and pressures that are energy-intensive, costly, and harmful to the environment. The compositions, methods, and systems of the present disclosure address the aforementioned needs and shortcomings, in some aspects, by providing compositions, methods, and systems for extracting, separating, and/or collecting metals from mineral sources, such as mineral materials including solid mineral materials, natural mineral materials, man-made mineral materials, rocks, ores, deposits, and/or other sources in an efficient, inexpensive, and scalable manner. In some cases, the disclosure further provides methods and systems for processing the extracted metals and/or using them in a product (e.g., rechargeable batteries). The extracted metal may be processed and turned into an industrial grade metal, battery grade metal, pharmaceutical grade metal, or other useful forms of metals.

[0005] In an aspect, provided herein is a method of extracting a metal from a mineral, the method comprising:

(a) contacting the mineral material with an enzyme having silicase activity under reaction conditions such that the metal contained within the mineral material is solubilized and released; and (b) collecting the released metal, thereby extracting the metal from the mineral material. In some embodiments, the mineral material comprises an ore, a rock, a natural mineral material, a man-made mineral material, or any combination thereof. In some embodiments, the mineral material comprises a silicate. In some embodiments, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, a tectosilicate, or any combination thereof. In some embodiments, the amorphous silicate is selected from the group consisting of: obsidian, coal fly ash, pumice, glass, and any combination thereof. In some embodiments, the tectosilicate comprises quarts, sand, or both. In some embodiments, the enzyme having silicase activity has a sequence identity of at least about at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more identity with a carbonic anhydrase. In some embodiments, the enzyme having silicase activity has a sequence identity of at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more identity with an alpha carbonic anhydrase. In some embodiments, the enzyme having silicase activity has a sequence identity at least at least about 30%, at least about 40%, about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more identity with a gamma carbonic anhydrase. In some embodiments, the enzyme having silicase activity is derived from an organism selected from the group consisting of: *Methanosarcina thermophila*, *Bacillus licheniformis* CG-B52, *Pelobacter carbinolicus*, *Syntrophus aciditrophicus*, *Methanosarcina barkeri*, *Methanosarcina mazei*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanosarcina acetivorans*, *Kofleriaeae bacterium SLC26A/SuP*, *Thermodesulfotimonas autotrophica*, *Fischerella thermalis/Mastigocladus laminosus*, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosynropha lipolytica*, isoleucine patch superfamily, *Desulfofundulus thermobenzoicus*, *Archaeoglobus veneficus*, *Suberites domuncula*, and any combination thereof. In some embodiments, the enzyme having silicase activity has a sequence identity of at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or more, with a *Methanosarcina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, *Pelobacter carbinolicus* gamma carbonic anhydrase, *Syntrophus aciditrophicus* gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, *Kofleriaeae bacterium SLC26A/SuP* transporter domain-containing protein, *Thermodesulfotimonas autotrophica* carbonic anhydrase/acyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly

protein CcmM, *Methanothrix thermoacetophila* carbonate dehydratase, *Thermosyntrropha lipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, Desulfovibrio thermobenzoicus transferase, *Archaeoglobus veneficus* carbonate dehydratase, Suberites domuncula carbonic anhydrase. In some embodiments, the enzyme having silicase activity has an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-18. In some embodiments, the enzyme having silicase activity is an engineered enzyme, and wherein the engineered enzyme has the sequence of any one of SEQ ID NOS: 19-402, or an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to any one of SEQ ID NOS: 19-402. In some embodiments, the enzyme having silicase activity is an enzyme having at least one amino acid variation as compared to a wild-type enzyme. In some embodiments, the enzyme having silicase activity has a pK_d of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a K_{cat} value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about 50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher. In some embodiments, the reaction conditions comprise a temperature from about 23 to about 85 degrees Celsius (C). In some embodiments, the reaction conditions comprise a temperature from about 45 to about 50 degrees Celsius (C). In some embodiments, the reaction conditions comprise a temperature of about 50 degrees Celsius (C). In some embodiments, the reaction conditions comprise a pH from about 4 to about 11. In some embodiments, the reaction conditions comprise a pH of about 5. In some embodiments, the reaction conditions comprise a pH of about 10. In some embodiments, the reaction conditions comprise contacting the enzyme having silicase activity with a co-factor. In some embodiments, the co-factor is selected from the group consisting of: iron, zinc, copper, nickel, and cobalt. In some embodiments, the co-factor is iron. In some embodiments, the enzyme having silicase activity depolymerizes silicate mineral in the mineral material. In some embodiments, the enzyme having silicase activity cleaves one or more Si—O bonds in the mineral material to generate silicic acid (Si(OH)₄). In some embodiments, the metal is lithium, aluminum, iron, nickel, cobalt, strontium, or a rare earth element. In some embodiments, the metal is lithium. In some embodiments, the metal is iron. In some embodiments, the metal is aluminum. In some embodiments, the metal is strontium. In some embodiments, the metal is released into a solution. In some embodiments, the method further comprises extracting the metal from the solution. In some embodiments, the method further comprises purifying the metal from the solution, thereby generating a purified metal.

In some embodiments, the purified metal has a purity of at least about 80%. In some embodiments, the purified metal has a purity of at least about 90%. In some embodiments, the purified metal has a purity of at least about 95%. In some embodiments, the purified metal has a purity of at least about 99%. In some embodiments, the purified metal has a purity of at least about 99.99%. In some embodiments, the purified metal has a purity of at least about 99.999%. In some embodiments, the purified metal is purified lithium. In some embodiments, the purified lithium is industrial grade, battery grade, or pharmaceutical grade. In some embodiments, the method is performed in situ or ex situ. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity is recombinantly produced in a host cell or in a cell-free production system. In some embodiments, the host cell is a bacterial cell or yeast cell. In some embodiments, the bacterial cell is *Escherichia coli* or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*. In some embodiments, the reaction conditions comprise a rock to liquid ratio from about 1-40% (w/v). In some embodiments, the reaction conditions comprise a rock to liquid ratio of about 30% (w/v). In some embodiments, the reaction conditions comprise a buffer. In some embodiments, the buffer is TRIS, PBS, citrate, monosodium glutamate, or a combination thereof.

[0006] In an aspect, provided herein is a method of extracting a metal from a mineral. The method comprises: extracting a metal from a mineral material, the method comprising: contacting the mineral material with an enzyme having silicase activity under reaction conditions such that the metal contained within the mineral material is solubilized and released, wherein the reaction conditions comprise a temperature from about 23-85 degrees Celsius (C), a pH from about 4-11, a co-factor, and a rock to liquid ratio from about 1-40% (w/v), and further comprises collecting the released metal, thereby extracting the metal from the mineral material. In some embodiments, the reaction conditions proceed for about 1-48 hours. In some embodiments, the reaction conditions proceed for about 48 hours. In some embodiments, the reaction conditions comprise a temperature of about 50 degrees Celsius (C). In some embodiments, the reaction condition comprises a pH of about 10. In some embodiments, the co-factor is zinc, iron, copper, cobalt, or any combination thereof. In some embodiments, the co-factor is iron. In some embodiments, the rock to liquid ratio is about 30% (w/v).

[0007] In an aspect, provided herein is a non-naturally occurring enzyme having silicase activity, the enzyme comprising at least one amino acid variation relative to a wild-type enzyme and having increased ability to release metals from mineral materials as compared to the wild-type enzyme. In some embodiments, the wild-type enzyme is selected from the group consisting of: *Methanosaerina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis*

CG-B52 gamma carbonic anhydrase, Pelobacter carbinolicus gamma carbonic anhydrase, Syntrophus aciditrophicus gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, Alkalihalobacillus *clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, Kofleriaceae bacterium SLC26A/SulP transporter domain-containing protein, Thermodesulfimonas *autotrophica* carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanotherix thermoacetophila* carbonate dehydratase, *Thermosyntrphalipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, Desulfovibrio thermobenzoicus transferase, *Archaeoglobus veneficus* carbonate dehydratase, Suberites domuncula carbonic anhydrase, and any combination thereof. In some embodiments, the non-naturally occurring enzyme comprises an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-18. In some embodiments, the wild-type enzyme is a carbonic anhydrase. In some embodiments, the carbonic anhydrase is a gamma carbonic anhydrase or alpha carbonic anhydrase. In some embodiments, the mineral materials comprise rock, ore, natural mineral, man-made mineral, or any combination thereof. In some embodiments, the mineral materials comprise a silicate. In some embodiments, the mineral materials comprise inosilicates, phyllosilicates, amorphous silicates, tectosilicates, or any combination thereof. In some embodiments, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some embodiments, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some embodiments, the amorphous silicate is selected from the group consisting of obsidian, coal fly ash, pumice, and any combination thereof. In some embodiments, the tectosilicate comprises sand, glass, quartz, or any combination thereof. In some embodiments, the non-naturally occurring enzyme has increased ability to depolymerize silicate mineral in the mineral material as compared to the wild-type enzyme, increased selectivity or specificity toward a mineral structure in the mineral material, or both. In some embodiments, the non-naturally occurring enzyme has increased ability to cleave one or more Si—O bonds in the mineral material to generate silicic acid (Si(OH)₄) as compared to the wild-type enzyme. In some embodiments, the metal comprises lithium, aluminum, iron, strontium, or any combinations thereof. In some embodiments, the metal comprises lithium. In some embodiments, the metal comprises iron. In some embodiments, the metal comprises aluminum. In some embodiments, the metal comprises strontium. In some embodiments, the non-naturally occurring enzyme is recombinantly produced in a host cell or in a cell-free production system.

In some embodiments, the host cell is a bacterial cell or yeast cell. In some embodiments, the bacterial cell is *Escherichia coli* or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*.

[0008] In an aspect, provided herein is a reaction mixture comprising a mineral material and a non-naturally occurring enzyme having silicase activity, wherein the non-naturally occurring enzyme comprises at least one amino acid variation relative to a wild-type enzyme and has increased ability to release metals from the mineral material as compared to the wild-type enzyme. In some embodiments, the mineral material comprises an ore, a rock, a natural mineral material, a man-made mineral material, or any combination thereof. In some embodiments, the reaction mixture has a pH from about 4 to about 11. In some embodiments, the reaction mixture has a pH of about 5. In some embodiments, the reaction mixture has a pH of about 10. In some embodiments, the reaction mixture has a temperature from about 23 to about 85 degrees Celsius (C). In some embodiments, the reaction mixture has a temperature from about 45 to about 50 degrees Celsius (C). In some embodiments, the reaction mixture has a temperature of about 50 degrees Celsius (C). In some embodiments, the reaction mixture further comprises a co-factor of the non-naturally occurring enzyme. In some embodiments, the co-factor is selected from the group consisting of: iron, zinc, copper, nickel, and cobalt. In some embodiments, the co-factor is copper. In some embodiments, the co-factor is iron. In some embodiments, the reaction mixture further comprises a buffered saline solution. In some embodiments, the reaction mixture further comprises an activator co-factor of the non-naturally occurring enzyme. In some embodiments, the activator co-factor is glycine. In some embodiments, the wild-type enzyme is selected from the group consisting of: *Methanosarcina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, Pelobacter carbinolicus gamma carbonic anhydrase, Syntrophus aciditrophicus gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, Alkalihalobacillus *clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, Kofleriaceae bacterium SLC26A/SulP transporter domain-containing protein, Thermodesulfimonas *autotrophica* carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanotherix thermoacetophila* carbonate dehydratase, *Thermosyntrphalipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, Desulfovibrio thermobenzoicus transferase, *Archaeoglobus veneficus* carbonate dehydratase, Suberites domuncula carbonic anhydrase, and any combination thereof. In some embodiments, the non-naturally occurring enzyme comprises an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-18. In some embodiments, the wild-type enzyme is a carbonic

anhydrase. In some embodiments, the carbonic anhydrase is a gamma carbonic anhydrase or alpha carbonic anhydrase. In some embodiments, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, a tectosilicate or any combination thereof. In some embodiments, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some embodiments, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some embodiments, the amorphous silicate is selected from the group consisting of: obsidian, coal fly ash, pumice, glass, and any combination thereof. In some embodiments, the non-naturally occurring enzyme has increased ability to depolymerize silicate in the mineral material as compared to the wild-type enzyme. In some embodiments, the non-naturally occurring enzyme has increased ability to cleave one or more Si—O bonds in the mineral material to generate silicic acid ($\text{Si}(\text{OH})_4$) as compared to the wild-type enzyme. In some embodiments, the metal comprises lithium. In some embodiments, the metal comprises aluminum. In some embodiments, the metal comprises iron. In some embodiments, the metal comprises strontium. In some embodiments, the non-naturally occurring enzyme is recombinantly produced in a host cell. In some embodiments, the host cell is a bacterial cell or a yeast cell. In some embodiments, the bacterial cell is *Escherichia coli* or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*. In some embodiments, the reaction mixture has a rock to liquid ratio from about 1-40% (w/v). In some embodiments, the reaction mixture has a rock to liquid ratio of about 30% (w/v). In some embodiments, reaction mixture has a buffer. In some embodiments, the buffer is TRIS, PBS, citrate, monosodium glutamate, or a combination thereof. In some embodiments, the reaction mixture proceeds for about 1-48 hours. In some embodiments, the reaction mixture proceeds for about 48 hours.

[0009] In an aspect, provided herein is a polynucleotide comprising a nucleotide sequence encoding the non-naturally occurring enzyme disclosed herein.

[0010] In an aspect, provided herein is a vector comprising the polynucleotide disclosed herein.

[0011] In an aspect, provided herein is a method of increasing silicase activity of an enzyme, the method comprising contacting the enzyme with a non-natural co-factor, wherein the non-natural co-factor increases silicase activity of the enzyme as compared to the enzyme in the presence of a natural co-factor. In some embodiments, the non-natural co-factor is copper. In some embodiments, the natural co-factor is zinc. In some embodiments, the natural co-factor is iron. In some embodiments, the method is performed in the absence of the natural co-factor. In some embodiments, the non-natural co-factor does not act as a co-factor for the enzyme having silicase activity in nature. In some embodiments, the method further comprises contacting the enzyme and the non-natural co-factor with a mineral material under reaction conditions such that a metal contained within the mineral material is solubilized and released from the mineral material. In some embodiments, the amount of metal solubilized and released from the mineral material is greater than an amount of metal solubilized and released from the mineral material when the enzyme is contacted with the natural co-factor.

[0012] In some embodiments, the mineral material comprises a rock, an ore, a natural mineral material, a man-made mineral material, or any combination thereof. In some embodiments, the mineral material comprises a silicate. In some embodiments, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, a tectosilicate, or any combination thereof. In some embodiments, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some embodiments, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some embodiments, the amorphous silicate is selected from the group consisting of: obsidian, coal fly ash, pumice, glass, and any combination thereof. In some embodiments, the enzyme having silicase activity is a carbonic anhydrase. In some embodiments, the carbonic anhydrase is a gamma carbonic anhydrase or alpha carbonic anhydrase. In some embodiments, the enzyme having silicase activity is derived from an organism selected from the group consisting of: *Methanosarcina thermophila*, *Bacillus licheniformis* CG-B52, Pelobacter carbinolicus, Syntrophus aciditrophicus, *Methanosarcina barkeri*, *Methanosarcina mazei*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanosarcina acetivorans*, Kofleriaceae bacterium, Thermodesulfutimonas autotrophica, *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosyntropha lipolytica*, Desulfovibrio thermobenzoicus, *Archaeoglobus veneficus*, Suberites domuncula, and any combination thereof. In some embodiments, the enzyme having silicase activity comprises an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-18. In some embodiments, the enzyme having silicase activity is an engineered enzyme, optionally wherein the engineered enzyme has the sequence of any one of SEQ ID NOS: 19-402. In some embodiments, the enzyme having silicase activity is an enzyme having at least one amino acid variation as compared to a wild-type enzyme. In some embodiments, the enzyme having silicase activity has a pKd of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a Kcat value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about 50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher. In some embodiments, the method is performed under reaction conditions. In some embodiments, the reaction conditions comprise a temperature from about 23 to about 85 degrees Celsius (C). In some embodiments, the reaction conditions comprise a temperature from about 45 to about 50 degrees Celsius (C). In some embodiments,

the reaction conditions comprise a temperature of about 50 degrees Celsius (C). In some embodiments, the reaction conditions comprise a pH from about 4 to about 11. In some embodiments, the reaction conditions comprise a pH of 5. In some embodiments, the reaction conditions comprise a pH of 10. In some embodiments, the enzyme having silicase activity depolymerizes silicate mineral in the mineral material. In some embodiments, the enzyme having silicase activity cleaves one or more Si—O bonds in the mineral material to generate silicic acid (Si(OH)₄). In some embodiments, the metal is selected from the group consisting of: lithium, aluminum, iron, nickel, cobalt, strontium, and rare earth metals. In some embodiments, the metal is lithium. In some embodiments, the metal is iron. In some embodiments, the metal is aluminum. In some embodiments, the metal is strontium. In some embodiments, the metal is released into a solution. In some embodiments, the method further comprises extracting the metal from the solution. In some embodiments, the method further comprises purifying the metal from the solution, thereby generating a purified metal, a solid metal complex, a metal precipitate, or any combination thereof. In some embodiments, the purified metal has a purity of at least about 80%, at least about 90%, at least about 95%, at least about 99%, at least about 99.99%, at least about 99.999% or greater. In some embodiments, the method is performed in situ or ex-situ. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity is recombinantly produced in a host cell or in a cell-free production system. In some embodiments, the host cell is a bacterial cell or a yeast cell. In some embodiments, the bacterial cell is *Escherichia coli* or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*. In some embodiments, the reaction conditions comprise a rock to liquid ratio from about 1-40% (w/v). In some embodiments, the reaction conditions comprise a rock to liquid ratio of about 30% (w/v). In some embodiments, the reaction conditions comprise a buffer. In some embodiments, the buffer is TRIS, PBS, citrate, monosodium glutamate, or a combination thereof.

[0013] In an aspect, provided herein is a reaction mixture comprising an enzyme having silicase activity, and a non-natural co-factor.

[0014] In some embodiments, the non-natural co-factor is bound to the enzyme having silicase activity. In some embodiments, the non-natural co-factor increases a function of the enzyme having silicase activity as compared to a reaction mixture comprising the enzyme having silicase activity and a natural co-factor. In some embodiments, the non-natural co-factor is copper. In some embodiments, the natural co-factor is zinc. In some embodiments, the natural co-factor is iron. In some embodiments, the reaction mixture does not contain the natural co-factor. In some embodiments, the non-natural co-factor does not act as a co-factor for the enzyme having silicase activity in nature. In some

embodiments, the reaction mixture further comprises a mineral material and reaction conditions such that a metal contained within the mineral material is solubilized and released from the mineral material. In some embodiments, the enzyme having silicase activity has increased ability to release metals from the mineral material in the presence of the non-natural co-factor as compared to the enzyme having silicase activity in the presence of the natural co-factor. In some embodiments, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, or any combination thereof. In some embodiments, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some embodiments, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some embodiments, the amorphous silicate is selected from the group consisting of: obsidian, coal, pumice, glass, and any combination thereof. In some embodiments, the enzyme having silicase activity has a sequence identity of at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more identity with a carbonic anhydrase. In some embodiments, the enzyme having silicase activity has a sequence identity of at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more identity with an alpha carbonic anhydrase or a gamma carbonic anhydrase. In some embodiments, the enzyme having silicase activity is derived from an organism selected from the group consisting of: *Methanoscincina thermophila*, *Bacillus licheniformis* CG-B52, *Pelobacter carbinolicus*, *Syntrophus aciditrophicus*, *Methanoscincina barkeri*, *Methanoscincina mazei*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanoscincina acetivorans*, *Kofleriaceae* bacterium SLC26A/SuIP, *Thermodesulfobacter autotrophic*, *Fischerella thermalis/Mastigocladus laminosus*, *Thermosynechococcus vestitus* BP-1/*Thermosynechococcus elongatus* BP-1 carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosyntrapha lipolytica*, isoleucine patch superfamily, Desulfofundulus thermobenzoicus, *Archaeoglobus veneficus*, *Suberites domuncula*, and any combination thereof. In some embodiments, the enzyme having silicase activity comprises an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-18. In some embodiments, the enzyme having silicase activity is an engineered enzyme, optionally wherein the enzyme has the sequence of any one of SEQ ID NOS: 19-402. In some embodiments, the enzyme having silicase activity is an enzyme having at least one amino acid variation as compared to a wild-type enzyme. In some embodiments, the enzyme having silicase activity has a pK_d of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a K_{cat} value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about

50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher. In some embodiments, the reaction mixture has a temperature from about 23 to about 85 degrees Celsius (C). In some embodiments, the reaction mixture has a temperature from about 45 to about 50 degrees Celsius (C). In some embodiments, the reaction mixture has a temperature of about 50 degrees Celsius (C). In some embodiments, the reaction mixture has a pH from about 4 to about 11. In some embodiments, the reaction mixture has a pH of 5. In some embodiments, the reaction mixture has a pH of 10. In some embodiments, the reaction mixture further comprises a buffered saline solution. In some embodiments, the reaction mixture further comprises an activator co-factor of the non-naturally occurring enzyme. In some embodiments, the activator co-factor is glycine or an iron ion. In some embodiments, the metal is lithium, aluminum, iron, nickel, cobalt, strontium, or a rare earth element. In some embodiments, the metal is lithium. In some embodiments, the metal is iron. In some embodiments, the metal is aluminum. In some embodiments, the metal is strontium. In some embodiments, the enzyme having silicase activity is recombinantly produced in a host cell. In some embodiments, the host cell is a bacterial cell or yeast cell. In some embodiments, the bacterial cell is *Escherichia coli* or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*. In some embodiments, the reaction conditions comprise a rock to liquid ratio from about 1-40% (w/v). In some embodiments, the reaction conditions comprise a rock to liquid ratio of about 30% (w/v). In some embodiments, the reaction conditions comprise a buffer. In some embodiments, the buffer is TRIS, PBS, citrate, monosodium glutamate, or a combination thereof. In some embodiments, the reaction conditions proceed for about 1-48 hours. In some embodiments, the reaction conditions proceed for about 48 hours.

INCORPORATION BY REFERENCE

[0015] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0017] FIG. 1 shows an example workflow according to the methods of the present disclosure;

[0018] FIG. 2 presents the rate of production of Si(OH)₄ corresponding to reaction rates of degrading silicate minerals (Alpha Spodumene and Beta Spodumene) using an enzyme having silicase activity according to the embodiments of the present disclosure;

[0019] FIG. 3 presents the rate of production of Si(OH)₄ corresponding to reaction rates of degrading silicate minerals (iron ore, platinum group metal (PGM) tailing, and

Bauxite) using an enzyme having silicase activity according to the embodiments of the present disclosure;

[0020] FIG. 4 presents the rate of production of Si(OH)₄ corresponding to reaction rates of degrading silicate minerals (Rhyolite and Olivine) using an enzyme having silicase activity according to the embodiments of the present disclosure;

[0021] FIG. 5 presents the rate of production of Si(OH)₄ corresponding to reaction rates of degrading silicate minerals (Hectorite mix, Clay, a silicate named Maverick source, and a Lepidolite) using an enzyme having silicase activity according to the embodiments of the present disclosure;

[0022] FIG. 6 presents the rate of production of Si(OH)₄ corresponding to reaction rates of degrading silicate minerals (crushed glass and Perlite) using an enzyme having silicase activity according to the embodiments of the present disclosure; and

[0023] FIG. 7 presents the rate of production of Si(OH)₄ corresponding to reaction rates of degrading silicate minerals (Oil Shale and Fly Ash) using an enzyme having silicase activity according to the embodiments of the present disclosure.

DETAILED DESCRIPTION

[0024] Metals such as lithium, aluminum, iron, nickel, cobalt, strontium, and rare earth elements have vast applications across various industries and in different products. The demand for such metals continues to increase, and there is an unmet need for efficient technologies to facilitate access to metal sources, and to extract and collect the metals for use in products and industries in need thereof and to meet demand. As an example, lithium is highly in demand for rechargeable batteries which can be used in a variety of products such as electronics, electric motors and electric vehicles, clean energy industry, solar panels, and beyond. As these industries advance and become more prominent in global markets, so does the demand for lithium. Lithium can be found in a number of sources, including in brine, for example, in brine deposits generated as a result of accumulations of saline groundwater enriched in dissolved lithium. However, brine sources of lithium are limited in abundance and can only be found in limited geographical locations, mostly located in South America.

[0025] Another prominent and abundant source of metals are mineral materials, such as natural minerals (e.g., rock, ore, clay) and man-made minerals that are commonly available across the world in a diverse range of geographical areas, constituting a major primary source of metals. The currently available technologies for extracting metals from solid mineral materials/sources, rocks, and ores are limited, inefficient, costly, and environmentally harmful. An example of such process is acid leaching or acid roasting which involves contacting a mineral with a strong acid (e.g., sulfuric acid) to extract a metal, such as lithium, from the mineral. Acid leaching/roasting usually requires reaction conditions involving highly acidic pH, high temperatures (e.g., 200 degrees Celsius (C) and above) and significant energy consumption (e.g., over 6000 megajoules (MJ) per ton of Li₂O extracted). This process is expensive, energy-inefficient, and harmful to the environment. Therefore, there is an unmet need for improved compositions, methods, and systems to address these shortcomings.

[0026] Provided herein are compositions, methods, and systems that can efficiently extract metals from minerals

(e.g., natural minerals (e.g., rock, ore, clay), man-made minerals) in an efficient, industrially scalable, inexpensive, and environmentally friendly fashion. For example, in some cases, the methods may avoid reaction conditions requiring substances (e.g., highly acidic solvents), high temperatures and pressures, and the like, which may cause harm to the environment and/or increase the cost, energy demands, and/or environmental footprint of the process. In some cases, this is accomplished by performing an enzymatic reaction on a mineral material, to extract and separate a metal (e.g., metal ion/atom) therefrom. The enzymatic reaction may have improved features such as higher reaction rate, specificity toward degrading a mineral material, acting on a certain substrate in the mineral material with high/improved substrate specificity, such that performing the reaction can be industrially scaled and implemented for releasing and collecting the metal. For example, in some cases, the reaction may not require temperatures that are significantly higher than room temperature, pressures significantly higher than atmospheric pressure, highly acidic or highly basic pH conditions, and other conditions that are environmentally harmful and costly. Instead, in many cases, the reactions of the present disclosure may be efficiently performed in near-ambient temperature, near-atmospheric pressure, and/or near-neutral pH conditions, reducing their cost, energy demand, and environmental footprint. The details of such reaction conditions are further elaborated on herein.

[0027] In some cases, the enzymatic reaction may comprise using one or more enzymes and/or co-factors. The enzymatic reaction may comprise an enzymatic degradation/digestion reaction performed with the aid of one or more enzymes and/or co-factors. The enzymes may catalyze the reaction and facilitate the extraction of the metal from the mineral material encasing it. For example, enzymes can be used to degrade, dissolve, and/or depolymerize silicates, and liberate metals (e.g., metal ions) therefrom at near-ambient temperatures without the need for an energy-intensive, high temperature acid separation process. This process significantly decreases the environmental impact of refining lithium and other metals deposited in mineral materials. Provided herein are also enzymes and co-factors with enhanced features and capabilities for performing such reactions. Such enzymes may be semi-synthetic and/or engineered enzymes with features, capabilities, sequences, methods of generation, and methods of use that are presented and further elaborated on in the present disclosure.

[0028] The term “sequence identity” as used herein generally refers to an exact nucleotide-to-nucleotide or amino acid-to-amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Typically, techniques for determining sequence identity include determining the nucleotide sequence of a polynucleotide and/or determining the amino acid sequence encoded thereby, and comparing these sequences to a second nucleotide or amino acid sequence. Two or more sequences (polynucleotide or amino acid) can be compared by determining their percentage (%) of “sequence identity”. The % of sequence identity of two sequences, whether nucleic acid or amino acid sequences, is the number of exact matches between two aligned sequences divided by the length of the longer sequence and multiplied by 100. Percent identity may also be determined, for example, by comparing sequence information using the advanced BLAST computer program,

including version 2.2.9, available from the National Institutes of Health. The BLAST program is based on the alignment method of Karlin and Altschul, Proc. Natl. Acad. Sci. USA, 87:2264-2268 (1990) and as discussed in Altschul, et al., J. Mol. Biol., 215:403-410 (1990); Karlin And Altschul, Proc. Natl. Acad. Sci. USA, 90:5873-5877 (1993); and Altschul et al., Nucleic Acids Res., 25:3389-3402 (1997). The program may be used to determine percent identity over the entire length of the proteins being compared. Default parameters are provided to optimize searches with short query sequences in, for example, with the blastp program. The program also allows use of an SEG filter to mask-off segments of the query sequences as determined by the SEG program of Wootton and Federhen, Computers and Chemistry 17:149-163 (1993). Ranges of desired degrees of sequence identity are approximately 50% to 100% and integer values therebetween. In general, this disclosure encompasses sequences with at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9% sequence identity with any sequence provided herein.

[0029] The terms “variant enzyme”, “enzyme variant”, “modified enzyme”, “synthetic enzyme”, “truncated enzyme”, and “engineered enzyme” are used interchangeably throughout to generally refer to non-naturally occurring polypeptides. The non-naturally occurring polypeptides have been designed and sequences included herein.

[0030] The term “about” or “approximately” generally means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, i.e., the limitations of the measurement system. For example, “about” can mean within 1 or more than 1 standard deviation, per the practice in the art. Alternatively, “about” can mean a range of up to 20%, up to 10%, up to 5%, or up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 5-fold, and more preferably within 2-fold, of a value. Where particular values are described in the application and claims, unless otherwise stated, the term “about” meaning within an acceptable error range for the particular value should be assumed.

[0031] In an aspect, provided herein is a method of extracting a metal from a mineral material (e.g., natural mineral material, man-made mineral material, rock, ore, clay and/or other kinds of mineral material). The method may comprise contacting the mineral material with an enzyme having silicase activity under reaction conditions such that the metal contained within the mineral material is solubilized and released. The method may further comprise collecting the released metal, thereby extracting the metal from the mineral material. In some cases, the mineral material comprises or is a natural mineral material or a man-made mineral material. In some cases, the natural mineral material comprises or is a rock, an ore, or a clay. In some cases, the metal is a metal ion or metal atom. FIG. 1 shows an example workflow according to the embodiments of the present disclosure.

[0032] In some cases, the enzyme comprises silicase activity such as the capability to digest or degrade a silicate. In some cases, the mineral material (e.g., rock/ore/clay) com-

prises a silicate. Silicate may comprise any kind of silicate. In some cases, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, or any combination thereof. In some cases, the mineral material comprises similar or near-similar unit cell geometries. In some cases, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some cases, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some cases, silicate may be an amorphous silicate. In some cases, the amorphous silicate is selected from the group consisting of a tectosilicate, obsidian, coal fly ash, pumice, glass, and any combination thereof.

[0033] In some cases, the enzyme having silicase activity disclosed herein is an engineered enzyme with improved characteristics compared to a wild-type enzyme, such that the modified enzyme exhibits improved ability (e.g., increased reaction rate, increased efficiency, increased ability to degrade silicates, increased specificity for a silicate type) to release metals from mineral materials. The enzyme used in the methods of the present disclosure are generally capable of degrading silicates. In some cases, the enzyme having silicase activity comprises or is a carbonic anhydrase, such as a gamma carbonic anhydrase, or an alpha carbonic anhydrase. In some cases, a wild-type enzyme may be used to perform the methods of the present disclosure. Alternatively or in addition, a modified, mutated, and/or engineered enzyme may be used to perform the methods of the present disclosure. In some cases, an enzyme used in a reaction/process of the present disclosure is a synthetic or semi-synthetic engineered enzyme. In some cases, an enzyme of the present disclosure may be a variant of a carbonic anhydrase, such as a gamma carbonic anhydrase, or alpha carbonic anhydrase. In some cases, an enzyme of the present disclosure may share some similarities (e.g., sequence identity, enzymatic activity) with a carbonic anhydrase. Any combination of wild-type and engineered/modified enzymes may be used.

[0034] In some cases, the enzyme having silicase activity is an engineered enzyme. In some cases, the enzyme having silicase activity is an enzyme having at least one amino acid variation as compared to a wild-type enzyme. In some cases, the enzyme having silicase activity may comprise an amino acid sequence having at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.5%, or greater, sequence identity to an amino acid sequence of a wild-type silicase enzyme. In some cases, the enzyme having silicase activity comprises an amino acid sequence having at most about 95%, at most about 90%, at most about 80%, at most about 70%, at most about 60%, at most about 50%, at most about 40%, at most about 30%, at most about 20%, or at most about 10% sequence identity to an amino acid sequence of a wild-type silicase enzyme. In some cases, the enzyme having silicase activity comprises an amino acid

sequence having about 95%, about 90%, about 85%, about 80%, about 75%, about 70%, about 65%, about 60%, about 55%, about 50%, about 45%, about 40%, about 35, about 30%, about 25%, about 20%, about 15%, or about 10% sequence identity to an amino acid sequence of a wild-type silicase enzyme.

[0035] In some cases, the enzyme having silicase activity is derived from an organism selected from the group consisting of: *Methanosarcina thermophila*, *Bacillus licheniformis* CG-B52, *Pelobacter carbinolicus*, *Syntrophus aciditrophicus*, *Methanosarcina barkeri*, *Methanosarcina mazei*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanosarcina acetivorans*, *Kofleriaceae* bacterium SLC26A/SuLP, *Thermodesulfitimonas autotrophica*, *Fischerella thermalis/Mastigocladus laminosus*, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosyntropha lipolytica*, isoleucine patch superfamily, *Desulfovibrio thermobenzoicus*, *Archaeoglobus veneficus*, *Suberites domuncula*, and any combination thereof.

[0036] In some cases, the enzyme having silicase activity has a sequence identity of at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or more with a *Methanosarcina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, *Pelobacter carbinolicus* gamma carbonic anhydrase, *Syntrophus aciditrophicus* gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, *Kofleriaceae* bacterium SLC26A/SuLP transporter domain-containing protein, *Thermodesulfitimonas autotrophica* carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila* carbonate dehydratase, *Thermosyntropha lipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, *Desulfovibrio thermobenzoicus* transferase, *Archaeoglobus veneficus* carbonate dehydratase, *Suberites domuncula* carbonic anhydrase.

[0037] In some cases, the enzyme having silicase activity has a sequence identity of at most about 80%, at most about 70%, at most about 60%, at most about 50%, at most about 40%, at most about 30%, at most about 20%, at most about 10% or less with a *Methanosarcina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, *Pelobacter carbinolicus* gamma carbonic anhydrase, *Syntrophus aciditrophicus* gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, *Kofleriaceae* bacterium SLC26A/SuLP transporter domain-containing protein, *Thermodesulfitimonas*

autotrophica carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis*/ *Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila* carbonate dehydratase, *Thermosyntrpho lipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, *Desulfofundulus thermobenzoicus* transferase, *Archaeoglobus veneficus* carbonate dehydratase, *Suberites domuncula* carbonic anhydrase.

[0038] In some embodiments, the enzyme having silicase activity comprises an amino acid sequence having at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 84%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-18 provided in Table 1.

TABLE 1

Library of Carbonic Anhydrase Enzymes			
SEQ ID NO:	Name Enzyme	Uniprot Accession number	SEQUENCE
1	γ Carbonic Anhydrase	P40881	MMFNKQIFTILILSLSLAGSGCI SEGAEDNVQAETITVDEFSNIRENP VTPWNPEPSAPVIDPTAYIDPQAS VIGEVTTIGANVMVSPMASIRSDE GMPIFVGDRSRNVQDGVVHLALE TINEEGEPTEIDNIEVEVDGKEYAVY IGNNVSLAHQSQVHGPAAVGDD TFIGMQAFVFHKSKVGNNCVLEPR SAAIGVTIPDGRYIPAGMVVTSQ AEADKLPEVTDDYASHTNEAV VYVNVLHAEQYKETS
2	γ Carbonic Anhydrase	T5H8M4	MKLSSKLILGLTVSSLAGKFLEKL LIQDNVSPNITASFNQEADIPDIDA SSYIHHFASVIGSVVIGRNVFIGF SSIRGDVGLKIFISHDCNIQDGVV LHGLKNYEYNSPVTEHSVFKDRE SYSIYIGEKVSLAPQCQIYGPVRID KNVFVGMQSLVFDAYIQEDTVIE PGAKIIGVTIPPKRFVVSAGRVISNQ EDANRLPEITDSYPYHDLNSKMT SVNLELAQGYKKEERQWKL
3	γ Carbonic Anhydrase	Q3A3H4	MIEKNVVTDFCSEASEPVIDASTY VHPLAAVIGNVILGKNIIMVSPTA VVRGDEGQPLHVGGDSNIQDGV VIHALETEMNGKPVAKNLYQVD GRSYGAYVGRVSLAHQVQIHG PAVVLDDTFVGMKSLLVFKSFVG KGCVIEPGSIVMGVTVADGRYVP AGSVIRTQEDADALPEIGADYPFR AMNPGVVHVNTALAKGYMVQ GN
4	γ Carbonic Anhydrase		MIGKNVLTDFAARASEPVIQGSFTF VHPLAAVIGNVILGDNIMVSPGA SIRGDEGQPLVVGSDSNVQDGVV IHALETELDGKPVKNLVEVDGK KYAVVVGVRVSLAHQVQVHGP AVIRDDTFVGMKSLLVFKSYVGSN CVIEPGVLLMGVTVADGRYVPA GSVVKTQEADALPVITDDYPM KEMNKGVVLHVNKAARGYLA GS
5	γ Carbonic Anhydrase	Q2LUP7	MRFNKQFTILILSLSALLGSGCI SEGEAEGNVQTQGITESEFSNIRE NPVTPWNPPVAPVIDPTAFIDPQ ASVIGNVTIGASVNMVSPMASIRSDE EGMPIFVGDRSRNVQDGVVHLALE ETIDEEGEPVENNIVEVGGKKYA VYIGENVSLAHQAOVHGPASVG NDTFIGMQAFVFHKSKVGNNCVLEPR PTSAIIGVTIPDGRYIPAGMVVT SQAEADNLSEITDDYASHTNEAV VYVNVLHAEQYKNA

TABLE 1-continued

Library of Carbonic Anhydrase Enzymes			
SEQ ID NO:	Name Enzyme	Uniprot Accession number	SEQUENCE
6	Carbonic Anhydrase	Q467M8	MALLLSSLAITLAGSGCVSQGEGA EEGENIEAEEVEANVEESNIRANP VTPWNPPEPTEPVIDTAYIHPQAS VIGDVTIGASVMVSPMASVRSDE GMPIFVGDECNIQDGVLILHALET VNEEGEPVEENQVEVDGKKYAV YIGERVSLAHQAQVHGPSLVGND TFIGMQTFVFKAKIGNNCVLEPTS AAIGVTVPDGRYIPAGTVVTSQD EADKLPEVTDDYAYKHTNEAVV YVNTNLAEGYNA
7	α Carbonic Anhydrase	Q8PSJ1	MKKYLWGKTCLVVSLSVMVTA CSSAPSTEPVDEPSETTHEETSGGA HEVHWSYTGTGPEHWAELDSE YGACAQGEQSPINLDKTEAIDT DTEIHVHYEPSSFTIKNNNGHTIQA ETTSOKNTIEIDGKEYTLVQFHFH IPSEHEMEGKNLDMELHFVHKNE NDELAFLGVLMKAGEENEELAQ LWSKLPAEETTEENISLDIDESIDLNV LLPESKEGFHYNGSLTTPCSEGIV KWTVLSEPITVSQEIQIDAFAEIFP DNHRPVQPWNDRDVYDVITE
8	α Carbonic Anhydrase	AOA0N9WRG3	MKRSHLFITSITLASVVTLATAPA ASAASFLSPLQALKASWSYEGET GPEFWGDLDEAFAAACSNGEQSP INLFYDREQTSKWNWAFSYSEAA FSVENNNGHTIQANVENEEDAGGLE INGEAYQLIQFHFPHTPSEHTIEETS FPMELHLVHANHAGDLAVLGVL MEMGNDHEGIEAVVWEVMPEEEG TAAYSISLDPNLFLPESVTAYQD GSLTTPPCSEGVKWTVLNDTISIS ETQLDAFRDIYPQNYRPVQELGD REIGFHYH
9	Carbonate dehydratase	Q5WD44	MKINRIFLALLFSLALTLAGSGCV SQGEAEGDGESESADTVESEVESNI RANPVTPWNPEPTEPVIDSTAYIH PQAAVIGDVTIGASVMVSPMASV RSDEGTPIFVGDETNIQDGVLVH ALETVNEEGEPVESNLVEVDGEEK YAVYVGERVSLAHQSQIHGPAY VGNNDTFIGMQALVFKANVGDCN VLEPKSGAIGVTIPDGRYIPAGTV VTSQAEADELPETVTDYGYKHT NEAVYYVNVLNAEGYNA
10	Kofleriaceae bacterium Carbonic Anhydrase	Q8TMW3	MRTNRVRTAGASKWGVSDIRT TLRERWSEIAAQGLSYHDVLAGL TVATVAIPLNVALAISAGLPPSAG LLAGAVGGLFAAAFGGSNFQVS GPAALALNMVFGVVAKFGLGGA AAAALVCGIVGIALGVSGLGLKYS NLMPKLVLAGFTTGVLGKLLDQ QIPILLGSDLALWHMLSNNFWAME WLREVEWFSVVCGLLVAWIIVG LAHLKSFPSALLGIVLATLIAYEL DWNVARVGEVDSLALALPSIA DGTSWFALIAVALPLAVLSSVES LISAKAVDAMANGKSGYSANTE LFGQCVGSIASALVGGMPLAGV VVRSSVNQQSGARTRLAAMCHA VFLGIVAYFFGGLLGVIPVAALA GLLVVIATRLMKSYFFSALREN KLHALAFLAAAIGTLLGYLISGLA LGCALVYIAHKLAHRPVKDAPVL RPSPTIRAVISOAGERAQDHTPSI DEQAKWSRHRVTRPKIHPTAYV

TABLE 1-continued

Library of Carbonic Anhydrase Enzymes			
SEQ ID NO:	Name	Uniprot Accession number	SEQUENCE
			HPTASVIGNVELGRENVIAADTS VRADEGAPFYVGDRSNVQDGVV IHALDKWVMVDGRRWAWIG SDVSLAHQALVHGPMIGRSRFIG FKAIHVDSVVGEGCFIGLAVVV GVEIPAGKRVPNGWIVDSPEKVR ELPDVEHAHAFNEDVVQVNRG LVVAYSRHVPTEELPQRTPSDPL FHLKPL
11	<i>Thermodesulfitimonas autotrophica</i> Carbonic Anhydrase	A0A7Y6PMB4	MRLPKMLTVAVGATLCFTAGC ASTQTTATKEPAK PANIRPNVVT TFNPPTETPVIAKDAYIDPLASVI GNVEIGSKVYVAPFASVRGDEGQ PIYYGEGSNVQDGGVHLALETED NGKPVEKNLVEYGGKYAVYIG KHVSLAHQAQVHGPAVLDDGTF VGMQALVFKAQVGKNCVIEPGA KLLNGVKVPDGRYVPAGTVVTT QAQADKLPVITDAYPLKLNKKG VLHVNEQLAEGYLKAQEGATGE TKSH
12	<i>Fischerella thermalis/ Mastigocladus laminosus</i> JSC-11 Carbonic Anhydrase	A0A3N5BJ34	MAVRSIAEAAPPPTPSRNLAEPIT HPSAFLHSFSNIIGDVRIGANVIIA PGTSVRADEGTPFYIGENTNLQD GVVVHGLEKGRVIGDDRQEYSV WIGKNCNITHMALIHGPACYIGDD CFIGFRSTVFNARVGAGCIVMMH ALIQDVEIPPGKYVPSGAITNQQ QADRLPDVQADDKEFAHHVVGI NQALRAGYLCAADSKCIRAIRDE LNNSYTSIEVDVLLERSDEVSSNSL GAETVEQVRYLLQQGYHICTEH VDQRRFRGWSWTSCCKPIEARSLG EAIAALEACLRDHSGEYVRLFGI DPKGKRVLLENI I QRPDGVVQAS SSLKAPAYSSNNNGSYNGNGSSRL SSETIDQIRQLLAGGYKIGTEHVD ERRFRGWSNQSCPPIESSSPGDVV AALEDCMDNHQGEYVRLIGIDPK AKRRVLESIIQRPNGPVSTPSSKST ATTTSYAAASGTTATATSSKLSSEA IEQLQOLLAGGFKISAEHVDGRR FRTGSWASCQIQANSIREAIAL EGYMNEYQGEYVRLIGIDPKVKR RVLELIVQRP
13	<i>Thermosynechococcus vestitus</i> BP- 1/(<i>Thermosynechococcus elongatus</i> BP-1 Carbonic Anhydrase	G6FUV4	MLRKNPRTSWNSQESMPSVATT AYVDETAVVIGDVRIGERVVVGP CASIRADEATPIVISEECNVQDGA IFHGLKGSSIKLGKKVSVAHGAV VHGPMTIIGDESFIGFNAVVHAST VGERCFIGHRALVMGVKLKDGS FVPHGSVIDTQDKADALGPVPDS LKGFNAEVVVEVNCEFAKGYRSL R
14	<i>Methanothrix thermoacetophila</i> Carbonic Anhydrase	Q8DKB5	MSENLRNPPQGDKPVIDPSSYVD PTAVIIGPVTIGKNCYIGPHTVIRA DEVDEKTGKVAPVIIGDNVNLDQ GVIIHALAGTSVEVGSNTSLAHG CVVHGPCKIEAGCFIGFRAVVFK TVIGSGSMVKHGAIVEGVNIPSG KLVPTGEIITSEDLVVLKEVGQA EKEFMQEVVHVNMELAHGYKK
15	<i>Thermosyntrropha lipolytica</i> Carbonic Anhydrase	A0B700	MSENLRNPPQGDKPVIDPSSYVD PTAVIIGPVTIGKNCYIGPHTVIRA DEVDEKTGKVAPVIIGDNVNLDQ GVIIHALAGTSVEVGSNTSLAHG

TABLE 1-continued

Library of Carbonic Anhydrase Enzymes			
SEQ ID NO:	Name	Uniprot Accession number	SEQUENCE
			CVVHGPCKIEAGCFIGFRAVVFK TVIGSGSMVKHGAIVEGVNIPSG KLVPTGEIITSEDLVVLKEVGQA EKEFMQEVVHVNMELAHGYKK
16	<i>Desulfofundulus thermobenzoicus</i> Carbonic Anhydrase	A0A1M5PQH8	MSENLRNPQGDKPVIDPSSYVD PTAVIIGPVITGKNCYIGPHTVIRA DEVDEKTGKVAPVIIGDNVNLDQ GVIHALAGTSVEVGNSNTSLAHG CVVHGPCKIEAGCFIGFRAVVFK TVIGSGSMVKHGAIVEGVNIPSG KLVPTGEIITSEDLVVLKEVGQA EKEFMQEVVHVNMELAHGYKK
17	<i>Archaeoglobus veneficus</i> Carbonic Anhydrase	A0A6N7IXF4	MLQKSPAVSWKPAGYPRISLAF VHPTAVLIGEVVIHDAIIPLAI RADEGFPIIIVGENTNIQDGVIIHCL KGRVEIGRRVSLAHGAVIHGPC VIGDETFVGFRAVMINSRIGRGCF IDHGALIEGVEIPDGKYIPGLTRV SSQEVSRLAGITEQQKDFAAEV LAVNGELKEAMQVIITSRDDAYP GQ
18	γ Carbonic Anhydrase	F2KNT3	MRWAIILTTVLFAALLLGCAAEK GAIEPLETPEEKASNINHANPITEW NDEQTMPDIDPTAFVHPYATVIG DVHIGKYVCISPHASVRGDEGMP IYVGDYSNIQDCVVIIHALETRDA EGNPIEKNLVGGDGKKYAVYIA DHVSLAHQSQVHGPAYVGSFTI GMQALVFKAKVGKNCVIEPGAK VIGVTIPDGRYVPAGMAVTNQSV ADNLPEITEDYPFKHTNEAVVHV NIELAKGYNAMFGGESTEGTEGE GGH

[0039] In some embodiments, an enzyme of the present disclosure is an engineered enzyme. In some cases, the engineered enzyme may have the sequence of any one of SEQ ID NOS: 19-402 provided in Table 2, or an amino acid sequence having at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 84%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity to any one of SEQ ID NOS: 19-402.

[0040] In some embodiments, an enzyme of the present disclosure is an engineered enzyme.

[0041] In some cases, the engineered enzyme may have the sequence of any one of SEQ ID NOS: 403-464 provided in Table 2, or an amino acid sequence having at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 84%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity to any one of SEQ ID NOS: 403-464.

TABLE 2

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
19	MQEITVTRFENIRPSVTPWNPEPRYPEIHPAYIDPAAVVQGD VKIGANVLVMANAVIRADEGYPIYIGDNSSVQDNVVLHAETR DADGRDLEENIVRVRGDERYAVVVGDNVLAHNQVHGPAAV GDNTFVGMNALVFRSRVGADCVLAPLAAAIGVTVPDGRYVPA GTVTTTQAAAALPAVTPDHPFAGLNARVVAVNVVALAKGYL ALS
20	MSKIYLAFCVCGPEQWHRFPTANGLRQSPIDIIPS KAVYDPKLR PLELKYPSTCLHLNNNGHSFQVEFDDSQDKSVLKGGLDGIY RLIQFPHWGSVDGQGSEHTVDKKKYAAELHLVHWNTKYGD

TABLE 2-continued

Library of modified or engineered enzymes

SEQ. ID.	NO	Sequence
		FGKAVQQPDPGLAVLGIFPLKVGRHKPELQKLVDALSSIKHKDTLVDFGMDPSCLMPTCPDWYTSGSLTTPLSESVTWIIKKQPVEDHDQEQRSLLFTSEGEKEKRMVDNRPLQPLMNTRRSSFR
21		MKRSLLVATIYGYPCEPWNDHQSEWGYGETNGPKTWTGKHFPEANGLQLQSPIDIKTEETQHDPNLRPLTLKYDPSTAKEELNNNGHSFQVTFVDDTDSSSLTDGPIGTGTYRLKQFHFHWGSDDKGSEHTVDGAKYPAELHLVHWNTQASFGEEASAKPDGLAVVGVLFKIGKEHPGLKLLTDALYMRVFKGTAQFTNFNPKCLLPTSLDWTYPSGSTTPPLSECVTWIVLKEPISVSSAQMEKFRNLLFTSEGEKACCMVDNYRPQQPLKG
22		MQEITVTNNYNNIRPSPVTWSNPTPKLPKIHPHTAYIDPAAVVQGDVTIGENVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALETVDADGNVLEENVVTGDKKYAVYIGKNVSLAHQAQVHGPAAVGDNFTIGMQAQFVFSVVGKDCVLMPLAAAIGVTIPDGKYIPAGTVTTQEEADKLPEVTPDHFPANTNKAVVAVNVELAKGYLALA
23		MRFFECSCSPFPSQLOSSFLTHLLILYTLSSSVEASSRNNYQWSYDSDVPGPDFWGLVEKDWWMCRKGRQLQSPIDIQPDRLLFDA5VKPVRLDKLPLVLSFVNQGMVRIIGYSTKKEPSVNITNGPLGYRYRVQRIDFHMGGRKGEMSEHTINGRRFPMEVQLVAFNTDLYPNFTAAKSPPHIAILSVLVDFAQTNQELTKLTIATASISYKQQRVQMDFEPWRLLPFTRDITIYEGSLTSPGCHETWIWIINLQPIFIREHFEWSHLYHTMGAEKVPVAPNYRKIQTENNRLVRTNIQHKV
24		MQEITVLEFSNVTKNEVTPWNPKPKPVTVIDPTAYIDPTATVIGDVТИGANCYIAASAVIRADEGKPIVIGDRSNVQDGVVVLHALESVDDGGKVRREDNNVIHGDNWYAVYIGENVS LAHQSQVHGPAYVGDDSFVGMKSLVFVKSIVGNSNCVIEPEAAAIGVTIPDGKYIPAGTVTTQAEADKLPEVTPDYAFYTQVAAVVTVNVNLCRAYRNLSS
25		MQEITVVAEYSNITKNEVTPWNPKPKPVTVIDPTSYVDPNATVIGDVТИGANCYIAASAVIRADEGKPIVIGDRSNVQDGVVVLHALESVDDGGMGIGDNNVVVEGDKYYAVYIGNNVVLKAHQSQVHGPMAVGDDSFVGMQS FVFN SIVGNSNCVIEPEAAAIGVTIPDGKYIPAGTVTTQAEADKLPEVTPDDAAFTKNAAVVNVNVGLAKAYREKA
26		MQEITVVAEYSNITKNEVTPWNPKPKPVTVIDPTSYVDPNATVIGDVТИGANCYIAASAVIRADEGKPIVIGDRSNVQDGVVVLHALESVDDGGMGIGDNNVVVEGDKYYAVYIGNNVVLKAHQSQVHGPMAVGDDSFVGMQS FVFN SIVGNSNCVIEPEAAAIGVTIPDGKYIPAGTVTTQAEADKLPEVTPDDAAFTKNAAVVNVNVGLAKAYREKA
27		MQEITVTRYENIQPSPVTPWNPKPKPVTVIDPTSYVDPNATVIGDVDTI GANVMSIPNASIRSDEGYPIKIGDNSNVQDNVVLHALETVDADGKRIEENIVKVGDEEYAVYIGDNVSLAHQAQVHGPAAVGDNTFVGMLNVFRSRVGKNCVLEHNAAAIGVTIPDGKYIPAGTVTTQEEADKLPEVTPDHFPYKLNERVVKVNVELAKGYLALAK
28		MLRKNPSPGHIPQVAETAFIDPTAII CGKVIIEDYVFIGPYAVIRADEVNQBGDMEAIVIKRDTNIQDGVVIHSKAGAAVTIGERSSSIAHRSIIHGP CWVGDDVF1GPNNSVVFNAKIGKGCVIRHNSVVDGLDLPENHVPPMNTNIGPFDLESISKVPPPEYSAFSESVVSANHELQGYRRIANEL
29		MGRSCLTLSRQAKVSANFLKRNVRMASWGYKT DNGPSQWHIGYPVAKTGTQRQSPVNIVPSTVTRD LLLKALKYEYTPSMIKMIN TGSSWRMDFSPEGNSNLSCGPGLDYDVKLQHMHAHWDGKAGR GSEHTMDGKMFDAELHIVHYNSKYGEP AIALDKPDGLAVLGMFIK TGTWSRSHPEFDKLCDNLKLIEMKGESLQLQEYLN PANCLPN NKTFTVY PGSLPFEVSTWVFLPEIEMSSKQLD S M RALKI GDTADCGCMVNNYRPCCALGNRKRIVKV
30		MSLVPPIERETARRGRPPVAPRALGALLALASAVAATPAIAWQS GIAV PDPNAMPQWRYTGERGPEHWS ELDPSYGACAH TDQSPV ALT ESM AVA VACRPLR PEYRSGPLVYVINDG RPLR LGYD RGS

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	HLLVEGLSYELVELRFHAPAEHVINGSRADAELOLIHANNRGD IAVVAVALMPGPRANSMLQRLLKHPRLSGESFYGRNVGVNP LFLLPGRKDYFAYRGSVTRPPCTEGVRWYVLRTPLEVADADL QRLVGFMEPNARPLQPLGGRRVTKACGP
31	MQEITVTRYENIRPSPVTPWNPEPKLPKIHPTAYIDPAAVVQGD VTIGANVMVSANASIRSDEGYPIYIGDNSVQDNVVLAETV DENGNVIEENVTVGDKKYAVAIGDNVSLAHQAQVHGPAG DNTFIGMQAFVFRSRVGKNCVLAPLAAIIGVTVPDGTYIPAGK VVTTQEEAAKLPKVTPDHFPANTNAAVVKVNVALAKGYLAL A
32	MQEITVHYSNVTKNEVTPTNPKPVIDPTSYVDPNATVIG DVTIGKVNLLIAANAVIRADEGAPIVIGDRSTVQDGVVHLAES VDDAGKVRDENVVIEGDEEYAVYIGKDVSLAHQSQVHGPAR VGDHSFVGMSLUVFKSIVGSNCVLEPEAAAIGVTVPDGKYIPAG GTVVTTQEEAAKLPVTPDHFPADLVARVVVKVNVELAKGYLAL LS
33	MAKTSFFPVVLSFIFILSYTMCINANATGKHEVDDEEPFSYLLG TAEGPYKWGTLLKPDWEICNTGLFQSPINFRNKTVKVTKH1PHF TPNYKIASATIMNRGHDIKLQWEGDAGSITLNGTVYKLIQCHW HTPSEHKVDGQSLAMEAHLIHQSVNGKLIAVIGILFNIGPPDPFL NELIHAKVVDHKGVGLVDPNKLGVKAEPFYRYIGSLTIPP CTEGIVWNVLHQPRTVMSMDQMMALRNAVNNDGFQANARPAQ GLRRRPVYLMV
34	MQEITVTTYNIRPSPVTSWNPEPRLPKIHPTAYIDPAAVVTGD VTIGANVLVMANAVIRADEGAPIVIGDNSVQDNVVLAETV DADGNVLEENVVLLVGDERYAVYVGDNVIAHNAQVHGPAG GDNTFVGMSNALVFRSRVGANCVLAPLAAIIGVTIPDGTYIPAG KVVTTQEEAAKLPVTPDHFPADLVARVVVKVNVELAKGYLAL S
35	MQEITVTDYSNITKNEVTSTNPKPPTVIDPTSYVDPNATVGD VTIGKVNMSIDSASIRSDEGRPIVIGDRSNVQDGVVHLAESVD DDGEILEDNVVVEVGDENYAVYVGKVNLSAHQSQVHGPAAVG DDSFIGMQAFVFKSKVGSNCVIEPDAAAIGVTVPDGKYIPAGT VVTTQEEAAKLPVTPDHFPADLVARVVVKVNVELAKGYLAL KEKS
36	MLAFVALVSLIFLGVQAQHGADWTYSEGMLDETHWPEEYPD CGGQRQSPIDLQRRKVRFNPDQLQPLLELTGYGDSQGSPFLMTNN GHTVQITLPPTMQLTADPGAVYKATQMHYHGGASYELSGS EHTIDGIRRIEMHLVHYNAKYESYDVAKD KPDGLAVMAAFV EIEEYAENTHYSSLISHLANIRYPGQTTLTDFDILDMLPGDMY HYTYNGSLTTPCCTQVWRWFVMSDSVKISKAQVIKLENSVM NHQNQTLHNGYRKTQPLHSRVVEANFPYFPNTMPGEGLRA KD PAREFGSRRHCYAWRGWQPAAAALEGHGEPRRRWRPLE EASTPPP
37	MQEITVTRYNNIRPSPVTPWNPEPKLPKIHPTAYIDPAAVVQGD VTIGANVMVSANASIRSDEGYPIYIGDNSVQDNVVLAETV DADGKRIEENVVKVGDKDYAVYVGDNVSLAHQAQVHGPAA VGDNTFTIGMOSFVFRSIVGKNCVLEPLAAIIGVTVPDNTYIPAG KVVTTQEEADKLPKVTPDHFPANTNAAVVKVNVALAKGYLA LA
38	MKNRRRIKPEIMTKFLFAILTLFFFSGCQFFDKNKSTEIESKPSS HEKWSYTGESGPEHWAELDQAVCDGQHQSPVNISIDIDIKPGK LIQESLDLSYQEVTTIKSITNNNGHTIQYNFANDSNLVSLLHDKQY KLKQFHPHSPSEHTINGTHSPLIEHLVHSEATNSYIVIAILVQQ GEPDDADFDLEKYLPIVNGETKEINSKYFGSTFPPEMYGKDTL NIYTYEGSLTTPCCTESVLWVVIKDPAYASSSQIVMLQKLMPK DNYREVQSLNNGRLIYNEIIIEDDISVLNH
39	MTKLSFAVIGPENWHRYCDQAQGDQQSPINIQTDRVHDPTL RPLTLRYDPSTAREIVNNNGHSFNVEFEDSTDRSVLRGGPLTDY RLTQFHFPHWGSSDDHGSSEHTVGDGVKYAELHLVHWNTKYGD FGEAASKPDGLAVGVFLKVGRHNPRLQKILDALHAIKTKGK RASFTNFDPSVLLPGCLDWTYSGSLSLTTPLSESVTWIVLREPIS VSPSQMAKFRSLLFTS

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
40	MQEITVTTYNNIQPSPPVTPWNPEPKLPKIHPTAYIHPKAVVQGD VTIGKVMVMSANASIRSDGYPIVIGDNSNVQDNVVLHALET DENGEIEENIVTVDGDKYAVYIGKNVSLAHQAQVHGPAIVG DNTFIGMQAFVFNNSVGSNCYLAPLAAAIGVTVPDGTYIPAGK VVTTQEEAKLPKITPDHPFYNTNAAVVKVNVALAKGYLALS
41	MQEITVDEFSNITKNEVTPFPNPKPPTIPVIDPTAYVDPNATVGD TIGKNCYIAPFASIRADEGKPIVIGDNSNVQDGVLVHalesidd GGKLIEENVVVEGEKRYAVYIGKNVSLAHQSQVHGPARVGDD SPVGMNSLVFNNSKVGNSNCVIEPFAAAIGVTVPDGYVPAVTVV TTQEEADKLPEITDDYAFAGTNEAVVKVNVLCKAYREKA
42	MQEITVLEYSNTKNEVTSQNPKPVTPVIDPTSYVDPNATVGD DVTIGENCCLVWPPTAVIRADEGRPIVIGNESSVQDGVLVHLES VDDGGELEDNVVVVGDKNYAVYVGKVNVLAHQAQVHGPA RVGDDSFVGMKSLVFKSDVGSNCVIIEPFAAAIGVTVPDGYIIP AGTVVTTQEEAAQLPEVTPDHAEYTTQATVVTVNVELNEAYR NQR
43	MTEKLWGYDSHNGPARWFQICVPAQGKRQSPIDIOPDKAVLD STLKPLELKYPDSTARTRIVNVGHSPHFVFEFDSTDKSVLQGGPLT GSYRLRQPHFWGKKDDVGSEHVLGVFKYSAELHVWHWNA DKYSSFVEAAHEPDGLVVLGVFLQIGDQHPLQRLTDALYAV RFKGTKBQFACFNPKCLLPTSRHYWTYPGSLTTPPLSESVTWI VLRPISVSRQMEKFRSLLFTSEDDERIHMVNNFRPLQPLMNR TVRSSF
44	MYHNALPLTPITVFYVAAHKFGYDAEDGPSTWRGVQCQTGKR QSPVDIARAFETIEIAPLPLQFLNQDLYLTGHITHLANNGHTVVGSGF ERWGEKRPYISGGGLNLNTYQLSQFHFWSQNDTGSEHTIASL HYPGEELHLVH1KEPSDEVNTIAVVAFTKLDDHAGSLHNLK PYVHNIRMPNTELVVPGSVSLLPEHRENFYRYEGSLTTPGCD EVVVWTLADPIAVTSPQMGAFHQVHFASGKTGHNWRPTQP LNGRKILFRPSITLRTFKSGGAMLKPVFFQPFISIWLGYIYHIIISVF
45	MQEITVTKNNIRPSPVTPWNPEPKLPEIHPPTAYIDPAAVVRGD VKIGENVLVMANAVIRADEGYPIYIGNNSSVQDNVVLHALET DENGNRIEENIVLVDGKEYAVYIGDNVVIAHNAQVHGPAAVG DNTFIGMNSLVFRSRVGSNCVLEPLAAAIGVTVPDGTYIPAGK VVTTQEEAKLPKITPDHPFANLNDRVVKNVALAKGYLAQA
46	MKMFPLDCILIPCCYFFFISTPHFANADVHIADWDHDHHHTHP DNWEGMCKEGQRQSPIDIIITNETTKEKWGOFIFHGYERKLSM NVKNNRHSMVVEDFDNDKKYEDIWIRGGGLGESKFRFAQLHFH WGSTDNGSEHTIDGKASPMEMMHIVHWNLDVGKDVEATEK DAYNSLEVLGVLFKLGKFNKDYDAIFNAARKVEKENTNATLE KDVRRLDLPEDTNAFYRYVGSLLTPPCNQIVMWTFIKDPIEIS QEOLDIMRKGSYRLLEGENDVRYIANNYRSTQTLYERDVLIDIT HIVHLACNSKGSTRYHPEEGSEGFGVHNTGNSLNSPIVTCLMFY LSIFVISMRLLH
47	MQEITVTRYENIRPSPVTPWNPEPRRPVIHPPTAYVDPLAYVQG DVTIGANVMVMSANASIRSDGYPIVIGDNSNVQDNVVLHALET RDADGRVLEENVVVVGDERYAVYVGDNVSLAHQAQVHGPA AVGDNFTIGMQAFVFRSRVGVKNCLIEPLAAAIGVTVPDGTYV PAGKVVTQEEAKLPVTPDHFPATTNAAVVAVNVALAK YLALA
48	MQEITVLEFSNITKNEVTSFNPEPKPTTPVIDPTSYIDPEATVGD TIGANVLIWPTAVIRADEGKPIVIGDRSNVQDGVLVHalesvd DGGKVRDNVVIEGDEYYAVYIGKNVTLAHQSQVHGPARVG DDSFVGMKSLVFNSDVGENCVIEPFAAAIGVTVPDGYIIPAGT VVTTQAEAAATLPEVTPDYAFYTQVAAVSVNVGLCQAYKNE A
49	MQEITVDEFSNVTKNEVTPWNPKPTTPVIDPTSYIDPEATVGD VTIGKNCYIAPFAVIRADEGSPIVIGDDSTIOPDGVLVHalesvd DGGKLIEDNVVLEGDDQYYAVYIGRNVVLAHQSQVHGPARVG DDSFVGMKSLVFNSTVGSNCVLEPNAAAIGVTVPDGYIIPAGQ VVTTQAEADNLPEVTTADDAYYTKVAAVVKVNVALCEAYREQ S

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
50	MQEITVTKYNNIRPSPVTPWNPEPKLPEIHPHTAYIDPAAVVQGD VTIGANVMVSANASIRSDEGYPIKIGDNSNVQDNVVLHALET DADGKELTENVTVGDEKYAVVGDNVSLAHQAQVHGPAA VGDNTFIGMQAFVFRSTVGKNCVLAPLAAAIGVTVPDGRYIPA GLVVTTQEEADKLKPVTPDHFPYNTNAAVVAVNVALAKGYL AQA
51	MSRPVALTIIFGYEDKNQWHCCYPSAQGNRQSPINIDIKKTVYD PKLKPPLSVDYPATAKIGILNNNGHSFNVEFEDSQDKSVLKCGPL TGTYRLIQFHFHWGATDDKGSEHTVDGVKYPSELHLVHN VKYSSFAEAASKPDGLAVLVGFLKVGDHNAAQLKLTDALYM VRFKGTKAQTGFNPCKLLPASLDYWTTSGSLTPPLLESVTW IVLKEPIVSSEQMAKFRSLLFTSEGEAECCMVDNYRPPQLKG R
52	MQEITVTTYTNIKSPVTSWNPTPKYPKIHPHTAYIDPAAVVQGD VTIGENVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET DANGNVIEENVTVGDKKYAVVGNNVSLAHQAQVHGPAA VGDNTFIGMQAFVFRNSRVGKNCVLEPLAAAIGVTVPDGTYIPA GEVVTTQEEADKLKPVTPDHFPANTNAAVVKVNIELAKGYLA QA
53	MQEITVTVYTNIQSPVTSWNPTPKLPKIDETAYVHPQAVVQG DVTIGKVMISANASIRSDEGYPIVIGDNSNVQDNVVLHALET VDADGKBEIEENVTVGDKKYAVVIGDNVSLAHQAQVHGPAA VGDNTFIGMQAFVFRNSVKGDCVLEPLAAAIGVTVPDGTYIPA GKVVTTQEEAKLPVTPDHFPYKTNAAVVKVNVELAKGYL ALA
54	MRLRNPSGHIAVIDQTAYIDETAIICGKVIIEANVFVGPYAVIRA DEVNEQDMEPIVIKRDTNIQDGVVIIHSKAGAAVTIGERSSIAH RSIIHGCPWCVGDDVFIGFNSVVFNAKIGKGCVIRHNSVVDGLD LPENFHVPPTMTNIGPDFDLNSISKVPEYESAFSESVVSANHEL QGYRRIANEL
55	MQEITVLEFSNITKNEVTPWNPKPSTPVIDPTSYVDPNATVGD VTIGKNCYIAASAVIRADEGKPIVIGDRSNVQDGVVHLAESV NDGGKIREDNVVLLEGDKYYAVVIGKNNVLAHQSQVHGPAAV GDDSFVGMKSLVFKSIVGSNCVIEPEAAAIGVTVPDCKYIPAGT VVTTQEEADKLPEITPDYAFYTQVAAVVKVNVDLCEAYRNKA
56	MQEITVTTYTNIKSPVTPWNPEPKLPEIHPHTAYVDPAAVVQGD VTIGKVMVSANASIRSDEGYPIKIGDNSNVQDNVVLHALET DEDGNIIEENVTVGDEKYAVVGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFRNSVGKNCYLAPLAAAIGVTIPDGTYIPAG TVVTTQEEAKLPKMTPDHGPYKTNAAVVKVNIALAKGYLS S
57	MQEITVDNFSNITKNEVTPTNPKPSTPVIDPTSYVDPNATVGD VTIGKNCNLIAANAKIRADEGKPIVIGDRSSVQDGVVHLAESVN DDGKVLEDNVVLLEGDEYYTGYIGKNNVLAHQSQVHGPAAVG DDSFVGMKALVFKSIVGSNCVIEPGAAAIGVTVPDCKYIPAG TVVTTQEEADKLPEITPDYPLSDANEAVVKVNVLCEAYRNK S
58	MQEITVTVTYENIRPSPVTPWNPEPKLPEIHPHTAYIDPLAYVQGD VTIGENVMVSANASIRSDEGYPIYIGNNNSNVQDNVVLHALET DKNGKVLEENVTVGDKKYAVVGDNVSLAHQAQVHGPAA VGDNTFIGMQAFVFRSTVGKNCYLAPLAAAIGVTVPDGTYIPA GKVVTTQEEAKLPKMTPDHGPYKTNAAVVNVNLCEAYRNKA ALA
59	MASKLLRRNLLFTIQRKRAVKSSVTRNSIPWLRKSAPSSNWGYN GSELDPEDWPKBYQCCNCQSPIDIDLSSLKVTSSESLPLESYPD NPKYMWMDGKNCNRIRHWRGETALSGGPLKGTYELVQLHFWGS AEGKGAAEHLVNGESVEGEAHLVHWNPKYGSIREALKHQDGIA VVGVFLKEADDGAESPLOSSILNRFPTLSKFMEKYIFENDVFNVG NLIPKNSDFICYDGGLTTPPLTECVQWIVLLKPLVVTKREMDIF RSLEGSFGNNFTDNFRPCQPVGDRVVSSSFEPEK
60	MKITALSVCWGPNEYEDHRQKWSNLYPPIAKGNRQSPINIVPGS AVYDSSLKPLKLKYDPSTCLEIWNNNGHSFQVTFEDTDDKSVLS GGPLTDKYKLQFHFHWGKTDDHGSEHTDGVVKYAAELHLV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	HWNNAKYGSFGEAADKPDGLAVVGIFLKIGREKGEFKLILDALD SIKTKGQTTFTNFDPSCLPFSCPDIYWTYSGSLTTPPLSESVTWI ILKQPIEVHDHQLEKFRTLLFTSEGEKEKRMVDNFRPLQPLMN RTVRSSFR
61	MQEITVTVYNNIRPSPVTPWNPEPKLPKIHPTAYVHPLADVTG DVTIGANVMVSAHASIRSDEGYPIYIGDNSNVQDNVVLHALET VDAAGKEIEKNIVTVDKKYAVYIGDNVSLAHQAQVHGPAAV GNNTFIGMQAFFNSVVGNCVLEPLAAGI GTVVPDGTYIPAG KVVTTQEEAAKLPKVTPDHFPFYNTNKAVVVAVNVALAKGYLA LA
62	MQEITVMEYSNVVKNEVTSTNPKPPTPKIDPTSYVDPNATVIG DVEIGKNVLIAPFAIRADEGSPIVIGDNSNVQDGVVHLAESV DDGGKINEDNVVVKGDKKYYAVYIGKNVNLAHQAQVHGPAY VGDDSFVGMKALVFKAKVGNNCVIEPNAAAIGVTPDGKYPAG AGTVVTTQEEADKLPEITEDYPFSTANEVvvVKVNVLAKAYR NLA
63	MQEITVTKFENIRESPTVTPWNPEPKKPEIHPTAYIDPAAVVIGD VTIGANVLVAARAVIRADEGSPIVIGDNSVQDNVVLHALET DEDGNIIEENVVEVGDKRYAVYIGDNVLAHNAQVHGPAAVG DNTFVGMSLVRSGVANCVLEPLAALGVVEVPDGYYVPG KVVTTQEEAARLPAVTPDHFPADLVARVVAVNVALAKGYLA LS
64	MAAHGAHWGYSGEAGPENWAKLTPEYGAUTGKQSPINLTG FIEAEELKPIKIAKAGAKEIVNNNGHTVQVNYQPGSFITIDGQQFE LKQFHFHAPSENTIEGKSFPLEAHFVHANSKGELAVVAVMYYE GKENPLIATAKAWQMPPEKAGEKNELKSTISAESLLPKDKDYRF SGSLTTPPCSEGVRWIVLKNYSTVSKEQVEQFLHTMHANNRP VQPVNARKVLK
65	MKSTLITAGFVCEQNPDHWYRQYPVAKGHHQSPIDIISHTAKYD PSLKPLSISYDPSTSLEI LNNNGHSFQVTFEDSNDKSVLKGGPLDG VYRLKQPHFHGWGKHKHSVGEHTVNGKSFPSLELHVHWNAV YESFGEAALEENGLAVGVFVLELGEHNAELQKITDALYMVRF KGTKTTSFCFNPKCLLPSLDYWTYSGSLTTPPLSESVTWIVLR EPISISPSQLAKFRSLLFTSEGEKAVCMVDNFRPLQPLMNRSVR SSFR
66	MQEITVTRYENIRPSPVTPWNPEPKLPPIHPTAYIDPKAVVQGD VRIGANVMVSAHASIRSDEGYPIVIGDNSNVQDNVVLHALET NENGEVIEENVVVEVGDERYAVVGDNVSLAHQAQVHGPAAV GDNFIGMQAFFNSVRSRVGKNCVLA PLAAGI GTVVPDGTYIPAG KVVTTQEEAAKLPKVTPDHFPANTNAAVVKVNVALAKGYLA LS
67	MSQIWSYTGDTGPEFWPELCEEYTAAQFPLQSPIALSYETQA LEEALKETYVEQNIYVQKVNETMHFVPUAASFVFAQNRYY LTDIHFMPSHEVINKQQAPLEFHLVHKDEGGNPLVCNFLDFL VENEDKCKNNDKLILEADKDKEQQLNPEI FL PENITYFHYEGSL TTPPTQGPVQWFVFDQIGVMSRSFIEDFKTSLLPNRNPLQNKNN QRPIFYKK
68	MKGTPSIAVF CYRQENWDHI FPIAAGNRQSPINIDTRKAKYDS SLKPLNLKYDPTSTSLEI LNNNGHSFQVNFEDTDNKSVLKGGPLT GSYRLRQPHFHGWGASDDKGSEHTVDGKVYASELHVHWNA VKYSSFAEAASKPDGLAVGVFVKGQHNPLQKITDALSSIK HKTQALFSNFDPSSLLPSCPDYWTYSGSLTTPPLSESVTWIVL KQPINVSPAQLAQFRSLLFTSEGEKACCMVDNYRPLQPLKGRQ VRASF
69	MSARLVTWGYKEDNGPHQWCIFFPEANGECQSPIDIITSETK HDPSLKPLSLSYNPATSK EII NVGHSHFVN FEDNDNRSV LKG GPLTDSYRLTQPHFHGWGKNDRGSEHTIDKKYSS ELHV HWNTKYGDFGKAVQQPDGLAVLGIFLKVKGKHNPSLQKVL DTLNSIKTKGKQTTFTNFDPSTLLPGCLDYWTYSGSLTTPPL LESVTWII LKEPISVSSEQMAKFRSLLFTSEGEKACCMVDNYRPLQPLKGRQ RPLQPLMNRTV RSSF
70	MQEITVSAFSNIRKNEVTPWNPEPSTPVIDPTAYVDPQATVIGD VTIGANVLVSASASIRADEGRPIVVGDRSNVQDGVVHLAESV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	DDGGEVIEDNVVLEGGELYAVYGENVSLAHQSQVHGPALV GDDSFVGCKSLVFKSKVGSNCVLEPGAAAIGVTIPDGKYIPAG TVVTQSQAEDNLPEVTPDYAYTTNEAVVKVNVALAEAYRN LS
71	MRLSAIFVTGWCPEKQDHNYQWGYGKHNQPEHWKDHFP ANGLQQSPIDQIISKVQHDPAKPLSLSYDPATARRILNNNGHSF NVEFDDSDQDAVLKGPGPLTGSYRLIQFHFHWGSADGQGSEHT VDKKKYAELHLVHWNNAVKYESFAEAAKQENGGLAVLGFLK VGEHNAQLQKLLDALSIAKHKGKQTAFTNFDPSCLLPACPDY WTYSGSLTTPLSESVTWIVLKEPIVSSEQMAKFRSLLFTSEGE TACCMVDNYRPPQPLKGRKVRAASF
72	MQEITVTRFENIRPSPVTSWNPEPKRPVIDPTAYIDPAAVVQGD VTIGKNMISANASIRSDEGYPIYIGDNNSVQDNVVLHALET DADGKRLEENVVKGDKKEYAVAIGDNVSLAHQAQVHGP GDNSFIGMQAFVFRSRVGKNCVLA PLAAAI GVEVPDGKYIPAG KVVTTQEEDAKLP EVTPDH PYATTNAAVVKVNVELAKGY L S
73	MARTVLCIGFCSPNKEWQYDHAKNGPEWKEYFPIADGDQOSP IEIKTKVEKHDSKLPLSISYNPATAKEILNVGHFSHVNPE NRSVLKGGPLSDSYRLSQFHFWGSDDHGSEHTVDGVKYAS ELHLVHWNNAKYGKFG EASKKPDGLAVVGIFLKVGSAKPG KVVDALGSIKTKGKQASFTNFDP SVLLPGCLDYWTYDGS LTT PLLESVTWIVLKEPIVS VSPSQMAKFRSLL FSS GEAACMV DNY RPPQPLKGRQVK
74	MPLPNARERRRDWRAVTTAAAVFGIVVPIGTGLHAEDWGYS GTHGPRFWAKTPGWEACAGTAATERQSPIDIDEV VADKELTR LQADLK ETPVAVVNN NGHTIEEYRLGSSL TLAGVRYDLKQFHF HTPSEHTV RGAHAAMEMHVVFKDAGSDKL VVI GVLFEV VKA NAFLS ALMADGLPGKRG EEVDAHS RPV NVAQAL TDT SQYYT Y PGSLTT PPCE N V T F V L K G R P E M S A E Q L A A F H R V L G D N A R P V Q K L N H R V A H E T V S G A R
75	MTSLOQYNNIRPNLAGDYPQIDPTALIDPSAQIIGNVKIDRVFV GPLTVIRADQRPNGKVSPIQIDREANIQDGVI IHTDPGASVI IGS KTTVAHGAIIHGPCTIGQECFIAIRASLYKVTLEDHVWL GIGAIA KLVTLHSFTRVPAGAVIRD SP EV L P L R L I T D K E R K Y M E E V W A A NSLLRTD Y L E L R D K V E S I R S T A K K G
76	MQEITVTRYENIRPSPVTPWNPEPKRPKI HPTAYIDPAAVV TGD VTIGENVLV MANAVI RADEGYPI V I G D N S V Q D N V V L H A E L T V DENGNRIE EN VV R V G D E D Y A V Y V G K N V L A H N A Q V H G P A A V G D N T F V G M N A L V F R S R V G K N C V L A P N A A I G V T V P D G T Y V P A G L V V T T Q E E A A K L P K V T P D H P Y N T N K A V V A N I A L A K G Y L A A
77	MQEITVTKFENIRPSPVTPWNPEPKRP EI HPTAYD PLAYV QGD VTIGANVM ISANAS IRS DEGY PI V I G D N S V Q D N V V L H A E L T V DANGNE I KEN I V T G D E K Y A V V G D N V L A H Q A Q V H G P A A V G D N T F I G M Q A F V F R S V V G K N C V L A P N A A I G V T V P D G K Y I P A G K V V T T Q E E A D K L P E I T P D Y A F Y T Q N E T V V K V N V A L C E A Y R E K A
78	MQEITVHHHHITKNEVPTNPKPTTPVIDPTSYIDPNATV G D V T I G K N V L I A P F A S I R A D E G S P I V I G D R S N V Q D G V V L H A E L T V DGGK V I E D N V V L E G D K Y Y A V Y I G R N V T L A H Q A Q V H G P A A V G D S F V G M K A L V P K A K V G K N C V L A P N A A I G V T V P D G K Y I P A G K V V T T Q E E A D K L P E I T P D Y A F Y T Q N E T V V K V N V A L C E A Y R E K A
79	MLSLSALLAATAFSASASAPHEYSGEAGPAHWASLTPEFGA CTGKNCSPVNLNTGFVDAKLKPIKFAYQAGGKSIVNNNGHTQV NYQPGSSITLDGVTFELKQFHFHAPS SENQIDGQSYPLEAHLV DKEGNLAVVALMFQGEANPELA KLWQAMPEKANQS QPLKA SIRADQLLP ENRYYRFSGSL TTPPCSEGVRWIVMKQ PITASAA QIEEF EHVMHHPNNR PVQPLNGKTIVTG LSS
80	MQEITVVFNSNEVTSQNPRPTTPVIDPTSYIDPNATV G D V T I G K N C Y I A A S A S I R G D E G R P I H I G D R S N V Q D G V V L H A E L T V DGEV L E D N V V L E G D E D Y A V Y I G K N V L A H Q S Q V H G P A R V G

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	DDSFIGMKSLSVFKSIVGSNCVLEPAAAIGVTVPDGKYIPAGTV VTTQAEADKLPEVTPDYAYYTNAAVVAVNVALCEAYRNQS
81	MLKIVSAFTGYPENWHRQFDKAAGSQSPIDIQTKDIQHDPCLQPLKLSYDPSTCLEIWNNGHSFLVQFEDSGDKSVIEGGPLEGVYRLKQFHFWGAKDSEGESEHTVDGVKFPCELHLVHNWNAKYGSFAEAAASKPDGLAVVGVLKIGKEAHEFQKLLDALDAIKTKGKQTTFTNFDPSCLLPACRDYTDGSLTTPPLLESVTWIVLKEPSVSPGQMAKFRSLLFTSEGEAACCMVDNYRPPQPLKGRHVRA SF
82	MQEITVLSFSNVQKNKVPTPTNPKPPTPVIDPTAYIDPDATVIGDVТИGKNCFIGAFAVIRADEGKPIVIGDRSNVQDGVVHLALESVDDEGKVIEDNVVVKGDKEYAVYIGKNVSLAHQSQVHGPARGDDSFVGMNATVPNSIVGSNCVIEPFAAAIGVVVPDNTYIPAGTVVTSQEEADKLPEVTPDYAYYTQVAAVVKVNVLCEAYREKA
83	MKITFLSAVCGWNYQDPERWHDDFPIAKGERQSPIDIDLKVQRDPSLKPLSPKYDPSTSRRILNNNGHSFNVEFEDSEDKSVLKGGLTGSYRLKQFHFWGATDDKGSEHTVDGVKYASELHLVHNAKYGDGEAASKPDGLAVVGVLKIGRHHEEFQKLLDALPAIKHKDTLVDPGSFDPSCLMPTCPDYWTYSGSLTTPPLLESVTWIVLKQPIEVHDQLEQFRTLLFTSEGEKEKRMVDNFRPLQPLMNRTVRSSFR
84	MQEITVDEFNSVTKNEVTPWNPKPSTPVIDPTSVIDPDATVIGDVТИGANLIGPNAVIRADEGKPIVIGDGSNVQDGVVHLALESVD DAGKVIEDNVVKGVGNNSYAVYVGKNVVLAHNAQVHGPAAVGDDSFVGMNAFVFNSIVGSNCVIEPNAAAIGVTVPDGKYIPA GTVVTQEEADKLPEITEDYEYYTKVAEVVEVNVALCEAYKEKA
85	MQEITVLLFSNVTKNEVTTTNPKPPTPVIDPTSVIDPDATVIGDVТИGANVMISANASIRSDEGRPIVIGDRSNVQDGVVHLALESVD DDGKIIBEENVIHGDEDYAVFIGKDVS LAHQAOQVHGPAYGDDSFVGMQSFVFKSKVGSNCVIEPEAAAIGVTVPDGKYIPAGTVVTTQEEADKLPEITPDYFTTNAEVVSVNVKLCEAYRNLKTTQAEAEKLPDVTPDHQAQYTTQAAVVTVNQLTKAYRNLK
86	MQEITVULKFSNVTKNEVTVTNPKPPTPVIDPTSVIDPDATVIGDVТИGKVLIAANATIRADEGKPIVVGDRSTVQDGVVHLALESVD VDTGKVIEENVVIKGNEDYAVYIGNNVSLAHQAQVHGPAAVGDDSFVGMKALVFKSKVGNKCVIEPDAAAIGVTVPDGKYIPA GTVVTQEEADKLPEITPDYFTTNAEVVSVNVKLCEAYKGEA
87	MIVRILVVTLVLSGFPA LSTSGTLQDKKAASECSDQPF SYDHGASGQQSWGRCNESGALPLPQAPINIPKIAESAQPAI VENGYNE NTSLVIYPHNPYNLKV D YKSSSNP VATIDIGSSANSRFKLLEFHFRPSEEAIDNRRFPMLHLVHLREVEGCEPGKPGVAAVILI KEGTPSQQTTDNLNALSHFP PPPDKPKDVEINLEGLLPPDHVNA GYWSYGGSLTTPCTENITFYLLKPMLTFSAAQIAEFERRYPTPNARDIQFLHDRHRVVRNHR
88	MIKSNPRGDLPLQVHETA FVDP TAILCGYVIVEENVFIGPYAVIRADETDADGRIAPIVIGAHNSNIQDGVVIHSKSGAWVTIGQRTSIA HRAIVHGPCTVGDGVFIGFNSVLFNCTIDDGVVRYNAVDGCHLPPGFYVRSTERIGPETDLAALPQVTADASDFSEDVARTNN ALVLGYKHIQNEF
89	MQEITVFEFSNVEKNEVSTNPKPPTPKIDPTSVIDPDATVIGDVTKIGKNCLIGASA VIRADEGHPIVIGDRSNVQDGVVHLALESVD QDGMVR EDNVVLEGDEYYAVYVGDRVSLAHQSQVHGPAKVGDDSFIGM QSFVFKSTVGSNCVIEPGAAAIGVTVPDGKYIPAGTVVTTQEEADKLPEITDDYPYFTSQAAVVEVNVLCEAYRGKA
90	MQEITVFD FS NVRK NKVGTGTNPKPPTPVIDPTSVIDPDATVIGDVTKIGKNCLIGASA VIRADEGHPIVIGDRSNVQDGVVHLALESVD VNDDGK I LEENVVIEGDEYYAVYVGKNNVLAHQSQVHGPAAVGDDSFVGMKSLVFRSIVGSNCVIEPNAAAIGVTVPDNKYIPA GTVVTQEEADNLPEITPDYFTSQAAVVEVNVLCEAYRGKA KE

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
91	MQEITVTRYENIRPSPVTPWNPEPRRPEIHP SAYIDPAAVVQGD VTIGANVVYAA NAVIRADEG PIVIGDNSSVQDNVVLHALET V DADGRRIEEN IVEVGGERYAVYVG ANVVL AHN A QVHGP AIVG DNTFVGMNALVFRSRVGANCVLMLA AAIGVTVPDGTYVPA GKVTTQEEAKLPK VPDHPFYKL NARVV AVNVALAKGYL ALS
92	MQEITVTKFENIQPS PVT PWNPEPKP EIDPTAYIHP AAVVQGD VKIGKNMISALASIR SDEGYPIVIGDNSSVQDNVVLHALET V DENGNVIEENVVTVG DEKYAVYIGKNVSLAHQAQVHGP AIVG DNTFIGMQAFVFRSKVGENCVLEPLA AIGVTIPNNTYI PAGKV VTTQEEAKLPK VPDHPFANTNAAVV KVNVLA KGYL ALS
93	MKSILAVFTGCGYQP NDEHWRYE DENGPEK WAEIEKNSDCGGK HQSPINI I HKETDSV HGP LQLQIN YEPSTLITEV RNN GH SI QFDPE KGDSINYKNETYYLKQIH FHEP SEHKINGI I YPI EMHL VH MNKS GK TIVL GILGEEGEES QLFEFPESFLPLKNGETKD I HQKIDLSSLF LEDKHY SYDGS LTT PCSEN VNWI VKEPIVLS VEEV I KL RNN MPLNNY RNEQP
94	MQEITVSLFSNVTKNEVTSWNPKPPTPVIDPTS FIDPNATV TG D VTIGKNCLIGPNAVIRADEGSPIVIGDRSNVQDG VVLHALESVN DEGKII EEN VVLYGSKLYAVYIGKNVSLAHQS QVHGP ARVGD DSFVGMSL VFN SIVG SNC VI EPNA AAI GVT VPDG KYI PAGTV VTSQAEADKLPEITPDHAYYTQNFAVVNVNVNL CRAYRNKS
95	MASSAFAAE GAHWG YTG HGG PAHW GDLSAD YATCKLGKQ SPIDIRGA KEADLPAI QFDYK ASPLK I LNN GH TVQVN YAP GSGI VVDGKPYELVQFHFKPSEEK IDGKAY PMVAH LVHRDAAGH LA VVA VLIKE GKENPLI KTLWPHLP AE EG P EQA VAG ATINAAD LL PADRGY YAFD GS LTPPCSEGV RWH VLQ P ITMSKA QID AF QK LYK P NARPLQPLN GRIM
96	MQEITVTRYENIRAS PVT PWNPEPKL PKI HPTAYIHP AAVVQGD VTIGENVL VMANAVIRADEG PIVIGDRSNVQDG VVLHALES IND DENGNEI EEN VVTVG DK KYA VYVG DN VVLA HNA QVHGP AAV GDNTFVGMNALVFRSRVGNCV LAPNAA AIGVTVPDG KYI PAGTV GKVTTQEEAKLP EITPDH PFA NLARVV KVNI ALAKGYLA QA
97	MQEITVLI FSNI TKNEV TSTNP KPKTP KIDPTSYIDPNAK VIGDV TIGKNV LIAFAF AVIRADEG KPIVIGDRSNVQDG VVLHALES IND DGKII EDN VVIEGNN HYA VYVG NN VSLAHQS QVHGP AHVG ND SFVGMKSLVFKSDVG DNCVIEPEAA AIGVTVPDG KYI PAGTV TTQEEAKLP EITDYP FYTKV AEVV KVNV DL CLAYRN KQ
98	MQEITVHHFSNRKNEV TPTNP KPTP VIDPTSYIDPNA T VIGDV VTIGKN CYVAHSAVIRADEG PIVIGDRSNVQDG VVLHALES V DDGGEI EDNV VEV GDES YAVYVG KNV VLA HQS QVHGP AAV GDDSFVGMKSLVFKS T VGS NC VIEPEAA AIGVTVPDG KYI PAG TVTVTSQAEAAKLPEITPDHADY TTQAA VVTVN VALCEAYKA QA
99	MGSYKTLTDIGKMM LKTLLA STVS AWTYS DQTA WG GECKT SKSQSPINIVTSSAVCKNSKDDPIKADS FVAEKLGGKH AMTLN NVTSSGTHSATWTFKTM PENS QLKC A QHHCHFDVAEHSMDG EKHFGECHVVC M QAKYADLGKALES KATDALA VFGFL LAKG TATTADH A VT KQ MIDAKKN YAEGK EYEM E PATTQ LADG YY RYNGGLTTPGCNEA VTVFKNVQYV SVAQY NEIMTWKDG N LRGNDRKVQPMNGRS LTFYKSSASKMMASLAIIGVMFM
100	MRFNRFVTTLLAACLMPLMTQ AAPW GYTG EGTGP A QWG KISK EYATC QTGIN QSPV D1 QTA TTSK LGLP ALN TQYIDN PTR FR S IN YTLRATM SSYNSNFIEI EGR LYY LKHFD FHAPSEHTL NGK TYPL ELQLVHKNQHGDIA IVA VMFDV GEPN QAIQNLW ESF PTM VDN SMPI FSDVDI NQ LLD PDKAY L YSGS LTT PCTEGV TWV VLKK PVALSAE QLDNF HYI VGP ANR PQQ PLN ARTITD SHSGN TEI LY
101	MQEITVTRFENIQPS PVT PWNPEPKL PEI HPTAYIHP AAVVQGD VTIGENVMV SANASIR SDEGYPIVIGDNSSVQDNVVLHALET V GDEGEV LEEN VVVG DERYA VYVG KNVSLAHQAQVHGP A

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	VGDNTFIGMQAFVFRSRVGKDCVLEPLAAAIGVTIPDGTYIPA GLVVTTQEEAAKLPKVTPDHFPANTNAAVVKVNVALAKGYL AQA
102	MQEITVLEFSNVTKNEVTPFNPKPETPVIDPTSYIDPNATVIGDV TIGKNCMISANASIRSDEGKPIVIGDRSNVQDGVVVLHALESVDD GGMVLGDNVVVHGNNSWFAVYVGKNVSLAHQAQVHGPAAV GDDSFIGMQSFWFNSIVGSNCVIEPNAAIIGTVPDNKYIPAGT VVTSQEEADKLPEVTEDDKYFTTQEAVVKVNVLAEAYRGLA
103	MKLKRISAFTVCGWNYYEDQHPEKWAISLFPLCAGKRQSPINIVTS EVVYDPKLKPLKLSYEPATCREIIVNNGHSFNFVFFDSQDKSVL KGGPLSGIYIRLKQFHPHWGAADDKGSEHTVDGAKYSAELHLV HWNACKYGDFAEAASKPDLGAVVGFLVKVGKANPELQKLDDA LGSIKTKGKQTRFTNFDPSLLPSSLWDYWTYDGSLLTPPLLESV TWIVLKEPISVSAPAQMEOFRLSLFTSEGETACCMVDNYRPPQPL KGRQVRASF
104	MIKTNPRGDLQPQVHESAFVDPTAILCGWVIVEEYVFIGPYAVIR ADELNADGDMPIVIGAHSNIQDGVIHSKSGAAVTIGRHTSIA HRAIVHGPCCRVCDDGVFIGFNSVLFNCTIIDDGCVVRYNAVUDG CHLPPGFYVRSTERIGPETDIALPQVTADASDFSEDVARTNN ALVLGYKHIQNEF
105	MQEITTVVFENIRPSPVTPWNPEPRLPEIHPHTAYIDPAAVVQGD VTIGENVMISANASIRSDEGYPIYIGNNSNVQDNVVLHALETVD ENGKRIEENIVTVGDKEYAVVYIGDNVSLAHQAQVHGPAAVGD NTFIGMQAFVFAWSRVGKNCVLAPLAAAIGTVPDGTYPAGK VVTTSQEEADKLKPMTPDHFYKTNDAVVKVNVALAKGYLAQ A
106	MKAISLVFTCGYWRENDPHOWHLTFPAAKGERQSPIDIQPAKA KYDPGLKPLKLSYDPATARRILNNNGHSFNVEFEDSQDKAVLKG GPLTGSYRLLQFHFWGSTDDHGSEHTVDGVKYASELHLVH WNAVKFSSFAEAAASKADGLAVIGVFLVKGEPAEMEKLNAL HAIKTKGKEAPFTNFDPSCLLPTCLDYWTYSGSLTTPPLLECVT WIVLKQPIVSSEQMAKFRSLLTSEGEKEKRMVDNFRPLQPL MNRTVRSSFR
107	MTRRAVLNRRGALAALLAVAGCAGSDPTAAAPHWDYDHE GPDHWADLGKQYATCRNGHAQSPIDLPAGEAHPTDDIDIVY RRIRTAUTNNGHAIQGVVPADSGNRIRRVDGTSFTLTQYHFHL PSEHTVAGAETAMELHVHTDAHGRЛАVLLRAQEAPAPL SAILAAAPDRVGATRTLSNIDPRAFLPDNRQAQFRYEGSLTTPPC TEGVAWIVLREPSPVAADVDRYRRLFPHSNRPTQPRNDRPVI LAGTN
108	MKIIISWLFIPLLLGACATDWSYSGRGSPQNWAIESNSNKFCIGY NQSPIDINLSMKNKDFILNDLKFDYKISEIEKVNEKYQKINFYSK SFVLRGKKYWLKYIEFRHPSEHFLDSPHSLEMQIYHKSEDE QWLATSYFLEIPAMNNNNENLYFNNNLIDFLKSKKIEDKFDSLKII DETSLSPFYEGSFTTPCCTEGVWKYIMKNPIFIISKEQMNIIKSTI FVKSASNARGIQKFNPEKF
109	MQPSAFHKLLLLPLAYHRTPNVGDDKDEHWNYYTNGKNWG GICASGERQSPISLSVQKSYIISIPRIVFGNYDIKLRGPLTITNNGH TAHMDIPETTNGKKPFITEGMLNRYVAESLHFHWGSPGSRG EHAINKQRYDVEMHIVHRNAKYKDMSEAVGKKDGLAVIGVM LKIVKNPKLMLGLHNVLGAVSRITTKAKTYVPGFSFLQV GIVNPRSYFTYRGSLTTPFCQEAVTWTVFTQVLPVSYTLVSKL WRLRDSEGHRLINNNFRDIQPTNRRAVFYRP
110	MQEITVTKYENIQASPVTPWNPEPKLPEIHPHTAYIHAAVVQGD VTIGANVLVMANAVIRADEGYPIVIGDNSSVQDNVVLHALETV DADGKVIEENVVTGDKKYAVYVGDNVLAHNAQVHGPAA VGDNTFVGMLALVFNSVVGKNCVLAPLAAAIGTVPDGKYIP AGKVTTQEEAAKLPETVTDHFYFYNLVDRVVAVNVALAAGY LAQA
111	MQEITVTRFENIQASPVTPWNPEPKLPEIHPHTAYVHPAAVVQGD VKIGKNVLIMANAVIRADEGYPIVIGDNSSVQDNVVLHALETV DENGNVIEENVVTGDEKYAVYVGDNVVIAHNAQVHGPAAV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	GDNTFVGMMNALVFRSTVGKNCYLAPNAAAIGVTVPDGTYVPA GTVVTTQEEAAKLPKITPDHPFANLNKRVVKVNVALAKGYLA LS
112	MSYSRVSTYLLALSVLCSVFVVVPTGVCQAINPPEKVOPGQH VHNGQHHMLHMMLGEEKCGPTYTYEEGVKGPSHWPEVCTTG KMQAPIDIQSTQKLPIINLKPNQPADLDVLNDCNQYRVLVKF PDNYWLMVGKKPYNLAEIHFREPGETAVNGKRPKMSIEFLHFS PEGVFLVIEVPVVAAGKENPMTQAILQNVPAAPGKEEKVAGVKIN PTDLLPIDRRSFYRYPGSSLTPDCTEVVTWYVMKTPIMESEAQI AEYSKHYHTARPLQPVNGRPVVEDQ
113	MTCTGKSTDYNYDNPS EWGTHFPAAANGLCQSPIDIDSHKTIR HVYPKFQFSKKYHSSELFKLINQTYQVTATLADRTYQGQNDNY LWFTGGGLEGTFYFVNFMHLHWGRDRRHGSEHEIDGHQFPAAEG HVFQNRQTKQAAVFAFLFTVADRFHKENKEWCKYADAASQ LTNDEDSIQCLFNLHDLMNVNDRLFYRYTGSLLTTPCTEGIVW TIFSQKIAIKQESLQKLKNILTKVYRPVQPLNDRIVYVKNH
114	MKLSNQIRFYGVATCPWEHDYPIADGDRQSPINIISSSQARYDP SLRPLELKYPDSTSLEI LNNNGHSFQVTFADDSDSSTLKDGPISGV YRLKQFHFWGAADDKGSEHTVDGVKYPAELHHLVHNNAVK YSSFAEAAASKENGLAVIGVFLKIGQHMANLQKIVDALNAIKTK GKQTTFTNFDPSTLLPGCLDYWTYDGSLTTPPLESVTWIVCK EPISVSSEQMAKFRSLLFS
115	MIRIMTRGALTGVLWMLSUVVGLQAAEPGSIIPWGYEGDLGPNH WGSLGSEFALCEKGMSQSPIDLVQTHKLALTDIQFSYRDAPFH VINTGHTLEELEPLSETVKSRSYPKHGQTVLHFQKDSTIVFDDDL YLLEQFHFSPEEHTLHEKHYPMELHLVHHNERHEAAVVAVF MKEGKHNPFFETFLDHAPKTGEFVEDRERVINPVNLLPKNHT YYRYFGSYTTPPCHEGVIWAVMHDPIEVSR EQVQRFRSLVGH DNARPTQPLHKRKVLENDVRAPGKLK
116	MSLKEWGYDAHNGPQTWCRCVPIAAEGKRQSPIDIQTKVEVESD LTLKPLKLNYEPASSLRILNNNGHSFOVEFDSTDKSVLTCGPLT GTYRLRQFHFWGSCDDHGSEHTVDGVKYASELHHLVHNNAK YESFAEAAKQPDGLAVVGVFLKIGKENPKLORVLDALNAIKT KGKQTTFTNFDPSTLLPGCLDYWTYHGSLTVPPPLLESVTWILK EPISVSSEQMSKFRSLLFT
117	MQEITVLYNSNIVKNEVTSTNPKPENVVIDPTSYIDPNATVGD VTIGKNCYIAAFARIADEGKPIIVIGDRSNVQDGVVLALESID DTGEVNNDNVVIEGNELYAVYIGDNVSLAHQSQVHGPARVGD DSFVGMMSLVFKSKVGSNCVIEPEAAAIGVTVPDNKYIPAGTV VTSQEEAAKLPVTPDHAETKNAAVNVNVALCEYKGKMK
118	MQEITVMDFSNITKNEITSWNPEPSTPKIDPTSYIDPNATVGD TIGKNCYIGPFAVIRADEGAPIVIGDESNVQDGVVLALESVDA GGKIREDNVVLHGDKLYAVYIGKNSLAHQAQVHGPAYVGD DSFVGMMSLVFKSKVGSNCVIEPEAAAIGVTVPDNKYIPAGTV VTTQAEADKLPEVTPDHAETKNAAVNVNVALCEYKGKSLA
119	MRRKRVSRFNAPQLPYMHKLAIAAALFLAAAIPSFAADDCAV PGYTVNDGMPATWGRYSAICASGLSQSPVKINNLLPSPATNLP TLSFQGGSRFRVKNNQHDLEVYPVNQWTLQPFGRALTKPHF HVPAEHLDGNTRHDAEAHFVYELGNRIFAIAVWIDQVNQGGN AALQKTAAVQRGLCLMSPLSLPAATLNLILDFLPDRNNYAYAH GSLTTTPCTENVTFFIMRTPTATATQINAATLVA PAPPGNARPV QQTKWRR
120	MQEITVLYNSNIVKNEVTPTNPKPENVVIDPTSYIDPNATVGD VTIGKNVLVMANAVIRADEGAPIVIGDRSNVQDGVVLALESV DENGNVLEENVVEVGDKRYAVYIGDNVLAHNAQVHGPAAV GDNTFVGMMNALVFRSRIGKNCVLAPLAAAIGVEVPDGTYIPAG TVTTQEEAAKLPKVTPDHPFANLNERVVKVNVALAKGYLA A
121	MQEITVLLFSNIRKNEVTPTNPKPENVVIDPTSYIDPNATVGD TIGANCFCVGPFAVIRADEGAPIVIGDRSNVQDGVVLALESV DGGKVREDNVVVHGDEWYAVYIGRNVSLAHQSQVHGPAAV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	GDDSFVGMKSLVFKSKVGSNCVIEPGAAALGVTVPDGKYIPA GTVVTTQAEADTLPEVTPDYAFYTTQAAVSVNVNLCEAYRA QA
122	MKRSLAFVTIGCQHNPEDWYPFIEGDEFGYSDSLQREWVMCK SGRMQSIPIDISPENLLFDPNLRLSQIDKHKSATLENLGQLPLLT INDSK1RPD5INISGGPASPYKYLHIIIIHFGRS1DEEKSEHTID HIRFPAAELQLLAYNTDLYSNFSEAMTQPRGLLAISIIVDICKITN TELRLKLTVASQSITYKGQKTIILKRFNAYGLLPETEDYITYEGSL TPFGCYETVTWVIMNNPIYITKEDLHIWNDLQQTEFKQPNPVF MPPNYRPLKPLNGLRLLRTNINIKYK
123	MQEITVLEFSNIKKNEVTSTNPKPPTPVIDPSSYVDPNATVGD TIGKNCLIGANAVIRADEGAPIVGIDNSNVQDGVLVHALESVDD GGKVREDNVVLYGDKYYAVYIGKNSLAHQSQVHGPARVGD DSFVGMSLVPNSIVGNNCVIEPNAAAIGVTVPDNKFIPAGTV VTSQAEADKLPEITPDHAFYTDIAKVVSVNVKLCAYLEKQ
124	MQEITVLTYSNVTKNEVTSTNPKPPTPVIDPSSYVDPNATVGD VTIGKNCLIGANAVIRADEGAPIVGIDNSNVQDGVLVHALESVDD DGGKVIEDNVVLUHGDNWYAVYVGKNVLAHNAQVHGPAYV GDDSFVGMKSLVFKAIVGNSNCVIEPDAAAIGVTVPDGKYIPAG TVTTTQEEADKLPEITPDHAKYTAKVAEVIAVNVALKAHREK A
125	MRKISFLVAGCTPENWHDYQPVAGGERQSPINIITKEAKYDPSL KPLSFTYDPSTSLEILNNGHSFQVTFADNSDSSLTGGLPTDKY RLTQFHFWGSTDHGSEHTVDGVKYASELHLVHWNAKDYS SPAEEASKPDGLAVLGVFLVKGEHNPSLQKLTDALYSVRFKG TKAQFTMFNPKCLLPSSLDWYTSGSLTTPLLESVTWIVLKEP ISVSSEQMEKFRSLLFSEGETACCMVDNYRPLQPLKGRKVRA SF
126	MVFSIATFGLLLLLGFCFLGDDFGYDGHNHGSHWGEEYHTCIGK HQSPINIEEHNVKNVSLPPLKLIGIDDPYQSFVTNNNGHTVMLKI NESKVIMLSGGPLGNKVVFEQLHFWGQNDFEGSEDLINNNH SFPMEMHAVFYKEDYKSMNEALNHSDGLAI LAYLYEVSPNPN VMYEPIVEVLPDIETVGSEKVLREPLMLRKLFISIDTTMQDYFT YNGSLTTPPCLEVIAWIDFKDHLRLSHEQIAAFRNLRSTECDKL THNFRPVQSLLEDRIVLHNIPREQNI PRNIPPKTYHRFDEHSQH NVEMPLSIIALAVLFAVILFAI
127	MTLFSKIRENVYGHAPQCDWCYESEGAPESWGLRLPFEATCA VGRRQSFIDIRDGIAVDLEPIRFDYRPTSFRIVDTGNTIQVNVP GNTIEVMGRYYELVQFHFHRPSEERIDGRQFDMVAHLVHKDG EGRЛАVAVVLLERGDDQPLVRTVWNNLPLEKGDEVAARTPID LNALLPEDRRYYTYMGSLTTPPCSEGVLWMVMKQPVOLS
128	MQEITVTTYNIRPSPVTPWNPEPKLPKIHPTAYVDPAAVVQG DVTIGKNVMISALASIRSDEGYPIYIGDNSNVQDNVVLHALET DENGNVIEENVVTVGDKYYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFRSNVGKDCVLEPLAAAIIGVTVPDGTYVPA GKVTTTQEEADKLPKVTPDHFPYKTNEAVVKVNVALAKGYL ALS
129	MQEITVLEFSNIKNEVTSTNPKPPTPVIDPSSYVDPNATVGD TIGANCYIGASAVIRADEGKPIVIGDDSNVQDGVLVHALESIND EGKVIEDNVVIIHGNKRYAVYVGKNSLAHQSQVHGPAAVGD DSFVGMSLVPNSKVGNSNCVIEPNAAAIGVTIPDGRIYIPAGTVV TSQAEADKLPEITPDYAKSNAVAVVNVNGLCEAYREEA
130	MQEITVGEFSNVTKNEVTNTNPKPETPVIDPSSYVDPSSTVGD VTIGKNCYIAANAVIRADEGAPIVGIDNSNVQDGVLVHALESV NDGGK1REDNVVLEGDEYYAVYVGKNVHLAHQSQVHGPAA VGDDSFVGMKSLVFNISVGSNCVIEPNAAAIGVVPDGKFI GTVVTTQEEADNLPDITPDHAAYTQAAVVKVNVALCEAYKA EA
131	MQEITVTKFENIRPSPVTPWNPTPKLPKIHPTAYIDPAAVVQGD VTIGENVMVSAANASIRSDEGYPIYIGDNSNVQDNVVLHALET DENKGRIEENIVRVGDKDYAVYIGDNVSLAHQAQVHGPAAV DNTFIGMQAFVFRSRVKGKNCVLEPLAAALGVEVPDGTYIPAGE VTTTQEEAAAKLPKITPDHPFANTNAAVVKVNVALAKGYLALS

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
132	MRARAVTGGIINGRIRSTLGAALLAPLFLAAGCGGECCCCGTGE ESGLAETHLAASWASHAGADGPDEWASLDPAYATCGTGERQSPI DIVGAKRRPFPVVELDYAPVRATLIDNNGHAI EAELEDGSASSI GGDEFTLEQFHHMPAEEVVVGKSFASISHLVHLDEDDGAAAV VGLLVEPGPENPVIERLAAEVPEETDEPVEVEGELDLAQLVPDG DAFRYEGSLTTPPCTEGITWTWTFEDPTMSPEQLEAFAGAYDA NARPVQARNGREISVGPGLG
133	MQEITVTVFENIRPSPVTPWNPTPRRPEIHPTAYVDPLATVGD VRIGANVMVSANASIRSDEGYPIVIGDNSNVQDNVVLHALET DAAGRRLEENVVEVGDELYAVYVGANVSLAHQAQVHGPAAV GDNTFIMQAFVFRSRVGANCVLEPLAAAIGVTIPDGTYIPAG KVTTQEEAAKLPKITPDHPFANTNAAVVAVNVALAAGYRAL A
134	MQEITVLTFSNVTKNDVTATNPKPVTPVIDPTSYVDPNATVGT TIGKNCYI GPF AVIRADEGAPIVIGDRSSVQDGVVHLALES DDGGELI EDNVVLEGD EYAVYI GKNVHLAHQSQVHGPAKG DDSFVGMKSTVFKSIVGSNCVIEPDAAAIGVTVPDGKYIPAGT VTTQEEADKLPEITPDHAKYTANAAVVTVNVALCEAYRNA
135	MQEITVLEFSNI TKNEVTPWNPKPKTPEIDPTSYIDPQATVGD TIGKNCYI GPF AVIRADEGAPIVIGDSSNVQDGVVHLALES KGEIIIEDNVVVIKGKNCYAVYI GKDVS LAHQSQVHGPARVG SFVGMNSLVFN SIVGDCNCVIEPNAAAIGVTVPDGKYIPAGT TSQAEADKLPEITPDHAYYT KNAAVVNVNALCRAYKSKE
136	MSTIPPWRLGAVFCNYQKHEDAVEEKEFSYDEGSERGPSRWGEI RPEWRTCGNGEMQSPIDLLNQRVEI VSKGLKLRDYKPSNATL KNRGHDISLEWKGGAGSIEINGTEYVLQQCHWHSPSEHTINGR RFDMELHMVHESRDGKAVAVGIVYKLGRPDLSFLSSLMHDLEA ISDTKDRERAVGVIDPRHIKF GSRKYYRYMGS LTVP PCTEN WTIVKRVRTVSREQLK
137	MKYGVVLILSFIQFTYAQNKKDWGYKDSGAPQYWANINPLY LGCTEGNQSPINII TKNVNKGAAHFELKYSVAKGVNLILSHNT FKMVYPGNFLEMNGNRYOLKEIYFKTPGENAIDS LRGMLEA QLLHEDSKGNV KILA VAFV FIEGRSNPIIDMLVKNLPTQPD KANFI ANVDVHQLLPSDLAS YCFDGSLT MPPCSQGVRWIVLK QTM TI TQS QVDSMRDITGVNSRPTQEI FNRLIVK
138	MQEITVLI FSNIRKNEVTPTNPKVPIVVIDPTSYVDPNATVGD TIGKNCYIAHSAVIRADEGKPIVIGDRSNVQDGVVHLALES DGGKIREDNVVI EGDEEYAVYI GKDVS LAHQSQVHGPARVG HSFVGMKSLVFN SIVGSCNCVIEPDAAAIGVTVPDNKYI PAGTV VTSQEEADKLPEITPDHAKYT AIAAVVNVNALCQAYKEKS
139	MKRTFLIAVSLCPGLIQYNHWDEWWTYEGISGPAYWGLINPA WSLCNKGRQSPV D1DPEKLLFDPNLKS LHL D KHVKSGTL ENT GQSLVFRVDKDTKHHVNISGGPLAYKYQFQE IYFHWGVDGL GSEHTINHQSPFAELQLYGFNSEL YSMSSEA QEKPHGVVG ISLL VQIGKTPNPELKI LTSQLEN IRYKGQS API KNFSLRGLL PNT EHY VTYEGSTTHPGCWETTVWVVLNKPVYI TQELYALRRLMQGS KEHPKA PLGNNA RPTQDLH HRTV RTNI
140	MQEITVTRYENI RESPVTPWNPTPRRPEIHPTAYVDPAAVVG DVTIGENVMISANASIRSDEGYPIVIGDNSNVQDNVVLHALET DAAGKRITENIVTVGDKEYAVYI GKNVSLAHQAQVHGPAAVG DNTFIGM QAFVPRSRVGKNCVLEPLAAAIGVTVPDGTYIPAG VTTQEEAAKLPKITPDHPFAKTNAAVVAVNVALAAGYRALA
141	MKLTSIAVFCGYPEQNRDH WGYQDHNGPEMWKEKFP SAGKG KQSPIDIOITAETTFDPKLKPLELKYPD STAKEI LNNGHSPQVTF DDTDSSTLKDGPISG IYRLKQFHFHWGASDDHGSEHTVDGVK YAAELHLVHWNAKYGKFGEAASQPDGLAVVGIFLKIGRHHEE FQKLLD ALD SIKTKGKQTTFTNFDPSTLLPGCL DYW TYFGSL TPPLLESVIWILKEPIVS SSEQ LAKFRSLLFTSEGEKEKRMVD FRPLQPLMNR
142	MQEITVAEFSNVTKNEVTPYNPKVTPVIDPTAYVDPEATVGD VTIGKDCMISANASIRSDEGHPIVIGDRSNVQDGVVHLALES DGGEVIEDNVVVEGNELYAVYVGKNVSLAHQAQVHGPAAVG

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	DDSFIGMQSFVFNSIVGSNCVIEPEAAAIGVIVPDNKYIPAGTVV TTQEEADKLPEITPDYAYYTTVAAVVNVALCKAYRRLM
143	MPAPAPKAAPKAGHGAKKAAPAKPAAPKAAPKAAPRAKVVK AAPAPPPEPAHAHWSYEGERAPARWQLKPEWKQCAVGTR QSPIDIRDGIVVDLDPIQFDYKASGFSVIDNGHTQVNLLAPGNFI TVLGRRYELVQFHFKPSEERINGKPYDMVAHLVHKDAEGLR AVVAVLLRPGEANPLIEKVWTYMPMLADGRVRMPTELIDLNO LLPADRAYFTYMGSLTPPCSEGVLWMVMKQPVPVSADQIAIF ARLYPMNARPLQAVSGKIIKETLM
144	MNRKKLNSLIAAVAVIFFATSAFSES PHWDHAEQSTWWAIEDTT QTYPKKRFPFAVCVGVCQHQSPIDLA AAEVIDTIQINPLELYDVD HAPVFFNSGHGIVQVNTSIEYSGKLKVGEELFPLIQFHFHAPGEH VIGDTKEPAELHYVHICQADGKIAVLAVAINIGDENSAFQTILEN VPSVSGGKNENSLQFDPAALLPPLDHPIKYYTVAGSLTTPPCS EGVQWYFLPTAITISEAQNLQRSLYADNNRLPQDVNGRSLLT Q
145	MQEITVTRYENIRESPVTPWNPTPRRKPIHPTAYVDPAAVVVG DVTIGANVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET VDADGKTLLEENVVTGDKYAVYVGDNVSLAHQAQVHGPA AVGNNTFIGMCAFVFRSTVGENCVLEPLAAAIGVTVPNGKYIP AGKVVTTQEEADKLPEVTPDHFPANTNAAVVKVNVALAAGY RALA
146	MQEITVDEFNSITKNEVTGTNPPEPSTPVIDPTAYVDPNATVIGD VTIGANVLVAANANAVIRADEGRPIVVGDRSSVQDGVLHales VDDEGEVREDNVVLVGDENYAVYVGKVNVLAHQAQVHGPA AVGDDSFVGMKANVFRSTVGSCVIEPDAAAIGVTVPDGKYIP AGTVVTTQEEADKLPEVTPDHAKSNDVAAVVAVNVNALCEAY REQS
147	MQEITVLLFSNTKNEVTPIPKPTTPVIDPTSYIDPNATVTGD TIGKNCMISANASIRSDEGKPIVIGDRSNVQDGVLHalesVDD GGMIIGDNVVVEGDEYAVYVGDNVSLAHQAQVHGPA DSFIGMQSFVFKSIVGSNCVIEPEAAAIGVTVPDGKYIPAGTV TTQEEADKLPEITTEDADYTTNVAVVNVALCKAYREKA
148	MQEITVTRFENIRPSVTPNPEPKRPIHPTAYVHPAAVVEGD VTIGANVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET DENGVLEENVVTGDKYAVYVGKVNVLAHQAQVHGPA VGDNTFIGMCAFVFRSTVGKDCVLEPLAAAIGVTVPDGTYIPA GKVVTTQEEAAKLPKITPDHFANTNAAVVKVNVALAKGYLA LA
149	MQEITVAVFSNVTKNEVTGTNPKPRTPVIDPTSYVDPNATVIG DVTIGANCYIAHSAVIRADEGRPIHVGDNSNVQDGVLHales VDADGERLEDNVVIEGDKRYAVYIGKVNVLAHQAQVHGPAR VGDDSFVGMKSLVFNSVVGSCVIEPNAAAIGVTVPDGKYIPA GTVVTTQEEADKLPEVTPDHAAYTEIAKVVTVNVNLCRAYRE QA
150	MQPIIHKEGKYKMYFFLPTILSSLTLSACNSNSKIVQEVPNKS IVSAARNEDWSYTGKTGPNYWSSINKKYALCSTGKQOSPVNID QAIKKSLPLGINYHNDLFKIERSQYTVKFIPVNHSNSINLNNTN YTLQFHFHTPSEHTLNGKQSDLEIHFINENSNSKIITIGVLVDR GRLNKEFQKILMANPMDEDLEGKVVKINLQSFIPYTSKKFSYT GSFTTPCTEGIKWIIFNKPIQFSEEQIHSYQNYFEPNSRPVQPLN GRDLFESW
151	MQEITVVFVSNVEKNEVTSTNPKPRTPVIDPTSYVDPNATVTGD VTIGANVMISASASIRSDEGKPIVIGDRSNVQDGVLHales DEGEVIEDNVVIHGDKNYAVYVGKVNVLAHQAQVHGPARVG DSFIGMQSFVFKSVDVGSCVIEPFAAAIGVTVPDGKYIPAGTV TTQEEADKLPEVTDYAYSDTNEAVVKVNVLCEAYKGKA
152	MNPTGHMPVVSETAFIDPTAIICGKVIIEDNVFIGPYAVIRADEV NEQGDMEAIVIKRDTNIQDGVVVIHSKAGAAVTIGERSIAHRSII HGPCQVCDDFVFIGFNSVVFNAVIGKGCVIRHNSVVDGLDLPEN FHVPPMTNIGADFDLNSISKVPEYSSFSESVVSANHTLVKGYK

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
153	MLSRKPGAVTPCIWNHQEYDVKMASWGYTKENGPATWYKD FPVANGPRQSPINIDPGSAKYDPGLKALTLYDPSTSLELNNG HSFQVTFAADDSDSSTLTDGPISGVYRLKQFHFHWGASDDKGSE HTVDGVKYAAELHLVHNAVKYSSFGEEAASKEKGLAVLGVF LKVGEHNNANLQKVLDALDSIKTKGKQAPFTNFDPLSTLLPASLD YWTYHGSLTTPLLESVTWIVLKEPISVSPAQMakersrlfesse GEKEKRMVDNFRPLQPLMNRTVRSSF
154	MKKGLVLICLSSLGAFGGEHWGYSKGVGPRYWGKLSRDY EICKSGKTQSPINIQHYHHSPDKEDLSFEYENTKPLSIAYSHYTL VAQFNEPGNAVIFRDHEYSLVNLHFFHIPMFAIHGKKQPLSMH LVHRDKEGDLVVVGIGFSIGKKNPFTPILNAYKVHTEPKLLAL KTLLPDTHYHENGSLTTPCSEGVTWFIIETLSISKEQFDEM QQIMHHQSNQRPLQKDYNRIVVKSSAIvreH
155	MQEITVDEFSNVTKNEVTATNPKPPTPVIDPTSYVDPEATVTG DVTIGKNCILIANAKIRADEGKPIVIGDRSSVQDGVVHLALESV DDGGKVIEDNVVLEGNELYAVVGENVVLAHNSQVHGPARV GDDSFVGMKSLSFKSDVGSNCVIEPFAAAIGVTVPDGKYIPAG TVVTTQEEAKLPEVTEDYPFYTKQAEVVVKVNVLCEAYRNK A
156	MIGVKPKSYPAQNKKKKWSYDGDNGPQNWGDSLADYLSCEV GLNQSPVDFSKSFSSPDLHSIRFNYSAGRVYLARGSITFKVIP GNVAYFKGKQWVLERVVLRTPEHSEHSIEGHSDFGEQLYHSYK GESFLWVSVLLEAGSALKPFRQIVDKAKGIGSASKLMGVDLRL LIPRRKNNYYFPGSDTIPPCKEGRSWVVLRQPVGASIKYIEHLE SQVGKGARPTQPLYARVPLRYD
157	MKGLCVMAIVALIGLQTATGYTRQDLSCGGRMDYSKPVCHNI PKHAHKKCDVYNQWSHHLFGTSQKCWGKLNACRGMRSQSPI NINEHKVEPNHNGDLCITGPHHLKVHIIHNTGHDLQAKLDESS SRATLVGGPLGNKKYRVLQFHFFASHPGGKGSEHSINCHFS DIEMHIVLQNVAYAGSFVDVAKDHDRDGLSVIAVMLSEDVRPNTV SNAMRNPPSWQYYINTLIYYASLRKHCDLHEVPGNTRFLFHN LLPSDYARNYYAGGSLTTPPCESVSWIIMRTRFHINRYHLLN LKDVSLLSRYHRGFEPMSQNKRNLQIINNRKVYYPAHGRCPSRG
158	MRLKSNIIVAGTCQPEDYHWGYEDHNGPATWAKHFPAAKGE KQSPIDIQLSNVKNVSPPPLVFPNFKDSTLKBIINVGHHSVQVNLE DSDNRSVLKGGLPLSGPYRLKQFHFHWGKTNDVGSEHTIDGKS FPSSELHLVHNAKKYASFGEASKPDGLAVVGVFLEIGDEHP EMNRLTDALYMRFKGTKAQFCNFNPCKLLPASRHWTYPGS LTTPPLSENVITWIVLREPISI SERQMEKFRSLLFTSEGEKEKRMV DNFRPLQPLMNR
159	MKFLTPSISFTSLRVARASAATGVKFYYNDQSOWPAVPATPEGTN VCDGQQQSPINIDTGFSCQADAQGYSFYTGDCCTLGDYEFPM NDHGLKASVEKSNCCEPKPMIIPGTGVYEVLFQFHIHTGCGENKF NNTGCDAAELHLVHIAKTDIALPAATTSDLPLDAVLGLMMYG VDEKHASVDALEDSWSEVCSNQKCMTSDDELKSQKFSPYSLI PSDTSIYNFQGSLTTPCWEVTTWVAEKPIKMSFKQVLAITN LINKYSGYRAEDGSCVADSTVADDAGITSRDVDQSLNQRQIVKN CEPLTVMSDFPAAQEQSPMTASSESSAQFLNIKIFGVVSVLA SIVLF
160	MQEITVTRYENIRPSPVTPWNPEPKLPKIHPTAYVDAAVQG DVTIGENVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET VDEDGKVLEENVTVGDKKYAVYVGKVNLSLAHQAVHGPA AVGDNTFIGMQAFVFRSVVGKDCVLEPLAAAIGVTVPDGTYIP AGKVVTTQEEAKLPKITPDHPFANTNAAVVKVNVALAKGYL ALA
161	MIVLIIPLLFIIVQSQTNTTTNTTTATTISYASQGSDWTSGVCSS STSQSPINLEVSSGTCDSNSMVLDIOPKKDAMQIVMERVQYTIQS KAAVSNLYATDINGNLGYTATSFMPHSPSEHTIEGTRYDLEM QIVHDLKSEFSATITKAIVSILFEVSSTDQFFFETYDFALVASAST NTTTNTNTNSTTTAAASVTSTIASINFNDLLGSQLDANPAYYT YVGSLTIPDCDENVNWYILD SilPITQTLDAFNTYFLSNSTFAS GNGNRRAIQSTNDRTIKKGGVACEEQFVYFFSFFILYIFINYFIF KLL

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
162	MQEITVLEFSNITKNEVTATNPKPPTPVIDPTSYVDPQATVIGD VTIGKNKYIAASAVIRADEGKPIYIGDRSNVQDGVLHAELEV NDGGKIREDNVVVHGDEYYAVYIGKNVVLAHQAQVHGPAAV GDDSFVGMSLKVFKSIVGSNCVIEPDAAAIGVTVPDNKYIPAG TVVTTQEEADNLPEITPDYAYYNDVAAVVKVNVDLCKAYREK A
163	MQEITVLEFSNVTKNEVTSTNPKPPTPVIDPTSYVDPNATVIGD VTIGKNKYIAASAVIRADEGKPIVIGDRSNVQDGVLHAELEV DDGGKVREDNVVLEGDDEYYAVYIGKNVVLAHQAQVHGPAA VGDDSFVGMSLKVFNISVGSNCVIEPEAAAIGVTVPDGKYIPAG GTVVTTQEAADKLPEITPDYAKSNAIAAVVKVNVALCEAYRN QS
164	MLKTNPRGDWPQVHASAFIEPTAILCGYVIVEENVFIGPYAVIR ADETDADGRIAPIVIGAHSNIQDGVIHSHSGASVFIGRHTSIAH RAIVHGPCKVGDGVFIGFNSVLFNCTIIDDGCVVRYNAAVVDGC HLPPGFYVRSTERIGPETDLAALPQVTADASDFSEDVARTNNA LVLGYKHIQNEF
165	MKRNFIAISTVCGYDPEQWHMDYPIANGNRQSPINIIITDAKY DPNLKPILTSDPATAKEIVNVGHSFNVFEDTDNKSVLKGP LTGSYRLTQFHFWGSDQGSEHTVDNVKYASELHLVHWN SVKFSSPAAEALKDNGLAFLKGFLKVEHNPHLQKITDILNSIK TKGKQTFTTNFDPSCLLPASLDYWTYHGSLTVPPLLESVTWIV LKEPISVSSEQLAKFRSLLFTSEGET
166	MQEITVTRYENIRPSPVTPWNPTPKLPKIDPTAYVDPLAYVQG DVTIGKNMVIASAHASIRSDEGYPIVIGDNSNVQDNVVLHALET VDANGNPLEANIVKVGDKDYAVYIGDNVSLAHQAQVHGPAA VGDNFTIGMQAFFVNSRVRGKDCYLAPLAAAIGVTVPDGTYIPAG GKVVTTQEEAAKLPKMTDHPFYNTNAAVVKVNVALAKGY ALA
167	MQEITVLFVFSNIRKNEVTENPEPVTPTVIDPTSYIDPKATVIGDV TIGKNKYIGASAVIRGDEGYPIVVGDESNVQDGVLHAEVD EQGKVIDNNVVRKGDKLYAYVVGKNVVLAHQAQVHGPAMV GDDSFVGMSLKVFKSRVGSNCVIEPYYAAIGVTVPDGKYIPAG TVVTTQEAADKLPEVTDYKPYTQVAAVVTVNVLCEAYRE QM
168	MGSSLILLPRVQTSRNGMKLFGILLSFGSVLGALAGNSWNYAG HGEYWPITSNAKSTGAESYWDCDGIRQSPIDINSSMVQDVYF WNQLNLANYAASYAGKFKNNNGHTLQFDLDDAETSGATLPTFS SPFMCTGCSYELQQFHFWGSTAYQGSEHTKEGIAFPMEHLHV HKKTSYSSVTASLSYNDGLAVIGIMPQLADTSAGLTEIINA AIKNAQDQHTHEAKSIDMSTFLYQTRGRSYYYYKGSLLTPC ETVDWHLMEGAIRITEADLEKLRLDTYDDAPLVDNYRLPMP LNNRIIKRVPN
169	MQEITVTRYNNIQPSPTSWNPTPKLPDIHPTAYIHPKAVVQGD VTIGKDMISANASIRSDEGYPIVIGDNSNVQDNVVLHALET DANGNRLEENIVTVGDEEYAVYIGKDVS LAHQQAQVHGPAAVG DNTFIGMSFVFRSRVGKDCVLEPLAAAIGVTVPDGTYVPAGK VVTTQEEAAKLPKITPDHPFANTNAAVVKVNVELAKGYLALA
170	MGLLDSKWWFVTQVLAAPVLPYSGPYPRTTSSYYDPNGFFQF ADKTHHRYNFYQHVTEAARAEKLI SNNEVWPSDKSIQMAS GSFSYREEDDYGPSNWGANATCEGMYQSP INLIANRSVIVQQ KRALELKGSRNVPAMMVENEGGAAAFPFRTEQPRLRGG PLRGEYLFYQFHYHLGS EHTFDKKRYS AEMHLVFYNELYGSF KAARDQANGVAVIALTFDVLKSRRI NSLNKWTRSLAEVVEAE SEYSIPRQELFSVSDVLDGMEWPYFAYEGSLTTPCSETVQWIV ASERQLLITRSELKTMRMLKGRGGDWVQTARPTQALNFRRVFI Y
171	MQEITVLEFSNVTKNEVTPTPNPKPTPVIDPTSYIDPQATVIGD VTIGKNKYIAASAVIRADEGKPIVIGDRSNVQDGVLHAELEV DDGGEIREENVVIEGDEEYAVYIGKNVSLAHQAQVHGPARVG D DSFVGMSLKVFNSDVGSNCVIEPFAAAIGVTVPDGKYIPAGT VVTTQEEAAKLPPEVTDYFPYTAI QEVVKVNVLCEAYREQK

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
172	MQEITVFEFSNVRKNEVTAWNPKPSPVPIDPTAYIDPNATVIGD VTIGKDCYIAASAVIRADEGSPIFIGDRSNVQDGVLHalesvn PDGMYREENVVLKGNNLYAVYVGRNVSLAHQAQVHGPAAV GDDSFVGMSLNFNSKVGNSCVIEPNAAIIGTVPDGKYIPAG TVTTQEEADKLPEITPDYAFYTQVAVVQVNVELCRAYRGK A
173	MQEITVTRYENI RPSPVTPWNPTPRLPKIHPTAYVDPLAYVQGD VTIGKVMISPHASIRSDEGYPIVIGDNSNVQDNVVLHALETVD ADGNEIEENIVTGVDEKYAVYIGDNVSLAHQAQVHGPAAVGD NTFIGMQAFVFKSRVGKNCVLEPLAAAIGTVPDGTYIPAGKV VTTQEEADKLPKVTPDPFNTNAAVVKVNVALAKGYLALK
174	MQEITVTRYENI QPSPVTPWNPEPKLPEIDPTAYIHAAVVQGD VTIGKVMVSALASIRSDEGYPIVIGDNSNVQDNVVLHALETV DADGKRLENIVTGVDEYEAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFRSTVGKNCVLEPLAAAIGTVPDGKYVPA GKVVTTQEEAAKLPEVTPDHFPANTNAAVVKVNVALAKGYL ALA
175	MQEITVTVFENIRESPVTPWNPTPRRPKIHPTAYVDPOAVVQGD VTIGANVMISANASIRSDEGYPIVIGDNSNVQDNVVLHALET VDENGKTLLENVVTVGDKKYAVYIGDNVSLAHQAQVHGPAA VGDNTFIGMQAFVFRSTVGKNCVLEPLAAAIGTVPDGKYIPA GTVVTTQEEADKLPEVTPDHFPANTNAAVVKVNVALAKGYL AQAA
176	MGSCQVHAGGSRHFSFVLTFGRAYNGVMLVPTS YLLL LVT LLPTFCADWSYKLGDSQGP DHWEYECKKEYQSPVNIPKGET TSTVFPALSFWNYELQPATATIENNGHTVKLATEPHRPKBTPLL SGGGLLHSYKFAQIHFWGAEDFKGSEHLVGD TQYPMEMHL VHYKAHD TIKDALAEGAYDSLAVIGIFFEVSEQRNPAL DLM PYLA KIAAHSEAATPFPPISSFLWGGDMSSFYRYNGSLTTPTC NEIVQWSVMKVPVPVTDQLEVFRQLMTDYEPPLVDNFRPPQ ALGGRDVLDVMTVEMLRKGSHSGCEILAGPAALLASL LILCC RTWDL
177	MQEITVTVYNNIRPSPVTPWNPEPRLPKIHPSAYIDPAAVVQGD VTIGENVMVSPNASIRSDEGYPIYIGDNSNVQDNVVLHALETV DENGEIEENIVTGVGDKKYAVAVGDNVSLAHQAQVHGPAAIVG DNTFIGMQAFVFRSKVGKNCVLEPLAAAIGTVPDGTYIPAGT VTTQEEAAKLPKVTPDHFPANTNAAVVKVNVALAKGYLAL K
178	MSTLVKAIRENP GCDWQYHFNPKISLIGRGHQSPIDIKTDAL FDPSLKLPSVSYDPATARL VNNGHTIQVEFEDSTD KSVV EGGP LEG PYR LKQFH FWGKKDG VGEHTVDGKSFPSELH LVHWN AEKYAS FGEAAAAPDGLA VLG VFLQVGEHHPSMNRLTD ALY MVRFKGTKAQFSCFPNKCLLPASRHYWTPGSLTT PPLSE SVT WIVLREPISV SERQMEKFRSLLFTSEGEKEKRMVDNFRPLQPL MNRTVRSSF
179	MSEKGPGAYWGEIKEEWAACSGNTMQSPIDLLNERVEVVPGLG ELKRN YKPSNATLKNRGHDIALEWNGEAGSILINGTPYFLKQC HWHS PSEHSINGR RYD MELH L VHQS PENKIAVIGILY EIGPPDT FLSSLMDH IKA VTD TTEAERSVG VGINPREIKRGSRKYYRYIGSL TVPPCTESVIWTVLAEIKKKIN
180	MLMRSLFIPTIVLSLILVSSNFAAEQDGADFDYNERGPEHWSQL DAKYKLCKDGERQSPINIFITSIDLAIKLPVNFIKQNTPNVKFPT ISMKKEGHATKFLPQQLIGSSFD SVRYI FNQVHFHTPSEH RFDGI HTDLEAHFVFEDSVTKY SVIGVLYEVDCAVGSSFFDSI IKLY NQDPNAKDNVPVDINSEVF SHIKEVY KYFGS LTT PNCTED VTW WVVKPLLI STSQLVLRKHIGFNSRPTQPRNGRKESNRL LIFH VKRFLLNYQVTVFAVFGLVGGITIE
181	MKLYTVIRGNPACSFHEDQWFAPS VQPGGHQSPINIVTSQTKY DPNLKPLTISYDPAT SLEI L NNGH S FQVTFD DTQDKS VL RGGPL DG VYRLVQFPHFWGSSD E QGSEHTVDKKYAAE LHLV HWN AVKYETPAEAAQEPDGLA VLG IFLK VGEHNAELQK ITD ILDSIK HKGKQTRFTNFDPICL LPPCPDYW TYPGSLTT PPLSE SVT WIVL KQPIEVPSQLAKFRSLLFTSEGETACC MV DN YRPLQPL MNRT VRSSF

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
182	MQEITVSFFSNVKNEVTSTNPKPVTPVIDPTSYVDPKATVIGD VHIGKNCYIAASAVIRADEGAPIYIIGDRSNVQDGVLHALESV ADGGKVLEDNNVLEGDENYAVVGKDVTLAHQAQVHGPAA VGDHSFVGMKALVFNAVKVGKNCVIEPEAAAIGVTVPDNKYIP AGTVVTTQEEADKLPEITPDHENYTKVAEVVAVNVKLCEAYK SKA
183	MLSVPVSIATRAPDAVDASAPGEWGYADSSNGPARWSILD ADGKASYPACGCAACQQSPIDLVRVTAAKGNVRVGSADRRLVA PAKPVTLAVSQKHGTNYVATDQNNDAAVVAPDGVRYTENS LHFHTPAENTVDGVANAMEMHMVHLSEAGDIAVLGVLFRHA DADLPANAEVTKLLRKIDADGKTKVAVDGLGLYDGGAGFW EWTGSLLTTPPCSGNVRWLLQKEVRGVNDARQAEAFKKHVGGF PGNARPTQPLNGRAVLSFDPTGIV
184	MQEITVPEFSNIATKNEVTSTNPKPVTPVIDPTSYIDPNATVIGDV TIGKNVMIWPTAVIRADEGKPIVIGDNSNVQDGVLHALESVN DGGKIREDNVVIEGNELIYAVVIGKNVTLAHQSQVHGPARVGD DSFVGGMKSLVFKSDVGSNCVIEGNAAAIGVTVPDGKYIPPGTV VTTQAEAEKLPEITEDYPFSDANQAVVEVNVLCKAYRGLQ
185	MLAAGAHWEYSGEAGPANWAKLTPEPGACSGKNQSPINLTGF IEAEELFLAFAYQASATQVLNNGHTQVNVAEGSTLTDQGTF TLKQFHPHSPSENRIEGKSFPLEAHFVHASEQGALAVVALMFQ EGAANPTELEKAWRVMPAHADQPVALPRPLDVQALLPKDHAY YRFNGSLTTPPCSEGVRWLVLKQPVBEASKQIEKFQKIMGYPN NRPVQPVNARTVLSS
186	MQEITVLEYSNVTKNEVTSTNPKPPTVTPVIDPTSYVDPNATVTG DTIGKNVLIGPNAVIRADEGAPIVIGDNSSVQDGVLHALESV DDDGEVIEDNVVLYGNKDYAVVVGKNVLAHQAQVHGPAA VGDDSFVGMKALVFKSIVGNSNCVIEPAAAIGVTVPDGKYIPA GTVVTSQEEAANLPEITPDHEDYTTQEAVVKVNVLCEAYRN QA
187	MMSVATAALLLSAVGTLAADWRYPTPGPDGSVGSPEWGG CDHGRQSPIDIAYAASVRGSYPEIFIDFSDYSLPD SAYIVNNGH TVQINLDSASSSVYCGGFRSKYVLEQLHFHWSEHTIEDRRY ALEMHLVHRQSYASVQEASSHKAGIAVLAFLFHDEHPNEA IQ LILNSTSPIKAKVDDRQPLRGSLHLNDLLPKDRTVYFRYEGS LTTPVCAESVWVTFPFESLPISLGQVQDFMTIHADNRTLVN YRPVQPLNTRVLVLVSDTEVEASGARRIASGMFAAVLSSL AIS LF
188	MKILVTFASCYEPRNDHWOEPWSYEGISGPDHGELNPEYS LCSTGKEQSPIDIDHTIKAQLPALKFDYKSEPLKYVINNGYTIRV NYHDAPGSGNFLIVDDTRYQLTQFHFHRPSSEYIHGKPYDMEL HLMHQSSDGKVAGVTFTIKTGRANSTTQKIWEHMPKTGQQE VAGVEINPADMLPHDTGYYVVMGSVTAPPCTEGVNWFVLQR PVEISADQIEAFAKLYPHDVRPLQPLNGR
189	MKN SLFATIVGCPERWDHQPVAPLGQRQSPIDIVPADAQYDS SLKPLKLQYDPTCLDLINNNGHSFOVTFVDDDSSTLTDGPISG VYRLKQFHFWGASDDKGSEHTVNGAKYAAELHLVHNNAV KYASFAAALEPNGLAVLGVLKVGEHNPALQKLTDILPSIKH KDTQASF GKFDPSCLMPTCPDYWTYAGSLTTPLSESTWIVL KEPIEVSEEQLGKFRSLLFTSEGEKEKRMVDNFRPLQPLMN R
190	MQEITVTLTYSNVTKNEVTATNPKPPTVTPVIDPTSYVDPNATVTG DTIGKNVLIAANAKIRADEGKPIVIGDRSTVQDGVLHALES VDDDGKVIIEENVVLEGDEYYAVVVGKNVVLAHNAQVHGPAA VGDDSFVGMNSL VFNSVVGGSNCVIEPNAAAIGVTVPDGKYIPA GTVVTTQEEADKLPEVTEDYEFYTQIAEVVKNVNLC EAYRK QA
191	MKFIATTALVAACALAI STVSAVSAVSEAGVKGAPWGYKPD DTTQASPQWADHYPD CNGTHQSPIDLVTDVKQQTKAQNT LRFRGDCA SFNL TQSAEGYKAEV VGGSCQVRGNKARYD LQF HVHAPSEHTLNCEPLDGEVHFVHSN KDG SALLV VGLFMEIDPS GNTDPWLET LIDGIDDV SPTKEV MLDL TSYSALVKKTVRGSSL FNYPGSLTTPGCSEIVDWV VVEKPMKISAKDLTRIRENQGEID LNYKSESARPVQPLNDRIVKS FQ

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
192	MINSRPLIFAVYDHGTAICGPADWKNSAHCVENTQSPINIKT DKIFMHMPYFDGFHFIVDNVVGSVGVLVNNGHATPLVIDQF ETPAITGGPWANKVYRLNQIHFHFGCDAKGSEHTVDGRVY SGEIHFPVTYNTKYFDHAAADKPDGLSVVAVFLLDNGDKSNW KQLTDEMKKI1KADSFTKVPMMYYINLYKMVPELRALFRAPFY YKGSLTTPPCYOSVKWVVLQNPVSTSRELMTAMRSLKHNHEGH SLCNNFRPTQPLNGRILAKHLKY
193	MSLKRIFGVATPEDQHNYCWCYEEENGPSWKEHFPPIANGPR QSPIDIKTSETKYDSSLKPLSVSYDPSTAREILNVGHSHFHTFED SENKSVLKDGPITGVYRLKQFHFWGAADDKGSEHTVDGAK YAAELHLVHVNAVKYKSFEAALEENGLAVIGVFLKLGHHE ELQKLVDLPAIKHKDALVTFGSFDPSCLMPTCPDYWTYPGSL TTPPLSESVTWIIKKQFVEVDHDQLEQFRTLLFTSEGE
194	MQEITVTRYENIQPSPPVTSWNPEPKLPEIHPTAYIHPPAAVQGD VTIGKNVLVMANAVIRADEGYPIYIGDNSSVQDNVVLHALET DKNGNTIEENVVTVGDEKYAVYVGDNVVLAHNAQVHGPAAV GDNTFVGMMALVFRSRVGKNCVLEPLAAAIGTVPDNKVYPA GTVVTTQEEADKLPEITPDHPFANLNKRVVEVNVELAKGYLAL S
195	MKLIRSAVTGFCPEWNDHYQYDGISGPAYWGLINPDWTLNC GKRQSPIDIDPNKLLFPNLKSLHIDKHKVSGVLENQSLVFR VDKDTKQHVNISGGPLAYKYQFHEIFIHYGLEDSNGSEHSV YSFPAEIQLYGYNSDLSYNSMSEAQEKSQGLVGISLLVQIGDMS NPELRVLTTEALEKVKYKGQTTRIRKENVRGLLPDTQHYMTYE GSTTHPGCWETTVWIILNKPIYITKQELYALRRLMQGSKEHPK APLGNNARPTQPLHHRTVRTNIDFKHKKD
196	MSQDEQKWSYAQDYLWKSPECTGSKQSPINIDTSQIQRGCVLC DLKLYLKSEKPSVEFTSQNDVILSFVNQSISITFNRYFNLRSIR VHVPSSLHTIDNSKTMEVVCLFDSGNNNETSSNDSLQNVAKG VQLCFMMNQSNNEYGNIEQFFNQFIHKIPTVQDELPIEVNVSS WSPPELLIPNKQNFYYYYEGSLAYPPCESEMYINIVYEIIGNIGVSNF RILKKYIRNNTRALKPKNNRVVVYSVDETNSASIQSNSVDKISD DRFLQCERRNNVVKTKQVIASETIPEDN
197	MWLFSFLFYVAVHKNSGKNLHIKVLRAPKMIALLSHTQGAQP SLPDRTYMPIAKKLPYTKHRLAAVILLIGMFVYHSALSSEEQP WHFTTPAKADDCCSQQSPSEGAPCGCGELQSPINIKHSLRAHLP VTRYSPGPATVKHIGHTEVRTEMKGHLTLGAKSYDFVQLHF HLPGVDLLIKGRSYPLVAHLVHRSSTGEVAVVAIVFKRGQENAN LAQLLAVMPRHKGDAFVLGKFDIAQLPQQRKYYAYKESMS AQPGIEGINWHILKTPMEVSDAQLHAFQLILPAHRRPAHPARN RSVRVGG
198	MQEITVLTFSNITKNEVTSTNPKPCTPIIDPTSYVHPLATVIGDV TIGKNCMISASASIRSDEGRPIYIGDNSSVQDGVVVLHALESVDD GGKIIIEENVVLEGNEYAVYIGKNVSLAHQSQVHGPARVGDD SFIGMQSFVFNSIVGSNCVIEPNAAAIGTVPDNKYIIPAGTVVT TQEEADNLPEITPKHAAFTTQEAVVKVNVLCRAYRNLA
199	MTTATDHDIDYGYGPTNGPHWTWCITCRTAAGTHQSPINIIITHNCH FDPTLTFFKVFSSHGHQIILSRKQHNFQVSFKTDRPTYVEGGP LKNKYNNLQLHFHWGCYDEWGSEHHIDGHSYAGELHLVFMN EKYANINQAFNDPEGLCVIGIFLKPSVEGCSAMAPMMAAMKS SKPGCETSVKGEIDINGLIPNNSRYFTYEGSLTTPPCVECRWIV CAKPLRLSKDQLAALRSMHCETCTNENFRPPPVPGDRVV CSFPQSIRPQKCDT
200	MQEITVTTFNNIQPSPPVWNPEPKLPEIHPTAYIHPPAAVQGD VTIGANVLVMANAVIRADEGYPIYIGDNSSVQDNVVLHALET DADGRRIEENVVTVGKEYAVYIGDNVVLAHNAQVHGPAAV GDNTFVGMMALVFNNSRIGANCVLEPAAAIGTVPDGRYIIPAG TVVTTQAAAALPAVTPDHPPATLNARVVAVNNALAAGYLA LA
201	MVAIILGVLMSSCEEVEVTVERHSPHWDYESTMWQNIGYTDG GIVQTPINIEETANTIKSADLSDVTFNNAFDIKIVDNGHTVQVN RDATAKTNNMVIDGVTYDFLQFHYHTHSEHEIDGATDEMEIHL VHQDPITKNLAVSVMLNANGTPNDFIESYLENFPSTEENEV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	ATTTSIDLDLLPSNHNYYTYTGSLLTPPCSQGLKIVLKDVK DVSVEQMHKFEETHGVNARPIQPLNGLRVLEKI
202	MQEITVLDFSNVTKNEVTSWNPKPPTVVIDPTSYVDPNATVIG DVTIGANCYIGPSASIRADEGKPIVIGDRSNVQDGVLHalesv DDGGKIREDNVVVGDEYYAVYIGKNVLAHQAQVHGPAAV GDDSFVGMKSLSVFKSDVGSNCVIEPFAAAIGVTVPDGKYIPAG TVTTQAEAAKLPEITPDHANYTQQEAVVKVNVLCRGYRRL Q
203	MQEITVLIYSNVEKNEVTSTNPKPPTVVIDPTSYVDpqATVIGD VTIGKNCYIAASAVIRAEGKPIVIGDNSNIQDGVLHalesv DGGKVLEDNVVIKGNLAYAVVIGKNVLAHQSQVHGPARV DDSFVGMNSLVFNSIVGSNCVIEPFAAAIGVTVPDNKYIPAGTV VTTQAEADQLPEVTDDHPFYTEVAAVVKVNVALCQAHKGLS
204	MLTPARSIFCGWKEQDHNSLSPTLRLPLVDGRQSPINIVPGN AVYDPRLKPLTLSYDPATSLEILNNGHSFQVTFDDSDQDKSVLK GGPLDGVYRLKQFHFWGASDDHGESHTVDGVKYPSELHLV HWNAKYDFGEAASKPDGLAVVGVLKIGHEKPHMQVKLDA LDAIKTKGKQTFTNFDPSLTLPGCLDYWTYDGSLLTPPLLESV TWIVLKEPISVSPAQMAKFRSLLFTSEGETACCMVDNYRPQP LKGRQVRASF
205	MSLKNIPTAVCGPEQWHDYFRKANGNFQSPINIDTKETKYDSS LKPLTLSYDPATAKEIILNNGHSFQVTFDDTDNKSVLKGGPLTG SYRLRQFHFWGATDEKGSEHTVDGVKYASELHLVHWNAV YASFAEAASKPDGLAVLGVLKIGKHHEELQKITDTLNSIKTP KQTTFTNFDPSCLLPSCLDYWTYFGSLTTPPLYESVTWIVCKQP ISVSSEQLAQFRSLLSNAEGERKACCMVDNYRPQPPLKGRKVR
206	MQEITVTNYNNIRQSPVTSWNPPTPKLPIHPTAYIDPAAVVTGD VTIGKNMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET DANGKEIIEENIVVVGDKKYAVYIGDNVSLAHQAQVHGPAAVG DNTFIGMQAFVFRSVVGKNCVLAAPLAAAIGVTVPDNTYIPAGK VTTQEEAKLPEITPDHPFANTNKAVVAVNVELAKGYLALS
207	MRSIKLLCLPALLATTIANAGASLDQWDYSSHGERYWRSHFPA CQGMQQSPINISTKRALKHPKAFFSLKPGVLDfspaaPVHIE NNNGHSIOPFEYRGNSLLHRGESYQLKQFHFWHASETTIDGKHS PLEVHFVHKSSQGHTLVIAVLLDSGRAENIILISSLKAADSSPQN GVNKSSFPKKLLPKBEDFYFFEGSLTTPCTEGVHWAVMKH KGLVSEQDVRYFAKFDY PANFRHTQFINGRSTYYFSDIDRSED DIKNSSGR
208	MQEITVSNFSNVTKNEVTYPNPKPPTVVIDPTSYIDPNATVIGD VTIGANCVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET NDEGKILEENIVVGDKEYAVYIGDNVVIAHNAQVHGPAAV GDDSFIGMQSFVFRSKVGSNCVIEPQAAIGVTIPDGKYIPAG VTTQAEADKLPEITPDYQAQSNTQAAVVTNVKLCEAYRNKQ
209	MQEITVTNYNTIQSPVTPWNPPEPKLPIHPTAYIDPAAVVQGD VKIGENVLMANAVIRAEGYPIYIGNNSSVQDNVVLHALET DENGNRIIEENIVVGDKEYAVYIGDNVVIAHNAQVHGPAAV DNTFIGMQSFVFRSKVGSNCVIEPQAAIGVTIPDGKYIPAG VTTQEEAKLPEITPDHPFANLNERNVVKVNIALAKGYLALA
210	MRKTLAVSIFCGWNYDPEHQWWDYDDQENGPHRWPKLYPEC GGNAQSPIDIKTETKYPDNKLPLTLVGYDKNGLEFSMTNNGH TVQISLSSSMYLKDSDGTVYIAKQMHFWGGDSSIESGSEHTID GMRYLIEHVHYNSKYKSYDVAQDAPDGLAVLAFFEVKD YAENTYYSNFINSHLENIKYPGQSTVLRGLDIQDMLPKNLHYYY SYLGSLLTPPCTENVHWFLADSVKLSKTQVWKLENSSLHDQ NKTIHNDYRKTQPLNHRVVEANF
211	MQEITVMEFSNVTKNAVTPNPKPPTVVIDPTSYVDPEATVIGD VTIGENCMSAFASIRSDEGKPIHIGRNSNVQDGVLHalesv PTGMVNNEENVVAGDELYAVYVGKNVSLAHQAQVHGPMV GDDSFIGMQSFVFKSIVGSNCVIEPMAAAIGVTVPDNKYIPAG VTTQAEADKLPEITPDYAYYTTVAAVVSVNVNLCKAYREQA
212	MKILTFASVCYGPENWHRDFQAAKGKRQSPIDIVPASAKYDSS LKPLTFTYEAGTSRCIVNNGHFSNFVFFDDSDQDKSVLSGGPLTD

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	KYRLTQFHFWGKTDEGESEHTVDGHSYPAELHLVHWNADK FASFGEAASKPDSLAVVGVLKVGDEHPGLKKVTDALYSVKF KGTKAEFKNFPNKCLLPASLDYWTDGSLLTPPLSECVTWIVL KEPISVSSGQMGKFRSLLFTSEGETECCMVNDYRPPQPLKGR
213	MQRKLPSVAIFCTGYENHDWGYEDHNGPEHWHELFPIANGDN QSPIELHTKEVKYDSSLQWPWSASYDPGSAKTIILNNGKTCRVVF DDTYDRSMLRGGLTGPYQLRQFHLHWGSSDDHGSEHTVDG VKYAAELHLHVHWNAVKFESFEAAAALEENGGLAVIGVFLKIGRH NPELQKLVDVLPAIKHDKTLVEFGSFDPSCLMPTCPDYWTYPG SLTTPPLESVTWILLKQPIEVHDHQLEQFRLLLFTSEGEKEKRM VDNFRPLQPLMNRTVRSSFRH
214	MLNSPSAANDERPEVEDGAWIHPASAALGVNVSIGSRAYVGQ ASIRADEPGPDSVAPVVISEANVQDGAVLHALGGTSVVRS RTSVAHGAHVHGPCQVGPGCFIGFNTVYDAELGEQVVMH GAVVENVEIPDGLLIVPSRAAVCCQEDVRALDEASESALAFADE VSRTNVHLAEVKNSEQTGYYE
215	MQEITVLEFSNRKNEVTPTNPKPPTPVIDPTSYVDPNATVGD VTIGANVLIWPTAVIRADEGRPIVIGDRSNVQDGVLHAELEV DDGGEIREDNVVRVGDENYAVYVGKNVSLAHQSQVHGPAAV GDDSFVGMKSLSVFKSKVGSNCVIEPDAAAIGVTVPDGKYIPAG TVVTTQEEAKLPEVTPDYAYTTVEEVVTVNVALCEAYREE A
216	MQEITVTRYENIRESPVTPWNPEPRRPEIHPTAYIDPKAVVQGD VTIGANVLVMANAVIRADEGYPIVIGDNNSSVQDNVVLHALET DENGNPIKENIVKVGDKDYAVYIGDNVIAHNAQVHGPAAVG DNTFIGMNALVFRSVVGKNCVLEPLAAAIGVTVPDGKYIPAG VVTTQEEADKLPKVTPDHFPANLNARVVKVNVALAKGYLAQ A
217	MQEITVTVYNNIQSPVTPWNPEPKLPKIDPTAYIHPKAVVIGD VTIGKNMISANASIRSDEGYPIYIGDNSNVQDNVVLHALET DENGNRIEENIVVVGDKKEYAVYVGDNVIAHNAQVHGPAAVG GDNTFIGMQAQFVFRSVVGKNCYLAPLAAAIGVTVPDGKYIPAG KVTTTQEEAKLPEMTPDHFPYKTNEAVVKNIALAKGYLAL K
218	MQEITVTRFENIQSPVTPWNPEPRRPEIHPTAYIHPPLAYVQGD VTIGENVLVAAHAVIRADEGYPIVVGNNNSIQDNVVLHALET DENGNRIEENIVTVGDEEYAVYVGDNVIAHNAQVHGPAAVG DNTFVGMNSLVFRSRVGKNCVLEPLAAAIGVTVPDGTYV VVTTQEEAKLPKITPDHPFANLNARVVKVNVALAKGYLAL S
219	MKIGTVLSIFLGMHAAVDDHSSPWNNTWGS DWGSLTAIAG NECGNRNQSPIDLPSVSDSSQIYASKSDNFNKMYTDQTNK WDGHTSKITIVMPGEDLQKFSSSFAKDYLQGPERFSGVQFHF HGSEHTIDGERHDLEMHTVHPDEGAKGGIKYAAMGIMFSVD KHTANABEWVKIIIDDFENLQWSSETTDPIVDLVSYGVMM MVDTDNRWVYKGSVTTPCATTLYWVNVRKIYPLKQKYLDQ FKNQLKRGSLTGNYREIQAQYDDHDLHII
220	MITFLVSLAALVCCEFVHSNLPLVACWYNNPACNFPNWPN QYCNGSSQSPIDIVTAQVQGNPNLQTFLTGFDANTTFTSIT TSVVSLDEDIMSVQGGLPGLYVSVQFHLHWGSSSLPGSEH TVDBGKQYAMELHVNLHSTYDGNVSAALAANDSSALAVLGFF IETGTDFADKTNSDIITSFLSNI PNSGNTYDIDMQIT GVNKTKYYRYQGSLLTTPCNEVDVIWTFKEPIKVNNNLIN TKVFAKATAKASDLNVNNFRGVQPLNGRVVTSQVEQT SLVPTSISSSLILLTLSCL
221	MQEITVYDYSNVTKNEVTSTNPKPPTPVIDPTSYVDPKATV DVTIGKVLIGFAVIRADEGAPIVIGDRSNVQDGVLHAELEV DDGGKVRDENVVRHGDELYAVYVGDNVSLAHQAQVHGP VGDDSFVGMKSLSVFRAKVGKNCVIEPGAAAIGVTVPDG AGTVVTTQEEAKLPEITPDHPNYSKVDEVVAVNVGLCEAYR ERA
222	MRSALVPIFYKGHQEDWNTCKNQGMQSPIDLLHERVEV GRLQKSYKPSNATLKNRGHDMMLRWGDAGGLEINGTEYVL

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	QOCHWHSPSEHTINGRRFDMELHMVHQSRDNKIAVIGIMYKIG RPDSFLSKLMDHISAIADTTEEEKAVGVIDPRNIKIGSRKYRYI GSLTVPPCTQNVWVTIVRKVRTVTRQVRLLRVAHVHD
223	MRPPPQRQGKTHREGKEMTTAAWKAIIFAMVLASVLLVDADD AHVKFGYSGSIGPEKWASLSPGYQMCMSKGERQSPVNIDKSKLA YNPGLAALERNYVPANATLVNKGYQIAALLFDKNVGTLLVVDGK NYSLKSVWHSPSEHTINGKRFIAVELHMVHMSDNGRIAVVAI LYQIGRDPFVVQIERKLKELAEEACKGDEEAYVVPGVVHTRS LKRHSSKYFRYSGSLTPPCENVIWSILGKVREMAEEQLAAL QAPLSQEENRNNAARPTQPLNYRAVQLYHESRKHDEYSR
224	MQEITVLEFSNTKNEVTPTNPKPPTPVIDPTSYVDPNATVTGD VTIGKVNMSIDSASIRSDEGKPIVIGDRSNVQDGVLHalesvd DDGEVIEDNVVYGDENYAVVGENVSLAHQAQVHGPAAVG DDSFIGMQAFVFKSTVGNSNCVIEPEAAAIGVTVPDGKYIPAGTV VTTQEEAKLPVTPDYPFYTTQAAVTVNVALCEAYRAER
225	MKKPKLFLNLLGTFAATFAYEYNPGNSDYPRENWAQMDSPNNI QCDWANQSPIDLQTQFVLIQSRAWSLITNLRTMPENVVLTNV GHGAETSEFANNDNMVVTGGPLNDQFIVAQAOQWHWGTAADC AGSEHMLNSQRYSAEVHIVTYNSKYASLEDAADKDYDGLAVLG FLYEVDRAANSDFPQSVQTSLLGGITFGCDSTTVSPFPLIDLFRTE FFDYIAYSGSLTPPCYQTVQWMVSTKPLKIWSSLDALRSIN DVNGSPLLRNFRPCQNSYSRALNGYYL
226	MQEITVLDFSNITKNEVTSWNPKPTTPVIDPTSYVDPNATVIGD VTIGENCLIGASAVIRADEGHPIVIGDRSNVQDGVLHalesvd DEGEYIEDNVVVKGDEEYAVYIGKNVSLAHQSQVHGPARVGD DSFVGMSLVPFKSDVGSNCVIEPFAAAIGVTVPDGKYIPAGTV VTSQEEAKLPVTPDYPFSTANEAVVKVNVALCEAYREQK
227	MQEITVTRYENIRPSPVTPWNPPEPKLPKIHPTAYVDPAAVVQGD DVTIGANVLIMANAVIRADEGHPIVIGDRSNVQDGVLHalesvd RDENGNLLEENVVKGDEEYAVYIGKNVSLAHQAQVHGPAAV AVGDNFTVGMNALVFRSVVGKNCVLEPLAAAIGVTVPDGTYIPAG PAGKVTTQEEADKLPKITPDHPHYNLNERVVKVNVALAKGYLK LAQA
228	MQEITVTVFNNIRPSPVTPWNPPEPKLPKIDPTAYIDPAAVVQGD VTIGKVNMSANASIRSDEGYPIYIGDNSNVQDNVVLHaleTV DENGVLEENVVTGDKKYAVYIGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFKSVVGKDCVLEPLAAAIGVTVPDGTYIPAG KVTTQEEADKLPKITPDHPFANTNAAVVKVNVALAKGYLK K
229	MKNWRITAFLFGCYHQPEDYFSYDGISGPAYWGEINPEWL CNQGMQSPIDLNNEREVVSKLERIKKNYKPSNATLKNRGH DMMLKWESEGAGSIHINGTEYVLKQCHWHSPSEHTINGRRYDM ELHMVHQSAVDNKTAIVGVTYKLGRPDSLSSIMKHKAISDTTE AEKAVGVIDPRHIKFGRSKYRYMGSLTVPPCTEGVWVTIVK KVRTVSREQLRLREAV
230	MELKVLSAHLFWILVGPLFVVIKAAEWSYADTSKWPKDYP SCSGYYQSPIDLTYKDSVYAPQLGQITITNLSKVEQTTYKVINN GHTVEVSFNEQWKISLGSDEDPYPIQMHPHWGGPTREGSE HLIGDLRHAMEHTIVCYNGRLYKSKEEATSSPONGLAVVGLHE EDKLAQTEQTERGKMGFETALASITTTKESKNIAAFDLAGLL GQVDTTQYFRYQGSLLTPPCQNVWTFITFVPTPAQLEL LRGLRTSSSTPLQDNYRPVQPLNDPHSPLPRTVYRTISAANRFT HSWWASFMLSFLACCSHGIL
231	MQEITVTEFENIQPSPVTSWNPTPKPVIHPTAYVHPAAVVQGD DVTIGKVNMSPLASIRSDEGYPIYIGDNSNVQDNVVLHaleTV DANGNTIEENVVTVGDKKYAVYIGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFRSIVGKNCVLEPLAAAIGVTIPDGTYIPAGT VTTQEEADKLPKITPDHPFANTNKAVVKVNVELAKGYLALS
232	MTLSLFAAAADVQECPPRYSYCGYSGPEQWKNIVFKDKRN ECNGTTQSPINLGTPTSGPTIHVEYVGNVAGNATIRNTGHD EVTPMRCNNKIKVGSRVYTLLQLHFHVPEHHVPRIGKAVAE

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	MHILHQDGTDYAVIGVMLTIGPTDSALAPVFENLPKEACA PPKPLEINFKKLLPEELTGYYTYVGSLTTPPCTEKETVTWYVL DAPREIPASDLKLKGALGKNARPIQTNPLTVTYVSPTPTPK
233	MQEITVAEFSNVVKNEVTPNPKPTTPEIDPTSYVDPNATVEGD VTIGANVLIHAFAVIRADEGRPIVIGDRSNVQDGVLHAEHSV DGGEIREDNVVLHGDDLYAVYVGKVNHLAHQAQVHGPARG DDSFVGMKSLVFKSDVGNSNCVIEPFSAIAIGVTIPDGKYIPAGTV VTTQEEAKLPEVTEDYAFSGQNEAVTVNVDLNEAYRQQR
234	MQEITVTFNNIRPSPVTPWNPEPKLPIIDPTAYVDPLATVTGD VTIGKVMISANASIRSDEGYPIYIGDNSVQDNVVLHAELEV DENGNRIEENVVTVGDKYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAQFVFRSNVGKNCVLEPLAAAIGVTIPDGTYIPAG KVTTQEEAKLPEVTPDHFPYKTNAAVVKVNVALAKGYLA LS
235	MLATFSRPNQGHVEIDYCKWTKYVSISGSSTWKDQFPPIANGNR QSPIDIKTSETKYDSSLKPLSVSYDPSTSLEILNNCHSFQVTFAD DSDSSTLKDGPIGTGVYRLKQFHFHWGASDDHGSEHTVDGVKY PAELHLVWHWNNTKYGDFGEAASKPDGLAVVGVFLKIGREKPEF QLVLDalesIKTKGKQASFNTNFDPSTLLPGCLDYWTYDGLTT PPLLESVTWIVLKEPIVSVPQAMAKFRSLLFTSEGETACCMVDN YRPPQPLKGRQVRASF
236	MIKTNPRGDLQVHESAFVDPTAILCGLVIVEEYVFIGPYAVIR ADETDAGRIAPIVIGHNSNIQDGVIHSKSGASVIGQRTSIA HRAIVHGPGRVGDGVFIGFNSVLFNCTIDDGVVRYNAVVDG CHLPPGFYVRSTERIGPETDLAALPQVTADASDFSEDVARTNN ALVLGYKHIQNEF
237	MQEITVTFNNIAESPVTPWNPEPKKPKIHPHTAYIHPLAYVQGD VTIGENVMVSANASIRSDEGYPIYIGNNSNVQDNVVLHAELEV DENGNRIEENVVTVGDKYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAQFVFRSTVKGDCVLEPLAAAIGVTIPDGTYIPAG KVTTQEEAKLPIKTPDHFPYKTNAAVVKVNVALAKGYLA A
238	MAAWAGGGPHWSYEGAGGPANWARLTPEFGACAGRQSPID LTGFIEAELPPLAFAYRAGGRSIVDNGHTVQVTYAPGSVLEV GRRFELQOQFHFTPSERERINGRSYPLVAVHLVHRDAAGHLAVVA VLFKQGAENPALAPLWAAMPKGAGETRALKAPLDAGALLPA RRDYFTYMGSLTTPPCSSEGVRWMVLRQPLEVSAAQVARFREV MGENARPVQPLNNGRTVLHRVM
239	MQEITVTFENIRPSPVTPWNPEPKLPIIHPHTAYIDPAAVVQGD VTIGKVMVSANASIRSDEGYPIYIGDNSVQDNVVLHAELEV DENGNRIEENVVTVGDKYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAQFVFRSTVKGDCVLEPLAAAIGVTIPDGTYIPAG GKVTTQEEAKLPIKTPDHFPYKTNAAVVKVNVALAKGYLA ALS
240	MQEITVTRYENIRESVTPWNPTPKRPEIHPHTAYVDPLAYVQG DVTIGANVMVSAHASIRSDEGYPIVIGDNSVQDNVVLHAELEV VDENGNEITEENITVVGDKYAVYVGDNVSLAHQAQVHGPAA VGDNTFIGMQAQFVFRNSVVGKNCFLAPLAAAIGVTIPDGTYIPAG GKVTTQEEAKLPIKTPDHFPYKTNAAVVKVNVALAKGYLA LS
241	MQEITVTLFNNIRPSPVTPWNPEPKLPIEHPTAYIDPAAVVQGD VTIGKVLIMANAVIRADEGYPIKIGDNSVQDNVVLHAELEV DENGNRIEENVVVGDERAYAVYVGDNVSLAHQAQVHGPAA VGDNTFIGMQAQFVFRSRVGKNCFLAPLAAAIGVEVPGDRYIP AGLVVTTQEEAKLPIKTPDHFPYKTNAAVVKVNVALAKGYLA ALK
242	MVPERCRRPTLLLTVSLAMAVAVSGACADDDKATAMRTAM PKPVSRASTASSAETVVTPTSVKEKRNTTSPHHGTQDSWSYD NVAAPATCAGNQQSMPMLRHPTADAHRGRSIRTLLTAATT RLRAVRDGSSIALLCNGYCGVVKVHGVTTHMIKNMHWHTPSE HTIDGRLDAELHMVAFAGGKIAVLSSLFKVANKNVLDRTIR

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	AMSGMRSMSATRKEVKDYFFSGAVKVSAAVYKGSLTTPPCTE GLSWVUNAKVSTMSKKQLSKIRELLGGHDNARPLQAPKGRV VEWMDVP
243	MKQNLFAITVSCYWREPGDHLWDKSAPSHWNKLYPIAQGNRQ SPINIITSQAVYSPSLKPYLESYDAATSLSITNNGHSVQVDFNDS DDRTVLKGGPLTGPYRLKQFHLHWGKDAVGSEHTVDGVKY ASELHLVHWNNAKYGKFGEAVVKQPDGLAVLGIFLKVGREKGEF QIFLDALDKVTKTGKEAPFTKFPDPSCLPACRDYTYHGSFTT PPCEECIVWLLKEPMTVSSDQMAKLRSLYSSAENEPPVPLVS NWRPPQPIKG
244	MIKKISLVLSTAALVLTCNYSEGGKPANVSAGYKKNWNYG TNNGPTHWEFSSTCGKGHQSPVNIIIPGKTLKMNHAYDLSMH DDITGLAKVIDNGHS1KVTPEHGGH1KLHGEIFDLLQYHFGKES EHTIDGKRFDMVAHMVHQNPKTQOLAVVAVFFEEGAKNKVL EKIINHVGSTVQldaQDFVPLQTEHYHYIIGSLTTTPCSENVQ WYLLKQPQEASEEQIKHFRKFYVDNERPVQELHDRFIEVN
245	MKITFLAVSCQHNEPDYWGRIKEDWKICKTGKMQSPIDLSNQ RVKIIISHLGDLKMNYSKSNATLKNRGHDIELEWKGGAGSIEIN GTEYVLQQCHWHSPSEHTINGRYYDLELHMVHESRDGKIAVI GILYKIGRPDSPLSKLMNIKSIISDTKDEERAVGVIDPRHIKIGS RKYYRYIGSLTPPCSQNVIVWTIVKKV
246	MQEITVLEFSNVTKNEVTSWNPKPTTPVIDPTSYVDPNATVIGD VTIGKNLIAASAVIRADEGAPIVIGDRSNVQDGVLHalesvn DGGKIREENVILHGDEEYAVVVGKDVS LAHQAOVHGPARG DDSFVGMKSLVFKSDVGNSNCVIEPFAAAIGVTVPDGKYIPAGT VVTTQAEAKLPEVTDYDYPFYTTQEEVVKVNVNLCEAYREQA
247	MSTPLVKWGYDEQNGAHIWCRFFPAANGKRQSPIDIDINTVKH DPSLKP LS VSYDP STAKEI LNVGHSFHVNFEDSDNRSLKG TGSYRLRQFHLLHWGSADDHGSEHTVDGVKYAAELHLVHWNP KYTFAEALKQPDGIAVVGVFLKIGREKGEFQILLDALDKIKTK GKEAPTTKFDPSCLFPACRDYWTYHGSLTVPPLLESVTWILKQ PISVSSEQLAKFRSLLCTSEGETAVFMLRNHRPPQPL
248	MQEITVLEFSNRKNEVTPWNPKPSTPVIDPTAYIDPQATVIGD VTIGANVLIGPMAVIRADEGAPIVIGDRSNVQDGVLHalesin EEGEVREDNVVVGNDENYAVYIGKNVSLAHQSQVHGPARG DDSFVGMKSLVFKSDVGNSNCVLEPGAAAIGVTVPDGKYIPAGT VVTTQAEAKLPEVTPDYPFYTAQEAVVEVNVALCQAYNEQS
249	MQEITVHHFSNVTKNEVTPWNPKPSTPVIDPTSYVDPNATVIGD VTIGKVLIAAFAVIRADEGAPIVIGDRSNVQDGVLHalesv DDDGKVIEDNVVIGHNKDYAVYIGKNVSLAHQSQVHGPARG GDDSFVGMNSL VFNSVVGNNCVIEPNAAI GVTVPDGKYIPAG TVVTTQEEAKLPEVTPDYPFYTAQEAVVEVNVALNEAHREQA
250	MQEITVHHFSNVTKNEVTPWNPKPSTPVIDPTSYVDPNATVIGD DVTIGENVLIGANAVIRADEGAPIVIGDRSNVQDGVLHales VDDGGEIEEDNVVIEGDEEYAVYIGKDVSLAHQSQVHGPARG GDDSFVGMKSTVFNSTVGENCVIEPDAAI GVTVPDGKYIPAG TVVTTQEEAKLPEVTPDYPFYTAQEAVVEVNVALNEAHREQA
251	MCDLN CIMTKMDNSDYMIVVCCVLLSIFLLEIWEWIFKVFTW TDNDVCLPPTFSFGYAHKNGPHTWKDLYPESAGSNQSPINITT RYAIVVQPS EPLRWINYN SVPLSTT L S NDGH T V I L RGFWDQSS WPQLQGGPLSDKYDFN IL FHWGPSN QEGSEHTLDYI RYPMEL QV I HMKH GLKSPK DAI I LGARDGIVI VSF L QINAMDNP YLDH VSNLWKISNP SHYK TNIPPF PLEWI FAPPFD RDY TY SGSL SQPPC NEBVTTW I QKEPIV ISALQ VEKFREIC SV DGPLL NCRPV QPLNE RDVYFYEESKL
252	MQEITVTVYNNIQPSPVTSWNPTPKLPEIHPTAYVHPAAVVG VKIGENVMISPHASIRSDEGMPIYIIGDNSNVQDGVLH ALET DANGNTIEENVTVGD K KYAVYVGK NVSLAHQSQVHGPAAV GDNTFIGMOSFVFKSVVGKNCVLEPLAAAIGVTVPDGTYVPA GKV VTT QEEAKL PKV TPDHPYANTNAAVVYVNV ELAKGYL ALA

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
253	MQEITVLVYSNVQKNEVTSQNPKPVPVIDPTSYVDPKATVIG DVTIGKNCMISASASIRSDEGPIVIGDRSNVQDGVLHAESEV NDGGMILEENVVLAGGEDYAVVVGKNVSLAHQSQVHGPAAK GDDSFIGMQSFVFNISIVGSNCVIEPNAAIIGTVPDNKYIPAGT VTTQEEADKLPEITPDHAYTTVAAVVNVNGLCRAYKNEA
254	MTWAVPLVLLPLVLASALGAVVEVPETCGAEAGACVDEESA MVQVKTPQSQRPSAATASGDVDYQGFQLGDWPEIAPLCAGG STTGFQAPINTIAVEGADYEKMPQASWPKFYAKEGGCDEAHFPV EKGTAWQVDFMNPKINLDCKNLEMEWKGKVYALVQFHFTL SEDTVDPQPTAMQMHHMVHLAADGSFAVVGVLIKTDGFFKNG FLEGIFETGFESDRMVTLLAKHRFNPYAGVLSKHGEFWHYEGS FTTPPCTEGVDFPLIAQSPPVTSKSYTSYMELKGNGKGNSYG QNHRPPIQPLNGREITTGRFLEVCPKKPAPDCGKLDPKKVQFCCE SA
255	MLSGPQTWYKRFAINCEDVHQSPINIVTKTI PDPNLKPLELTY DATTTRTIVNNGHSVQVDFEDSSNRTVITGGPLTGPYRLKQFH PHWGASDDKGSEHTVDGVKYASELHLVHWNAEKYSSFVEAA HEPDGLVVLGVFLKIGEHNPNLQKLTDALYSVRFKGTKAQFT NPNPKCLLPPSLDYWTYPGSLTTPPLLESVTWIVLKEPISVSPSQ LAKFRSLLFSEGETACCMVNDYRPLQPLMNMRKVRAF
256	MQEITVTRFENIAPSPTPWNPEPKLPKIHPHTAYVHPLAYVQGD VTIGENVLIAPLASIARAEGYPIYIGDNSSVQDNVVLHALETVD ENGNVLEENVVTVGDKKYAVVIGKNNVIAHLAQVHGPAAVG DNTFVGMLALVFKSNVGKNCVLEPLAAAIGVTIPDGKYIPAGK VTTQEEAKLPEVTPDHFPYKLNERVVKVNVALAKGYLAQA
257	MLGMKNTENHSAVLVQGHPAPANGGQIKVINNQEEGPSTWA ESYPDYCNGSSQSPIDDDWEVSPNPCLDSFVNVDLPLFTGYWK NNGHALQFTLDDGSGAVVSGPCLGNSTYQLLQVHFWGSAK GQGSEHTIEGKQHDLEMHMVHTNTAYETDEAANYKDGYLV GVLFDEAKQNKIRGFERTFRNFVKKSSKLQDSDEGLTAMFDV SDILRKSGVARSHFQYGSLSLTPSCNEVVTWILATKILKEKRSE LNALRSLQTHDEALVDNFRPTQELNGRKIMMF
258	MQEITVAEYNSVTKNEVTPTNPKPTTPVIDPSSYVDPNATVTG DVTIGKNCMISASASIRAEGAPIVIGDNSSVQDGVLHAESEV DDDGEVIEDNVVLYGNEDYAVVVGKNVSLAHQSQVHGPAA VGDDSFVGMKALVFKSIIVGSNCVIEPDAAIIGTVPDNKYIPA GTVVTTQEEAKLPEVTPDHEYYTEVAEVVKVNVALCEAHLA KA
259	MQEITVTRFENIQPSPTPWNPTPKLPEIHPTAYIHPAAVQGD VTIGANVLVMANAVIARAEGYPIVIGDNSSVQDNVVLHALETVD DANGNVIENVVVVGDERYAVVVGDNVVL AHLAQVHGPAA VGDNTFVGMLSJVFRSRVGKNCFLAPLAAAIGVTIPDGKYIPA GKVVTTQEEAKLPEITPDHPGANLNRVAVNVNALAAGYL QA
260	MQEITVTEFSNITKNEVATNPPEVTPVIDPTSYVDPNATVTGD VTIGKNCMISASASIRAEGAPIVIGDRSSVQDGVLHAESEV DEGMPIEENVVLEGDKYYAVVIGENVTLAHQSQVHGPARVGD DSFVGMKSLVFKSDVGSNCVIEPFAAIIGTVPDGKYIPAGTV VTTQEEADKLPEVTPDHFYNTAAVVKVNVALCEAYRNKA
261	MQEITVLEFSNVRKNEVTPTNPKPTTPVIDPTSYVDPNATVGD VTIGKNCMISASASIRAEGAPIVIGDRSSVQDGVLHAESEV DGGKLIEDNVVLEGNFYAVVIGNNVVL AHLAQVHGPAA DDSFVGMKSLVFKSKVGSNCVIEPEAAAIGTVPDGKYIPAGT VTTQEEADKLPEVTPDHFYNTAAVVKVNVALCEAYKKL S
262	MQEITVTKYENIRPSPTPWNPEPKLPPIHPTAYVDPAAVQGD DVTIGANVMVSAHASIRSDEGPIYIGDNSSVQDGVLHAELET VDEAGNVIENVVTVGDKKYAVVVGDNVSLAHQSQVHGPAA VGDNTFIGMQAFVFKSVVGKNCVLEPLAAAIGTVPDGKYIPA GTVVTTQEEAKLPEVTPDHFYNTAAVVKVNVALAKGY ALS
263	MCQLENAIEIDIFELKEDIVQCQWTPLVTITIVNEGTGEIEAQPN KIELQKVQNLCTIVKTEWMYQGADNQNDKWPQNCPSCDASL

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	EGNERQSPIDLNQPQMTNMVTKTLPKLTFPNPQNGDTLKGKFENK VNTIQFTANDLSQNKMHGGLSCEYSFWQMHCWKGKTNYEP GTTEPTKVEQHGSEHWIDGKQYDAECHWVHFNNKYATVGDA IASGDADALSIVGVMLEIDETNGQDEVEWIGTVKDAASALVTP DDGPAEDAPFNVYGFQLDQLGDSQCFCGGYYNYLGGLTTPGCNQ LVSFIIIDTPIRINMAQVKNVKYNKIESFCSIYVRQY
264	MQEITVLRFSNVTKNAVATATNPKPPTPVIDPTAYVDPNATVIG DVTIGKNCYIAAFARI TRADEGRPIVIGDRSNVQDGVLHalesI DDAGKVIEDNVVVEGNKLYAVYVGRNVS LAHQSQVHGPARV GDDSFVGMKSLSVFKSDVGSNCVIEPFAAAIGVTVPDGKYIPAG TVVTTQAEADALPEVTPDYAFYTQVAAVVTVNVALCEKYKA QA
265	MKLINFVGTACSPYEQWRDHYPIDAGNRQSPIDIVPGSASYDS GLKPPLTLKYDPSTSLEI LNNNGHSFQVTFVDDSDSSTLKGGPISG VYRLKQPHFHGWSSDDHGSEHVVDGVKYAAELHVWHWNAA KYSSFVEAAHEPDGLAVLGVPLKVGEHNSQLQKITDILNSIKEK GKQTRFTNFDPICLLPPCPDYWTYPGSLTVPPLESVTWIVLKQ PISVSSSQLAARNLFTSEGEKACCMVNYYRPLQPLMNRTVR SSFR
266	MQEITVLVYSNVTKNERTSYNPKPPTVVIDPTS YVDPNATVIG DVKIGKN CYIAAFAVIRADEGKPIVIGDRSNVQDGVLHalesI VDAGGKLIEDNVVIHGDNWFAVYVGKNNVLAHRAQVHGPAA VGDDSFVGMNSLVFN SKVGSNCVIEPFAAAIGVTVPDGKYIPAG GTVVTSQAEADKLPEITPDYAYYTQNAAVVNVNIGLCRGYKR LA
267	MQEITVTVFENIRESPVTPWNPTPKRPIIHPTAYIDPAAVVQGD VTIGANVMVSANASIRS DEGYPIYIGDRSNVQDNVVLHAETV DANGKRIEENVVRVGDKDYAVYIGDRSNVLAHQAOVHGPAAV GDNTFIGMQAFVFRSRVGANCVLEPLAAAIGVTVPDGTYVPA GKVVTTQEEADKLPKVTPDHFPATTNAAVVAVNVALAKGYL AQK
268	MQEITVLEFSNVTKNEVTSWNPKPVTPVIDPTS YVDPDATVIG DVTIGENVLIAAGATIRADEGKPIYIGDRSSVQDGVLHalesR DDGMENGDNVVIHGNTLYAVYVGNNVSLAHQSQVHGPAA VGDDSFVGMNSLVFN SKVGSNCVIEPNAAAIGVTVPDGKYIPAG GTVVTSQAEADKLPEITPDYEEYYTAVAKVVGVNVALCEAYQE LQ
269	MTAALLSASA PWAAPHWEYSGEAGPANWAKLTPEFGACAGKN QSPINLTGFTQAQLKPLKFNYQADAKSILNNNGHTVQVNFKPGN YLELDGORFELKQFHFHAPSSENLI ECKSFPLEAHFVHANQGE LAVLALMF KPGKANPELA KAWQQMPEKAGEETV LKAPINAQ DLLPKNLEYYYRSGSLTTPPCSEGVRWLVMKQPVELSQEQIDA FKEIMHHPPNNRPLQPLNNGRPVLT S
270	MQEITVTVYNNIRESPVTPWNPTPRRPQIHPTAYIDPAAVVQGD VKIGKNMVSANASIRS DEGYPIYIGDRSNVQDNVVLHAETV DEDGNEIEENIVTVGDEKYAVYVGDRSNVLAHQAOVHGPAAVG DNTFIGMQAFVFRSVVGKNCVLEPLAAAIGVTVPDGTYIPAGK VVTITQEEADKLPKVTPDHFPYKTNEAVVKVNI ELAKGYLAQS
271	MQEITVTRYENIRESPVTPWNPTPRRPQIHPTAYIDPAAVVQGD VTIGANVMVSPLASIRS DEGYPIYIGDRSNVQDNVVLHAETV DAAGKTLLEENVTVGDEKYAVYVGDRSNVLAHQAOVHGPAA VGDNTPFIGMQAFVFKSTVGKNCVLA PLAAAIGVTVPDGTYVPA AGTVVTTQEEAAKLPKVTPDHFPATTNAAVVAVNVALAAGY RALA
272	MRSSAFAVPAVAALAVAGLSAALAFAAQANEPAK PAAAGHH EVYDYPHQEAQWQALHDKSQSPIDIVTAGAAAADPAE PRAIEFS HTHGAIDKIEDNGH A VQDVTHATEATIRGRHFKLAQFHFHQAS EHTLDGKHFPLEGHFVKAQDGRLAVVGVMYE QGKANAVAQ EV LDDL KPGKAKPAQPEIDIEG LLPKAH GYYHYLGS LTT PPLTE NVEWYVMPPTPVMSKQQIDGFLSHYRRNNRNQPLN GRLIRY EG
273	MARKPSGH LT IYEQDVNC FWSFIEPIEGTGQSPIDLHTKEIKYDS SLKPLSVKYDPSTAKEISNTGHSFQVTFEDNDNKSVL RGGLT

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	DSYRLSQFHFGWGSDEHGSEHVVGDGVKYAAELHLVHWNAA KYSSFAAAAHEDPGLAVLGFLKVGEHNQQLQKVIDALNSIKT KGKRAPFTNFDSTLLPSSLWDYTDSLTPPLLESVTWIVLK EPISVSSEQMSKFRSLLFTSEGETACCMVDNYRPPQPLKGRQV R
274	MQEITVTRFENIRESPVTWNPTPKPKIHPHTAYVDPLASVGD VTIGENVIMISPHASIRSDEGMPIYIGDNSNVQDGVLVLAETD DNGNVIIEENVVVVGDEKYAVYIGENVSLAHQSQVHGPAAIGD NTFIGMQSFVKSKVGNCKVLMPLAAAAGVEVPDNKYIPAGK VVTTQEEADKLPEITPDHPYYNTNKAVVYVNVELAKGYLALS
275	MQEITVTVYNNIQASPVTPWNPTPKLPEIHPHTAYVHPAAVQQG DTIGENVYIAANANAVIRADEGKPIVIGDNSSVQDNVVLHALET VDEDGNIIEENVVVKVGDKDYAVYVGKNNVLAHNAQVHGPAA AVGDNTFVGMNALVFRSTVGKNCFLAPNAAAIGVTPDGTYIPAGK PAGKVVTTQEEAKLPKITPDHPGANLNERVVKVNVVALAKGYLAQA
276	MQEITVTKYENIRESPVTWNPTPKPKIHPHTAYIDPAAVVQGD VTIGKNMVSANASIRSDEGYPIKIGDNSNVQDNVVLHALET DENGEKEEENIVVVVGDEKYAVYIGDNEVSLAHQAQVHGPAAVG DNTFIGMQAFFVPRSRVKGKNCVLEPLAAAIGVTPDGTYIPAGK VVTTQEEADKLPKITPDHPFANTNAAVVKVNVALAKGYLAQA
277	MQEITVPIFSNVEKNEVETENPKPVVPKIDPTSYIDPNATVIGDV TIGENCYIAPFASIRADEGKPIVIGDRSNIQDGVLVLAESVDDN GEIIIEENMVLEGDEYYAVYIGKNCVSLAHQSQVHGPAAVG VGMKSLVFNSIVGSNCVIEPNAAAIGVTPDGKYIPAGTVVTT QEEADSLPEVTPDHAAYTAKIAAVVTVNVSLCLAYLGES
278	MSAPVIRWTYEGDKGPHFWNLCEEEYIAKTGKNQSPIDIHME KVMEVQGAPPLELNPKPTKTYTVRRVENSVHLFPKDKEQGLTF NGKRYNLIIAFHHIPSEHTLNEHYFAIEWHLVHMNEAGERLVL GIWMEKELEGSDFGELAEIFPEVFADEGKIEKEISLDVSGFLPEER AYFTYQGSLTTPPTFEGVTWIVLRNATSIS
279	MVASLSSLCLVLASLVGQTLATSPCDVDKTSPECDKTGVRNA SWGYAAENGPATWAANYPDFCAGDMQSPIDLDSSKAVTMDP GPIITMVGYNLQAGKIEENNHTLGFCAFASGSTPYIMGGRLPAG DRFDFVQLHWGSDSSKGSEHTMNGKEYPIEVHVLHANTK YYVNGAAPSNDNLVMPDGLAVLGIFYEVSTEDNANLTNIVSKV NEVAVEQRRRRRKQGRAGSNEVLDLMTLALDSFLPADTTqyyyy gggLTTPSCHEAVLWTMMKSTQTISEAQLEVFRSMTDSGICITLN MNYRPPQPLNNRTIYTTGTSTAGSSNMFTELLNTAFTAATV GLVGIVAPLFAAPPSQQRSDAASARAEOALRAGRDOQWGGY G
280	MQEITVLTFSNVTKNEVTATNPKPPTPVIDPTSYVDPNATV DVTIGKNCFIGANAVIRADEGKPIVIGDNSNVQDGVLVLAES VDDGGKVREDNVVHGNEWYAVYIGKNCVSLAHQSQVHGPAA YVGDDSFVGMKSLVFKSIVGSNCVIEPEAAAIGVTPDGKYIP AGTVVTTQEEADKLPEITPDHPFANTNAAVVKVNVALAKGY KA
281	MQEITVTRYTNIRSPVTPWNPEPKLPEIHPHTAYIDPLAYVQGD VTIGENVIMISANASIRSDEGYPIVIGNNSNVQDNVVLHAETD ENGNRLEENVVVKVGDEYYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAFFVPRSRVKGKNCYLAPLAAALGVTPDGTYIP GKVVTTQEEAKLPITPDHPFANTNAAVVKVNVALAKGY QA
282	MFKSSLILLATLSVVLCGDDAKSWGYRNKGRNIVPEKWGEMQ PKCLGSVQSPINVDFASTQFDANLGKLNINKKHGNETEQWDVK NNGHSVVFPTVNTDFSFVIYPQKEEFKLLQLHFHWRGSEHFVN GIKYAGELHLVHQSKTNPQFSVIGFLQLVNADNLKMKAVID VLADVTYEATKKIDNFELNDMVPFEVENFFRYSGSLTTPGCD EFPEVNLADKPVIGLSENQILEFQSLLDNHKPILSNSRPVQE NDRIVKRSFYPFEAKARTHGASGYSVSGANKFQFTSVFFT SAFCFYSL
283	MQEITVLEFSNVTKNEVTPTNPKPVTPVIDPTSYVDPDATV DVTIGANVLIWPKAIRADEGKPIVIGDRSNVQDGVLVLAES

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	VDDGGEIREDNVVLVGDENYAVYVGNNVSLAHQSQVHGPAR VGDSFVGMSLUVFKSDVGSNCVLEPNAAAIGVTVPDGKYIP AGTVVTTQEEAKLPETDDYPFYTAQDAVVEVNVLCEAY KGQA
284	MQEITVDTFSNVTKNEVTSTNPEPVTVIDPTSYVDPNATVTGD VTIGKNCYIGANAVIRADEGAPIVIGDRSNVQDGVLHAELEV DDEGEIREDNVVVHGDENYAVYIGEDVSLAHQSQVHGPARVG DDSFVGMSLUVFNSTVGENCVIEPEAAAIGVTVPDGKYIPAGT VVTQAEADKLPEVTDPDYAFYTEVAEVVTNVNALCEAHREQK
285	MIGRSSLRARLATAASAGLVLSAVPVAAPVTAAAAATPVMSIM AGETAEWNHDPASPIGPTHGELDPAWSACRSVQDQSPPIAVT PTREADRPVLLVLDYPRTPLVRNRTGHVIEVPAPPGGGTLLVG GHSYRLLQWHTHVPSEHVVNVNGHRADLEIHLVHQDEQGEIAVL AVFADVVSGLGEAAPRMPAADLLRTTVQAAPOSTAGEEIDLQDK VSAAALLGATVEDGEQRAITNYLSYTGSLLTPPCGGVWRWFL LPGIIGVDPASVQPLHALIASFPGYDGYPDNNRPVQPVGSRMV ERRVGWPVSGGVTSGAA
286	MSPLCWGYEKDNGAHVWRQTFIAAEGRQSPIDIQTSKAVPDL TLKPLTLSYDPATSLEILNNGHSFQVTFADDSDSSTLTEGPVSGI YRLKQFHFWGASDDKGSEHTVDGVKYPAELHLVHNNAVKE KSFGEALEENGLAVVGVFLKIGKHPELQKLVDALPAIKHKD TLVKFGSFDPSCLMPTCPDYWTYPGSLTTPLSESVTWIVLREP ISVSPEQL
287	MAAPSASKGHDVHWSYEGDNGPANWGKIKPEWAKCSTGNR QSPIDIRDGMKVELDQIQFDYRPPSSFSVIDNGHTVQGVGSGGN YITVQNMRYELQOFHFHRPSEERINGKAFEMVIHLVHKDAEGR LAVALVLERGAPQPVIQTVWNHLPLEKFETMQPTILLDPAEL LPARRDYFTYMGSLTTPCTEGVLWVMREPIQASSEQIAIFA RLYPMNARPIQETNGRMIWKSKEYS
288	MRLSTIFVAGYCPEKWDHQNPITGGEHQSPNIISSQTKYDPNL KPLNISYDPSTSLEILNNGHSFQVTFKDNDNRSVLKGGPLDDV YRLEQFHFHWGKDKAEGSEHTVDGVKYSSSELHLVHNNAVKY SSFEEAASKENGLAVLGVFLKVGEHNPKLQIIDALNSIKTKKG QTTFTNFDPSTLLPSSLWDYTSGSLTTPPLSECVTWIVLKEPIS VSPAQMACKRSLLFTSEGEKACCMVDNYRPPQPLKGRKVRAS F
289	MQEITVLFSSNVTKNEVTATNPKPVTVIDPTSYVHPEATVIGD VTIGENCYIAFPASIRADEGSPIVIGNDNSVQDGVLHAEVD DGGKLIEDNVVLEGHKNYTVYIGKNVSLAHQSQVHGPARVG DSFVGMSNFVFN SKVGSNCVIEPNAAAIGVTIPDGKYIPAGTVV TSQAEADNLPEITEDYKYYTQIAAVNVNVGLCRAYREKA
290	MKNVTGHLSSARCFCQIEDYPWSYDNDLGGPDFWGLINKHWK LCAIGKMQSPIDIDPNILLYDPNLKPIHIDKHKVSGTLENTGQSL VFRVDKETKHHVNISGGPLAYKYQFHEFYIHFGLHDHILGSEHS IDRYSFPAEIQLYGFNSDLYNNMSEAQEKSQGLVGVSLSMVQIG ETPNPELRIITSTFNKVIYRGKSAVPKRLSVRSLLPDTKDYVTYE GSTTHPCGCWETTVWIILNKPIYITKQELYALRKLMQGSKSHPK APLGNNARPIQDLHGRTRVTNI
291	MQEITVTRYENIRPSPTWPWNPTPRRPRIHPTAYVDPAAVVQG DVTIGANVLVMANAVIRADEGSPIVIGDNSSVQDNVVLHALET VDAAGGRLEENVVRVGDEDYAVYVGANVVLAHNAQVHGPA AVGDNTFVGMLALVFRSRVGANCVLAPNAAAIGVTVPDGTYVPA VPAGLVVTTQEEARLPRVTPDHFPANLNARVVAVNVALAAG YRALA
292	MQEITVTKYENIRPSPTWPWNPEPKLPEIHPHTAYIDPAAVVQGD VTIGANVMVSANASIRSDEGYPIVIGDNSVQDNVVLHALET DADGKVLEENVVKVGDERYAVYVGDNVSLAHQAQVHGPA VGDNTFIGMQSFVFRSVVGKNCVLEPLAAAIGVTVPDGTYVPA GKVVTTQEEAKLPKITTDPHFPANTNAAVVAVNVALAKGYLA QS
293	MAGSSARALAALVALVLVAVAVIAEPRQQQLKTALLRIEGGP ADTFAAAAEAEAAAAKAAEAAAACPWSYEGANGPANWGTIC GKIFSECATGMQSPINIKLLRMHQGPQSMIGWKIPSDAYNK

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	FVTFGGGGDYLESYDGHSFVVSHADALFPFGGVTYKLOSFHT HTVSEHTIDGEHYDMEMQFVHKTVDGAKFSTGLKGELGQTLI VSVMFQVGKGQGSPHWLRLQLAKAVPSVTNEASAQVILPDLFTEV AQSVMVGTLPQDARFKDFKPNNHYYGTGSLLAPPCTQGV OWLVLANPIYAEAEDIQAFKDLEGDNFRPVQRINGRIVTQRYC GLSCE
294	MAFTRLSISLLSGLILSAGMPAQAAPETVMVPEVTAMALEK WPADWSYQGENGPAPHGELHPSYSKCARGRVQSPVDSLKGAT TRSRRSTVRVAFHPIREIIFNDGRGIRAVPLEAQHPPIRIDRHDT LKHIVFRAPSEHTFQGRHYPLEAQLVYEADDGALAVLATVSP GHSNPSLAALTROPLAEGQLDKPMGTRVLLPRRLPHRLNGSL TPPPCTEGVNWWVFTQPVQATRAQIDAMTRLIGHPNRNPVQP AHRRRLMVEEMR
295	MKRTSLFAVIGECPOWNYDHQEEWKIVFPQANGDQQSPINIEP SSAVYDSALKPLELKYPDSTSLEILNNGHFSQVTFVDDSDSSTL KDGPITGTVYRLLKQFHFWGAADDKGSEHTVDGVKYPAELHL VHWNAKYGSFGEAASKPDGLAVVGVLKIGKHHPGLQKLTD ALYSIRFKGTKAEFSGFNPKCLLPASLDYWTPGSLTTPPLSES VTWIVLKEPISVSPEQMAKFRSLLFTSEGETACCMVDNYRPLQ PLKGRKVRAASF
296	MQEITVLEFSNITKNEVTSWNPKPKTPVIDPTSYIDPNATVIGDV TIGKNCYIGASAVIRADEGRPIVIGDRNSNVQDGVVLALESVN DDGKVIEDNVVULEGDNKYYAVYIGKNVVLAHQSQVHGPAAVG DDSFIGNNSLVFRSIVGSNCVIEPNAAAIGVTVPDNKYIPAGTV VTTQEEADKLPEITEDYAYWNTIAEVVKVNVLCEAYKNEA
297	MQEITVLEYSNVRKNEVTTTNPKPKTPVIDPTSYVDPKATVIGD VTIGENVLIGPFAVIRADEGRPIVIGDRSNVQDGVVLALESVD DDGKIIEDNVVUEGDEYYAVYIGKNVVLAHQAOVHGPARVG DDSFVGMNALVFNSIVGDNCVIEPNAAAIGVTVPDGKYIPAGT VTTQEEADKLPEITPDDEYYTKIAEVVKVNVALCEAYREKA
298	MQEITVLTFSNVRKNEVTPQNPKPVTPVIDPTSYVDPKATVIGD DVTIGANVMSANASIRSDEGYPIVIGDRNSNVQDNVVLHALET VDENGNIKENVVKVGDYAVYIGKNVSLAHQAOVHGPAAV VGDNFTIGMQAFVFRSNVGKNCVLMPLAAAIGVTIPDGTYIPA GKVVTTQEEADKLPKVTPDHFPYKTNEAVVKVNVELAKGYL AMA
299	MQEITVLTFSNVRKNEVTPQNPKPVTPVIDPTSYVDPKATVIGD VTIGENVLIGASAVIRADEGHPIVIGDRSSVQDGVVLALESVD DDGKIIEDNVVULEGDEYYAVYVGGRNVVLAHQSQVHGPAAVG DDSFVGMKSLVFRSIVGSNCVIEPEAAAIGVTVPDGKYIPAGTV VTTQEEADKLPEITPDHPYTTAVEKVVEVNVLCKAYRNKE
300	MKNSCATYSVVVMTLSLILVLTISLGYQNPFAMGQDTINDTII SKQWPNIIMSNVNTFVVENVTSRIDDATAYIHPFAIIIGDCSIGKK VLVAPTAVCRADEGIPIHGDYNSNIQDGVLHALDAVRDGTNV DNKRFQSQEDRLLGNDTRFDEGYAIYLSGNVSLAHDSLHGPV WIGNNNTLIGVKSALDSKIGMNVIRVGSIIITGVEIPDNTLVPPG SVLTNQSQVATLPSVIGSPSQNLNQGDLKNSQALATAVDNTNI ER
301	MQEITVLSFSNVTKNEVTSNPKPTPKIDPTSYVDPKATVGD VTIGKNCYIGPFAVIRADEGAPIVIGDRNSNVQDGVVLALESVD DDGKIIIEENVVLYGNKYYAVYIGKNVVLAHQAOVHGPARVG DDSFVGMNSLVFRSIVGSNCVIEPNAAAIGVTVPDNKYIPAGT VTTQEEADNLPEITPDHPYTTAVEKVVEVNVLCKAYRNKE
302	MQEITVTKYENIQESPVTPWNPTPKRPVIDPTAYVHPAAVQG DVTIGKNCYIGPFAVIRADEGAPIVIGDRNSNVQDGVVLALESVD VDADGNEIEENIVTVGDKKYAVYIGDNVSLAHQAOVHGPAAV GDNTFIGMQAFVFRSNVGKNCVLAPlAAAIGVTVPDGTYVPA GTVVTTQEEADKLPKVTPDHFPANTNAAVVKVNVALAKGYL ALS
303	MRGCLEKTGEGAIAGILVMAGPPQIQGSNFHSGFIFLKNFIMNS TQHCTLLAISFCFALLLFACNGANKEQQQSTSNSIKDHPKAD TLLGDNEVKAEPDANSKAEQGYALPQHTDRLAQSPIDIISVK ADKTVKEQISFAFHSDINAALKNLGHТИEFPKEGSTCKVNGKD

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	YASRQFHFHTPSEHLDVGITFPPEMHIVNILADSVNTNKPSYLV LAVLFKIGTENKFIKEFFNKIPNKEGEENTLQTGDVRLDDLLSQ FTPNDIKSYYTYQGSLLTPPPTESVQWVILKHIVEASEEQIMAIE KMEGNNNARHVQAINDRKIYSH
304	MSRP GTVLAI FCWNHQE KYDMKKV LAVA ALLALGGVAAEA SHWGYEGEGAPEHWGALDEAYKACQAGKNQSPINIEHALKA HHGQLD LAFKPGAAQ QIVNNGHTI QVNVSAGNTL TDGDTFTL QOFHFHAPSENEIDGKQFP LEAHFVYKD KDGALVULALMFQQ GKANPQLAQAWQ QM PAAIDQVATLNQPV DIKALLPKEFNFYR FSGSLTTT PCEGVRWLVDQPV SASAEQI QQFR AVV HAN NR PVQPLHGRVIVD
305	MQEITVLD FSNI TKNEV TPTNPEP ITPVID PTSYIDPNATVGDV TIGKNVLIIGPNAVIRADEG RPIVV GDRSNVQDG VV LHALESVD DEGEPIEDNVVEKGDEL YAVYIGK NVSLAHQS QVHG PARVGD DSFVG MKSLVFKSDVGENC VIEPE SAAIGVTIPDGKYI PAGTVV TSQAEAAKLPEVTPDYA S DTNEAVV KVNV GLCEAYKEQA
306	MQEITVTRFENIRPS PVT PWNP TPKR PVIH PTAYV DPAAV VQG DVTIGANVMISALAS IRS DEG YPI YIG DNSN VQDN VV LHA LETV DADGKRIEEN VVKGD KDYAVYIGDNVSLAHQAQVHGPAAV GDNTFIGM QAFV FRS RIGK NCYLAP LAAA IGV E VP DGT YI PAG KVTTQEEAAKLPK MTPDHPF YKT NEAVV AVNVALAKGYLA LA
307	MKRSLV ATIFG CYEP NHDQ WGYT KDN GPATWAKSFPAANGP RQSPIDIKPSET KYDSS LKPLS LKYDP STALEI LNNGHSQV TPK DSEN KSVL QGGP LEG TYRLEQ FHFHWG SSDE HGSEH VDGVK YASELHV VV HNAKY GDFGEAV KHDGLAV LGIFL KV GKHH P EFQKLL DALNS I KNKG KQASFTN FDP SVLL PA CLDY WT YSGSL TTPPLLES VTWIVL KEP ISV SPA QMBO FRSL LFT SE GEKE KRM V DNFRPLQPLMNRT VRSS FR
308	MTLSRAFI VGC PQED HKNW YNQ YPIAK GNRQ SPINIE T KQ A QY DSSLKPLTFSYDP STAKEI VN VGH S FVN FED NDN QSVLS GGPL TG SY RLKQ FHFHWG ASDE HGSE HTD GLK YPAEL HLHV WN A KYGSFSE AAS QPD GLAV VGVFL KIGDEN PKL QK II DALES I KTK GKQTRFTN FDP STLL PSC LDYWTY HGS LTT PPLLES VTWII CKE PISVSPSQ MEK PRS LLFT SE GEKE CCMV DN YRPLQPL MNRT VR SSFR
309	MQEITVTRYENIRPS PVT PWNP TPKR PVIH PTAYV DPAAV VQG VTIGANVLM ANAVIRADEG YPI YIG DNSN VQDN VV LHA LETV DEN GNRIEEN VVR VG DED YAVYVG KNVV LAHNAQVHGPAAV GDNTF VGM NALV FRS RVG KDC VLM PNA AAIGV T VP DGT YV P AGL VVTTQEEAAKLPK VTPDHPF ANLARV KVNV VALAKGY LALA
310	MQEITVTRYENIRPS PVT PWNP TPKR PVIH PTAYV DPAAV VQG DVTIGANVM VSANAS IRS DEG YPI YIG DNSN VQDN VV LHA LETV VDAAGRRL EEN VVR VG DDE YAVYVG DNV S LAHQAQVHGPAAV AVGDNTFIGM QAFV FRS RVG KNC VLE PLAAA IGV T VP DGT YV P AGT VVTTQEEADKL PKVTPDHPF YKT NAA VV KVNV VALAKGY YLAQA
311	MGS SHAWSYS GSG PHE WAS LTPEY GACAGR NQSPV DLAGFI EADL API AFHYQAGGTE VV NN GHTV QV NYA PGS AIEL DGHR F ELKQFHFHAPSEN LIDGKS YPLEM HLV HADEA GH LAVV ALMF KAGA ENA ALA KLW KAM PEQ PG ETVHL APLV SAE AL LPK DRD YYRFNGSLTTT PCEGVRWL VMK EPV S ASAEQIA AFE KRL PHP NNRPLQPTNARL VLK
312	MQEITVLF FSNTKNEV TPTNPK P STPV ID PTSYIDPNATVGD VTIGANV LVAANATI RADEG KPIVIGD RSSV QDG VV LHAESV DDEGEI KEDN VV VGNK NYA VYIGK NVSLAHQS QVHG PAHV GDDSFV GMKSLV FKSDV GSNC VIEPF AAA IGV T VP DGT YI PAG TVTTQEEADKL PEVTPD YAES NTNEAVV KVNV GLCEAYK N S
313	MAWNRRNFLGSFACFG LSLAT GRALAV TSCK PEEQ PCW GYH GDEGP DHWGR LHPD WVA CEGSE QSPIALAGEEV KPTA ERFA LHYQPTTARL SDN VHT VRID MEGPSQ LLG DRT FSLRQFHFHT

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	PSEHLWSDTADLGELHLVHVADSREIAVLGVALRPDAAQAFP DSFWNWLQAAEAGESLTLDPAGLVRQGRLVGYRGSFTTPC TEGVNWLLAMEPMAMGPEEQRWLEQRMGRNARPVQLGSR TVHTVLREGS
314	MQEITVTRYENIRESPVTSWNPEPRRPEIHPHTAYVDPAAVVQG DVTIGENVMVSAHASIRSDEGYPIVIGNNSNVQDNVVLHALET VDENGNEIEENIVTVGDKKYAVYVGDNVSLAHQAQVHGPAA VGDNTFIGMQAQFVFRSRVGKDCYLAPLAAAIGVTVPDGTYP GKVVTTQEEAAKLPKMTPDHPFYKTNAAVVKVNVELAKGYL AQA
315	MQEITVTVFNNIQPSPVTPWNPEPKLPEIHPHTAYVHPLAYVQGD VKIGENVMISALASIRSDEGYPIVIGNNSNVQDNVVLHALETVD ENGNETEENIVTVGDEKYAVVIGDNVSLAHQAQVHGPAAVGD NTFIGMQAQFVFNSIVGKNCVLEPLAAAIGVTIPDGTYIPAGKVV TTQEEADKLPKVTPDHPFANTNAAVVKVNVALAKGYLALS
316	MIRKMFTIIAVALAGLFASSEQLSQQNPLASKSPEPAKTESNT KPAEEAKQEEHAKHDWTENGPDKWAGLDPQNKLCSEGKM QSPIDITNPKPQDLPESVIEPPAVERSMTHNEHVKDIEENNHTIQ VDFDEKNTDTLKIGNAKYSLSQFHFSSEHTVNGKSFPMEMH LVHKAGDNFAVLGIFIEEGPEDNKAPEPIWSKLPQKGKTEENIN IDINQFLPKSRTTYRVEGSLITTPKCGEAVKWIIVFAEPIRMSSGQI AKFRSIVVKNNRPTQPLNERVVQTDIIEEKDSK
317	MLTSLFLLSALFSTAWSCPCKHDNYQSHPHLGRQRQIRVDKGREP KDWNYDVSDADWATINPEYVLCQSGTHQSPINIAQQDLSTLHKP NPEGYQSVKIPGNFFNWQFAPAWTPHHPEGDVTGLPSFNEDGE EVFNIGWHIAPSEHLDGKRSRAEIHMVHVTAEERHEAAVIGIR LAVGPQESAFIKQLGPMIHYNDTAQLEGLEVNLRLAIDEVGGV EEFWTYKGSLTTPPCSEGLRFPLPKQELIVSEQQMVEILAASRF SHRVEQPVWLHDINL
318	MRLSVVFATICGYQPEHWNDKYKMASGKRQSPIDIQPKDTKYD SSLKLITISYDPSTSKEILNNGHFSQVTFEDSNNSVULKGGPLTD SYRLTQFHFWHGASDEHGSEHVVDGAKYSAELHLVHWNSDK YSSFAEAASKPDLGAVLGFLVKVGKBEHAELQKLTDALPSIKHK DTLAKFGNFDPSCLMPSCPDYWTYAGSLTTPPLLESVTWILKE PISVSPSQMAKPRSSLFTSEGEKEKRMVNDNPRPLQPLMNRTVR SSF
319	MQEITVTKYENIQPSPVTPWNPEPKPPEIHPHTAYIHAAVVG VKIGENVMVSAHASIRSDEGYPIVIGDNSNVQDNVVLHALET DENGNIEEENIVTVGDEKYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAQFVFRSRVGKNCVLEPLAAAIGVTVPDGTYP GKVVTTQEEAAKLPKVTVDHPFYNTNAAVVKVNVALAKGYL ALS
320	MQEITVDEYSNTKNEVTPYNPKPITPPVIDPTSYVDPNATVTG DVTIGKVNVLIGAFARIRADEGQPIVIGDRSNVQDGVVLHALESV DDDGEVLEDNVVLHGDEDYAVVVGKDVSLAHQSQVHGPAR VGDDSFVGMKSLVFNSDVGDNVICIEPFAAAIGVTVPDGTYP GTVVTTQEEAAKLPPEITPDHAASNAQAAVVEVNQQLNQAYRG QA
321	MQEITVTKFENIQPSPVTSWNPEPKLPKIDPTAYIHPLATVGD VTIGKVNVLIGAFARIRADEGQPIVIGDRSNVQDGVVLHALESV DENGNRIEENIVVVGDKKEYAVYIGKNSVLAHQQAQVHGPAAVG DNTFIGMQAQFVFRSVVGKNCVLEPLAAAALGVTVPDGTYP KVVTTQEEADKLPKITPDHPFATTNAAVVKVNVELAKGYLAL K
322	MKRISGVLATFCWPEQHNDYLLLHLLYVLKMNSWGYNESNG PATWHEHYPIANGDRQSPIDIKTKEVKYDSSLRPLSIKYDSTA KEILNNGHFSFNEFEDSQDKSVLKGGPLTGSYRLQFHFWGS ADDHGSEHTVDGVKYPSEHLHVHWNNAVKFSSFGEAALLEENGL AVIGVFLKLGRHGEFDKIVDALDSIKTKGKQASFTNFDPSCLL PPCPDWTYSGSLTTPPLSESVTWILKQPIISVDSEQLAKFRSLL SSSEGEKASFMLSNNHRLQPLKGRKVRSSF
323	MQEITVFNYSNTKNEVTPENPKPTTPEIDPTAFVDPDATVGD VTIGKVNVLIGAFARIRADEGQPIVIGDRSNVQDGVVLHALESV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	ENGKVLEDNVVLEGDEWYAVYVGKNVSLAHQSQVHGPAMV GDGSFIGMOSFVFKSHVGSNCVIEPDAAIIGTVVPDGKYIPAGT VTTQEEADKLPEVTPDYAYYTTVAAVVEVNVLAAQAYKSK A
324	MQEITVTRYENIRPSPVTPWNPEPKLPEIHTPASYIDPAAVVQGD VTIGANVLVMANAVIRADEGYPIVIGDNSSVQDNVVLHALET DAAGRVLLEENVVKVGDERYAVYVGANVLAHQAVHGPAA VGDNTFVGMQALVFRSTVGANCVLAPLAAAIGTVVPDGTVVP AGLVVTTQAEAAALPRVTPDHPFAIDLARVVAVNVNALAAGY RALA
325	MQEITVTRYENIRPSPVTPWNPEPKLPEIHTPASYIDPAAVVQGD VTIGANVLVMANAVIRADEGYPIVIGDNSSVQDNVVLHALET DENGNRIEENVVVVGDKKYAVYIGKNNVIAHNAQVHGPAAVG DNTFVGMNALVFRSEVGKDCYLAPNAAAIGVKVPDGTYIPAG KVTTQEEAAKLPKMTPDHPGYKLNERVVVKVNIALAKGYLALS S
326	MQEITVTKNNIRPSPVTPWNPEPKLPEIHTPASYIDPAAVVQGD VTIGANVLVMANAVIRADEGYPIVIGDNSSVQDNVVLHALET DENGNRIEENIVKVGDEEYAVYIGKNNVIAHLAQVHGPAAVG DNTFVGMNALVFRSEVGKDCYLAPNAAAIGVKVPDGTYIPAG VTTQEEADKLPEVTPDHPLYNLARVVVKVNVALAKGYLALS
327	MKLIFTVASGQEYDPNHWRGRGYPIAKGNRQSPIDIDTKSAKYD SSLKPLTVSYDPATAREIVNVGHFSFNVTFDDSQDKSVLRGGPL TGVYRLRFQFHFHWGS SDDHGSEHVDGVVKYSAELHLVHWNA KYGSFAEAARHPDGLAVVGFLKIGREKGEFQIILDAIKT KGKQTRFTNFDPSCLFPPPCRDIWTYSGSLTTPPLSESVTWIVLK QPIEVHDQLEKFRTLLFTSEGE
328	MITKLFAGSVQRQCYPEPDNWHRYYPVANGNSIDIEAAETQYDSS LKPLTISYNPATAKEILNVGHFFTVHFEDKDQNQAQKGGPLDG VYRLIQFHFWHSIDQGKSEHTVDKKYAAELHLVHWNAKY GDFGEAAQQPDGLAVLGIFLKVGSAKPGLOQKVDALNSIKTK GKSADFTNFDPSTLLPGCLDYWTYDGSLTTPPLLESVTWIVLK EPISVSSEQMSKFRSLLFTSEGEAACMVNDNYRPPQPLKGR
329	MDNNLAAAVRIVVEVLLFVIFICILIWWVIQSKREEATLQVKLA GAQVQINTATEKLATTEAAFAEAEHKLDKAAKGALWEYEGRF GPDFWGKVFPCTGIGKSQAPLDIIRGFPGAKAKIqvDyKLSGL KLIHNGHTVQVNVAAPGSRLLVTDGVAYELLQFHFHRPSEEWIEG KPSDMSLHLVHKSADGKLAVLGVLLQAMAADNQQLVPIWTH LPSAEGPEQSFPETNVDPAKLIPSNLAYYQEGSLTTPPCTEGV TFFILKTCKMPISKQLDAFPIPHSNARPVQPLNGRTIYSSS
330	MRIKRLGLSRLGIGLLSITVVGTTASAEGVLATEAGPPAQGATLA WQYEQEQQPSHWGTLAPTTASCEKGTHQSPINIRTASHPHGD GMLIQYRAASGHVGTSHTVVEVDFQSGGTLELSGRSYSLSKEFH FPHPSEHQLNGRIPMEAHLVHRDESGHLVVLAILMELGTEATA PLADVWERIPSGKQEEVRDLLLFPQDLLPKDLHHYAYDGSLLT PPCTEGVHWIVLKEPIHITAHLERFVSLIGHNARPVQPLNERE VDEE
331	MQEITVTRYENIRPSPVTPWNPEPKLPEIHTPASYIDPAAVVQGD VTIGANVMVASANASIRSDEGYPIVIGDNSSVQDNVVLHALET DAAGRELEENVTVGDEKYAVYVGANVSLAHQAQVHGPAA VGDNTFVGMQAFVNSRVGANCVLMLPAAAIGTVVPDGTYIP AGLVVTTQEEAAKLPKVTVDHPFATTNAAVVKVNVALAAGY RALA
332	MQEITVLFVFSNRKNEVTPWNPKPETPKIDPTSYIDPEATVIGD VTIGKNCYIAASAVIRADEGGRPIVIGDRSNVQDGVLHALES DDGGKVREENIVLEGGKYYAVYVGKNNVLAHQAVHGPAA VGDNTFVGMKSLVFKAIVGNCVLEPEAAAIGTVVPDGKYIPA GTVVTTQEEADKLPEVTPDDAKYTANVAVVNVNVNLAKAYR ELA
333	MLNSAGIFPKRVTQECYHWDYKGKHEWEKTTPPSAAGNRQSPI NIPQPREAQFDPSLKPLTLKYDPSTSLEILNNNGHSFQVTFVDDTD SSTLTGGPITGTYRLKQFHFHWGAADDKGSEHTVDGVKYPCE LHLVHWNAVYKASFAEAAAEPDGLAVVGFLKIGQHHEELQ

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	KLVDALPSIKHKDTLVTGSPDPSCLMPTCPDYWTYSGSLTTPP LSESVTWIICKQPVEVDHDQLEQFRTLILFTSEGE
334	MKSLIAVFGTCHWNYDEQRPEEWHNDYPVANGLRQSPIDIKP AETQYDSTLRPLSFKYDPSTAKEIILNNGHFSFQVTFDSSDKSVL SGGPLTGTYRKLQFHFHWGASDEHGSEHTVDGVVKYAAELHL VHWNSDKYASFAEEAAAKPDGLAVVGFLKIGEANPALQKLL DALSSIKTKGKQTTFTNFDPSTLLPSSLDYWTYLGSLTVPPLE SVTWIVLKEPISVSPAQLAKFRSLLCSGEGEAACMVDNYRPP QPLKGR
335	MQEITVTRFENIRPSPVTPWNPTPKLPKIHPTAYIDPAAVVQGD VTIGENVLVMANAVIRADEGYPIYIGDNSSVQDNVVLHALETW DENGNRIEENIVTVGDKEYAVYIGKNVVIAHNAQVHGPAPIVG NTFIGMNALVFRSKVGNKCVLEPLAAIGVTIPDGTYIPAGKV VTTQEEADKLPKVTDPHFYKLNERVVKVNIALAKGYRALS
336	MLRSAPGVFICTNWQEKYDHVAEQSEQSPINIVTDKAVYDSTL KPLELKVDASTALEIVNNGHSVQVKFDDSSDKAVLKGGPLTGP YRLKQFHFWGKDDVGSEHTVDGVVKYASELHLVHWNAKY GSFGEAASQPDGLAVVGVFLKIGSAKPLQKVVDALNSIKTKG KSADFTMFDPSTLLPSSLDYWTYDGSLTTPPLLESVTWIVLKEPI F VSSEQMSKFRSLLFTSEGEAACMVDNYRPPQPLKGRQVRAS
337	MQEITVLEFSNITKNEVTPWNPEPVTPTVIDPTAYIDPQATVIGD VTIGANCYIAASAVIRADEGKPIVIGDRSNVQDGVVLHALESIN DGGMVREDNVVEVGDENYAVYVGKNNVLAHQSQVHGPAAV GDDSFVGMKSLVFKSIVGSNCVIEPBAAAIGVTVPDGKYIPAGT VTTQEEAKLPEVTPDHDAAYSQIAAVVAVNVALCQAYRDQ A
338	MVLFFLSSSYLISASTAHGEVEDESEFTYDEGSEKGPKNWGKI KPQWKACSTGKLQSPIDLLDQRVQVLPNLGELKREYKPAV KNRGHDITIKWKGDAKGKIKINGDFKLQQCHWHPSEHTFNGS RYNLEMHIVHLQAQNKAIAVIALYKGRDPFLSRLFHHIKTVG TEERDIGIINPGEIKFGSRKYYRYIGSLTTPPCTEGVIWTVFK
339	MQEITVLLFSNVQKNEVTTTNPKPTPTVIDPTSYVDPNATVVG DVTIGKNVLIWATAVIRADEGKPIVIGDRSNVQDGVVLHALES VDDGGKIRTNDVNLVHGEDLYAVYIGNNVSLAHQAQVHGPAA VGDDSFVGMKSLVFKSKVGSNCVIEPFAAAIGVTIPDGKYVPS GTVVTTQEEAKLPEITADHAQYTQQAQVSVNVRLCKAYRE OK
340	MQEITVTLYENIRPSPVTPWNPTPKRPVIDPTAYIDPAAVVQGD VTIGKNVLMANAVIRADEGYPIVIGDNSSVQDNVVLHALETW DENGNVIEENVVEVGDKKYAVYVGDNVVLAHLAQVHGPAA GDNTFVGMALAVFRSRVGKNCVLEHLAAIGVTVPDNTVPA GTVVTTQEEAKLPMTPDHPHYNLVERVVKVNVELAKGY ALS
341	MKLNSFVAIGCTPREQYHWDEVIKGGPNSWAEYFPLANGDKQ SPIDIVPGSAKYDGLKPLTLKYDPSTSLEILNNGHFSFQVTFSDD TDSSTLTGPISGVYRKLQFHFHWGASDDKGSEHTVDGVVKYA AELHLVHWNAVKYSSGEAASKPDGLAVLGFLKVGKHHGE FEKIVNALGSIKHDTLATFENFDPSCLMPACPDYWTYDGSLT TPPLLESVTWIVLKEPIVSPSQMAKFRSLLFTSEGEKACCMVD NYRPPQPLKGRQVRASF
342	MQEITVTVFENIQPSPVTPWNPEPKRPEIHPTAYIHAAVQGD VTIGANVLVMANAVIRADEGYPPIVVGDNNSAVQDNVVLHALET VDASGKELEENIVTVGDKEYAVYVGDNVVLAHNAQVHGPAA VGDNTFVGMNALVFRSRVGANCVLEHLAAALGVTVPDGRYV PAGRVTITQEEARLPAVTPDHPHADLNARVVAVNVALAKG YLALA
343	MKKTIMLVPVLVFVFIAMTCDNKTNHHKDVKHSKETKEEMK KETAKKDCDQVHWSHHKGEHGPNWANLCEGFKDNGEKQ SPIDIKEAVKGEDLKPLEFETYGKTKVNIINNGHTVQFNIDKGSS MMVDGKKYDQQFHYHATSEHTIKGEYSPLEVHFVHRADD

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	DFAVLGIMYEEGEANDLFNKYLKHFFPADKGEYTSDEKFDLDA LLPDNLSSYYHYGGSLLTPPCSEVVSWYLLQNPRLRASQEIQKDF SEILDKNFRPIQELNNGRTIYKFGE
344	MKR LASVFTICGWNYQDPEHWFPTAKGNHQSPINIETRK IYDSTLKLPLTFSYEATTSRRIVNNGHSFQVEFEDTDNKSVLKGG PLTDRYRLTQFHFHWGSSDDHGEHTVDGLKYPAEHLHVW NAKYGSFGEAASKPDGLAVGVFLKIGRENAEFQLVLDALDSI KTKGKQTPFTNFDPSCLFPACRDYWTYSGLTTPPLESVTWIV LKQPIEVSPRQLSKFRSLLFTSEGEKEKRMVDNFRPLQPLMNRS VRSSF
345	MITRLPAVTAVLAMFVUCMSAHDPWNTDYTSQRGPLFWGOR PEFKMCGLGREQSPINIRRSSTIYQDFPPLAFELKSPIVHSNIENK GSATAAPPLSDIPILSGGPLGNRKYRVYNVHLHFGNYSFRAAE HAFDGVRTTGEFHIVTYDSRYPHIKAALGSGRRGALAVLGVM FEARNVSNIDMGVTNLLIELSSNVNTYKGDHYMTGIDFSNLVSEV DMGYYYAYNGSLTTPCTNEVQQWMVIDRIHYVLPEТАDILLE LKTGYREHHSIPIFGNTRPLQPLYGRKVLRSGPVTVDHDQG EEIVYSSADLVGPLGRVMLLALAAIAFVVIKA
346	MKLTSAFIVCGYQNHEPRDWHEVAPSAGNRQSPINIQRD VYDPGLKPLTISYDPAACLHIWNNGYSFLVEFEDSTDKSVKGG PLENNYRLKQFHFHWGATDDHGEHTDVGVKYSABELHLHVW NADKFDSFVEAAHEKDGLAVLGVFLKIGEHNAQLQKITDILDSI KEKGKQTRFTNFDPVCLLPPCPDYWTYPGSLTVPPLESVTWII LKQPINISSQQLAKFRLLFTSEGETA
347	MNNRPIQPLNDRSIWINRIKTEKCEFGWCPPVEEPEKASKkvek dddsksaskqgksdkkgkssqgdksgkksqgksnkkkePPQWNYASVQRWED DYSMCGGKKQSPVNANTSJKIQSVQGPAGGLVSRMAYSAVGP NAGFQFKNNNGKSLVLECNWGTLLRPDGDYIATKSIKFHFPEHA VDGVLAAGEMHIVHQRSDATGTDGLAVIAIILLRDSDLLGQAG PVGFDFRLGFSSRLPVEGETVILGADTVLDIGAI FAPQLGGKYW HYEGSLTTPPCSETVHWYLMQTPAGINKAMVNNFKSLFPSPAN NRPVQGMYGRAIVVTELSSKEFD
348	MKFAAAVASIVFAVSGAAAIAAPEGAJVGDGLPEKWSI TNEAYGACDAGNMQSPIDLLANTRGEIEFASSYEETTGELKT GPSKVQVDVAPGMGMISSQHFLS LVQFHFBHTPSEHRLHGORY PLTVHLVHGTTATGDFAVLGVFMEEGDENPALARILSGIDGGSK NVAVDVRELVPENIDVYRYMGSLLTTPCTEGVLWLILKOPASI SAEQLRLFSQLYPNNARPVQSLNGRPVRDALLIAPGGRP
349	MQEITVTKYENIRPSPVTPWNPEPKLPKIHPTAYIDPAAVVQGD VTIGANVMVMSANASIRSEDEGYPIYIGDNNSNVQDNVVLHALET DENGPLEENIVKVGDKDYAVYVGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFRSRVGKNCVLEPLAAAIGTVPDGTYVPA GTVVTTQEEAAKLKPVTPDHPFYKTNEAVVKVNIALAKGYLA LK
350	MQEITVLTYSNTKNEVTSTNPKPPTPVIDPTSYVDPNATVTG DVTIGKNCFIGAFAVIRADEGKPIVIGDRSNVQDGVLHalesv DDGGEIREDNVVVHGDEYYAVYIGKNVSLAHQAQVHGPAAV GDDSFVGMKSLVFNSIVGDNCVIEPDAAIIGTVPDGKYIPAG TVVTTQEEAAKLPEITPDHEFYQTQIAAVVQVNVDLCKAYRDK K
351	MLKEWGYASHNGPDTWQI FRCARGNNQSPIELKTDIKHDP SLQPLSVSYDPCTAKEIVNVGHSFHVNFEDSDNRSVLKDGPITG SYRLRQFHFHWGASDDHGEHHVVDGVRYAAELHVWHWNAD KYPSFVBAAHEDGLAVLGVLKIGEHNPQLQKITDVLVYAVKF KGTKAQFTNFPKCLLPASLDYWTYPGSLTTPPLESCTWIVL KEPISVSPSQMAKFRSLLFSSGETACCMVDNYRPPQPLKGRT VRASF
352	MQEITVLEFSNITKNEVTPTNPKPSTPVIDPTSYVDPNATVGD VIGKVLIAANAVIRADEGAPIVIGDRSNVQDGVLHalesvd DDGKILEDNVVKGDEYYAVYIGKNVHLAHQAQVHGPARVG DDSFVGMKSLVFNSKVGNCVIEPDAAIIGTVPDNQYIPAGT VVTTQEEADKLPEVTVDYAYSDTNEAVVTNVNDLNEAYRNQ Q

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
353	MQEITVTKYENIRPSPVTSNPEPKLPKIHPTAYIDPAAVVQGD VTIGENVMISALASIRSDEGYPIYIGNNSNVQDVVLHAETVD ENGNVLEENVVTVGDKKYAVYIGDNVSLAHQAQVHGPAAVG NNTFIGMQSFVFRSVVGENCVLEPLAAAIGVTVPDGTYVPAGT VVTTQEEADKLKPVTPDHFPYNTNAAVVKVNVELAKGYLAL K
354	MQEITVNLNSNIEKNEVTSTNPKPPTPVIDPTSYIDPNATVTGD VTIGKNYCIGPFAVIRADEGAPIVIGDNSNVQDGVVVLHALESVD DGGKIRKDNNVEVGDNNYAVYVGKNVSLAHQSQVHGPARV GDDSFVGMNATVFNSIVGSNCVIEPNAAAIGVTVPDGTYIPAG TVVTTQEEADKLPEITEDYPFYTAVEEVVKVNVALCKAYREK K
355	MLSRKPAGHTDIYEQFVCNWKNNGGKLHRSSATDPEGERQSPI DIQTSKVEVDQKLQPLTLTYDPSTSLEILNNNGHSQVTFKDKD NRSVLUKGGLTGPYRLKQFHFHWGKDDVGSEHTVDGAKFA SELHLVHNNAKYSSFAEAASKSDGLAFLGVFLQVGEHNAQ LQKITDILDSIKEKGKQTRFTNFDPDLSSLPPCRDYWTYHGSLTV PPLLESVTWIIILKQPISVSSQQLAKFRSLLCTSEGEKAVPMLSNH RPPQPLKGRQVRASF
356	MTMKLSQLGQLFLVICCLTVVINAMPNPQAQAPSGALVATAE SGHF SYDPPNKWEHNSLCAGEHQSPINIDTRKSRTDKFPFRF HNYAKGLPENLENNGHTVQLTIDNLIKDLPТИSGGGLEGPYEFA QMHFHWGEDEFGSEHKINNKQYAGEVHVHNWKYGNFVNA TKHNDGLAFLGLIIDLQDKENIAFSHIEQFDEIRDASKNEKLP YSVPLKDLLPSNTASFFRYEGSLTDARCNEDTVGFPLHQFTSP IIQLQNLNDEGEPLSKNRVPTQEEHDRIVTVSGRAMQCGTCSTA TADRSSLERSDSESGESKEITKSCTRHYGY
357	MQEITVTRYENIRPSPVTPWNPEPKLPKIHPTAYIDPAAVVQGD VRIGANVMVSALASIRSDEGYPIVIGDNSNVQDVVLHAETVD DADGKVLEENVVVEGDERYAVYIGDNVSLAHQAQVHGPAAV GDNTFIGMQAFVFRSRVKGDCVLMPLAAAIGVEVPDGRYIPA GKVVTTQEEADKLKPVTPDHFPANTNAAVVAVNVALAKGYL ALA
358	MQEITVTTNNIRPSPVTPWNPEPKLPKIHPTAYIDPAAVVQGD VTIGENVLVMANAVIRADEGYPPIVIGDNSNVQDVVLHAETVD DEDGKRIEENVVKGDKDYAVYVGDNVVLAHNAQVHGPAA VGDNTFVGMNALVFHSNVGKNCVLAAPAAAIGVTVPDGTYIP AGKVVTTQEEADKLPEVTPDHFPANTNAAVVAVNVALAKGY LALA
359	MAMLNKKRKEWMRGRVFFALILAMCLSVAGYSLYEKEQNQ HDEERIEDVYYSYDEHGPDAANVCERGMMQSPVQITRKDALQ NQSPEIEIHYGEGRFEI IKKAHTAEAVSKSGQNYLILIDHQOYKLE SFHFHLPSEHQUEQSYEMELHFVHENKNQEAVMAVFIQEG QANEMVKEIWSRLQDGFSKKDNVSI RLPEFIPKERRAFYTGS LTPPCTEGVKWIVFEMPVEFSEEQIGTFHRLFGNNSRQVQPLN GRKIYQLTVR
360	MKHCTLLAILLSGLLSAAVETDFSYADQGAWQTLPNQCGGR RQSPVDDLRLNVTVDKILQDQLACTWQQNKAVIDGLVNTGR TIELDVRSPHTCRGVPGSPSAHFRLAAVHIHYGSASDQGSEHTI NGRTSALEVHMVHFDTFASLDKARBQPGGIMVAGLLFDEAD EAIANPELTKMAVISGTALRSTGGVLASRLNAAPLIEGTGLDKA RARFLTYAGSLTTPTCNEVVTWIVAEPGLVGHQTMHLLRTV TGLGNKTISPNNFRQVQPLNGRTITSSFQPACGLHGRC
361	MLKNPAGDWSYEQTVHIFRCTDFIPAVILPGGARQSPINIVTSQ AVYSPSLKPLELSYEACTSLSITNNNGHSVQVEFNIDSTDRTVIKG GPLEGPYRLKQFHFWGARDSRGSEHTVDGARYPSELHLVHW NAKYASFGEAASQPDGLAVVGVFLKIGREKPGQLQKVLDALDA IKTKGKQTRFTNFDPSTLLPGCLDYWTYDGSLTTPPLLESVTW VLKEPISVSSGQMAKFRSLLFTSEGETACCMVDNYRPQPQLKG RQVRASF
362	MQEITVLEYSNIRKNEVTWPWNPKPSTPVIDPTSYIDPNATVIGD VTIGANVLIGPNAVIRADEGRRPIVIGDRSNVQDGVVVLHAESVN DEGMEIGDNVLEGNSYYAVYIGKNVLAHQSQVHGPAAVG

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	DDSFVGMQSLVFNSIVGSNCVIEPNAAAIGVTVPDGKYIPAGT VVTTQAEADKLPEVTPDHAFYTDVAKVSVNVNLCRAYKEQ S
363	MIRKNPSGHLPVIAETAFIGDQTAIICGKVIIYDNVFVGPYAVIRA DEVNEHGDMEAIVIKRDTNIQDGVIHSKAGAAVTIGERSSIAH RSIIHGCPWCWVGDDVFIGFNSVVFNAKIGKGCVIRHNSVVDGLD LPEHFHVPPMTNIGADFDLSSISKVPPPEYSAFSESVVSANHEL QGYRRRIANEL
364	MRILVLTACFYPNSEHDGQKWANIKEPEWKTCHGKMQSPIDLS SHRVSLVHDQWTWNRDYKPAVAVINRGHDIMVSWKEDAGKV TIHQTDYKLVQCHWHSPSEHTVNGTRYDLELHMVHTSAQGKT AVIGVLYKLGRPNEFLAKLLDGKISVGKEEKDLGIVDPRTIGFH TDKFYRYVGSLLTPPCTEGVIWTVKKVNTVSMEQLAALREA V
365	MQEITVTRYENIRPSPVTSWNEPKLPKIDPTAYVDPAAVVQG DVTIGKVNVMVASANASIRSDEGYPIYIGDNSNVQDNVLHALET VDADGKRIEKVNITVGDKEYAVYVGDNVSLAHQAQVHGPAA VGDNTFIGMOSFVFNSTVGKNCYLAAPLAAAIGVTIPDGTYIPAG KVTTQEEAAKLPKITPDHPFANTNAAVVKVNVELAKGYLAL K
366	MSTPLVRWGYKEDNGAHQWCIFFPEACKGKRQSPINIQTSKV YDPGLRPLNLNYDPSTSLEILNNGHHSVQVNFKETDRSVLSGG PVTGTYRLRQFHFWGAKDCRGSEHTVAGVKYPSELHLVHW NAVKEYSEFAEALEENGLAVIGVFLKLGHDELQKLVDALP SIKHKDTLVEFGSFDPSCLMPTCPDYWTYSGLTTPPLSESVTW IKKQPVEVDHDQLEQFRSLLLFTSE
367	MSSTFVVGRPCDTRLPRGRSRKEPARVPHGFAAGIATVVSALL CLAGGCAHAPVPREAGRSAVAQSEADYSDALAPWTYPEGPS WGAACAKQOPPPQQSPIDLTRTTAPWASSAVITQATFDGHDQN VVFQASPGPSVTMAPGVDGSGRAFYTVAGFHFYRNEHvia CNPVYELHIIKTVTDQHGGVAVPAVLWTADDAAGEDPTLAAAY RSLAPPDSVVAVDLGRALWRFGQQPFYSYVGSLLTPCCTGI RWFVLOPPIRTSSASIGRLNALIARGMPRDNVRTVTPVVAQPO PVVYLVTPK
368	MQEITVLEFSNITKNEVTPTNPKPTTPVIDPTS YVDPNATVTGD VTIGKVNLIQPNNAVIRADEGRPIVIGDNSSVQDGVLVLAESVD DEGKIIEDNVVLYGNKYAYVYIGKVNVLQAHQAQVHGPAAVG DSFVGMSNLVFNSIVGSNCVIEPNAAAIGVTVPDGKYIPAGTV VTTQEEADKLPEVTEDYKFYTQVAKVVTVNVLCEAYRNQA
369	MQEITVTTFTNIRPSPVTPWNPTPKLPKIHPHTAYVDPAAVVQD VTIGENVMISANASIRSDEGYPIYIGDNSNVQDNVLHALETVD ENGKVIIEENVVTVGDKYYAYVYIGDNVSLAHQAQVHGPAAVG DNTFIGMOSAFVFKSNIGKNCVLEPLAAAIGVTVPDNKYIPAGT VVTTQEEAAKLPVTEPDHPFANTNAAVVKVNNAAGYLA
370	MKLSNVFIAGCTYQEPWDHREWDSKKGPATWGLINSAWSL CSIGKRQSPIDIELNQLLYDPFLPPLRLSSGGKKLGGTMINTGR HVSFRPDKAQLVNISGGPLSYSHRLEEIRLHFGSEDSQGSEHLL NGEAFSGEVQLIHYNQELYSNFSEARPKPNGLLIISIFMKVADT SNPFLNRLNRDTITRISYKNDAYFLMNLNIELLYPESFGFITY QGSMSTPPCYETATWILIDRPINITSLQMHSLLSQNLPSQIFLS MSDNSRPLQPLAHRALRGNR
371	MQEITVTRYENIRASPPTWPWNPTPKLPKIHPHTAYVHPLAEVVG DVTIGANVMVASANASIRSDEGYPIYIGDNSNVQDNVLHALET VDANGNRIEENIVKVGDEEYAYVYVGDNVSLAHQAQVHGPAA VGDNTFIGMOSAFVFRSVVGKNCYLAAPLAAAIGVTVPDNTYIPAG GKVVTTQEEADKLKPMTPDHFYNTNKAVVKVNVALAKGY ALA
372	MRSPLAGWTIVFCQKDEYNHLDGILGGPGYWGGLINPEWRMCS KGKMQSPIDIDPKVLLYDPNLSAVHLDKHKVSGTLENTGQSLV FRVDKGSRQHVNISGGPLAYRYQFHEIFLHYGLKDSMGSEHRI NGYSFPAAEIQLYGFNSELYHNMSSEAQHKSQGIVGVSLMVQIGE

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	TPNPELRLTSQLERVRYRGOSAPIHHLSLRGLLPDTEHYMTYE GTTTHPGCWETTVWVILNKPIYITRQELYALRRLMQGSQSOPK APLGNNARPVQDLHGRTVRTNI
373	MLISRATGHPVKENDCYQWPGPNGEKGPDWKWGKINPKWKV CGEGKLQSPIDLLNQRVQILPNLGKLQKDYPAPAVLKNRGH DIMVKWKGDAKLNLINGTYKLVQCHWHTPSEHTTINGTKFD MELHAVHKSSKGETAVIYIGWIKIGRPDSFLSKLLKNIKSVGDK EIDLGVINPGDIKFGSRKYYRYMGSLTVPPCTEGVIWTIVKKVR TVSREQLRAL
374	MKRSLIFAVGTCPCQEDWHYNYDEASGRGPSRWGLLKPEWRT CSVGKLQSPIDIGTVQVSSSELGDLQRNYRSAPALLRNRTEDVA VIWLGNAKSITINGVVYRVVNCHWHSPEHTFNGTRLPLEIHIV HRSSQNRIAVVGILYKGDPDFLSKLHFSIKSLGKEEKNLGIV NPESIGFQDKYYRYIGSLTTPPCSEGVVWTVFKKVRTVSREQ LKALKDAVD
375	MQEITVTRFENIRPSPVTPWNPEPKLPKIHPTAYIDPAAVVQGD VTIGANVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET DENGNVLEENVVTVGDEKYAVYVGDNVSLAHQAQVHGPAIV GDNTFIGMQAFVFRSRVGKNCVLAAPLAAAIGVTVPDGTYVPA GKVVTTQEEAAKLPKTPDHFPANTNAAVVKVNVALAKGYL ALA
376	MQEITVTKYNNIRASPVTPWNPTPKLPNIHPTAYIDPAAVVQGD VTIGANVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET VDENGNPNIKENIVKVGDKDYAVYVGDNVSLAHQAQVHGPA VGDNFIGMQSFVFASEVGKNCVLAAPLAAAIGV рр KVPDNTYIPA GKVVTTQEEAAKLPKTPDHFPANTNAAVVKVNVALAKGYL QS
377	MQEITVLIYSNVTKNEVTTWNPKPKTPKIDPTS YVDPKATVGD VTIGANCMISPFASIRSDEGYPIYIGDNSNVQDNVVLHALET TNGKIIEDNVVIKGDKRYAVYVGDNVSLAHQAQVHGPARVGD DSFIGMQSFVFKSIVGSNCVIEPNAAAIGVTVPDNKYIPAGT TTQEEADKLPEITEDYKYYNTNDAVVVNVKLCKAYRNKS
378	MQEITVTFNFFNIIQSPSPVTPWNPEPKLPKIHPTAYIHPLAVQGD VTIGENVLVMANAVIRADEGYPIYIGDNSNVQDNVVLHALET DENGNRIEENIVKVGDEEYAVYIGDNVVLAHNAQVHGPAAVG DNTFVGMLALVFNSTIGKNCVLAAPLAAAIGVTVPDGTYIPAG VTTTQEEAAKLPKTPDHFPANTNAAVVKVNVALAKGYLALS
379	MRKSLFACTVIGWNYEDQPHWESELDPAYAACATGKEQSPIDIR GARRADLPLRFEYRSAPLKVKVINNGYTIRVNYHDSPGSGNF VGDARYQLTQFHFRPRSEEVYHGKPYTMELHLMHQSSDGEV AGVAVLLKAGRANATIQRLWEHMPATEGGQEQLLAGVTIDPAG LLPRETGYYVYMGSVTAPPCTEGVTWFVLKTPVEISAEQIAV ARLYPHDVRPLQPL
380	MQEITVTRYENIRPSPVTPWNPEPKLPKIHPTAYIDPKAVVQGD VTIGENVLVMANAVIRADEGYPIYIGDNSNVQDNVVLHALET DENGNRNLKENVVTVGDKKEYAVYIGKNNVIAHLAQVHGPAAV GDNTFVGMLALVFNSTIGKNCVLAAPLAAAIGVTVPDGTYIPAG TVTTTQEEAAKLPKTPDHFPADLNARVVKNIALAKGYLALA
381	MQEITVTRYENIRPSPVTPWNPEPKLPKIHPTAYIDPKAVVQGD DVRIGANVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET VDAAGNRIENIVTVDDEEYAVYVGDNVSLAHQAQVHGPA VGDNFIGMQAFVFRSVVGKDCVLEPLAAAIGVTVPDGTYIPAG AGKVVTTQEEAAKLPKTPDHFPANTNAAVVAVNVELAKGY LALA
382	MQEITVTRYENIRPSPVTPWNPEPKLPKIHPTAYIDPKAVVQGD DVTIGANVMVSANASIRSDEGYPIYIGDNSNVQDNVVLHALET VDENGKVIENVVTVGDKKYAVYIGKNNVSLAHQAQVHGPA VGDNFIGMQAFVFRSVVGKDCVLEPLAAAIGVTVPDGTYIPAG GKVVTTQEEAAKLPKTPDHFPANTNAAVVAVNVELAKGY LA
383	MQEITVFEFSNITKNEVPTNPKPTTPVIDPTS YIDPNATVTGD TIGKNNLIGPNAVIRADEGAPIYIGDNSNVQDGVLHALESVDD

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	EGEI IEDNNVLEGDEYYAVYIGKNNVLAHQAQVHGPAMVGDD SFVGMKALVFVKSGNCVIEPEAAAGTVTVDGKYIPAGTVV TTQAEADKLPEVTDDYFYTAVEEVVENVNLAEAYREQS
384	MQEITVMDFSNIVKNEVTPTNPKPPTPVIDPTSYIDPNATVGD VTIGKNCYIGPFAVIRADEGAPIVIGDSNVQDGVLHALESVD AGGKIREDNVVTVGDRSYAVVVGKNVSLAHQSQVHGPARG DDSFVGMNSLVFNSIVGNCVIEPGAAAIGTVTVDGKYIPAGT VVTQAEAAKLPEVTDPHAAYSANADEVNVNVALSEAYRNL K
385	MVKRNILADFSPEGQTHWCYDCFIRPLPPVKWAKLFPKAKGN FQSPINIESRETRYDPSLKPLTLKYDPLSTAKLISNSGHSPNVDFD DTEDKSVLRRGGPLTGSYRLRQFHHLWGSADDHGSEHAVDGV KYAAELHVHVNAVKPFESFEEAALEENGGLAVIGVFLKLGEBHN PHLQKITDILYSIKFKDTLAEFTNFNPKCLLPTSDLTYWTYSGSLT TPPLLESVTWIVLKEPIVSSEQMAKRSLLFTSEGETACCMVD NYRPPQPLKGRQ
386	MLSKRIFGVATCOPENWHDDYKKANGEKQSPINIVTKETKYD SSLKPLTFKYPDSTAKEIVNVGHSFHVNFEDSENKSVLKGGPLT GTYRLKQFHFHWGSADDKGSEHTDGVVKYPSELHLVHWNAV KFESFABAALEEENGGLAVIGVFLKLGEBHHKELQKLTDLPSIKHK DTLANFGSFDPSCLMPTCPDYWTYPGSLTTPLSESVTWIVLK QPIEVSEEQLAAFRSLLFTSEGEK
387	MQEITVLEFSNTKNEVTSWNPKPSTPVIDPTSYVDPNATVGD VTIGKNCYIAASAVIRADEGKPIVIGDNSNVQDGVLHALESVD DDGGKIREDNVVVIHGDKWYAVYIGKNNVSLAHQSQVHGPAYV DDSFVGMNSLVFNSIVGNCVIEPNAAAIGTVTVDGKYIPAG TVTTQAEADKLPEITPDYAFYTQVAAVVKVNVLCRAYRNQ A
388	MQEITVLIYSNTKNEVTSTNPKPPTPVIDPTSYVDPNATVGD VTIGKNCNCLIGPSAVIRADEGAPIVIGDRSNVQDGVLHALESVD DEGGKIIBEENVVVHGDKYAVYIGKDVLVLAHQAQVHGPARG DHSFVGMKSLVFNLSIVGNCVIEPNAAAIGTVTVDGKYIPAGT VVTQEEAAKLPEITPDHEKYTKIAEVVTVMNVNLCRAYRNKA
389	MIKLSVAFCTGNQRPEWDYHNNNGHKEEWPEEYPSCGGQLQS PIDLHGDILQYDASLTPLQFQGYNSATEQFTLTNNNGHSVQLS PSDMYLKGGLPSRYTATQCLHLHWGKKGDLEGSEHQINSEATAA ELHIVHYDSEKYSNISEAMNKPQGLAVLGLIIEVGETENPAYDH ILSLRLHIERYDQKTSVPGFNIRELLPEQLEEEYYRYQGSLLTPPC YQSVLWTLFNRRAQISMGQOLEKLQETLSSTESEPSEPLVQNYR VPQPLNQRTVFAZF
390	MGHTWCNDEEGTRGRSEGPTAAAGVRVERMIREGGSR AATPHVRGCVLYAVRGVPMARSWLTASALTVAAVTLIGCAQ AAPAETAPTERVAEPAHWSYDGDGPESWAGLDDAFQACEA GTDQSPIDLPAAVPAPSTSIELSAAEEAGDVFDGSHAVEIETDG QGETLTFADDYDSLQQLHAAHVPSHTVAGOPAAAEELHLVHAD ADGNLLVGLVLTEGAASDALTPFIEAASHLADDEEVTLDDAA VLPASLENYEYSGSLLTPPCTEDVQWVVMGTPISMSAEQIGTL AGAHNNNARPTQPLGDRTVVGGAGKVEITG
391	MARKNPSPGHLPQVSETAFIDPTAIICGVIIIEDYVFIGPYAVIRA DELNAAGDMEPIVIGAHSNIQDGVVIIHSKSGAAVTIGEFSSIAH RSIVHGPWCIGDRVFIGFNSVLFNCHIQSGCVVRYNAVDGVT LPENTYIPSTERVGPDSDSLRYQVDRGALQFSEEVATNVEL VRGYQALRNEF
392	MQEITVTRYENIRESPVTPWNPTPKRPKIHPHTAYIDPLAYQGD VTIGENVMVSALASIRSEGYPIYIIGNNSNVQDNVVLHALET DENGEKEEENIVTVGDEKYAVAIGDNVSLAHQAQVHGPAPIVG NTFIGMQAFVFRSKVGKNCVLEPLAAAIGTVPDNTYIPAGTV VTTQEEAAKLPKVTPDHPFANTNAAVVKVNVALAKGYLALA
393	MNPITSFNPVQRYPKIDKTAFISPSSVIGDVRIKDNVYVAPNVS IRADEGTPFYIGSNTNLQDGVLILHGLLINKFVTVDKKSITYIGN QVSIAHDALIHGPACYIGDKVFVGFKAIVYNAIVGKGTVISYNAV VTNGVRIAPNRVPPGANIDTQEKA DALSRVPKDEEEFAREVQ RVNQEFFPASYHLLFGENRCSCGLS

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
394	MQEITVLDFSNVTKNEVTPTNPKPCTPVIDPTSYIDPNATVIGD VTIGKNMVWPSAVIRADEGKPIVIGDNSSVQDGVLHalesv DDGGKVIEDNVVLEGNKRYAVYIGKNTLAHQSQVHGPAYV GDSSFVGMSSEVFNPKGSNCVIEPNAAAIIGVTVPDGKYIPAG TVVTSQAEDAKLPEITDDYPYSNAIAAVVKVNVLCEAYKAQ A
395	MQEITVLRFSNIRKNEVTPEPETPVIDPTSYIDPNATVIGDV TIGANCYIGPFARIRADEGRPPIVIGDRSNVQDGVLHalesvda EGEIIIEDNVVIEGDELYAVYIGRDVSLAHQSQVHGPARVGDS FVGMSLVFKSDVGSNCVIEPFAAAIGVTIPDGKYIPAGTVV QAEAEKLPEITEDYPFTTIEEVVKVNVLAKAYREQK
396	MQEITVMEFSNVTKNEVTSTNPKPCTPVIDPTSYVDPEATVIGD VTIGKNCYIGPFARIRADEGAPIVIGDSSVQDGVLHalesvd ADGKIIEDNVVHLGDKLYAVHIGKNVSLAHQAQVHGPARVGD DSFVGMSLSVFNSSVVGNSNCVIEPNAAAIIGVTVPDGKYIPAGTV VTTQEEADKLPEITPDYAKSTAIAAVEVNVALCEAYREQA
397	MQEITVAEFSNIKTKEVTSWNPKPKTPVIDPTSYVDPNATVIGD VTIGKNCYIAPFASIRADEGTPPIVIGDSSVQDGVLHalesvd ADGKILEDNVVHLGDKRYAVYIGKNVSLAHQSQVHGPAHVGD DSFVGMSLSVFKSKVGNNCVIEPGAAAIGVTVPDGKYIPAGT VTTQAEADKLPEITPDYAKSNQVAAVVKVNVALCEAYRKQS
398	MQTYDSSLRESLLPLPDKKESVRYWLILGGFTAAAAVAVFVIA ARSGSHADASVLSALIAVAPHFEYAEANCDETKEASEIVQL DTWSWAPTCITGRAQSPIDIVTKEVATAGLLEDDAISLISIGSATL VPSNTGCHGFQLTSTGTPPSAMFRGEKFNFQKTHWHTPSENTV DGEHAAMEGHFVFQLDPLWVNTTLNLAVMAVFFELGDCNQ HLSAVWDTPVDRRLGTGSGTFSGETLASLLASVLCGGYYQFTG SLTTPPCTEGVAWNVMKRTTVCQDQVDRLKHALSATANG DISNRVUQPLHQRVVTQTSR
399	MSRLTGKIAVFCYQNPEHWDYDSPIAKGKNRQSPIDIDLWSAKY DPGLKPLTFTGYDKKSLRTLLNNNGHSVSVQFEDSEDKAVALSGG PLTGVYRLKQFHFWGAADDKGSHTVDGVKYPSELHLVHW NAVKFSSFAEAASKPDGLAVVGVFLKIGKEHVELNKLTDALY MVRFKGTKAQFSCFNPKCLLPASRHYWTYPGSLTTPPLSESVT WIVLREPISVSERQMEKFRSLLFTSEDDERIHMVNNFRPLQPLM NRTVRSSFR
400	MVPYPYPIVYQNPPVAEVTSVSYPKISRKAIGTDSMIIGDITIA DDVYIGFKNLLRADSGHPPYVGPYTNIQDYVLMVHVPGREHV VVNNQKGVFLEGMSNSVLUHAAVHGPLFIGKNTFIGQHANIY DAVIGRDCVVMHGATVTNGVKIADNRFVAPGQSVWQQSEAD KLPPVPEKFDLNRISIVDHYYRLGKSYGLNTPLAYSYSGG
401	MLALTLLAIALLLNARAVLSSCAHGTYLRLRAIDDNKPIKLPNFG YGPFDGPTNWHSLSEDNILCGTGRQSPIDIDDTISQVAAGFV MDVPIQDVSFLNLRLTTVEVILKGSTRINGREFVLEQFHFPHTPSE HVLNGEIFVAEVHFVHSNKENPKELAVITLMVQVSADHSTRSL DRVIGETRISTPGNKVAIPALNIGDITSLVNKQQLFTYGSLLTP PCTEGVQFFIIPQPIPMPRATVFNALKSVTGHNARFLQNNNATR PNVLVAGCQVIAAEVWSNATQYSR
402	MLAATVPAGTALADEWGYAGDGAPVNWGALSPDFAVCSAG VQQSPVLDLPGIIADGVRPVLDFAVGVEAERSAHGVTYHVP SGSAQLSLNNGRSFDLILQPHFHAASEHWVEGQSYPLEVHFVTAS EGDLAVGVGLPERGEAHATDVLWDAIGEPGDREEIDGPVSLA SLLPQDQAAFRYEGSLTPPCSEIVSWTVFTTPLSVSDAQIDAF VETVGENARPPQPLNRRYVLLDN
403	TAYIDPQASVIGEVTIGANVMSPMASIRSDEGMPIFVGDRSNV QDGVLHaleTINEEGEPIEDNIVEVDGKEYAVYIGNVSLAH QSQVHGPAVGDDTFIGMQAFVFKSKVGNNCVLEPRSSAAIGV TIPDGRYIPAGMVVTQSQAEADKLPEVTTDYAYSHTNEAVVYV NVHLAEGYKETS
404	TAIFIAPNAEVIGDVTIEGNAMISPNAStRADEGMPIYLGKDVL QDNVQLHaleTVDEEGNLIEENLVEVNGKKYAVYLGENVSLG HQAQVHGPAYVGKDTFIGMNAVVFKSRIGNNCVLEPNATVIG

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	VTIPDGRYVKAGTVIRTQADLPKLLDLKEVPEVKKKVDEYHN KLKELIKAKKAAA
405	TAYIHPQAQVIGEVEIGANVMSPMASIRSDEGMPYIYIGDNAN VQDGVLQLHALETVNEEGELIBENVVVEVDGKKYAVVGENVSL AHQAQVHGPAAVGKDTFIGMGAVFKSTVGNGCVLEPGAEVI GVTIPDGRYVPAGTVVRTQEQIPSREMTPDPPLLAVRDRVIA ENLKRAAELKARA
406	TAYIAEGAEVIGEVEYIGENVMISPNAISIRSDEGMPYIYIGENANV QDGVELHCALETKDEEGNLIEENVVVEVGKKYAVVGENVSLA HQAOQIHGPARVGKDTFIGMGAVVRGSTLGENVLLGEGVVIE VTIEEGTLVEEECTVITKQEDVKKLRKLPSDKMVKIKKEVLEK NKKLWEKLKEEE
407	TAYIHPSATVIGPVRIEEGVMISPNAISIRSDEGMPYIYIGDNVQ DGVTLHCLEVKREEGRVDESVPVEVDGKDYCIVLGEVGSLGH QATIHGPFAKVGDDTFIGMGATVFRSTIGEGCVLEPGATVIGVTI PEGRYVPAGKTVTQAEADALPLITDSYPYRETENVVAVNL ALAEAARAAA
408	TAYIHPQAQVIGEVQIGANVMSPMASIRSDEGMPYIYIGDNAN VQDGVLQLHALEARNEECVEDESAWVEVNKGKRYRVVGENVS LAHQAOQVHGPAAVGKDTFIGMGASVFKSRLGNNGCVLEPGATV IGVTIPDGRYLPAGTVLRGRPIEEEIELREVTEELRARHQAVVE ANLARAELKARA
409	TAYIHPSAEVIGEVEIGANVMSPMASIRSDEGMPYIYIGDNANV QDGVLHCALEALDEEGEDEEAYVEVDGKRYRVVLYGNNVSL AHQAQVHGPAAVGKDTFIGMGASVFKSILGNNGCVLEPGATV GVTIPDGRYIIPAGAVLNVEDAEKTRELPEVTPELRAKRAAVLA ANAARYAELRAAA
410	TAYIHPQAQVIGDVQIGANVMSPMASIRSDEGMPYIYIGDNAN VQDGVLQLHALEARNEEGEDEEAYVEVNKGKRYRVVLYGNNVSL LAHQAOQVHGPAAVGKDTFIGMGASVFKSRLGNNGCVLEPGATV IGVTIPDGRYLPAGVLEGETAEAVAALPEVTPEMREAAQO AAAAAQYAAKAAA
411	TAYIAPSAAEVIGEVTIEDDCMISPNAISIRAEGMPYIYLGNGTNV QDGVLHGLEVKREEGEDEEAYVEVNKGKYYVYLGDNVSL GHQAQIHPAKVGDDTFIGMGATVFKSVIGNGCVLEPGATVIG VTIPDGRYVPAGATVTTQAEADALPLMTPDYALYHTNERVVA VNRALAAEARAAA
412	TAYIHPASAVIGDVEIGANVMSPMASIRSDEGMPYIYIGDNANV QDGVLHGLEVKNEEGEDEEAYVEVNKGKYYVYLGKNVSL AHQAQVHGPASVGSDFIGMGASVFKSRLGNNGCVLEPGATV VTIPDGRYLPAGTVLPGRLEDNTPLREVTPPEQREAHKAVVT KNLKLAKLLKELS
413	TAYIHPQAQVIGPVQIGANVMSPMASIRSDEGMPYIYIGDNANV QDGVLQLHALEARDEEGEDEEAYVEVNKGKRYVYIGENVSL AHQAQVHGPASVGSDFIGMGASVFKSRLGNNGCVLEPGATV GVTIPDGRYLPAGTVLPGRLEDNTPLREVTPPEQREAHKAVVT ENLARATELKAA
414	TASIAPSATVIGDVEIADNVMSISPNAISIRSDEGMPYIYLGANANIQ DNVTLHCALETKDEEGNLIEENYVEVNKGKYYAVVYIGDGSTLPA GLTIKGNGYVEVLAGPGEELLVVTTEPYKVEITSPEPVVLVRLSP EVRELLEVSPDSERLLAREADGGTALFAAFDARRAALKAAAL AANAAAVALTASIAPSATVIGDVEIADNVMSISPNAISRSDEG MPIYLGANANIQDNVTLHALETKDEEGNLIEENYVEVNKGKYY AVVYIGDGSTLPAGLTIKGNGYVEVLAGPGEELLVVTTEPYKVEITS PEPVVLVRLRLSPEVRELLEVSPDSERLLAREADGGTALFAAFDA RRAALKAAANAAAVALTASIAPSATVIGDVEIADNVMS PNASIRSDEGMPYIYLGANANIQDNVTLHALETKDEEGNLIEENY VEVNKGKYYAVVYIGDGSTLPAGLTIKGNGYVEVLAGPGEELLV TEPYKVEITSPEPVVLVRLRLSPEVRELLEVSPDSERLLAREADG GTALFAAFDARRAALKAAANAAAVAL
415	TAYIHPASAVIGDVEIGENVMISPNAISIRSDEGMPYIYLGENDV QDNVTLHGLEVYTEEELIEENLVEVNKGKRYVYVYTGKNVSLG

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	HQAQIHGPAKVGDDTFI GMNATVFKS VIGNNCV LEPNATV IGV TIPDGRYVPAGKT VTT QAEADALPVL TPDY ALYHT NERV NAV NLKLAQEA NAAATAYI HPSAS VIGDVE IGENVM ISPNAS IR SDE GMPI YLGENVN VQDN VT LH GLEV YTEEGELIE ENLVE VN GKR XVVYTGK NVSL GHQ A QIHGP A KVGD DTFI GMNATV FKSV IGN NCV LEPNATV IGV TIPDGRYVPAGK VTT QAEADALPVL TPDY ALYHT NERV NAVNLKLAQEA NAAATAYI HPSAS VIGDVE IGEN VMISP NASIR SDEGM PI YLGENVN VQDN VT LH GLEV YTEEGELI EENLVE VN GKR VVYTGK NVSL GHQ A QIHGP A KVGD DTFI GM NATV FKSV IGN NCV LEPNATV IGV TIPDGRYVPAGK VTT QAE ADALPVL TPDY ALYHT NERV NAVNLKLAQEA NAA
416	TAYIAPGAEVIGEVEIGANVMVSPMASI RSDEGMPIYLGDN TQDGVT LH GLEVE DEEGEE DESVYVEVN GKKYRVYI GNNVSL AHQAQVHGPAYVGDDTFI GMGATV FKS RIGNGC VL EPGATV GVTIPDGRYVPAGKT VTT QAEADALPVL TPDY AMYHT NETVV AVNLALAAA KAAATAYIAPGAEVIGEVEIGANVMVSPMASI RSDEGMPIYLGDN TNVQDGVT LH GLEVE DEEGEE DESVYVE NGKKYRVYI GNNVSLAHQAQVHGPAYVGDDTFI GMGATV F SRIGNGC VL EPGATV IGV TIPDGRYVPAGKT VTT QAEADALP LTPDY AMYHT NETVV AVNLALAAA KAAATAYIAPGAEVIGE VEIGANVMVSPMASI RSDEGMPIYLGDN TNVQDGVT LH GLE EDEEGEE DESVYVEVN GKKYRVYI GNNVSLAHQAQVHGPAY VGDDTFI GMGATV FKS RIGNGC VL EPGATV IGV TIPDGRYVP GKT VTT QAEADALPVL TPDY AMYHT NETVV AVNLALAAA AAA
417	TAYIAPTAEVIGDVII GDNV MISP NASI RSDEGMPIYIGEN VN DGV TITADRTK DEAGNDI P ENW VTV NGKKYAVY LGK NV HNATVNGRTV LGENV L VQENATL TASTL GENV VQENATL TG VTVAEGK VVEAGKT ITT QAEADKLKD LT KDHPL YNK KEV AKN LAI LEEKKK LETAYIAPTAEVIGDVII GDNV MISP NASI RD EGM PIYI GENVN VQDG VTI TADRTK DEAGNDI P ENW VTV NG KYAVY LGK NVVLA HNATVNGRTV LGENV L VQENATL TASTL GENV VQENATL TGTV VAEGK VVEAGKT ITT QAEADKLKD LT KDHPL YNK KEV VAKN LAI LEEKKK LETAYIAPTAEVIGDVII DN VMISP NASI RSDEGMPIYI GENVN VQDG VTI TADRTK DEAG NDI P ENW VTV NGKKYAVY LGK NVVLA HNATVNGRTV LGENV L VQENATL TASTL GENV VQENATL TGTV VAEGK VVEAGKT IT QAEADKLKD LT KDHPL YNK KEV VAKN LAI LEEKKK LE
418	TAYIAPTAEVIGDVII GDNV MISP NASI RSDEGMPIYIGEN ANLQ DNV NLH ALET K DEEGNDI EEN VVEVDGKKYAVY IGRV S LGH OQI IHGP ALV GDDTFI GMNAK FKS RIGN RC VL EPNAQV IGV TIPDGRYVPAGKV TT QEEADKLPL LTPD YAM LALAAE RALATAYIAPTAEVIGDVII GDNV MISP NASI RSDEG MPIYI GENANL QDN VVL HALE T K DEEGNDI EEN VVEVDGKKY AVY IGRV S LGH QAOQI HGPA LV GDDTFI GMNAK FKS RIGN RC VLEPNAQV IGV TIPDGRYVPAGK VTT QEEADKLPL LTPD YAM YHT NERV NAVN LALAAE RALATAYIAPTAEVIGDVII GDNV MISP NASI RSDEGMPIYI GENANL QDN VVL HALE T K DEEGNDI EN WVEVDGKKYAVY IGRV S LGH QAOQI HGPA LV GDDTFI GMN AKV FKS RIGN RC VL EPNAQV IGV TIPDGRYVPAGK VTT QEEA DKLPL LTPD YAM YHT NERV NAVN LALAAE RAL
419	TAYIAPTAEVIGDVII GDNV MISP NASI RADEGMPIV IEN VN QDG VET ALRSDL PEEE VE KLDL QEV DGKK VRAY FGK GAVLA HGAKI L VAST RL KVEP VP GVT VL KQDN VL RNV LL TEM HGL L EVNA ETGS IVI RESS DP ALES KAKT W KVTP EDK KAKIA AVIA A ARQE ALAAA ATAYIPTA EVIG DVII GDNV MISP NASI RADEG MPIV IEN VN VQDG VET ALRSDL PEEE VE KLDL QEV DGKK V AYFGK GAVLA HGAKI L VAST RL KVEP VP GVT VL KQDN VL R VLL TEM HGL L ILEV NAET GS IVI RESS DP ALES KAKT W KVTP EDK AKIA AVIA A AARQE ALAAA ATAYIPTA EVIG DVII GDNV M SPNASI RADEGMPIV IEN VN VQDG VET ALRSDL PEEE VE KLD L QEV DGKK VRAY FGK GAVLA HGAKI L VAST RL KVEP VP GVT LKQDN VL RNV LL TEM HGL L ILEV NAET GS IVI RESS DP ALES KA TW KVTP EDK KAKIA AVIA A AARQE ALAAA
420	TAYIEPNAEVIGDVK IGENV MISP NASI RSDEGMPIV IEN VN QDG VVINA K LKKN ENGEV D ESQL NTING EKV QIYLE KNV QLA HNVTI ED S VVL KEN VLL QEN VVL KNSTL GEGV VLA EN VV IEN TL PENT VV EAGT VIK NQEEV KTL KQL TAD SPAI VQL QAVL K

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	AALWEELKAAETAYIEPNAEVIGDVKIGENVMISPNAISRSDEG MPTIVIKENVNQDGVVINAKLKKNENGEVDESQLNTINGEKV QIYLEKNVQLAHNVTIEDSVVLKENVLQENVVLKNSTLGEVG VLAENVVIENVTLPENTVVEAGTVIKNQEEVKTLKQLTADSPA IVQLQAVLAKNAALWEELKAAETAYIEPNAEVIGDVKIGENV MISPNAIRSDEGMPIVIKENVNQDGVVINAKLKKNENGEVD ESQLNTINGEKVQIYLEKNVQLAHNVTIEDSVVLKENVLQEN VVLKNSTLGEGVVLAENVVIENVTLPENTVVEAGTVIKNQEEV KTLKQLTADSPAIVQLQAVLAKNAALWEELKAAE
421	TAYIHPSAEVIGDVTIGDNVMISPNAIRADEGMPYIYLDGNANV QDGVTLHGLETKDEEGNIIIEENLVEVNGKKYAVYVGDNVSLA HQAQIHGPAlVGDDTFIGMGTVRSSILGDGVLLGEVGQIENA TLPAGLCLGPGRVIRTPEELVDDCTEEQRAELKKKHAEVVAKN LALHEELKAAATAYIHPSAEVIGDVTIGDNMISPNAIRADEG MPIYLGDNANVQDGVTLHGLETKDEEGNIIIEENLVEVNGKKY AVYVGDNVSLAHQAOIHGPAIVGDDTFIGMGTVRSSILGDG VLLGEGVQIENATLPAGLCLGPGRVIRTPEELVDDCTEEQRAEL KKKHAEVVAKNLALHEELKAAATAYIHPSAEVIGDVTIGDNV MISPNAIRADEGMPYIYLDGNANVQDGVTLHGLETKDEEGNIIIE ENLVEVNGKKYAVYVGDNVSLAHQAOIHGPAIVGDDTFIGMG ATVRRSILGDGVLLGEGVQIENATLPAGLCLGPGRVIRTPEELV DCTEEQRAELKKKHAEVVAKNLALHEELKAA
422	TAYIAPNAQVIGEVTINGENVMISPNAIRSDEGMPYIYIGENANLQ DNVVLHGLEVYTEEGLIEENLVEVDGKKVYYIGKNVSLGH QAQIHGPAlVGDDTFIGMNAKVFKSIGNRCVLEPNATVIGVT IPDGRYVPAGKVTTQAEADALPVLTDPYALYHTNELVNEVN LALAAEGRAAATAYIAPNAQVIGEVTINGENVMISPNAIRADEG MPIYIGENANLQDNVVLHGLEVYTEEGLIEENLVEVDGKKYV VYIGKNVSLGHQAOIHGPAVGDDTFIGMNAKVFKSIGNRC VLEPNATVIGVTIPDGRYVPAGKVTTQAEADALPVLTDPYAL YHTNELVNEVNLAALAEGRAAATAYIAPNAQVIGEVTINGEN MISPNAIRSDEGMPYIYIGENANLQDNVVLHGLEVYTEEGLIE ENLVEVDGKKVYYIGKNVSLGHQAOIHGPAVGDDTFIGMN AKVFKSVIGNRCVLEPNATVIGVTIPDGRYVPAGKVTTQAEA DALPVLTDPYALYHTNELVNEVNLAALAEGRAAA
423	TAYIHPSAEVIGDVEIADNVMISPNAIRADEGMPYIYLGENTNV QDGVSLLALENSSEEDEDENWVEVNGKKYRVTIGNNVSLG HQAQIHGPAlVGDDTFIGMGAKFVKSTIGNCVLEPGVTIVG TIPDGRYLEAGTVLRSQADIEKAKPIKEDMPTYKKVKEHKEKL KEEREKLKKERTAYIHPSAEVIGDVEIADNVMISPNAIRADEG MPIYLGENTNVQDGVSLLALENSSEEDEDENWVEVNGKKY RVYIGNNVSLSGHQAOVHGPAIVGDDTFIGMGAKFVKSTIGNG CVLEPGVTIVGVTIPDGRYLEAGTVLRSQADIEKAKPIKEDMPT YKKVKEHKEKLKEEREKLKKERTAYIHPSAEVIGDVEIADNV MISPNAIRADEGMPYIYLGENTNVQDGVSLLALENSSEEDED NWVEVNGKKYRVTIGNNVSLSGHQAOVHGPAIVGDDTFIGMG AKVFKSTIGNGC VLEPGVTIVGVTIPDGRYLEAGTVLRSQADIE KAKPIKEDMPTYKKVKEHKEKLKEEREKLKKER
424	TAIIAPGATVIGEVHIADGMISPNAIRADEGMPYIYLGETYTNLQ DNVVLHGLETYDEEGNLIIEENLVEVNGKKYAVYVGKNVSLG HQAQIHGPAlVGDDTFIGMNAKVFIRSTLGEGVVLEENVVVEGQ TLEKGTYLEKGMLLTPEDLKKAKKIKEEDPVKKLEAHIKEQ KAQAKAAQAAATAIIAPGATVIGEVHIADGMISPNAIRADE GMPIYLGETYTNLQDNVVLHALETYDEEGNLIIEENLVEVNGKK YAVYVGKNVSLGHQAOQHGPITVGDFTFIGMNAKVFIRSTLGE GVVLEENVVVEGQTLTEKGTYLEKGMLLTPEDLKKAKKIKEE DPVKKKLEAHIKEQKAQAKAAQAAATAIIAPGATVIGEVHIAD GMISPNAIRADEGMPYIYLGETYTNLQDNVVLHALETYDEEGN LIEENLVEVNGKKYAVYVGKNVSLGHQAOQHGPITVGDFTFIG MNAKVFIRSTLGEGVVLEENVVVEGQTLTEKGTYLEKGMLLT EDLKKAKKIKEEDPVKKLEAHIKEQKAQAKAAQAAA
425	TAYIHPSAEVIGEVEIGANVMSPMASIRSDSEGMPYIYGDNVN QDGVVLLHGLETKNEEGEIIEENLVEVDGEKYVYVYLGKNVSLA HQAQVHGPSIVGDDTFIGMGAKEVGSTLGDGVFLGEGETVTG LTIPAGAVVSPGTVLTPAOLASLKP LTADPPLLKKKDGVVN NLATAAAALKALETAYIHPSAEVIGEVEIGANVMSPMASIRSD EGMPYIYGDNVNQDGVLHGLETKNEEGEEIEENLVEVDGEK YVYVYLGKNVSLAHQAOVHGPSIVGDDTFIGMGAKEVGSTLGD

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	GVFLGEGATVTGLTI PAGAVVSPGTVLTPAQLASLKP LTADD PLKKKKDV VENN LATAAALKALE TAYIHPSA E VIGEVEIGAN VMVSPMASIRSD EGMPIKIGDNVN VODGVVLHGLETKNEEGE EIEENLV EVDGEKYVY LGKNVSLAHQAQVHG P SIVGDDTFIG MGA KVEGSTLGDGVFL GEGATVTGLTI PAGAVVSPGTVL T AQLASLKP LTADDPLKKKKDV VENN LATAAALKALE
426	TAYIHP SASVIGD V EIADNV MISP NASIRADE GMPIKIGP NAN QDG VTLH GLET YDEEGN LIEE NYVEVNG ERYV VYI GD NVSLG HQAOI HGP AKVG DDTFIG MKATV FKSV IGN NC VLEPG ATV G V TIPD GRV VPA GKV VTT QAEAD ALP VL TDY A LYHT NLK LAEKAR LEATAYIHPSASVIGD V EIADNV MISP NASIRADE GMPIKIGP NANVQDG VTLH GLET YDEEGN LIEE NYVEVNG ERY V VYI GD NVSLG HQAOI HGP AKVG DDTFIG MKATV FKSV IGN CV LEPG ATV G V TIPD GRV VPA GKV VTT QAEAD ALP VL TDY LYHT NERV NA VNLK LAEKAR LEATAYIHPSASVIGD V EIADNV MISP NASIRADE GMPIKIGP NANVQDG VTLH GLET YDEEGN LIE EN YVEVNG ERYV VYI GD NVSLG HQAOI HGP AKVG DDTFIG MK ATV FKSV IGN NC VLEPG ATV G V TIPD GRV VPA GKV VTT QAE DALP VL TDY A LYHT NERV NA VNLK LAEKAR LEA
427	TAYIAPS AEVIGD V EIAGAN VMVSP MASIRADE GMPIYI GD NAN VQDG VVLH ALEY TDEEGN LIEE AY VEDG K KYA VV GD NVS LAHQAOI HGP AKVG D EFT FIG MGAK VVG STLG KG VFLA EG VVV ENATL PEGTILEKG TVT PSD KELPKA PEEL RAKL AEEHK AVV AANIAAAA AKAATAYIAPS AEVIGD V EIAGAN VMVSP MASIR ADEGMPIYI GD NANVQDG VVLH ALEY TDEEGN LIEE AY VED GKKY AVV GD NVSLA HQAOI HGP AKVG D EFT FIG MGAK VVG TLG KG VFLA EG VV VENATL PEGTILEKG TVT PSD KELPKA PE ELRAKL AEEHK AVV AANIAAAA AKAATAYIAPS AEVIGD V EIAGAN VMVSP MASIRADE GMPIYI GD NANVQDG VVLH ALEY DEEGN LIEE AY VEDG K KYA VV GD NVSLA HQAOI HGP AKV GEDT FIG MGAK VVG STLG KG VFLA EG VV VENATL PEGTILEKG TVT PSD KELPKA PEEL RAKL AEEHK AVV AANIAAAA AKA A
428	TAYIAPG AEVIGD V EIAGAN VMVSP MASIRADE GMPIYV GD NAN VQDG VVLH GLET LDEEGN LIEE NW VEDG K KYV VY LGKNV LAHQAOI HGP AKVG D EFT FIG MGQALV FK STI GN CG VLE PG GV TIPD GRV VPA GAVV TS QAEAD ALP KMTPD YAYA HTNETV VAVNN NALA AGY KAAATAYIAPG AEVIGD V EIAGAN VMVSP MA SIRADE GMPIYV GD NANVQDG VVLH GLET LDEEGN LIEE NW EV DG K KYV VY LGKNVSLA HQAOI HGP AKVG D EFT FIG MGQALV FK STI GN CG VLE PG A V IGV TIPD GRV VPA GAVV TS QAEAD LPK MTPD YAYA HTNETV VAVNN NALA AGY KAAATAYIAPG AE VIGD V EIAGAN VMVSP MASIRADE GMPIYV GD NANVQDG VVLH GLET LDEEGN LIEE NW VEDG K KYV VY LGKNVSLA HQAOI HGP PAKVG D EFT FIG MGQALV FK STI GN CG VLE PG A V IGV TIPD GRV VPA GAVV TS QAEAD ALP KMTPD YAYA HTNETV VAVNN NALA GY KAAA
429	TAYIHP SATV I GQVN I GAN VMVSP MASIRADE GMPIYI GEN AN VQDG VL IQNESLK N ESEI DYS KV HKPN KRIES I VL KKNV SLA QATV YNT ELS EGV F LQEG VV VKN S VIEGRV V LQRG VTV EN YIGEEV VIA EGT V LKG DED LKTT L APLT P EQVA QI QAVIA QN AAAAAA KAAATAYIHP SATV I GQVN I GAN VMVSP MASIRADE GMPIYI GEN ANVQDG VL IQNESLK N ESEI DYS KV HKPN KRIES I VL KKNV SLA HQATV YNT ELS EGV F LQEG VV VKN S VIEGRV LQRG VTV EN VY I GEEV VIA EGT V LKG DED LKTT L APLT P EQ QI QAVIA QN LAAAAA KAAATAYIHP SATV I GQVN I GAN VM VSP MASIRADE GMPIYI GEN ANVQDG VL IQNESLK N ESEI DYS KV HKPN KRIES I VL KKNV SLA HQATV YNT ELS EGV F LQEG VKNS VIEGRV V LQRG VTV EN VY I GEEV VIA EGT V LKG DED LK TTL APLT P EQVA QI QAVIA QN LAAAAA KAA
430	TAYIAPG A QVIGD V EIADNV MISP NASIRADE GMPIYI GEN AN QDNV QLH GLEV YTEEG E LIEE NF VEDG K KYV VY I GRV S LA HQAOI HGP AKVG DDTFIG MGNA KV FK SIV GN C VLE PNATV G V TIPD GRV VPA GKT VTT QAEAD ALP VL TDY A LYHT NEL V VNL LAL AEEA RAATAYIAPG A QVIGD V EIADNV MISP NASIR ADEGMPIYI GEN ANLQDNV QLH GLEV YTEEG E LIEE NF VEDG K KYV VY I GRV S LAHQAOI HGP AKVG DDTFIG MGNA KV FK SIV NRC VLE PNATV I G V TIPD GRV VPA GKT VTT QAEAD ALP VL TD

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
	YALYHTNELVNAVNLALAAEARAAAATAYIAPGAQVIGDVEIA DNVMISPNASIRADEGMPYIYGENANLQDNVQLHGLEVYTEEG ELIENEVFVEVDGKKYVYYIGRRVSLAHQAQVHGPAGKVGDDTFI GMNAKVFKSIVGNRCVLEPNATIVGTVIPDGRYVPAGKTVTQ AEADALPVLTPDYALYHTNELVNAVNLALAAEARAAA
431	TAYIHPHTARVIGEVТИAAGVMISPAGSIRADEGMPIVIGENANV QDGVLHGLEVYDEEGNLIEENLVEVNGEKYVYYIGENVSLG HQAQIHGPALVGDDTFIIMGAKVTRSLILGEGVILEEGAQLTNVI VPGAYVKSGQVFVSTGEPVVLSLKQTPEQKEKLAQLAEE RAARAQQAAATAYIHPHTARVIGEVТИAAGVMISPAGSIRADE GMPIVIGENANVQDGVS LHGLEVYDEEGNLIEENLVEVNGEKY VYYIGENVSLGHQAQIHGPALVGDDTFIIMGAKVTRSLILGEGV ILEEGAQLTNVIVPDGAYVKSGQVFVSTGEPVVLSLKQTPEQ KEKLAQLAEEAERAQQAAATAYIHPHTARVIGEVТИAAGV MISPAGSIRADEGMPIVIGENANVQDGVS LHGLEVYDEEGNLIE ENLVEVNGEKYVYYIGENVSLGHQAQIHGPALVGDDTFIIMG AKVTRSLILGEGVILEEGAQLTNVIVPDGAYVKSGQVFVSTGEP VVLSELKQTPEQKEKLAQLAEEAERAQQAA
432	TAYIHPHTAEVIGNVKIGENVISMSPNASIRSDEGMPIVKENANV QDGVVIRADPTKDENGNDIEENWVTNVNGEKYAVYLEKNVVL AHNAVVEGRTVLKEGVLVQENA VVRSTLGEGVILQENAVLE GTVADGKIVPAGATIRTQAEADTTLATLTDHPLYNLNKVN AKNLALLKENLAAKTAYIHPHTAEVIGNVKIGENVISMSPNASIRS DEGMPIVKENANVQDGVVIRADPTKDENGNDIEENWVTNVNG EKYAVYLEKNVVLAHNAVVEGRTVLKEGVLVQENA VVRST LGEGLQENAVLEGTVADGKIVPAGATIRTQAEADTTLATL PDHPLYNLNKVNNAKNLALLKENLAAKTAYIHPHTAEVIGNVKI GENVMISPNASIRSDEGMPIVKENANVQDGVVIRADPTKDENG GNDIEENWVTNVNGEKYAVYLEKNVVLAHNAVVEGRTVLKEG VLFQENAVVRRSTLGEGLQENAVLEGTVADGKIVPAGATI RTQAEADTTLATLTDHPLYNLNKVNNAKNLALLKENLAAK
433	TAIIAPGATVIGEVEIGDNVMISPNASIRSDEGMPIVLGEGANLQ DNVELHALEVYDEEGNLIEENYVEVNKGKYAVYIGNNVSLGH QAQIHGPAPIVGDDTFIGMNAEVFKSIIIGNGCVLEPNARIVGTIP DGRYVKAGTTIDQAEIPS LKQLKDSDPIKAKVEAHKAALKAE RERLLAERTAI IAPGATVIGEVEIGDNVMISPNASIRSDEGMPIV LGEGLQENAVLEGTVADGKIVPAGATIRTQAEADTTLATL GNNVSLGHQAQIHGPAPIVGDDTFIGMNAEVFKSIIIGNGCVLEP NARIVGTIPDGRYVKAGTTIDQAEIPS LKQLKDSDPIKAKVE AHKAALKAEERLLAERTAI IAPGATVIGEVEIGDNVMISPNASI RSDEGMPIVLGEGLQENAVLEGTVADGKIVPAGATIRTQAEADT NGKKYAVYIGNNVSLGHQAQIHGPAPIVGDDTFIGMNAEVFKSII IGNGCVLEPNARIVGTIPDGRYVKAGTTIDQAEIPS LKQLKD SDPIKAKVEAHKAALKAEERLLAER
434	QEITVDEFSNIRENPVTPWNPEPSAPVIDPTAYIDPQASVIGEV GANVMVSPMASIRSDEGMPIVFGDRSNVQDGVLHALETINEE GEPIEDNIVEVDGKEYAVYIGNNVSLAHQSQVHGPAAVGDDT FIGMQAFVFKSKVGNNCVLEPRSAI GVTIPDGRYI PAGMVVT SQAEADKLPEVTDYDAYSHTNEAVVYVNVHLAEGYKETS
435	GKVVYKKPFIPARHIPS DKTII EPEIDEA VIEEGAI ITGGVIIKG RVYIASGATIRSDEGVPVIBENSSIQD GALVHADETVD EGDNP EENIVEVNKGKYAVYIGENVVLEHNATVHGPAAVGKNSLIGE ALVRNSVIGENCVLEEGASAENVTI PAGRYVPAGVTTQAAA AALPAVTPDHPLYKRNEELVKENLEKVKKANAAA
436	GSVLVEPSDIQCSPPNKYHKEPRCPTIAKGAYIEKGALIEGDVII EENVYIESGAIIRSDEGTPYIYGKNSVIQDGALVHADETVD EGD NPIEENIVEVNKGKYAVYIGENVVLEHNAEVHGPAAVGKNSLI GEGALVRSIIGENCVLEEGASAENVTI PAGRYVPAGKVT AEAAALPKMTPDHPLYKRNEELVKENLEKVKKANAAA
437	GVVLVEEGIRPSPATPRYPEPRAPII HPSAYVADGALITGEV DNVLIARGAVIRSPNDEGTPYIYGKNSVQDGAVIHADETVD AE EIEENIVEVNKGKYAVYIGENVVIEH GATVHGPAKIGENSLIGR GALVENS VIGKNCVLEEGASAIGVTIPEGRYI PAGVTTQ DALPEVTPDHPDYNRVAELVAKNIALAKELNAAR

TABLE 2-continued

Library of modified or engineered enzymes

SEQ. ID. NO	Sequence
438	PAPVRGHEAVFEDSLHPVTGKLLVTIAETAYIEEGATISGAVI LADNVYVESGATIRSDEGIPIYVGENSAIQDGAVLHADETVD DGNIPENIVEVNGEPEYAVVIGENVLEHGTAVHGPAAVGKNS LIGKNAVRNSVVGNCVLEEGASAENVTIPAGRYPAGVKT TTQEADALPEVTPDHPLRNEKLVAENNAKVKAAYAAR
439	GVVLTIVSDIRPSAPTAKESKAPTIHPSAYIAPGATIVGDVTI AANVYVEAGATIRSDEGVPIYVGENSAVQDGAVLHADETVD NGNPIENEENIVEVNGKKYAVVGENVLEHGTAVHGPAAVGAN SLVGEGLVANSIVGANCVLEPGASAINVTIPAGRYPAGVTV TTQAAADALPAVTPDHPLANRNAELVAKNVAKAKAAVAR
440	GTVVVATSPIRPSEPTPWRKESRAPTLAPGAYVHPDATVEGAV ILEEGALVQGGATIRSDEGVPIYVGRNSVIQDGATLHADETVD EGNIPENIVEVDGKPYAVVGENVVIQHGATIHGPAAVGENS LIGENALVENSVVGKNCVQIPEGGAARNVTIPAGRYPAGVTV TQAEDALPKVTPDHPLNKNAAALVAENLARRAELLAAR
441	MVVLVEEAGLRPSPPTRHREPRAPTLAEGAWVAPGATIEGEV HIAAGAYATIDGATIRSDEGVPIYVGRNSVIQDGALLHADETVD DGKVIENVTVNGEPEYAVVGENVVIQHGATIHGPAAVGANS LIGENALVRHSIIGENCVLEEGASAINTIPAGRYPAGVTVTT QAEAAALPKVTPDHPLNKNAAALVAENLALNKALVAAA
442	MLLVEEEPLIRPSEPTPWRGTRREPTIAEGAYIEPGAVITGDTIIE AGAYIESGAVIRSDEGVPIYIGANSAIQDGAVLHADETVDENG NLIEENVVVEVNGKKYAVVYVGANVIEHNAVIHGPAAVGANS IPEGAAVVRNSIVGANCVLEPGASVENVTIPAGRYPAGVVRT TQAADALPAVTPDHPLANRNAELVAKNVAKVKAANAAK
443	GLKKRKLTPAELRKPDPRYTGPRTSTIGETCLFAGAVISPGBT LGENVYIESGAVIRSDEGRPIVVGDNNSVIQDGAVLHADETVD DGNPENIPENITVNGKPYAVVYVGSNNVIDHGATIHGPAAVGANT LIGEGATVRNSTVGSNCVLEPGASAIGVTIPAGRYPAGVTVTT QAEADALPAVTPDHPLNKNAAALVAENLAKVKAANAAR
444	GVVVAAPVSDIQCSPPTPRFPESRCPTLHPSAYIEEGATIIGEVITG DNVLEKGATIRSDEGVPIYIGENSIQDGATLHADETVDAGN PIEENIVTVNGKKYAVVYVGENVIEHGTAVHGPAAGRNSLIGE GATVRNSIVGENCVLEEGASAIGVTIPAGRYPAGVTVTTQEEA AALPEVTPDHPLNKNAAALVAENLAKVKAANAAR
445	TAYIHPHSATVIGDVIEADNAMISPNSIRADEGMPKIEKNAAV QDNATIEAKPTKDAGNLIEENIVEVNGKKYAVVYVGENVSLAH NATLEGTTIIGKNNLVQENATLTNSTLGENVIVQENATLTGVTI AEGKIVPEGATITQEEAEKLAPLTDHPLYNKRAEIVAKALAE REAAALAAA
446	TAYIHPHSATVIGDVIEGANVMVSPMASIRSDEGMPKIEENANV QDGVKIEGKRVYSASGELIEENIVEVNGKKYVYVYVGENVSLAH QATIIGGTVLKKNVFIQEGAYIENSVLGENVIVQKNATIIGVTIK EGKVVPEGAVITTTQEEAEKLAPLTDHPLYNLNAQVVAANI AAALKAAAE
447	TAYIHPHTATVIGNVKIGENVMISPEASLRADEGMPVILEENVNV QDGVVIRGDRVLDAGNLIEENLVEVNGERYVYVYLGKGVVLA HGA伟VEGTSVGLVQEGAVLRRSTLGERVIVQEGAVLEG VTVAPGAVVPAGAVIRTQEEAATLAALTDPHPLYNENARVVA KNLALLEELKALE
448	TAYIHPHSATVIGDVIIIGKNAIMSPNASIRSDEGMPVILEENAVQ DNATITAKPTKTAGSELIEENIVEVNGKKYAVVYVGENVSLAH ATIEGGTGKNNLVQENATLTGSTLGENVIVQENATITGVTIA EGAVTPEGATITQEEAEKLEKLTPDHPLYNLNAELNAAKALAL RDLLLALS
449	TAYIHPHSATVIGDVIEGENAMISPNSIRSDDEGMPVILEKNVV QDNATIEANPVLDENGELIEENREVNGKKYAVVYLEEGVVLQ KNATIKGTTVVKNNLVQENATLTNSTLGENVIVQENATLTG VTVAEKGKVVPEGATITQEEAEKLEKLTPDHPLYNLGAERAK AAALARELKLALE

TABLE 2-continued

Library of modified or engineered enzymes

SEQ. ID.	NO	Sequence
450		TAYIHP SAKVEGEVEIGANVMVSPM ATINSTE GEPI F LGD RVNV QDG VIT CEP VYNA DGE LDE SKL VEIDG K KYCV YVA ENV SLA HQ STLS GTVLKKNF VQEG A VLK N STL G ENVV VRE NAVIEG VTI EGTVAEE GTV VLTE EDL A KLR PLT P EDPL LEI HK KV VEE IA KAKA LKAAA
451		TAYIHP SAEVIGD VEGE IGA NVM MISPN ASIR A DEG MP IVL GD NT NV QDG VSL HALE TL DEEGN LIEEN VVEV DGKK YAVY VGD NV S LA HQ AQV HGPA I VG DFT FIG MG AV RRS VLG KG VIL REG AT VEG VTI EGT VV EENT VLT KQ EEV KKL KLT PEH PY YNL NK KV VEE QNI KK VQA RAAA
452		TAVIHP SATVIGD VTIA DNV M ISPN ASIR A DEG MP IVL GEN VNL QDN VSL HALE TL DEEGN LIEEN VVEV NGKK YAVY LG EGV S LA HQ AQV HGPA I VG DFT FIG MN A KVG S IL GEG VIL QDN AT VEGA TIA EGK VV PEG AV IT TQE EAD KLA PLT PDH PY YEL V K RTREE N LRL RD LLL ELE
453		TAYIHP SAKVIGD VEGE IGA NVM MISPN ASIR A DEG MP IK L EKN VIV QDN AVI EAD RI YD E N G E L I E S A V T VNGKK YAVY LG E N V I L QK NAT RRG T VLG K N V L V Q E N A V L T N S T L G E N V I V Q E N A T V T G A TL K E G T I V P E G A T I T T Q E E A D K L E K L T P D H P Y Y E L V K R T R E E N A L R D L L L E L E
454		TAYIHP SAEVIGD VTIG ANVM VSPM ASIR A DEG MP IVL GN VN VQDG VVL HLG E LV L N E E G E L I E EN VVEV DGKK YV VV GEG V S L AH QAT VVG AT VLG KGV FV GEG VV L E R S I L G E G V I V G E N A V I K GVTIA EGK VV KEG T VTT Q E E A D K L E K L T P D H P Y Y E L N A R V V A E N I A K A R L L K L E
455		TAYIAPGAS VIGE VEIGD NV M ISPN ASL R S D E G M P I K L G D N V N V QDG VTL H G L E T K D E E G N L I E E N V V E V N G E K Y V V V G K N V V L A H N V T L S T R T V V E D N V Y L E E N V T L T R S T L G K V V V E V G K V V I E G V T I K E G M Y A K E G T V I R T Q E D V K S L E M I K D L A K H K A K V Q A V I D A N L R I H Q E A L A A T A T Y I A P G A S V I G E V E I G D N V M I S P N A S L R S D E G M P I K L G D N V N V Q D G V T L H G L E T K D E E G N L I E E N V V E V N G E K Y V V V V G K N V V L A H N V T L S T R T V V E D N V Y L E E N V T L T R S T L G K Y V V V E K G V V I E G V T I K E G M Y A K E G T V I R T Q E D V K S L E M I K D L A K H K A K V Q A V I D A N L R I H Q E A L A A T A T Y I A P G A S V I G E V E I G D N V M I S P N A S L R S D E G M P I K L G D N V N V Q D G V T L H G L E T K D E E G N L I E E N V V E V N G E K Y V V V V G K N V V L A H N V T L S T R T V V E D N V Y L E E N V T L T R S T L G K V V V E K G V V I E G V T I K E G M Y A K E G T V I R T Q E D V K S L E M I K D L A K H K A K V Q A V I D A N L R I H Q E A L A A A
456		TAYIHP TAT VIG S VTI I ADG VM I SPY ASIR A D E G M P I Y I G E G A N V QDG VTL H G L E T K D E E G N L I E E N V V E V N G E K Y V V V I G K G V S L G HQ AQV HGPA I VG DFT FIG MG A Q V T G A I L P E G L V L A E G V R V E S V D L S G Y R Y L P P G T V I R T Q A D K E R V R E D E S L A A E V E A R R A A L A A E R A A E A R A A A T A T Y I H P T A T V I G S V T I I A D G V M I S P Y A S I R A D E G M P I Y I G E G A N V D Q G V L H G L E T R D E E G N L I E E N V V E V N G K Y V V V I G K G V S L G H Q A V Q H G P A I V G D D T F I G M G A Q V T G A I L P E G L V L A E G V R V E S V D L S G Y R Y L P P G T V I R T Q A D K E R V R E D E S L A A E V E A R R A A L A B R A A E A R A A A T A T Y I H P T A T V I G S V T I I A D G V M I S P Y A S I R A D E G M P I Y I G E G A N V D Q G V Q L H G L E T R D E E G N L I E E N V V E V N G K Y V V V I G K G V S L G H Q A Q V H G P A I V G D D T F I G M G A Q V T G A I L P E G L V L A E G V R V E S V D L S G Y R Y L P P G T V I R T Q A D K E R V R E D E S L A A E V E A R R A A L A A E R A A A A R A A A
457		TA F I H P S A T V I G D V T I G A N V M I S P M A S I R S D E G M P I Y V G A N A N L Q D Q V T L H A L E V F D E E G N L I E E N V V E V N G E K Y A V Y L G D N V S L A H Q A Q V H G P A I V G D T F I G M Q A S V F K S T I G N G C V L E P G A A V I G V T I P D G R Y V P A G K V V T S Q A E A D A L P K M T P D Y A Y Y H T N E K V V A V N R A L A A G Y R A A Q T A F I H P S A T V I G D V T I G A N V M I S P M A S I R S D E G M P I Y V G A N A N L Q D Q V T L H A L E V F D E E G N L I E E N V V E V N G E K Y A V Y L G D N V S L A H Q A Q V H G P A I V G D T F I G M Q A S V F K S T I G N G C V L E P G A A V I G V T I P D G R Y V P A G K V V T S Q A E A D A L P K M T P D Y A Y Y H T N E K V V A V N R A L A A G Y R A A Q T A F I H P S A T V I G D V T I G A N V M I S P M A S I R S D E G M P I Y V G A N A N L Q D Q V T L H A L E V F D E E G N L I E E N V V E V N G E K Y A V Y L G D N V S L A H Q A Q V H G P A I V G E D T F I G M Q A S V F K S T I G N G C V L E P G A A V I G V T I P D G R Y V P A G K V V T S Q A E A D A L P K M T P D Y A Y Y H T N E K V V A V N R A L A A G Y R A A

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
458	TAYIHPSPSATVIGDVTIGANVMSPMASIRSDEGMPYIYLGDNVN VQDGVSLLHGLETVDEEGNVIENLVEVDGKYYVYLGDNVSL AHQAQVVEGGTVLGENVFLQEGVRVRSTLGEGVILREGATVE GVTIAPGKVVAAAGQTVTQAAAADALPTLTASDPLYSEHATVV AANIAAAAAAKAAATAIHPSPATVIGDVTIGANVMSPMASIR SDEGMPYIYLGDNVNQDGVSLLHGLETVDEEGNVIENLVEVD GKYYVYLGDNVSLAHQAQVVEGGTVLGENVFLQEGVRVRSS TLGEGVILREGATVEGVTIAPGKVVAAAGQTVTQAAAADALPTL TASDPLYSEHATVVAAANIAAAAAAKAAATAIHPSPATVIGDVT IGANVMSPMASIRSDEGMPYIYLGDNVNQDGVSLLHGLETVD EEGNVIEENLVEVDGKYYVYLGDNVSLAHQAQVVEGGTVLG ENVFLQEGVRVRSTLGEGVILREGATVEGVTIAPGKVVAAAGQ TVTTQAAADALPTLTASDPLYSEHATVVAAANIAAAAAAKAA
459	TAYIAPSATVIGDVTIGANVMSPMASIRADEGMPYIKVGDNN VQDQVTLHALETKDDEGNDIEENWVEVNGEKYAVYVGANVS LAHQAOQLHGPCIVGDDTFIGMQARVFKSSIGNGCVLEPQAAVI GVTIPDGRYVPAGAVVTSQAEADALPKLTDDYAYAHTNEKV AVNLALAKGYLTTPAYIAPSATVIGDVTIGANVMSPMASIRA DEGMPYIKVGDNNVQDQVTLHALETKDDEGNDIEENWVEVN GEKYAVYVGANVSLAHQAQQLHGPCIVGDDTFIGMQARVFKSS IGNGCVLEPQAAVIGVTIPDGRYVPAGAVVTSQAEADALPKLT DDYAYAHTNEKVVAVNLAQALAKGYLTTPAYIAPSATVIGDVTI GANVMSPMASIRADEGMPYIKVGDNNVQDQVTLHALETKDE EGNDIEENWVEVNGEKYAVYVGANVSLAHQAQQLHGPCIVGD DTFIGMQARVFKSSIGNGCVLEPQAAVIGVTIPDGRYVPAGAV VTSQAEADALPKLTDDYAYAHTNEKVVAVNLAQALAKGYLTTP
460	TAYIHPSPAVVIGQVEIGANVMSPMASIRSDEGMPYIKEANAN QDGVLIQSLVSKENDKELLEKLKLNNGEYNNIYLEEGVSLAH QATILNSCYLSSGCFLAEGVVLENSVLNDAVFLGRGVTVTNAE VLEPHVFEAGDVITEEKVEPVIEPEELRAIAAAQRAAVIAANLA AAAAAAKAAATAIHPSPAVVIGQVEIGANVMSPMASIRSDEG MPIKIEANANVQDGVLIQSLVSKENDKELLEKLKLNNGEYNN IYLEEGVSLAHQATILNSCYLSSGCFLAEGVVLENSVLNDAVFL GRGVTVTNAEVLEPHVFEAGDVITEEKVEPVIEPEELRAIAAQ RAAVIAANLAAAAAAKAAATAIHPSPAVVIGQVEIGANVMVS PMASIRSDEGMPYIKEANANVQDGVLIQSLVSKENDKELLEKL KKLNNGEYNNIYLEEGVSLAHQATILNSCYLSSGCFLAEGVVL ENSVLNDAVFLGRGVTVTNAEVLEPHVFEAGDVITEEKVEPV IPEELRAIAAAQRAAVIAANLAAAAAAKAA
461	TAYIHPQANVIGDVEIGANVMSPMASIRSDEGMPYIVFGENAN VQDQVTLHALETYDEEGNPYIENIVEVDGKYYVYLGKNVSL AHQAQIHGPSIVGDDTFIGMQALVFVFKSVLGNNCVLEPQAAAIG VTIPDGRYIPAGKVVTSQAEADALPEVTPDYAYYHTNEQVY VNTQLAEGYRAAATAYIHPQANVIGDVEIGANVMSPMASIRS DEGMPYIVFGENANVQDQVTLHALETYDEEGNPYIENIVEVDGK KYAVYLGKNVSLAHQAQIHGPSIVGDDTFIGMQALVFVFKSVLG NNCVLEPQAAAIGVTIPDGRYIPAGKVVTSQAEADALPEVTPD YAYYHTNEQVYVNTQLAEGYRAAATAYIHPQANVIGDVEIG ANVMSPMASIRSDEGMPYIVFGENANVQDQVTLHALETYDEE GNPIEENIVEVDGKYYAVYLGKNVSLAHQAQIHGPSIVGDDTFI GMAQALVFKSVLGNNCVLEPQAAAIGVTIPDGRYIPAGKVVTSQ AEADALPEVTPDYAYYHTNEQVYVNTQLAEGYRAAA
462	TAYIHPSPAEVIGSVEIGENVMSPNASIRSDEGMPYIVGDNANVQ DGVTIHLGLETKTEEGELIEENYVEVDGKYYVYIGENVSLAH QAQIHGPSIVGDDTFIGMGATVQTSILGEGVLLREGAQITGVT LAPGTVVDRGTVLTTQADVASLRKLEPSDPLLKENEEVRKKN LALWEELKKAETAYIHPSPAEVIGSVEIGENVMSPNASIRSDEG MPIVGDNNVQDGVLHGLETKTEEGELIEENYVEVDGKYY VYIGENVSLAHQAQVHGPAGVGEDTFIGMGATVQTSILGE VLLREGAQITGVTIAPGTVVDRGTVLTTQADVASLRKLEPSDP LLKENEEVRKKNLALWEELKKAETAYIHPSPAEVIGSVEIGEN MISPNASIRSDEGMPYIVIGDNANVQDGVLHGLETKTEEGELIE ENYVEVDGKYYVYIGENVSLAHQAQVHGPAGVGEDTFIGM GATVQTSILGEGVLLREGAQITGVTIAPGTVVDRGTVLTTQAD VASLRKLEPSDPLLKENEEVRKKNLALWEELKKAETAYIHPSPAEVIGSVEIGEN
463	TAVIAPNAQVIGEVHIGDNVMSPNASIRSDEGMPYIYIGENANL QDNVQLHGLEVLDEEGNVIIEALVEVDGKYYVYIGKNVSLG HQQAQIHGPALVQDGDTFIGMNAKVFKSRIIGNGCVLEPNAQVIGV

TABLE 2-continued

Library of modified or engineered enzymes	
SEQ. ID. NO	Sequence
464	TIPDGRYVPAGKVTTQAEADALPVLPDYAMAHTNERVVAV NLALAAAARAATAVIAPNQVIGEVHIGDNVMISPNAISRSD EGMPIYIGENANLQDNVQLHGLEVLDEEGNVIEEALVEVDGK KYVYIYGKNSVLGHQAQIHGPALVGDDTFIGMNAKFKSIG NGCVLEPNAQVIGVTIPDGRYVPAGKVTTQAEADALPVLPD YAMAHTNERVVAVNLALAAAATAVIAPNQVIGEVHIG DNVMISPNAIRSDEGMPYIYIGENANLQDNVOLHGLEVLDEEG NVIEEALVEVDGKKYVYIYGKNSVLGHQAQIHGPALVGDDTFI GMNAKVFKSRIGNGCVLEPNAQVIGVTIPDGRYVPAGKVTT QAEADALPVLPDYAMAHTNERVVAVNLALAAAARAAA TAYIHPQATVIGDVTIGANVMVSPMASIRSDEGMPIFVGDNAN VQDGVTLHALEYDDEEGNPPIEENWVEVDGKKYAVYLGDNVS LAHQAQVHGPAAVGEDTFIGMQATVFKSKLGNNCVLEPGAA AIGVTIPDGRYIIPAGKVTSQAEADALPEVTPDYYHTNEDV VYVNIALAEGYKKLSTAYIHPQATVIGDVTIGANVMVSPASI RSDEGMPIFVGDANVQDGVTLHALEYDDEEGNPPIEENWVEV DGKKYAVYLGDNVSLAHQAQVHGPAAVGEDTFIGMQATVFK SKLGNNCVLEPGAAAIGVTIPDGRYIIPAGKVTSQAEADALPE VTPDYYHTNEDVYVNVIALAEGYKKLSTAYIHPQATVIGD VTIGANVMVSPMASIRSDEGMPIFVGDANVQDGVTLHALET YDEEGNPPIEENWVEVDGKKYAVYLGDNVSLAHQAQVHGPA VGEDTFIGMQATVFKSKLGNNCVLEPGAAAIGVTIPDGRYI GKVVTSQAEADALPEVTPDYYHTNEDVYVNVIALAEGYK KLS

[0042] The enzyme comprising silicase activity may be specific or substantially specific to a substrate in the silicate such that the enzyme acts specifically on that substrate and facilitates extracting the metal from the mineral material. In some cases, the enzyme having silicase activity may degrade, digest, and/or disintegrate the silicate. As a result, metals, such as in the form of metal ions, metal atoms, or metal precipitates, may be released from the mineral material (e.g., into a solution). In some cases, the method may comprise collecting the metal or the solution containing the metal. In some cases, the method may comprise separating the metal from the solution. In some cases, the metal may be water soluble. Alternatively or in addition, the metal may precipitate in the solution. The solution may be an aqueous solution comprising water and/or a buffer described anywhere herein.

[0043] In some embodiments, the enzyme having silicase activity has a pKd of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a Kcat value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about 50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher.

[0044] In some cases, the specificity of the enzyme having silicase activity to the substrate may be higher than a wild-type version of the enzyme. For example, a wild-type enzyme may be engineered to improve its specificity for a substrate. In some cases, the enzyme provided herein may be engineered by directed evolution. In some cases, machine learning and artificial intelligence may be used for performing such enzyme engineering and directed evolution methods to design the enzymes of the present disclosure. The engineered enzyme may be synthesized or semi-synthesized.

In some embodiments, the enzyme (e.g., the engineered enzyme) has the sequence of any one of SEQ ID NOS: 19-402, or an amino acid sequence having at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity to any one of SEQ ID NOS: 19-402. In some embodiments, the enzyme (e.g., the engineered enzyme) has the sequence of any one of SEQ ID NOS: 403-464, or an amino acid sequence having at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity to any one of SEQ ID NOS: 403-464.

[0045] In some embodiments, the enzyme having silicase activity comprises a purification tag. The purification tag can comprise commonly used tags known in the art to aide in the purification of the enzyme having silicase activity from a host cell. The purification tag can comprise, for example, a GST tag, a His tag, a NEXT tag, a FLAG tag, or any other tags known in the art. In some cases, the purification tag is conjugated to the N-terminus of the enzyme having silicase activity. In some cases, the purification tag is conjugated to the C-terminus of the enzyme having silicase activity. In some cases, the purification tag is cleaved from the enzyme having silicase activity after purification. In some cases, the purification tag is not cleaved from the enzyme having silicase activity after purification. In some cases, the purification tag aides in enzyme stability. In some cases, the purification tag does not affect enzymatic efficacy. In some

cases, the purification tag does not affect the enzyme having silicase activity polymerization.

[0046] In some cases, the enzyme having silicase activity may have a catalytic activity that is superior to the wild-type version of the same enzyme. For example, the enzymes provided herein may have a higher catalytic rate. This may decrease the time required to extract a given amount of metal from the mineral material, compared to when using a wild-type enzyme. In some cases, the enzymes provided herein may have reduced energy requirements, as compared to a wild-type enzyme. In some cases, catalytic activity/rate/efficiency may be characterized by using one or more metrics.

[0047] In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher.

[0048] In some embodiments, the enzyme having silicase activity has a pKd of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a Kcat value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about 50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher.

[0049] The methods of the present disclosure, such as the enzymatic reactions provided herein, may be performed under a set of reaction conditions. In some cases, the reaction conditions may comprise a reaction temperature (e.g., a temperature under which the enzymatic reaction, or a portion thereof, is performed). In some cases, the reaction temperature is from about 20 to about 90 degrees Celsius (C). In some cases, the reaction temperature is from about 23 to about 90 degrees Celsius (C). In some cases, the reaction temperature is from about 23 to about 85 degrees Celsius (C). In some cases, the reaction temperature is from about 30 to about 90 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 30 to about 80 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 30 to about 70 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 30 to about 60 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 30 to about 50 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 45 to about 55 degrees Celsius (C). In some

cases, the reaction conditions comprise a temperature from about 45 to about 50 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 20 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 23 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 25 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 30 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 35 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 40 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 45 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 50 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 55 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 60 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 70 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 75 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 80 degrees Celsius (C). In some cases, the reaction conditions comprises a temperature about 85 degrees Celsius (C). In some cases, the methods of the present disclosure may be performed in near-ambient temperatures and/or pressures. In some cases, the temperature ranges of the methods of the present disclosure may be significantly lower than temperatures required in acid roasting. (e.g., 200 degrees Celsius (C) and above). This may reduce the energy requirements of the process performed using the methods of the present disclosure

[0050] In some cases, the enzymatic reaction may be performed at a pH from about 4 to about 11. In some cases, the enzymatic reaction may be performed at a pH from about 4 to about 10. In some cases, the enzymatic reaction may be performed at a pH from about 4 to about 9. In some cases, the enzymatic reaction may be performed at a pH from about 4 to about 8. In some cases, the enzymatic reaction may be performed at a pH from about 4 to about 7. In some cases, the enzymatic reaction may be performed at a pH from about 4 to about 6. In some cases, the enzymatic reaction may be performed at a pH from about 5 to about 11. In some cases, the enzymatic reaction may be performed at a pH from about 5 to about 10. In some cases, the enzymatic reaction may be performed at a pH from about 5 to about 9. In some cases, the enzymatic reaction may be performed at a pH from about 5 to about 8. In some cases, the enzymatic reaction may be performed at a pH from about 5 to about 7. In some cases, the enzymatic reaction may be performed at a pH from about 5 to about 6. In some cases, the enzymatic reaction may be performed at a pH from about 6 to about 11. In some cases, the enzymatic reaction may be performed at a pH from about 6 to about 10. In some cases, the enzymatic reaction may be performed at a pH from about 7 to about 11. In some cases, the enzymatic reaction may be performed at a pH from about 7 to about 10. In some cases, the enzymatic reaction may be performed at a pH from about 8 to about 11. In some cases, the enzymatic reaction may be performed at a pH from about 8 to about 10. In some cases, the enzymatic reaction may be performed at a pH from about 9 to about 11. In some cases, the enzymatic reaction may be performed at a pH from about 9 to about 10. In some cases, the enzymatic reaction may be performed at a pH of 4. In some cases, the enzymatic

reaction may be performed at a pH of 5. In some cases, the enzymatic reaction may be performed at a pH of 6. In some cases, the enzymatic reaction may be performed at a pH of 7. In some cases, the enzymatic reaction may be performed at a pH of 8. In some cases, the enzymatic reaction may be performed at a pH of 9. In some cases, the enzymatic reaction may be performed at a pH of 10. In some cases, the enzymatic reaction may be performed at a pH of 11. In some cases, the methods of the present disclosure may be performed in pH ranges that are substantially neutral, or in other words, not highly/strongly acidic or highly/strongly basic. In some cases, the method/reaction of the present disclosure may not comprise using a strong acid, such as is used in acid leaching. Instead, the enzymes presented throughout the disclosure may perform enzymatic degradation of the mineral material in neutral pH conditions.

[0051] In some cases, the methods provided herein comprise crushing or grinding the rocks or ores to achieve a particulate size. In some cases, the ground ores comprise a size of about 50 μm to 1 mm. In some cases, the ground ores comprise a size from about 50 μm to 750 μm . In some cases, the ground ores comprise a size from about 50 μm to 500 μm . In some cases, the ground ores comprise a size from about 50 μm to 250 μm . In some cases, the ground ores comprise a size from about 50 μm to 150 μm . In some cases, the ground ores comprise a size from about 50 μm to 100 μm . In some cases, the ground ores comprise a size of about 50 μm . In some cases, the ground ores comprise a size of about 100 μm . In some cases, the ground ores comprise a size of about 150 μm . In some cases, the ground ores comprise a size of about 250 μm . In some cases, the ground ores comprise a size of about 500 μm . In some cases, the ground ores comprise a size of about 750 μm . In some cases, the ground ores comprise a size of about 1 mm.

[0052] In some cases, the methods provided herein comprise creating a slurry of crushed rock and liquid. In some cases, the rock to liquid ratio is from about 1-40% (w/v). In some cases, the rock to liquid ratio is from about 1-35% (w/v). In some cases, the rock to liquid ratio is from about 1-30% (w/v). In some cases, the rock to liquid ratio is from about 1-25% (w/v). In some cases, the rock to liquid ratio is from about 1-20% (w/v). In some cases, the rock to liquid ratio is from about 1-15% (w/v). In some cases, the rock to liquid ratio is from about 1-10% (w/v). In some cases, the rock to liquid ratio is from about 1-5% (w/v). In some cases, the rock to liquid ratio is from about 10-40% (w/v). In some cases, the rock to liquid ratio is from about 10-35% (w/v). In some cases, the rock to liquid ratio is from about 10-30% (w/v). In some cases, the rock to liquid ratio is from about 10-25% (w/v). In some cases, the rock to liquid ratio is from about 15-35% (w/v). In some cases, the rock to liquid ratio is from about 15-30% (w/v). In some cases, the rock to liquid ratio is from about 20-35% (w/v). In some cases, the rock to liquid ratio is from about 20-30% (w/v). In some cases, the rock to liquid ratio is from about 25-35% (w/v). In some cases, the rock to liquid ratio is from about 25-30% (w/v). In some cases, the rock to liquid ratio is about 1% (w/v). In some cases, the rock to liquid ratio is about 5% (w/v). In some cases, the rock to liquid ratio is about 10% (w/v). In some cases, the rock to liquid ratio is about 15% (w/v). In some cases, the rock to liquid ratio is about 20% (w/v). In some cases, the rock to liquid ratio is about 25% (w/v). In some cases, the rock to liquid ratio is about 30%

(w/v). In some cases, the rock to liquid ratio is about 35% (w/v). In some cases, the rock to liquid ratio is about 40% (w/v).

[0053] In some cases, the methods provided herein comprise an enzymatic reaction that proceeds for a set period of time. In some cases, the method comprises the enzymatic reaction proceeding for about 1-72 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1-60 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1-48 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1-36 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1-24 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1-12 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1-6 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 12-72 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 12-60 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 12-48 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 12-36 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 12-24 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 24-72 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 24-60 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 24-48 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 24-36 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 36-72 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 36-60 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 36-48 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 48-72 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 48-60 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 1 hour. In some cases, the method comprises the enzymatic reaction proceeding for about 6 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 12 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 24 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 36 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 48 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 60 hours. In some cases, the method comprises the enzymatic reaction proceeding for about 72 hours.

[0054] In some cases, the methods provided herein comprise contacting the enzyme having silicase activity with a co-factor. The co-factor may help further increase the reaction rate when used in combination with the enzyme having silicase activity. In some cases, the co-factor is selected from the group consisting of: iron, zinc, copper, nickel, cobalt, and any combination thereof. Such co-factor may be used with any enzyme disclosed anywhere in the present disclosure. In some cases, the co-factor may be a non-natural co-factor, such as a co-factor that is typically not used by an enzyme as a co-factor in nature.

[0055] In some cases, the enzyme having silicase activity depolymerizes silicate mineral in the mineral material (e.g., ore/rock). In some cases, the enzyme having silicase activity cleaves one or more Si—O bonds in the mineral material to generate silicic acid (Si(OH)4). In some cases, the metal is lithium, aluminum, iron, nickel, cobalt, strontium, and/or a rare earth element. In some cases, the metal is lithium. In some cases, the metal is aluminum. In some cases, the metal is iron. In some cases, the metal is strontium. As a result of enzymatic degradation and/or disintegration of the mineral material, the metal may be released and extracted from the mineral, in some cases, in a solution, in some cases in the form of a metal ion or a metal atom. The solution may be an aqueous solution.

[0056] In some cases, the method comprises extracting the metal from the solution. In some cases, the method comprises purifying the metal from the solution, thereby generating a purified metal, a metal ion, a metal atom, a solid metal complex, a metal precipitate, or any combination thereof. In some cases, the purified metal has a purity of at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 99%, at least about 99.9%, at least about 99.99%, at least about 99.999%, at least about 99.9999%, or higher purity. In some cases, the purified metal is lithium, aluminum, iron, nickel, cobalt, strontium, a rare earth element, and/or uranium. In some cases, the purified metal is industry-grade, battery-grade, and/or pharmaceutical grade. In some cases, the purified metal is industry-grade lithium, battery-grade lithium, and/or pharmaceutical-grade lithium.

[0057] In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher.

[0058] In some aspects, the enzyme having silicase activity is recombinantly produced in a host cell or in a cell-free production system. In some cases, the host cell is a bacterial cell or yeast cell. In some cases, the bacterial cell is *Escherichia coli*. In some cases, the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*.

[0059] In some embodiments, the methods of the present disclosure comprise performing a reaction involving an enzyme and a mineral material, as described throughout the disclosure. The reaction may be performed inside any suitable container. In some cases, the reaction may be performed on a rock or ore. In some cases, the mineral material may be placed inside a container and added to a solution comprising the enzyme, water, a buffer, and/or potential other reagents for performing the reaction. In some cases, the reaction may

be performed in one or more of a container, a dish, a beaker, a device, a tank, a reactor, and/or any combination thereof. The containers (e.g., one or more reactors and/or tanks) may be connected to one another to perform one or more reactions according to the embodiments of the present disclosure. The containers may also be reaction units and/or process units each of which may serve a function as part of the method and/or in combination with the method. For example, one or more tanks, reactors, and/or processing units, may be connected to each other with any configuration, such as in series, in parallel, or any combination thereof to perform the method steps such as contact the enzyme with the mineral, extracting the metal, separating the metal from the solution, purifying the metal, processing the metal, and converting the metal into an industry-grade, battery-grade, or pharmaceutical-grade metal. In some cases, the method further comprises grinding the mineral material (e.g., rock/ore) prior to performing the reaction (e.g., the enzymatic degradation). In some cases, the method further comprises using a filtration/chelating system, a precipitation system, a recycle system, or any combination thereof.

[0060] In an aspect, provided herein is a non-naturally occurring enzyme having silicase activity, the enzyme comprising at least one amino acid variation relative to a wild-type enzyme, and having increased ability to release metals from a mineral material (e.g., rock/ore) as compared to the wild-type enzyme. In some cases, the enzyme having silicase activity is used in a reaction/process of the present disclosure for metal extraction, as described anywhere in the present disclosure. In some cases, a wild-type carbonic anhydrase, gamma carbonic anhydrase, or alpha carbonic anhydrase may be used as a starting point for the enzyme engineering and performing the modifications to design and synthesize the non-naturally occurring enzyme having silicase activity. The non-naturally occurring enzyme having silicase activity may in some cases be a modified, engineered, and semi-synthetic enzyme (e.g., the enzyme having silicase activity for performing the methods and reactions of the present disclosure). In some cases, a wild-type carbonic anhydrase, gamma carbonic anhydrase, or alpha carbonic anhydrase may be used as a starting point for the enzyme engineering and performing the modifications to design and synthesize the non-naturally occurring enzyme (e.g., the enzyme having silicase activity for performing the methods and reactions of the present disclosure). As such, the resulting modified enzyme may have some similarities, for example with respect to characteristics and sequence, to a wild-type Carbonic Anhydrase, gamma Carbonic Anhydrase, or alpha Carbonic Anhydrase, and some differences, for example with respect to characteristics and sequence, to a wild-type carbonic anhydrase, gamma carbonic anhydrase, or alpha carbonic anhydrase.

[0061] In some cases the wild-type enzyme is selected from the group consisting of: *Methanosarcina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, *Pelobacter carbinolicus* gamma carbonic anhydrase, *Syntrophus aciditrophicus* gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, Alkalihalobacillus *clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, Kofleriaceae bacterium SLC26A/SulP transporter domain-containing protein, Ther-

modesulfimonas *autotrophica* carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila* carbonate dehydratase, *Thermosyntrphpha lipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, Desulfovibrio thermobenzoicus transferase, *Archaeoglobus veneficus* carbonate dehydratase, *Suberites domuncula* carbonic anhydrase, and any combination thereof.

[0062] In some cases, the non-naturally occurring enzyme is derived from an organism selected from the group consisting of: *Methanoscincus thermophilus*, *Bacillus licheniformis* CG-B52, *Pelobacter carbinolicus*, *Syntrophus aciditrophicus*, *Methanoscincus barkeri*, *Methanoscincus mazei*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanoscincus acetivorans*, *Kofleriaceae* bacterium, *Thermodesulfimonas autotrophica*, *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosyntrphpha lipolytica*, *Desulfovibrio thermobenzoicus*, *Archaeoglobus veneficus*, *Suberites domuncula*, and any combination thereof.

[0063] In some cases, the non-naturally occurring enzyme comprises an amino acid sequence having at least about 10%, at least about 20%, at least about 30%, at least about 40%, having at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-402. In some cases, the non-naturally occurring enzyme comprises an amino acid sequence having at least about 10%, at least about 20%, at least about 30%, at least about 40%, having at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 403-464. In some cases, the wild-type enzyme is a carbonic anhydrase. In some cases, the carbonic anhydrase is a gamma carbonic anhydrase or alpha carbonic anhydrase.

[0064] In some cases, the methods of the present disclosure are performed on a mineral material. In some cases, the mineral material comprises or is a rock, an ore, a deposit, a clay, a natural mineral material, a man-made mineral material, or any combination thereof. The method may be according to the embodiments described anywhere herein. According to the embodiments described anywhere in the present disclosure, in some cases, an enzyme having silicase activity acts on a mineral material. The enzyme and the method of the present disclosure may degrade, digest, or disintegrate the mineral material and extract a metal therefrom. The mineral material such as a rock, ore, natural mineral materials, and/or man-made mineral materials may be abundant sources of valuable metals such as lithium, aluminum, iron,

nickel, cobalt, copper, strontium, rare earth elements, uranium, and other metals with vast industrial use and applications. The methods and enzymes of the present disclosure facilitate access to such sources. In some cases, the mineral material comprises a silicate. In some cases, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, a tectosilicate or any combination thereof. In some cases, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some cases, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some cases, amorphous silicate is selected from the group consisting of obsidian, coal fly ash, pumice, glass, and any combination thereof. In some cases, the tectosilicate comprises quartz, sand, or glass.

[0065] In some cases, the non-naturally occurring enzyme has an increased ability to depolymerize silicate mineral in the mineral material, rock, ore, or other kind of mineral material as compared to the wild-type enzyme, increased selectivity or specificity toward a mineral structure in the mineral material, or both. In some cases, the non-naturally occurring enzyme has increased ability to cleave one or more Si—O bonds in the mineral material to generate silicic acid (Si(OH)₄) as compared to the wild-type enzyme. In some cases, the metal comprises lithium, aluminum, iron, nickel, cobalt, or a rare earth element. In some cases, the metal comprises lithium. In some cases, the metal comprises aluminum. In some cases, the metal comprises iron. In some cases, the metal comprises strontium. In some cases, the non-naturally occurring enzyme is recombinantly produced in a host cell or in a cell-free production system. In some cases, the host cell is a bacterial cell or yeast cell. In some cases, the bacterial cell is *Escherichia coli*. In some cases, the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*.

[0066] In an aspect, provided herein is a reaction mixture comprising a mineral material and a non-naturally occurring enzyme having silicase activity, wherein the non-naturally occurring enzyme comprises at least one amino acid variation relative to a wild-type enzyme, and has increased ability to release metal from the mineral material as compared to the wild-type enzyme. The mineral material may be according to any embodiment described anywhere herein. It may comprise silicates and/or Si—O bonds. In some cases, the mineral material comprises silicates. In some cases, the mineral material may comprise an inosilicate, a phyllosilicate, an amorphous silicate, or any combination thereof. In some cases, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some cases, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some cases, the amorphous silicate is selected from the group consisting of obsidian, coal fly ash, pumice, glass, and any combination thereof. The mineral material may be a source of a metal.

[0067] The metal may be extracted from the mineral material (in some cases a rock or ore) by using the methods and enzymes described anywhere in the present disclosure. The enzyme having silicase activity may be any enzyme disclosed anywhere in the present disclosure. In some cases,

the reaction mixture has a pH from about 4 to about 11. In some cases, the reaction mixture has a pH from about 4 to about 10. In some cases, the reaction mixture has a pH from about 4 to about 9. In some cases, the reaction mixture has a pH from about 4 to about 8. In some cases, the reaction mixture has a pH from about 4 to about 7. In some cases, the reaction mixture has a pH from about 4 to about 6. In some cases, the reaction mixture has a pH from about 5 to about 11. In some cases, the reaction mixture has a pH from about 5 to about 10. In some cases, the reaction mixture has a pH from about 5 to about 9. In some cases, the reaction mixture has a pH from about 5 to about 8. In some cases, the reaction mixture has a pH from about 5 to about 7. In some cases, the reaction mixture has a pH from about 5 to about 6. In some cases, the reaction mixture has a pH from about 6 to about 11. In some cases, the reaction mixture has a pH from about 6 to about 10. In some cases, the reaction mixture has a pH from about 7 to about 11. In some cases, the reaction mixture has a pH from about 7 to about 10. In some cases, the reaction mixture has a pH from about 8 to about 11. In some cases, the reaction mixture has a pH from about 8 to about 10. In some cases, the reaction mixture has a pH from about 9 to about 11. In some cases, the reaction mixture has a pH from about 9 to about 10. In some cases, the reaction mixture has a pH of 4. In some cases, the reaction mixture has a pH of 5. In some cases, the reaction mixture has a pH of 6. In some cases, the reaction mixture has a pH of 7. In some cases, the reaction mixture has a pH of 8. In some cases, the reaction mixture has a pH of 9. In some cases, the reaction mixture has a pH of 10. In some cases, the reaction mixture has a pH of 11. In some cases, the reaction mixture has a temperature from about 20 to about 90 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 23 to about 90 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 23 to about 85 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 30 to about 90, from about 30 to about 80, from about 30 to about 70, from about 30 to about 60, or from about 30 to about 50 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 45 to about 55 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 45 to about 50 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 20 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 23 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 25 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 30 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 35 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 40 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 45 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 50 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 55 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 60 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 70 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 75 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 80 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 85 degrees Celsius (C). In some cases, the reaction mixture further comprises a co-factor of the non-naturally occurring enzyme.

In some cases, the co-factor is selected from the group consisting of iron, zinc, copper, nickel, and cobalt. In some cases, the co-factor is copper. In some cases, the co-factor is iron. In some cases, the reaction mixture further comprises a buffered saline solution. In some cases, the buffered solution comprises saline, glycine, iron ions, or any combination thereof. In some cases the buffered solution comprises TRIS, PBS, citrate, monosodium glutamate, or any combination thereof. In some cases, the reaction mixture further comprises an activator co-factor of the non-naturally occurring enzyme. In some cases, the activator co-factor is glycine. The reaction mixture may be used to perform any method described anywhere herein using any enzyme, any co-factor, and/or any reaction condition disclosed anywhere herein.

[0068] In some cases, the reaction mixture provided herein comprise crushing or grinding the rocks or ores to achieve a particulate size. In some cases, the ground ores comprise a size of about 50 µm to 1 mm. In some cases, the ground ores comprise a size from about 50 µm to 750 µm. In some cases, the ground ores comprise a size from about 50 µm to 500 µm. In some cases, the ground ores comprise a size from about 50 µm to 250 µm. In some cases, the ground ores comprise a size from about 50 µm to 150 µm. In some cases, the ground ores comprise a size from about 50 µm to 100 µm. In some cases, the ground ores comprise a size of about 50 µm. In some cases, the ground ores comprise a size of about 100 µm. In some cases, the ground ores comprise a size of about 150 µm. In some cases, the ground ores comprise a size of about 250 µm. In some cases, the ground ores comprise a size of about 500 µm. In some cases, the ground ores comprise a size of about 750 µm. In some cases, the ground ores comprise a size of about 1 mm.

[0069] In some cases, the reaction mixture provided herein comprise creating a slurry of crushed rock and liquid. In some cases, the rock to liquid ratio is from about 1-40% (w/v). In some cases, the rock to liquid ratio is from about 1-35% (w/v). In some cases, the rock to liquid ratio is from about 1-30% (w/v). In some cases, the rock to liquid ratio is from about 1-25% (w/v). In some cases, the rock to liquid ratio is from about 1-20% (w/v). In some cases, the rock to liquid ratio is from about 1-15% (w/v). In some cases, the rock to liquid ratio is from about 1-10% (w/v). In some cases, the rock to liquid ratio is from about 1-5% (w/v). In some cases, the rock to liquid ratio is from about 10-40% (w/v). In some cases, the rock to liquid ratio is from about 10-35% (w/v). In some cases, the rock to liquid ratio is from about 10-30% (w/v). In some cases, the rock to liquid ratio is from about 10-25% (w/v). In some cases, the rock to liquid ratio is from about 15-35% (w/v). In some cases, the rock to liquid ratio is from about 15-30% (w/v). In some cases, the rock to liquid ratio is from about 20-35% (w/v). In some cases, the rock to liquid ratio is from about 20-30% (w/v). In some cases, the rock to liquid ratio is from about 25-35% (w/v). In some cases, the rock to liquid ratio is from about 25-30% (w/v). In some cases, the rock to liquid ratio is about 1% (w/v). In some cases, the rock to liquid ratio is about 5% (w/v). In some cases, the rock to liquid ratio is about 10% (w/v). In some cases, the rock to liquid ratio is about 15% (w/v). In some cases, the rock to liquid ratio is about 20% (w/v). In some cases, the rock to liquid ratio is about 25% (w/v). In some cases, the rock to liquid ratio is

about 30% (w/v). In some cases, the rock to liquid ratio is about 35% (w/v). In some cases, the rock to liquid ratio is about 40% (w/v).

[0070] In some cases, the reaction mixture provided herein comprise an enzymatic reaction that proceeds for a set period of time. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-24 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-12 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-6 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-24 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 48-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 48-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1 hour. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 6 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 72 hours.

[0071] The reaction mixture comprises a non-naturally occurring enzyme described anywhere herein. As described throughout the present disclosure, in some cases, the non-naturally occurring enzyme may be an engineered and/or semi-synthetic enzyme having a modification compared to a wild-type enzyme. In some cases, the wild-type enzyme is selected from the group consisting of: *Methanosarcina ther-*

mophila gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, *Pelobacter carbinolicus* gamma carbonic anhydrase, *Syntrophus aciditrophicus* gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, *Kofleriaceae bacterium* SLC26A/SulP transporter domain-containing protein, *Thermodesulfotimonas autotrophica* carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila* carbonate dehydratase, *Thermosyntrapha lipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, *Desulfovibrio thermobenzoicus* transferase, *Archaeoglobus veneficus* carbonate dehydratase, *Suberites domuncula* carbonic anhydrase, and any combination thereof.

[0072] In some cases, the non-naturally occurring enzyme comprises an amino acid sequence having at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80% at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-402. In some cases, the non-naturally occurring enzyme comprises an amino acid sequence having at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80% at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 403-464. In some cases, the wild-type enzyme is a carbonic anhydrase. In some cases, the carbonic anhydrase is a gamma carbonic anhydrase or alpha carbonic anhydrase.

[0073] In some cases, the non-naturally occurring enzyme has increased ability to depolymerize silicate mineral in the mineral material as compared to the wild-type enzyme. In some cases, the non-naturally occurring enzyme has increased ability to cleave one or more Si—O bonds in the mineral material (e.g., rock/ore) to generate silicic acid (Si(OH)₄) as compared to the wild-type enzyme. In some cases, the metal comprises lithium. In some cases, the metal comprises aluminum. In some cases, the metal comprises iron. In some cases, the metal comprises strontium. In some cases, the metal may comprise lithium, aluminum, nickel, iron, cobalt, copper, a rare earth element, uranium, strontium, another metal, or any combination thereof. In some cases, the non-naturally occurring enzyme is recombinantly produced in a host cell. In some cases, the host cell is a bacterial cell or yeast cell. In some cases, the bacterial cell is *Escherichia coli*. In some cases, the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*.

[0074] In an aspect, provided herein is a polynucleotide comprising a nucleotide sequence encoding the non-naturally occurring enzyme of any one of the preceding embodiments. In an aspect, provided herein is a vector comprising the polynucleotide comprising the nucleotide sequence encoding the non-naturally occurring enzyme. The non-naturally occurring enzyme may be according to any embodiment mentioned anywhere in the present disclosure. The polynucleotide and vector may be designed and engineered. The polynucleotide and the vector may get synthesized. The polynucleotide and/or vector may be used to generate and/or produce the non-naturally occurring enzyme of the present disclosure.

[0075] In an aspect, provided herein is a method of increasing silicase activity of an enzyme, the method comprising contacting or combining the enzyme with a non-natural co-factor. In some cases, the enzyme and the co-factor may be added to a solution. In some cases, the co-factor may be brought in proximity of the enzyme. In some cases, the enzyme and the co-factor may be part of the same system, the same reaction mixture, or the same kit for performing the methods of the present disclosure. In some cases, the non-natural co-factor increases silicase activity of the enzyme as compared to the enzyme in the presence of a natural co-factor. In some cases, the non-natural co-factor may be copper. In some cases, natural co-factor is zinc. In some cases, natural co-factor is iron. In some cases, the method is performed in the absence of the natural co-factor. In some cases, the non-natural co-factor does not act as a co-factor for the enzyme having silicase activity in nature. In some cases, the method further comprises contacting the enzyme and the non-natural co-factor with the mineral material under reaction conditions such that a metal contained within the mineral material is solubilized and released from the mineral material such as rock/ore.

[0076] As an example, a method of the present disclosure comprises using an enzyme having silicase activity (wild-type or engineered/modified/semi-synthetic) to degrade a mineral material such as a rock/ore comprising metal-bearing silicates so as to extract the metal from the mineral material. Zinc may act as a natural co-factor for the enzyme comprising silicase activity in nature. For example, a natural silicate rock may get degraded by a wild-type silicase enzyme such as a gamma carbonic anhydrase in nature, zinc may act as a co-factor for the wild-type enzyme, catalyze the digestion/degradation reaction, and speed it up and/or increase its efficiency. Alternatively, in some cases, the method of the present disclosure may comprise bringing an enzyme having silicase activity to a mineral material such as a rock/ore comprising metal-bearing silicates, and further provide a co-factor other than zinc (the natural co-factor) to increase the catalytic effects of the enzyme having silicase activity on the mineral material. The co-factor other than zinc may be a non-natural co-factor. The non-natural co-factor is in some cases, copper, iron, nickel, cobalt, or glycine. In some cases, the non-natural co-factor may work better than the natural co-factor. For example, copper, iron, nickel, cobalt, or glycine may work better than zinc in increasing the catalytic efficiency of the enzyme and increasing the reaction rate. The enzyme used in the method of the present disclosure may comprise using a wild-type enzyme or a modified enzyme described anywhere in the present disclosure.

[0077] In some cases, the amount of metal extracted, solubilized/precipitated in the extraction solution, and/or released from the mineral material (e.g., ore/rock) is greater than an amount of metal extracted from the mineral material when the enzyme is contacted with the natural co-factor (e.g., in unit time when other conditions are equal). In some cases, the amount of metal extracted from the mineral material is greater than an amount of metal extracted from the mineral material when the enzyme is contacted with the natural co-factor. In some cases, the mineral material comprises silicate. In some cases, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, a tectosilicate, or any combination thereof. In some cases, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some cases, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some cases, the amorphous silicate is selected from the group consisting of obsidian, coal fly ash, pumice, glass, and any combination thereof. In some cases, the enzyme having silicase activity is a carbonic anhydrase. In some cases, the carbonic anhydrase is a gamma carbonic anhydrase or an alpha carbonic anhydrase. In some cases, the enzyme is a wild-type enzyme. In some cases, the enzyme is a modified or engineered enzyme.

[0078] In some cases, the enzyme having silicase activity is derived from an organism selected from the group consisting of: *Methanosarcina thermophila*, *Bacillus licheniformis* CG-B52, *Pelobacter carbinolicus*, *Syntrophus aciditrophicus*, *Methanosarcina barkeri*, *Methanosarcina mazei*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanosarcina acetivorans*, *Kofleriaceae* bacterium, *Thermodesulfitimonas autotrophica*, *Fischerella thermalis/Mastigocladus laminosus* JSC-11 carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosyntropha lipolytica*, *Desulfovulum thermobenzoicus*, *Archaeoglobus veneficus*, *Suberites domuncula*, and any combination thereof.

[0079] In some cases, the enzyme having silicase activity comprises an amino acid sequence having at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, having at least about 50%, at least about 60%, at least about 70%, tale at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-402. In some cases, the enzyme having silicase activity comprises an amino acid sequence having at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, having at least about 50%, at least about 60%, at least about 70%, tale at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 403-464. In some cases, the enzyme

having silicase activity is an engineered enzyme. In some cases, the enzyme having silicase activity is an enzyme having at least one amino acid variation as compared to a wild-type enzyme.

[0080] In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher. In some embodiments, the enzyme having silicase activity has a pKd of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a Keat value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about 50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher.

[0081] In some cases, the reaction conditions comprise a temperature from about 20 to about 90 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 23 to about 90 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 23 to about 85 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 30 to about 90, from about 30 to about 80, from about 30 to about 70, from about 30 to about 60, or from about 30 to about 50 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature from about 45 to about 55 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 45 to about 50 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 20 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 23 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 25 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 30 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 35 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 40 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 45 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 50 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 55 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 60 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 70

degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 75 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 80 degrees Celsius (C). In some cases, the reaction conditions comprise a temperature about 85 degrees Celsius (C). In some cases, the reaction conditions comprise a pH from about 4 to about 11. In some cases, the reaction conditions comprise a pH from about 4 to about 10. In some cases, the reaction conditions comprise a pH from about 4 to about 9. In some cases, the reaction conditions comprise a pH from about 4 to about 8. In some cases, the reaction conditions comprise a pH from about 4 to about 7. In some cases, the reaction conditions comprise a pH from about 4 to about 6. In some cases, the reaction conditions comprise a pH from about 5 to about 11. In some cases, the reaction conditions comprise a pH from about 5 to about 10. In some cases, the reaction conditions comprise a pH from about 5 to about 9. In some cases, the reaction conditions comprise a pH from about 5 to about 8. In some cases, the reaction conditions comprise a pH from about 5 to about 7. In some cases, the reaction conditions comprise a pH from about 5 to about 6. In some cases, the reaction conditions comprise a pH from about 5 to about 5. In some cases, the reaction conditions comprise a pH from about 7 to about 11. In some cases, the reaction conditions comprise a pH from about 7 to about 10. In some cases, the reaction conditions comprise a pH from about 8 to about 11. In some cases, the reaction conditions comprise a pH from about 8 to about 10. In some cases, the reaction conditions comprise a pH from about 9 to about 11. In some cases, the reaction conditions comprise a pH from about 9 to about 10. In some cases, the reaction conditions comprise a pH of 4. In some cases, the reaction conditions comprise a pH of 5. In some cases, the reaction conditions comprise a pH of 6. In some cases, the reaction conditions comprise a pH of 7. In some cases, the reaction conditions comprise a pH of 8. In some cases, the reaction conditions comprise a pH of 9. In some cases, the reaction conditions comprise a pH of 10. In some cases, the reaction conditions comprise a pH of 11. In some cases, the reaction conditions comprise contacting the enzyme having silicase activity with a co-factor. In some cases, the co-factor is selected from the group consisting of: Iron, zinc, copper, nickel, and cobalt.

[0082] In some cases, the reaction conditions provided herein comprise crushing or grinding the rocks or ores to achieve a particulate size. In some cases, the ground ores comprise a size of about 50 µm to 1 mm. In some cases, the ground ores comprise a size from about 50 µm to 750 µm. In some cases, the ground ores comprise a size from about 50 µm to 500 µm. In some cases, the ground ores comprise a size from about 50 µm to 250 µm. In some cases, the ground ores comprise a size from about 50 µm to 150 µm. In some cases, the ground ores comprise a size from about 50 µm to 100 µm. In some cases, the ground ores comprise a size of about 50 µm. In some cases, the ground ores comprise a size of about 100 µm. In some cases, the ground ores comprise a size of about 150 µm. In some cases, the ground ores comprise a size of about 250 µm. In some cases, the ground ores comprise a size of about 500 µm. In some cases, the ground ores comprise a size of about 750 µm. In some cases, the ground ores comprise a size of about 1 mm.

[0083] In some cases, the reaction conditions provided herein comprise creating a slurry of crushed rock and liquid.

In some cases, the rock to liquid ratio is from about 1-40% (w/v). In some cases, the rock to liquid ratio is from about 1-35% (w/v). In some cases, the rock to liquid ratio is from about 1-30% (w/v). In some cases, the rock to liquid ratio is from about 1-25% (w/v). In some cases, the rock to liquid ratio is from about 1-20% (w/v). In some cases, the rock to liquid ratio is from about 1-15% (w/v). In some cases, the rock to liquid ratio is from about 1-10% (w/v). In some cases, the rock to liquid ratio is from about 1-5% (w/v). In some cases, the rock to liquid ratio is from about 10-40% (w/v). In some cases, the rock to liquid ratio is from about 10-35% (w/v). In some cases, the rock to liquid ratio is from about 10-30% (w/v). In some cases, the rock to liquid ratio is from about 10-25% (w/v). In some cases, the rock to liquid ratio is from about 15-35% (w/v). In some cases, the rock to liquid ratio is from about 15-30% (w/v). In some cases, the rock to liquid ratio is from about 20-35% (w/v). In some cases, the rock to liquid ratio is from about 20-30% (w/v). In some cases, the rock to liquid ratio is from about 25-35% (w/v). In some cases, the rock to liquid ratio is from about 25-30% (w/v). In some cases, the rock to liquid ratio is about 1% (w/v). In some cases, the rock to liquid ratio is about 5% (w/v). In some cases, the rock to liquid ratio is about 10% (w/v). In some cases, the rock to liquid ratio is about 15% (w/v). In some cases, the rock to liquid ratio is about 20% (w/v). In some cases, the rock to liquid ratio is about 25% (w/v). In some cases, the rock to liquid ratio is about 30% (w/v). In some cases, the rock to liquid ratio is about 35% (w/v). In some cases, the rock to liquid ratio is about 40% (w/v).

[0084] In some cases, the reaction conditions provided herein comprise an enzymatic reaction that proceeds for a set period of time. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-72 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-60 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-48 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-36 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-24 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-12 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1-6 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 12-72 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 12-60 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 12-48 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 12-36 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 12-24 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 24-72 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 24-60 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 24-48 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 24-36 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 36-72 hours. In some cases, the reaction conditions comprise the enzymatic

reaction proceeding for about 36-60 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 36-48 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 48-72 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 48-60 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 1 hour. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 6 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 12 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 24 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 36 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 48 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 60 hours. In some cases, the reaction conditions comprise the enzymatic reaction proceeding for about 72 hours.

[0085] In some cases, the enzyme having silicase activity depolymerizes silicate mineral in the mineral material (e.g., ore/rock). In some cases, the enzyme having silicase activity cleaves one or more Si—O bonds in the mineral material to generate silicic acid ($\text{Si}(\text{OH})_4$). In some cases, the metal (e.g., metal ion) extracted from the mineral material is lithium, aluminum, iron, nickel, cobalt, uranium, strontium, a rare earth element, or any combination thereof. In some cases, the metal is lithium. In some cases, the metal ion is aluminum. In some cases, the metal ion is iron. In some cases, the metal ion is strontium.

[0086] In some cases, the metal is released into a solution. In some cases, the metal is extracted and released in form of metal ion. In some cases, the metal is extracted and released in form of a metal atom. In some cases, the metal is solubilized in a solution comprising water and/or buffer. In some cases the buffer comprises TRIS, PBS, citrate, monosodium glutamate, or any combination thereof. In some cases, the metal precipitates in the solution. In some cases, the metal is released and/or extracted in form of a metal complex. In some cases, the method further comprises extracting, and/or separating the metal from the solution. Any proper separation technique may be used. In some cases, an electromagnetic force may be used to separate metal ions from the solution. In some cases, a solid-liquid separation technique may be used to separate a metal precipitate from the solution. Any combination of separation and processing methods may be used. The method may comprise collecting the metal from the mineral material (e.g., source rock/ore) and from the system or solution used to perform the extraction according to the embodiments of the present disclosure and provide the metal for use in its intended application. In some cases, the metal may be processed as an industry-grade metal, battery-grade metal, or pharmaceutical-grade metal. An example of this may comprise industry-grade metal, battery-grade metal, or pharmaceutical-grade lithium.

[0087] In some cases, the method further comprises comprising purifying the metal from the solution, thereby generating a purified metal, a metal ion, a metal atom, a solid metal complex, a metal precipitate, or any combination thereof. In some cases, the purified metal ion a purity of at least about 50%, at least about 60%, at least about 70%, at

least about 80%, at least about 90%, at least about 95%, at least about 99%, at least about 99.9%, at least about 99.99%, at least about 99.999%, at least about 99.9999% or greater.

[0088] In some cases, the method is performed in situ or ex-situ. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher.

[0089] In some cases, the enzyme having silicase activity is recombinantly produced in a host cell or in a cell-free production system. In some cases, the host cell is a bacterial cell or a yeast cell. In some cases, the bacterial cell is *Escherichia coli* or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*.

[0090] In an aspect, provided herein is a reaction mixture comprising an enzyme having silicase activity, and a non-natural co-factor. In some cases, the non-natural co-factor is bound to the enzyme having silicase activity. In some cases, the non-natural co-factor increases a function of the enzyme having silicase activity as compared to a reaction mixture comprising the enzyme having silicase activity and a natural co-factor. In some cases, the non-natural co-factor is copper, iron, nickel, cobalt, or glycine. In some cases, the natural co-factor is zinc. In some cases, the natural co-factor is iron. In some cases, the reaction mixture does not contain the natural co-factor. In some cases, the non-natural co-factor does not act as a co-factor for the enzyme having silicase activity in nature. In some cases, the reaction mixture further comprises the mineral material comprising silicate. In some cases, the reaction mixture has reaction conditions such that a metal contained within the mineral material is extracted, released, or solubilized, or precipitated into a solution from the mineral material. For example, a solution may be provided in proximity of a mineral material comprising a metal-bearing silicate. An enzyme having silicase activity and a non-natural co-factor according to the embodiments disclosed anywhere herein may be present in the solution. The enzyme may facilitate breaking Si—O bonds in the mineral material, thereby digesting and/or degrading the mineral material (e.g., rock/ore) and releasing the metal encased in the mineral material in form of metal ion, metal atom, metal solubilized in solution, metal precipitated in solution, or any combination thereof. The non-natural co-factor combined with or bound to the enzyme may further enhance the catalytic efficiency of the enzyme in releasing the metal from the mineral material in any of the mentioned forms.

[0091] In some cases, the enzyme having silicase activity has increased ability to release metal in any form mentioned

anywhere herein, from mineral materials (e.g., ore/rock) in the presence of the non-natural co-factor as compared to the enzyme having silicase activity in the presence of the natural co-factor. In some cases, the mineral material may comprise silicates. In some cases, the mineral material may comprise a metal bearing silicate. In some cases, the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, or any combination thereof. In some cases, the inosilicate is selected from the group consisting of: spodumene, wollastonite, balangeroite, eveslogite, holmquistite, jadeite, shattuckite, augite, tremolite, and any combination thereof. In some cases, the phyllosilicate is selected from the group consisting of: lepidolite, hectorite, kaolinite, vermiculite, muscovite, montmorillonite, and any combination thereof. In some cases, the amorphous silicate is selected from the group consisting of obsidian, coal fly ash, pumice, glass, and any combination thereof.

[0092] In some cases, the enzyme having silicase activity has a sequence identity of at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50% or more identity with a carbonic anhydrase. In some cases, the enzyme having silicase activity has a sequence identity of at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50% or more identity with an alpha carbonic anhydrase or a gamma carbonic anhydrase. In some cases, the enzyme having silicase activity is derived from an organism selected from the group consisting of: *Methanoscincina thermophila*, *Bacillus licheniformis* CG-B52, *Pelobacter carbinolicus*, *Syntrophus aciditrophicus*, *Methanoscincina barkeri*, *Methanoscincina mazae*, *Bacillus halodurans*, *Alkalihalobacillus clausii* (strain KSM-K16) (*Bacillus clausii*), *Methanoscincina acetivorans*, *Kofleriacaceae* bacterium SLC26A/SuLP, *Thermodesulfotimonas autotrophica*, *Fischerella thermalis/Mastigocladus laminosus*, *Thermosynechococcus vestitus* BP-1/*Thermosynechococcus elongatus* BP-1 carboxysome assembly protein CcmM, *Methanothrix thermoacetophila*, *Thermosyntrapha lipolytica*, isoleucine patch superfamily, Desulfofundulus thermobenzoicus, *Archaeoglobus veneficus*, *Suberites domuncula*, and any combination thereof.

[0093] In some cases, the non-naturally occurring enzyme comprises an amino acid sequence having at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-402. In some cases, the non-naturally occurring enzyme comprises an amino acid sequence having at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, at least about 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 403-464. In some cases, the enzyme having silicase activity is an engineered enzyme. In some cases, the enzyme

having silicase activity is an enzyme having at least one amino acid variation as compared to a wild-type enzyme.

[0094] In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 98% at least about 99%, at least about 99.5% or higher. In some embodiments, the enzyme having silicase activity has a catalytic efficiency of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher. In some embodiments, the method has a maximum metal extraction rate of at least about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.5, 6, 6.5, 7, 8, 9, 10 times or higher.

[0095] In some embodiments, the enzyme having silicase activity has a pKd of at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, or higher. In some embodiments, the enzyme having silicase activity has a Kcat value of at least about 2 mol per second (mol/s), at least about 10 mol/s, at least about 50 mol/s, at least about 100 mol/s, at least about 200 mol/s, at least about 300 mol/s, at least about 400 mol/s, at least about 500 mol/s, at least about 600 mol/s, at least about 700 mol/s, at least about 800 mol/s, at least about 900 mol/s, at least about 1000 mol/s, or higher.

[0096] In some cases, the reaction mixture has a pH from about 4 to about 11. In some cases, the reaction mixture has a pH from about 4 to about 10. In some cases, the reaction mixture has a pH from about 4 to about 9. In some cases, the reaction mixture has a pH from about 4 to about 8. In some cases, the reaction mixture has a pH from about 4 to about 7. In some cases, the reaction mixture has a pH from about 4 to about 6. In some cases, the reaction mixture has a pH from about 5 to about 11. In some cases, the reaction mixture has a pH from about 5 to about 10. In some cases, the reaction mixture has a pH from about 5 to about 9. In some cases, the reaction mixture has a pH from about 5 to about 8. In some cases, the reaction mixture has a pH from about 5 to about 7. In some cases, the reaction mixture has a pH from about 5 to about 6. In some cases, the reaction mixture has a pH from about 6 to about 11. In some cases, the reaction mixture has a pH from about 6 to about 10. In some cases, the reaction mixture has a pH from about 7 to about 11. In some cases, the reaction mixture has a pH from about 7 to about 10. In some cases, the reaction mixture has a pH from about 8 to about 11. In some cases, the reaction mixture has a pH from about 8 to about 10. In some cases, the reaction mixture has a pH from about 9 to about 11. In some cases, the reaction mixture has a pH from about 9 to about 10. In some cases, the reaction mixture has a pH of 4. In some cases, the reaction mixture has a pH of 5. In some cases, the reaction mixture has a pH of 6. In some cases, the reaction mixture has a pH of 7. In some cases, the reaction mixture has a pH of 8. In some cases, the reaction mixture has a pH of 9. In some cases, the reaction mixture has a pH of 10. In some cases, the reaction mixture has a pH of 11. In some cases, the reaction mixture has a temperature from

about 20 to about 90 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 23 to about 90 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 23 to about 85 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 30 to about 90, from about 30 to about 80, from about 30 to about 70, from about 30 to about 60, or from about 30 to about 50 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 45 to about 55 degrees Celsius (C). In some cases, the reaction mixture has a temperature from about 45 to about 50 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 20 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 23 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 25 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 30 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 35 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 40 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 45 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 50 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 55 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 60 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 70 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 75 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 80 degrees Celsius (C). In some cases, the reaction mixture has a temperature about 85 degrees Celsius (C). In some cases, the buffered solution comprises saline, glycine, iron ions, or any combination thereof. In some cases the buffered solution comprises TRIS, PBS, citrate, monosodium glutamate, or any combination thereof. In some cases, the reaction mixture further comprises an activator co-factor of the non-naturally occurring enzyme. In some cases, the activator co-factor comprises glycine, iron ion, or both. In some cases, the metal is lithium, aluminum, iron, nickel, cobalt, strontium, or a rare earth element. In some cases, the metal is lithium. In some cases, the metal is aluminum. In some cases, the metal is iron. In some cases, the metal is strontium. In some cases, the enzyme having silicase activity is recombinantly produced in a host cell or in a cell-free production system. In some cases, the host cell is a bacterial cell or yeast cell. In some cases, the bacterial cell is *Escherichia coli*, or the yeast cell is *Pichia pastoris* or *Saccharomyces cerevisiae*.

[0097] In some cases, the reaction mixture provided herein comprise crushing or grinding the rocks or ores to achieve a particulate size. In some cases, the ground ores comprise a size of about 50 µm to 1 mm. In some cases, the ground ores comprise a size from about 50 µm to 750 µm. In some cases, the ground ores comprise a size from about 50 µm to 500 µm. In some cases, the ground ores comprise a size from about 50 µm to 250 µm. In some cases, the ground ores comprise a size from about 50 µm to 150 µm. In some cases, the ground ores comprise a size from about 50 µm to 100 µm. In some cases, the ground ores comprise a size of about 50 µm. In some cases, the ground ores comprise a size of about 100 µm. In some cases, the ground ores comprise a size of about 150 µm. In some cases, the ground ores comprise a size of about 250 µm. In some cases, the ground ores comprise a size of about 500 µm. In some cases, the

ground ores comprise a size of about 750 μm . In some cases, the ground ores comprise a size of about 1 mm.

[0098] In some cases, the reaction mixture provided herein comprise creating a slurry of crushed rock and liquid. In some cases, the rock to liquid ratio is from about 1-40% (w/v). In some cases, the rock to liquid ratio is from about 1-35% (w/v). In some cases, the rock to liquid ratio is from about 1-30% (w/v). In some cases, the rock to liquid ratio is from about 1-25% (w/v). In some cases, the rock to liquid ratio is from about 1-20% (w/v). In some cases, the rock to liquid ratio is from about 1-15% (w/v). In some cases, the rock to liquid ratio is from about 1-10% (w/v). In some cases, the rock to liquid ratio is from about 1-5% (w/v). In some cases, the rock to liquid ratio is from about 10-40% (w/v). In some cases, the rock to liquid ratio is from about 10-35% (w/v). In some cases, the rock to liquid ratio is from about 10-30% (w/v). In some cases, the rock to liquid ratio is from about 10-25% (w/v). In some cases, the rock to liquid ratio is from about 15-35% (w/v). In some cases, the rock to liquid ratio is from about 15-30% (w/v). In some cases, the rock to liquid ratio is from about 20-35% (w/v). In some cases, the rock to liquid ratio is from about 20-30% (w/v). In some cases, the rock to liquid ratio is from about 25-35% (w/v). In some cases, the rock to liquid ratio is from about 25-30% (w/v). In some cases, the rock to liquid ratio is about 1% (w/v). In some cases, the rock to liquid ratio is about 5% (w/v). In some cases, the rock to liquid ratio is about 10% (w/v). In some cases, the rock to liquid ratio is about 15% (w/v). In some cases, the rock to liquid ratio is about 20% (w/v). In some cases, the rock to liquid ratio is about 25% (w/v). In some cases, the rock to liquid ratio is about 30% (w/v). In some cases, the rock to liquid ratio is about 35% (w/v). In some cases, the rock to liquid ratio is about 40% (w/v).

[0099] In some cases, the reaction mixture provided herein comprise an enzymatic reaction that proceeds for a set period of time. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-24 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-12 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1-6 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12-24 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24-48 hours. In some cases, the reaction mixture comprises

the enzymatic reaction proceeding for about 24-36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36-48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 48-72 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 48-60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 1 hour. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 6 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 12 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 24 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 36 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 48 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 60 hours. In some cases, the reaction mixture comprises the enzymatic reaction proceeding for about 72 hours.

[0100] In some cases, provided herein are engineered enzymes. In some cases, the method of enzyme engineering comprises performing directed molecular evolution on an enzyme sequence and generating an evolved enzyme sequence, wherein the evolved enzyme sequence has a higher specificity to a substrate in a mineral material (e.g., a silicate rock), a higher catalytic rate for acting on the mineral material, or both, compared to the first enzyme sequence. The first enzyme sequence may be a wild-type enzyme. In some cases, the wild-type enzyme is a carbonic anhydrase, a gamma carbonic anhydrase, or an alpha carbonic anhydrase.

[0101] The evolved enzyme, the wild-type enzyme, or both may cleave Si—O bonds in the substrate and extract a metal from the mineral material, in some cases a silicate rock. In some examples, directed molecular evolution is performed using a Machine Learning (ML) or Artificial Intelligence (AI) Algorithm. In some cases, performing directed molecular evolution comprises deoxyribonucleic acid (DNA) shuffling. In some cases, the ML or AI algorithm comprises one or more of structural sequence generation, sequence ranking, and sequence fine-tuning. In some cases, the ML or AI algorithm comprises a transformer model system. In some cases, the ML or AI algorithm comprises using natural language processing (NLP). In some cases, the evolved enzyme sequence is the sequence of the synthetic enzyme used in the methods of any of the embodiments of the present disclosure.

EXAMPLES

Example 1. Methods for Enzymatic Degradation Assay

Materials

[0102] Buffer recipe: 50 micro-Molar (μM) amino acid activator, 250 micro-Molar (μM) co-factor, and 0.15 Molar (M) Sodium Chloride (NaCl) diluted in distilled water

[0103] Sample comprising mineral material and enzyme in buffer (positive sample): 0.175 grams (g) of mineral material (e.g., ore or rock or other mineral), 7 milliliters (mL) of buffer, 350 microliters (μ L) of purified enzyme (0.51 mg/mL enzyme). The enzyme having silicase activity according to the embodiments and sequences described anywhere in the present disclosure.

[0104] Negative control sample: 0.175 g of mineral material, 7350 μ L of buffer.

Procedure

[0105] Mineral samples were crushed and sifted to a grain size of 150 μ M. they were subsequently washed with distilled water and ethanol. Samples were then centrifuged, and the pellets dried for 12 hours at 100° C. 2.5% (weight/volume (w/v)) solutions were made for both the positive sample and the negative control. Samples were resuspended in 96-well flat bottom plates and placed in an OT-2 heater shaker set to 300 rounds per minute (rpm) and a temperature from about 50 to about 60° C., overnight with periodic samples taken at regular time intervals. Samples were degraded and assayed in triplicate. The molybdenum blue photometry method in solution was used to determine the concentration of colloidal silica and soluble silica in the samples as well as for the standard curve. The assays were conducted with an automated procedure on an OT-2 Open-trons and absorbance taken on a Byuonoy Absorbance 96.

[0106] Positive reaction rates minus the negative baseline rates were calculated and normalized based on an established silica concentration reference curve.

Results

[0107] The method was performed on a variety of mineral materials, and the results are present in FIGS. 2-7.

[0108] FIG. 2 presents the rate of production of Si(OH)_4 corresponding to reaction rates of degrading silicate minerals(Alpha Spodumene and Beta Spodumene) using an enzyme having silicase activity according to the embodiments of the present disclosure.

[0109] FIG. 3 presents the rate of production of Si(OH)_4 corresponding to reaction rates of degrading silicate minerals (iron ore, platinum group metal (PGM) tailing, and Bauxite) using an enzyme having silicase activity according to the embodiments of the present disclosure.

[0110] FIG. 4 presents the rate of production of Si(OH)_4 corresponding to reaction rates of degrading silicate minerals (Rhyolite and Olivine) using an enzyme having silicase activity according to the embodiments of the present disclosure.

[0111] FIG. 5 presents the rate of production of Si(OH)_4 corresponding to reaction rates of degrading silicate minerals (Hectorite mix, Clay, a silicate named Maverick source, and a Lepidolite) using an enzyme having silicase activity according to the embodiments of the present disclosure.

[0112] FIG. 6 presents the rate of production of Si(OH)_4 corresponding to reaction rates of degrading silicate minerals (crushed glass and Perlite) using an enzyme having silicase activity according to the embodiments of the present disclosure.

[0113] FIG. 7 presents the rate of production of Si(OH)_4 corresponding to reaction rates of degrading silicate miner-

als (Oil Shale and Fly Ash) using an enzyme having silicase activity according to the embodiments of the present disclosure.

Example 2. Inosilicate Degradation with Enzymes Having Silicase Activity

[0114] The enzyme Gamma Carbonic Anhydrase from *M. thermophila* degrades silicate mineral material which allows for the extraction of metals such as lithium and aluminum, for example. Enzymes having silicase activity were designed from gamma carbonic anhydrase to improve the efficiency of the degradation reaction of silicate mineral material, specifically inosilicates, such as alpha spodumene, augite, and tremolite.

[0115] The 17 amino acid residue signal sequence as well as part of the disordered region (about residues 18 to 64, starting from the N-terminus) of wildtype Gamma Carbonic Anhydrase from *M. thermophila* were truncated. The wild-type truncation is as shown in SEQ ID NO: 403. From there, further mutations were generated to optimize for enzymatic efficacy, as shown in SEQ ID NOs: 404-433. Table 3 shows the percentage identity, as calculated by comparing sequence information using the advanced BLAST computer program, of the enzymes having silicase activity compared to wildtype gamma carbonic anhydrase from *M. thermophila*.

TABLE 3

Percentage Identity of Enzymes Having Silicase Activity to Wildtype Gamma Carbonic Anhydrase	
SEQ ID NO:	% Identity to Gamma Carbonic Anhydrase from <i>M. thermophila</i> (SEQ ID NO: 1)
403	100
404	65.0
405	67.8
406	54.7
407	61.1
408	65.4
409	73.6
410	71.5
411	67.6
412	66.5
413	64.3
414	58.0
415	69.5
416	72.8
417	46.1
418	70.5
419	51.7
420	38.3
421	60.1
422	71.6
423	67.1
424	50.0
425	58.9
426	68.9
427	58.2
428	74.3
429	42.9
430	69.3
431	58.7
432	46.3
433	67.5

[0116] Enzymes having silicase activity of SEQ ID NOs: 403-433 were generated comprising a GST tag and

expressed in *E. coli* BL21 using a pGEX-6P1 GST codon-optimized vector. *E. coli* cultures were grown at 37° C. with shaking and induced. After induction, the cells were harvested by centrifugation and lysed. The lysate was supplemented with ferrous gluconate to provide a source of Fe. The lysate was heated to 55° C. to aide in protein folding and stability. Enzymes were generated comprising an N-terminal GST tag. Other common purification tags, such as NEXT or 6-HIS, or no tags may be utilized in purification and experimental use of the enzymes. The enzymes were purified using a GST affinity column. The GST tag was found to not affect enzymic activity under reaction conditions.

[0117] The degradation reactions were tested for the various enzymes having silicase activity with alpha spodumene, augite, or tremolite. Degradation reactions were conducted in plastic containers to avoid silicate dissolution from glass. A range of reaction conditions were tested. The reaction was operational in a buffer comprising TRIS, PBS, 0.1 M citrate, or 0.9% monosodium glutamate in a pH range of 4-11, the rock to liquid rock ratio was tested between 1-40% (w/v), the minerals were crushed with a small grinder to ground ore sizes between 50 µm to 1 mm, the reaction was shaken with a range of 1-220 RPM, at a temperature between 23-85° C., the enzymes having silicase activity of SEQ ID NOs: 403-433 with GST, NEXT, 6-His or no N-terminal tag were tested, Zn, Fe, Cu, or Co metal cofactors were included, and the reaction ran for a time range of 1-48 hours. The range of reaction conditions tested resulted in degradation of silicate material. Data not shown.

[0118] Optimal reaction conditions were developed and used to compare the enzymes having silicase activity of SEQ ID NOs: 403-433. The enzymes were tested with alpha spodumene, augite, and tremolite. Optimized reaction conditions were found to be the following: the minerals were crushed with a small grinder and sifted to achieve a particulate size between 50 and 150 µm. The reaction proceeded in a 0.1 M TRIS buffer at pH 10 in a rock to liquid rock ration of 30% (w/v) at a temperature of 51° C. and shaking at 220 RPM for 48 hours. Reactions were completed in triplicate. After the reaction proceeded for 48 hours, the suspensions were centrifuged at 14,000 RPM for 15 minutes. The supernatant was filtered using a 45 µm, 13 mm diameter syringe filter.

[0119] The elemental composition of the supernatant was determined using a Laser Induced Breakdown Spectroscopy (LIBS) lithium brine analyzer and X-ray fluorescence analyzer. The results of the extracted metals were measured as PPM in solution as shown in Table 4. Degradation results were normalized to compared to a truncated wildtype Gamma Carbonic Anhydrase from *M. thermophila*, SEQ ID NO: 403.

[0120] The hydrolytic activity of the enzymes having silicase activity on the crystalline structure was also assessed using a silica degradation assay. The assay measured the amount of free silica (Si(OH)_4 , orthosilicic acid) using a molybdenum blue assay. The reaction proceeded as described above. 100 µL of the supernatant was deposited into a 96-well plate. 10 µL 1:1 sulfuric acid solution was added to the sample and mixed with the sample. 20 µL of 5% ammonium molybdate solution was added to the acidified sample and allowed to rest. Next, 20 µL of 0.5% ascorbic acid reducing reagent was added to the mixture and allowed the color to develop for 10 minutes. The molybdenum blue assay reaction mixture was transferred to a microcuvette and

the absorbance was measured at 810 nm. The amount of free orthosilicic acid was calculated against a calibrated standard curve. The results of the degradation of enzymes having silicase activity of SEQ ID NOs: 404-433 were normalized to activity of SEQ ID NO: 403 as shown in Table 5. The results show superior extraction of Fe, Li and Al as well as enzyme degradation activity in the enzymes having silicase activity of SEQ ID NOs: 404-433 as compared to the designed truncated wildtype enzyme having silicase activity of SEQ ID NO: 403.

TABLE 4

Metal Extraction Reaction Results	
SEQ ID NO:	Degradation activity compared to truncated wildtype enzyme
Degradation of alpha spodumene	
403	1
404	2.3
405	4.6
406	1.6
407	3.5
408	1.7
409	1.5
410	2.1
411	2
412	1.5
413	1.1
Degradation of augite	
403	1
414	3.9
415	1.4
416	5
417	1.5
418	3.4
419	1.3
420	6.9
421	2.1
422	1.5
423	3.2
Degradation of tremolite	
403	1
424	2.1
425	1.2
426	1.2
427	1.8
428	1.4
429	4.2
430	1.2
431	3.2
432	2.5
433	2

TABLE 5

Degradation Activity of Enzymes Having Silicase Activity			
SEQ ID NO:	Fe (PPM)	Li (PPM)	Al (PPM)
Metal extraction of alpha spodumene			
403	29177	2500	29744
404	33654	3128	35912
405	58434	4970	71002
406	31598	2774	33592
407	51460	4350	62887
408	32134	2802	34201
409	31025	2659	32378

TABLE 5-continued

Degradation Activity of Enzymes Having Silicase Activity			
SEQ ID NO:	Fe (PPM)	Li (PPM)	Al (PPM)
410	33380	3020	35312
411	33014	2982	34789
412	30896	2640	32157
413	29756	2536	30298
Metal extraction of augite			
403	21072	2877	31841
414	41234	5604	62197
415	23918	3265	36029
416	51043	6820	77102
417	24368	3321	36901
418	39692	5382	59748
419	22996	3104	34219
420	68129	9072	102432
421	30112	4098	45412
422	24560	3350	37129
423	37850	5137	57092
Metal extraction of tremolite			
403	27594	29727	31841
424	31267	33564	39753
425	28345	30218	32053
426	28409	30301	32198
427	30567	32674	31252
428	29123	31089	34506
429	35981	38374	45098
430	28390	30296	39587
431	34012	36102	39584
432	32878	34906	38128
433	31856	33870	37656

Example 3. Inosilicate Degradation with Host Cells Expressing Enzymes Having Silicase Activity

[0121] The enzyme Gamma Carbonic Anhydrase from *M. thermophila* degrades silicate mineral material which allows for the extraction of metals such as lithium and aluminum, for example. Enzymes having silicase activity are designed to improve the efficiency of the degradation reaction of silicate mineral material, specifically inosilicates, such as alpha spodumene, augite, and tremolite.

[0122] Enzymes having silicase activity are generated comprising a tag and expressed in a bacteria host cell, such as *E. coli*, using a host cell appropriate vector. Host cell cultures are grown and induced. After induction, the cells are harvested.

[0123] The degradation reactions are tested using the host cells expressing the enzymes having silicase activity with inosilicate materials, such as alpha spodumene, augite, and tremolite. Degradation reactions are conducted in plastic containers to avoid silicate dissolution from glass. A range of reaction conditions are tested. The reaction is tested in a buffer comprising TRIS, PBS, 0.1 M citrate, or 0.9% monosodium glutamate in a pH range of 4-11, the rock to liquid rock ratio is tested between 1-40% (w/v), the minerals are crushed with a small grinder to ground ore sizes between 50 µm to 1 mm, the reaction is shaken with a range of 1-220 RPM, at a temperature between 23-85° C., Zn, Fe, Cu, or Co metal cofactors are included, and the reaction is run for a time range of 1-48 hours.

[0124] The elemental composition of the supernatant is determined using a Laser Induced Breakdown Spectroscopy (LIBS) lithium brine analyzer and X-ray fluorescence analyzer. The results of the extracted metals are measured as PPM in solution.

[0125] The hydrolytic activity of the enzymes on the crystalline structure is also assessed using a silica degradation assay. The assay measures the amount of free silica (Si(OH)₄, orthosilicic acid) using a molybdenum blue assay. Supernatant is deposited into a 96-well plate. 1:1 sulfuric acid solution is added to the sample and mixed with the sample. 5% ammonium molybdate solution is added to the acidified sample and allowed to rest. 0.5% ascorbic acid reducing reagent is added to the mixture and allowed the color to develop for 10 minutes. The molybdenum blue assay reaction mixture is transferred to a microcuvette and the absorbance is measured at 810 nm. The amount of free orthosilicic acid is calculated against a calibrated standard curve.

Example 4. Phyllosilicate Degradation with Enzymes Having Silicase Activity

[0126] The enzyme gamma carbonic anhydrase from *M. thermophila* degrades silicate mineral material which allows for the extraction of metals such as lithium and aluminum, for example. Enzymes having silicase activity were designed from Gamma Carbonic Anhydrase to improve the efficiency of the degradation reaction of silicate mineral material, specifically phyllosilicates, such as lepidolite, montmorillonite, and muscovite.

[0127] The 17 amino acid residue signal sequence or the 17 amino acid residue signal sequence and part of the disordered region (about residues 18 to 64, starting from the N-terminus) of wildtype Gamma Carbonic Anhydrase from *M. thermophila* were truncated (SEQ ID NO: 403 and SEQ ID NO: 434 respectively). From there, further mutations were generated to optimize for enzymatic efficacy, as shown in SEQ ID NOs: 435-464. Table 6 shows the percentage identity, as calculated by comparing sequence information using the advanced BLAST computer program, of the enzymes having silicase activity compared to wildtype gamma carbonic anhydrase from *M. thermophila*.

TABLE 6

Percentage Identity of Enzymes Having Silicase Activity to Wildtype Gamma Carbonic Anhydrase	
SEQ ID NO:	% Identity to Gamma Carbonic Anhydrase from <i>M. thermophila</i> (SEQ ID NO: 1)
403	100
434	100
435	52.2
436	51.3
437	54.2
438	52.6
439	55.1
440	54.4
441	48.8
442	49.3
443	53.3
444	54.2
445	42.8
446	50.6
447	43.3
448	43.6
449	42.8
450	43.9
451	59.0
452	59.0
453	41.1

TABLE 6-continued

Percentage Identity of Enzymes Having Silicase Activity to Wildtype Gamma Carbonic Anhydrase	
SEQ ID NO:	% Identity to Gamma Carbonic Anhydrase from <i>M. thermophila</i> (SEQ ID NO: 1)
454	53.9
455	45.5
456	56.5
457	73.3
458	55.3
459	74.9
460	41.1
461	81.7
462	51.2
463	66.7
464	84.2

[0128] Enzymes having silicase activity of SEQ ID NOS: 403 and 434-464 were generated comprising a GST tag and expressed in *E. coli* BL21 using a pGEX-6P1 GST codon-optimized vector. *E. coli* cultures were grown at 37° C. with shaking and induced. After induction, the cells were harvested by centrifugation and lysed. The lysate was supplemented with ferrous gluconate to provide a source of Fe. The lysate was heated to 55° C. to aide in protein folding and stability. Enzymes were generated comprising an N-terminal GST tag. Other common purification tags, such as NEXT or 6-HIS, or no tags may be utilized in purification and experimental use of the enzymes. The enzymes were purified using a GST affinity column. The GST tag was found to not affect enzymic activity under reaction conditions.

[0129] The degradation reactions were tested for the various enzymes having silicase activity with lepidolite, montmorillonite, and muscovite. Degradation reactions were conducted in plastic containers to avoid silicate dissolution from glass. A range of reaction conditions were tested. The reaction was operational in a buffer comprising TRIS, PBS, 0.1 M citrate, or 0.9% monosodium glutamate in a pH range of 4-11, the rock to liquid rock ratio was tested between 1-40% (w/v), the minerals were crushed with a small grinder to ground ore sizes between 50 µm to 1 mm, the reaction was shaken with a range of 1-220 RPM, at a temperature between 23-85° C., the enzymes having silicase activity of SEQ ID NOS: 403 and 434-464 with GST, NEXT, 6-His or no N-terminal tag were tested, Zn, Fe, Cu, or Co metal cofactors were included, and the reaction ran for a time range of 1-48 hours. The range of reaction conditions tested resulted in degradation of silicate material. Data not shown.

[0130] Optimal reaction conditions were developed and used to compare the enzymes having silicase activity of SEQ ID NOS: 403 and 434-464. The enzymes were tested with lepidolite, montmorillonite, and muscovite. Optimized reaction conditions were found to be the following: the minerals were crushed with a small grinder and sifted to achieve a particulate size between 50 and 150 µm. The reaction proceeded in a 0.1 M TRIS buffer at pH 10 in a rock to liquid rock ration of 30% (w/v) at a temperature of 51° C. and shaking at 220 RPM for 48 hours. Reactions were completed in triplicate. After the reaction proceeded for 48 hours, the suspensions were centrifuged at 14,000 RPM for 15 minutes. The supernatant was filtered using a 45 µm, 13 mm diameter syringe filter.

[0131] The elemental composition of the supernatant was determined using a Laser Induced Breakdown Spectroscopy (LIBS) lithium brine analyzer and X-ray fluorescence analyzer. The results of the extracted metals were measured as PPM in solution as shown in Table 7. Degradation results were normalized to compared to a truncated wildtype Gamma Carbonic Anhydrase from *M. thermophila* (either of SEQ ID NOS: 403 or 434).

[0132] The hydrolytic activity of the enzymes having silicase activity on the crystalline structure was also assessed using a silica degradation assay. The assay measured the amount of free silica (Si(OH)₄, orthosilicic acid) using a molybdenum blue assay. The reaction proceeded as described above. 100 µL of the supernatant was deposited into a 96-well plate. 10 µL 1:1 sulfuric acid solution was added to the sample and mixed with the sample. 20 µL of 5% ammonium molybdate solution was added to the acidified sample and allowed to rest. Next, 20 µL of 0.5% ascorbic acid reducing reagent was added to the mixture and allowed the color to develop for 10 minutes. The molybdenum blue assay reaction mixture was transferred to a microcuvette and the absorbance was measured at 810 nm. The amount of free orthosilicic acid was calculated against a calibrated standard curve. The results of the degradation of enzymes were normalized to activity of a truncated wildtype Gamma Carbonic Anhydrase from *M. thermophila* as shown in Table 8. The results of the degradation using enzymes having silicase activity of SEQ ID NOS: 435-464 were normalized to activity of SEQ ID NOS: 403 or 434 as shown in Table 5. The results show superior extraction of Fe, Li and Al as well as enzyme degradation activity in the enzymes having silicase activity of SEQ ID NOS: 435-464 as compared to the designed truncated wildtype enzyme having silicase activity of SEQ ID NO: 403 and SEQ ID NO: 434.

TABLE 7

Metal Extraction Reaction Results	
SEQ ID NO:	Degradation activity compared to SEQ ID NO: 403 (truncated wildtype)
Degradation of lepidolite	
434	1
435	2
436	2.2
437	1.9
438	1.5
439	1.7
440	1.5
441	1.6
442	1.7
443	1.7
444	1.6
Degradation of montmorillonite	
434	1
445	3.6
446	2.4
447	1.2
448	1.1
449	2
450	1.5
451	2.2
452	2.4
453	1.3
454	1.2

TABLE 7-continued

Metal Extraction Reaction Results	
SEQ ID NO:	Degradation activity compared to SEQ ID NO: 424 (truncated wildtype)
Degradation of muscovite	
403	1
455	1.7
456	2.8
457	2
458	1.5
459	1
460	3
461	1.7
462	1.4
463	4
464	2.4

TABLE 8

Degradation Activity of Enzymes Having Silicase Activity				
SEQ ID NO:	Fe (PPM)	Li (PPM)	Al (PPM)	Sr (PPM)
Metal extraction of lepidolite				
434	21287	3514	24903	N.D.
435	24021	3598	25968	N.D.
436	24341	3678	26245	N.D.
437	23123	3627	25873	N.D.
438	21786	3552	25514	N.D.
439	22259	3642	26031	N.D.
440	21892	3557	25487	N.D.
441	22018	3589	25716	N.D.
442	22230	3638	25955	N.D.
443	22242	3643	26028	N.D.
444	22011	3594	25732	N.D.
Metal extraction of montmorillonite				
434	21061	450	25105	2194
445	41584	789	55613	4216
446	32235	654	46147	3798
447	23018	478	26695	2389
448	23240	461	26821	2453
449	34012	652	37334	3728
450	24287	634	27568	3560
451	34763	658	32849	3851
452	35047	662	38312	3917
453	23391	592	26743	2329
454	23674	594	27058	2290
Metal extraction of muscovite				
403	20364	29624	24959	N.D.
455	21547	31789	28125	N.D.
456	25432	34812	38912	N.D.
457	23489	32950	34968	N.D.
458	22015	30970	27605	N.D.
459	20456	29730	24964	N.D.
460	26710	35890	40025	N.D.
461	21570	31810	28060	N.D.
462	21030	30200	25302	N.D.
463	28020	37250	46390	N.D.
464	24080	33420	32705	N.D.

N.D. = no data

Example 5. Phyllosilicate Degradation with Host Cells Expressing Enzymes Having Silicase Activity

[0133] The enzyme Gamma Carbonic Anhydrase from *M. thermophila* degrades mineral material which allows for the extraction of metals such as lithium and aluminum, for

example. Enzymes having silicase activity are designed to improve the efficiency of the degradation reaction of silicate mineral material, specifically phyllosilicates, such as lepidolite, montmorillonite, and muscovite.

[0134] Enzymes having silicase activity are generated comprising a tag and expressed in a bacteria host cell, such as *E. coli*, using a host cell appropriate vector. Host cell cultures are grown and induced. After induction, the cells are harvested.

[0135] The degradation reactions are tested using the host cells expressing the enzymes with phyllosilicate materials, such as lepidolite, montmorillonite, and muscovite. Degradation reactions are conducted in plastic containers to avoid silicate dissolution from glass. A range of reaction conditions are tested. The reaction is tested in a buffer comprising TRIS, PBS, 0.1 M citrate, or 0.9% monosodium glutamate in a pH range of 4-11, the rock to liquid rock ratio is tested between 1-40% (w/v), the minerals are crushed with a small grinder to ground ore sizes between 50 µm to 1 mm, the reaction is shaken with a range of 1-220 RPM, at a temperature between 23-85° C., Zn, Fe, Cu, or Co metal cofactors are included, and the reaction is run for a time range of 1-48 hours.

[0136] The elemental composition of the supernatant is determined using a Laser Induced Breakdown Spectroscopy (LIBS) lithium brine analyzer and X-ray fluorescence analyzer.

[0137] The results of the extracted metals are measured as PPM in solution.

[0138] The hydrolytic activity of the enzymes on the crystalline structure is also assessed using a silica degradation assay. The assay measures the amount of free silica ($\text{Si}(\text{OH})_4$, orthosilicic acid) using a molybdenum blue assay. Supernatant is deposited into a 96-well plate. 1:1 sulfuric acid solution is added to the sample and mixed with the sample. 5% ammonium molybdate solution is added to the acidified sample and allowed to rest. 0.5% ascorbic acid reducing reagent is added to the mixture and allowed the color to develop for 10 minutes. The molybdenum blue assay reaction mixture is transferred to a microcuvette and the absorbance is measured at 810 nm. The amount of free orthosilicic acid is calculated against a calibrated standard curve.

[0139] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

SEQUENCE LISTING

Sequence total quantity: 464

SEQ ID NO: 1 moltype = AA length = 247
FEATURE Location/Qualifiers
source 1..247
mol_type = protein
note = Carbonic Anhydrase P40881
organism = synthetic construct

SEQUENCE: 1
MMPNKKQIFTI LILSLSLALA GSGCISEGAE DNVAQEITVD EFSNIRENPV TPWNPEPSAP 60
VIDPTAYIDP QASVIGEVTI GANVMVSPMA SIRSDEGMPI FVGDRSNVQD GVVLHALETI 120
NEEGEPIEDN IVEVDGKEYA VYIGNNVSLA HQSQVHGPAA VGDDTFIGMQ AFVFKSKVGN 180
NCVLEPRSSAA IVGTIPDGRY IPAGMVVTQS AEADKLPEVT DDYAYSHTNE AVVYVNVLHA 240
EGYKETS 247

SEQ ID NO: 2 moltype = AA length = 236
FEATURE Location/Qualifiers
source 1..236
mol_type = protein
note = Carbonic Anhydrase T5H8M4
organism = synthetic construct

SEQUENCE: 2
MKLSSKLILG LTVSSLAGKF LEKLLIQDNV SPNITASFNQ EADIPDIDAS SYIHHFASVI 60
GSVVIIGRNVF IGPFESSIONGD VGLKIFISHD CNIQDGIVLH GLKNYEYNSP VTEHSVFKDR 120
ESYSIYIGEK VSLAPQCQIY GPVRIDKNNF VGMQSLVFPDA YIQEDTVIEP GAKIIGVTIP 180
PKRFVSGRVS INQEDANRL PEITDSPPYH DLNSKMTSVN LELAKGYKKE ERQWKL 236

SEQ ID NO: 3 moltype = AA length = 205
FEATURE Location/Qualifiers
source 1..205
mol_type = protein
note = Carbonic Anhydrase Q3A3H4
organism = synthetic construct

SEQUENCE: 3
MIEKNVVTDF CSEASEPVID ASTYVHPLAA VIGNVILGKIN IMVSPTAVVR GDEGQPLHVG 60
DDSNIQDGVVH IHALETEMNG KPVAKNLYQV DGRSYGAVVG CRVSLAHQVQ IHGPAVVLDD 120
TFVGMKSLVF KSFVGKGCVI EPGSIVMGVT VADGRYVPAG SVIRTQEDAD ALPEIGADYP 180
FRAMNPGVHV VNTALAKGYM VKQGN 205

SEQ ID NO: 4 moltype = AA length = 204
FEATURE Location/Qualifiers
source 1..204
mol_type = protein
note = Carbonic Anhydrase
organism = synthetic construct

SEQUENCE: 4
MIGKNVLTDF SARASEPVIG SFTFVHPLAA VIGNVILGDN IMVSPGASIR GDEGQPLYVG 60
SDSNVQDGVVH IHALETELGD KPVEKNLVEV DGKKYAVYVG NRVSLAHQVQ VHGPAPIRDD 120
TFVGMKSLVF KSYVGSNCVI EPGVLLMGVT VADGRYVPAG SVVKTQEQQAD ALPVITDDYP 180
MKEMMNKGVLH VNKAALKGYL AAGS 204

SEQ ID NO: 5 moltype = AA length = 248
FEATURE Location/Qualifiers
source 1..248
mol_type = protein
note = Carbonic Anhydrase Q2LUP7
organism = synthetic construct

SEQUENCE: 5
MRPNKKQFTTI LILSLSLALL GSGCISEGEG AEGNVVTQGIT ESEFSNIREN PVTPWNPV 60
APVIDPTAFI DPQASVIGNV TIGASVMSP MASIRSDEGM PIFVGDRSNV QDGVLHCALE 120
TIDEEGEPVE NNIVEVGGKK YAVVYGENVS LAHQAQVHGPAA ASVGNDTFIG MQAFVFKSKI 180
GNNCVLLEPTS AAIGVTVPDG RYIPAGMVVT SQAEADNLSE ITDDYAYKHT NEAVVYVN 240
LAEGYNA 248

SEQ ID NO: 6 moltype = AA length = 243
FEATURE Location/Qualifiers
source 1..243
mol_type = protein
note = Carbonic Anhydrase Q467M8
organism = synthetic construct

SEQUENCE: 6
MALLLSLAIT LAGSGCVSOG EGAAEENIE AEEVEANVVE SNIRANPVTW WNPEPTEPVI 60
DPTAYIHPOA SVIGDVTIGA SVMSPMASV RSDEGMPIFV GDECNIQDGV ILHALETVNE 120
EGEPVEENQV EVDGKKYAVY IGERVSLAHQ AQVHGPSLVG NDTFIGMQTF VFKAIGNNC 180
VLEPTSAAG VTVPDGRYIP AGTVVTSQDE ADKLPEVTDD YAKHTNEAV YVVTNLAEV
YNA 240
243

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SEQ ID NO: 7      moltype = AA length = 275
FEATURE          Location/Qualifiers
source           1..275
                 mol_type = protein
                 note = Carbonic Anhydrase Q8PSJ1
                 organism = synthetic construct

SEQUENCE: 7
MKKYLWGKTC LVVSL SVMVT ACSSAPSTEP VDEPSETHEE TSGGAHEVHW SYTGTGPEH 60
WAELDSEYGA CAQGEEQSPI NLDKTEAIDT DTEIHVHYEP SSFTIKNNGH TIQABTTSDK 120
NTIEIDKEY TLVQFHFPN SEHEMEGKJL DMELHVFVHN ENDELAVLGV LMKAGEENEE 180
LAQLWSKLPA EETEENISLD ESIDLNVLLP ESKEGFHYNG SLTTPCSEG VKWTVLSEPI 240
TVSQEQIDAF AEIFPDNHNP VQPWNDRDVY DVITE                           275

SEQ ID NO: 8      moltype = AA length = 263
FEATURE          Location/Qualifiers
source           1..263
                 mol_type = protein
                 note = Carbonic Anhydrase A0AON9WRG3
                 organism = synthetic construct

SEQUENCE: 8
MRSRSHLTSI TLASVTLAT APAASAASPL SPLQALKASW SYEGETGPEF WGDLDEAFAA 60
CSNGKEQSPI NLFYDREQTS KWNWAFSNSYH TIQANVENED AGGLEINGEA 120
YOLIQQFHHT PSEHTIEETS FPMELHLVHA NHAGDLAVLG VLMMEMGNDHE GIEAVWEVMP 180
EEEETAAASI SLDPNLFLPE SVTAYQYDGS LTTPPCSEG VWTVLNDTIS ISETQLDAFR 240
DIYPQNYRPV QELGDREIGF HYH                           263

SEQ ID NO: 9      moltype = AA length = 247
FEATURE          Location/Qualifiers
source           1..247
                 mol_type = protein
                 note = Carbonate dehydratase Q5WD44
                 organism = synthetic construct

SEQUENCE: 9
MKINRIFLAL LFSLALTLAG SGCVSQGEA EDGESADTEV ESEVSIRAN PVTPWNPEPT 60
EPVIDSTAYI HPQAAVIGDV TIGASVMVP MASVRSDEGT PIFVGDETNI QDGVLVHAE 120
TVNEEGEPVE SNLVEVDGEK YAVYVGERVS LAHQSQIHPG AYVGNDTFIG MQALVFKANV 180
GDNCVLEPKS GAIGVTIPDG RYIPAGTVVT SQAEADELPV VTDDGYKHT NEAVVYVN 240
LAAGYNA                           247

SEQ ID NO: 10     moltype = AA length = 666
FEATURE          Location/Qualifiers
source           1..666
                 mol_type = protein
                 note = Kofleriaceae bacterium Carbonic Anhydrase Q8TMW3
                 organism = synthetic construct

SEQUENCE: 10
MRTNRVRTAG ASKWSGVSDI RTTLRERWSE IAAQGLSYHD VLAGLTVATV AIPLNVALAI 60
SAGLPPSAGL LAGAVGGLFA AAFFGGSNFOV SGPAALNVM VFGVVAKFGL GGAAAALVC 120
GIVGIALGVs GLGKYSNLMP KLVLAGFTTG VGLKLLDQQI PILLGSDLAL WHMLSNFWAM 180
EWLREWFVS VVCGLLVAWI TVGLAHLKSF PSALLGIVLA TLIAYELDWN VARVGEVDLS 240
DLALALPSIA DGTSWFLALIA VALPLAVLSS VESLISAKAV DAMANGKSGY SANTELFQGG 300
VGSIASALVG CMPLAGVVVS SSVNQQSGAR TRLAAMCHAV FLGIVAYFFG GLLGVIPVAA 360
LAGLLVVIAT RLMKLSYFFS ALRENKLHAL AFLAAAIGTL LGYLISGLAL GCALVYIAHK 420
LAHRPVKDAP VLRPSPITRA VISQAGERAQ DHPTPSIDEQKA KWSRHVRTRP KIHPTAYVHP 480
TASVIGWVEL GREVNIAADT SVRADEGAPF YVGDRSNVQD GVVIHALKDK WVMVDGRWA 540
VWIGSDVSLA HQALVHGPN IGSRSFIGFK AIVHDSVVG ECFIGLGA VGVIEPAGKR 600
VPNGWIVDSP EKVRELDPVE HAHAHFNEDV VQVNGLVVA YSRHVPTEEL PQRTPSDSL 660
FHLKPL                           666

SEQ ID NO: 11     moltype = AA length = 251
FEATURE          Location/Qualifiers
source           1..251
                 mol_type = protein
                 note = Thermodesulfobacterales autotrophica Carbonic Anhydrase
                 AOA7Y6PMB4
                 organism = synthetic construct

SEQUENCE: 11
MRPLPKMLTVV AVGATLCTFA GCASTQTTAT KEPAK PANIR PNVVTTFNPT TETPVIAKDA 60
YIDPLASVIG NVEIGSKVY APFASVRGDE GQPIYVGEGS NVQDGVLH A LETEDNGKPV 120
EKNLVEYGGK KYAVYIYGKHV SLAHOAQVHG PALVDDGTFV GMQALVFKAQ VGKNCVIEPG 180
AKLLNGVKVP DGRYVPAGTV VTTQAQADKL PVTDAYPLK NLNKGVLVN EQLAEGYLKA 240
QEGETGETKS H                           251

SEQ ID NO: 12     moltype = AA length = 547
FEATURE          Location/Qualifiers

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source          1..547
mol_type = protein
note = Fischerella thermalis/Mastigocladus laminosus JSC-11
Carbonic Anhydrase AOA3N5BJ34
organism = synthetic construct

SEQUENCE: 12
MAVRSIAEAA PPTPWSRNLA EPTIHPSAFL HSFSNIIGDV RIGANVIIAP GTSVRADEGT 60
PFYIGENTNL QDGVVVHGLE KGRVIGDDRQ EYSVWIGKNN CITHMALIHG PCYIGDDCFI 120
GFRSTVFNAR VGAGCIVMMH ALIQDVEIPP GKYVPSGAI TNQQQADRPL DVQADDKEFA 180
HHVVGINQAL RAGYLCAADS KCIRAIRDEL NNSYTSIEVD VLERSDEVSS NSLGAEETVEQ 240
VRVLLQQGYH IGTEHVQDRR FRTGSWTSCK PIEARSILGEA IAALEACLRD HSGEVVRLFG 300
IDPKGKRRLV ENIIQRPDG VQASSSLKAP AYSNNNGSYN GNGSSRLSSE TIDQIRQLLA 360
GGYKIGTEHV DERRFRRTGSW QSCKPIESSS PGDVVALEED CMDNHQGEYV RLIGIDPKAK 420
RVLLESVIIQR PNGPVSTPSS KSTATTTSYA ASGTTATATSS SKLSSEIAIEQ LQQLLAGGFK 480
ISAEHVGDRR FRTGSWASCG QIQANSIREA IAALEGYMNNE YQGEYVRLIG IDPKVKRRLV 540
ELIVQRP          547

SEQ ID NO: 13      moltype = AA length = 183
FEATURE
source          1..183
mol_type = protein
note = Thermosynechococcus vestitus
BP-1/(Thermosynechococcus elongatus BP-1 Carbonic
Anhydrase GeFUV4
organism = synthetic construct

SEQUENCE: 13
MLRKNPRTSW NSQESMPSSVA TTAVYDETAV VIGDVRIGER VYVGPCASIR ADEATPIVIS 60
EECNVQDGAI PHGLKGSSIK LGKKVSVAHG AVVHGPMТИ DESFIGFNAY VHASTVGERC 120
FIGHRALVMG VKLKDGSFVP HGSVIDTQDK ADALGPVPDS LKGFNAEVVE VNCEFAKGYR 180
SLR          183

SEQ ID NO: 14      moltype = AA length = 185
FEATURE
source          1..185
mol_type = protein
note = Methanothrix thermoacetophila Carbonic Anhydrase
Q8DKB5
organism = synthetic construct

SEQUENCE: 14
MSENLRNLPQ GDKPVIDPSS YVDPTAVIIG PVTIGKNCYI GPHTVIRADE VDEKTGKVAP 60
VIIGDNVNLO DGVIHALAG TSVEVGSNTS LAHGCVVHGP CKIEAGCFIG FRAVVFKTVI 120
GSGSMVKHGA IVEGVNIPSG KLVPTGEIIT SEDHLVKLKE VGQAEKEFMQ EVVHVNMLEA 180
HGYKK          185

SEQ ID NO: 15      moltype = AA length = 185
FEATURE
source          1..185
mol_type = protein
note = Thermosynropha lipolytica Carbonic Anhydrase A0B700
organism = synthetic construct

SEQUENCE: 15
MSENLRNLPQ GDKPVIDPSS YVDPTAVIIG PVTIGKNCYI GPHTVIRADE VDEKTGKVAP 60
VIIGDNVNLO DGVIHALAG TSVEVGSNTS LAHGCVVHGP CKIEAGCFIG FRAVVFKTVI 120
GSGSMVKHGA IVEGVNIPSG KLVPTGEIIT SEDHLVKLKE VGQAEKEFMQ EVVHVNMLEA 180
HGYKK          185

SEQ ID NO: 16      moltype = AA length = 185
FEATURE
source          1..185
mol_type = protein
note = Desulfofundulus thermobenzoicus Carbonic Anhydrase
AOA1M5PQH8
organism = synthetic construct

SEQUENCE: 16
MSENLRNLPQ GDKPVIDPSS YVDPTAVIIG PVTIGKNCYI GPHTVIRADE VDEKTGKVAP 60
VIIGDNVNLO DGVIHALAG TSVEVGSNTS LAHGCVVHGP CKIEAGCFIG FRAVVFKTVI 120
GSGSMVKHGA IVEGVNIPSG KLVPTGEIIT SEDHLVKLKE VGQAEKEFMQ EVVHVNMLEA 180
HGYKK          185

SEQ ID NO: 17      moltype = AA length = 192
FEATURE
source          1..192
mol_type = protein
note = Archaeoglobus veneficus Carbonic Anhydrase A0A6N7IXF4
organism = synthetic construct

SEQUENCE: 17

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MLQKSPAVSW KPGYPRISS LAFVHPTAVL IGEVVIHDGA IIPLAIIRA DEGFPIIVGE	60
NTNIQDGVI HCLKGGRVEI GRRVSLAHLGA VIHGPCVIGD ETFVGFRAMV INSRIGRCF	120
IDHGALIEGV EIPDGKYIPG LTRVSSQEQQ SRLAGITEQQ KDFAAEVLAV NGELKEAMQV	180
IITSRDDAYP GQ	192
 SEQ ID NO: 18	
FEATURE	moltype = AA length = 256
source	Location/Qualifiers
	1..256
	mol_type = protein
	note = Carbonic Anhydrase F2KNT3
	organism = synthetic construct
SEQUENCE: 18	
MRWAIILTTV LFAALLGCA AEKGIAEPLE TPEEKASNIH ANPITEWNDE QTMPDIDPTA	60
FVHPYATVIG DVHIGKYVICI SPHASVRGE GMPIYVGDD NIQDCVVIHA LETRDAEGNP	120
IEKNLVGVDD GKYYAVYIAD HVSLAHQSQV HGPAYVGSQT FIGMQLVFK AKVGKNCVIE	180
PGAKVIGVTI PDGRYVPGM AVTNQSVADN LPTEIDYPF KHTNEAVVHV NIELAKGYNA	240
MFGGESTEGT EGEGGH	256
 SEQ ID NO: 19	
FEATURE	moltype = AA length = 214
source	Location/Qualifiers
	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 19	
MQEITVTRFE NIRPSPVTPW NPEPRPEIH PTAYIDPAAV VQGDVKIGAN VLVMANAVIR	60
ADEGYPIYIG DNSVQDNVV LHALETRDAD GRDLEENIVR VGDERYAVVV GDNVVLAHNA	120
QVHGPAAVGD NTFVGMNALV FRSRVGADC LAPLAAAIGV TVPDGRYVPA GTVVTQAAA	180
AALPAVTPDH PFAGLNARVV AVNVALAKGY LALS	214
 SEQ ID NO: 20	
FEATURE	moltype = AA length = 259
source	Location/Qualifiers
	1..259
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 20	
MSKIYLAFVC GPEQNMHRDFP TANGLRQSPPI DIIPSKAVVD PKLRPLELKQ DPSTCLHLIN	60
NGHSFQVEFD DSQDKSVLKG GPLDKIYRLI QFHFWGSVD GQGSEHTVDK KKYAAELHLV	120
HWNTKYGDFG KAVQQPDGLA VLGIIFLKVRG HKPELQKLVD ALSSIKHKDT LVDFGNFDPS	180
CLMPTCPDYW TYSGSLTTPP LSESVTWIIC KQPVEVDHDQ LEQFRSLLFT SEGEKEKRMV	240
DNFRPLQPLM NRTVRSSFR	259
 SEQ ID NO: 21	
FEATURE	moltype = AA length = 270
source	Location/Qualifiers
	1..270
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 21	
MKRSVLATIF GYCPEWNDHQ SEWGYGETNG PKTWGKHFPPE ANGLLQSPID IKTEETQHDP	60
NLRPLTLKYD PSTAKEILNN GHFSQVTFV DTDSSLTDG PITGTYRLKQ FHFWGSDD	120
KGESEHTVDDA KYPAELHLVH WNTKYASFGE AASKPDGLAV VGVFLKIGKE HPGLKLLTD	180
LYMVRFKGTQ AQFTNFNPKC LLPTSLDYWT YPGSLTTPPPL SECVTWIVLK EPISVSSAQW	240
EKFPRNLFLTS EGEKACCMVD NYRPPQPLKG	270
 SEQ ID NO: 22	
FEATURE	moltype = AA length = 214
source	Location/Qualifiers
	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
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MQEITVTVNYN NIRPSPVTSW NPTPKLPKH PTAYIDPAAV VQGDVTIGEN VMVSANASIR	60
SDEGYPIYIG DNSVQDNVV LHALETVDDA GNVLEENVVT VGDKKYAVVI GKNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FNSVVGKDCV LMPLAAAIGV TIPDGKYIPA GTVVTQEEA	180
DKLPEVTPDH PFANTNKAVV AVNVELAKGY LALA	214
 SEQ ID NO: 23	
FEATURE	moltype = AA length = 310
source	Location/Qualifiers
	1..310
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 23	
MRFFECSCSP FFSQLSSFLT HLLILYTLSS SVEASSRNYY QWSYDSDVFG GPDFWGLVEK	60

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DWWMCRKGRL QSPIDIQPDR LLFDASVKPV RLDKLPVLSE FVNTGQMVRI RIGYSTKKPS	120
VNITNGPLYG YRYRVRQRIDF HMGRGKENG S EHTINGRRFP MEVQLVAFNT DLYPNFTAAS	180
KSPHGIAILS VLVDFGAQTN QELTKLTIAT ASISYKDQRV QMADFEWRL LPFTRDITY	240
EGSLTSPGCH ETVTWIILNQ PIFITREHFE EWSHLYHTME GAEKPVAPN YRKIQETNNR	300
LVRTNIQHKV	310
 SEQ ID NO: 24	moltype = AA length = 214
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source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 24	
MQEITVLEFS NITKNEVTPW NPKPVTPTVID PTAYIDPTAT VIGDVTIGAN CYIAASAVIR	60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GKVNEDNVVI HGDNWYAVYI GENVSLAHQS	120
QVHGPAYVGD DSFVGGMKSLV FKSIIVGSNCV IEPEAAAIGV TIPDGKYIPA GTVVTITQAEA	180
DKLPEVTPDY AFYTQVAAVV TVNVNLCRAY RNLS	214
 SEQ ID NO: 25	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 25	
MQEITVVAEYS NITKNEVTPW NPKPSTPVID PTSYVDPNAT VIGDVTIGKN CYIAASAVIR	60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GMIIGDNVVV EGDKYYAVYI GNNVVLAAHQ	120
QVHGPAMVGD DSFVGGMQSFV FNSIIVGSNCV IEPEAAAIGV TVPDGKYIPA GTVVTITQAEA	180
DKLPEVTPDD AAFTKNAAVV NVNVGLAKAY REKA	214
 SEQ ID NO: 26	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 26	
MQEITVTVNYN NIRPSPVTSW NPEPKLPEIH PTAYIDPAAV VQGDVTIGEN VLVMANAVIR	60
ADEGKPIVIG DNSAVQDNVV LHALETVDEN GNRIEENIVK VGDEEYAVYI GKNVVLAAHN	120
QVHGPAAVGD NTFVGMMNALV FRSRVGKNCV LEHNAAAIGV TVPDGKYIPA GTVVTITQEEA	180
DKLPEVTPDH PHYKLNERVV KVNVELAKGY LALK	214
 SEQ ID NO: 27	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 27	
MQEITVTRYE NIQPSPVTPW NPTPKRPQIH PTAYVHPLAY VQGDVTIGAN VMISPNASIR	60
SDEGYPKIVG DNSNVQDNVV LHALETVDAD GRKRIEENIVK VGDEEYAVYI GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSIIVGKNCV LEPLAAAIGV TIPDGTYIPA GTVVTITQEEA	180
DKLPKVTPDH PFAKTMNAAVV AVNVALAKGY LALA	214
 SEQ ID NO: 28	moltype = AA length = 186
FEATURE	Location/Qualifiers
source	1..186
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 28	
MLRKNPSLGHQ PQVAETAFID PTAAICGKV IIEDYVFFIGPY AVIRADEVNE QGDMEAIVIK	60
RDTNIQDGVV IHSKAGAAVT IGERSSIAHR SIIHGPCWVG DDVFIGRNSV VFNAKIGKGC	120
VIRHNSVVDG LDLPENFHVP PMTNIGPGFD LESISKVPP EYAFSESVVS ANHELVQGYR	180
RIANEL	186
 SEQ ID NO: 29	moltype = AA length = 281
FEATURE	Location/Qualifiers
source	1..281
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 29	
MGRSCLTLSR YQAKVMSANFL KNRVMASWGY KTDNGPSQWH IGYPVAKTGT RQSPVNIVPS	60
TVTRDDLLKA LKYEYTPSMI KMINTGSSWR MDFSPEGSNL SGGPLGDDYK VLQMHAHWGD	120
KAGRGESEHTM DGKMFDAELH IVHYNSNSKYGE PAIALDKPDG LAVLGMFIKT GWRSHPEFDK	180

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LCDNLKLIEM KGESIQLQEQY LNPANCLPNN KTFVTYPGSL TPPPLFESVT WIVFLEPIEM SSKQLDSMRA LKIGDTADCG CMVNNYRPPC ALGNRKIRVK V	240 281
SEQ ID NO: 30	moltype = AA length = 282
FEATURE	Location/Qualifiers
source	1..282
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 30	
MSLVPIERET ARRGRPPVAP RALGALLALA SAVAATPAIA WQSGIAVPDP NAMPQWRYTG ERGPGEHWSEL DPSYGACAHT DTQSPVALTE SMAVAVACEP LRFRYRSGPL YVTNDGRALR LGYDRGSHLL VEGLSYELVE LRFHPAAEHV INGSRADAEL QLIHANNRGD IAVVAVALMP GPRANSMQLR LLKHAPRLSG ESFYGRNVGV NPFLFLPGRK DYFAYRGSVT RPPCTEGVRW YVLRTPLEVA DADLQRLVGF MEPNARPLQP LGGRRVTKAC GP	60 120 180 240 282
SEQ ID NO: 31	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 31	
MQBKITVTRYE NIRPSPVTPW NPEPKLPKIH PTAYIDPAIA VQGDVTIGAN VMVSANASIR SDEGYPIYIG DNSNVQDNVV LHALETVDEN GNVIENVTT VGDKKYAVAI GDNVSLAHQA QVHGPAIVGD NTFIGMQAFV FRSRVGKNCV LAPLAAAIGV TVPDGTYIPA GKVVTTQEEA AKLPKVTPDH PFANTNAAVV KVNVLAQGY LALA	60 120 180 214
SEQ ID NO: 32	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 32	
MQBKITVHHYS NVTKNEVTPT NPKPVTPVID PTSYVDPNAT VIGDVITIGKN VLIAANAVIR ADEGAPIVIG DRSTVQDGVV LHALESVDDA GKREDNVVI EGDEEYAVVI GKDVSLAHQS QVHGPARVGD HSFVGMKSLV FKSIVGSNCV LEPEAAAIGV TVPDGKYIPA GTVVTTQEEA AKLPEITPDY PLYHANQVVV NVNVLLCQAY KALS	60 120 180 214
SEQ ID NO: 33	moltype = AA length = 269
FEATURE	Location/Qualifiers
source	1..269
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 33	
MAKTSFFPVV LSFIFILSYT MCINANATGK HEVDDEEFFS YLLGTAEGPY KWGTLKPDWE ICNTGLFQSP INFRNKTIVKV TKHIPHFTPN YKIASATIMN RGHDIKLQWE GDAGSITLNG TVYKLIQCHW HTPSEHKVDG QSLAMEAHLI HQSVNGKLIA VIGILFNIGP PDPFLNELIH HAKKVDHKKGK KVGLVDPNKL GVKAEPFYRY IGSLTIPPC EGIWVNVLHQ PRTVSMQMM ALRNAVNDGF QANARPAQGL RRRPVPYLV	60 120 180 240 269
SEQ ID NO: 34	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 34	
MQBKITVITYN NIRPSPVTSW NPEPRLPKIH PTAYIDPAIA VTGDVTIGAN VLVMANAVIR ADEGAPIVIG DNSNVQDNVV LHALETVDA GNVIENVVL VGDERYAVVV GDNVVIAHNA QVHGPAIVGD NTFIGMNAHV FRSRVGANCV LAPLAAAIGV TIPDGTYIPA GKVVTTQEEA AKLPRVTPDH PFADLVARVV KVNVLAQGY LALS	60 120 180 214
SEQ ID NO: 35	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 35	
MQEITVTDYS NITKNEVTST NPKPTTPVID PTSYVDPNAT VTGDVTIGKN VMISDSASIR SDEGRPIVIG DRSNVQDGVV LHALESVDDD GEILEDNVVE VGDENYAVVV GKNVSLAHQS QVHGPAAVGD DSFIGMQAFV FKSKVGNSNCV IEPDAAAIGV TVPDGKYIPA GTVVTTQEEA AKLPEITPDY EYSDTVEAVV EVNVALREAY KEKS	60 120 180 214

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SEQ ID NO: 36      moltype = AA  length = 343
FEATURE          Location/Qualifiers
source           1..343
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 36
MLAFVALVSL IFLGVQAQHG ADWTYSEGML DETHWPEEYP DCGGQRQSPI DLQRRKVRFN 60
PDLQPLELTG YGDSQGSPFL MTNNGHTVQI TLPPTMQLTA PDGAVYKATQ MHYHWGGASY 120
ELSGSEHTID GIRDVIEMLH VHYNAKYESY DVAKDKPDGL AVMAAFVEIE EYAENTHYSS 180
LISHLANIRY PGQTTYLTDV DILDMLPGDM YHYYTYNGSL TTPPCQTQNRV WFVMSDSVKI 240
SKAQVIKLEN SVMNHQNQTL HNGYRKTQPL HSRVVEANFP YFPNTMPGEG SGLRAKDPAR 300
EFGSRRHCYA WRGWQPAAA ALEGHGEPRR RWRPLETEAST PPP                343

SEQ ID NO: 37      moltype = AA  length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 37
MQEITVTRYN NIRPSPVTPW NPEPKLPEIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR 60
SDLEGYPPIYG DNSNVQDNVV LHALETVDAD GKRIEENVVK VGDKDYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQSFV FRSIVGKNCV LEPLAAAIGV TVPDNTYIPA GKVVTQEEA 180
DKLPKVTPDH PFANTNAAVV KVNVLAKGY LALA                214

SEQ ID NO: 38      moltype = AA  length = 291
FEATURE          Location/Qualifiers
source           1..291
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 38
MKNRRIKPEI MTKKFLFAIL TLFFFSGCQF FDKNKSTEIE SKPSSHEKWS YTGESGPHEW 60
AELEDQAVCD GHQHQSPVNIS DIDIKPGKLQI QESLDLSYQE VTTIKSITNN GHTIQYNFDA 120
NSNLVSLHDK QYKLKQFHFB SPSEHTINGT HSPLIEHLVH HSEATNSYIV IAILVQQGEP 180
DDAFDFLEKY LPINVGETKE INSKYFGST FPEMYGKDTL NIYTYEGSLT TPPCTESVLW 240
VVIKDPAYAS SSQIVMLQKL MPKDNYREVQ SLNGRLIYNE IIEDDISVLN H                291

SEQ ID NO: 39      moltype = AA  length = 230
FEATURE          Location/Qualifiers
source           1..230
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 39
MTKLSFAVIG PENWHRYCDQ AQGDOQSPIN IQTRDVKHDP TLRPLTLRYD PSTAREIVNN 60
GHSFVNVEFED STDRSVLRGG PLTDRYRLTQ FHPHWGSSDD HGSEHTVDGV KYAABLHLVH 120
WNTKYGDFGE AASKPDGLAV VGVFLKVGRH NPRLQKILDA LHAIKTKGKR ASFTNFDPNV 180
LLPGCLDYWT YSGSLSLPPPL SESVTWIVLR EPISVSPSQM AKFRSLLFTS                230

SEQ ID NO: 40      moltype = AA  length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 40
MQEITVTRYN NIQPSPVTPW NPEPKLPIH PTAYIHPKAV VQGDVTIGKN VMVSANASIR 60
SDLEGYPPIYG DNSNVQDNVV LHALETVDEN GNEIEENIVT VGDKKYAVVI GKNVSLAHQA 120
QVHGPAIVGD NTFIGMQAFV FNSNVGSNCY LAPLAAAIGV TVPDGTYIPA GKVVTQEEA 180
AKLPKITPDH PFYNTNAAVV KVNVLAKGY LALS                214

SEQ ID NO: 41      moltype = AA  length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 41
MQEITVDEFS NITKNEVTPF NPKPTIPVID PTAYVDPNAT VIGDVTIGKN CYIAPFASIR 60
ADEGKPIVIG DNSNVQDGVV LHALESIDDG GKLIENVV EGEKRYAVVI GKNVSLAHQS 120
QVHGPARVGD DSFVGMSLW FNSKVGSNCV IEPFAAAIGV TVPDGKYVPA GTVVTTQEEA 180
DKLPKITEIDDY AFAGTNEAVV KVNVKLCKAY REKA                214

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SEQ ID NO: 42      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 42
MQEITVLEYS NVTKNEVTSQ NPKPVTVID PTSYVDPNAT VVGDVTIGEN CLVWPTAVIR 60
ADEGRPIVIG NESSVQDGVV LHALESVDDG GELVEDNVVV VGDKNYAVVV GKNVSLAHQA 120
QVHGPARVGD DSFVGMSLKV FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTQEEA 180
AQLPEVTPDH AEYTTQATVV TVNVELNEAY RNQR                      214

SEQ ID NO: 43      moltype = AA length = 261
FEATURE          Location/Qualifiers
source           1..261
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 43
MTEKLWGYDS HNGPARWFQI CVPAQGKRQS PIDIQPDKAV LDSTLKPYLE KYDPSTARRI 60
VNNGHSFHVE FEDSTDKSVL QGGPLTGSYR LRQFHFHWGK KDDVGSEHVL DGVKYSSELH 120
VWHWNADKYS SFVEAAHEPD GLVULGVFLQ IGQHHPGLQR LTDALYAVRF KGTKAQFACF 180
NPKCLLPTSR HYWTYPGSLT TPPLSESVTW IVLREPISVS ERQMEKFRSL LFTSEDDERI 240
HMVNNFRPLQ PLMNRTVRSS F                           261

SEQ ID NO: 44      moltype = AA length = 302
FEATURE          Location/Qualifiers
source           1..302
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 44
MHNALFLTP ITVFYVAAHK FGYDAEDGPS TWRGVCQTGK RQSPVDIRAF EIEIAPLDPL 60
QFLNYDLTGH IHLANNHGTW VGSGFERWGE KRPyISGGGL NGTYQLSQFH FHWSQQNDTG 120
SEHTIASLHY PGELHVLVHIK KEPSPDEVNT IAVVAAFIKL DDHAGSLHNL KPYVHNIRMP 180
NTELVVPGFS VSSLLEPREH NFYRVEGSLT TPGCDEVVWW TLMADPIAVT PSQMGAFHQV 240
HFASGKTGHN WRPTQPLNGR KILFRPSITL RTFKSGGAML KPVFQPFI SI WLYGIYHII S 300
VF                                         302

SEQ ID NO: 45      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 45
MQEITVTKYN NIRPSPVTPW NPEPKLPEIH PTAYIDPAAV VRGDVKIGEN VLVMANAVIR 60
ADEGYPIYIG NNSSVQDNVV LHALETVDEN GRNRIEENIVL VGDKEYAVVI GDNVVIAHNA 120
QVHGPAAVGD NTFIGMNSLV FRSRVGSNCV LAPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
AKLPKITPDH PFANLNDRVV KVNVLAKG Y LAQA                      214

SEQ ID NO: 46      moltype = AA length = 353
FEATURE          Location/Qualifiers
source           1..353
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 46
MKMFPLDCLI LPCCYFFFIS TPHFANADVH IADWDHDHHH THPDNWEGMC KEGQRSPID 60
ITNETTKEK WQGPFIFHGY ERKLSMNVKE NRHSMVVEFD NDKKEYIDI RGGLGESKF 120
RFQQLHFWG STNDQGSEHT IDGKASPMEM HIVHWNLDVG KDVKEATEKD AYNSLEVLG 180
LFKLGKFNKD YDAIFNAARK VEKENTNATL EKDVRRLDLL PEDTNAFYRY VGSLTTPCN 240
QIVMWTFIKD PIEISQEQLD IMRKGSYRL EGENDVRVYIAN NYRSTQTLYE RDVLDIDTHI 300
VHLACNSKGS TRYHFEEGSE GFVHNTGNSL NSPIVTCMLF YLSIFVISM R LLH        353

SEQ ID NO: 47      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 47
MQEITVTRYE NIRPSPVTPW NPEPRRPVIH PTAYVDPLAY VQGDVTIGAN VMVSANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETRDAD GRVLEENVVV VGDERYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSRVGNKCV LEPLAAAIGV TVPDGTYVPA GKVVTTQEEA 180
AKLPKVTPDH PFATTNAAVV AVNVALAKGY LALA                      214

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SEQ ID NO: 48      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 48
MQEITVLEFS NITKNEVTSF NPEPVTPVID PTAYIDPNAT VIGDVTIGAN VLIWPTAVIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GKVRDENVVI EGDEEYAVYI GKNVTLAHQS 120
QVHGPAAVGD DSFVGGMKSLV FNSDVGGENCIEPFAAAIGV TVPDGKYIPA GTVVTTQAEA 180
ATLPEVTPDY AFYTQVAAVV SVNGLCQAY KNEA 214

SEQ ID NO: 49      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 49
MQEITVDEFS NVTKNEVTPW NPKPTTPVID PTSYIDPEAT VIGDVTIGKN CYIAPFAIVR 60
ADEGSPPIVIG DDSTIQDGVV LHALESVDDG GKLIEDNVVL EGDQYYAVYI GRNVVLAHQ 120
QVHGPAAVGD DSFVGGMKSLV FKSTVGSNCV LEPNAAAIGV TVPDGKYIPA GQVTTQAEA 180
DNLPEVTADD AYYTKVAAVV KVNVVALCEAY REQ 214

SEQ ID NO: 50      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 50
MQEITVTKYN NIRPSPVTPW NPEPKLPEIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR 60
SDEGYPIKIG DNSNVQDNVV LHALETVDAD GKELTENVVT VGDEKYAVYV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSTVKGKNCV LAPLAAAIGV TVPDGRYIPA GLVTTQEEA 180
DKLPKVTPDH PFYNTNAAVV AVNVALAKGY LAQA 214

SEQ ID NO: 51      moltype = AA length = 256
FEATURE          Location/Qualifiers
source           1..256
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 51
MSRPVALTIF GYEDKNQWHC CYPSAQGNRQ SPINIDIKKT VYDPKLKPLE LSYDPATAKG 60
ILNNNGHSFNV EFEDSQDKSV LKGGPLTGTY RLIQFHFWHG ATDDKGSEHT VDGVKYPSEL 120
HLVHWNAVKY SSFAEAASKP DGLAVLGVL KVGDHNAAALQ KLTDALYMRV FKGTKAQFTG 180
FNPKCLLPAS LDYWTYSGSL TTPPLLESVT WIVLKEPISV SSEQMAKFRS LLFTSEGEAE 240
CCMVVDNYRPP QPLKGR 256

SEQ ID NO: 52      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 52
MQEITVTTYT NIRKSPVTSW NPTPKYPKH PTAYIDPAAV VQGDVTIGEN VMVSANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDAN GNVIENVVT VGDKKYAVYV GNNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FNSRVGKNCV LEPLAAAIGV TVPDGTYIPA GEVTTQEEA 180
DKLPKVTPDH PFANTNAAVV KVNIELAKGY LAQA 214

SEQ ID NO: 53      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 53
MQEITVTVYT NIQPSPVTSW NPTPKLPKID ETAYVHPQAV VQGDVTIGKN VMISANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDAD GKEIEENVVT VGDKKYAVYI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSNVGKDCV LEPLAAAIGV TVPDGTYIPA GKVTTQEEA 180
AKLPKVTPDH PFYKTNAAVV KVNVELAKGY LALA 214

SEQ ID NO: 54      moltype = AA length = 186
FEATURE          Location/Qualifiers

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source          1..186
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 54
MLRKNPSGHI AVIDQTAYID EТАIICGKVI IEANVFVGPY AVIRADEVNIE QGDMEPIVIK 60
RDTNIQDGVV IHSKAGAAVT IGERSSIAHR SIIHGPCWVG DDVFIGFNSV VFNAKIGKGC 120
VIRHNSVVDG LDLPENFHVP PMTNIGPFD LNSISKVPPE YSAFSESVVS ANHELVQGYR 180
RIANEL                                              186

SEQ ID NO: 55      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 55
MQBITEVLEFS NITKNEVTPW NPKPSTPVID PTSYVDPNAT VIGDVTIGKN CYIAASAVIR 60
ADEXGKPIVG DRSNVQDGVV LHALESVNDG GKIREDNVNL EGDKYYAVYY GKNVVLAHQA 120
QVHGPAAVGD DSFVGMSLKV FKSIIVGSNCV IEPEAAAIVG TVPDGKYIPA GTVVTTQAEA 180
DKLPEITPDY AFYTQVAAVV KVNVDLCEAY RNKA                                              214

SEQ ID NO: 56      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 56
MQBITEVITYT NIRPSPVTPW NPEPKLPEIH PTAYVDPAAV VQGDVTIGKN VMVSANASIR 60
SDEGKPIKG DSNVQDNVV LHALETVDDED GNVIEENVTT VGDEKYAVYY GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFAV FRSNVGKNCY LAPLAAAIVG TIPDGTYIPA GTVVTTQEEA 180
AKLPKMTPDH PGYNTNAAVV KVNLALAKGY LALS                                              214

SEQ ID NO: 57      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 57
MQEITVVDNF NITKNEVTPPT NPKPSTPVID PTSYVDPNAT VTGDTIGKN CLIAANAKIR 60
ADEXGKPIVG DRSSVQDGVV LHALESVNDG GKVLEDNVNL EGDEYYTVYY GKNVVLAHQA 120
QVHGPAAVGD DSFVGMSKALV FKSKVGNKNCV IEPGAAAIVG TVPDGKYIPA GTVVTTQEEA 180
DKLPEITPDY PLSDANEAVV KVNVGLCEAY RNKS                                              214

SEQ ID NO: 58      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 58
MQEITVTKYE NIRPSPVTSW NPTPKLPIH PTAYIDPLAY VQGDVTIGEN VMVSANASIR 60
SDEGYPPIYG NNSNVQDNVV LHALETVDKN GKYLEENVTT VGDKKYAVYY GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFAV FRSTVGNKNCY LAPLAAAIVG TIPDGTYIPA GKVVTTQEEA 180
AKLPKMTPDH PGYKTNEAVV EVNVELAKGY LALA                                              214

SEQ ID NO: 59      moltype = AA length = 293
FEATURE
source          1..293
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 59
MASKLLRRNL LFTIQKRAVK SSVTRNSIPW LRKSAPSSNW GYNGSELDPE DWPKEYQCGN 60
CQSPIDIDL KVTYSSSELSP LEYSYPDNFK YMVNDGKNIR IHWRGETALS GGPLKGTYEL 120
VQLHFHWGSA EGKGAEHLVN GESVEGEAHL VHWNPKYGSI REALKHQDGI AVVGVLKEA 180
DDGAESPLSS ILNRFPTLSK FNEKYIFEND VFNVGNLIPK NSDFICYDGG LTPPPLTECV 240
QWIVLLKPLV VTKREMDIFR SLEGSGFGNNF TDNFRPCQPV GDRVVSSSFE PEK                                              293

SEQ ID NO: 60      moltype = AA length = 266
FEATURE
source          1..266
mol_type = protein
note = Library of modified or engineered enzymes

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SEQUENCE: 60
organism = synthetic construct
MKITALSVFC WGPNEYEDHRQ KWSNLIPYIAK GNRQSPINIV PGSAYDSSL KPLKLKYDPS 60
TCLEIWNNGH SFQVTFEDTD DKSVLSGGPL TDKYKLQFH FHWGKTDDHG SEHTVDGVKY 120
AAELHLVHWN AKYGSFGEAA DKPDGLAVVG IFLKIGREKG EFKLILDA LD SIKTKGKQTT 180
FTNFDPSCLF PSCP DYWTYS GSLTTPPLE SVTWWIILKQP IEVDHDQLEK FRTLLFTSEG 240
EKEKRMVDFN RPLQPLMNRT VRSSFR 266

SEQ ID NO: 61      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 61
MQEITVTYVN NIRPSPVTPW NPEPKLPKH PTAYVHPLAD VTGDVTIGAN VMVSAHASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDAA GKEIEKNIVT VGDKKYAVVI GDNVSLAHQA 120
QVHGPAAVGN NTFIGMCAAFV FNSVVGENCV LEPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
AKLPKVTPDH PFYNTNKAVV AVNVALAKGY LALA 214

SEQ ID NO: 62      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 62
MQEITVTYMEYS NVVKNEVTST NPKPTTPKID PTSYVDPNAT VIGDVEIGKN VLIAPFAIR 60
ADEGSPIVIG DNSNVQDGVV LHALESVDDG GKINEDNNVV KGDKYYAVVI GKNVHLAQA 120
QVHGPAYVGD DSFVGMKALV FKAKVGNNCV IEPNAAAIGV TVPDGKYVPA GTVVTTQEEA 180
DKLPEITEDY PFSTANEVVV KVNVLNLAKAY RNLA 214

SEQ ID NO: 63      moltype = AA length = 226
FEATURE           Location/Qualifiers
source            1..226
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 63
MAAHGAHWGY SGEAGPENWA KLTPEYGA CT GKNQSPINLT GFIEAEKP I KIAYKAGAKE 60
IVNNNGHTVQV NYQPGSFITI DGQQFELKQF HFHAPSENTI EGKSFPLEAH FVHANSKGEL 120
AVAVAMYEEG KENPLIAKAW QQMPEKAGEK NELKSTISAE SLLPKDKDYY RFSGSLTTPP 180
CSEGVRWIVL KNYSTVSKEQ VEQFLHTMH ANNRPVQPVN ARKVLK 226

SEQ ID NO: 64      moltype = AA length = 226
FEATURE           Location/Qualifiers
source            1..226
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 64
MAAHGAHWGY SGEAGPENWA KLTPEYGA CT GKNQSPINLT GFIEAEKP I KIAYKAGAKE 60
IVNNNGHTVQV NYQPGSFITI DGQQFELKQF HFHAPSENTI EGKSFPLEAH FVHANSKGEL 120
AVAVAMYEEG KENPLIAKAW QQMPEKAGEK NELKSTISAE SLLPKDKDYY RFSGSLTTPP 180
CSEGVRWIVL KNYSTVSKEQ VEQFLHTMH ANNRPVQPVN ARKVLK 226

SEQ ID NO: 65      moltype = AA length = 263
FEATURE           Location/Qualifiers
source            1..263
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 65
MKSTLIAFGV CEQNPDHWYR QYPVAKHHQ SPIDIISHTA KYDPSLKPLS ISYDPSTSLE 60
ILNNNGHSFQV TFEDSNKSV LKGGLDGVY RLKFHFHWG KKHSVGEHT VNGKSFPSEL 120
HLVHWNAVYK ESFGEALEE NGLAVVGFL ELGEHNABELQ KITDALYMRV FKGTKTFSC 180
FNPKCLLPPS LDYWTSYSGSL TTPPLSESVT WIVLREPISI SPSQLAKFRS LLFTSEGEKA 240
VCMVDNFRPL QPLMNRSVRS SFR 263

SEQ ID NO: 66      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 66

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SEQ ID NO: 67	moltype = AA length = 224
FEATURE	Location/Qualifiers
source	1..224
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 67	
MSQIWSYSGD TGPEFWPELC EEFYTAQQFP LQSPIALSYE ETQALEEALK FTYVEQNIYV	60
QKVNETMHFV PVDAASFVFE AQNRYLTDI HFHMPSHEVI NKQQAPLEFH LVHKDEGGNP	120
LVCALVFLDV ENEDKKCNKD KLILEADKDK EQLLNPEIFL YVQWVFDQI GVMSRSFIED FKTSLLPNNR	180
PVQWVFDQI PLQNKNRQPI FYKK	214
SEQ ID NO: 68	moltype = AA length = 262
FEATURE	Location/Qualifiers
source	1..262
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 68	
MKGGLTPSIAV FCYRQEENWDH IFPIAAGNRQ SPINIDTRKA KYDSSLKPLN LKYDPSTSLE	60
ILMNNGHSFQV NFEDTDNKS VLGKGGPLTGSY RLQFHFHWG ASDDKGEHT VDGVKYASEL	120
HVVHHNAVKY SSFAEEASKP DGLAVGVFL KVGHNPQLQ KITDALSSIK HKDTQALFSN	180
FDPSSLPLSC PDYWTYSGSL TTPLLSESVT WIVLKQPINV SPAQLAQFRS LLFTSEGEKA	240
CCMVVDNYRPL QPLKGRQVRA SF	262
SEQ ID NO: 69	moltype = AA length = 262
FEATURE	Location/Qualifiers
source	1..262
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 69	
MSARLVTWGY KEDDNGPHQWC IFFPEANGEC QSPIDIITSE TKHDPSLKPL SLSYNPATSK	60
EIIINVGSFH VNFEDEDNDRS VLKGGLPTDS YRLTQFHFHW GKKNDRGSEH TIDKKKYSSE	120
LHLVHWNNTKY GDFGKAVQQP DGLAVLGIFL KVGHNPQLQ KVLDTLNSIK TKGQTTFTN	180
FDPSTLLPGC LDYWTYSGSL TTPLLSESVT WIILKEPISV SSEQMAKFRS LLFTSEGEKA	240
CCMVVDNYRPL QPLMNRTVRS SF	262
SEQ ID NO: 70	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 70	
MQEITVSAFS NIRKNEVTPW NPEPSTPVID PTAYVDPQAT VIGDVTIGAN VLVSASASIR	60
ADEGRPIVVG DRSNVQDGVV LHALESVDDG GEVIEDNVVL EGGELYAVVV GENVSLAHQS	120
QVHGPAVLGD DSFVGMSKLV FKSKVGSNCV LEPGAAAGV TIPDGKYIPA GTVVTSQAEA	180
DNLPEVTPDY AYYTTNEAVV KVNVLAEEAY RNLS	214
SEQ ID NO: 71	moltype = AA length = 278
FEATURE	Location/Qualifiers
source	1..278
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 71	
MRLSAIFVTG WCPEKQDHNY YQWGYGKHNG PEHWKDHFP ANGLQQSPID IQISKVQHDP	60
ALKPLSLSYD PATARRILNN GHSHNFNEFDD SQDKAVLKGG PLTGSYRLIQ FHFHWGSADG	120
QGSEHTVDKK KYAAELHLVN WNAVAKYESFA EAAKQENGIA VLGVFLKVGE HNAQLQKLLD	180
ALSAIKHKGK QTAFTNFDP CLLPACPDW TYSGSLTTPP LSESVTWIVL KEPISVSEQ	240
MAKFRSLLFT SEGETACCMV DNYRPPQPLK GRKVRASF	278
SEQ ID NO: 72	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 72	
MQEITVTRFE NIRPSPVTSW NPEPKRPVID PTAYIDPAAV VQGDVTIGKN VMISANASIR	60

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SDEGYPIYIG DNSNVQDNVV LHALETVDAD GKRLEENVVK VGDKEYAVAI GDNVSLAHQA 120	
QVHGPAIVGD NSFIGMQAFV FRSRVGKNCV LAPLAAAIGV EVPDGKYIPA GKVTTQEEA 180	
DKLPEVTPDH PYATTNAAVV KVNVELAKGY LALS 214	
SEQ ID NO: 73	moltype = AA length = 268
FEATURE	Location/Qualifiers
source	1..268
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 73	
MARTVLGIFC SPNKEWQYDH AKNGPEVWKE YFPIADGDQQ SPIEIKTKEV KHDSSLKPLS 60	
ISYNPATAKE ILNVGHFSHV NFEDNDNRSV LKGGLPLSDSY RLSQFHFHWG SSDDHGSEHT 120	
VDGVKYASEL HLHVHNNAKYG KFGEAASKPD GLAVVGIFLK VGSACKPLQK VVDALGSIKT 180	
KGKQASFTNF DPSVLLPGCL DWTYDPSVTL TPPLLESVTW IVLKEPISVS PSQMAKFRL 240	
LFSSEGEAAC CMVDNYRPPQ PLKGRQVK 268	
SEQ ID NO: 74	moltype = AA length = 268
FEATURE	Location/Qualifiers
source	1..268
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 74	
MPLPNARERR RDWRAVVTAA AVFGIVVPIG TGLHAEDWGY SGTHGPRFWA KTPGWEACAG 60	
TAATERQSP1 DIDEVVADKE LTRLQADLKE TPVAVNNH TIEEYRLGS SLTLAGVRYD 120	
LKQFHFHTPS EHTVRGAHAA MEMHVVFKDA GSDKLVVIGV LFEVGVKANAF LSALMADGLP 180	
GKRGEEVDAH SRPVNVAQAL TDTSQYYTYP GSLTTPPCSE NVTWFVULKGR PEMSAEQLAA 240	
FHRVLGDNAR PVQKLNHRVA HETVSGAR 268	
SEQ ID NO: 75	moltype = AA length = 204
FEATURE	Location/Qualifiers
source	1..204
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 75	
MTSLQYNNIR PNLADGYPOI DPTALIDPSA QIIGNVVKIDR DVFVGPLTVI RADQRGPNGK 60	
VSPIQIDRE4 NIQDGREA KTTVAHGAII HGPCTIGQEC FIAIRASLYK 120	
VTLEDHVWLIG IGAIAKLVTL HSFTRVVPAGA VIRDSPVELP LRLITDKERK YMEEVWAANS 180	
LLRTDYLERL DKVESIRSTA KKKG 204	
SEQ ID NO: 76	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 76	
MQEITVTRYE NIRPSPVTPW NPEPKRPKI PTAYIDPAAV VTGDTVIGEN VLVMANAVIR 60	
ADEGYPIVIG DNSSVQDNVV LHALETVDEN GNRRIEENVRR VGDEDYAVVV GKNVVLAHNA 120	
QVHGPAAVGD NTFVGMMALV FRSRVGKNCV LAPLAAAIGV TVPDGTYVPA GLVTTQEEA 180	
AKLPKVTPDH PFANLNARVV KVNVELAKGY LALA 214	
SEQ ID NO: 77	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 77	
MQEITVTKFE NIRPSPVTPW NPTPKRPEIH PTAYIDPPLAY VQGDVTIGAN VMISANASIR 60	
SDEGYPIVIG DNSNVQDNVV LHALETVDAN GNEIKENIYT VGDEKYAVVV GDNVSLAHQA 120	
QVHGPAAVGD NTFIGMQAFV FRSRVGKNCV LEPLAAAIGV TIPDGTYIPA GKVTTQEEA 180	
DKLPKMTPDH PFYNTNKAVV AVNIALAKGY LALS 214	
SEQ ID NO: 78	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 78	
MQEITVHHHH HITKNEVTPT NPKPTTPVID PTSYIDPNAT VIGDVTIGKN VLIAPFASIR 60	
ADEGSPIVIG DRSNVQDGVV LHALETVDDG GKVIEDNVVL EGDKYYAVVI GRNVTLAHQA 120	
QVHGPAAVGD DSFVGMKALV FKAKVGKNCV IEPDAAAIGV TVPDGKYIPA GTVTTQEEA 180	

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DKLPEITPDY AFYTQNETVV KVNVLC EAY REKA	214
SEQ ID NO: 79	moltype = AA length = 244
FEATURE	Location/Qualifiers
source	1..244
	mol_type = protein
	note =
	MLSLSALLAATAFSASASAPSHWEYSGEAGPAHWASLTPEFGACTGKNQSPVNLTGFVDA
	KLKPIKFAYQAGGKSIVNNGHTVQVNYQPGSSITLDGVTFELKQFHAPSENQIDGQS
	YPLAEAHLVHADKEGNLAVVALMFQGEANPELAKLWQAMPEKANQSQPLKASIRADQLL
	PENRDYRFSGSLTTPPCSEGVRWIVMKQPITASAQIEEPEHVMMHPNNRPVQPLNGK
	TIVTG LSS
	organism = synthetic construct
SEQUENCE: 79	
MLSLSALLAATAFSASASAP HWEYSGEAGP AHWASLTPEF GACTGKNQSP VNLTGFVDAK	60
LKPIKFAYQAGGKSIVNNGH TVQVNYQPGS SITLDGVTFELKQFHAPSENQIDGQS	120
LEAHLVHADK EGNLAVVALM FKQGEANPEL AKLWQAMPEK ANQSQPLKAS IRADQLL PEN	180
RDYRFSGSL TPPCSEGVR WIVMKQPITA SAAQIEEPEH VMHHPPNNRPV QPLNGKTIVT	240
GLSS	244
SEQ ID NO: 80	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 80	
MQBKITVTVS NVEKNEVTSQ NPPRPTTPVID PTSYIDPNAT VIGDVTIGKN CYIAASASIR	60
GDEGRPIIHG DRSNVQDGVV LHALESVTD GEVLEDNVVL EGDEDYAVVI GKNVSLAHQS	120
QVHGPARVGD DSFIGM KSLV FKSIVGSNCV LEPDAAAIGV TVPDGKYIPA GTVVT TQAEA	180
DKLPEVTPDY AYYTKNAAVV AVNVALCEAY RNQS	214
SEQ ID NO: 81	moltype = AA length = 259
FEATURE	Location/Qualifiers
source	1..259
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 81	
MLKIVSAFTG YCPENWHRQF DKAAGSQOSP IDIQT KDIQH DPCLQPLKLS YDPSTCLEIW	60
NNGHHSFLVQF EDSDGDKSVIE GGPLEGVYRL KOFHFHWGAK DSEGSEHTVD GVFP CELHL	120
VHWNNAKYGSF AEAASKPDGL AVVGFLKIG KEHAEFQKLL DALDAIKTKG KQTPTNFDP	180
SCLLPACRDY WTYDGSLLTP PLLESVTWIV LKEPISVSPG QMAKFRSLLF TSEGEAACM	240
VDNYRPPQPL KGRHVRASF	259
SEQ ID NO: 82	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 82	
MQBKITVLSFS NVQKNKVPTPT NPKPPTTPVID PTAYIDPDAT VIGDVTIGKN CFIGAFAVIR	60
ADEGKPIVIG DRSNVQDGVV LHALESVDE GKVIEWDNVV KGDKEYAVVI GKNVSLAHQS	120
QVHGPARVGD DSFIGM MNAT FNSIVGSNCV IEPFAAAIGV VVPDNTYIPA GTVVT SQEEA	180
DKLPEVTPDY AYYTQVAAVV KVNVLC EAY REKA	214
SEQ ID NO: 83	moltype = AA length = 264
FEATURE	Location/Qualifiers
source	1..264
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 83	
MKITFLSAVC GWNYQDPERW HDDFPPIAKGE RQSPIDIDLIS KVQRDP SLKP LSFKYDPSTS	60
RRILNNNGHSF NVEFEDSEDK SVLKGGPLTG SYRLKQFH FH WGATDDKGSE HTVDGVYAS	120
ELHLVHWNAK YGDFGEAASK PDGLAVGVVF LKIGRHHEEF QKLLDALPAI KHKD TLDVFG	180
SFDPSCLMPT CPDYWTYSGS LTTPPLLESV TWIVLKQPIE VDH DQLEQFR TLLLFTSEGEK	240
EKRMVDNFRP LQPLMNRTVR SSFR	264
SEQ ID NO: 84	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct

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SEQUENCE: 84
MQEITVDEFNS NVTKNEVTPW NPKPSTPVID PTSYIDPDAT VIGDVTIGAN VLIGPNAIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVDDA GKVIEDNVVK VGNNSYAVVV GKNVVLAHNA 120
QVHGPAAVGD DSFVGGMNAFV FNSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTQEEA 180
DKLPEITEDY EYYTKVAEVV EVNVALCEAY KEKA 214

SEQ ID NO: 85      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 85
MQEITVLLFS NVTKNEVTTT NPKPTTPVID PTSYVDPNAT VTGDTIGAN VMISANASIR 60
SDEGRPIVIG DRSNVQDGVV LHALESVDDD GKIIENVVI HGDEDYAVFI GKDVS LAHQ 120
QVHGPAAVGD DSFIGMOSFV FKSKVGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTTQEEA 180
EKLPDVTPDH AQYTTQAAVV TVNVQLTAK RNLK 214

SEQ ID NO: 86      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 86
MQEITVLFNS NVTKNEVTTT NPKPTTPVID PTSYVDPKAT VTGDTIGKN VLIAANATIR 60
ADEGKPIVVG DRSTVQDGVV LHALESVDDT GKVIENVVI KGNEDYAVVI GNNVSLAHQA 120
QVHGPAAVGD DSFVGGMKALV FKSKVGSNCV IEPDAAAIGV TVPDGKYIPA GTVVTTQEEA 180
AKLPEITPDY PFYTTNAEVV SVNVKLCEAY KGEA 214

SEQ ID NO: 87      moltype = AA length = 282
FEATURE
source          Location/Qualifiers
1..282
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 87
MVRILVVTL LVLSGPPLS TSGTLQDKKA ASECSQDPFYS YDHGASQQS WCGRCNESGA 60
LPLPQAPINI PKIAESAQPA IVFNGYNENT SLVIYPHNPY NLKVDYKSSS NPVATIDIGS 120
SANSRFKLLE FHFHRPSEEA IDNRNRPMPVL HLVLHLREVEG CEPGKPGCVA AVAILIKEGT 180
PSQQTDLNLL ALFSHPPPPD KPKDVEINLE GLLPPDHVNA GYWSYGGSLT TPPCTENITF 240
YLLKPMMLTFS AAQIAEFERR YPTPNARDIQ PLHDRHRVVN RH 282

SEQ ID NO: 88      moltype = AA length = 186
FEATURE
source          Location/Qualifiers
1..186
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 88
MIKSNPGRGL PQVHETAFVD PTAILCGYVI VEENVFIGPY AVIRADETTA DGRIAPIVIG 60
AHSNIQDGVV IHSKSGAWVT IQRTSIAHR AIVHGPCTVG DGVFIGFNSV LFNCTIDDGC 120
VVRYNAAVVG CHLPPGFYVR STERIGPETD LAALPQVTD ASDFSEDVAR TNNAVLGYK 180
HIQNEF 186

SEQ ID NO: 89      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 89
MQEITVFEFS NVEKNEVTT NPKPTTPKID PTSYVDPNAT VIGDVTIGEN CMISATASIR 60
SDEGRPIVIG DRSNVQDGVV LHALESVDDQ GMVREDNVVL EGDEYYAVVV GDRVSLAHQS 120
QVHGPAAVGD DSFIGMOSFV FKSTVGSNCV IEPGAAAIGV TVPDGKYIPA GTVVTTQEEA 180
DKLPEITDDY PFYSTQAAVV EVNVGLCEAY RGKA 214

SEQ ID NO: 90      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 90
MQEITVFDTS NVRKNKVTGT NPKPVTPVID PTSYVDPNAT VIGDVKIGKN CLIGASAVIR 60
ADEGHPIVIG DRSNVQDGVV LHALESVNDD GKILEENVVI EGDEYYAVVV GKNVVLAHQS 120

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QVHGPAAVGD DSFVGGMKSLV FRSIVGSNCV IEPNAAAIGV TVPDNKYIPA GTVVTTQEEA	180
DNLPEITPDY PYYDTVEQVV KVNVNLCEAY REKE	214
SEQ ID NO: 91	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 91	
MQEITVTRYE NIRPSPVTPW NPEPDRPEIH PSAYIDPAAV VQGDVTIGAN VYVAANAVIR	60
ADEGYPIVIG DNSVQVDNVV LHALETVAD GRRIEENIVE VGGERYAVVV GANVVLAHNA	120
QVHGPAIVGD NTFVGMMALV FRSRVGKNCV LMHLAAAIGV TVPDGTYVPA GKVVTTQEEA	180
AKLPKVTPDH PFYKLNARVV AVNVALAKGY LALS	214
SEQ ID NO: 92	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 92	
MQEITVTKFE NIQPSPVTPW NPEPKKPEID PTAYIHPAAV VQGDVKIGKN VMISALASIR	60
SDEGYPIVIG DNSVQVDQVV LHALETVDEN GNVIENVVT VGDEKYAVVI GKNVSLAHQA	120
QVHGPAIVGD NTFIGMQAFV FRSKGGENCV LEPLAAAIGV TIPNNNTYIPA GKVVTTQEEA	180
AKLPKITPDH PFANTNAAVV KVNVNLAKGY LALS	214
SEQ ID NO: 93	moltype = AA length = 233
FEATURE	Location/Qualifiers
source	1..233
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 93	
MKSILAVFTG CYQPNDHEHWR YEDENGPEKW AEIEKNSDCG GKHQSPINII HKETDSVHGP	60
LDLQINYEPS TLITEVRNNG HSIQFDPEKG DSINYKNETY YLKQIHHEP SEHKINGIIY	120
PIEMHLVHMN KSGKITVGLI LGEEEESQL FEFPEFLPL KNGETKDIHQ KIDLSSLFLE	180
DKHYYSYDGs LTTPPCSENV NWIVFKPEIV LSVEEVIKLR NNMPLNNYRN EQP	233
SEQ ID NO: 94	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 94	
MQEITVSLFS NVTKNEVTSW NPKPTTPVID PTSFIDPNAT VTGDTVTIGKN CLIGPNAIVR	60
ADEGSPIVIG DSRNVQDGVV LHALESVNDL GKIIEENVVL YGSKLYAVVI GKNVSLAHQS	120
QVHGPARVGD DSFVGMMALV FNSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTSQAEA	180
DKLPPEITPDH AYYTQNFAVV NVNVNLCRAY RNKS	214
SEQ ID NO: 95	moltype = AA length = 230
FEATURE	Location/Qualifiers
source	1..230
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 95	
MASSAFAAEG AHWGYTGHGG PAHVGDLSDAD YATCKLGKHQ SPIDIRGAKE ADLPAIQFDY	60
KASPLKILNN GHTVQVNYP GSGIVVVDGKP YELVQFHFK PSEEKIDGKA YPMVAHLVHR	120
DAAGHLAVVA VLIKEGKENP LIKTLWPHLPL AEEGPEQAVA GATINADLL PADRGYYAFD	180
GSLTTPPCSE GVRWHVLKQP ITMSKAQIDA FQKLYKPNAR PLQPLNGRIM	230
SEQ ID NO: 96	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 96	
MQEITVTRYE NIRASPVTPW NPEPKLPIH PTAYIDPAAV VQGDVTIGEN VLVMANAVIR	60
ADEGYPIVIG NNSSVQDNVV LHALETVDEN GNEIEENVVT VGDKKYAVVV GDNVVLAHNA	120
QVHGPAIVGD NTFVGMMALV FRSRVGKNCV LAPNAAAIGV TVPDGKYIPA GKVVTTQEEA	180
DKLPPEITPDH PFANLNARVV KVNLALAKGY LAQA	214
SEQ ID NO: 97	moltype = AA length = 214

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FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 97	
MQEITVLIFS NITKNEVTST NPKPKTPKID PTSYIDPNAK VIGDVTIGKN VLIAAFAVIR	60
ADEGKPIVIG DRSNVQDGVV LHALESINDD GKIIEDNVVI EGNNNHYAVVV GNNVSLAHQS	120
QVHGPAHVGN DSFVGMKSLV FKSDVGDNCV IEPEAAAIVG TVPDGKYIPA GTVVTQEEA	180
AKLPTEITEDY FYTAKVAEVV KVNVDLCLAY RNKQ	214
SEQ ID NO: 98	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 98	
MQEITVHHFS NVRKNEVTPT NPKPTTPVID PTSYIDPNAT VIGDVTIGKN CYVAHSAVIR	60
ADEGHPIVIG DRSNVQDGVV LHALESVDDG GEIREDNVVE VGDESYAVVV GKNVVLAHQS	120
QVHGPAAVGD DSFVGMKSLV FQSTVGSNCV IEPEAAAIVG TVPDGKYIPA GTVVTQEEA	180
AKLPTEVTPDH ADYTTQAAVV TVNVALCEAY KAQA	214
SEQ ID NO: 99	moltype = AA length = 287
FEATURE	Location/Qualifiers
source	1..287
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 99	
MGSYKTLTDI GKMLKTLLL ASTVSAWTYS DQTAWGGECK TSKSQSPINI VTSSAVCKNS	60
KDDPIKADSF VAEKLGGKHA MTLNNNTSSG THSATWTFKT MPENSQLKCA QHHCHFDVAE	120
HSMDEGEKHFG ECHVVCMQAK YADLGKALES KATDALAVFG FLLAKGTATT ADHAVTKQMI	180
DAKKNYAEKG EYEMEIATT QLADGYYRYN GGLTTPGCNE AVTWTVFKNV QYVSVAQYNE	240
IMTWKDGMLR GNDRKVQPMN GRSLTFYKSS ASKMMMASLAI IGVMPMF	287
SEQ ID NO: 100	moltype = AA length = 258
FEATURE	Location/Qualifiers
source	1..258
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 100	
MRFNRFVTTL LAACLMPLMT QAAPWGYTGE TGPAQWKGKIS KEYATCQTGI NQSPVDIQT	60
TTSKGLGPAL NTQYIDNPTR FRSINYTLRA TMSSYSSNFI EIEGRILYYLK HFDFHAPSEH	120
TLNGKTYPLE LQLVHKNQHG DIAIVAVMFD VGEPNQAIQN LWESFPMTVD NSMPIFSDVD	180
INQLLPDNKA YWLXSGSLTT PPCTEGVTVW VLKKPVALSA EQLDNFHYIV GPANNRPPQP	240
LNARTITDSH SGNTILEY	258
SEQ ID NO: 101	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 101	
MQEITVTRFE NIQPSPVTPW NPEPKLPEIH PTAYIHPAAV VQGDVTIGEN VMVSANASIR	60
SDEGYPIVIG DRSNVQDNVV LHALETVGED GEVLEENVVV VGDERYAVVV GKNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSRVGKDCV LEPLAAAIVG TIPDGTYIPA GLVVTQEEA	180
AKLPKVTPDH PFANTNAAVV KVNVVALAKGY LAQA	214
SEQ ID NO: 102	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 102	
MQEITVLEFS NVTKNEVTTF NPKPETPVID PTSYIDPNAT VIGDVTIGKN CMISANASIR	60
SDEGKPIVIG DRSNVQDGVV LHALESVDDG GMVLGDNVVV HGNSWFAYVV GKNVSLAHQA	120
QVHGPAAVGD DSFIGMQSFV FNSIVGSNCV IEPNAAAIVG TVPDNKYIPA GTVVTQEEA	180
DKLPTEVTEEDY KYFTTQEAVV KVNVNLAEAY RGLA	214
SEQ ID NO: 103	moltype = AA length = 266
FEATURE	Location/Qualifiers
source	1..266

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mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 103
MLKRISAFTV CGWNYEDQHP EKwasLFPLC AGKRQSPIN1 VTSEVVYDPK LKPLKLSYEP 60
ATCREIVNNG HSFNVFDD5 QDKSVLKGGP LSGIYRLKQF HFHWGAADDK GSEHTVDGAK 120
YSAELHLVHW NAKYGDFAEA ASKPDPGLAVV GVFLKVGKAN PELQKLLDAL GS1KTKGKQT 180
RFTNFDPSTL LPSSLDYWTY DGSLLTPPLL ESVTWIVLKE PISVSPAQME QFRSLLFTSE 240
GETACCMVDN YRPPQPLKGR QVRASF 266

SEQ ID NO: 104      moltype = AA length = 186
FEATURE
source          Location/Qualifiers
1..186
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 104
MIKTNPRGDL PQVHESAFVD PTAILCGWVI VEEYVFIGPY AVIRADELNA DGDMEPIVIG 60
AHSNIQDGVV IHSKSGAAVT IGRHTSIAHR AIVHGPCRVG DGVFIGFNSV LFNCTIDDGC 120
VVRYNAAVVDG CHLPPGFYVR STERIGPETD LAALPQVTAD ASDFSEDVAR TNNALVLGYK 180
HIQNEF 186

SEQ ID NO: 105      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 105
MQB1TVTVFEE NIRPSPVTPW NPEPRLPEIH PTAYIDPAAV VQGDVTIGEN VMISANASIR 60
SDEGYPIYG NNSNVQDNVW LHALETVDEN GKRIEENIVT VGDKEYAVVI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FASRVGKNCV LAPLAAAIVG TVPDGTYVPA GKVVTTQEEA 180
DKLPKMTPDH PFYKTNDAVV KVNVLAKGY LAQA 214

SEQ ID NO: 106      moltype = AA length = 266
FEATURE
source          Location/Qualifiers
1..266
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 106
MKAISLVFTC GYWRENDPHQ WHLTFPAAKG ERQSPIDIQP AKAKYDPGLK PLKLSYDPAT 60
ARRILNNNGH FSNEFEDSQD KAVLKGGPML GSYRLLQFHF HWGSTDDHGS EHTVTDGVKYA 120
SELHLVHWNA VKFSSFAEAA SKADLAGIV VFLKVGEPA EMKEKLLNALH AIKTKGKEAP 180
FTMFDPSCLL PTCLDYWTYS GSLTTTPLLC CVTWIVLKQP ISVSSEQMAK FRSLLLFTSEG 240
EKEKRMVDNF RPLQPLMNRT VRSSFR 266

SEQ ID NO: 107      moltype = AA length = 260
FEATURE
source          Location/Qualifiers
1..260
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 107
MTTRAVLNRR GALAALALLA VAGCAGSDPT AAAPHWDYDH EGPDHWADLG KQYATCRNGH 60
AQSPIDLDPD GEAHPTEID IVYRRIRTAT LTNNNGHAIQV GVPADSGNRI VVDGTSFTLT 120
QYHFHLPSEH TVAGABTAME LHLVHTDAHG RLAVLAVLLR AQEAPAPLSA ILAAAPDRVGV 180
ATRTTLSNIDP RAFLPDNRAQ FRYEGSLTP PCTEGVAWIV LREPSPVAVA DVDRYRRLFP 240
HSNRPTQPRN DRPVILAGTN 260

SEQ ID NO: 108      moltype = AA length = 239
FEATURE
source          Location/Qualifiers
1..239
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 108
MKIIISWLIF LLGACATDWS YSGRGSPQNW AEISESNKFC KIGYNQSPID INLSMNKDFI 60
LNDLKFDYKI SEIEKVNEKY YQKINFYSKS FVLRGKKKYW LKYIEFRHPS EHFLDSSPHS 120
LEMQIYHKSE DEQWLATSYF LEIPAMNNNE NLYFNNLIDF LKSKKIEDKF DLSKIIDETS 180
LSFFYEGSFT TPPCTEGVKW YIMKNPIFIS KEQMNTIJKS TIFVKSNARG IQKFNPEKF 239

SEQ ID NO: 109      moltype = AA length = 288
FEATURE
source          Location/Qualifiers
1..288
mol_type = protein

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note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 109

MQPSAFHKLL	LLLPLAYHRT	PNVGDDKDEH	WNYETNGKNW	GGICASGERQ	SPISLSVQKS	60
YIISIPRIVF	GNYDIKLGRP	LTIITNNGHTA	HMDIPETTNG	KKPFITEGML	NGRYVAESLH	120
FHWGSPGSRG	SEHAINKQRY	DVEMHVHRN	AKYKDMSEAV	GKKDGLAVIG	VMLKIVKNPK	180
LMFLGLHNVL	GAVSRITKTK	AKTYVPGSFS	LGQVLGIVNP	RSYFTYRGSL	TTPFCQEAVT	240
WTVFTQVLPV	SYTLVSKLWR	LRDSEGHLRI	NNFRDIQPTN	RRAVFYRP		288

SEQ ID NO: 110 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 110

MQEITVTKYE	NIQASPVTPW	NPEPKLPEIH	PTAYIHPAAV	VQGDVTIGAN	VLVMANAVIR	60
ADEGYPIVIG	DNSSVQDNVV	LHALETVDAD	GKVIEENVVT	VGDKKYAVVV	GDNVVLAHNA	120
QVHGPAAVGD	NTFVGGMNALV	FNSVVGKNCV	LAPLAAAIGV	TVPDGKYIPA	GKVTTQEEA	180
AKLPEVTPDH	PFYNLNVDRVV	AVNVALAAGY	LAQA			214

SEQ ID NO: 111 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 111

MQEITVTRFE	NIQPSPVTPW	NPEPKLPEID	ETAYVHPAAV	VQGDVKIGKN	VLIIMANAVIR	60
ADEGYPIVIG	DNSSVQDNVV	LHALETVDEN	GNVIEENVVT	VGDEKYAVVV	GDNVVIAHNA	120
QVHGPAAVGD	NTFVGGMNALV	FRSTVGKNCY	LAPNAAAIGV	TVPDGTYVPA	GTVVTTQEEA	180
AKLPKITPDH	PFANLNKRVV	KVNVALAKGY	LALS			214

SEQ ID NO: 112 moltype = AA length = 283
 FEATURE Location/Qualifiers
 source 1..283
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 112

MSYSRSVSTYL	LALSVLCFSV	FVVVPTGVCO	AINPPEKVPQ	GQHVHNGQHH	MLHMMLGEEK	60
CGPTYTYEEG	VKGPSHWPBV	CTTGKMQAPI	DIQSTQKLPI	NNLKFNQYPA	DLDILNDCNQ	120
YRVLVKEPDN	YWLMVGKKPV	NLAETHFRREP	GETAVNGKRP	KMSIEFLHFS	PEGVFLVIEV	180
PVAGKENPT	MQAILQNVPV	PGKEEKVAGV	KINPDTLLPQ	DRRSFYRYPG	SLTPDCTEV	240
VTWYVMKTP	EMSEAQIAEY	SKHYHDTARP	LQPVNGRPPV	EDQ		283

SEQ ID NO: 113 moltype = AA length = 252
 FEATURE Location/Qualifiers
 source 1..252
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 113

MTCTGKSTDY	WNYDNPSEWG	THFPAAAGLC	QSPIDIDSHK	TIRHVYPKFQ	FSKKYHSSEL	60
FKLINQTYQV	TATLADRTYG	QNDNDLWFTG	GGLEGTFYVV	NFHLLHWGRDD	RHGSEHEIDG	120
HQFPKAEGHVV	QPNRQTKQAA	VFAFLFTVAD	RFHKENKEWC	KYADAASQLT	NDEDSIQCLF	180
NLHDLMEHVNND	RLFYRYTGSL	TTPPCTEGIV	WTIFSQKIAI	KQESLQKLK	NILTkvYRPV	240
QPLNDRIVYK	NH					252

SEQ ID NO: 114 moltype = AA length = 234
 FEATURE Location/Qualifiers
 source 1..234
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 114

MKLSNQIRFY	GVATCPEWHD	YYPIADGDRQ	SPINIISSQA	RYDPSLRPLE	LKYDPSTSLE	60
ILMNNGHSFQV	TFADDSDSST	LKDGPISGVY	RLKQFHFWHG	AADDKGSEHT	VDGVKYPHEL	120
HIVHWNNAVKY	SSFAEAASKE	NGLAVIGVFL	KIGQHNNANLQ	KIVDALNAIK	TKGKQTTFTN	180
FDPSTLLPGC	LDYWTYDGSL	TTPPLESVT	WIVCKEPISV	SSEQMAKFRS	LLFS	234

SEQ ID NO: 115 moltype = AA length = 282
 FEATURE Location/Qualifiers
 source 1..282
 mol_type = protein
 note = Library of modified or engineered enzymes

-continued

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SEQUENCE: 115          organism = synthetic construct
MRIMTRGALT GVLWMLSLVVG LQAAEPGSIP WGYEGDLGPN HWGSLGSEFA LCEKGMSQSP 60
IDLVQTHKLA LTDIQFSYRD APFHVINTGH TLEELEPPLSE TVKSRYPKHG QTVLHFQKDS 120
TIVFDDDLYL LEQFHFHSPS EHTLHEKHYP MELHLVHHNE RHEAAVVAVF MKEGKHNPFF 180
ETFLDHAPKT VGEFVEDRER VINPVNLIPK NHHTYYRYFGS YTTPPCHEGV IWAVMHDPIE 240
VSREQVQRFR SLVGHDNARP TQPLHKRFVL ESNDVRAPGK LK 282

SEQ ID NO: 116          moltype = AA length = 232
FEATURE           Location/Qualifiers
source            1..232
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 116          moltype = AA length = 232
MSLKEWGYDA HNGPOTWCVR FIAAEKGROS PIDIQTKEVE SDLTLKPLKL NYEPASSLRI 60
LNNGHFSFQVE FDDSTDKSVL TGGPLTGTYR LRQFHFHWGS CDDHGSEHTV DGVKYASELH 120
LVHWNAYKES FAEAAKQPQDG LAVVGVFLKI GKENPKLQRV LDALNAIKTK GKQTTFTNFD 180
PSTLLPPCLD YTWTYHGSLTV PPLLESVTWI ILKEPISVSP SQMSKFRSLL FT 232

SEQ ID NO: 117          moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 117          moltype = AA length = 214
MQBKITVLNYS NIVKNEVTST NPKPEVPVID PTSYVDPNAT VIGDVTIGKN CYIAAFARIR 60
ADEGKPIVIG DRSNVQDGVV LHALESIDDT GEVNKDNNVI EGNELYAVYI GDNVSLAHQS 120
QVHGPARYGD DSFVGMNSLV FKSDVGDNCV IEPAAAIGV TVPDNKYIPA GTVVTTSQEEA 180
AKLPPEVTPDH AYYTTQEAVV EVNVALTEAY KGKM 214

SEQ ID NO: 118          moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 118          moltype = AA length = 214
MQEITVMDFS NITKNEITSW NPEPSTPKID PTSYIDPNAT VIGDVTIGKN CYIGPFAIR 60
ADEGAPIVIG DESNVQDGVV LHALESVDAG GKIREDNVVL HGDKLYAVYI GKNVSLAHQA 120
QVHGPAYGD DSFVGMNSLV FKSKVGSNCV IEPAAAIGV TVPDGKYIPA GTVVTTSQEEA 180
DKLPEVTPDH AEYTKNAAVV NVNVALCEGY KSLA 214

SEQ ID NO: 119          moltype = AA length = 265
FEATURE           Location/Qualifiers
source            1..265
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 119          moltype = AA length = 265
MRRKRVSRFN APQLRPMYHK LAIAAALFLA AAIPSFAADD CPVPWGYTVD NGPATWGRYS 60
AICASGLSQS PVKINNLLPS PATNLPTLSF QGGPSRFRVK NNQHDLLEVYP VNQWTLQPF 120
ARLTKFHFHV PAEHLDGNTR HDAAEHFVYE LGNRIFAIAV WIDQVNQGGN AALQKIAAVQ 180
RPGLCCLMSPY SLPAATLNIL DFLPDRNNYA AYHGSLLTPP CTENVTFFIM RTPITATATQ 240
INALTLVAPA PPGNARPVQQ TKWR 265

SEQ ID NO: 120          moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 120          moltype = AA length = 214
MQEITVTNYN NIRPSPVTPW NPEPKLPEIH PTAYIDPKAV VQGDVTIGKN VLVMANAVIR 60
ADEGYPPIVIG DNSSVQDNVV LHALETVDEN GNVLLEENVVE VGDCKRYAVYI GDNVVLAHNA 120
QVHGPAAVGD NTFVGMNALV FRSRIGKNCV LAPLAAAIGV EVPDGTYIPA GTVVTTSQEEA 180
AKLPKVTPDH PFANLNERVV KVNVLAQGY LALA 214

SEQ ID NO: 121          moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 121

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-continued

MQEITVLLFS	NIRKNEVTPT	NPKPTTPVID	PTSYIDPNAT	VIGDVTIGAN	CFVGPFIAIR	60
ADEGAPIVIG	DRSNVQDGVV	LHALESVDDG	GKVREDNVVV	HGDEWYAVVI	GRNVSLAHQS	120
QVHGPAGVD	DSFVGGMKSLV	FKSKVGSNCV	IEPGAAALGV	TVPDGKYIPA	GTVVTTQAEA	180
DTLPVTPDY	AFYTTQAAVV	SVNVNLCEAY	RAQA			214
 SEQ ID NO: 122		moltype = AA	length = 291			
FEATURE		Location/Qualifiers				
source		1..291				
		mol_type = protein				
		note = Library of modified or engineered enzymes				
		organism = synthetic construct				
SEQUENCE: 122						
MKRSLAFTI	GCQHNPEDWY	PFIEGDEFGY	SDSLQREWWM	CKSGRMQSPI	DISPENLLFD	60
PNLRSRQIDK	HKKVSAATLENL	GQLPLLTIND	SKIRPDSINI	SGGPASPQKY	RLHHIIIIHFG	120
RSIDEEKGSE	HTIDHIRFP	ELQLLAYNTD	LYSNFSEAMT	QPRGGLAISI	IVDIGKITNT	180
ELRKLTVASQ	SITYKGQKTI	LKRFNAYGLL	PETEDYIYTE	GSLTFPGCYE	TVTWVIMNNP	240
YIYTKEKDLHI	WNDLQQTEFK	QPNPVFMFPN	YRPLKPLNGR	LLRTNINIKY	K	291
 SEQ ID NO: 123		moltype = AA	length = 214			
FEATURE		Location/Qualifiers				
source		1..214				
		mol_type = protein				
		note = Library of modified or engineered enzymes				
		organism = synthetic construct				
SEQUENCE: 123						
MQEITVLEFS	NIKKNEVTSY	NPKPTTPVID	PTSYIDPNAT	VIGDVTIGKN	CYIGPFIAIR	60
ADEGAPIVIG	DNSNVQDGVV	LHALESVDDG	GKVREDNVVV	YGDKYYAVVI	GRNVSLAHQS	120
QVHGPAGVD	DSFVGGMNSLV	FNSIVGNNCV	IEPNAAAIGV	TVPDNKFIPIA	GTVVTSQAEA	180
DKLPEITPDH	AFYTDIAKVV	SVNVKLCKAY	LEKQ			214
 SEQ ID NO: 124		moltype = AA	length = 214			
FEATURE		Location/Qualifiers				
source		1..214				
		mol_type = protein				
		note = Library of modified or engineered enzymes				
		organism = synthetic construct				
SEQUENCE: 124						
MQEITVVLTYS	NVTKNEVTST	NPKPTTPVID	PSSYVDPNAT	VTGDTVIGKN	CLIGANAVIR	60
ADEGAPIVIG	DNSSVQDGVV	LHALESVDDG	GKVIEDNVVV	GDHNWYAVVV	GRNVVLAHNA	120
QVHGPAGVD	DSFVGGMNSLV	FKAIVGNSCN	IEPDAAAIGV	TVPDGKYIPA	GTVVTSQEEA	180
DKLPEITPDH	AKYTKVAEVI	AVNVALCKAH	REKA			214
 SEQ ID NO: 125		moltype = AA	length = 260			
FEATURE		Location/Qualifiers				
source		1..260				
		mol_type = protein				
		note = Library of modified or engineered enzymes				
		organism = synthetic construct				
SEQUENCE: 125						
MRKISFLVAG	CTPENWHDYQ	PVAGGERQSP	INIITKEAKY	DPSLKPLSFT	YDPSTSLEIL	60
NNGHSFOVTF	ADNSDSSTLT	GGPLTDKYRL	TQPHFHGWGST	DDHGSEHTVD	GVKYASELHL	120
VHWNAKYSS	FAEAASKPDG	LAVLGVFLKV	GEHNPSLQKL	TDALYSVRFK	GTKAQFTNFN	180
PKCLLPSSLD	WTYTSGSLTT	PPLLESVTWI	VLKEPISVSS	EQMEKFRSLL	FTSEGETACC	240
MVDNYRPLQP	LKGRKVRASF					260
 SEQ ID NO: 126		moltype = AA	length = 325			
FEATURE		Location/Qualifiers				
source		1..325				
		mol_type = protein				
		note = Library of modified or engineered enzymes				
		organism = synthetic construct				
SEQUENCE: 126						
MVFSIATFGL	LLLLGFCLGD	DFGYDGNHGP	SHWGEEYHTC	IGKHQSPINI	EEHNVKNVSL	60
PPPLKLIGIDD	EYQSFVTNNG	HTVMLKINES	KVIMLSGGPL	GNKVVYFEQL	HFHWGQNDFE	120
GSEDLINNH	PMEMHAVFY	KEDYKSMNEA	LNHSDGLAIL	AYLYEVSPNP	NVMYEPIVEV	180
LPDIETVGSE	KVLREPLMLK	KLFISDITMM	QDYFTYNGSL	TPPPCLEVAI	WIDFKDHRL	240
SHEQIAAFRN	LRSTEGDKLT	HNFRPVQSLE	DRIVLHNIPR	EQNIPRNIPP	KTYHRFDEHS	300
GQHNVEMPLS	IIALAVLFAV	ILFAI				325
 SEQ ID NO: 127		moltype = AA	length = 210			
FEATURE		Location/Qualifiers				
source		1..210				
		mol_type = protein				
		note = Library of modified or engineered enzymes				
		organism = synthetic construct				
SEQUENCE: 127						

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MTLFSKIREN VYGHAPQCDW CYEGEGAPES WGRLRPEFAT CAVGRRQSPI DIRDGIAVDL	60
EPIRFDRYPT SFRIVDTGNT IQVNVPAGNT IEVMGRRYEL VQFHFRPSE ERIDGRQFDM	120
VAHLVHKDGE GRLAVVAVLL ERGDDQPLVR TVWNNLPLEK GDEVAARTPI DLNALLPEDR	180
RYTYTGYMSLT TPPCSEGVLW MVMKQPVQLS	210
SEQ ID NO: 128	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 128	
MQEITVTYTN NIRPSPVTPW NPEPKLPKH PTAYVDPAAV VQGDVTIGKN VMISALASIR	60
SDEGYPIYIG DNSNVQDNVV LHALETVDEN GNVIENVVT VGDKKYAVYY GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSRVGKDCV LEPLAAAIGV TVPDGTYVPA GKVVTTQEEA	180
DKLKPVTPDH PFYKTNEAVV KVNVLAKG Y LALS	214
SEQ ID NO: 129	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 129	
MQEITVLEFS NITKNEVTPW NPKPKTPVID PTSYIDPDAT VIGDVTIGAN CYIGASAVIR	60
ADEGKPIVIG DNSNVQDGVV LHALESINDE GKVIDENVVI HGNKRYAVYY GKNVSLAHQS	120
QVHGPAAVGD DSFVGMQSLV FNSKVGGSNCV IEPNAAAIGV TIPDGTYIPA GTVVTSQAEA	180
DKLPEITPDY AKSNAVAAVV NVNVGLCEAY REEA	214
SEQ ID NO: 130	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 130	
MQEITVGEFS NVTKNEVTTT NPKPETPVID PSSYVDPSSST VIGDVTIGKN CYIAANAVIR	60
ADEGAPIVIG DNSNVQDGVV LHALESVNDG GKLREDNVUL EGDEYYAVYY GKNVHLAHQA	120
QVHGPAAVGD DSFVGMKSLV FNSIVGSNCV IEPNAAAAGV VVPDGKFIPIA GTVVTTQEEA	180
DNLPDITPDH AAYTTQAAVV KVNVLAKG Y KAEA	214
SEQ ID NO: 131	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 131	
MQEITVTKFE NIRPSPVTPW NPTPKLPKH PTAYIDPAAV VQGDVTIGEN VMVSANASIR	60
SDEGYPIYIG NNNSNVQDNVV LHALETVDEN GKRIEENIVR VGDKDYAVYY GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSRVGKNCV LEPLAAAALGV EVPDGTYIPA GEVVTTQEEA	180
AKLPKITPDH PFANTNAAVV KVNVLAKG Y LALS	214
SEQ ID NO: 132	moltype = AA length = 277
FEATURE	Location/Qualifiers
source	1..277
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 132	
MRARAVITGGI HGRIRSTLGA ALLAPLFLAA GCGGEGGGGT GEESGLAETH LAAWSHAGAD	60
GPDEWASLDP AYATCGTGER QSPIDIVGAK RRPFPVVELD YAPVRATLID NGHAIIEAEL	120
DSGSSARIGG DEFTLEQFHF HMPAAEVVGG KSFASIIHLV HLDEDGGAAC VGLLVEPGPE	180
NVPIERLAAE VPEETDEPVE VEGELDLAGL VPDPGDAFRYE GSLTTPPCTE GITWTFEDP	240
VTMSPEQLEA FAGAYDANAR PVQARNGREI SVGPGGLG	277
SEQ ID NO: 133	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 133	
MQEITVTVFE NIRPSPVTPW NPTPRREIH PTAYVDPLAT VVGDVRIGAN VMVSANASIR	60
SDEGYPIVIG DNSNVQDNVV LHALETVDAA GRRLEENVVE VGDELYAVYY GANVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSRVGANCV LEPLAAAIGV TIPDGTYIPA GKVVTTQEEA	180

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AKLPKITPDH PFANTNAAVV AVNVALAAGY RALA	214
SEQ ID NO: 134	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 134	
MQEITVLTFS NVTKNVTAT NPKPVTPTVID PTSYVDPNAT VTGDTIGKN CLIEANATIR	60
ADEGHPIVIG DRSSVQDGVV LHALESVDDG GELIEDNVVL EGDEEYAVVI GKNVHLAHQS	120
QVHGPARKGD DSFVGGMKSTV FKSIVGGSNCV IEPDAAAIGV TVPDGKYIPA GTVVTTSQEEA	180
DKLPEITPDH AKYTANAAVV TVNVALCEAY RNEA	214
SEQ ID NO: 135	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 135	
MQEITVLEFS NITKNEVTWP NPKPKTPEID PTSYIDPQAT VIGDVTIGKN CYIGPFAIR	60
ADEGAPIVIG DDSNVQDGVV LHALESINEK GEIIEDNVVI KGNKRYAVVI GKDVSLAHQS	120
QVHGPARKGD HSFVGMNSLV FNSIVGDSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTSQEEA	180
DKLPEITPDH AYYTKNAAVV NVNVALCRAY KSKE	214
SEQ ID NO: 136	moltype = AA length = 230
FEATURE	Location/Qualifiers
source	1..230
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 136	
MSТИPWRLGA VFCNYQKHED AVEEKEFSYD EGSERGPSRW GEIRPEWRTC GNDEMOSPID	60
LINQRVEIVS KLGKLKRDKYK PSNATLKNRG HDISLEWKGG AGSIEINGTE YVLOQCHWHS	120
PSEHTINGRR PDMELHMVHE SRDGKVAVVG IVYKLGRPDS FLSSLMMDHLE AISDTKDRER	180
AVGVIDPRHI KFGSRKYYRY MGSLTVPPCT ENVIWTIVKR VRTVSREQLK	230
SEQ ID NO: 137	moltype = AA length = 243
FEATURE	Location/Qualifiers
source	1..243
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 137	
MYGVVLVLIL SFIQFTYAQN KKDWDGYKDSG APQYWANINP LYLGCTEGNQ QSPINIITKN	60
VNKGAAHFEL KYSVAKGVNL ILSHNTFKMV YPGNFLEMGN GNRYQLKEIY FKTPGENAID	120
SIRGMLEAQI LHEDSKGNKV ILAVFFIEGR SNPIIDMLVK NLPTQPDKAN FIANVDVHQL	180
LPSDLASYQF DGSLTMPPCS QGVRWIVLKQ TMTITQSQVD SMRDITGVNS RPTQEIFNRL	240
IVK	243
SEQ ID NO: 138	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 138	
MQEITVLFIS NIRKNEVTPT NPKPVIPVID PTSYVDPNAT VIGDVTIGKN CYIAHSAVIR	60
ADEGKPIVIG DRSSVQDGVV LHALESVNDG GKIREDNVVI EGDEEYAVVI GKDVSLAHQS	120
QVHGPARKGD HSFVGMNSLV FNSIVGGSNCV IEPDAAAIGV TVPDGKYIPA GTVVTTSQEEA	180
DKLPEITPDH AKYTAIAAVV NVNVALCQAY KEKS	214
SEQ ID NO: 139	moltype = AA length = 285
FEATURE	Location/Qualifiers
source	1..285
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 139	
MKRTFLIAVS LCPGLIQYNH WDEWWTYEGI SGPAYWGLIN PAWSLCNKGR RQSPVDidPE	60
KLLFDPNLKS LHLDKHKVSG TLENTGQSLV FRVDKDTKH VNISGGPLAY KYQFQEYIFH	120
WGVHDGLGSE HTINHQSFPA ELQLYGFNSE LYSNMSEAOE KPHGVVGISL LVQICKTPNP	180
ELKILTSQLE NIRYKGQSAP IKNFSLRGLL PNTEHYVTYE GSTTHPGCWE TTVWWVVLNKP	240
YYITKQELYA LRRLMQGSKE HPKAPLGNNA RPTQDLHHRT VRTNI	285

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SEQ ID NO: 140      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 140
MQEITVTRYE NIRESPVTPW NPTPRRPEIH PTAYVDPAAV VVGDVTIGEN VMISANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDAA GKRITENIVT VGDKEYAVVI GKNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSRVGKNCV LEPLAAAIGV TVPDGTYIPA GKVTTQEEA 180
AKLPKITPDH PFAKTNAAVV AVNVALAAGY RALA 214

SEQ ID NO: 141      moltype = AA length = 268
FEATURE
source
1..268
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 141
MKLTSIAVFC GYPEQNDRHW GYQDHNGPEM WKEKFPSAGG KKQSPIDIQT AETTFDPKLK 60
PLELKYDPST AKEILNNNGHS FQVTFVDDTD SSTLKDGPIS GIYRLKQFHF HWGASDDHGS 120
EHTVDGVKYA AELHLVHWNA KYKGKGEAAS QPGLAVVGI FLKIGRHHEE FQKLDDALDS 180
IKTKGKQTTF TNFDPSTLLP GCLDYWTYFG SLTTPPLLES VIWIVLKEPI SVSSEQLAKF 240
RSLLFTSEGE KEKRMVNDNR PLQPLMNR 268

SEQ ID NO: 142      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 142
MQEITVAEFS NVTKNEVTPY NPKPVTPVID PTAYVDPPEAT VIGDVTIGKD CMISANASIR 60
SDEGHPIVIG DRSNVQDGVV LHALESVNND GEVIEDNVVV EGNELYAVVV GKNVSLAHQA 120
QVHGPAAVGD DSFIGMQSFV FNSIVGSNCV IEPEAAAIGV IVPDNKYIPA GTVVTQEEA 180
DKLPEITPDY AYYTTVAAVV NVNVALCKAY RRLM 214

SEQ ID NO: 143      moltype = AA length = 278
FEATURE
source
1..278
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 143
MPAPAPKAAP KAGHGAKKAA PAPKAAPKAA PKAAPRAKVV KAAPAPPPP PAHAHWSYEG 60
EGAPARWQGL KPEWKQCAVG TRQSPIDIRD GIKVLDLPIQ FDYKASGFV IDNGHTVQVN 120
LAPGNFITVLR GRYYELVQFH FHKGPEERIN GKPYDMVAHL VHKAEGRLA VVAVLLRPGE 180
ANPLIEKVWT YMLDAGDRV RMPTELIDLQ QLLPADRAYF TYMGSLTTPP CSEGVLWMVM 240
KQPVPVSADQ IAIFARLYPM NARPLQAVSG KIIKETLM 278

SEQ ID NO: 144      moltype = AA length = 264
FEATURE
source
1..264
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 144
MNRKKLNSLI AAVIVFFATS AFSESPHDH AEQSTWWAIE DTTQTYPPKR FPFAVCVGQ 60
HQSPIDLAALAA EVIDTIQINP LEILYDWDHA PVFFNSGHGI QVNTSIEYSG KLKVGEELFP 120
LIQFHFHAPG EHVGIDTKFP AELHYVHIQA DGKIAVLAVA INIGDENSAF QTILENVPSV 180
SGGKNENNSGL QFDPAALLPP LDHPIKYYTV AGSLTTPPCS EGVQWYFLPT AITISEAQLN 240
QLRSLYADNN RLPQDVNGRS LLTQ 264

SEQ ID NO: 145      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 145
MQEITVTRYE NIRESPVTPW NPTPRRPIKH PTAYVDPAAV VVGDVTIGAN VMVSANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDA D GKTLEENVVT VGDKEYAVVV GDNVSLAHQA 120
QVHGPAAVGN NTFIGMQAFV FRSTVGENCV LEPLAAAIGV TVPNGKYIPA GKVTTQEEA 180
DKLPEVTPDH PFANTNAAVV KVNVVALAAGY RALA 214

SEQ ID NO: 146      moltype = AA length = 214

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FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 146	
MQEITVDEFS NITKNEVTGT NPEPSTPVID PTAYVDPNAT VIGDVTIGAN VLVAANAVIR	60
ADEGRPIIVVG DRSSVQDGVV LHALESVDE GEVREDNVLL VGDENYAVVV GKNVSLAHQA	120
QVHGPAAVGD DSFVGMKANV FRSTVGSNCV IEPDAAAIGV TVPDGKYIPA GTVVTTOQAEA	180
DKLPDVTPDH AKSNDVAAVV AVNVALCEAY REQS	214
SEQ ID NO: 147	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 147	
MQEITVLLFS NITKNEVTPI NPKPTTPVID PTSYIDPNAT VTGDTIGKN CMISANASIR	60
SDEGKPIIVG DRSNVQDGVV LHALESVDD GMIIGDNVVV EGDEYYAVVV GDNVSLAHQA	120
QVHGPAYVGD DSFIGMOSFV FKSIVGSNCV IEPEAAAIGV TVPDGKYIPA GTVVTTOQEEA	180
DKLPEITEDD ADYTTNVAVV NVNVALCKAY REKA	214
SEQ ID NO: 148	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 148	
MQEITVTRFE NIRPSPVTPW NPEPKRPVIH PTAYVHPAAV VEGDVTIGEN VMVSANASIR	60
SDEGYPIYIG DNSNVQDNVV LHALETVDEN GKYLEENVVT VGDKKYAVVV GKNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSTVGDCKV LEPLAAAIGV TVPDGKYIPA GKVVTTOQEEA	180
AKLPKITPDH PFANTNAAVV KVNVLAKGY LALA	214
SEQ ID NO: 149	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 149	
MQEITVAVFS NVTKNEVTGT NPKPTTPVID PTSYVDPNAT VIGDVTIGAN CYIAHSAVIR	60
ADEGRPIHVG DRSSVQDGVV LHALESVDAD GERLEDNVVI EGDKRYAVVI GKNVSLAHQA	120
QVHGPARVGD DSFIGMOSFV FNSVVGGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTOQAEA	180
DKLPEVTPDH AAYTEIAKVV TVNVNLCRAY REQA	214
SEQ ID NO: 150	moltype = AA length = 274
FEATURE	Location/Qualifiers
source	1..274
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 150	
MYPIIHIKEG KYKMNYFFLF TILSSLTLSA CSNSKIVQEV HPNKSIVSAA RNEDWSYTGK	60
TGPNEYWSIN KYALCSTGK QQSPVNIDQA IKKSLPLGIN YHNDLFKIER SQYTVKFIPV	120
NHSNSNSINLNG TNYTLLQFH HTPSEHTLNG KQSDLEIHIFI NENSNSKSIIT IGVLVDRGRL	180
NKEFQKILNA NPMDEDLEGK VVKINLQSF1 PYTSKKFSYT GSFTTPPCTE GIKWIIFNKP	240
IQFSEEQIHS YQNYFEPNSR PVQPLNGRDL FESW	274
SEQ ID NO: 151	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 151	
MQEITVVFIS NVEKNEVTST NPKPTTPVID PTSYVDPNAT VTGDTIGAN VMISASASIR	60
SDEGKPIIVG DRSSVQDGVV LHALESVDE GEVIEDNVVI HGDKNYAVVV GKNVSLAHQA	120
QVHGPARVGD DSFIGMOSFV FKSDVGSNCV IEPFAAAAIGV TVPDGKYIPA GTVVTTOQEEA	180
DKLPEVTDY AYSDTNEAVV KVNVNLCEAY KGKA	214
SEQ ID NO: 152	moltype = AA length = 177
FEATURE	Location/Qualifiers
source	1..177
	mol_type = protein

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note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 152
 MNPTGHMPVV SETAFIDPTA IICGKVIIED NVFIGPYAVI RADEVNEQGD MEAIVIKRDT 60
 NIQDGVVIHS KAGAAVTIGE RSSIAHRSII HGPCQVCDDV FIGFNSVVFN AVIGKGCVIR 120
 HNSVVDGLDL PENFHVPPMT NIGADFDLNS ISKVPPEYSS FSESVVSANH TLVKGYK 177

SEQ ID NO: 153 moltype = AA length = 281
 FEATURE Location/Qualifiers
 source 1..281
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 153
 MLSRKPGAVT FCIWNHQEYD VKMASWGYTK ENGPATWYKD FPVANGPRQS PINIDPGSAK 60
 YDPGLKALTL KYDPSTSLEI LNNNGHSFOVT FADDSDSSTL TDGPISGVYR LKQFHFHWGA 120
 SDDKGSEHTV DGVKYAAELH LVHNNAVKYS SFGEAASKEK GLAVLGVLK VGEHNANLQK 180
 VLDALDSIKT KGKQAPFTNF DPSTLLPASL DYWTYHGSLT TPPLLESVTW IVLKEPISVS 240
 PAQMAKFRSL LFSSEGEKEK RMVDNFRPLQ PLMNRTVRSS F 281

SEQ ID NO: 154 moltype = AA length = 249
 FEATURE Location/Qualifiers
 source 1..249
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 154
 MKKGLVLICL SLSLLGAFGG EHWGYSKGVG PRYWGKLRSR YEICKSGKTQ SPINIQHYYH 60
 SPDKEDLSFE YENTKPLSIA YSHYTLVAQF NEPGNAVIFR DHEYSLVNLH FHIPMFAIH 120
 GKKQPLSMHL VRDKEGDLL VVGIGFSIGK KNPFFTPILN AYKYHTEPKL LALKTLLPDT 180
 IHYYHFNGSL TPPCSEGVT WFIIETLSI SKEQFDEMQQ IMHHQSNQRP LQKDYNRVIV 240
 KSSAIVREH 249

SEQ ID NO: 155 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 155
 MQEITVDEFS NVTKNEVTAT NPKPTTPVID PTSYVDPEAT VTGDTVIGKN CLIAANAKIR 60
 ADEGKPIVIG DRSSVQDGVV LHALESVDDG GKVIDEDNVVL EGNELYAVVV GENVVLAHNS 120
 QVHGPARVGD DSFVGMSLKV FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTTQEEA 180
 AKLPVEVTEDY PFYTKQAEVV KVNVGLCEAY RNKA 214

SEQ ID NO: 156 moltype = AA length = 237
 FEATURE Location/Qualifiers
 source 1..237
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 156
 MIGVKPKSYA AQNKKKKWSY DGDNGPQNWG DLSADYLSCE VGLNQSPVDF SKSFSSPDHL 60
 SIRFNYGISA GRVYLARGSI TFKVIPGNVA YFKGKQWVLE RVVLRTPSEH SIEGHSDGE 120
 LQLYHSYKGE SFLWVSVLLE AGSALKPFRQ IVDKAKGISING ASKLMGVDLR LLIPRRKNYY 180
 FYPGSDTIPP CKEGRSWVVL RQPVGASIKY IEHLESQVGK GARPTQPLYA RVPLRYD 237

SEQ ID NO: 157 moltype = AA length = 343
 FEATURE Location/Qualifiers
 source 1..343
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 157
 MKGLCVMAIV ALIGLQTATG YTRQDLS CGG RMDYSKPVCH NIPKHAHKKC DVYNQWSHHL 60
 FGTSQKCGWK LNPACRGMHQ SPININEHKV EPNHNYGDLC ITGPHHLKVH IHNTGHDLQA 120
 KLDEESSSRAT LVTGGPLGNK KYRVLQFHFH FASHPGKGSS EHSINCHFSD IEMHIVLQNV 180
 AYGSFDVAKD HRDGLSIAV MLSEDVRPNT VSNAMERNPNPS WSQYYINTLI YYASLRKHCD 240
 LHENVGNTRF SLFHLLPSDY ARNYYAYGGS LTTPPCSESV SWIIMRTRFH INRYHLLNK 300
 DVSLLSRYHR GFEPMSQNKR NLQLLNNRKV YYPAGHGRCP SRG 343

SEQ ID NO: 158 moltype = AA length = 268
 FEATURE Location/Qualifiers
 source 1..268
 mol_type = protein
 note = Library of modified or engineered enzymes

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organism = synthetic construct
SEQUENCE: 158
MRLKSNIFVA GTCQPEDYHW GYEDHNGPAT WAKHFPAAKG EKQSPIDIQL SNVKNVSFPP 60
LVEPNYKDSTL KEIINVGHSV QVNLEDSDNR SVLKGGPLSG PYRLKQFHFB WGKTNDVGSE 120
HTIDGKSFPS ELHLVHWNAK KYASFGEAAS KPDGLAVGVF FLEIGDEHPE MNRLTDALYM 180
VRFKGTAQF SCFNPKCLLP ASRHYWTVPG SLTTPPLSEN VTWIVLREPI SISERQMEKF 240
RSLLFTSEGE KEKRMVDNFR PLQPLMNR 268

SEQ ID NO: 159      moltype = AA length = 348
FEATURE           Location/Qualifiers
source            1..348
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 159
MKFLTPSIFF TSLRVASAAT GVKFYYNDQS QWPAPVATPE GTNVCDGQQQ SPINIDTGDF 60
SCQADAQGYS FYTGDCTLGD YEFTMNDHGL KASVEKSNC E KPKMIIPIGTG KVYEVLFQHFI 120
HTGCENKEPNN TGCDABLHLV HIAKTDIALP AATTSDLPLD LAVLGLMMYG VDEKHASVDA 180
LIDSWEVSC SNQKCMVSD ELKSQKFSFY SLIPSDTSIY NFQGSLSLTPP CWEVVTWNVA 240
EPIKIKMSFKQ VLAITNLINK YSGYRAEDGS CVADSTVADD AGITSRDVQS LNGRQIVKNC 300
EPLTVMSDFP AAAQEQQSPMT ASSESSAQFL NIKNIFGVVS VLASIVLF 348

SEQ ID NO: 160      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 160
MQBKITVTRYE NIRPSPVTPW NPEPKLPKIH PTAYVDPAAV VQGDVTIGEN VMVSANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETPDED GKVLLEENVTT VGDKKYAVVV GKNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVVGKDCV LEPLAAAIGV TVPDGTYIPA GKVTTQEEA 180
AKLPKTPDH PFANTNAAVV KVNVVALAKGY LALA 214

SEQ ID NO: 161      moltype = AA length = 316
FEATURE           Location/Qualifiers
source            1..316
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 161
MIVLIIPLLF IVQSOOTTNTT NTNTTTTATTI SYASQGSDWT SGVCSSSTSQ SPINLEVSSG 60
TCDDNSMVLDI QFKKDAMQIV MERVQYTIQS KAAVSNLYYT DINGNLYGTT ATSFMFHSPS 120
EHTIEGTRYD LEMQIVHDLK SEFSATITKA IVSILFEVSS TDQPFPTTYD FALVASASTN 180
TTTTNTTNST NTTTAASVTS TIASINFNDL LGSQLDANPA YYTYVGSLLTI PDCDENVNWY 240
ILDSILPITQ TQLDAFNTYF LSNSTFASGN GNNRAIQSTN DRTIKGGVA CEEQFVYFFS 300
FFILYIIFINY PIFKLL 316

SEQ ID NO: 162      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 162
MQEITVLEFS NITKNEVTAT NPKPVTVPVID PTSYVDPQAT VIGDVTIGKN CYIAASAVIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVNDG GKIREDNVV HGDEYYAVVI GKNVVLAHQA 120
QVHGPAAVGD DSFVGMKSLV FKSIVGSNCV IEPDAAAIGV TVPDNKYIPA GTVVTTOQEEA 180
DNLPEITPDY AYYNDVAAVV KVNVDLCKAY REKA 214

SEQ ID NO: 163      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 163
MQEITVLEFS NVTKNEVTST NPKPVTVPVID PTSYVDPNAT VIGDVTIGKN CYIAASAVIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GKIREDNVVL EGDEYYAVVI GKNVVLAHQA 120
QVHGPAAVGD DSFVGMKSLV FNSIVGSNCV IEPEAAAIGV TVPDGKYIPA GTVVTTOQEEA 180
DNLPEITPDY AKSNAIAAVV KVNVALCEAY RNQS 214

SEQ ID NO: 164      moltype = AA length = 186
FEATURE           Location/Qualifiers
source            1..186
mol_type = protein

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note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 164
 MLIKTNPRGDW PQVHASAFIE PTAILCGYVI VEENVFIGPY AVIRADETDA DGRIAPIVIG 60
 AHSNIQDGVV IHSKSGASVT IGRHTSIAHR AIVHGPCKVG DGVFIGFNSV LFNCTIDDGC 120
 VVRYNAVVDG CHLPPGFYVR STERIGPETD LAALPQVTAD ASDFSEDVAR TNNALVLGYK 180
 HIQNEF 186

SEQ ID NO: 165 moltype = AA length = 240
 FEATURE Location/Qualifiers
 source 1..240
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 165
 MKRNFLAIST VCGYDPEQWH MDYPIANGNR QSPINIIITKD AKYDPNLKPL TLSYDPATAK 60
 EIVNVGHFSN VEFEDTDNKS VLKGGLPTGS YRLTQFHFWH GSVDGQGSEH TVDNVKYASE 120
 LHLLVHWNSVK FSSFABAALK DNGLAVLGF LVKGEEHNPIL QKITDILNSI KTKGQTTFT 180
 NFDPSCLLPA SLDDWTYHGS LTVPPPLESV TWIVLKEPIVS VSSEQLAKFR SLLFTSEGTT 240

SEQ ID NO: 166 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 166
 MQBKITVTRYE NIRPSPVTPW NPTPKLPKID PTAYVDPLAY VQGDVTIGKN VMISAHASIR 60
 SDEGYPIVIG DNSNVQDNVV LHALETV DAN GNPLEANIVK VGDKDYAVYYI GDNVSLAHQA 120
 QVHGPAAVGD NTFIGMQAFV FNSRVGKDCV LAPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
 AKLPKMTPDH PFYNTNAAVV KVNVLA KGY LALA 214

SEQ ID NO: 167 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 167
 MQEITVLVFS NIRKNEVTPE NPEPVTPVID PTSYIDPKAT VIGDVTIGKN CYIGASAVIR 60
 GDEGYPIVVG DESNVQDGVV LHALESVDEQ GKVIEDNVVR KGDKLYAVYYI GKNVVLAHQA 120
 QVHGPAAVGD DSFVGMSLV FKSRVGSNCV IEPYAAAIGV TVPDGKYIPA GTVVTTQEEA 180
 DKLPEVTDY KFYTQVA VVV TVNVKLCEAY REQM 214

SEQ ID NO: 168 moltype = AA length = 310
 FEATURE Location/Qualifiers
 source 1..310
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 168
 MGSSLILLPR VQTSRNGMKL FGILLSFGSV LGALAGNSWN YAGHGEYWPT SHAKSSTGAE 60
 SYWDCDGIRQ SPIDINSSMV QDVYFWNQLN LANYAASYAG KFKNNNGHTLQ FDLDAAETSG 120
 ATLPTFSSPF MCTGCSYELQ QFHFHWGSTA YQGSEHTKEG IAFTPMLHLV HKKTSYSSVT 180
 ASLSYNDGLA VIGIMPQLAD TSDAGLTEII NAAVAIKNAA DQHTHKEAKS IDMSTFLYQT 240
 GRSYYYYYKGS LTTPPCTETV DWHLMEGAIR ITEADLEKLR DLTYTDDAPL VDNYRLPMPL 300
 NNRIIKRVPN 310

SEQ ID NO: 169 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 169
 MQBKITVTRYN NIQPSPVTSW NPTPKLPDIH PTAYIHPKAV VQGDVTIGKD VMISANASIR 60
 SDEGYPIVIG DNSNVQDNVV LHALETV DAN GRNRIEENIVT VGDEEYAVYYI GKDVSLAHQA 120
 QVHGPAAVGD NTFIGMQSFV FRSRVGKDCV LEPLAAAIGV TVPDGTYVPA GKVVTTQEEA 180
 AKLPKITPDH PFANTNAAVV KVNVLA KGY LALA 214

SEQ ID NO: 170 moltype = AA length = 340
 FEATURE Location/Qualifiers
 source 1..340
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

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SEQUENCE: 170
MGLLDSKWF VTQVLAAPVPL VYSGPYPRRT SSYYDPNGFF QFADKTHHRF YNFYQHVTEA 60
ARAEKLISNN EVWPSDKSIS QMASGSFSYR EEDDYGPSNW GALNATCEGM YQSPINLIAN 120
RSVIVQQKRA LELKGSRNVP MAMVENEGB AAAFFPEPRT NEQPRLRGGP LRGEYLFYQF 180
HYHLGSEHTF DKKRYSAEMH LVFVNELYGS FKAARDQANG VAVIALTFDV LKSRRINSLN 240
KWTRSLAEVV EAESSEYSIPR QELFSVSDVL GDMEWPYPAY EGSLTTPPCS ETVQWIVASE 300
RQLLTRSELK TMRMLKGRGG DWVQTARPQ ALNFRRRVFIY 340

SEQ ID NO: 171 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 171
MQEITVLEFS NVTKNEVTPW NPKPKTPVID PTSYIDPQAT VIGDVTIGKN CYIAASAVIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GEIREENVVI EGDEEYAVYI GKNVSLAHQA 120
QVHGPARVGD DSFVGMSLKV FNSDVGGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTQEEA 180
AKLPEVTDY PFYTAIQEVV KVNVKLCEAY REQK 214

SEQ ID NO: 172 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 172
MQEITVFEFS NVRKNEVTAW NPKPSVPVID PTAYIDPNAT VIGDVTIGKD CYIAASAVIR 60
ADEGSPPIFG DRSNVQDGVV LHALESVNPD GMYREENVVL KGNNLHYAVVV GRNVSLAHQA 120
QVHGPAAVGD DSFVGMSLKV FNSDVGGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTQEEA 180
DKLPEITPDY AFYTQVAAVV QVNVELCRAY RGKA 214

SEQ ID NO: 173 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 173
MQEITVTRYE NIRPSPVTPW NPTPRLPKIH PTAYVDPLAY VQGDVTIGDN VMISPHASIR 60
SDEGYPIVIG NNSNVQDNVV LHALETVDAD GNEIEENIVT VGDEEYAVYI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FKSRVGKNCV LEPLAAAIGV TVPDGKYIPA GKVVTTQEEA 180
DKLPKVTPDH PFYNTNAAVV KVNVVALAKGY LALK 214

SEQ ID NO: 174 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 174
MQEITVTRYE NIQPSPVTPW NPEPKLPEID PTAYIHPAAV VQGDVTIGKN VMVSALASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDAD GKRLENIVT VGDEEYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSTVGKNCV LEPLAAAIGV TVPDGKYVPA GKVVTTQEEA 180
AKLPEVTPDH PFANTNAAVV KVNVVALAKGY LALA 214

SEQ ID NO: 175 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 175
MQEITVTVFE NIRESPVTPW NPTPRRPKIH PTAYVDPQAV VQGDVTIGAN VMISANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDEN GKTLEENVVT VGDKKYAVYI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSTVGKNCV LEPLAAAIGV TIPDGKYIPA GTVVTQEEA 180
DKLPEVTPDH PFANTNAAVV KVNVVALAKGY LAQA 214

SEQ ID NO: 176 moltype = AA length = 346
FEATURE Location/Qualifiers
source 1..346
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 176
MGSCQVHAGG SRHFSFVLTF GRAYNGVVML VPTSYLLLLL VTLLTPTFCA DWSYKLGDQS 60

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GPDHWEYECK KEYQSPVNIP KGETTSTVFP ALSFWNYELQ PATATIENNG HTVKLATEPH 120	
RPKETPLLSG CGLLHHSYKFA QIHFPWGAED FKGSEHLVGD TQYPMEMHLV HYKAVHDTIK 180	
DALAEAGAYDS LAVIGIFFEV SEQRNPALDL LMPYLAKIKA AHSEAAATPF PISSFLWGKD 240	
MSSFYRYNGS LTTPTCNEIV QWSVMKVPVP VTVDQLEVFR QLMTKDYEPL VDNFRPPQAL 300	
GGRDVLDVMT VEMLRKGSHS GCEILAGPAA LLASLILICL CRTWDL 346	
 SEQ ID NO: 177 moltype = AA length = 214	
FEATURE Location/Qualifiers	
source 1..214	
mol_type = protein	
note = Library of modified or engineered enzymes	
organism = synthetic construct	
 SEQUENCE: 177	
MQBITVTVYN NIRPSPVTPW NPEPRLPKIH PSAYIDPAAV VQGDVTIGEN VMVSPNASIR 60	
SDEGYPIYIG NNSNVQDNVV LHALETVDEN GKEIEENIVT VGDKKYAVAV GDNVSLAHQA 120	
QVHGPAIVGD NTFIGMQAFV FRSKVGKNCV LEPLAAAIGV TVPDGTYIPA GTVVITQEEA 180	
AKLPKVTPDH PFANTNAAVV KVNVLAKG Y LALK 214	
 SEQ ID NO: 178 moltype = AA length = 264	
FEATURE Location/Qualifiers	
source 1..264	
mol_type = protein	
note = Library of modified or engineered enzymes	
organism = synthetic construct	
 SEQUENCE: 178	
MLTUVKAIRE NPGCDWQYHF NPDKISLIGRQ QHQSPIDIHT KDALFDPSLK PLSVSYDPAT 60	
ARLVNNNHTI QVEFEDSTDK SVVEGGPLEG PYRLKQFHFB WGKKDGVGSE HTVDGKSFPS 120	
EILHLVHWNAE KYASFGEAAA APDGLAVLGV FLQVGEHHPS MNRLTDALYM VRFKGTKAQF 180	
SCFNPKCLLP ASRHWTYPG SLTTPPLSES VTWIVLREPI SVSERQMEKF RSLLFTSEGE 240	
KEKRMVDNFR PLQPLMNRTV RSSF 264	
 SEQ ID NO: 179 moltype = AA length = 195	
FEATURE Location/Qualifiers	
source 1..195	
mol_type = protein	
note = Library of modified or engineered enzymes	
organism = synthetic construct	
 SEQUENCE: 179	
MSEKGPAYWG EIKEEWAACS NGTMQSPIDL LNERVEVVPG LGELKRNYKP SNATLKNRGH 60	
DIALEWNGEA GSILINGTPY FLKQCHWHP SEHSINGRYY DMELHLVHQZ PENKIAVIGI 120	
LYB1GPPDTF LSSLMDHIKA VTDTEAERS VGVINPREIK RGSRKYYRYI GSLTVPPCTE 180	
SVIWTVLAEI KKKIN 195	
 SEQ ID NO: 180 moltype = AA length = 290	
FEATURE Location/Qualifiers	
source 1..290	
mol_type = protein	
note = Library of modified or engineered enzymes	
organism = synthetic construct	
 SEQUENCE: 180	
MLMRSFLIPT IVLSSLILVSS NFIAEQDGAD FDYNERGPEH WSQLDAKYKL CKDGERQSPI 60	
NFITSIDLAI KLPNVNFIKQ NTPNVKFPTI SMKKEGHATK FLPQQLIGSS FDSVRYIFNQ 120	
VHFPHTPSEHR FDGIHTDLEA HFVFFEDSVTK KYSVIGVLYE VDCAVGSSSF FDSIIKLYNQ 180	
DPNAKDNVPV DINSEVFISHI KEVYKYFGSL TTPNCTEDVTW WVVVNKPILLI STSQLVQLRK 240	
HIGFNSRPTQ PRNGRKESNR LILFHVKRFL LNYQVTVFAV FGLVGGITIE 290	
 SEQ ID NO: 181 moltype = AA length = 263	
FEATURE Location/Qualifiers	
source 1..263	
mol_type = protein	
note = Library of modified or engineered enzymes	
organism = synthetic construct	
 SEQUENCE: 181	
MKLYTVIRGN PACSFHEDQW FAPSVQPGGH QSPINIVTSQ TKYDPNLKPL TISYDPATSL 60	
EILNNNGHSFQ VTFDDTQDKS VLRRGPLDGV YRLVQFHFHW GSSDEQGSEH TVDKKKYAAE 120	
LHLVHWNAVX YETFABAQAE PDGLAVLGIF LKVGEHNAEL QKITDILDSI KHKGQTRFT 180	
NFDPICLCLPP CPDYWTYPGS LTTPPLSES VTWIVLKQPIE VSPSQLAKFR SLLFTSEGET 240	
ACCMVNDNYRP LQPLMNRTV SSF 263	
 SEQ ID NO: 182 moltype = AA length = 214	
FEATURE Location/Qualifiers	
source 1..214	
mol_type = protein	
note = Library of modified or engineered enzymes	
organism = synthetic construct	
 SEQUENCE: 182	

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MQEITVSFFS NVSKNEVTST NPKPVTPVID PTSYVDPKAT VIGDVHIGKN CYIAASAVIR ADEGAPIYIG DRSNVQDGVV LHALESVADG GKVEDNVNL EGDENYAVVV GKDVTLAHQ QVHGPAAVGD HSFGVMKALV FNAKVGKNCV IEPEAAAIVG TVPDNKYIPA GTVVTQEEA DKLPEITPDH ENYTKVAEVV AVNVLCEAY KSKA	60 120 180 214
SEQ ID NO: 183 FEATURE source	moltype = AA length = 272 Location/Qualifiers 1..272 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
 SEQUENCE: 183 MLSVPVSIAI ATRAPDAVDA SAPGEWGYAD SSNGPARWSD ILDADGKASY PACGCAACQQ SPIDLVRATAA KGNVRVGSIA DRLVAPAKPV TLAVSQKHGT PNYVATDQNN DAAVVPADGV RYTFNSLHFH TPAENTDVGV ANAMEMHMVH LSEAGDIAVGLVFRHADAD LPANAETVTL LRKIDADGGK TKVAVDLGGL YDGAGFWEW TGSLTTPCS GNVRWLLQKE VRGVDARQAE AFKKHVGGFP GNARPTQPLN GRAVLSFDPT GV	60 120 180 240 272
SEQ ID NO: 184 FEATURE source	moltype = AA length = 214 Location/Qualifiers 1..214 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
 SEQUENCE: 184 MQEITVPEFS NITKNEVTST NPKPVTPVID PTSYIDPNAT VIGDVТИGKN VMIWPTAVIR ADEGKPIVIG DNSNVQDGVV LHALESVNNDG GKIREDNVVI EGNELYAVVI GKNVTLAHQS QVHGPARVGD DSFVGMSKLV FKSDVGSNCV IEGNAAAIVG TVPDGKYIPP GTVVTQAEA EKLPEITEDY PFSDANQAVV EVNVKLCKAY RGLQ	60 120 180 214
SEQ ID NO: 185 FEATURE source	moltype = AA length = 227 Location/Qualifiers 1..227 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
 SEQUENCE: 185 MIAAGAHWEY SGEAGPANWA KLTPEFGACS GKNQSPINLT GFIEAELPL AFAYQASATQ VLLNGHTQV NYAEGSTLTL DGQFTPLKQF HFHSPSENRI EGKSFPLEAH FVHASEQGAL AVVALMFQEG AANPELEKAW RVMPRPLDQVQ ALLPKDHAYY RFNGSLTTPP CSEGVRWLVL KQPVEASKAQ IEKFQKIMGY PNNRPVQPVN ARTVLLSS	60 120 180 227
SEQ ID NO: 186 FEATURE source	moltype = AA length = 214 Location/Qualifiers 1..214 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
 SEQUENCE: 186 MQEITVLEYS NVTKNEVTST NPKPTTPVID PTSYVDPNAT VTGDTIGKN VLIGPNAVIR ADEGAPIVIG DNSVQDGVV LHALESVNNDG GEVIEDNVNL YGNKDYAVVV GKNVVLAHQS QVHGPAAVGD HSFGVMKALV FKSIVGSNCV IEPDAAAIVG TVPDGKYIPA GTVVTQEEA ANLPEITPDH EDYTTQEAVV KVNVGLCEAY RNQA	60 120 180 214
SEQ ID NO: 187 FEATURE source	moltype = AA length = 302 Location/Qualifiers 1..302 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
 SEQUENCE: 187 MMSVATALL LSAVGTLLAAD WRYPTPGPDG SVGSPENWGG SCDHGRQQSP IDIAYAASVR GSYPEFIFDS YDSLPSAYI VNNGHTVQIN LDSSASSSSVY GGGFRSKYVL EQLHPHWSSSE HTIEDRRYAL EMHLVHRQSR YASVEQASSH KAGIAVLAVL FHVDEHPNEA IQLILNSTSP IKAKVDDRQP LRGSILHNLNDL LPKDRTVYFR YEGSLTTPVC AESVWVTFVFP ESLPISLGQV QDFMTIHAD NRTLVVNYRP VQPLNTRVLV LVSDTEVEAS GARRIASGMF AAVLLSLAIS LF	60 120 180 240 300 302
SEQ ID NO: 188 FEATURE source	moltype = AA length = 242 Location/Qualifiers 1..242 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
 SEQUENCE: 188 MKILVTFASC GYEPRNDHWQ EPWSYEGISG PDHWGELNPE YSLCSTGKEQ SPIDIDHTIK	60

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AQLPALKFDY KSEPLKYVIN NGYTIRVNYH DAPGSGNFLI VDDTRYQLTQ FHFHRPSEEY IHGKPYDMEL HLMHQSSDJK VAGVTFVIKT GRANSTTQKI WEHMPKTEGQ QEVAEGVEINP ADMPLPHDTGY YVYMGSVTAP PCTEGVNWFW LKTPVEISAD QIEAFAKLYP HDVRPLQPLN GR	120 180 240 242
 SEQ ID NO: 189 FEATURE source	 moltype = AA length = 255 Location/Qualifiers 1..255 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
SEQUENCE: 189 MKNSLFATIV GYCPEWRDHQ PVAPLGQRQS PIDIVPADAQ YDSSLKPLKL QYDPSTCLDI LNNGHFSQVT FVDDTDSSLT TDGPISGVYR LKQFHFHWGA SDDKGSEHTV NGAKYAAELH LHWNAVAKYA SFEEAALEPN GLAVLGVFLK VGEHNPALQK LTDILPSIKH KDTQASFHKF DPSCCLMPTCY DPWTYAGSLT TPPLESVTW IVLKEPIEVS EEQLGKFRL LFTSEGEKEK RMVDNFNRPLQ PLMNR	60 120 180 240 255
 SEQ ID NO: 190 FEATURE source	 moltype = AA length = 214 Location/Qualifiers 1..214 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
SEQUENCE: 190 MOEITVLTYS NVTKNEVTAT NPKPTTPVID PTSYVDPNAT VTGDTVIGKN VLIAANAKIR ADEGKPIVIG DRSTVQDGVV LHALESVDDD GKVIIEENVLL EGDEYYAVVV GKNVVLAHNA QVHGPAAVGD DSFVGGMNSLV FNSVVGGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTQEEA DKLPEVTEDY EFYTQIAEVV KVNVNLCEAY RKQA	60 120 180 214
 SEQ ID NO: 191 FEATURE source	 moltype = AA length = 277 Location/Qualifiers 1..277 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
SEQUENCE: 191 MKPIATTAL VAACALAIST VSAVSAVSEA GVKGAPWGYK PDDTTQASPV QWADHYPDCN GTHQSPIDLV TADVKQQTKA QNTLRFGRGDC ASFNLQTQSAE GYKAEVVGGS CQVRGNKARY DLLQFHVHAP SEHTLNGEPL DGEVHFVHSN KDGSALLVVG TDPWLETLLID 180 GIDDVSPTKE VMDDLTSYSA LVKKTVRGGS LFNYPGSLTT PGCSEIVDWV VVEKPMKISA KDLTRIRENQ GEIDLNYKSE SARPVQPLND RIVKSQ	60 120 180 240 277
 SEQ ID NO: 192 FEATURE source	 moltype = AA length = 279 Location/Qualifiers 1..279 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
SEQUENCE: 192 MINSRPFLIF AVYDHGTAIC GPADWKNSA HCVENTQSPI NIKTDKIFMH MFYPFDGFHF IVDNVVGVS GVLVNNGHAP TLVIDQFETP AILTGGPWAN KVYRLNQIHF HFGCDASKGS EHTVDGRVYS GEIHFVTYNT KYDFDHAAAD KPDGLSVVAV FLIDNGDKSN WKQLTDEMKK IIKADSFTKV PMYYINLYKM VPELRALFRA PFYTYKGSLT TPPCYQSVKW VVLQNPVSTS RELMTAMRSL KNHEGHSLCN NFRPTQPLNG RILAKHLKY	60 120 180 240 279
 SEQ ID NO: 193 FEATURE source	 moltype = AA length = 251 Location/Qualifiers 1..251 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
SEQUENCE: 193 MSLKRIFGVA TPEDQHNYCW CYEEENGPS E WKEHFPIANG PRQSPIDIKT SETKYDSSLK PLSVSYDPST AREILNVGHS FVHTFEDSEN KSVLKDGPIT GYVRLKQFHF HWGAADDKGS EHTVDGAKYA AELHLVHWNA VKYKSFEAAA LEENGLAVIG VFLKLGHHE ELQKLVDTLP AIKHKDALVT FGSFDPSCLM PTCPDFWYTP GSLTTPPLSE SVTWIICKQP VEVDHDQLEQ FRTLLFTSEG E	60 120 180 240 251
 SEQ ID NO: 194 FEATURE source	 moltype = AA length = 214 Location/Qualifiers 1..214 mol_type = protein note = Library of modified or engineered enzymes organism = synthetic construct
SEQUENCE: 194	

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MQEITVTRYE NIQPSPVTSW NPEPKLPEIH PTAYIHPAAV VQGDVTIGKN VLVMANAVIR	60
ADEGYPIYIG DNSSVQDNVV LHALETVDKN GNTIEENVVT VGDEKYAVYY GDNVVLAHNA	120
QVHGPAAVGD NTFVGMMNALV FRSRVGKNCV LEPLAAAIGV TVPDNKYVPA GTVVTQEEA	180
DKLPEITPDH PFANLNKRKV EVNVELAKGY LALS	214
SEQ ID NO: 195	moltype = AA length = 287
FEATURE	Location/Qualifiers
source	1..287
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 195	
MKLIRSAVTG FCPEWNDHYQ YDGISGPAYW GLINPDWTLC NSGKRQSPID IDPNKLLFDP	60
NLKLSLHIDKH KVSGVLENTQ QSLSVFRVDKD TKQHVNISGG PLAYKYQFHE IFIHYGLEDS	120
NGSEHSVDGY SFPAEIQLYG YNSDLSNMS EAQEKSQGLV GISLLVQIGD MSNPELRVLT	180
TALEKVKYKG QTTRIRKFNV RGLLPDTQHY MTYEGSTTHP GCWETTVWII LNKPIYITKQ	240
ELYALRRLMQ GSKEHPKAPL GNNARPTQPL HHRTVRTNIID FKHKKDQ	287
SEQ ID NO: 196	moltype = AA length = 292
FEATURE	Location/Qualifiers
source	1..292
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 196	
MSQDEQKWSY AQDYLWKSPS CTGSQSPIN IDTSQIQRCG VLCDLKLYLK SEKPSVEFTS	60
QNQVILSVFVN AQQSITFNNR YFNLRSRVH VPSSLHTIDNS KTDMEVCLF DSGNNNETSS	120
NDSLQNVAKG VOLCFMMNQS NNEYGNIEQF FNQFIHKIPT VQDELPIEVN VSSSWSPELL	180
IPNKQNFFYY EGSLAYPPCS EMYINIVYEE IGNIGVSNFR ILKKYIRNNT RALKPKNNRV	240
VYYSVDETNs ASIQSNSVDK ISDDRFLQCE RRNNVVTKK QVIASETIPE DN	292
SEQ ID NO: 197	moltype = AA length = 305
FEATURE	Location/Qualifiers
source	1..305
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 197	
MWLFSSFLFYV AVHKNSGKNL HIKVLRAPKM IALLSHTQGA QPSLPDRTYM PIAKKLPYTK	60
HHRLAAVILL IGMFVYHSAL SEEQPWHFTT PAKADDCCSQQ SPEGAPCGCG ELQSPINIKH	120
SIRAHLPLEV TRYSPGPATV KHIGHTLEVR TEMKGHLTLG AKSYDFVQLH FHLPGVDLIK	180
GRSYPLVAHL VHRSSTGEVA VVAIVFKRGQ ENANLAQLLA VMPRHKGDAF VLGKFDIAQL	240
LPOQRKYAY KESMSAQPGI EGINWHILKT PMEVSDAQLH AFQLILPAHR RPAHPARNRS	300
VRVGG	305
SEQ ID NO: 198	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 198	
MQEITVLTFS NITKNEVTST NPKPKTPIID PTSYVHPLAT VIGDVTIGKN CMISASASIR	60
SDEGRPIYIG DNSNVQDGVV LHALESVDDG GKIIENVVL EGNEYYYAVVI GKNVSLAHQS	120
QVHGPARVGD DSFIGMQSFV FNSIVGSNCV IEPNAAAIGV TVPDNKYIPA GTVVTQEEA	180
DNLPEITPKH AAFTTQEAVV KVNVNLCRAY RNLA	214
SEQ ID NO: 199	moltype = AA length = 271
FEATURE	Location/Qualifiers
source	1..271
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 199	
MTTATDHIDY GYGPPTNGPHT WCITCRTAAG THQSPINIIT HNCHFDPTLT PFKVFVSHHG	60
HQILLSRKQHNN PQVSFKTDRP TYVEGPLKN KYNLLQLHFH WGCYDEWGSE HHIDGHSYAG	120
ELHLVFMNEK YANINQAFND PEGLCVIGIF LKPSVEGCSA MAPMMAAMKS SKPGCETSVK	180
GEIDINGLIP NNSRYFTYEG SLTTPPCVEC VRWIVCAKPL RLSKDQLAAL RSMHCETCY	240
TNENFRPPVP VGDRVVVCSF PQSIRPQKCD T	271
SEQ ID NO: 200	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct

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SEQUENCE: 200
MQEITVTFN NIQPSPVTPW NPEPRLPEIH PTAYVHPAAV VQGDVTIGAN VLVMANAVIR 60
ADEGYPIYIG DNSSVQDNVV LHALETVDAD GRRIEENVVT VGDKEYAVVI GDNVVLAHNA 120
QVHGPAAVGD NTFVGMMALV FNSRIGANCV LEPNAAAIGV TVPDGRYIPA GTVTTQAAA 180
ALPAVTPDH PFATLNARVV AVNNALAAGY LALA 214

SEQ ID NO: 201 moltype = AA length = 247
FEATURE
source Location/Qualifiers
1..247
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 201
MVAIILGVLM SCEEVEVTVE RHSPHWYTES TMWQNIGYTD CGGIVQTPIN IETANTIKA 60
DLSDVTFNYN AFDIKIVDNG HTVQVNDRAT KTNNMVIDGV TYDFLQFHYH THSEHEIDGA 120
TDEMEIHLVH QDPITKNLAV VSVMLNANGT TPNDFIESYL ENFPSTEENE VATTTSIDLD 180
DLLPSNHNYY TYTGSLLTPP CSQGLKWIVL KDKVDVSVEQ MHKFEETHGV NARPIQPLNG 240
RLVLEKI 247

SEQ ID NO: 202 moltype = AA length = 214
FEATURE
source Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 202
MQEITVLDFS NVTKNEVTWSW NPKPPTVPPVID PTSYVDPNAT VIGDVTIGAN CYIGPSASIR 60
ADEGRPIVIG DRSNVQDGVV LHALESVDDG GKIREDNVVH HGDEYYAVVI GKNVVLAHQA 120
QVHGPAAVGD DSFVGGMKSLV FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GTVTTQAEA 180
AKLPEITPDH ANYTQQEAVV KVNVKLRCRGY RRLQ 214

SEQ ID NO: 203 moltype = AA length = 214
FEATURE
source Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 203
MQEITVTLIYS NVEKNEVTST NPKPPTVPPVID PTSYVDPQAT VIGDVTIGKN CYIAASAVIR 60
ADEGKPIVIG DNSNIQDGVV LHALESVDDG GKLEDNVVI KGNKLYAVVI GKNVALAHQS 120
QVHGPARVGD DSFVGGMNSLV FNSIVGSNCV IEPFAAAIGV TVPDNKYIPA GTVTTQAEA 180
DQLPEVTDDH PFYTEVAAVV KVNVALCQAH KGLS 214

SEQ ID NO: 204 moltype = AA length = 266
FEATURE
source Location/Qualifiers
1..266
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 204
MLTPARSIFC VGWKEQDHNY SLSPLTRLPLV DGDROSPINI VPGNAVYDPR LKPLTLSYDP 60
ATSLEILNNNG HSFQVTFDDS QDKSVLKGGP LDGVYRLKQF HFHWGASDH GSEHTVDGVK 120
YPSELHLVHW NAKYGFGEA ASKPDGLAVV GVPBKIGHEK PHMQKVLDAL DAIKTKGKQT 180
TFTNFDPSTL LPGCLDYWTY DGSLTTPPLL ESVTWIVLKE PISVSPAQMA KFRSLLFTSE 240
GETACCMVDN YRPPQPLKGR QVRASF 266

SEQ ID NO: 205 moltype = AA length = 257
FEATURE
source Location/Qualifiers
1..257
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 205
MSLKNIFTAV CGPEQWHDYF RKANGNFQSP INIDTKETKY DSSLKPLTLS YDPATAKEIL 60
NNNGHSFQVTF DDTDNKSVLK GGPLTGSYRL RQFHFHWGAT DEKGSEHTVD GVKYASELHL 120
VHWNNAVKYAS FAEAAASKPDG LAVLGVFLKI GKHHHEELQKI TDTLNSIKTK GKQTTFTNFD 180
PSCLLPSCLD YTWTYFGSLTT PPLYESVTWI VCKQPISVSS EQLAQFRSLL SNAEGEKACC 240
MVDNYRPPQP LKGRKVR 257

SEQ ID NO: 206 moltype = AA length = 214
FEATURE
source Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 206

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MQEITVTNYN NIROSPVTSW NPTPKLPKIH PTAYIDPAAV VTGDTVIGKN VMVSANASIR	60
SDEGYPIIYG DNSNVQDNVV LHALETVDAN GKBIEENIVV VGDKEYAVYI GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSVVGKNCV LAPLAAAIGV TVPDNTYIPA GKVVTTQEEA	180
AKLPKIPDHH PFANTNKAVV AVNVELAKGY LALS	214
 SEQ ID NO: 207	moltype = AA length = 267
FEATURE	Location/Qualifiers
source	1..267
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 207	
MRSIKLLCLP ALLATTIANA GASLDQWDYS SHGERYWRSH FPACQGMQQS PINISTKRAL	60
KHPKAFLPLK PGPVLDFSPK AAPVHFEYRGN YSLLHRGESY QLKQPHFHHA	120
SETTIDGKHS PLEVHFVHK SQQGHTLVIAV LLDSGRAENI LISSGKAAADS SPQNGVNKSS	180
FNPKKLPLKE KDFYYFEGSL TPPCTEGVH WAVMKHKGLV SEQDVRYFAK FDYPANFRHT	240
QPINGRSTYY FSDIDRSEDD IKNSSGR	267
 SEQ ID NO: 208	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 208	
MQEITVSNFS NVTKNEVTPY NPKPVTVPID PTSYIDPNAT VIGDVTIGAN CMVSANASIR	60
SDEGKPIIVG DRSNVQDGVV LHALESVNDN GKIILEENVV VGDRNYAVVV GKNVSLAHQS	120
QVHGPAAVGD DSFIGMQSFV FRSKVGSNCV IEPQAAAIGV TIPDGKYIPA GTVVTTQAEA	180
DKLPEITPDY AQSNNTQAAVV TVNVKLCEAY RNKQ	214
 SEQ ID NO: 209	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 209	
MQEITVTNYT NIQPSPVTPW NPEPKLPEIH PTAYIHPPAAV VQGDVKIGEN VLVMANAVIR	60
ADEGYPIIYG NNSSNVQDNVV LHALETVDEN GNRIEENIVK VGDKEYAVYI GDNVVIAHNA	120
QVHGPAAVGD NTFVGGMNSLV FRSKVGSNCV LEPLAAAIGV EVPDGKYIPA GTVVTTQEEA	180
AKLPVTPDH PFANLNERVV KVNLAKGY LALA	214
 SEQ ID NO: 210	moltype = AA length = 277
FEATURE	Location/Qualifiers
source	1..277
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 210	
MRKTLAISIF CGWNYDPEHQ RWDYDQQENG PHRWPKLYPE CGGNAQSPID IKTKEKTYDP	60
NLKPLTVLGV DKNGGLEFSMT NNGHTVQISL PSSMYLKDSL GTVYIAKQMH FHWGGSSEI	120
SGSEHTIDGM RYLIEHVHVH YNSKYKSYDV AQDAPDGLAV LAAFVEVKDY AENTYYSNFI	180
SHLENIKYPG QSTVLRGLDI QDMPLPKNLHH YYSYLGLSLTT PPCTENVHWF VLADSVKLSK	240
TQVWKLENSL LDHQNKTIHN DYRKTOPLNH RVVEANF	277
 SEQ ID NO: 211	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 211	
MQEITVMEFS NVTKNAVTPT NPKPVTVPID PTSYVDPEAT VIGDVTIGEN CMISAFASIR	60
SDEGKPIIHG NRSNVQDGVV LHALESVNP GMVNEENVVV AGDELYAVVV GKNVSLAHQA	120
QVHGPMVGD DSFIGMQSFV FKSIVGNSNCV IEPNAAAIGV TVPDNKYIPA GTVVTTQAEA	180
DKLPDITPDY AYYTTVAAVV SVNVNLCKAY REQA	214
 SEQ ID NO: 212	moltype = AA length = 254
FEATURE	Location/Qualifiers
source	1..254
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 212	
MKILTFASVC YGPENWHRDF QAAKGKRQSP IDIVPASAKY DSSLKPLTFT YEAGTSRCIV	60
NNGHSFNVEF DDSQDKSVLS GGPLTDKYRL TQPHFHGWKT DDEGSEHTVD GHSPYPAELHL	120

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VHWNADKFAS	FGEAASKPDG	LAVGVFLKV	GDEHPGLKKV	TDALYSVKFK	GTKAEFKNFN	180
PKCLLPASLD	YWTYDGSLLT	PPLSECVTWI	VLKEPISVSS	QOMGKFRSLL	FTSEGETECC	240
MVDNYRPPQP	LKGR					254
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SEQ ID NO: 213	moltype = AA	length = 277				
FEATURE	Location/Qualifiers					
source	1..277					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
SEQUENCE: 213	organism = synthetic construct					
MQRKLPVAI	FCTGYENHDW	GYEDHNGPEH	WHELFPIANG	DNQSPIELHT	KEVKYDSSLQ	60
PWSASYDPGS	AKTILNNNGKT	CRVFDDTYD	RSMLRGGPLT	GPYRLRQFHL	HWGSSDDHGS	120
EHTVDGVKYA	AELHLVHWNA	VKFESFEAAA	LEENGLAVIG	VFLKIGRHNP	ELQLKLVDVLP	180
AIKHKDTELVE	FGSFDPSCLM	PTCPDYWTYP	GSLTTPPLSE	SVTWIIKLQP	IEVDHDQLEQ	240
FRFLLLFTSEG	EKEKRMVDFN	RPLQPLMNR	VRSSFRH			277
<hr/>						
SEQ ID NO: 214	moltype = AA	length = 191				
FEATURE	Location/Qualifiers					
source	1..191					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
SEQUENCE: 214	organism = synthetic construct					
MLNSPSAAND	ERPEVEDGAW	IHPSPAALVGN	VSIGSRAYVG	PQASIRADEP	GPDGSVAPVV	60
IESEANVQDG	AVLHALGGTS	VVRSRTSVA	HGAVVHGPQCQ	VGPGCFIGFN	TVVYDAELGE	120
QVVMMHGAVV	ENVEIPDGLI	VPSRAAVCCQ	EDVRALDEAS	ESALAFADEV	SRTNVHLAEV	180
KNSEQQTGYY	E					191
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SEQ ID NO: 215	moltype = AA	length = 214				
FEATURE	Location/Qualifiers					
source	1..214					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
SEQUENCE: 215	organism = synthetic construct					
MQEITVLEFS	NVRKNEVTPT	NPKPTTPVID	PTSYVDPNAT	VIGDVTIGAN	VLIWPTAVIR	60
ADEGRPIVIG	DRSNVQDGVV	LHALESVDDG	GEIREDNVVR	VGDENYAVYY	GKNVSLAHQS	120
QVHGPAAVGD	DSFVGMKSLV	FKSKVGSNCV	IEPDAAAIGV	TVPDGKYIPA	GTVVTTQEEA	180
AKLPPEVTPDY	AYYTTVVEVV	TVNVALCEAY	REEA			214
<hr/>						
SEQ ID NO: 216	moltype = AA	length = 214				
FEATURE	Location/Qualifiers					
source	1..214					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
SEQUENCE: 216	organism = synthetic construct					
MQEITVTRYE	NIRESPTVTPW	NPEPRRPEIH	PTAYIDPKAV	VQGDVTIGAN	VLMANAVIR	60
ADEGYPIVIG	DNSSVQDNVV	LHALETVDEN	GNPIKENIVK	VGDKEYAVYY	GDNVIAHNA	120
QVHGPAAVGD	NTFIGMNALV	FRSVVGKNCV	LEPLAAAIGV	TVPDGKYIPA	GTVVTTQEEA	180
DKLPKVTPDH	PFANLNARVV	KVNVALAKGY	LAQA			214
<hr/>						
SEQ ID NO: 217	moltype = AA	length = 214				
FEATURE	Location/Qualifiers					
source	1..214					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
SEQUENCE: 217	organism = synthetic construct					
MQEITVTVYN	NIQPSPVTPW	NPEPKLPKID	PTAYIHPKAV	VIGDVTIGKN	VMISANASIR	60
SDEGYPIVIG	NNSSIQDNVV	LHALETVDEN	GNRIEENIVV	VGDKEYAVYY	GDNVSLAHQA	120
QVHGPAAVGD	NTFIGMQAFV	FRSVVGKNCV	LEPLAAAIGV	TVPDGKYIPA	GTVVTTQEEA	180
AKLPPEMTPDH	PFYKTNEAVV	KVNIALAKGY	LALK			214
<hr/>						
SEQ ID NO: 218	moltype = AA	length = 214				
FEATURE	Location/Qualifiers					
source	1..214					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
SEQUENCE: 218	organism = synthetic construct					
MQEITVTRFE	NIQPSPVTPW	NPEPRRPEIH	PTAYIHPLAY	VQGDVTIGEN	VLVAAHAVIR	60
ADEGYPIVVG	NNSSIQDNVV	LHALETVDEN	GNRIEENIVV	VGDKEYAVYY	GDNVIAHNA	120
QVHGPAAVGD	NTFIGMNLSV	FRSVVGKNCV	LEPLAAAIGV	TVPDGTYVPA	GTVVTTQEEA	180
AKLPKITPDH	PFANLNARVV	KVNVALAKGY	LALS			214

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SEQ ID NO: 219      moltype = AA length = 281
FEATURE          Location/Qualifiers
source           1..281
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 219
MKIGTVLSIF LGMAHAAVDD HSSPWNYNTW GSDWGSILTAI AGNECGNRNQ SPIDLPSVVD 60
SSQIYASKSD NFNKMYTDQT NAKIYWDGHT SKITIVNPGE DLQKFSSFA KDYLQGPERF 120
SGVQFHFHHG SEHTIDQF DLEMHTVHPV DEGAKGGIKY AAMGIMFSVD KHTANAEEWE 180
VKIIIDDFFEN LQWSETTDP IVDLVSYGVK MMMVDTDNRW VYKGSVTPPP CATALVWNVV 240
RKIYPLKQKY LDQFKNQLKR GSLTGNYREI QAYDDHDLHI I 281

SEQ ID NO: 220      moltype = AA length = 324
FEATURE          Location/Qualifiers
source           1..324
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 220
MTFLVSLFLA ALVCEPVHSI NLPVAWCYNN PACNFPNPNP IAPQYCNGSS QSPIDIVTAQ 60
VQGNPNLNTQF ILTGFDANTT FTTSITNSGTS VVVSLLDEDIM SVQGGDLPGL YVSVQFHLLHW 120
GSSSSLPGSE HTVDGKQYAM ELHIVNLHST YDGNVSAALA ANDSSALAVL GFFFIEGTDEA 180
DKTNNSWIDFT SFLSNIPNSG NTYTDIMDQI TMNSLLEGVN KTKYYRYQGS LTTPPCNEDV 240
IWTVFKEPIK VNINNLLNRFK TKVFAKATAK SDLNVNNPRG VQPLNGRVVT SQVEQTGSSA 300
APSLVPTIS SLSLILLLTS LSCL 324

SEQ ID NO: 221      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 221
MQEITVYDYS NVTKNEVTST NPKPTTPVID PTSYVDPKAT VTGDTIGKN VLIGPFAIR 60
ADEGAPIVIG DRSNVQDGVV LHALESVDDG GKVRDENVVR HGDELYAVYV GRNVSLAHQA 120
QVHGPARVGD DSFVGGMKSLV FRAKVGKNCV IEPGAAAIGV TVPDGKYIPA GTVVTTQAEA 180
AKLPEITPDH PNYSKVDEVV AVNVGLCEAY RERA 214

SEQ ID NO: 222      moltype = AA length = 208
FEATURE          Location/Qualifiers
source           1..208
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 222
MRSALVIPFY KGHQEDWNTC KNNGMQSPID LLHERVEVVS HLGRQLQSKYK PSNATLKNRG 60
HDMMMLRGDA CGYLEINGTE YVLQQCHWHS PSEHTINGRR FDMELHMVHQ SRDNKIAVIG 120
IMYKIGRPDS FLSKLMDHIS AIADTTEEKK AVGVIDPRNI KIGSRKYYRY IGSLTVPPCT 180
QNVVWTIVRK VRTVTRREQVR LLRAVAVHD 208

SEQ ID NO: 223      moltype = AA length = 291
FEATURE          Location/Qualifiers
source           1..291
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 223
MRPPPQRQGK THREGKEMTT AAWKAIFAMV LASVLLVDAD DAHVKGFGYSG SIGPEKWASL 60
SPGYQMCSKG ERQSPVNIDK SKLAYNPGLA ALERNYVPAN ATLVNKGYQI ALLFDKVNVT 120
LVDGKNSYL KSVWHHSPSE HTINGKRFAV ELHMVHMSDN GRIAVVAILY QIGRRDPFVV 180
QIERKELA EEARCKGDEEA YVPVGVVHTR SLKRHSSKYF RYSGSLLTPP CTENVIWSIL 240
GKVRREMAEQQ LAALQAPLSQ ENRNNNARPTQ PLNYRAVQLY HESRKHDEYS R 291

SEQ ID NO: 224      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 224
MQEITVLEFS NVTKNEVTPT NPKPTTPVID PTSYVDPNAT VTGDTIGKN VMISDSASIR 60
SDEGKPIVIG DRSNVQDGVV LHALESVDDD GEVIEDNVVI YGDENYAVYV GENVSLAHQA 120
QVHGPAAVGD DSFIGMGAQFV FKSTVGSNCV IEPEAAAIGV TVPDGKYIPA GTVVTTQEEA 180
AKLPEITPDY PFYTTQAAVV TVNVALCEAY RAER 214

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SEQ ID NO: 225      moltype = AA length = 283
FEATURE
source
1..283
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 225
MKKP KLFNLL GTFAATFAYE YNPGNNSDYRP ENWAQMDSPN NIQCDWANQS PIDLQTOFVL 60
IQSRANLSI TNLRTPMENV VLTVNGHGAE ISFEFANNND MVVTGGPLND QFIVAQAOWH 120
WGHTADCA GSE HMLNSQRYSA EVHIVTYNSK YASLEDAADK YDGLAVLGFL YEVDEAANS 180
FPQSVQTS LG GITFGCDS TT VSPFPLIDL F RTEFFD YIA SGSLTTPPCY QTQWMVSTK 240
PLKI WSSD ALRSINDVNG SPLLRNFRPC QNSYSRALNG YYL 283

SEQ ID NO: 226      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 226
MQBITVLD FS NITKNEVTSW NPKPTTPVID PTSYVDPNAT VIGDVTIGEN CLIGASAVIR 60
ADEGHPIVIG DRSNVQDGVV LHALETRDEN GNLLNEENVK VGDEEYAVYI GKNVSLAHQS 120
QVHGPARVG D DSFVGMSL V FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTSQEEA 180
AKLPVETDDY PFSTANEAVV KVNV ALCEAY REQK 214

SEQ ID NO: 227      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 227
MQBITVTRYE NIRPSPVTPW NPEPKLPKI PTAYVDPAAV VQGDVTIGAN VLIMANAVIR 60
ADEGHPIVIG DNSVQDNVV LHALETRDEN GNLLNEENVK VGDEEYAVYV GDNVLAHNA 120
QVHGPAAVGD NTFIGMQAFV FRSVVGKNCV LEPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
DKLPKIPDH PHYNLNERVV KVNV ALAKGY LAQA 214

SEQ ID NO: 228      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 228
MQEITVTFN NIRPSPVTPW NPEPKLPKID PTAYIDPAAV VQGDVTIGKN VMVSANASIR 60
SDEGYPIVIG DNSVQDNVV LHALETRDEN GVKEENVVT VGDKKYAVYI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVVGKDCV LEPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
AKLPKIPDH PFANTNAAVV KVNV ALAKGY LALK 214

SEQ ID NO: 229      moltype = AA length = 229
FEATURE
source
1..229
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 229
MKNSWRITAV LFGCYHQPED YFSYDGISGP AYWGEINPEW SLCNQGKMQS PIDLLNERVE 60
VVKSLERIKK NYKPSNATLK NRGHDMMLKW ESGAGSTIHIN GTEYVLIKQCH WHSPSEHTIN 120
GRRYDMELHM VHQSADNKTA VIGVTVKLGR PDSFLSSIMK HIKAI SDTTE AEKAVGVIDP 180
RIKFGSRKY YRYMGSLTVP PCTEGVVWTI VKKVRTVSR EQLRLRREAV 229

SEQ ID NO: 230      moltype = AA length = 320
FEATURE
source
1..320
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 230
MELKVLSAHL PSWILVGPLF VVHIKAAEWS YADTSKWPKD YPSCSGYYQS PIDLTYKDSV 60
YAPQLGQITI TNLSKVEQT YKVTNGHHT EVSFNEKOWK ISLGSDEDPY YPIQMHHFWG 120
GPTREGSEHL IGDLRHAMET HIVCYNGRLY KSKEEATSSP NGLAVVGILH EEDKLAQTEQ 180
TERGKGMGEFE TALASITTTK ESKNIAAFDL AGLLGQVDTT QYFRYQGSLT TPPCTQNVMW 240
TVFTTFVPTV PAQLELLRGL RTSSSTPLQD NYRPVQPLND PHSPLPRTVY RTISAANRFT 300
HSWWSFVMLS FLACCSHGIL 320

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SEQ ID NO: 231      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 231
MQEITVTEFE NIOPSPVTWS NPTPKPVIH PTAYVHPAAV VQGDVTIGKN VMISPLASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETV DAN GNTIEENV VT VGDKEYAVYYI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSIVGKNCV LEPLAAAIGV TIPDGTYIPA GTVVTTQEAE 180
DKLPKITPDH PFANTNKAVV KVNVELAKGY LALS                         214

SEQ ID NO: 232      moltype = AA length = 256
FEATURE          Location/Qualifiers
source           1..256
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 232
MTLSLFAAAA FADVQECPPR YSYCGYSGPE QWKNIVFKDK RNECNQTTQS PINLGTPPTPT 60
SGPTIHVEYV GNVAGNATIR NTGHDIEVTP MRGNNAKIKVG SRVYTLQLH FHVPNEHHVP 120
RICKAEMH ILHQLDGGTD YAVIGVMLTI GTPTDSALAP VFENLPKEAC APPKPLEINF 180
KKLLPEELTG YYTYVGSLLT PPCTEKETV TWYVLDAPRE IPASDLKLKG ALGKNARPIQ 240
TNPLTVTYVS PTPTPK                         256

SEQ ID NO: 233      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 233
MQEITVAEFS NVVKNEVTPT NPKPPTPEID PTSYVDPNAT VEGDVTIGAN VLIHAFAVIR 60
ADEGRPIVIG DRSNVQDGVV LHALESVDDG GEIREDNVVL HGDDLYAVYYV GKNVHLAHQA 120
QVHGPARVGD DSFVGGMKSLV FKSDVGSNCV IEPFSAAIGV TIPDGKYIPA GTVVTTQEAE 180
DKLPPEVTDY AFSGQNEAVV TVNVDLNEAY RQQR                         214

SEQ ID NO: 234      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 234
MQEITVTFNFN NIRPSPVTPW NPEPKLPKID PTAYVDPPLAT VTGDTIGKN VMISANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETV DEN GNRIEENV VT VGDKEYAVYYV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSNVGKNCV LEPLAAAIGV TVPDNKYIPA GKVVTTQEAE 180
AKLPEVTPDH PFYKTNAAVV KVNVELAKGY LALS                         214

SEQ ID NO: 235      moltype = AA length = 275
FEATURE          Location/Qualifiers
source           1..275
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 235
MLATFSRPNQ GHVEIDYCKW TKYVSISSGSS TWKDQFPPIAN GNRQSPIDIK TSETKYDSSL 60
KPLSVSYDPN TSLEILNNGH SFQVTFADDN DSSTLKDGPI TGVYRLKQFH FHWGASDDHG 120
SEHTVDGVKY PAELHLVHN TKYGDFGEAA SKPDGLAVVG VFLKIGREKP EFQLVLDAL 180
SIKTKGKQAS FTNFDPSTLL PGCLDYWTYD GSLTTPPLLE SVTWIVLKEP ISVSPAQM 240
FRSLLFTSEG ETACCMVDNY RPPQPLKGQ VRASF                         275

SEQ ID NO: 236      moltype = AA length = 186
FEATURE          Location/Qualifiers
source           1..186
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 236
MIKTNPRGDL PQVHESAFVD PTAILCGLVI VEEYVFFIGPY AVIRADETDA AGRIAPIVIG 60
AHNSNIQDGVV IHSKSGASVW IGQRSTIAHR AIVHGPCRVG DGVFIGFNSV LFNCTIDDG 120
VVRYNAVVDG CHLPPGFYVR STERIGPETD LAALPQVTAD ASDFSEDVAR TNNALVLGYK 180
HIQNEF                         186

SEQ ID NO: 237      moltype = AA length = 214
FEATURE          Location/Qualifiers

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source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 237
MQEITVTNPN NIAESPVTPW NPEPKPKIH PTAYIHPPLAY VQGDVTIGEN VMVSANASIR 60
SDEGYPIYIG NNSNVQDNVV LHALETVDEN GNEIEENIVK VGDKKYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVGKNCV LEPLAAAIGV TIPDNTYIPA GKVVTTQEEA 180
AKLPKITPDH PFYKTNEAVV KVNVVALAKGY LALA 214

SEQ ID NO: 238      moltype = AA length = 231
FEATURE
source          1..231
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 238
MAAWAGGGPH WSYEGAGGPA NWARLTPEFG ACAGRQNQSPI DLTGFIEAEL PPLAFAYRAG 60
GRSIVDNGHT QVVTYAPGSV LEVGRRFEL QQFHFPHTPSE ERINGRSYPL VAHLVHRDAA 120
GHLAVVAVLF KQGAENPALA PLWAAMPKA GETRALKAPL DAGALLPARR DYFTYMGSLT 180
TPPCSEGVRV MVLRQPLEVS AAQVARFREV MGENARPVQP LNGRTVLHRV M 231

SEQ ID NO: 239      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 239
MQEITVTVFE NIRPSPVTPW NPEPKLPKIH PTAYIDPAAV VQGDVTIGKN VMVSANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDEN GNVIENVV VGDKKYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSTVGKDCV LEPLAAAIGV TVPDGTYVPA GKVVTTQEEA 180
AKLPKMTPDH PFYKTNEAVV KVNVVALAKGY LALS 214

SEQ ID NO: 240      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 240
MQEITVTRYE NIRESPVTPW NPTPKRPEIH PTAYIDPPLAY VQGDVTIGAN VMVSAHASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDEN GNEITENIVT VGDKKYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVGKNCV LAPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
AKLPKITPDH PFANTMNAAVV KVNVVALAKGY LALS 214

SEQ ID NO: 241      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 241
MQEITVTLFN NIRPSPVTPW NPEPKLPKIH PTAYIDPAAV VQGDVTIGKN VLIMANAVIR 60
ADEGYPKIKIG DNSNVQDNVV LHALETVDEN GNVIENVV VGDERYAVVV GDNVVLAHQA 120
QVHGPAAVGD NTFVGMQALV FRSRVGKNCV LAHQAAAIGV EVPDGRYIPA GLVVTTQEEA 180
AKLPVTPDH PFANLVDRVV KVNVVALAKGY LALK 214

SEQ ID NO: 242      moltype = AA length = 300
FEATURE
source          1..300
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 242
MVPERCRRTP TLLLFVSLAM AVAVSGACAD DDKATAMRTA MPKPVSRRAS TASSAETVVT 60
PSVKEKRNTT PSPHGHGTQDS WSYDNVAWP ATCAGNQQSP MPLRHTPADA HGRGSIRTL 120
TAATTLLRLRA VRDGSSIAALL CNGYCGVVKV HGVTMIIKNM HWHTPSEHTI DGRRLDaelH 180
MVAFAGGKIA VLSSLFKVAN KNVLVDRTIR AMSGMRSMSA TRKEVKDYFF SGAVKVSAAV 240
YKGSLTTPPC TEGLSWVVNA KVSTMSKKQL SKIRELLGGH DNARPLQAPK GRVVEWMVP 300

SEQ ID NO: 243      moltype = AA length = 266
FEATURE
source          1..266
mol_type = protein
note = Library of modified or engineered enzymes

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SEQUENCE: 243          organism = synthetic construct
MKQNLFAITV SCYWREPGDH LVDKSAPSHW NKLKYPIAQGN RQSPINIIITS QAVYSPSLKP 60
LELSYDAATS LSITNNGHHSV QVDFNDSDDR TVLKGGPLTG PYRLKQFHHLH WGKKDAVGSE 120
HTVDGVKYAS ELHLVHWNAK YGKFGEAVKQ PDGLAVLGIN LKGREKGEF QIFLDALDKV 180
KTKGKEAPFT KFDPSCLFPQ CRDWTYHGS FTTPPCEECI VWLLLKEPMT VSSDQMAKLR 240
SLYSSAENEP PVPLVSNWRP PQPIKG 266

SEQ ID NO: 244          moltype = AA length = 253
FEATURE               Location/Qualifiers
source                1..253
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 244          moltype = AA length = 253
MKIKISLVLs IAALVLTGCN YSEGGKPKAN VSAGYKKNNW YGTNNNGPTHW EEFSSTCGKG 60
IHQSPVNIIIP GKTLKMNHAY DLSMHDDITG LAKVIDNGHS IKVTPEHGGH IKLHGEIFDL 120
LQYHFHGKSE HTIDGRFDL VAHMVHQNPK TKQLAVVAVF FEEGAKNKVL EKIINHVGST 180
VQLDAQDFVP LQTEHYHHYI GSLTTPPCSE NVQWYLLKQP QEASEEQIKH FRKFYVDNER 240
PVQELHDRFI EVN 253

SEQ ID NO: 245          moltype = AA length = 199
FEATURE               Location/Qualifiers
source                1..199
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 245          moltype = AA length = 199
MKITFLAVSC QHNEPDYWGRI IKEDWKICKT GKMSPIDLs NQRVKIISHL GDLKMNYKPS 60
NATLKNRGRHD ILEWKGGAG SIEINGTEVV LQOCHWHSPS EHTINGRYYD LELHMVHESR 120
DGKIAVIGIL YKIGRPDSFL SKLMKNIKSI SDTKDEERAV GVIDPRHIKI GSRKYYRYIG 180
SLTPPPCSQN VIWTIVKVV 199

SEQ ID NO: 246          moltype = AA length = 214
FEATURE               Location/Qualifiers
source                1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 246          moltype = AA length = 214
MQBITIVLEFS NVTKNEVTSW NPCKPTTPVID PTSYVDPNAT VIGDVTIGKN CLIAASAVIR 60
ADEGAPIVIG DRSNVQDGVV LHALESVNNDG GKIREENVIL HGDEEYAVVV GKDVSLAHQA 120
QVHGPARVGD DSFVGMSLKV FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTTQAEA 180
EKLPEVTDY PFYTTQEEVV KVNVNLCEAY REQA 214

SEQ ID NO: 247          moltype = AA length = 253
FEATURE               Location/Qualifiers
source                1..253
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 247          moltype = AA length = 253
MSTPLVKWGY DEQNGAHIBC RFFPAANGKR QSPIDIDINT VKHDPSSLKPL SVSYDPSTAK 60
EILNVGHFSH VNFEQEDNRs VLKGGPLTGS YRLRQFHLHW GSADDHGSEH TVDGVKYAAE 120
LHLVHWNPKY NTFAEALKQP DGIAVGVFL KIGREKGEFQ ILLDALDKIK TKGKEAPFTK 180
FDPSCLFPAC RDYWTYHGSL TVPPLLESVT WIILKQPISV SSEQLAKFRS LLCTSEGETA 240
VFMRLRNHRPP QPL 253

SEQ ID NO: 248          moltype = AA length = 214
FEATURE               Location/Qualifiers
source                1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 248          moltype = AA length = 214
MQBITIVLEFS NVRKNEVTPW NPCKPSTPVID PTAYIDPQAT VIGDVTIGAN VLIGPMAVIR 60
ADEGAPIVIG DRSNVQDGVV LHALESINEE GEVREDNVVE VGDENYAVVI GKNVSLAHQS 120
QVHGPARVGD DSFVGMSLKV FKSDVGSNCV LEPGAAAIGV TVPDGKYIPA GTVVTTQAEA 180
AKLPEVTDY PFYTAQEAVV EVNVALCQAY NEQS 214

SEQ ID NO: 249          moltype = AA length = 214
FEATURE               Location/Qualifiers
source                1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

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SEQUENCE: 249
 MQEITVYEFNS NVTKNEVTPT NPKPSVPVID PTSYIDPNAT VIGDVTIGKN VLIAFAVIR 60
 ADEGRPIVVG DRSTVQDGVV LHALESVDDD GKVIEDNVVI HGNKDYAVYI GKNVVLAHQS 120
 QVHGPARVGD DSFVGGMNSLV FNSVVGNNCV IEPNAAAIVG TVPDGKYIPA GTVVTQEEA 180
 DKLPEVTPDY AFYTKNEVVV NVNVDLCKAY KEKA 214

SEQ ID NO: 250 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 250
 MQEITVHHFS NVTKNEVTSW NPKPSTPVID PTSYVDPNAT VIGDVTIGEN VLIGANAVIR 60
 ADEGAPIVIG DRSNVQDGVV LHALESVDDG GEEIEDNVVI EGDEEYAVYI GKDVS LAHQ 120
 QVHGPAAVGD DSFVGGMKSTV FNSTVGENCV IEPDAAAIVG TVPDGKYIPA GTVVTQEEA 180
 AKLPVTPDH PSHDEIEAVV EVNVALNEAH REQA 214

SEQ ID NO: 251 moltype = AA length = 317
 FEATURE Location/Qualifiers
 source 1..317
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 251
 MCDLNCIMTK MDNSDYMIVV CCVLLSIFLL FEIVEWIFKV FTWTDNDVCL PPTPSFGYAH 60
 KNGPHTWKDL YPESAGSNQS PINITTRYAI VVQPSEPLRW INYNSVPLST TLSNDGHTVI 120
 LRGFWWDQSSW PQLQQGPLSD KYDFFNILPH WGPSNQEGSE HTLDYIRYPM ELQV1HMKHG 180
 LKSPKDAAIIL GARDGIVIVS FFLQINAMDN PYLDHIVS NL WKISNP SHYK TNIPPFPLEW 240
 IFAPFDRDYY TYSGSLSQPP CNEVVTWIIQ KEPIVISALQ VEKFREICSV DGPLLNCRP 300
 VQPLNERDVY FYEESKL 317

SEQ ID NO: 252 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 252
 MQEITVTVYN NIQPSPVTSW NPTPKLPEIH PTAYVHPAAV VIGDVKIGEN VMISPHASIR 60
 SDEGMPYIYG DNSNVQDGVV LHALETV DAN GNTIEENV VT VGDKKYAVYV GKNVSLAHQS 120
 QVHGPAAVGD NTFIGMQS FV FKSVVGKNCV LEPLAAAIVG TVPDGTYVPA GKVVTTQEEA 180
 AKLPKVTPDH PYANTNAAVV YVNVELAKGY LALA 214

SEQ ID NO: 253 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 253
 MQEITVLVYS NVQKNEVTSQ NPKPVPVID PTSYVDPKAT VIGDVTIGKN CMISASASIR 60
 SDEGHPYIYG DRSNVQDGVV LHALESVNDG GMILEENV VL AGGEDYAVYV GKNVSLAHQS 120
 QVHGPAKVGD DSFIGMQS FV FNSIVGSNCV IEPNAAAIVG TVPDNKYIPA GTVVTQEEA 180
 DKLPEITPDH AYYTTVA VVV NVNGLCRAY KNEA 214

SEQ ID NO: 254 moltype = AA length = 339
 FEATURE Location/Qualifiers
 source 1..339
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 254
 MTWAVPLVLL PLVLASALGA VVEV PETCGA EAGACVDEES AMVQVKTOPS QRAPS AATAS 60
 GDV DYQGFQL GDWPEIAPLC AGGSTTGFQA PINIAVEGAD YEKMPQASWP KFYAKEGGCD 120
 EAHFVEKGTA WQVDFMNP KNL DCKNLEM E WKGKVYALVQ FHFHTLSEDT VDFQPTAMQM 180
 HMVHLAADGS FAVVGVLIKT DGFFKNGFLE GIFTGFESD RMV TLLAKHR FN PYAGVLSK 240
 HGGEFWHYEGS FTTPPCTEGV DFLIAQSPVV TSKSYVTSY M EYLKGNGKGN SYGQNHRPIQ 300
 PLNGREITTG RFLEVCPKKP APDCGKLDPK KVQFCEESA 339

SEQ ID NO: 255 moltype = AA length = 253
 FEATURE Location/Qualifiers
 source 1..253
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

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SEQUENCE: 255
 MSLGPQTWYK RFAINCEDVH QSPINIVTKK TIPDPNLKPL ELTYDATTTR TIVNNNGHSVQ 60
 VDFEDSSNRT VITGGPLTGP YRLKQFHFW GASDDKGSEH TVDGVKYASE LHLVHWNAEK 120
 YSSFVEAAHE PDGLVVLGVF LKIGEHNPNL QKLTDALYSV RFKGTKAQFT NFNPKCLLPP 180
 SLDYWTYPGS LTPPLLESV TWIVLKEPIS VSPSQLAKFR SLLFTSEGET ACCMVDNYRP 240
 LQPLMNRKVR ASF 253

SEQ ID NO: 256 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 256
 MQEITVTRFE NIAPSPVTPW NPEPKLPKH PTAYVHPLAY VQGDVTIGEN VLIAPLASIR 60
 ADEGYPIYIG DNSSVQDNVV LHALETVDEN GNVLEENVTT VGDKKYAVVI GKNVVI AHLA 120
 QVHGPAAVGD NTFVGMLALV FKSNVGKNCV LEPLAAAIGV TIPDGKYIPA GKVVTTOEEA 180
 AKLPEVTPDH PFYKLNERVV KVNVLA KGY LAQA 214

SEQ ID NO: 257 moltype = AA length = 286
 FEATURE Location/Qualifiers
 source 1..286
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 257
 MLGMKNTENH SAVLVQGHPA PANGGQIKVI NNQEEGPSTW AESYPDYCNG SSQSPIDIDD 60
 WEVSPNPDCD SFVNVDLPLFT GYWKNNGHAL QFTLDDGSGA VVSGPCLGNS TYQLLQVHFH 120
 WGSAGKGQGSE HTIEGKQHDL EMHMVHTNTA YETDEAANYK DGYLVGVLF DEAKQNKRIG 180
 FERTFNRNFVK KSSKLQDSDE GTLTAMFDVS DILRKSGVAR SHFQYSGSLT TPSCNEVVTW 240
 ILATKILKEK RSELNALRSL QTHDDEALVD NFRPTQELNG RKIMMF 286

SEQ ID NO: 258 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 258
 MQEITVAEYS NVTKNEVTPT NPKPTTPVID PSSYVDPNAT VTGDVTIGKN CLIGASAVIR 60
 ADEGAPIVIG DNSSVQDGVV LHALESVDDD GEVIEDNVVL YGNEDYAVYY GKNVLAHQ 120
 QVHGPAAVGD DSFVGGMKALV FKSIVGSNCV IEPDAAAIGV TVPDNKYIPA GKVVTTOEEA 180
 AKLPEVTPDH EYYTEVAEVV KVNVLA CEAH LAKA 214

SEQ ID NO: 259 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 259
 MQEITVTRFE NIOPSPVTPW NPTPKLPTEH PTAYIHPAAV VQGDVTIGAN VLVMANAVIR 60
 ADEGYPIVIG DNSSVQDNVV LHALETVDDN GNVIEENVVY VGDERYAVYY GDNVLAHLA 120
 QVHGPAAVGD NTFVGMLSLV FRSRVGKNCF LAPLAAAIGV TVPDGKYIPA GKVVTTOEEA 180
 DKLPEITPDH PGANLNARVV AVNVALAAGY LAQA 214

SEQ ID NO: 260 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 260
 MQEITVTEFS NITKNEVTAT NPEPVTVID PTSYVDPNAT VTGDVTIGKN CLIAANAVIR 60
 ADEGKPIVIG DRSSVQDGVV LHALESVDDN GMPIEENVVL EGDKYYAVVI GENVTLAHQS 120
 QVHGPARVGD DSFVGMSKSLV FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GKVVTQAEA 180
 DKLPEVTDYD PFSTAQEAVV EVNVNLCEAY RNKA 214

SEQ ID NO: 261 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 261
 MQEITVLEFS NVRKNEVTPT NPKPTTPVID PTSYVDPNAT VIGDVTIGEN CYIAPFASIR 60

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ADEGSPIVIG NNSNVQDGVV LHALESVNDG GKLIEDNVVL EGNEYYYAVYI GNNVLAHQ	120
QVHGPAVGD DSFVGMSLV FKSKVGSNCV IEPAAAIGV TVPDGKYIPA GTVVTTQAEA	180
DKLPEVTPDY AKSNAQEAVV KVNVALCEAY KKLS	214
SEQ ID NO: 262	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 262	
MQEQITVTKYE NIRPSPVTPW NPEPKLPEIH PTAYVDPAAV VQGDVTIGAN VMVSAHASIR	60
SDEGYPIYIG DNSNVQDGVV LHALETVDDEA GNVIEENVTT VGDKKYAVVV GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FKSVVGKNCV LEPLAAAIGV TVPDGKYIPA GTVVTTQEEA	180
AKLPEVTPDH PFYNTNAAVV KVNVVALAKGY LALS	214
SEQ ID NO: 263	moltype = AA length = 333
FEATURE	Location/Qualifiers
source	1..333
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 263	
MCQLENAIED IFELKEDEVQ CQWTVPVLTI TIVNEGTGEI EAQPNKIELQ KVQNLCTIVK	60
TEWMYQGADN QNDKWPQNCP SCDALEGNE RQSPIDLNQPM MTNMVTKLTP KLTFTPNNPNG	120
DTLGKFENKV NTIQFTANDL SQNKMHGGPL SGBEYFSFWQMHH CHWGKTNYEP GTTEPTKVEQ	180
HGSEHWIDGK YDAAECHWVH FNNKYATVGD AIASGDADAL SVIGVMLEID ETNGQDEVEW	240
IGTVVKDAASA LVTPDDGPAAE DAPFNVYGPL DQLGDQSQCFC GYYNYLGGLT TPGENQQLVSF	300
IIDTPIRIN MAQVKNVKYN KIESFCSIYV RQY	333
SEQ ID NO: 264	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 264	
MQEQITVLRFS NVTKNAVTAT NPKPTTPVID PTAYVDPNAT VIGDVVTIGKN CYIAAFARIR	60
ADEGRPIVIG DNSNVQDGVV LHALESIDDA GKVIDENVTT EGNKLYAVVV GRNVSLAHQA	120
QVHGPARVGD DSFVGMSLV FKSKVGSNCV IEPAAAIGV TVPDGKYIPA GTVVTTQAEA	180
DALPEVTPDY AFYTQVAAVV TVNVALCEKY KAQA	214
SEQ ID NO: 265	moltype = AA length = 262
FEATURE	Location/Qualifiers
source	1..262
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 265	
MKLINFVGTA CSPYEQWRDH YPIADGNRQS PIDIVPGSAS YDSGLKPLTL KYDPSTSLEI	60
LNNGHFSQVT FVDDDSSTL KGGPFISGVVR LKQFHFWGSS SDDHGSEHVV DGVKYAAELH	120
VVHWNAAKYS SEVEAAHEPD GLAVLGVFNLK VGEHNSQLQK ITDLSNIKE KGKQTRFTNF	180
DPICLLPPCP DYWTYPGSLT VPPLLESVTW IVLKQPISVS SQQLAAFRNL LFTSEGEKAC	240
CMVNNYRPLQ PLMNRTVRSS FR	262
SEQ ID NO: 266	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 266	
MQEITVLYS NVTKNERTSY NPKPTVPVID PTSYVDPNAT VIGDVKIGKN CYVAAFAVIR	60
ADEGKPIVIG DRNSNVQDGVV LHALESVAG GKLIEDNVVI HGDNWFAVVV GKNVVLAHRA	120
QVHGPAAVGD DSFVGMSLV FNSKVGSNCV IEPAAAIGV TVPDGKYIPA GTVVTSQAEA	180
DKLPEITPDY AYYTQNAAVV NVNIGLCRGY KRLA	214
SEQ ID NO: 267	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 267	
MQEITVTVFE NIRESPVTPW NPTPKRPVIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR	60
SDEGYPIYIG DNSNVQDNVV LHALETVDAN GKRIEENVVR VGDKDYAVYI GDNVSLAHQA	120

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QVHGPAAVGD NTFIGMQAFV FRSRVGANCV LEPLAAAIGV TVPDGTYVPA GKVVTQEEA	180
DKLPKVTVDH PFATTNAAVV AVNVALAKGY LAQK	214
SEQ ID NO: 268	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 268	
MQEITVLEFS NVTKNEVTSW NPKPVTVID PTSYVDPDAT VIGDVTIGEN VLIAAGATIR	60
ADEGKPIYIG DRSSVQDGVV LHALESRDDG GMENGDNVVI HGNTLYAVVV GNNVSLAHQS	120
QVHGPAAVGD DSFVGGMNSLV FNSKVGNSCV IEPNAAAIGV TVPDGKYIPA GTVVTSQAEA	180
DKLPEITPDY EYYTAVAKVV GVNVLCCEAY QELQ	214
SEQ ID NO: 269	moltype = AA length = 235
FEATURE	Location/Qualifiers
source	1..235
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 269	
MTAALLSASA WAAPHWEYSG EAGPANWAKL TPEFGACAGK NQSPINLTGF TQAQLKPLKF	60
NYQADAKSIL NNGHTVQVN KPGNYLELDG QRPELKQPHF HAPSENLLIEG KSFPLEAHFV	120
HANAQGELAV LALMFPGKA NPELAKAWQQ MPEKAGEETV LKAPINAQDL LPKNLEYYRF	180
SGSLTTPPCS EGVRWLVMKQ PVELSQEQID AFKEIMHHPN NRPLQPLNGR PVLTS	235
SEQ ID NO: 270	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 270	
MQEITVTVYN NIRESPTVSW NPEPKKPEID PTAYIDPKAV VRGDVKIGKN VMVSANASIR	60
SDEGYPIYIG DNSNVQDNVV LHALETVDDED GNBIEENIVT VGDEKYAVVV GENVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FRSVVGKNCV LEPLAAAIGV TVPDGTYIPA GKVVTQEEA	180
DKLPKVTVDH PFYKTNEAVV KVNIELAKGY LAQS	214
SEQ ID NO: 271	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 271	
MQEITVTRYE NIRESPTVTPW NPTPRRPQIH PTAYIDPAAV VQGDVTIGAN VMVSPLASIR	60
SDEGYPIVIG DNSNVQDQVV LHALETVDAA GKTLLEENVVT VGDEKYAVVV GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FKSTVGKNCV LAPLAAAIGV TVPDGTYIPA GKVVTQEEA	180
AKLPKVTVDH PFATTNAAVV AVNVALAAGY RALA	214
SEQ ID NO: 272	moltype = AA length = 257
FEATURE	Location/Qualifiers
source	1..257
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 272	
MRSSAFAVPA VAALAVAGLS AALAFAAQAN EPAKPAAGH HEVYDYDHQE AWQALHDKSQ	60
SPIDIVTAGA AAADPAEPRLA IEFSHTHGAI DKIEDNGHAV QVDTHATEAT IRGRHFKLAQ	120
FHPHQAQSEHT LDGKHHPLEG HFVFKAQDGR LAVVGVMYEQ GKANAVAAQEV LDDLKPGKAK	180
PAQPEIDIEG LLPKAHGYHH YLGSLLTTPPL TENVEWYVMP TPVTMSKQQI DGFLSHYRRN	240
NRNIQPLNGR PLIRYEG	257
SEQ ID NO: 273	moltype = AA length = 260
FEATURE	Location/Qualifiers
source	1..260
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 273	
MARKPSGHLT IYEQDVNCFW SFIEPIEGTG QSPIDLHTKE IKYDSSLKPL SVKYDPSTAK	60
EISNTGHSFQ VTFEDNDNKS VLRGGPLTDS YRLSQFHFW GSSDEHGSEH VVDGVKYAAE	120
LHLVHWNAAK YSSFAEAHE PDGLAVLGVF LKVGEHNQPL QKVIDALNSI KTKGKRAPFT	180
NFPDPSTLLPS SLGYWWTYDG5 LTTPPPLLESV TWIVLKEPIS VSSEQMSKFR SLLLFTSEGFT	240
ACCMVVDNYRP PQPLKGRQVR	260

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SEQ ID NO: 274      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 274
MQEITVTRFE NIRESPVT SW NPTPKPKIH PTAYVDPLAS VIGDVTIGEN VMISPHASIR 60
SDEGMPYIYG DNSNVQDGVV LHALETVDDN GNVIEENVVV VGDEKYAVYI GENVSLAHQS 120
QVHGPAIVGD NTFIGMQSFV FKSKVGNKCV LMPLAAAIGV EVPDNKYIPA GKVVTTQEEA 180
DKLPPEITPDH PYYNTNKAVV YVNVELAKGY LALS 214

SEQ ID NO: 275      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 275
MQEITVTVYN NIQASPVT PW NPTPKLPEIH PTAYVHPAAV VQGDVTIGEN VYIAANAVIR 60
ADEGYPPIVG DNSSVQDNVV LHALETVDED GNVIEENVVK VGDKDYAVYV GKNVVLAHNA 120
QVHGPAAVGD NTFIGMQAFV FRSTVGNKCF LAPNAAAIGV TVPDGTYIPA GKVVTTQEEA 180
AKLPKIPTPDH PGANLNERVV KVNVLA KGY LAQA 214

SEQ ID NO: 276      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 276
MQEITVTKYE NIRESPVT PW NPTPKPPEIH PTAYIDPAAV VQGDVTIGKN VMVSANASIR 60
SDEGYPPIKG DNSNVQDNVV LHALETVDEN GKEIEENIVV VGDEKYAVYI GDNVSLAHQA 120
QVHGPAKVGD NTFIGMQAFV FRSRVGNKCV LEPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
DKLPKIPTPDH PFANTNAAVV KVNVLA KGY LAQA 214

SEQ ID NO: 277      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 277
MQEITVPIFS NVEKNEVTET NPKPVVPKID PTSYIDPNAT VIGDVTIGEN CYIAPFASIR 60
ADEGKPPIVG DRSNIQDGVV LHALESVDDN GEIIEENVVL EGDEYYAVYI GKNVSLAHQS 120
QVHGPAKVGD DSFVGMKSLV FNSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTQEEA 180
DSLPEVTPDH AAYTKIAAVV TVNVSCLAY LGES 214

SEQ ID NO: 278      moltype = AA length = 203
FEATURE          Location/Qualifiers
source           1..203
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 278
MSAPVIRWTY EGDKGPHFWN QLCCEEYEIAK TGKNQSPIDI HMEKVMEVQG APPLELNYKP 60
TKYTVRVEN SVHLFPKDKE QGLTFNGKRY NLIAFHGHIP SEHTLNEHYF AIEWHLVHMN 120
EAGERLVLGI WMEKELEGSD FGELAEIFPE VFADFGIEKE ISLDVSGFLP EERAYFTYQG 180
SLTTPPTFEG VTWIVLRNAT SIS 203

SEQ ID NO: 279      moltype = AA length = 382
FEATURE          Location/Qualifiers
source           1..382
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 279
MVASSLSSLC LVLASLVGQT LATSPCDVDK TSPECDFDTGV NRASWGYAAS NGPATWAANY 60
PDFCAGDMQS PIDLDSSKA V TMDPGPITMV GYNLKQAGKI ENNGHTLGFA FASGSTPYIM 120
GGRLPAGDRF DFVQLHWHWG SDSSKGSEHT MNCGKEYPIEV HLHVANTKYY VNGAPSNDNL 180
VMPDGLAVLG IFYEVSTEDN ANLTNIVSKV NEVAVEQRRL RKQGRAGSNE VDLDMTLALD 240
SFLPAPDTTQY YYQQGLLTTP SCNEAVLWTN MKSTQTISEA QLEVFRSMTD SDGITLNNNY 300
RPPQPLNNRT IYTTGTSTTA GSSNMFTELL NTAFTA AVVT GLVGIVAPLF APPPSQQRSD 360
AASARAEQAL RAGR DQWGGY WG 382

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SEQ ID NO: 280      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 280
MQEITVLTFS NVTKNEVTAT NPKPTTPVID PTSYVDPNAT VTGDTIGKN CFIGANAVIR 60
ADEGKPIVIG DNSNVQDGVV LHALESVDDG GKVRDENVVH GNEWYAVVI GKNVSLAHQS 120
QVHGPAVGD DSFVGMSLKV FKSVGSNCV IEPEAAAIVG TVPDGKYIPA GTVVTQEEA 180
DKLPEITPDY AFYTQIAEVV KVNVGLCKAY REKA                         214

SEQ ID NO: 281      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 281
MQEITVTRYT NIRPSPVTPW NPEPKLPEIH PTAYIDPLAY VQGDVTIGEN VMISANASIR 60
SDEGYPIVIG NNSNVQDNVV LHALETVDEN GNRLEENVVK VGDEEYAVVV GDNVSLAHQA 120
QVHGPAVGD NTFIGMQAFV FRSRVGKNCY LAPLAAALGV TVPDGKYIPA GKVVTQEEA 180
AKLPEITPDH PFANTNAAVV KVNVVALAKGY LAQA                         214

SEQ ID NO: 282      moltype = AA length = 309
FEATURE           Location/Qualifiers
source            1..309
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 282
MFKSSLILLA TLSVVLCGDD AKSWGYRNKG RNIVPEKWGE MQPKCLGSVQ SPINVDFAST 60
QFDANLGKLN IKKHGNETEQ WDVKNNGHSV VFTPVNTDFS FVIYPQKEEF KLLQLHFHW 120
GSEHVFVNGIK YAGELLHLVHQ SKTNPQNQFSV IGPLLQLVNA DNLMKMAVID VLADVTEYE 180
TKKIDNPELN DMVPFEVENF FRYSGSLTTP GCDEFVEWNL ADKPVIGLSE NQILEFQSSL 240
DHNHKYPILSN SRPVQEINDR IVKRSFYPFE AKARTHGASG YSVSGANKFQ FTSSVFFTLI 300
ASAFCFYSL                                         309

SEQ ID NO: 283      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 283
MQEITVLEFS NVTKNEVTPT NPKPVTPVID PTSYVDPDAT VVGDVTIGAN VLIWPKAVIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GEIREDNVVL VGDENYAVVV GNNVSLAHQS 120
QVHGPARVGD DSFVGMSLKV FKSDVGSNCV LEPNAAAIVG TVPDGKYIPA GTVVTQEEA 180
AKLPEVTDY FFYTAQDAVV EVNVDLCEAY KGQA                         214

SEQ ID NO: 284      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 284
MQEITVDTFS NVTKNEVTST NPEPVTPVID PTSYVDPNAT VTGDTIGKN CYIGANAVIR 60
ADEGAPIVIG DRSNVQDGVV LHALESVDE GEIREDNVVL HGDENYAVVI GEDVSLAHQS 120
QVHGPARVGD DSFVGMSLKV FNSTVGENCV IEPEAAAIVG TVPDGKYIPA GTVVTQAEA 180
DKLPEVTPDY AFYTEVAEVV TVNVALCEAH REKQ                         214

SEQ ID NO: 285      moltype = AA length = 314
FEATURE           Location/Qualifiers
source            1..314
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 285
MIGRSSLRAR LATASAGLVL SAVPVAAPVT AAAAATPVMS IMAGETAewn HDPASPIGPT 60
HWGELDPAWS ACRSVQDQSP IAVPTTREAD RPVLLVDYPR TPLVVRNTGH VIEVPAPGG 120
GGTLLVGGHS YRLLQWHTHV PSEHVNNGHR ADLEIHLVHQ DEQGEIAVLA VFADVSSLGE 180
AAPRMPAAVL LRRTVQAAPS TAGEEIDLQ KVSAALLGA TVEDGEQRRA ITNYLSYTGS 240
LTTPPCTGGV RWFLLPGIIG VDPASVQPLH ALIASFPGYD GYPDNNRPVQ PVGSRMVER 300
VGWPSVGGVT SGAA                                         314

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SEQ ID NO: 286      moltype = AA length = 224
FEATURE           Location/Qualifiers
source            1..224
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 286
MSPLCWGYEK DNGAHWWRQT FIAAEQPRQS PIDIQTSAKV PDLTLPKPLTL SYDPATSLEI 60
LNNNGHSFQVT FADDSDSSTL TEGPVSGIYR LKQFHFWGGA SDDKGSEHTV DGVKYPALH 120
LVHWNNAVKFK SFGEAALEEN GLAVVGVFLK IGKHHPPELQK LVDALPAIKH KDTLVKFGSF 180
DPSCLMPTCP DYWTYPPGSLT TPPLSESVTW IVLREPISVS PEQL                224

SEQ ID NO: 287      moltype = AA length = 237
FEATURE           Location/Qualifiers
source            1..237
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 287
MAAPSAKGH DVHWSYEGDN GPANWGKIKP EWAKCSTGNR QSPIDIRDGM KVELDQIQFD 60
YRPSSFSVID NGHTTVQVGVS GGNYITVQNR MYELQQFHFH RPSEERINGK AFEMVIHLVH 120
KDAEGRALAV AVLLERGAPQ PVIQTVWNHL PLEKFETMQP TILLDPAEELL PARRDYFTYM 180
GSLTTPPCTE GVLWMVMREP IQASSEQIAI FARLYPMNAR PIQETNGRMI WKS KYLS    237

SEQ ID NO: 288      moltype = AA length = 260
FEATURE           Location/Qualifiers
source            1..260
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 288
MRSLSTIFVAG YCPEKWDHQN PITGGEHQSP INIISSQTKY DPNLKPLNIS YDPSTSLEIL 60
NNGHSFQVT FDNDNRNSVLK GGPLDDVYRL EQPHFHNGKK DAEGSEHTVD GVKYSSLELH 120
VHWNNAVKYSS FEEAASKENG LAVLGVFLKV GEHNPKLQKI IDALNSIKTK GKQTTFTNFD 180
PSTLLPSSLQ YWTYSGSLTT PPLSECVTWI VLKEPISVSP AQMAKFRSLL FTSEGEKACC 240
MVDNYRPPQP LKGRKVRASF                                260

SEQ ID NO: 289      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 289
MQEITVLFNS NVTKNEVTAT NPKPVTPVID PTSYVHPEAT VIGDVTIGEN CYIAPFASIR 60
ADEGSPIVIG NDNSNVQDGVV LHALESVDDG GKLIEDNVNL EGHKNYTVYI GKNVSLAHQS 120
QVHGPARVGD DSFVGMSNFV FNSKVGSNCV IEPNAAAIGV TIPDGKYIPA GTVVTSQAEA 180
DNLPEITEDY KYYTQIAAVV NVNVGLCRAY REKA                214

SEQ ID NO: 290      moltype = AA length = 282
FEATURE           Location/Qualifiers
source            1..282
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 290
MNVTGHLSA RCFQIEDYPW SYDNDLLGGP DFWGLINKHW KLCAIGKMQS PIDIDPNILL 60
YDPNLKPIHI DKHKVSGTLE NTGQSLVFRV DKEKTHHNVI SGGPLAYKYQ FHEFYIHFG 120
HDHLGSEHSI DRYSFPAEIQ LYGFNSDSL VN NMSEAQEKSQ GLVGVSLSMVQ IGETPNPELR 180
ITSTFNKVI YRGKSAPVKR LSVRSLLPDT KDYVTVYEGST THPGCWETTV WIILNKPIYI 240
TKQELYALRK LMQGSKSHPK APLGNNARPI QDLHGRTVRT NI                282

SEQ ID NO: 291      moltype = AA length = 214
FEATURE           Location/Qualifiers
source            1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 291
MQEITVTRYE NIRPSPVTPW NPTPRPRIH PTAYVDPAAV VQGDVTIGAN VLVMANAVIR 60
ADEGYPIVIG DNSSVQDNVV LHALETVDAA GRRLEENVVR VGDEDYAVYV GANVVLAHNA 120
QVHGPAAVGD NTFVGMNALV FRSRVGANCV LAPNAAAIGV TVPDGTYVPA GLVVTQEEA 180
ARLPRVTPDH PFANLNARVV AVNVALAAGY RALA                214

SEQ ID NO: 292      moltype = AA length = 214
FEATURE           Location/Qualifiers

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source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 292
MQEITVTKYE NIRPSVTWP NPEPKLPEIH PTAYIDPAAV VQGDTIGAN VMVSANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVAD GKVLEENVVK VGDERYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMOSFV FRSVGKNCV LEPLAAAIGV TVPDGTYVPA GKVVTTQEEA 180
AKLPKITPDH PFANTNAAVV AVNVALAKGY LAQS                         214

SEQ ID NO: 293      moltype = AA length = 341
FEATURE
source          1..341
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 293
MASSARALA ALVALVLVAV AVIAEPRQQQ LKTALLRIEG GPADTFAAAA EAEAAAAKAA 60
EAAAACPWSY EGANGPANWG TICGKIFSEC ATGMQQSPIN IKLLRMHQGP QGSMIGWKIP 120
SDAYNKFVTF GGGGDYLESY DGHSFVVSHA DALFPFGGVV YKLQSFTHT VSEHTIDGEH 180
YDMEMQFVHK TVDGAFKSTG LKGELGQTLI VSVMFQVGKQ QGSPHWRQL AKAVPSVTNE 240
SAQVIPLDFT EVAQSVMVGT LPQDARFKDF KPNYNHYGGY TGSLLAPPCT QGVQWLVLAN 300
PIYAEAEDIQ AFKDLEGDNF RPVQRINGRI VTQRYCGLSC E                         341

SEQ ID NO: 294      moltype = AA length = 268
FEATURE
source          1..268
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 294
MAFTRLSISL LLSGLLISAG MPAQAAPETV MVPEVTAMAL EGKWPADWSY QGENGPAAHWG 60
ELHPSYSKCA RGRVQSPVDL GKATTRSRRS TVRVAFHPIR YEIFNDGRGI RAVPLEAQHP 120
IRIDRHDYTL KHIVFRAPSE HTFQGRHYPL EAQLVYEAADD GALAVLATVF SPGHSNPSLA 180
ALTROPLAEG QLDKPMGTRV LLPQRLPMLR LNGSLTTPPC TEGVNWWVFT QPVQATRAQI 240
DAMTRLIGHP NNRPVQPAHR RLMVEEMR                         268

SEQ ID NO: 295      moltype = AA length = 267
FEATURE
source          1..267
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 295
MKRTSLFAVI GECPOWNYYDH QEEWKIVFPQ ANGDQQSPIN IEPSSAVYDS ALKPYLELKDY 60
PSTSLEILNN GHSFQVTFVD DSDSSTLKDQ PITGVYRLKQ FHFHWGAADD KGSEHTVDGV 120
KYPAEHLVH WNAKYGSFGE AASKPDGLAV VGFLKIGKH HPGLQKLTD AYSIRFKGTK 180
AEFGSGNPKC LLPASLDYWT YPGSLTTPPPL SESVTWIVLK EPISVSPEQM AKFRSLLFTS 240
EGETACCMVD NYRPLQPLKG RKVRASF                         267

SEQ ID NO: 296      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 296
MQEITVLEFS NITKNEVTSW NPKPKTPVID PTSYIDPNAT VIGDVTIGKN CYIGASAVIR 60
ADEGRPIVIG DNSNVQDGVV LHALESVND GKVIEDNVNL EGNKYYAVVI GKNVVLAHQS 120
QVHGPAAVGD DSFIGMNSLV FRSIVGNSCN IEPEAAAIGV TVPDGKYIPA GTVVTQEEA 180
DKLPEITEDY AYWNTIAEVV KVNVNLCEAY KNEA                         214

SEQ ID NO: 297      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 297
MQEITVLEYS NVRKNEVTTT NPKPKTPVID PTSYVDPKAT VIGDVTIGEN VLIGPFAIVR 60
ADEGRPIVIG DRSNVQDGVV LHALESVDDD GKIIEDNVV EGDEYYAVVI GKNVVLAHQA 120
QVHGPARVGD DSFVGMLALV FNSIVGDNVC IEPEAAAIGV TVPDGKYIPA GTVVTQEEA 180
DTLPEITPDD EYYTKIAEVV KVNVNLCEAY REKA                         214

SEQ ID NO: 298      moltype = AA length = 214
FEATURE

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source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 298
MQEITVTNYN NIQASPVTSW NPEPKLPEIH PTAYIHPKAV VQGDVTIGAN VMISANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDEN GNVIKENVVK VGDKDYAVVI GKNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSNVGKNCV LMPLAAAIVG TIPDGTYIPA GTVVTTQEEA 180
DKLPKVTPDH PFYKTNEAVV KVNVELAKGY LAMA 214

SEQ ID NO: 299      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 299
MQEITVLFFS NVRKNEVTPQ NPKPVPVID PTSYVDPNAT VIGDVTIGEN CLIGASAVIR 60
ADEGHPIVIG DRSSVQDGVV LHALESVDDG GKIIEDNVVL EGDEYYAVVV GRNVVLAHQ 120
QVHGPAAVGD DSFVGMSL VFRSIVGSNCV IEPEAAAIVG TVPDGKYIPA GTVVTTQEEA 180
DKLPKVTPDH ADYTKQAEVV KVNVGLCEAY RELS 214

SEQ ID NO: 300      moltype = AA length = 265
FEATURE
source          1..265
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 300
MNNSCATYSV VVMTLSSLILV LTISLGYQNP FAMGQDTIND TSIISKQWPN IMSNVNTFVV 60
ENVTSRPTT TAYIHPFAII IGDCSICKKV LVAPTAVCRA DEGIPIHIGD YSNIQDGVL 120
HALDAVRDGT NVDNKRFQSE GDRLLGNDTR FDEGYAIYLS GNVSLAHDSL IHGPVWIGNN 180
TLIGVKSAVL DSKIGNNVVI RVGSIITGV E IPDNTLVPPG SVLTNQSQVA TLPSVIGSPS 240
QNLNQGDLKN SQALATAYDN TNIER 265

SEQ ID NO: 301      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 301
MQEITVLSFS NVTKNEVTST NPKPTTPKID PTSYVDPKAT VTGDVТИGKN CLIGPFAIR 60
ADEGAPIVIG DNSNVQDGVV LHALESVDDG GKIIIEENVVL YGNKYYAVVI GKNVSLAHQA 120
QVHGPARVGD DSFVGMSL VFRSIVGSNCV IEPNAAAIVG TVPDGKYIPA GTVVTTQEEA 180
DNLPEITPDH PYYTAKEVVA EVNVNLCKAY RNKE 214

SEQ ID NO: 302      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 302
MQEITVTKYE NIQESPVTPW NPTPKRPVID PTAYVHPAAV VQGDVTIGKN VMISANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDAD GNEIEENIVT VGDKKYAVVI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSNVGKNCV LAPLAAAIVG TVPDGTYVPA GTVVTTQEEA 180
DKLPKVTPDH PFANTNAAVV KVNVELAKGY LALS 214

SEQ ID NO: 303      moltype = AA length = 328
FEATURE
source          1..328
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 303
MRGCLEKTGE GAIAGILVMA GPPQIQGSNF HSGFIFLKNF IMNSTQHCTL LAISFCFALL 60
LIFACNGANK EQQQSSTSNI SKDHPKADTL LGDNEVKAEE PDANSKAEQG YALPQHTDRL 120
AQSPIDIISV KADKTVKEQI SFAPHSNDINA AKNLGHTIEL EFKEGSTCKV NGKDYASRQF 180
HFHTPSEHLV DGITFPMEMH IVNILADSVN TNKPSYLVLA VLFKIGTENK FIKEFFNKP 240
NKEGEENTLQ TGDRVRLDDLL SQFTPNDIKS YYTYQGSLLT PPFTESVQWV ILKHIVEASE 300
EQIMAIEKME GNNARHVQAI NDRKIYSH 328

SEQ ID NO: 304      moltype = AA length = 263
FEATURE
source          1..263

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mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 304
MSRPGTVLAI PCWNHQEKYD MKKVLAVAAA LLALGGVAAE ASHWGYEGEG APEHWGALDE 60
AYKACQAGKN QSPINIEHAL KAHHGQLDLA FKPGAQQIVN NGHTIQVNVS AGNTLTLGKD 120
TFTLQQFHFH APSENEIDGK QFPLEAHFVY KDKDGALVVL ALMFQQGKAN PQLAQAWQQM 180
PAAIDQVATL NQPVDIKALL PKEFNFYRFS GSLTTPPCSE GVRWLVLDDQP VSASAEQIQQ 240
FRAVVHHANN RPVQPLHGRV IVD 263

SEQ ID NO: 305      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 305
MQB1ITVLDFS NITKNEVTPT NPEPITPVID PTSYIDPNAT VTGDTVTIGKN VLIGPNAIR 60
ADEGRPIVVG DRSNVQDGVV LHALESVDE GEPIEDNVVE KGDELYAVVI GKNVSLAHQS 120
QVHGPAAVGD DSFVGMKSLV FKSDVGENCV IEPESAAIGV TIPDGKYIPA GTVVTSQAEA 180
AKLPKVTDPY AYSDTNEAVV KVNVGLCEAY KEQA 214

SEQ ID NO: 306      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 306
MQB1ITVTRFE NIRPSPVTPW NPTPKRPVIH PTAYVDPAAV VQGDVTIGAN VMISALASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDAK GKRIEENVVK VGDKDYAVVI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSRIGKNCY LAPLAAAIGV EVPDGTYIPA GKVVTTQEEA 180
AKLPKMTPDH PFYKTNEAVV AVNVALAKGY LALA 214

SEQ ID NO: 307      moltype = AA length = 275
FEATURE
source          Location/Qualifiers
1..275
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 307
MKRSLVATIF CCYEPNDHQW GYTKDNGPAT WAKSFPAANG PRQSPIDIKP SETKYDSSLK 60
PLSLKYDPST ALEILNNGHF FQVTFKDSEN KSVLQGGPLE GTYRLQFHFW HWGSSDEHGS 120
EHVVDGVKYA SELHVWNNA VGYDFGEAVK HPDGLAVLGI FLKVGKHHE FQKLLDALNS 180
IKNKGKQASF TNFDPSPVLLP ACLDYWTYSG SLITPPILLES VTWIVLKEPI SVSPAQMEOF 240
RSLLFTSEGE KEKRMVDNFR PLQPLMNRTV RSSFR 275

SEQ ID NO: 308      moltype = AA length = 263
FEATURE
source          Location/Qualifiers
1..263
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 308
MTLSRAFIGV CPQEDHKNWY NQYPIAKGNR QSPINIEKTQ AQYDSSLKPL TFSYDPSTAK 60
EIVNVGHFSH VNFEVDNDQS VLSGGPLTGS YRLKQFHFHW GASDEHGSEH TVDGLKYPAE 120
LHLVHVNAKY GSFSEASQP DGLAVGVFL KIGDENPKLQ KIIDALESIK TKGKQTRFTN 180
FDPSTLLPSC LDYWTYHGSL TPPPLLESVT WIICKEPISV SPSQMEKFRS LLFTSEGEKE 240
CCMVVDNYRPL QPLMNRTVRS SFR 263

SEQ ID NO: 309      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 309
MQEITVTRYE NIRPSPVTPW NPEPKRPKIH PTAYIDPAAV VVGDVTIGEN VLVMANAVIR 60
ADEGYPIVIG DNSVVQDNVV LHALETVDEN GNRIEENVVR VGDEDYAVVV GKNVVLAHNA 120
QVHGPAAVGD NTFVGMNALV FRSRVGKDCV LMPNAAAIGV TVPDGTYVPA GLVVTTQEEA 180
AKLPKVTDPH PFANLNARVV KVNVGLCEAY LALA 214

SEQ ID NO: 310      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein

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note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 310
 MQEITVTRYE NIRPSPVTPW NPTPKLPKIH PTAYVDPAAV VQGDVTIGAN VMVSANASIR 60
 SDEGYPIVIG DNSNVQDNVV LHALETVDAA GRRLEENVVR VGDEEYAVYY GDNVSLAHQA 120
 QVHGPAAVGD NTFIGMQAFV FRSRVGKNCV LEPLAAAIGV TVPDGRYVPA GTVVTTQEEA 180
 DKLPKVTPDH PFYKTNAAVV KVNVLAKEGY LAQA 214

SEQ ID NO: 311 moltype = AA length = 225
 FEATURE Location/Qualifiers
 source 1..225
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 311
 MGSIAHWSYS GASGPHEHWAS LTPEYGACAG RNQSPVVDLAG FIEADLAPIA FHYQAGGTEV 60
 VNNGHTVQVN YAPGSAIELD GHRFELKQFH FHAPSENLLID GKSYPLEMHL VHADEAGHLA 120
 VVALMFKAGA ENAALAKLWK AMPEQPGETV HLAPLVSAAE LLPKDRDYYR FNGLSTTPPC 180
 SEGVRWLVMK EPVSASAEQI AAFEKRLPHP NNRPLQPTNA RLVLK 225

SEQ ID NO: 312 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 312
 MQEITVLFSS NVTKNEVTPT NPKPSTPVID PTSYVDPNAT VTGDVTIGAN VLVAANATIR 60
 ADEGKPIVIG DRSSVQDGVV LHALESVDE GEIKEDNNVV VGNKNYAVYY GKNVSLAHQS 120
 QVHGPAVGD DSFVGGMKSLV FKSDVGSNCV IEPFAAAIGV TVPDGKYIPA GTVVTTQEEA 180
 DKLPEVTPDY AESNTNEAVI KVNVGLCEAY KNKS 214

SEQ ID NO: 313 moltype = AA length = 260
 FEATURE Location/Qualifiers
 source 1..260
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 313
 MAWNRRNFLG SFACFGQLSLA TGRALAVTSC KPEEQPCWGYY HGDEGPDHWG RLHPDWVACA 60
 EGSEQSPIAL AGEEVKPTAE RFALHYQPTT ARLSDNVHTV RIDMEPGSQL LLGDRTFSLR 120
 QFHHTPSEH LWSDTADLGE LHLVHVADSR EIAVLGVALR PDAAQAFPDS FWNLQAAEA 180
 GESLTLDAG LVPROGRLVG YRGSFSTTPPC TEGVNWLAM EPMAMGPEEQ RWLEQRMGGRN 240
 ARPVQPLGSR TVHTVLRREGS 260

SEQ ID NO: 314 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 314
 MQEITVTRYE NIRESPVTSW NPEPRRPEIH PTAYVDPAAV VQGDVTIGEN VMVSAHASIR 60
 SDEGYPIVIG NNNSNVQDNVV LHALETVDEN GNEIEENIVT VGDKKYAVYY GDNVSLAHQA 120
 QVHGPAAVGD NTFIGMQAFV FRSRVGKDCY LAPLAAAIGV TVPDGTYIPA GKVVTTQEEA 180
 AKLPKMTPDH PFYKTNAAVV KVNVLAKEGY LAQA 214

SEQ ID NO: 315 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 315
 MQEITVTVFN NIQPSPVTPW NPEPKLPEIH PTAYVHPLAY VQGDVKGGEN VMISALASIR 60
 SDEGYPIVIG NNNSNVQDNVV LHALETVDEN GNEIEENIVT VGDEKYAVYY GDNVSLAHQA 120
 QVHGPAAVGD NTFIGMQAFV FNSIVGKNCV LEPLAAAIGV TIPDGTYIPA GKVVTTQEEA 180
 DKLPKVTPDH PFANTNAAVV KVNVLAKEGY LALS 214

SEQ ID NO: 316 moltype = AA length = 294
 FEATURE Location/Qualifiers
 source 1..294
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 316

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MIRKMFCII AVALAGLFAS	SEQLSQQNPL ASKSPEPAKT	ESNTKPAEEA KQEEHAKHWD	60
YTENGPDKWA GLDPQNKLC	EGKMQSPIDI TNPKPDQLPE	VSIEFPFAV SMTNEHVKD	120
IENNGHTIQV DFDEKNTDTL	KIGNAKYSLS QFHFHSSEH	TVNFKSFPM E MHLVHKAGDN	180
FAVLGIFIEE GPEDNKAFEP	IWSKLHQK TEENINIDIN	QFLPKSRTTY RYEGSLTTPK	240
CGEAVWKWIVF AEPIRMSSGQ	IAKFRSIVVKK NNRPTQPLNE	RVVQTDIIEE KDSK	294
 SEQ ID NO: 317	moltype = AA length = 275		
FEATURE	Location/Qualifiers		
source	1..275		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
 SEQUENCE: 317			
MLTSLFLLSA LFSTAWSCP KHDNYQSHPHL	GRRQIRVDKG REPKDWNYDV	SADWATINPE	60
YVLCQSGTHQ SPINIAQDQ	STLHKPNFEG YQSVKIPGNF	FNWQFAPAWT PHHPEGDVTG	120
LPSFNFDGEE VENIGWHIHA	PSEHLIDGKR SRAEIHMVHV	TAEEHEAAVI GIRLAVGPQE	180
SAFIKQLGPM IHYNDTAQLE	GLEVNRLALI DEVGGVEEFW	TYKGSLLTPP CSEGLRWFLP	240
KQBLIVSEQQ MVEILAASRF	SHRVEQPVWL HDINL		275
 SEQ ID NO: 318	moltype = AA length = 261		
FEATURE	Location/Qualifiers		
source	1..261		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
 SEQUENCE: 318			
MRLSVFATIC GYQPEHWNDK	YKMASGKRQS PIDIQPKDTK	YDSSLKPLTI SYDPSTSKEI	60
LNNGHFSQVT FEDSNNNKSVL	KGGPLTDSYR LTQFHFWGA	SDEHGSEHVV DGAKYSAELH	120
LHWNSNDKYS SFAEAASKPD	GLAVLGVLK VGKEHAELQK	LTDALPSIKH KDTLAKFGNF	180
DPSCLMPSCP DYWTYAGSLT	TPPLLESVTW IILKEPISVS	PSQMAKFDSL LFTSEGEKEK	240
RMVDNFRPLQ PLMNRTVRSS F			261
 SEQ ID NO: 319	moltype = AA length = 214		
FEATURE	Location/Qualifiers		
source	1..214		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
 SEQUENCE: 319			
MQEITVTKYE NIQPSPVTPW	NPEPKKPTEIH PTAYIHPAAV	VIGDVKIGEN VMVSANASIR	60
SDEGYPIVIG DNSNVQDNVV	LHALETVDEN GNIEEENIVT	VGDEKYAVVV GKNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV	FRSRVGKNCV LEPLAAAIGV	TVPDGTYVPA GKVVTTQEEA	180
AKLPKVTPDH PFYNTNAAVV	KVNVALAKGY LALS		214
 SEQ ID NO: 320	moltype = AA length = 214		
FEATURE	Location/Qualifiers		
source	1..214		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
 SEQUENCE: 320			
MQEITVDEYS NVTKNEVTPY	NPKPTTPVID PTSYVDPNAT	VTGDTIGKN VLIGAFARIR	60
ADEGQPIVIG DRSNVQDGVV	LHALESVDDD GEVLEDNVVL	HGDDEDYAVVV GKDVS LAHQ	120
QVHGPAAVGD DSFVGMKSLV	FNSDVGDNVC IEPFAAAIGV	TVPDGKYIPA GTVVTTQEEA	180
AKLPKVTDPH AASNAQAAVV	EVNVQLNQAY RGQA		214
 SEQ ID NO: 321	moltype = AA length = 214		
FEATURE	Location/Qualifiers		
source	1..214		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
 SEQUENCE: 321			
MQEITVTKFE NIQPSPVTSW	NPEPKLPKID PTAYIHPPLAT	VVGDTIGKN VMISANASIR	60
SDEGYPIVIG DNSNVQDNVV	LHALETVDEN GRNIEEENIVV	VGDKEYAVVI GKNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV	FRSVVGKNCV LEPLAAALGV	TVPDGRYIPA GKVVTTQEEA	180
DKLPKITPDH PFATTNAAVV	KVNVELAKGY LALK		214
 SEQ ID NO: 322	moltype = AA length = 289		
FEATURE	Location/Qualifiers		
source	1..289		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
 SEQUENCE: 322			
MKRISGVLAT PCWPEQHNDY	LLLHLLYVLK MNSWGYNESN	GPATWHEHYP IANGDRQSPI	60

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DIKTKEVKYD SSLRPLSIKY DPSTAKEILN NGHSFNVEFE DSQDKSVLKG GPLTGSYRLR 120
 QFFFHFGSAD DHGSEHTVDG VKYPSELHLV HWNAVKFSSF GEAALEEENG AVIGVFLKLG 180
 RHHGEFDKIV DALDSIKTKG KQASFTNFDP SCLLPPCPDY WTYSGLSLTP PLSESVTWII 240
 LKQPISVDSL SSEGEKASFM LSNHRPLQPL KGRKVRSSF 289

SEQ ID NO: 323 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 323 MQEITVFNYS NVTKNEVTPE NPKPTTPEID PTAFFVDPDAT VIGDVTIGKN VMISASASIR 60
 SDEGKPPIVG DRSNVQDGVV LHALESVDEN GKVLLEDNVVL EGDEWYAVVV GKNVSLAHQS 120
 QVHGPAMVGD DSFIGMGSFV FKSHVGNSCV IEPDAAAIGV TVPDGKYIPA GTVVTQEEA 180
 DKLPEVTPDH AYYTTVAAVV EVVNVLQAQY KSKA 214

SEQ ID NO: 324 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 324 MQEITVTRYE NIRPSPVTPW NPTPKRPKI PTAYIDPAAV VQGDVTIGAN VLVMANAVIR 60
 ADEGYPIVIG DNSVQDNVV LHALETVDAA GRVLEENVVK VGDERYAVVV GANVVLAHQA 120
 QVHGPAAVGD NTFVGMQALV FRSTVGCNCV LAPLAAAIGV TVPDGTYVPA GLVVTTQEEA 180
 AALPRVTPDH PFADLNARVV AVNVALAAGY RALA 214

SEQ ID NO: 325 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 325 MQEITVTRFE NIRPSPVTPW NPEPKLPTEIH PTAYIDPAAV VQGDVTIGEN VLVMANAVIR 60
 ADEGYPIVIG DNSVQDNVV LHALETVDEN GNEIEENVV VGDKKYAVVI GKNVIAHNA 120
 QVHGPAAVGD NTFVGMNALV FRSEVGKDCY LAPNAAAIGV KVPDGTYIPA GKVVTTQEEA 180
 AKLPKMTPDH PGYKLNERVV KVNLAKGY LALS 214

SEQ ID NO: 326 moltype = AA length = 214
 FEATURE Location/Qualifiers
 source 1..214
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 326 MQEITVTKYN NIRPSPVTPW NPEPKLPTEIH PTAYIDPAAV VQGDVTIGEN VLVMANAVIR 60
 ADEGYPIVIG DNSVQDNVV LHALETVDEN GNRIEENIVK VGDEEYAVVI GKNVIAHLA 120
 QVHGPAAVGD NTFIGMLALV FNSIVGKNCV LAPLAAAIGV TIPDGKYIPA GKVVTTQEEA 180
 DKLPEVTPDH PLYNLNARVV KVNLAKGY LALS 214

SEQ ID NO: 327 moltype = AA length = 237
 FEATURE Location/Qualifiers
 source 1..237
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 327 MKLIFTVASG QEQYDPNHWR CRGYPIAKGNRQ SPIDIDTKSA KYDSSLKPLT VSYDPATARE 60
 IVNVGHFSNV TFDDSQDKSV LRGGLPTGVY RLRFHFHWG SSDDHGSEHV VDGVKYSAEL 120
 HLVHWNAYKG SPAEARHPD GLAVVGVFLK IGREKGEFQI LLDALDAIKT KGKQTRFTNF 180
 DPSCLFPCCR DYWTYSGSLT TPPLSESVTW IVLKQPIEVHD HQLEKFRTL LFTSEGE 237

SEQ ID NO: 328 moltype = AA length = 253
 FEATURE Location/Qualifiers
 source 1..253
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 328 MITKLFAGSV QRKYEPDNWH RYYPVANGNS IDIEAAETQY DSSLKPLTIS YNPATAKEIL 60
 NVGHFFTVHF EDKDNQAQEK GGPLDGVYRL IQFHFHWGSI DGQGSEHTVD KKKYAAELHL 120
 VHWNAKYGDF GEAAQQPDGL AVLGIPLKVG SAKPGLQKVW DALNSIKTKG KSADFTNFDP 180
 STLLPGCLDY WTYDGSLLTP PLLESVTWIV LKEPISVSSE QMSKFRSLLF TSEGEAACCM 240

-continued

VDNYRPPQPL KGR	253
SEQ ID NO: 329	moltype = AA length = 297
FEATURE	Location/Qualifiers
source	1..297
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 329	
MDNNLAAAVR IVVEVLLFVF ICILIWWVIQ SKREEAATLQV KLAGAQVQIN TATEKLATTE	60
AAFAEAEAHKL DKAAGALWE YEGRGCPDFW GKVPTCCIG KSQAPLDIIG PFGKAKAKIQ	120
VDYKLSGLKL IHNGHTVQVN VAPGSRLLV DGVAYELLQFH FHRPSEEWIE GKPSDMSLHL	180
VHKSADGKLA VLGVLLQAMA ADNQGLVPIW THLPSAEGPE QSFPETNVDP AKLIPSNLAY	240
YQVEGSLTTP PCTEGVTFPI LKTAKMPISKG QLDAFPPIHS NARPVQPLNG RTIYSSS	297
SEQ ID NO: 330	moltype = AA length = 264
FEATURE	Location/Qualifiers
source	1..264
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 330	
MRIKRLGLSR LGIGLLSITV VGTASAEGVL ATEAGPPAQG ATLAQWYEGER QGPHWGTLA	60
PTTASCEKGT HQSPINIRTA SHPHGHDGML IQYRAASGHV GTSHHTVEVD FQSGGTLELS	120
GRSYSLSKEFH FHEPSEHQLN GRIYPME AHL VHRDESGHVL VLAILMELGT ETAPLADVWE	180
RIPSGKQEV RDLLFNQPDL LPKDLDHHAY DGSLTTPPCT EGVHWIVLKE PIHITAHL	240
RFVSLIGHNA RPVQPLNERE VDEE	264
SEQ ID NO: 331	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 331	
MQEITVTRFE NIRPSPVTPW NPEPRLPRIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR	60
SDEGYPIVIG DNSNVQDNVV LHALETRDAA GRELEENVVT VGDEKYAVYV GANVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FNSRVGANCV LMPLAAAIGV TVPDGKYIPA GTVVTTOEEA	180
AKLPKVTPDH PFATTNAAVV KVNVLAAGY RALA	214
SEQ ID NO: 332	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 332	
MQEITVLFVS NVRKNEVTPW NPKPETPKID PTSYIDPEAT VIGDVTIGKN CYIAASAVIR	60
ADEGRPIVIG DRSNVQDGVV LHALESVDDG GKREENIVL EGGKYYAVYV GKNVVLAHQA	120
QVHGPAAWGD DSFVGGMKSLV FKAIVGSNCV LEPEAAAIGV TVPDGKYIPA GTVVTTOAEA	180
DKLPPEVTPDD AKYTANVAVV NVNVNLAKAY RELA	214
SEQ ID NO: 333	moltype = AA length = 247
FEATURE	Location/Qualifiers
source	1..247
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 333	
MILNSAGIFPK RVTQECYHWD YGKHMWEKFT FPSAAGNRSQ PINIQPREAQ FDPSLKPPLT	60
KYDPSTSLEI LNNGHHSFQVT FVDDDSSTL TGGPITGYR LKQFHFWGA ADDKGSEHTV	120
DGVKYPCEHL LVHWNNAVKYA SFAEEAAEPD GLAVGVFLK IGQHHEELQK LVDALPSIKH	180
KDTLVTGFSD DPSCLMPTCP DYWTYSGSLT TPPLSESVTW IIKKQPVEVD HDQLEQFRTL	240
LFTSEGE	247
SEQ ID NO: 334	moltype = AA length = 261
FEATURE	Location/Qualifiers
source	1..261
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 334	
MKSLIAVEGT CHWNYDQEQR PEEWHNDYPVA NGLRQSPIDI KPAETQYDST LRPLSLFKYDP	60
STAKEILNNG HSFQVTFDDS SDKSVLSGGP LTGTYRLKOF HFHWGASDEH GSEHTVGDVK	120
YAAELHLVHW NSDKYASFAE AAAKPDGLAV VGVFLKIGEA NPALQKLLDA LSSIKTKGKQ	180
TTFTNFDPST LLPSSLQDWT YLGSLTVPPPL LESVTWIVLK EPISVSPAQL AKFRSLLCG	240

-continued

EGEAACCMVD NYRPPQPLKG R	261
SEQ ID NO: 335	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 335	
MQEITVTRFE NIRPSPVTPW NPTPKLPKIH PTAYIDPAAV VQGDVTIGEN VLVMANAVIR	60
ADEGYPIYIG DNSSVQDNVV LHALETVDEN GNRIEENIVT VGDKEYAVVI GKNVVIAHNA	120
QVHGPAIVGD NTFIGMNALV FRSKVGKNCV LEPLAAAIGV TIPDGTYIPA GKVVTTQEEA	180
DKLPKVTPDH PFYKLNERVV KVNIALAKGY RALS	214
SEQ ID NO: 336	moltype = AA length = 258
FEATURE	Location/Qualifiers
source	1..258
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 336	
MIRSAPGVFI CTNWQKYDH VAEGSEQSPI NIVTDKAVID STLKPLEKY DASTALEIVN	60
NGHSVQVKFD DSSDKAVLKG GPLTGPYRLK QFHFHWGKKD DVGSEHTVDG VKYASELHLV	120
HWNNAKYGSFG EAASQPDGLA VVGVLKIGS AKPGLQKVDD ALNSIKTKGK SADFTNFDPS	180
TLLPSSLSDYW TYDGSLTTPP LLESVTWIVL KEPISVSSEQ MSKFRSLLFT SEGEAACMV	240
DNYRPPQPLK GRQVRASF	258
SEQ ID NO: 337	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 337	
MQEITVLEFS NITKNEVTPW NPEPPTPVID PTAYIDPQAT VIGDVTIGAN CYIAASAVIR	60
ADEGKPIVIG DRSNVQDGVV LHALESINDG GMVREDNVVE VGDENYAVVV GKNVVLAHQS	120
QVHGPAIVGD DSFVGGMKSLV FKSIVGSNCV IEPEAAAIGV TVPDGKYIPA GTVVTQAEA	180
AKLPEVTPDH AAYSQIAAVV AVNVALCQAY RDQA	214
SEQ ID NO: 338	moltype = AA length = 217
FEATURE	Location/Qualifiers
source	1..217
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 338	
MVLFFLSSS YLISASTAHG EVEDESEFTY DEGSEKGPKN WGKIKPQWKA CSTGKLQSPI	60
DLDQRVQVL PNLGELKREY KPAPAVIKNR GHSTITWKWG DAGKIKINGT DFKLQQCHWH	120
SPSEHTFNGS RYNLEMHVH LSAQNKIAVI AILYKYGRPD FPLSRLFHHI KTVGTEERDI	180
GIINPGEIKF GSRKYYRYIG SLTTPPCTEG VIWTVFK	217
SEQ ID NO: 339	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 339	
MQEITVLLFS NVQKNEVTTT NPKPTTPVID PTSYVDPNAT VVGDVTIGKN VLIWATAVIR	60
ADEGKPIVIG DRSNVQDGVV LHALETDNNV GKIRTDNNV HGDELYAVVI GNNVSLAHQA	120
QVHGPAIVGD DSFVGGMKSLV FKSIVGSNCV IEPFAAAIGV TIPDGKYVPS GTVVTQEEA	180
AKLPEITADH AQYTQQAQVV SVNVRLCKAY REQK	214
SEQ ID NO: 340	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 340	
MQEITVTLYE NIRPSPVTSW NPTPKRPVID PTAYIDPAAV VQGDVTIGKN VLVMANAVIR	60
ADEGYPIVIG DNSSVQDNVV LHALETVDEN GNVIEENVVE VGDKEYAVVV GDNVVLAHLA	120
QVHGPAIVGD NTFIGMNLALV FRSRVGKNCV LEHLSAAAIGV TVPDNTYVPA GTVVTQEEA	180
AKLPKMTPDH PHYNLVERVV KVNVELAKGY LALS	214
SEQ ID NO: 341	moltype = AA length = 274

-continued

FEATURE	Location/Qualifiers
source	1..274
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 341	
MKLNNSFVAIG CTPREQYHWD EVIKGGPNW AEYFPLANG KQSPIDIVPG SAKYDSGLKP	60
LTLKYDPSTS LEILNNNGHSF QVTFSDDTDS STLTEGPISG VYRLKQFH FH WGASDDKGSE	120
HTVDGVKYAA ELHLVHWNAV KYSSFGEAAS KPDGLAVLGV FLKVGKHGE FEKIVNALGS	180
IHKKDTLATF ENFDPSCLMP ACPDYWTYDG SLTTPPLSES VTWIVLKEPI SVSPSQMAKF	240
RSLLFTSEGE KACCMVDNYR PPQPLKGRQV RASF	274
SEQ ID NO: 342	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 342	
MQEITVTVFE NIQPSPVTPW NPEPKRPEIH PTAYIHPAAV VQGDVTIGAN VLVMANAVIR	60
ADEGYPIVVG DNSAVQDNVV LHALETVDAS GKELEENIVT VGDEKYAVVV GDNVVLAHNA	120
QVHGPAVGD NTFVGMNALV FRSRVGANCV LEHLAAALGV TVPDGRYVPA GRVVTQEEA	180
ARLPAPVTPDH PHADLNARVV AVNVALAKGY LALA	214
SEQ ID NO: 343	moltype = AA length = 276
FEATURE	Location/Qualifiers
source	1..276
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 343	
MKKTIMLVPV LFVFIAIFMT CDNKTNHHKD VKHSKETKEE MKKETAKKDC DQVHWSHHKG	60
EHGOPENWANL CEGFKDCNGE KQSPIDIKEA VKGEDLKPLE FEYGKTKVNI INNNGHTVQFN	120
IDKGSSMMVD GKKYDLLQFH YHATSEHTIK GEYSPLEVHF VHRHADDFA VLGINMYEEGE	180
ANDLFNKYLK HFPADKGEYT SDEKFDDAL LPDNLSYYHY GGSLTTPPCS EVVSWYLLQN	240
PLRASQEIQIK DFSEILDKNF RPIQELNGRT IYKFGE	276
SEQ ID NO: 344	moltype = AA length = 264
FEATURE	Location/Qualifiers
source	1..264
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 344	
MKRKLASVFTI CGWNYQDPEH WHELFPTAKG NHQSPINIEF RKTIYDSTLK PLTFSYEAT	60
SRRIVNNNGHS PQVEFEDTN KSVLKGGLPT DRYRLTQFH FH WGSSDDHGS EHTVDGLKYP	120
AELHLVHWNA KYGSFGEAAS KPDGLAVVGV FLKIGRENAE FQLVLDALDS IKTKGKQTDF	180
TNFDPSCLLP ACRDYWTYSG SLTTPPLSES VTWIVLQKPI EVSPRQLSKF RSLLFTSEGE	240
KEKRMVDNFR PLQPLMNRSF RSSF	264
SEQ ID NO: 345	moltype = AA length = 332
FEATURE	Location/Qualifiers
source	1..332
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 345	
MITRLPAVTA VLAMFVVCMS AHDPWNTDYT SQRGPLFWGQ RPEFKMCGLG REQSPINIRR	60
STTIYQDFPP LAFELKSPIV HSNIENKGSA TAAFPLSDIP ILSGGGLGNR KYRVYNVHLH	120
FGNYSFRAAE HAFDGVRTTG EFHIVTYDSR YPHIKAALGS GRRGALAVLG VMFEARNVSN	180
IDMGVTNLIE LLSNVNTYKGD HYMTGIDFSN LVSEVDMGYY YAYNGSLTTP TCNEVQQWMV	240
IDRIHYVLPE TADLLELKT GYRREHSIPI FGNTRPLQPL YGRKVLRSGF PVVTDVHDQG	300
EEIVYSSADL VGPLGRVMLL ALAAIATFVI KA	332
SEQ ID NO: 346	moltype = AA length = 242
FEATURE	Location/Qualifiers
source	1..242
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 346	
MKLTSAFIVC GYQNHEPRDW HEVAPSAGN RQSPINIQWR DSVYDPGLKP LTISYDPATC	60
LHIWNNGYSF LVEFEDSTDK SVIKGGPLEN NYRLKQFH FH WGATDDHGSE HTVDGVKYS	120
ELHLVHWNAF KFDSFVEAAH EKDGGLAVLGV FLKIGEHNAQ LQKITDILDS IKEKGKQTRF	180
ELHFLVHWNAF KFDSFVEAAH EKDGGLAVLGV FLKIGEHNAQ LQKITDILDS IKEKGKQTRF	240
TA	242

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SEQ ID NO: 347      moltype = AA length = 335
FEATURE
source
1..335
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 347
MNNRPIQPLN DRSIWINRIK TEKCEFGWCP PVEEEPEKAS KKVEKDDSK ASSKQGKSDK 60
KGKSSGDKKS GKKSGKSNKK EKEPPQWNYA SVQRWEDDYS MCGGKKQSPV NANTSKIQSV 120
QGPAGLVLVR MAYSAVGPNA GFQPKNNGKS LVLEGNWCTL RLPDGDIAK SIKFHFPSEH 180
AVDGVLAAGE MHIVHQRSDA TGTGGLAVIA ILLRDSDLIG QAGPVGFDR LGFSSRLPVE 240
GETVILGADT VLDIGAIFAP QLGGKYWHYE GSLTTPPCSE TVHWYLMQTP AGINKAMVNN 300
FKSLFPSPAN NRPVQGMYGR AIVVTELSVS SKEFD 335

SEQ ID NO: 348      moltype = AA length = 252
FEATURE
source
1..252
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 348
MKFAAAVASI VFAVSGAAAI AAPEGAVDWV YGDGDLPEKW SITNEAYGAC DAGNMQSPID 60
LDLANTRGEI EFASSYEETT GELKTGPKV QVDVAPGMG ISGQHLFLSLV QFHFPSEH 120
RLHGQRYPLT VHLVHGTATG DFAVLGVMFE EGDENPALAR ILSGIDGGSK NVAVDVRELV 180
PENIDVYRYM GSLTTPPCTE GVLWLILKQP ASISAEQLRL FSQSLYPNNAR PVQSLNRPV 240
RDALLIAPGG RP 252

SEQ ID NO: 349      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 349
MQEITVTKYE NIRPSPVTPW NPEPKLPKIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR 60
SDEGYPIYIG DNSNVQDNVV LHALETVDEN GKPLEENIVK VGDKDYAVYY GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSRVGKNCV LEPLAAAIGV TVPDGTYVPA GTVVTTOEEA 180
AKLPKVTPDH PFYKTNEAVV KVNIALAKGY LALK 214

SEQ ID NO: 350      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 350
MQEITVLTYS NVTKNEVTST NPKPTTPVID PTSYVDPNAT VTGDTIGKN CFIGAFAVIR 60
ADEGKPIVIG DRSNVQDGVV LHALESVDDG GEIREDNVV HGDEYYAVVI GKNVSLAHQA 120
QVHGPAHVGD DSFVGMKSLV FNSIVGDNVCN IEPDAAAIGV TVPDGKYIPA GTVVTTOEEA 180
AKLPVTPDH FFYTQIAAVV QVNVDLCKAY RDKK 214

SEQ ID NO: 351      moltype = AA length = 260
FEATURE
source
1..260
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 351
MLKEWGYASH NGPDWTWQIF RCARGNNQSP IELKTKDIKH DPSSLQPLSVS YDPGTAKEIV 60
NVGHSHFHVNF EDSDRNRSVLK DGPITGSYRL RQPHFHVGAS DDHGSEHVV DGVRYAELHV 120
VHNWADKYPY FVEAAHEPDG LAVLGVFLKI GEHNPHLQKI TDVLYAVKFK GTKAQFTNFN 180
PKCLLPASLD YTWTYPSLTT PPLSECVTWI VLKEPISVSP SQMAKFRSLL FSSEGETACC 240
MVDNYRPQQP LKGRTVRASF 260

SEQ ID NO: 352      moltype = AA length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 352
MQEITVLEFS NITKNEVTPT NPKPSTPVID PTSYVDPNAT VIGDVTIGKN VLIAANAVIR 60
ADEGAPIVIG DRSNVQDGVV LHALESVDDD GKILEDNVVE KGDEYYAVVI GKNVHLAHQA 120
QVHGPARVGD DSFVGMKSLV FKSKVGSNCV IEPDAAAIGV TVPDNKYIPA GTVVTTOEEA 180
DKLPVTPDY AYSDTNEAVV TVNVDLNEAY RNQQ 214

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SEQ ID NO: 353      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 353
MQEITVTKYE NIRPSPVTSW NPEPKLPKI PTAYIDPAAV VQGDVTIGEN VMISALASIR 60
SDEGYPIIVIG NNNSNVQDQVV LHALETVDEN GNVLEENVTE VGDKKYAVYI GDNVSLAHQA 120
QVHGPAAVGN NTFIGMQSFV FRSGVGENCV LEPLAAAIGV TVPDGTVPA GTVVTTQEEA 180
DKLPKVTPDH PFYNTNAAVV KVNVLA KGY LALK 214

SEQ ID NO: 354      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 354
MQEITVNLNS NIEKNEVTST NPKPTTPVID PTSYIDPNAT VTGDTIGKN CYIGPFAIR 60
ADEGAPIIVIG DNSNVQDGVV LHALESVDDG GKIRKDNNVE VGDNNYAVYV GKNVSLAHQS 120
QVHGPAAVGD DSFVGMMATV FNSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTQEEA 180
DKLPEITEDY PFYTAVEEVV KVNVLA KGY REKK 214

SEQ ID NO: 355      moltype = AA length = 272
FEATURE          Location/Qualifiers
source           1..272
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 355
MLSRKPAGHT DIYEQFVCNW KNNGGKLHRS SATDPEGERQ SPIDIQTSKV EVDQKLQPLT 60
LTYPDSTSLE ILNNNGHSVQV TFKDKDNRSV LKGGLPTGPY RLKQFHFWG KKDDVGSEHT 120
VDGAKFASEL HLHVHNNAKKY SSFAEEAASKS DGLAVLGVFV QVGEHNAQLQ KITDILDSIK 180
EKGKQTRFTN FDPLSSLPPC RDYWTYHGSL TVPPLLESVT WIILKQFISV SSQQLAKFRS 240
LLCTSEGEKA VPMLSNSHRPP QPLKGRQVRA SF 272

SEQ ID NO: 356      moltype = AA length = 333
FEATURE          Location/Qualifiers
source           1..333
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 356
MTMKLSQLGQ LFLVICCLTV VINAMPNPQA QAPSGALVAT AESGHFSYDD PNKWKEHNSL 60
CAGEHQSPIN IDTRKSRTDK FPPFRFHNYA KGLPENLENM GHTVQLTIDN LIKDLPTISG 120
GGLEGPYFEA QMHFPWGEDE FGSEHKINNK QYAGEVHIVH WNKKYGNFVN ATKHNDGLAV 180
LGILIDLQDK ENIAFSHIEQ FDEIRDASKK NEKLPPYSVPL KDLLPSNTAS FFRYEGSLTD 240
ARCNEDVTGP FLKHQFTSPI IRQLNDEGE PLSKNVRPTQ EEHDRIVTYS GRAMQCGTCS 300
TATADRSSEG RSDSSSESGES KEITKSKTRH YGY 333

SEQ ID NO: 357      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 357
MQEITVTRYE NIRPSPVTPW NPEPLRPEIH PTAYIDPAAV TVGDVRIGAN VMVSALASIR 60
SDEGYPIIVIG DNSNVQDQVV LHALETVDAD GKVLEENVTE VGDERYAVYI GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSGVKDCV LMPLAAAIGV EVPDGRYIPA GKVVTQEEA 180
DKLPKVTPDH PFANTNAAVV AVNVALAKGY LALA 214

SEQ ID NO: 358      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 358
MQEITVTTYN NIRPSPVTPW NPEPKLPKI PTAYIDPAAV VQGDVTIGEN VLVMANAVIR 60
ADEGAPIIVIG NNSSVQDNVV LHALETVDDED GKRIEENVVK VGDKDYAVYV GDNVVLAHNA 120
QVHGPAAVGD NTFVGMMALV FHSNFGKNCV LAPNAAAIGV TVPDGKYIPA GKVVTQEEA 180
DKLPEVTPDH PFYDLNARVV KVNVLA KGY LALA 214

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SEQ ID NO: 359      moltype = AA length = 267
FEATURE
source          Location/Qualifiers
1..267
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct
SEQUENCE: 359
MAMLNKKRKE WKMRGRVFFA LILAMCLSAVA GYSLYEKEQON QHDEERIEDV YYSYDEHGPD 60
AANVCERGMM QSPVQITRKD ALQNQSPEIE IHYGEGRFEI IKKAHTAEAV SKSGQNYILI 120
DHQQYKLESF HHFLPSEHQV EGQSYEMELH FVHENKNGEQ AVMAVFQEG QANEMVKEIW 180
SRLQDGFSKK DNVSIRLPEF IPKERAFYY TGSLTTPCCT EGVKWIVFEM PVEFSEEQIG 240
TFHRLFGNNS RQVQPLNGRK IYQLTVR 267

SEQ ID NO: 360      moltype = AA length = 293
FEATURE
source          Location/Qualifiers
1..293
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct
SEQUENCE: 360
MKHCTLLAIL LSGLLSAAVE TDFSYADQGA WQTLSPNSQCG GRRQSPVLDL LRNVTVDKIL 60
GQDLACTWQQ NKAVIDGDLV NTGRTIELDV RSPHTCRGVP GSPSAHFRLA AVHIHYGSAS 120
DQGSEHTING RTSALEVHMV HFDTRFASLD KAREQPGGIM VAGLLFDEAD EAIAHPELTK 180
MAVISGTALR STGGVLASRL NAAPLIEGTG LDKARARPLT YAGSLTTPTC NEVVTWIVAA 240
EPGLVGHQTM HLLRTVTGLG NKTISPNNFRQ VQPLNGRTIT SSFQPACGLH GRC 293

SEQ ID NO: 361      moltype = AA length = 266
FEATURE
source          Location/Qualifiers
1..266
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct
SEQUENCE: 361
MLKNPAGDWS YEQTvhFIRC TDFIPAVILP GGARQSPINI VTSQAVYSPS LKPLELSYE 60
CTSLISITNNG HSVQVEFNDS TDRTVIKGPP LEGPYRLKQF HFHWGARDSR GSEHTVDGAR 120
YPSELHLVHW NAKYASFGEA ASQPDGLAVV GVPBKIGREK PGLQKVLDAL DAIKTKGKQT 180
RFTNFDPSTL LPGCLDYWTY DGSLTTPPLL ESVTIVLKE PISVSSGQMA KFRSLLFTSE 240
GETACCMVDN YRPPQPLKGR QRASF 266

SEQ ID NO: 362      moltype = AA length = 214
FEATURE
source          Location/Qualifiers
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct
SEQUENCE: 362
MQEITVLEYS NIKRNNEVTPW NPKPSTPVID PTSYIDPNAT VIGDVTIGAN VLIGPNAIVR 60
ADEGRPIVIG DRSNVQDGVV LHALESVNDE GMEIGDNVVL EGNSYYAVVI GKNVVLAHQS 120
QVHGPAAVGD DSFVGGMQSLV FNSIVGNSCNV IEPNAAAIGV TVPDGKYIPA GTVVTTQAEC 180
DKLPEVTPDH AFYTDVAKVV SVNVNLCRAY KEQS 214

SEQ ID NO: 363      moltype = AA length = 186
FEATURE
source          Location/Qualifiers
1..186
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct
SEQUENCE: 363
MIRKNPSGHL PVIAETAFID QTAAICGKVI IYDNVFVGPY AVIRADEVNE HGDMEAIVIK 60
RDTNIQDGVV IHSKAGAAVT IGERSSIAHR SIIHGPCWVG DDVFIGFNSV VFNAKIGKGC 120
VIRHNSVVDG LDLPEHFHVP PMTNIGADFD LSSISKVPPE YSAFSESVVS ANHELVQGYR 180
RIANEL 186

SEQ ID NO: 364      moltype = AA length = 212
FEATURE
source          Location/Qualifiers
1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct
SEQUENCE: 364
MRILVLTACFY PNSEHDGQKW ANIKPEWKTC GHGKMQSPID LSSHVRVSLHV DQTWNRDYKP 60
APAVIVNRGH DIMVSWKEDA GKVTIHQTDY KLVQCHWHSP SEHTVNGTRY DLELHMVHTS 120
AQGKTAIVGV LYKLGRPNEF LAKLLEDGIGS VGKEEKDLGI VDPRTIGFHT DKFYRYVGSL 180
TTPPCTEGVI WTVVKKVNTV SMEQLAALRE AV 212

SEQ ID NO: 365      moltype = AA length = 214

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FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 365	
MQEITVTRYE NIRPSPVTSW NPEPKLPKID PTAYVDPAAV VQGDVTIGKN VMVSANASIR	60
SDEGYPIYIG DNSNVQDNVV LHALETVAD GKRIEKNIVT VGDKEYAVYY GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQSFV FNSTVGKNCY LAPLAAAIGV TIPDGTYIPA GKVTTQEEA	180
AKLPKITPDH PFANTNAAVV KVNVELAKGY LALK	214
SEQ ID NO: 366	moltype = AA length = 237
FEATURE	Location/Qualifiers
source	1..237
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 366	
MSTPLVRWGY KEDNGAHQWC IFFPEACGKR QSPINIQTSK VVYDPGLRPL NLNYDPSTSL	60
EILNNNGHSVQ VNFKETDDRS VLSGGPVGTG YRLRQFHFHW GAKDCRGSEH TVAGVKYPSE	120
LHLVHWNAVX YESFAEAALE ENGLAVIGVF LKLGKHHDEL QKLVDALPSI KHKDTLVEFG	180
SPDPSCLMPT CPDYWTYSGS LTPPPLSESV TWIIKKQPVE VDHQDQLEQFR SLLFTSE	237
SEQ ID NO: 367	moltype = AA length = 305
FEATURE	Location/Qualifiers
source	1..305
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 367	
MSSTFVVGRP CDTRLPRGSR KEPARVPHGF AAGIATVVSL ALLCLAGGCA HAPVPREAGR	60
SVAQSEADYY SDALAPWTYP EGPSWGAACA KQPPPQQSPI DLTRVTTAPW SASSVITQAT	120
FDGHDQNVFV QASPGPSVTM APGVGDGSRA FVYTVAGFH HYRNEHVIAG NPVYELHIKT	180
VQHGHHVAVF AVLWTADAA GEDPTLAAAY RSLSAPPDSV VAVDLGRALW RFGQQPFYSY	240
VGSLLTTPCCT TGIRWFVLQT PIRTSSASIG RLNAALIARG MPRDNVRTVR PVAQPQPVVY	300
LVTPK	305
SEQ ID NO: 368	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 368	
MQEITVLEFS NITKNEVTPT NPKPTTPVID PTSYVDPNAT VTGDVTIGKN VLIGPNAVIR	60
ADEGRPIVIG DNSSVQDGVV LHALESVDE GKIIEDNVVL YGNKYYAVYY GKNVVLAHQS	120
QVHGPAAVGD DSFVGMLS LV FNSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVTTQEEA	180
DKLPEVTDY KPYTQVAKVV TVNVNLCEAY RNQA	214
SEQ ID NO: 369	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 369	
MQEITVTTFT NIRPSPVTPW NPTPKLPKH PTAYVDPAAV VQGDVTIGEN VMISANASIR	60
SDEGYPIYIG NNSNVQDNVV LHALETVDEN GKVIENVVT VGDKKYAVYY GDNVSLAHQA	120
QVHGPAAVGD NTFIGMQAFV FKSNIGKNCV LEPLAAAIGV TVPDNKYIPA GTVTTQEEA	180
AKLPPEVTPDH PFANTNAAVV KVNNNALAAGY LALS	214
SEQ ID NO: 370	moltype = AA length = 283
FEATURE	Location/Qualifiers
source	1..283
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 370	
MKLSNVFIAG CTYQEPWDHR EWDYSSKGPA TWGLINSAWS LCSIGKRQSP IDIELNQLLY	60
DPFLPPLRLS SGGKKLGGTM YNTGRHVSFR PDKAQLVNIS GGPLSYSHRL EEIRLHFGSE	120
DSQGSEHLLN GEAFSGEVQL IHYNQELYSN FSEAAARKPNQ LLIISIFMKV ADTSNPFLNR	180
MLNRDTITRI SYKNDAYFLM NLNIELLYPE SFGFITYQGS MSTPPCYETA TWILIDRPIN	240
ITSLSQMHSLR LLSQNLPSQI FLSMSDNSRP LQPLAHRALR GNR	283
SEQ ID NO: 371	moltype = AA length = 214
FEATURE	Location/Qualifiers

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source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 371
MQEITVTRYE NIRASPVTPW NPTPKLPKIH PTAYVHPLAE VVGDTVIGAN VMVSANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDAN GNRIEENIVK VGDEEYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVVGKNCY LAPLAAAIGV TVPDNTYIPA GKVVTTQEEA 180
AKLPKMTPDH PFYNTNKAVV KVNVVALAKGY LALA 214

SEQ ID NO: 372      moltype = AA length = 280
FEATURE
source          1..280
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 372
MRSPLAGWTI VFCQKDEYNH LDGILGGPGY WGLINPEWRM CSKGKMQSPI DIDPKVLLYD 60
PNLSAVHLDK HKVSGTLENT GQSLVFRVDK GSRQHVNISSG GPLPLAYRYQFH EIFLHYGLKD 120
SMGSEHRING YSFPAIBQLY GFNSELYHN M SEAQHKSGQI VGVSLMVQIG ETPNPELRIL 180
TSQLERVRYR GQSAPIHHLS LRGLLPDTEH YMITYEGSTTH PGCWETTVWV ILNKPIYITR 240
QELYALRRRLM QGSQSOPKAP LGNNARPVQD LHGRRTVRNTI 280

SEQ ID NO: 373      moltype = AA length = 221
FEATURE
source          1..221
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 373
MLISRFATGH PKENDCYQW FGPNGEKGPD KWGKINPKWK VCGEGKLQSP IDLLNQRVQI 60
LPNLGKLQKD YKPAPAVLKN RGHDIMVKWK GDAGKLNING TYKKLVQCHW HTPSEHTING 120
TKFDMELHLAV HKSSKGGETAV IGIWYKIGRP DSFLSKLLKN IKSVGDKIED LGVINPGDIK 180
FGSRKYYRYM GSLTVPPCTE GVIWTIVKKV RTVSREQLRA L 221

SEQ ID NO: 374      moltype = AA length = 224
FEATURE
source          1..224
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 374
MKRSLIFAVG TCPQEDWHYN YDEASGRGPB RWGLLKPEWR TCSVGKLQSP IDIGTVQVSS 60
ELGDLQRNYR SAPALLRNRT EDVAWIWLGN AGSITINGVVY YRVVNCHWHS PSEHTFNGTR 120
LPLEIHTVHR SSQNRRIAVVG ILYKYGLPDP FLSKLFHSIK SLGKEEKNLG IVNPESIGFQ 180
DKKYYRYIGS LTTPPCSEGV VWTVFKKVRT VSREQLKALK DAVD 224

SEQ ID NO: 375      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 375
MQEITVTRFE NIRASPVTPW NPEPKLPKIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDEN GNVLLEENVVT VGDEKYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVVGKNCY LAPLAAAIGV TVPDGTYVPA GKVVTTQEEA 180
AKLPKVTDPH PFANTNAAVV KVNVVALAKGY LALA 214

SEQ ID NO: 376      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 376
MQEITVTKYN NIRASPVTPW NPTPKLPNIH PTAYIDPAAV VQGDVTIGAN VMVSANASIR 60
SDEGYPIVIG DNSNVQDNVV LHALETVDEN GNPIKENIVK VGDKDYAVVV GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQSFV FASEVVGKNCY LAPLAAAIGV KVPDNTYIPA GKVVTTQEEA 180
AKLPKITPDH PFANTNAAVV KVNVVALAKGY LAQS 214

SEQ ID NO: 377      moltype = AA length = 214
FEATURE
source          1..214
mol_type = protein
note = Library of modified or engineered enzymes

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SEQUENCE: 377 organism = synthetic construct
MQEITVLIYS NVTKNEVTW NPKPKTPKID PTSYVDPKAT VIGDVTIGKN CMISPFASIR 60
SDEGMPIVIG DNSNVQDGVV LHALETVDTN GKIIEDNVII KGDKRYAVYY GKNVSLAHQS 120
QVHGPARVGD DSFIGMQSFV FKSIVGSNCV IEPNAAAGV TVPDNKYIPA GTVVTTOEEA 180
DKLPKITEPDY KYYNTNDAVV YVNVKLCKAY RNKS 214

SEQ ID NO: 378 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 378
MQEITVTFN NIQPSPVTPW NPEPKLPIH PTAYIHPLAY VQGDVTIGEN VLVMANAVIR 60
ADEGYPIVIG NNSSVQDNVV LHALETVDEN GNRIEENIVK VGDEEYAVVI GDNVVLAHNA 120
QVHGPAAVGD NTFVGMNALV FRSRVGKNCV LEPLAAAAGV TIPDGTYIPA GKVVTTOEEA 180
AKLPKITPDH PFYNNLVDRVV KVNVLAQGY LALS 214

SEQ ID NO: 379 moltype = AA length = 227
FEATURE Location/Qualifiers
source 1..227
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 379
MKSLFLFACTV IGWNYEDQPH WSELDPAYAA CATGKEQSPI DIRGARRADL PPLRFEYRSA 60
PLKYVINNGY TIRVNYHDSP GSGNPLIVGD ARYQLTQPHF HRPSEEVHVG KPYTMELHLM 120
HQSSDGEVAG VAVLLKAGRA NATIQLWEH MPATEGQEQV LAGVTIDPAG LLPRETGYV 180
YMGSVTAPPC TEGVTFWVFLK TPVEISAEQI AVFARLYPHD VRPLQPL 227

SEQ ID NO: 380 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 380
MQEITVTRYE NIRPSPVTPW NPEPRLPEIH PTAYIDPKAV VQGDVTIGEN VLVMANAVIR 60
ADEGYPIVIG DNSSVQDNVV LHALETVDEN GNRLKENVVT VGDKEYAVVI GKNVIAHQA 120
QVHGPAAVGD NTFVGMALV FNSTIGKNCY LAPLAAAAGV TVPDGTYIPA GTVVTTOEEA 180
AKLPKITPDH PFADLNARVV KVNVLAQGY LALA 214

SEQ ID NO: 381 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 381
MQEITVTRYE NIRESPTSW NPTPRRPEIH PTAYVDPAAV VVGDVRIGAN VMVSANASIR 60
SDEGYPPIVIG DNSNVQDNVV LHALETVDAA GNRITENIVT VGDEEYAVYY GDNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSNVGKNCV LEPLAAAAGV TVPDGTYVPA GKVVTTOEEA 180
AKLPKVTPDH PFANTNAAVV AVNVLAQGY LALA 214

SEQ ID NO: 382 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 382
MQEITVTRYE NIRPSPVTPW NPEPKLPIH PTAYVDPAAV VVGDVTIGAN VMVSANASIR 60
SDEGYPPIVIG DNSNVQDNVV LHALETVDEN GKVIENVVT VGDKKYAVVI GKNVSLAHQA 120
QVHGPAAVGD NTFIGMQAFV FRSVVGKDCV LEPLAAAAGV TVPDGTYIPA GKVVTTOEEA 180
AKLPKITPDH PFANTNAAVV KVNVLAQGY LALA 214

SEQ ID NO: 383 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 383
MQEITVFEFS NITKNEVTPT NPKPTTPVID PTSYIDPNAT VTGDVTIGKN VLIGPNAVIR 60
ADEGAPIVIG DNSNVQDGVV LHALESVDDE GEIIEEDNVVL EGDEYYAVVI GKNVVLAHQA 120

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QVHGPAMVGD DSFVGGMKALV FKSIVGSNCV IEPEAAAIGV TVPDGKYIPA GTVVTTQAEA	180
DKLPEVTDY PFYTAVEEVV EVVNVLAEAY REQS	214
SEQ ID NO: 384	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 384	
MQEITVMDF NIVKNEVTPT NPKPTTPVID PTSYIDPNAT VIGDVTIGKN CYIGPFAIR	60
ADEGAPIVIG DDSNVQDGVV LHALESVDAG GKIREDNVVT VGDRSYAVYY GKNVSLAHQS	120
QVHGPARVGD DSFVGGMNSLV FNSIVGDNVCV IEPGAAAIGV TVPDGKYIPA GTVVTTQAEA	180
AKLPEVTPDH AAYSANAAVV EVNVALSEAY RNLK	214
SEQ ID NO: 385	moltype = AA length = 271
FEATURE	Location/Qualifiers
source	1..271
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 385	
MVKRNILADF SPEGQTHWCY DCFIRPLPPV KWAKLFPKAK GNFQSPINIE SRETRYDPSL	60
KPLTLKDYPS TAKLISNSGH SFNVDFFDTE DKSVLRGGPL TGSYRLRQFH LHWSADDHG	120
SEHAVDGKVY AAELHHVHWN AVKFESFEEA ALEENGLAVI GVFLKLGEHN PHLQKITDIL	180
YS1KFKDTLA EPTNFPKCL LPTSLDYWTY SGSLTTPLL ESVTWIVLKE PISVSSEQMA	240
KFRSLLFTSE GETACCMVDN YRPPQPLKGR Q	271
SEQ ID NO: 386	moltype = AA length = 238
FEATURE	Location/Qualifiers
source	1..238
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 386	
MLSKRIFGVA TCQOPENWHDY YKNANGEKQS PINIVTKETK YDSSLKPLTF KYDPSTAKEI	60
VNVGHSHFHVN PEDSENKSVL KGGPLTGTYR LKQFHFWGGS ADDKGSEHTV DGKVYPSELH	120
LHVHNAVKFE SFAEEAALEEN GLAVIGVFLK LGEEHHKELQK LTDTLPSIKH KDTLANFGSF	180
DPSCLMPTCP DYWTYPGSLT TPPLSESVTW IVLKQPPIEVs EEQLAAFRSL LFTSEGEK	238
SEQ ID NO: 387	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 387	
MQEITVLEFS NVTKNEVTSW NPKPSTPVID PTSYVDPNAT VIGDVTIGKN CYIAASAVIR	60
ADEGKPIVIG DNSNVQDGVV LHALESVDDG GKIREDNVVI HGDKWYAVYYI GKNVSLAHQS	120
QVHGPAYVGD DSFVGGMNSLV FKSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTQAEA	180
DKLPEITPDY AFYTQVAAVV KVNVNLCRAY RNQA	214
SEQ ID NO: 388	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 388	
MQEITVLIYS NVTKNEVTST NPKPSTPVID PTSYVDPNAT VTGDVTIGKN CLIGPSAVIR	60
ADEGKPIVIG DRSSNVQDGVV LHALESVDE GKIEENVVH HGDKWYAVYYI GKDVLHWAHQ	120
QVHGPARVGD HSFVGGMKSLV FNSIVGSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTQEEA	180
AKLPEITPDH EKYTKIAEVV TVNVNLCRAY RNKA	214
SEQ ID NO: 389	moltype = AA length = 274
FEATURE	Location/Qualifiers
source	1..274
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 389	
MKLSVAFCT GNQRPEWDYH NNHGKKEEW PEEYPSGGQL QSPIDLHGDI LQYDASLTPL	60
QFQGYNVSAT EQFTLTTNGH SVQLSLPSDM YLKGLPSRTY ATQLHLHWGK KGDLGSEHQ	120
INSEATAAEL HIVHYDSEKY SNISEAMNKP QGLAVLGLIY EVGETENPAY DHILSRHETI	180
QYKDQKTSVP GFNIRELLPE QLEEEYYRYQG SLTTPPCYQGS VLWTLFNRRQ QISMGQLEKL	240
QETLSSTESE PSEPLVQNYR VPQPLNQRTV FASF	274

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SEQ ID NO: 390      moltype = AA  length = 327
FEATURE
source
1..327
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 390
MGHTWCNDEE GTRGRSEGP TPAAAGVRVE RMIREGGSRR RAATPHVRCG VLYAVRGVPM 60
SARSWLTASA LTVAATVLIG CAQAPAPAETA PTERPVABPA HWSYDGDSGP ESWAGLDDAF 120
QACEAGTDQS PIDLPAAVPA PSTSIELSAE EAEGDVFDSG HAVEIETDGQ GETLTFADD 180
YSLQQLHAHV PSEHTVAGQP AAAELHLVHA DADGNLLVLG VLVTEGAASD ALTPFIEAAS 240
HILADEEVTL DLAAVLPLSL ENYEYSGSLT TPPCTEDVQW VVMGTPISMS AEQIGTLAGA 300
HHHNARPTQP LGDRTVVGGA GKVEITG 327

SEQ ID NO: 391      moltype = AA  length = 186
FEATURE
source
1..186
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 391
MARKNPMSGHL PQVSETAFID PTAAICGKVI IEDYVFIGPY AVIRADELNA AGDMEPIVIG 60
AHNSNIQDGVV IHSKSGAAVT IGEFSIAHR SIVHGPCWIG DRVFIGFNSV LFNCHIQSGC 120
VVRYNAVVDG VTLPENTYIP STERVGPDSL LSLYRQVDRG ALQFSEEVAA TNVELVRGYQ 180
ALRNEF 186

SEQ ID NO: 392      moltype = AA  length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 392
MQEITVTRYE NIRESPTVTPW NPTPKRPKIH PTAYIDPLAY VQGDVTIGEN VMVSALASIR 60
SDEGYPIYIG NNSNVQDNVV LHALETVDEN GBIEENIVT VGDEKYAVAI GDNVSLAHQA 120
QVHGPAIVGD NTFIGMQAFV FRSKVGKNCV LEPLAAAIGV TVPDNTYIPA GTVVTQEEA 180
AKLPKVTPDH PFANTNAAVV KVNVLAKG 214

SEQ ID NO: 393      moltype = AA  length = 200
FEATURE
source
1..200
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 393
MNPIITSFNPV QRYPKIDKTA FISPFSVG DVRIKDNNVV APNVSIRADE GTPFYIGSNT 60
NLQDGVLHG LLNKFVTVND KKYSIYIGNQ VSIAHDALIH GPCYIGDKVF VGFKAIIVYNA 120
IVVGKGTVISY NAVVTNGVRI APNRFVPPGA NIDTQEKAADA LSRVPKDEEE FAREVQRVNQ 180
EFPSAYHLLF GENRCSCGLS 200

SEQ ID NO: 394      moltype = AA  length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 394
MQBKITVLDFS NVTKNEVTPPT NPKPKTPVID PTSYIDPNAT VIGDVTIGKN VMWPSAVIR 60
ADEGKPIVIG DNSSVQDGVV LHALESVDAG GKVIEDNVLL EGNKRYAVYI GKNVTLAHQS 120
QVHGPAIVGD DSFVGMSFFV FNSKVGNSCV IEPEAAAIGV TVPDGKYIPA GTVVTSQAEA 180
DKLPEITDDY PYNSNAIAAVV KVNVQLCEAY KAQA 214

SEQ ID NO: 395      moltype = AA  length = 214
FEATURE
source
1..214
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 395
MQBKITVLRFS NIRKNEVTPE NPEPEPTPVID PTSYIDPNAT VIGDVTIGAN CYIGPFARIR 60
ADEGRPIVIG DRSNVQDGVV LHALESVDAE GEIIEDNVVI EGDELYAVYI GRDVSLAHQS 120
QVHGPARVGD DSFVGMSFLV FKSDVGSNCV IEPFAAAIGV TIPDGKYIPA GTVVTSQAEA 180
EKLPEITEDY PYFTTIEEVV KVNVNLAKAY REQK 214

SEQ ID NO: 396      moltype = AA  length = 214

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FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 396	
MQEITVMEFS NVTKNEVTST NPKPKTPVID PTSYVDPEAT VIGDVTIGKN CYIGPFAIR 60	
ADEGAPIVIG DDSSVQDGVV LHALESVAD GKIIEDNVVL HGDKLYAVHI GKNVSLAHQA 120	
QVHGPARGD DSFVGGMNSLV FNSVVGNSNCV IEPNAAAIGV TVPDGKYIPA GTVVTTOEEA 180	
DKLPEITPDY AKSTAIAAVV EVNVALCEAY REQA 214	
SEQ ID NO: 397	moltype = AA length = 214
FEATURE	Location/Qualifiers
source	1..214
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 397	
MQEITVAEFS NITKNEVTSW NPKPKTPVID PTSYVDPNAT VIGDVTIGKN CYIAPFASIR 60	
ADEGTPIVIG DDSNVQDGVV LHALESVAD GKILEDNIVL HGDKRYAVVI GKNVSLAHQS 120	
QVHGPAGVD DSFVGGMMSLV FKSKVGNNSCV IEPGAAAIGV TVPDGKYIPA GTVVTTOQAEA 180	
DKLPEITPDY AKSNQVAAVV KVNVALCEAY RKQS 214	
SEQ ID NO: 398	moltype = AA length = 317
FEATURE	Location/Qualifiers
source	1..317
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 398	
MQTYDSSLRE SLLPLPDKE SVRYWLILGG FVTAAAVAVF VIAARSGSHA DASVLSALI 60	
AVAPHFEYAE ANCDETKCEA SEIVQLDTWS WAPTCITGRA QSPIDIVTKE VATAGLLDDA 120	
ISLSIGSATL VPSNTGHGFQ LTSTGGTPSA MFRGEKFNFQ QTHWHTPSEN TVDGEHAAME 180	
GHFVFLQDDP LWVNNTTLNLA VMAVFFELGD CNQHLSAWVD TFPVDRLLGTG SGTFSGEILA 240	
SILLASVLGGG YYQFTGSLTT PPCTEGVAWN VMKKRTTVCQ DQVDRKLHAL SATANGVDIS 300	
NRVVQPLHQR VVTQTSR 317	
SEQ ID NO: 399	moltype = AA length = 265
FEATURE	Location/Qualifiers
source	1..265
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 399	
MSRLTGKIAV PCYQNPEHWD YDSPIAKGNR QSPIDIDLWS AKYDPGLKPL TFTGYDKKSL 60	
RTLNNNGHSV SVQFEDSEDK AVLSGGPLTG VYRLKQFHFW WGAADDKGSE HTVDGVKYPS 120	
ELHLVHWNAV KFSSFAEAS KPDGLAVGV FLKIGKEHVE LNKLTDALYM VRFKGKTAQF 180	
SCFPNPCKLLP ASRHWTYPG SLTTPPLSES VTWIVLREPI SVSERQMEKF RSLLFTSEDD 240	
ERIHMVNNRTV RSSFR 265	
SEQ ID NO: 400	moltype = AA length = 210
FEATURE	Location/Qualifiers
source	1..210
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 400	
MVPYPYPIVY QNPPVAEVTS VSYPKISRKA VIGTDMSMIIG DITIADDVYI GFKNLLRADS 60	
GHPYYYVGPYT NIQDYVLMHV HPGREHVVVN NQKQWGVPLEG MNSVLHHAACV HGPLFIGKNT 120	
FIGQHANIYD AVIGRDCVVM HGATVTNGVK IADNRFVAPG QSVWQQSEAD KLPPVPEKFK 180	
DLNRSIVDHY YRLGKSYGLN TPLAYS YSGG 210	
SEQ ID NO: 401	moltype = AA length = 288
FEATURE	Location/Qualifiers
source	1..288
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 401	
MLALTLAILL LLNARAVLSS CAHGTYLLRR AIDDNKPILK PNFGYGPFDG PTNWHSLSED 60	
NILCGTGRQ SPIDIDDTIS QVAAGFVMSD VPIQDVSPFLN LRTTVEVILK GSTRINGREF 120	
VLEQFHFTP SEHVLNGEIF VAEVHFVHSN KENPKELAVI TLMVQVSADH STRSLDRVIG 180	
EITRISTPGRN KVAIPALNIG DITSLVNKQQ LFVYTGSLLT PPCTEGVQFF ILPQPPIPRA 240	
TVFNALKSVT GHNARFLQNN NATRPNVLVA GCQVIAAEWV SNATQYSR 288	
SEQ ID NO: 402	moltype = AA length = 236

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FEATURE	Location/Qualifiers
source	1..236
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 402	
MIAATVPAGT ALADEWGYAG DGAPVNWGAL SPDFAVCSAG VQQSPVLDVP GIIADGVRPV	60
LDFADVSQVE AERSAHGVTY HVPSGSAQLS LNGRSFDLLQ FHFHAASEHW VEGQSYPLEV	120
HFVTASEGDL AVVGVLFERG EAHATVDTLW DAIGEPGDRE EIDGPVSLAS LLPQDQAAFR	180
YEGLSLTTPPC SEIVSWTVFT TPLSVSDAQI DAPFETVGEN ARPPQPLNRR YVLLDN	236
SEQ ID NO: 403	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 403	
TAYIDPQASV IGEVTIGANV MVSPMASIRS DEGMPIFVGD RSNVQDGVVL HALETINEEG	60
EPIEDNIEVE DGKEYAVYIG NNVSLAHQSQ VHGPAAVGDD TFIGMQAFVF KSKVGNNCVL	120
EPRSAAIGVT IPDGRYIPAG MVVTSQAED KLPEVTDDY YSHTNEAVVY VNVHLAEGYK	180
ETS	183
SEQ ID NO: 404	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 404	
TAIFIAPNAEV IGDVTIEGNA MISPNASIRA DEGMPYLGK DVNLQDNVQL HALETVDEEG	60
NLIEENLVEV NGKKYAVYLG ENVSLGHQAQ VHGPAYVGKD TFIGMNAVVF KSRIGNNCVL	120
EPNATVIGVT IPDGRYVKAG TVIRTQADLP KLLDLKEVPE VKKKVDEYHN KLKELIKAKK	180
AAA	183
SEQ ID NO: 405	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 405	
TAYIHPSAQV IGEVEIGANV MVSPMASIRA DEGMPIVLGD NANVQDGVQL HALETVNEEG	60
ELIEENVVEV DGKKYAVYVG ENVSLAHQAQ VHGPAAVGKD TFIGMGAKVF KSTVGNVCV	120
EPGAEVIGVT IPDGRYVPAG TVVRTQEIQIP SLREMTPDDP LLAVRDRVIA ENLKRAAEELK	180
ARA	183
SEQ ID NO: 406	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 406	
TAYIAEAGAEV IGEVYIGENV MISPNASIRS DEGMPIYIGE NANVQDGVEL HALETKDEEG	60
NLIEENVVEV NGKKYAVYVG ENVSLAHQAQ IHGPARVGKD TFIGMGAVVR GSTLGENVLL	120
GEGVVIENVT IEEGTTLVEEG TVITKQEDVK KLRKLKPSDK MVKIKKEVLE KNKKLWEKLK	180
EEE	183
SEQ ID NO: 407	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 407	
TAYIHPSATV IGPVRIEEGV MISPNASIRA DEGGPIYLGE NVNVQDGVTI HCLEVKREEG	60
RVDSEVFVEV DGEKYCVYLG EGVLGHQAT IHGPAKVGKD TFIGMGATVF RSTIGEGCVL	120
EPGATVIGVT IPEGGRYVPAG KTVTTQAEAD ALPLITDSYP YRETNNENVVA VNLALAEAAAR	180
AAA	183
SEQ ID NO: 408	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes

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SEQUENCE: 408          organism = synthetic construct
TAYIHPSAQV IGEVQIGANV MVSPMASIRS DEGMPYIYGD NANVQDGQL HALEARNEEG 60
VEDESAWVEV NGKRYRVYVG ENVSLAHQAQ VHGPAAVGKD TFIGMGASVF KSRLGNGCVL 120
EPGATVIGVT IPDGRYLPAG TVLRLGRPIEE EIELREVTE LRARHQAVVE ANLARAELK 180
ARA                                         183

SEQ ID NO: 409          moltype = AA length = 183
FEATURE
source
1..183
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 409          moltype = AA length = 183
TAYIHPSAEV IGEVEIGANV MVSPMASIRS DEGMPYIYGD NANVQDGVL HALEALDEEG 60
EEDEEAYVEV DGKRYRVYLG ENVSLAHQAQ VHGPAAVGRD TFIGMGASVF KSILGNGCVL 120
EPNATVIGVT IPDGRYIPAG AVLNVEDAEK TRELPEVTPE LRAKRAAVLA ANAARYAELR 180
AAA                                         183

SEQ ID NO: 410          moltype = AA length = 183
FEATURE
source
1..183
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 410          moltype = AA length = 183
TAYIHPSAQV IGDVQIGANV MVSPMASIRS DEGMPYIYGD NANVQDGQL HALEARDEEG 60
VEDEEAYVEV NGKRYRVYLG ENVSLAHQAQ VHGPAAVGRD TFIGMGATVF KSILGNGCVL 120
EPQATVIGVT IPDGRYLPAG AVLEGETAEA VAALPEVTPE MREAVAAQQA AAAAQYAAAK 180
AAA                                         183

SEQ ID NO: 411          moltype = AA length = 183
FEATURE
source
1..183
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 411          moltype = AA length = 183
TAYIAPSAAEV IGEVTIEDDC MISPNASIRA DEGMPYILGN GTNVQDGVTL HGLEVKREEG 60
EEDESAYVEV NGKKYVVYLG DNVSLGHQAQ IHGPAKVGDD TFIGMGATVF KSVIGNGCVL 120
EPGATVIGVT IPDGRYVPAG ATVTTQAEAD ALPLMTPDYA LYHTNERVVA VNRALAAEAR 180
AAA                                         183

SEQ ID NO: 412          moltype = AA length = 183
FEATURE
source
1..183
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 412          moltype = AA length = 183
TAYIHPSASV IGDVEIGANV MVSPMASIRS DEGMPYIHGD NANVQDGVL HGLEVKNNEG 60
EEDESQYVEV NGKKYVVYLG KNVSLAHQAQ IHGPAKVGDD TFIGMGAFVF KSTLGNNCVL 120
EPGATVIGVT IPDGRYLPAG TTVTGKPLAE DVTVRPVTEE QRNKHKKVVE KNLKLAKLLK 180
ELS                                         183

SEQ ID NO: 413          moltype = AA length = 183
FEATURE
source
1..183
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 413          moltype = AA length = 183
TAYIHPSAQV IGPVQIGANV MVSPMASIRS DEGMPYIYGD NANVQDGQL HALEARDEEG 60
VEDEAAAYVEV NGKRYRVYIG ENVSLAHQAQ VHGPASVGSD TFIGMGASVF KSRLGNGCVL 120
EPQATVIGVT IPDGRYLPAG TVLLPGRLED NTPLREVTEP QREAHKAVVT ENLARATELK 180
AAL                                         183

SEQ ID NO: 414          moltype = AA length = 549
FEATURE
source
1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 414          moltype = AA length = 549
TASIAPSATV IGDVEIADNV MISPNASIRS DEGMPYILGA NANIQDNVTL HALETKDEEG 60
NLIEENYVEV NGKKYAVYIG DGSTLPAGLT IKGNGYVEVL AGPGEELLVVT EPYKVEITSP 120

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EPVLVLRRLS	PEVRELLEVS	PDSERLLARE	ADGGTALFAA	FDARRAALKKA	ANLAANAAAV	180
AALTASITAPS	ATVIGDVEIA	DNVMISPNA	IRSDEGMPIY	LGANANIQDN	VTLHALETKD	240
EEGNLIEENY	VEVNGKKYAV	YIGDGSTLPA	GLTIKGNGYV	EVLAGPGELL	VVTTEPYKVEI	300
TSPEPVLVLR	RLSPEVRELL	EVSPDSERLL	AREADGGTAL	FAAFDARRAA	LKAANLAANA	360
AAVAALTASI	APSATVIGDV	EIADNMISP	NASIRSDEGM	PIYLGANANI	QDNVTLHALE	420
TKEEGLNIE	ENYVEVNGKK	YAVYIGDGT	LPAGLTICKN	GYVEVLAGPG	ELLVVTEPYK	480
VEITSPEPVL	VLRRRLSPEVR	ELLEVSPDSE	RLLAREADGG	TALFAAFDAR	RAALKAANLA	540
ANAAAVALA						549

SEQ ID NO: 415	moltype = AA	length = 549				
FEATURE	Location/Qualifiers					
source	1..549					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
	organism = synthetic construct					
SEQUENCE: 415						
TAYIHPASAV	IGDVEIGENV	MISPNASIRS	DEGMPIYLGE	NVNQDNVTL	HGLEVYTEEG	60
EILEENLVEV	NGKRYVYVTG	KNVLGHQAQ	IHGPARKVGD	TFIGMNATVF	KSRIGNCWL	120
EPNATVIGVT	IPDGRYVPAG	KTVTTQAEAD	ALPVLTDPYA	LYHTNERVNA	VNLKLAQEAN	180
AAATAYIHP	ASVIGDVEIG	ENVMSISPNA	IRSDEGMPIY	LGENVNVQDN	VTLHGLEVYT	240
EEGELIEENL	VEVNGKRYVV	YTGNVSLGH	QAQIHGPALK	GDDTFIGMNA	TVFKSVIGNN	300
CYLEPNTAVI	GVTIPDGRYV	PAGKTVTQA	EADALPVLT	DYALYHTNER	VNAVNLKLAQ	360
EANAAATAYI	HPSASVGDV	EIGENMISP	NASIRSDEGM	PIYLGENVNV	QDNVTLHGLE	420
VYTEEGLIE	ENLVEVNGKR	YVVTGKNN	LGHQAQIHGP	AKVGDDTFIG	MNATVFKSVI	480
GNNCVLEPNA	TVIGVTIPDG	RYVPAGKTVT	TQAEADALPV	LTPDYALYHT	NERVNAVNLK	540
LAQEANAAA						549

SEQ ID NO: 416	moltype = AA	length = 549				
FEATURE	Location/Qualifiers					
source	1..549					
	mol_type = protein					
	note = Library of modified or engineered enzymes					
	organism = synthetic construct					
SEQUENCE: 416						
TAYIAPGAEV	IGEVEIGANV	MVSPMASIRS	DEGMPIYLG	NTNVQDGVT	HGLEVEDEEG	60
EEDESVXEV	NGKKYRVYIG	NNVSLAHQAQ	VHGPAYVGD	TFIGMGATVF	KSRIGNCWL	120
EPGATVIGVT	IPDGRYVPAG	KTVTTQAEAD	ALPVLTDPYA	MYHTNETVVA	VNLALAAA	180
AAATAYIAPG	AEVIGDVEIG	ANVMVSPMAS	IRSDEGMPIY	LGDNTNVQDG	VTLHGLEVED	240
EEGEDESVY	VEVNGKKYRV	YIGNVSLAH	QAQVHGPAYV	GDDTFIGMGA	TVFKSRIGN	300
CYLEPGATVI	GVTIPDGRYV	PAGKTVTQA	EADALPVLT	DYAMYHTNET	VNAVNLALAA	360
AAKAAATAYI	APGAEVIGEV	EIGANMVSP	MASIRSDEGM	PIYLGNDNTV	QDGVTLHGLE	420
VEDEEGEDE	SVYVEVNGKK	YRVYIGNNVS	LAHQAQVHGP	AYVGDDTFIG	MGATVFKSRI	480
GNNCVLEPGA	TVIGVTIPDG	RYVPAGKTVT	TQAEADALPV	LTPDYAMYHT	NETVVAVNL	540
LAQAAKAAA						549

SEQ ID NO: 417	moltype = AA	length = 549
FEATURE	Location/Qualifiers	
source	1..549	
	mol_type = protein	
	note = Library of modified or engineered enzymes	
	organism = synthetic construct	
SEQUENCE: 417		

TAYIAPTAEV	IGDVIIGDNV	MISPNASIRS	DEGMPIYIGE	NVNQDGVTI	TADRTKDEAG	60
NDIPENWTV	NGKKYAVYLG	KNVVLAHNAT	VNGRTVLC	VLVQENATLT	ASTLGENVIV	120
QENATLTVGT	VAEGKVVEAG	KTITTTQAEAD	KLKDLTKDHP	LYNKRNKEVVA	KNLAI	180
KLETAYIAPT	AEVIGDVIIG	DNVMSISPNA	IRSDEGMPIY	IGENNVNVQDG	VITADRTKD	240
EAGNDIPEW	WTVNGKKYAV	YLGKNNVLAH	NATVNGRTV	GENVLQENA	TLTASTLGEN	300
VIVQENATLT	GVTVAEGKVV	EAGKTITTQA	EADKLKDLTK	DHPLYNKNKE	VVAKNL	360
EKKKLETAYI	APTAEVIGDV	IIGDNVMSISPNA	NASIRSDEGM	PIYIGENVNV	QDGVTITADR	420
TKDEAGNDIP	ENWVTVNGKK	YAVYLGKNNV	LAHNATVNGR	TVLGENVLVQ	ENATLTASTL	480
GENVIVQENA	TLTGTVVAEG	KVVEAGKTIT	TQAEADKLKD	LTKDHP	LYNK NKEVVKNL	540
ILEEKKKLE						549

SEQ ID NO: 418	moltype = AA	length = 549
FEATURE	Location/Qualifiers	
source	1..549	
	mol_type = protein	
	note = Library of modified or engineered enzymes	
	organism = synthetic construct	
SEQUENCE: 418		

TAYIAPTAEV	IGDVEIADNV	MISPNASIRS	DEGMPIYIGE	NANLQDNVVL	HALETKDEEG	60
NDIEENWVEV	DGKKYAVYIG	RRVSLGHQAQ	IHGPALVGD	TFIGMNAKVF	KSRIGNRCVL	120
EPAQNVIGVT	IPDGRYVPAG	KVVTQAEAD	KLPLLTPYA	MYHTNERVNA	VNLALAAEAR	180
ALATAYIAPT	ATVIGDVEIA	DNVMSISPNA	IRSDEGMPIY	IGENANLQDN	VVLHALETKD	240
EEGNDIEENW	VEVDGKKYAV	YIGRRVSLGH	QAQIHGPALV	GDDTFIGMNA	KVFKSRIGNR	300
CVLEPNAQVI	GVTIPDGRYV	PAGKVVTTQ	EADKLPLLTP	DYAMYHTNER	VNAVNLALAA	360

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SEQ ID NO: 419	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 419	
TAYIHPTAEV IGDVEIGDNV MISPNASIRA DEGMPIVIE NVNVQDGVEI TALRSDLPEE 60	
EVEKQLDQEVGK KGAVALAHGAK ILVASTRLKV EPVPGVTVLK QDNAVLRNVL 120	
LTEMHGLILE VNAETGSIVI RESSDPALES KAKTWKTWPE DKAKIAAVIA ANAAARQEAL 180	
AAATAYIHT AEVIGDVEIG DNVMSPNAS IRADEGMPIV IEENVNQDG VEITALRSDL 240	
PEEEVEKLQLDQEVGK YFGKGAVLAH GAKILVASTR LKVEPVPGVT VLKQDNAVLR 300	
NVLLTEMHGLILE LLEVNAETGS IVIRESSDPALES KAKTWKTWPE DKAKIAAVIA ANAAARQEAL 360	
EALAAATAYI HPTAEVIGDV EIGDNVMISP NASIRADEGM PIVIEENVNV QDGVEITALR 420	
SDLPEEEVEKLQLDQEVGK YFGKGAVLAH GAKILVASTR LKVEPVPGVT VLKQDNAVLR 480	
VLRNVLLTEMHGLILE VLAENVNAE TGSIVIRESS DPALESKAKT WKVTPEDKAK IAAVIAANAA 540	
ARQEALAAA 549	
SEQ ID NO: 420	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 420	
TAYIEPNAEV IGDVKIGENV MISPNASIRS DEGMPIVIKE NVNVQDGVVII NAKLKKNENG 60	
EVDESQINTI NGEKVQIYLE KNVQLAHNVIT IEDSVVLLKEN VLLQENVVLK NSTLGEVVLL 120	
AENVVIENVT LPENTVVEAG TVIKNQEEVK TLKQLTADSP AIVQLQAVLA KNAALWEEKL 180	
AAETAYIETPN AEVIGDVKIG ENVMSPNAS IRSDEGMPIV IKENVNQDG VVINAKLKKN 240	
ENGEVDESQINTINGEKVQI YLEKNVQLAH NVTIEDSVVLL KENVLLQENV VLKNSTLGEV 300	
VVLAAENVIE NVTLPENTVV EAGTVIKNQEV KIGENVMISP NASIRADEGM PIVIENVNQ QDGVVINAKL 360	
ELKAAETAYI EPNAEVIGDV KIGENVMISP NASIRADEGM PIVIENVNQ QDGVVINAKL 420	
KKNENGKEDV SQLNTINGEK VQIYLEKNVQ LAHNVTIEDS VVLKENVLLQ ENVVLKNSTL 480	
GEGVVLAAENV VIENVTLPEV TVVEAGTVIK NQEEVKTLLQ LTADSPAIVQ LQAVLAKNAA 540	
LWEELKAAE 549	
SEQ ID NO: 421	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 421	
TAYIHPSAEV IGDVTIGDNV MISPNASIRA DEGMPYILGD NANVQDGVTL HGLETKDEEG 60	
NIIEENLVEV NGKKYAVYVG DNVSLAHQAQ IHGPAIVGDD TFIGMGATVR RSILGDGVLL 120	
GEGVQIENAT LPAGLCLGPV RVRVTPPEELV DDCTEEQRAE LKKKHAEVVA KNLALHEELK 180	
AAATAYIHPSE AEVIGDVTIG DNVMSPNAS IRSDEGMPIV LGDNANVNQDG VTLHGLETKD 240	
EENNIIEENNE VEVNGKYYAV YVGDNVSLAH QAQIHGPAPIV GDDTFIGMGA TVRRSILGDG 300	
VLLGEVGQIE NATLPLAGLCL GPGRVIRTPV ELVDDCTEEQ RAEKKKHAEE VVAKNLALHE 360	
ELKAAATAYI HPSEAEVIGDV TIGDNVMISP NASIRADEGM PIYLGDNANVN QDGVTLLHGLE 420	
TKDEEGNIE ENLVEVNGKK YAVYVGDNVS LAHQAOIHGP APIVGDDTFIG MGATVRRSIL 480	
GDGVLLGEGV QIENATLPG LCLGPGRVIR TPEELVDDCT EEQRAELKKK HAEVVAKNLA 540	
LHEELKAAA 549	
SEQ ID NO: 422	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 422	
TAYIAPNAQV IGEVTIGENV MISPNASIRS DEGMPYIGE NANLQDNVVL HGLEVYTEEG 60	
ELIEENLVEV DGKKYVYVG KNVSLGHQAQ IHGPAKVGGD TFIGMNAKVF KSVIGNRCVL 120	
EPNATVIGVT IPDGRYVPAG KVVTQAEAD ALPVLTDPYA LYHTNELVNE VNLLALAAEGR 180	
AAATAYIAPN AQVIGEVTIG ENVMSPNAS IRSDEGMPIV IGENANLQDN VVLHGLEVYT 240	
EEGELIEENL VEVGDGKYYV YIGKNVSLGH QAQIHGPAPIV GDDTFIGMNA KVFKSIGNR 300	
CVLEPNATVI GTIPDGRYV PAGKVTTQAEAD ALPVLTDPYA LYHTNELVNE VNLLALAAEGR 360	
EGRRAATAYI APNAQVIGEV TIGENVMISP NASIRADEGM PIYIGENANL QDNVVLHGLE 420	
VYTEEGERLIE ENLVEVNGKK YVYVIGKNVS LGHQAOIHGP APIVGDDTFIG MNAKVFKSVI 480	
GNRCVLEPNA TVIGVTIPDG RVYPAGKVVT TQAEADALPV LTPDYALYHT NELVNEVNLA 540	
LAAEGRAAA 549	

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SEQ ID NO: 423      moltype = AA length = 549
FEATURE
source
1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 423
TAYIHPSAEV IGDVEIADNV MISPNASIRA DEGMPYLGE NTNQDGDSL HALENSSEEG 60
EDEDESNWVEV NGKKYRVYIG NNVLGHQAO VHGPAGVDD TFIGMGAKVF KSTIGNCVL 120
EPGVTVIGVT IPDGRYLEAG TVLRSQADIE KAKPIKEDMP TYKKVKEHKE KLKEEREKLK 180
KERTAYIHPS AEVIGDVEIA DNMISPNA S IRADEGMPI LGENTNVQDG VSLHALENSS 240
EEGEDEDSNW VEVNGKKYRV YIGNNVSLGH QAQVHGPAIV GDDTFIGMGA KVFKSTIGNG 300
CVLEPGVTVI GVTIPDGRYV EAGTVLRSQDIE KAKPIKEDMP TYKVKKVKH KHEKLKEERE 360
KLKKERTAYI HPSAEVGDV EIADNMISP NASIRADEGM PIYLGENTNV QDGVLSHALE 420
NSSEEDEDE SNWVEVNGKK YRVYIQQVHGP AIVGDDTFIG MGAKVFKSTI 480
GNGCVLEPGV TVIGVTIPDG RYLEAGTVLR SQADIEKAKP IKEDMPTYKK VKEHKEKLKE 540
EREKLKKER 549

SEQ ID NO: 424      moltype = AA length = 549
FEATURE
source
1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 424
TAIIAPGATV IGEVHIAIDGV MISPNASIRA DEGMPYLGE YTNLQDNVVL HALETYDEEG 60
NLIENLVEV NGKKYAVYVG KNVSLGHQAO LHGPPTIVGDD TFIGMNAKVI RSTLGEGVV 120
EENVVVEGQT LEKGTYLEKG MKLLTPEDLK KAKKIKEEDP VKKKLEAHIK EQKAQAKAAQ 180
AAATAIIAPG ATVIGEVHIA DGVNMISPNA S IRADEGMPI LGEYTNLQDN VVLHALETYD 240
EEGNLIEENL VEVNGKKYAV YIGNNVSLGH QAQVHGPTIV GDDTFIGMNA KVIRSTLGE 300
VVLLEENVVVE GOTLEKGTYL EKGMLLTPE DLKKAKKIKE EDPVKKKLEA HIKEQKAQAK 360
AAQAAATAII APGATVIGEV HIADGVMISP NASIRADEGM PIYLGEYTNL QDNVVLH 420
TYDEEGNLIE ENLVEVNGKK YAVVYIGKNVS LGHQAOQLHGP TIVGDDTFIG MNAKVIRSTL 480
GEGVVLEENV VVEGQTLKGK TYLEKGKMLL TPEDLKKAKK IKEDPVKKK LEEHIKEQKA 540
QAKAAQAAA 549

SEQ ID NO: 425      moltype = AA length = 549
FEATURE
source
1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 425
TAYIHPSAEV IGEVEIGANV MVSPMASIRS DEGMPIKIGD NVNVQDGVL HGLETKNEEG 60
EEIEENLVEV DGEKYVYLG KNVSLAHQAQ VHGPASIVGDD TFIGMGAKEV GSTLGDGVFL 120
GEGATVIGLT IPAGAVVSPG TVLTTPAOLA SLKPLTADDP LLKKKKDVNE NNLATAAALK 180
ALETAYIHPS AEVIGEVEIG ANVMVSPMAS IRSDEGMPK IGDNVNVQDG VVLHGLETKN 240
EEGEEIEENL VEVDGEKYVV YLGKVNLSLAH QAQVHGSPIV GDDTFIGMGA KVEGSTLGDG 300
VFLGEGATVT GLTIPAGAVV SPGTVLTTPA QLASLKP LTADPLKKKD VVENNLATAA 360
ALKALETAYI HPSAEVIGEV EIGANMVSP MASIRSDEGM PIKIGDNVNV QDGVLHGLE 420
TKNEEGEEIE ENLVEVDGEK YVYVYIGKNVS LAHQAOQLHGP SIVGDDTFIG MGAKVEGSTL 480
GDGVFLGEGA TVTGLTIPAG AVVSPGTVLT TPAQLASLKP LTADPLKKKD VVENNLATAA 540
TAAALKALE 549

SEQ ID NO: 426      moltype = AA length = 549
FEATURE
source
1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 426
TAYIHPSASV IGDVEIADNV MISPNASIRA DEGMPIKIGP NANVQDGVTL HGLETYDEEG 60
NLIENNYVEV NGERYVYVYIG DNVSLGHQAO IHGPAKVGDD TFIGMKTAVF KSVIGNNCVL 120
EPGATVIGVT IPDGRYVPAG KVTTQAEAD ALPVLTPDYA LYHTNERVNA VNLKLAEKAR 180
LEATAYIHPS ASVIGDVEIA DNMISPNA S IRADEGMPI IGPNANVQDG VTLHGLETKN 240
EEGNLIEENY VEVNGERYVV YIGDNVSLGH QAQIHGPARK GDDTFIGMKA TVFKSIVGN 300
CVLEPGATVI GVTIPDGRYV PAGKVTTQA EADALPVLT DYALYHTNER VNAVNLKLA 360
KARLEATAYI HPSASVIGDV EIADNMISP NASIRADEGM PIKIGPNANV QDGVTLHGLE 420
TYDEEGNLIE ENYVEVNGER YVYVYIGDNVS LGHQAOQLHGP AKVGDDTFIG MKATVFKSVI 480
GNNCVLEPGA TVIGVTIPDG RVYPAGKVVT TQAEADALPV LTPDLYALYHT NERVNAVN 540
LAEKARLEA 549

SEQ ID NO: 427      moltype = AA length = 549
FEATURE
source
1..549

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mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 427
TAYIAPSAEV IGDVEIGANV MVSPMASIRA DEGMPYIGD NANVQDGVL HALETYDEEG 60
NLIEEAYVEV DGKKYAVYVG DNVS LAHQAQ IHGPAKVGED TFIGMAGKVV GSTLGKVFL 120
AEGVVVENAT LPEGTILEKG TVTPSDKEL PKAPEELRAK LAAEHKAVVA ANIAAAAAAK 180
AAATAYIAPS AEVIGDVEIA ANVMVSPMAS IRADEGMPY IGDANVQDG VVLHALETYD 240
EEGNLIEEAY VEVDGKKYAV YVGDNVSLAH QAQIHGPCKV GEDTFIGMGA KVVGSTLGKG 300
VFLAEGVVVE NATLPEGTIL EKGTVPVTPSD KELPKAPEEL RAKLAEHKV VVAANIAAAA 360
AAKAAATAYI APSAEVIGDV EIGANVMVSP MASIRADEGM PIYIGDNANV QDGVLVHGLE 420
TYDEEGLNIE EAYVEVDGKK YAVVYGDNVS LAHQAQIHGPCKV GEDTFIG MGAKVVGSTL 480
GKGVFLAEGV VVENATLPEG TILEKGTVVT PSDKELPKAP EELRAKLAEE HKAVVAANIA 540
AAAAAKAAA 549

SEQ ID NO: 428      moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 428
TAYIAPGAEV IGDVEIGANV MVSPMASIRA DEGMPYVGD NANVQDGVL HGLETLDDEG 60
NLIEENWVEV DGKKYVYVLG KNVSLAHQAQ IHGPAKVGED TFIGMQLVF KSTIGNGCVL 120
EPGAAGIVGT VPDGRYVPAG AVVTSQAEAD ALPKMTPDYA YAHTNETVVA VNNALAAGYK 180
AAATAYIAPG AEVIGDVEIA ANVMVSPMAS IRADEGMPY VGDANVQDG VVLHGLETLID 240
EEGNLIEEENW VEVDGKKYIV YLGKVNLSAH QAQIHGPCKV GEDTFIGMGA LVFKSTIGNG 300
CVLEPGAAVI CTVTPDGRYV PAGAVVTSQA EADALPKMTP DYAYAHTNET VVAVNNALAA 360
GYKAAATAYI APGAEVIGDV EIGANVMVSP MASIRADEGM PIYVGDNANV QDGVLVHGLE 420
TLEDEEGLNIE ENWVEVDGKK YVYVLGKNSV LAHQAQIHGPCKV GEDTFIG MGALVFKSTI 480
GNGCVLEPGA AVIGVTVPDG RVYPAGAVVT SQAEADALPK MTPDYAYAHT NETVAVNNAA 540
LAAGYKAAA 549

SEQ ID NO: 429      moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 429
TAYIHPSATV IGGVNIGANV MVSPMASIRA DEGMPITLED NVNVQDGVLI QNESLKNESG 60
EDYISKVHPK NKRIESIVLK KNVSLAHQAT VYSNTELSEG VFLQEGVVVK NSVIEGRVVL 120
QRGVTVENVY IGEVVIAEG TVLKGDEDLK KTTLAPLTPE QVAQIQAVIA QNLAAAAAK 180
AAATAYIAPG ATVIGQVNIG ANVMVSPMAS IRADEGMPY LEDNVNVQDG VLQIQNESLN 240
ESGEIDYSKV HPKNKRIEST VLKKNVSLAH QATVYSNTTEL SEGVFLQEGV VVKNSVIEGR 300
VVLQRGVTVE NYVIGEEVVI AEGTVLKGDE DLKKTTLAPL TPEQVAQIQA VIAQNLAAAA 360
AAKAAATAYI HPSATVIGQV NIGANVMVSP MASIRADEGM PITLEDNVNV QDGVLQNES 420
LKNESGEIDY SKVHPKNKRI ESIVLKKNSV LAHQATVYSN TELSEGVFLQ EGVVVKNSVI 480
EGRVVLQRGV TVENVYIGEE VVIAEGTVLK GDEDLKTTT APLTPEQVAQ IQAVIAQNL 540
AAAAAKAAA 549

SEQ ID NO: 430      moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 430
TAYIAPGAQV IGDVEIADNV MISPNASIRA DEGMPYIGE NANLQDNVQL HGLEVYTEEG 60
ELIEENFVEV DGKKYVYVYIG RRVSLAHQAQ VHGPCKV GDDTFIGMNA KSIVGNRCVL 120
EPNATVIGVTVT IPDGRYVPAG KTVTQAEAD ALPVLTQDYA LYHTNELVNA VNLLAEEAR 180
AAATAYIAPG AQVIGDVEIA DNMVISPNA IRADEGMPY IGENANLQDN VQLHGLEVYT 240
EEGELIEENF VEVDGKKYIV YIGRGRVSLAH QAQVHGPCKV GDDTFIGMNA KVFKSIVGNR 300
CVLEPNTAVI CTVTPDGRYV PAGKVTITQA EADALPVLTPE QVAVNLALAA 360
EARAAATAYI APGAQVIGDV EIADNVMISP NASIRADEGM PIYIGENANL QDNVQLHGLE 420
VYTEEELIE ENFVEVDGKK YVYVYIGRRVS LAHQAQVHGPCKV GDDTFIG MNAKVKFSIV 480
GNRCVLEPNA TVIGVTIPDG RVYPAGKTVT TQAEADALPV LTPDYALYHT NELVNAVNL 540
LAAEAAAAA 549

SEQ ID NO: 431      moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 431

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TAYIHPTARV	IGEVТИAAGV	MISPGASIRA	DEGMPIVIGE	NANVQDGDSL	HGLEVYDEEG	60
NLIEENLVVE	NGEKVVYVIG	ENVSLGHQAQ	IHGPALVGDD	TFIGMGAKV	RSLIAGEGVIL	120
EEGAQLTNVI	VPDGAYVKSG	QVFVSTGEPV	VSELKQTPE	QKEKLAQLA	AERAARAAAQ	180
AAATAYIHPT	ARVIGEVTIA	AGVMISPGAS	IRADEGMPIV	IGENANVQDG	VSLHGLEVYD	240
EEGNLIEENL	VEVNGEKYVV	YIGENVSLGH	QAQIHGPALV	GDDTFIMGMA	KVTRSILEGEG	300
VILEEGQQLT	NVIVPDGAYV	KSGQFVSTG	EPVVLSELKQ	TPEQKEKLA	QLAABRAARA	360
AAQAAATAYI	HPTARVIGEV	TIAAGVMISP	GASIRADEGM	PIVIGENANV	QDGVSLHGLE	420
VYDEEGNLIE	ENLVNNGEK	YVYVGENVS	LGHQAQIHGP	ALVGDDTFIG	MGAKVTRSIL	480
GEGVILEEGA	QLTNVIVPDG	AYVKSGQVFV	STGEPVVLS	LKQTPEQKEK	LAAQLAERA	540
ARAAAQAAA						549

SEQ ID NO: 432 moltype = AA length = 549
 FEATURE Location/Qualifiers
 source 1..549
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 432

TAYIHPTAEV	IGNVKIGENV	MISPNASIRS	DEGMPIVIKE	NANVQDGVVI	RADPTKDENG	60
NDIEENWTVT	NGEKYAVYLE	KNVVLNAHV	VEGRTVLKEG	VLVQENAVVR	RSTLGEVIL	120
QENAVLEGVT	VADGKIVPAG	ATIRTQAEAD	TLATLTPDH	LYNLNKVVNA	KNLALLKENL	180
AAKTAYIHPT	AEVIGNVKIG	ENVNMISPNA	IRSDEGMPIV	IKENANVQDG	VVIRADPTKD	240
ENGNDIEENW	TVVNGEKYAV	YLEKNVVLAH	NAVVEGRTVL	KEGVLVQENA	VVRRSTLGE	300
VILQENAVLVE	GVTVADGKIV	PAGATIRTQ	EADTLATLTP	DHPLVNLNKV	VNAKNLALLK	360
ENLAAKTAYI	HPTAEVIGNV	KIGENVMISP	NASIRSDEGM	PIVIKENANV	QDGVVIRADP	420
TKDENGNIDIE	ENWVTVNNGEK	YAVYLEKNVV	LAHNAAVEGR	TVLKEGLVQ	ENAVVRRSTL	480
GEGVILQENA	VLEGVTVADG	KIVPAGATIR	TQREADTLAT	LTPDHPLYNL	NKVVNAKNLA	540
LLKENLAAK						549

SEQ ID NO: 433 moltype = AA length = 549
 FEATURE Location/Qualifiers
 source 1 .. 549
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 433

TAIIAPGATV	IGEVEIGDNV	MISPNASIRS	DEGMPIVLG	GANLQDNVEL	HALEVYDEEG	60
NLIEENYVVE	NGKKYAVYIG	NNVSLGHQAQ	IHGPAlVGD	TFIGMNAEVF	KSIICNGCWL	120
EPNARVIGVT	IPDGRYVKAG	TTITDQAEIP	SLKQLKDSDP	IKAKVEAHKA	ALKAERERLL	180
AERTAIAPG	ATVIGEVEIG	DNVMSPNAS	IRSDEGMPIV	LGEGANLQDN	VELHALEVYD	240
EENGLIEENY	VEVNGKKYAV	YIGNNNVSLGH	QAQIHGPAlV	GDDTFIGMNA	EVFKSIIING	300
CVLEPNARVI	GVTIPDGRYV	KAGTTITDQ	EIPSLKQLKD	SDPIKAKVEA	HKAALKAERE	360
RLLAERTAI	APGATVIGEV	EIGDNVMISP	NASIRSDEGM	PIVLGEGANL	QDNVELHALE	420
VYDEEGNLIE	ENYVEVNGKK	YAVYIGNNVS	LGHQAQIHGP	AVGDDTFIG	MNAEVFKSII	480
GNGCVLEPNA	RVIGVTPDGY	RYVKAGTTIT	DQAEIPSLKQ	LKDSDPIKAK	VEAHKAALK	540
ERERLLAER						549

SEQ ID NO: 434 moltype = AA length = 213
 FEATURE Location/Qualifiers
 source 1..213
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 434

QEITVDEFSN	IRENPVTPWN	PEPSAPVIDP	TAYIDPQASV	IGEVТИGANV	MVSPMASIRS	60
DEGMPIFVGD	RSNVQDGVL	HALETINNEG	EPIEDNIVEV	DKEYAVYIG	NNVSLAHQSQ	120
VHGPAAVGDD	TFIGMQAFVF	KSKVGNNCWL	EPRSAAlGVT	IPDGRYIPAG	MVVTSQAEAD	180
KLPEVTDDYA	YSHTNEAVVY	VNVHLAEGYK	ETS			213

SEQ ID NO: 435 moltype = AA length = 212
 FEATURE Location/Qualifiers
 source 1..212
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 435

GKVVVKKPF	IPARHIPS	DKTIIPEIDE	AVIEEGAIIT	GGVIKGRVY	IASGATIRSD	60
EGVPIVIEEN	SSIQDGALVH	ADETVDEDGN	PIEENIVEVN	GKPYAVYIGE	NVVLHNATV	120
HGPAAVGKNS	LIGEGALVRN	SVIGENCVLE	EGASAENVTI	PAGRYVPAGV	TVTTQAAAAA	180
LPAVTPDHP	YKRNEELVKE	NIEKAELL	EA			212

SEQ ID NO: 436 moltype = AA length = 212
 FEATURE Location/Qualifiers
 source 1..212
 mol_type = protein
 note = Library of modified or engineered enzymes

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SEQUENCE: 436          organism = synthetic construct
GSVLVEPDSI QCSPPNKYHK EPRCPTIAKG AYIEKGALIE GDVIIIEENVY IESGAIIRSD 60
EGTPIYIGKN SVIQDGALVH ADETVDEDGN PIBENIVEVN GKPYAVYIGE NVVLEHNAAEV 120
HGPAAVGKNS LIGEGALVRN SIIGENCVLE EGASAENVTI PAGRYVPAGK TVTTQAEAAA 180
LPKVTDPDHPL YKRNEELVKE NLEKVKKANA AA                           212

SEQ ID NO: 437          moltype = AA length = 212
FEATURE               Location/Qualifiers
source                1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 437          organism = synthetic construct
GVVLVEEEGI RPSPATPRYP EPRAPIIHPS AYVADGALIT GEVIIEDNVL IAEGAVIRSD 60
EGRPIYIGKN SSVQDGAVIH ADETVDAECK EIBENIVEVN GKKYAVYIGE NVVIEHGATV 120
HGPAKIGENS LIGRGALVEN SVIGKNCVLE EGASAIGVTI PEGRYIPAGV TVTTQEEADA 180
LPEVTPDHPD YNRVAELVAK NIALAKELNA AR                           212

SEQ ID NO: 438          moltype = AA length = 212
FEATURE               Location/Qualifiers
source                1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 438          organism = synthetic construct
PAPVRGHEAV PEDSLHPTVG KKLVTTIAET AYIEEGATIS GAVILADNVY VESGATIRSD 60
EGIPIYVGEN SAIQDGAVLH ADETVDADGN PIPENIVEVN GEPYAVYIGE NVVLEHGATV 120
HGPAAVGKNS LIGKNAVVRN SSVGENCVLE EGASAENVTI PAGRYVPAGK KVTTQEEADA 180
LPEVTPDHPD YKRNEKLVAE NNAKVKAYNA AR                           212

SEQ ID NO: 439          moltype = AA length = 212
FEATURE               Location/Qualifiers
source                1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 439          organism = synthetic construct
GVVLTPVSDI RPSAPTPRYK ESKAPTIHPS AYIAPGATIV GDVTIAANVY VEAGATIRSD 60
EGVPIYVGAN SAVQDGAVLH ADETVDENGN PIEENIVEVN GKKYAVYVGE NVVLEHGATV 120
HGPAAGIGNS LVGEGALVRN SIVGANCVLE PGASAINVTI PAGRYVPAGV TVTTQAAADA 180
LPAVTPDHPD ANRRAELVAK NVAKAKAAVA AR                           212

SEQ ID NO: 440          moltype = AA length = 212
FEATURE               Location/Qualifiers
source                1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 440          organism = synthetic construct
GTVVVATSPI RPSEPTPWKR ESRAPTLAPG AYVHPDATVE GAVILEEGAL VQGGATIRSD 60
EGVPIYVGRN SVIQDGATLH ADETVDEEGN PIPENIVEVD GKPYAVYVGE NVVIQHGATI 120
HGPAAVGNS LIGENALVEN SSVGKNCVIQ EGGAARNVTI PEGRYIPAGK TVTTQAEADA 180
LPKVTDPDHPY YNKNAALVAE NLARRELLA AR                           212

SEQ ID NO: 441          moltype = AA length = 212
FEATURE               Location/Qualifiers
source                1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 441          organism = synthetic construct
MVLVLEEAFL RPSPPPTPRHR EPRAPTLAEG AWVAPGATIE GEVHIAAGAY IADGATIRSD 60
EGTPIYVGAN SVIQDGALLH ADETVLDGK VIEENVVTVN GEPYAVYIGE NVVIEHNATI 120
HGPAAVGANS LIGENALVRN SIIGENCVLE EGASAINVTI PAGRYVPAGK TVTTQAEAAA 180
LPKVTDPDHPN YNKNAALVAE NLALNKLVA AA                           212

SEQ ID NO: 442          moltype = AA length = 212
FEATURE               Location/Qualifiers
source                1..212
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 442          organism = synthetic construct
MLLVVEEPLI RPSEPTPWRG TRREPTIAEG AYIEPGAVIT GDTIIEAGAY IESGAVIRSD 60
EGVPIYIGAN SAIQDGAVLH ADETVDENGN LIEENVVEVN GKKYAVYVGA NVVIEHNAVI 120

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HGPAAVGANS	LIGEGAVVRN	SIVGANCVLE	PGASVENVTV	PAGRYPAGV	RVTTQAAADA	180
LPAPVTPDHPL	ANRVAELVAK	NVAKVKAANA	AK			212

SEQ ID NO: 443 moltype = AA length = 212
 FEATURE Location/Qualifiers
 source 1..212
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 443
 GLKKRKRLTPA ELRKPDPRYT GPRVSTIGET CLFAPGAVIS PGVTLGENVY IESGAVIRSD 60
 EGRIPIVVGDN SVIQDGAVLH ADETVDADGN PIPENIVTVN QOPYAVVVG S NVVIDHGATI 120
 HGPAAVGANT LIGEGATVRN STVGSNCVLE PGASAIGVTI PAGRYPAGK TVTTQAEADA 180
 LPAPVTPDHPL ANRVAELVAK NLAKVKAANA AR 212

SEQ ID NO: 444 moltype = AA length = 212
 FEATURE Location/Qualifiers
 source 1..212
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 444
 GVVVAPVSDI QCSPPTPRFP ESRCPTLHPS AYIEEGATII GEVTIGDNVL IEKGATIRSD 60
 EGVPIYIGEN SSIQDGATLH ADETVDEAGN PIEENIVTVN GKPYAVVIGE NVVIBHGATV 120
 HGPAAIGRNS LIGEGATVRN SIVGANCVLE EGASAIGVTI PAGRYPAGK VVTTQEEAAA 180
 LPAPVTPDHPL YKRVEELVAK NIALVKALLA AR 212

SEQ ID NO: 445 moltype = AA length = 183
 FEATURE Location/Qualifiers
 source 1..183
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 445
 TAYIHPSATV IGDVEIADNA MISPNASIRA DEGMPIKIEK NAVVQDNATI EAKPTKDADG 60
 NLIEENIEEV NGKKYAVYIG EGAVLQKNAT LEGGTIICKN VLVQENATLT NSTLGENVIV 120
 QENATLTGVT IAEGKIVPEG ATITTQEEAE KLAPLTPDHP LYNKRAEIVA KALAREEAAL 180
 AAA 183

SEQ ID NO: 446 moltype = AA length = 183
 FEATURE Location/Qualifiers
 source 1..183
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 446
 TAYIHPSAKV IGDVEIGANV MVSPMASIRS DEGMPIKIEE NANVQDGVKI EGKRVYSASG 60
 ELIEENIEEV NGKKYVYVYIG ENVSLAHQAT IIIGGTVLKNN VFIQEGAYIE NSVLGENVIV 120
 QKNATIIGVT IKEGKVVPEG AVITTOQEEAD KLPKLTPEHP LYNLNAQVVA ANIKAALK 180
 AAE 183

SEQ ID NO: 447 moltype = AA length = 183
 FEATURE Location/Qualifiers
 source 1..183
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 447
 TAYIHPTATV IGNVKIGENV MISPEASLRA DEGMPIVLEE NVNVQDGVVI RGDRVLDEAG 60
 NLIEENLVVE NGERYVYVYLG KGVLVLAHGAV VEGSTVLGEG VLVQEGAVLR RSTLGERVIV 120
 QEGAVLEGVT VAPGAVVPAG AVIRTOQEEAA TLAALTPDHP LYNNENARVVA KNLALLEELK 180
 ALE 183

SEQ ID NO: 448 moltype = AA length = 183
 FEATURE Location/Qualifiers
 source 1..183
 mol_type = protein
 note = Library of modified or engineered enzymes
 organism = synthetic construct

SEQUENCE: 448
 TAYIHPSATV IGDVIIGKNA MISPNASIRS DEGMPIVLEE NAIQVDNATI TAKPTKTASG 60
 ELIEENVVEV NGKKYAVYLG ENAILQKNAT IEGGTIVVGKVN VLVQENATLT GSTLGENVIV 120
 QENATITGVT IAEGAIVPEG ATITTQEEAE KLEKLTPDHP LYNLNAELNA KALALRDLL 180
 ALS 183

SEQ ID NO: 449 moltype = AA length = 183

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FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 449	
TAYIHPSATV IGDVEIGENA MISPNASIRS DEGMPIVLEK NVVVQDNATI EANPVLDENG	60
ELIEENREV NGKKYAVYLE EGVLQKNAT IKGGTVVKNN VLVQENATLT NSTLGENVIV	120
QENATLTVGT VAEKGKVVPEG ATITQAEAE KLAPELTPDHP LYNLGAEIRA KALALRELKL	180
ALE	183
SEQ ID NO: 450	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 450	
TAYIHPSAKV EGEVEIGANV MVSPMATINS TEGEPIFLGD RVNVQDGVTI TCEPVYNADG	60
ELDESKLVEI DGKKYCVYVA ENVSLAHQST LSGTQLKNN VFVQEGAVLK NSTLGENVV	120
RENAVIEGV TIEEGTVAAEG TVVLTEEDLA KLRPLTPEDP LLEIHKKVVE ENIAKAKALK	180
AAA	183
SEQ ID NO: 451	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 451	
TAYIHPSAEV IGDVEIGANV MISPNASIRA DEGMPIVLGD NTVNQDGVSL HALETLDDEG	60
NLIEENVVEV DGKKYAVYVG DNVSLAHQAQ VHGPAAIVGED TFIGMGAIVR RSVLGKGVIL	120
REGATVEGVT IEEGTVAEEN TVLTKQEEVK KLKKLTPEHP YYNLNKKVVE QNIKKVQAAR	180
AAA	183
SEQ ID NO: 452	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 452	
TAVIHPSATV IGDVTIADNV MISPNASIRA DEGMPIVLGE NVNLQDNVSL HALETLDDEG	60
NLIEENVVEV DGKKYAVYLG EGVS LAHQAT VHGPAAIVGKD TFIGMNAKVS GSILGEGVIL	120
QDNATVEGAT IAEGKVVPEG AVITTQEEAD KLAPELTPDHP YYELVKRTRE ENLRLRDLL	180
ELE	183
SEQ ID NO: 453	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 453	
TAYIHPSAKV IGDVEIGENV MISPNASIRA DEGMPIKLEK NVVQDNAVI EADRIYDENG	60
ELIESAVTVT NGKKYAVYLG ENVIQKNAT VRGGTVLGKNN VLVQENAVLT NSTLGENVIV	120
QENATVTVGT LKEGTIVPEG ATITQEEAD KLEKLTPDHP LYNLHALLA AGLALRDL	180
ALE	183
SEQ ID NO: 454	moltype = AA length = 183
FEATURE	Location/Qualifiers
source	1..183
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 454	
TAYIHPSAEV IGDVTIGANV MVSPMASIRA DEGMPIVLGN NVNVQDGVVL HGLEVLNEEG	60
ELIEENVVEV DGKKYVYVG EGVS LAHQAT VVGGATVLGKG VFVGEVGVL RSVLGEGVIV	120
GENAVIKVGT IAEGKVVKEG TT VTTQEEAD KLEKLTPDHP YYELNARVVA ENIAKARLLK	180
LLE	183
SEQ ID NO: 455	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes

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SEQUENCE: 455          organism = synthetic construct
TAYIAPGASV IGEVEIGDNV MISPNASLRS DEGMPIKLGD NVNVQDGVTL HGLETKDEEG 60
NLIEENVVEV NGEKYVYVG KNVVLAHNVT LTSRTVVEDN VYLEENVTLT RSTLGKYYVV 120
EKGVIVIEGVT IKGEMYAKEG TVIRTQEDVK SLEMICKDLAK HKAKVQAVID ANLRIHQEAL 180
AAATAYIAPG ASVIGEVEIG DNVIMSPNAS LRSDEGMPIK LGDNVNQDG VTLHGLETKD 240
EEGNLIEENV VEVNGEKYVV YVGKNNVLAH NVTLTSRTVV EDNVYLEENV TLTRSTLGKY 300
VVEKGVIVIE GVTIKEGMYA KEGTVIRTOE DVKSLEMIKD LAKHKAKVQA VIDANLRHQ 360
EALAAAATAYI APGASVIGEV EIGDNVMISP NASLRSDEGM PIKLGDNVNV QDGVTLHGLE 420
TKDEEGNLIE ENVVEVNGEY YVYVVGKNNV LAHNVLTSLR TVVEDNVYLV ENVTLTRSTL 480
GKVVYVEKGV VIEGVTIKEG MYAKEGTVIR TQEDVKSLEM IKDLAKHKAK VQAVIDANLR 540
IHQEALAAA 549

SEQ ID NO: 456          moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 456          moltype = AA length = 549
TAYIHPTATV IGSVTIADGV MISPYASIRA DEGMPYIIGE GANVQDGQL HGLETRDEEG 60
NLIEENVVEV NGKKYVYVG KGKSLGHQAQ VHGPAPIVGD TFIGMGAQVT GAILPEGLVL 120
AEGRVRVESVD LSGYRVLPPG TVIRTPQAD RVREDES LAAVEARRAALA AERAAAEEAAR 180
AAATAYIHT ATVIGSVIA DGMVISPYAS IRADEGMPIY IEGEGANVQDG VQLHGLETRD 240
EEGNLIEENV VEVNGKKYVV YIGKGVS LAAVEEARRA ALAAABRAAAE 360
LVAEGRVRE SVDSLGYRVL PPGTVIRTOE DKERVREDES LAAVEEARRA ALAAABRAAAE 360
AARAATAYI HPTATIVGSV TIADGVMISP YASIRADEGM PIYIGEGANV QDGVQLHGLE 420
TRDEEGNLIE ENVVEVNGKK YVYVYGKGVIS LGHQAQVHGP AIVGDDTFIG MGAQVTGAIL 480
PEGLVLAEVG RVESVDSLGY RYLPPGTIVR TQADKERVRE DESLAAEVEA RRAALAAERA 540
AAEAARAAA 549

SEQ ID NO: 457          moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 457          moltype = AA length = 549
TAFIHPSPATV IGDVTIGANV MISPMASIRS DEGMPYIVGA NANLQDQVTL HALEVFDEEG 60
NLIEENVVEV NGEKYAVYLG DNVSLAHQAQ VHGPAPIVGED TFIGMQASFV KSTICNGCVL 120
EFGAAAVIGVT IPDGRYVPAG KVVTSQAEAD ALPKMTPDYA YYHTNEKVV A VRNRLAAGYR 180
AAQTAFIHPS ATVIGDTVIG ANVMISPMAS IRSDEGMPIY VGANANLQDQ VTLHALEVFD 240
EEGNLIEENV VEVNGEYKAV YLGDNVSLAH QAQVHGPAPIV GEDTFIGMQA SVFKSTIGNG 300
CVLEPGAAVI GVTIPDGRYVG PAGKVWTSQA EADALPKMTP DYAYYHTNEK VVAVNRALAA 360
GYRRAAQTAIFI HPSATVIGDV TIGANVMISP MASIRSDEGM PIYVGANANL QDQVTLHALE 420
VFDEEGNLIE ENWVEVNGEK YAVYLGDNVS LAHQAQVHGP AIVGEDTFIG MQASVFKSTI 480
GNGCVLEPGA AVIGTIPDG RYVPGAKVVT SQAEADALPK MTPDYAYYHT NEKVVAVNRA 540
LAAGYRAAQ 549

SEQ ID NO: 458          moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 458          moltype = AA length = 549
TAYIHPSPATV IGDVTIGANV MVSPMASIRS DEGMPYILGD NVNVQDGVS L HGLETVDEEG 60
NVIEENLVEV DGKKYVYVLG DNVSLAHQAQ VEGGTVLGEN VFLQEGVRV RSTLGEGVIL 120
REGATVEGVT IAPGKVAAG QTVTQAAAD ALPTLTASDP LYSEHATVVA ANIAAAAAAAK 180
AAATAYIHP ATVIGDTVIG ANVMSPMAS IRSDEGMPIY LGDNVNQDG VSLHGLETVD 240
EEGNVIEENV VEVDGKYYVV YLGDNVSLAH QAVVEGGTIVL GENVFLQEGV RVRRLSTLGE 300
VILREGATVE GVTIAPGKVV AAGQTVTQA AADALPLTA SDPLYSEHAT VVAANIAAAA 360
AAKAAATAYI HPSATVIGDV TIGANVMSP MASIRSDEGM PIYLGDNVNV QDGVSLHGLE 420
TVDEEGNVIE ENLVEVDGKK YVYVLGDNVS LAHQAVVVEGG TVLGENVFLQ EGVRVRRSTL 480
GEGVILREGA TVEGVTIAPG KVVAAGQTWT TQAAADALPT LTASDPLYSE HATVVAANIA 540
AAAAAKAAA 549

SEQ ID NO: 459          moltype = AA length = 549
FEATURE          Location/Qualifiers
source           1..549
mol_type = protein
note = Library of modified or engineered enzymes
organism = synthetic construct

SEQUENCE: 459          moltype = AA length = 549
TAYIAPSATV IGDVTIGANV MISPMASIRA DEGMPIKVGD NANVQDGVTL HALETKDEEG 60
NDIEENWVEV NGEKYAVYVG ANVSLAHQAQ LHGPCIVGDD TFIGMQARVF KSSIGNGCVL 120

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EPQAAVIGVT IPDGRYVPAG	AVVTSQAEAD ALPKLTDDYA	YAHTNEKVVA VNLALAKGYL	180
TPTTAYTAPS ATVIGDTVIG	ANVMISP MAS IRADEGMPKI	VGDNANVQDQ VTLHALETKD	240
EEGNDIEENW VEVNGEKYAV	QAQLHGPCIV GDDTFIGMQA	RVFKSSIGNG	300
CVLEPQAAVI GVTIPDGRYV	PAGAVVTSQA EADALPKLTD	DYAYAHTNEK VVAVNLALAK	360
GYLTTPTAYI APSATVIGDV	TIGANVMISP MASIRADEGM	PIKVGDNANV QDQVTLH	420
TDKEEGNDIE ENWVEVNGEK	YAVVVGANS LAHQAOQLHGP	CIVGDDTFIG MQARVFKSS	480
GNGCVLEPQA AVIGVTIPDG	RYVPGAVVT SQAEADALPK	LTDYYAYAHT NEKVVAVNL	540
LAKGYLTP			549

SEQ ID NO: 460	moltype = AA length = 549		
FEATURE	Location/Qualifiers		
source	1..549		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
SEQUENCE: 460			
TAYIHPSAVV IGGVEIGANV	MVSPMASIRS DEGMPIKIEA NANVQDGVL	I QSLVSKENDK	60
ELLEKLLKKLN NGEYYNIYLE	EGVSLAHQAT IILNSCYLSSG	CFLAEGVVL NSVLNDAVFL	120
GRGVTVTNAE VLEPHVFEAG	DVITEEKVEP VEIPEELRAA	IAAQRAAVIA ANLAAAAAAK	180
AAATAYIHP AVVIGOVEIG	ANVMISP MAS IRSDEGMPKI	IEANANVQDG VLIQSLVSKE	240
NDKELLEKLK KLNNGEYYNI	YLEEGVSLAH QATILNSCYL	SSGCFLAEVG VLLENVLNDA	300
VFLGRGVTVT NAEVLPHVF	EAGDVITEEK VEPVEIPEEL	RAAIAAQRAA VIAANLAAA	360
AAKAAATAYI HPSAVVIGQV	EIGANVMVSP MASIRSDEGM	PIKIEANANV QDGVLIQSLV	420
SKENDKELLE KLKKLNNGEY	YNIYLEEGVS LAHQATILNS	CYLSSGCFLA EGVVLENSVL	480
NDAVFLGRGV TVTNAEVLEP	HVFEAGDVIT EEKVEPVEIP	EELRAAIAAQ RAAVIAANLA	540
AAAAAKAAA			549

SEQ ID NO: 461	moltype = AA length = 549		
FEATURE	Location/Qualifiers		
source	1..549		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
SEQUENCE: 461			
TAYIHQPQANV IGDVEIGANV	MVSPMASIRS DEGMPIFVGE NANVQDQVTL	HALEYDDEEG	60
NPIEENIEVEV DGKKYAVYLG	KNVSLAHQAO IHGPSIVGDD	TFIGMQALVF KSVLGNNCVL	120
EPQAAAIGVT IPDGRYIPAG	KVVTTSQAEAD ALPEVTPDYA	YYHTNRQVVY VNTQLAEGYR	180
AAATAYIHPQ ANVIGDVEIG	ANVMISP MAS IRSDEGMPIF	VGENANVQDQ VTLHALEYTD	240
EEGPNPIEVEV DGKKYAVYLG	VEVDGKYYAV YLGKNVSLAH	QAQIHGPSIV GDDTFIGMQA LVFKSVLGN	300
CVLEPQAAAI GVTIPDGRYI	PAGKVVTSQA EADALPEVTP	DYAYYHTNEQ VVYVNTQLAE	360
GYRAAATAYI HPQANVIGDV	EIGANVMVSP MASIRSDEGM	PIFVGENANV QDGVTLH	420
TYDEEGNPIE ENIVEVDGKK	YAVVYLGKNS LAHQAOQIHGP	SIVGDDTFIG MQALVFKS	480
GNNCVLEPQA AAIQVTIPDG	RYVPGAVVT SQAEADALPE	VTPDYAYYHT NEQVYVNTQ	540
LAEGYRAAA			549

SEQ ID NO: 462	moltype = AA length = 549		
FEATURE	Location/Qualifiers		
source	1..549		
	mol_type = protein		
	note = Library of modified or engineered enzymes		
	organism = synthetic construct		
SEQUENCE: 462			
TAYIHPSAEV IGSVEIGENV	MISPNASIRS DEGMPIVIGD NANVQDGVT	L HGLETKTEEG	60
ELIEENYVEV DGKKYVYIG	ENVSLAHQAO VHGPVKGED	TFIGMGATVT QSILGEVLL	120
REGAQQTGTVT LAPGTVVDRG	TVLTTQADVA SLRKLEPSDP	LLKENEERVK KNLALWEELK	180
KAETAYIHP AVIGSVEIG	ENVMSPNAS QAQVHGPVKG	EADALPEVTP D GDDTFIGMQA	240
EEGELIEENY VEVDGKYYVY	YIGENVSLAH QAOVHGPVKG	GEDTFIGMA TVTQSILGEG	300
VLLREGAQIT GTVLAPGTVV	DRGTVLTTQA DVASLRKLEP	SDPLLKENEE VRKKNLALWE	360
ELKKAETAYI HPSAEVIGSV	EIGENVMISP NASIRSDEGM	PIVIGDNANV QDGVTLHGLE	420
TKTEEGELIE ENYVEVDGKK	YVYVYIGENVS LAHQAOQVHGP	AKVGEDTFIG MGATVTQSIL	480
GEGVLLREGA QTGVTLAPG	TVVDRGTVLT TQADVASLRK	LEPSDPLLKE NEEVRKKNL	540
LWEELKKA			549

SEQ ID NO: 463	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 463	

TAVIAPNAQV IGEVHGIDNV	MISPNASIRS DEGMPIVIGE NANLQDNVQL	HGLEVLDEEG	60
NVIEEALVEV DGKKYVYIG	KNVSLGHQAO IHGPALVGD	TFIGMNAKVF KSRIGNGCVL	120
EPNAQVIGVT IPDGRYVPAG	KVVTTSQAEAD ALVLTPDYA	MAHTNERVVA VNLALAAAAR	180
AAATAVIAPN AQVIGEVHIG	DNVMISP NAS IRSDEGMP	PIY GENANLQDN VQLHGLEVLD	240
EEGNVIEEAL VEVDGKYYVY	YIGKNVSLGH QAQIHGPALV	GDDTFIGMNA KVFKSRIGN	300
CVLEPNAQVI GVTIPDGRYV	PAGKVVTTQA EADALPVLT	DYAMAHTNER VVAVNLALAA	360

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AARAAATAVI APNAQVIGEV HIGDNVMISP NASIRSDEGM PIYIGENANL QDNVQLHGLE	420
VLDDEEGNIE EALVEVDGKK YYVYIGKNS LGHQAQIHGP ALVGDDTFIG MNAKVFKSRI	480
GNGCVLEPNA QVIGVTIPDG RYVPAGKVVT TQAEADALPV LTPDYAMAHT NERVVAVNL	540
LAAAAARAAA	549
SEQ ID NO: 464	moltype = AA length = 549
FEATURE	Location/Qualifiers
source	1..549
	mol_type = protein
	note = Library of modified or engineered enzymes
	organism = synthetic construct
SEQUENCE: 464	
TAYIHPQATV IGDVTIGANV MVSPMASIRS DEGMPIFVGD NANVQDGVTL HALETYDEEG	60
NPIEENWVEV DGKKYAVYL DGNSLAHQAQ VHGPAAVGED TFIGMQATVF KSKLGNNCVL	120
EPGAAAIGVT IPDGRYIPAG VFTSQAEAD ALPEVTPDYA YYHTNEDVVY VNIALAEGYK	180
KLSTAYIHPQ ATVIGDTVIG ANVMSPMAS IRSDEGMPIF VGDNANVQDG VTLHALETYD	240
EENPPIEENW VEVDGKKYAV YLGDNVSLAH QAQVHGPAAV GEDTFIGMQA TVFKSKLGN	300
CVLEPGAAAI GVTIPDGRYI PAGKVVTCSQ EADALPEVTP DYAYYHTNED VVYVNIALAE	360
GYKKLSTAYI HPQATVIGDV TIGANVMVNS MASIRSDEGM PIFVGDNANV QDGVTLHCALE	420
TYDEEGNPIE ENWVEVDGKK YAVYLGDNVS LAHQAQVHGP AAVGEDTFIG MQATVFKSKL	480
GNNCVLEPNA AAIQVTIPDG RYIPAGKVVT SQAEEADALPE VTPDYAYYHT NEDVVVNVIA	540
LAEGYKKLS	549

What is claimed is:

1. A method of extracting a metal from a mineral material, the method comprising:
 - (a) contacting the mineral material with an enzyme having silicase activity under reaction conditions such that the metal contained within the mineral material is solubilized and released; and
 - (b) collecting the released metal, thereby extracting the metal from the mineral material.
2. The method of claim 1, wherein the mineral material comprises an ore, a rock, a natural mineral material, a man-made mineral material, or any combination thereof.
3. The method of claim 1, wherein the mineral material comprises a silicate.
4. The method of claim 1, wherein the mineral material comprises an inosilicate, a phyllosilicate, an amorphous silicate, a tectosilicate, or any combination thereof.
5. The method of claim 1, wherein the enzyme having silicase activity has a sequence identity of at least about 30%, at least about 40%, about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more with an amino acid sequence of a gamma carbonic anhydrase.
6. The method of claim 1, wherein the enzyme having silicase activity has a sequence identity of at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or more, with an amino acid sequence of an enzyme selected from the group consisting of: *Methanosarcina thermophila* gamma carbonic anhydrase, *Bacillus licheniformis* CG-B52 gamma carbonic anhydrase, *Pelobacter carbinolicus* gamma carbonic anhydrase, *Syntrophus aciditrophicus* gamma carbonic anhydrase, *Methanosarcina barkeri* gamma carbonic anhydrase, *Methanosarcina mazei* carbonic anhydrase, *Bacillus halodurans* alpha carbonic anhydrase, Alkalihalobacillus *clausii* (strain KSM-K16) (*Bacillus clausii*) alpha carbonic anhydrase, *Methanosarcina acetivorans* carbonate dehydratase, *Kofleriaceae* bacterium SLC26A/SuP transporter domain-containing protein, Thermodesulfitimonas *autotrophica* carbonic anhydrase/acetyltransferase-like protein (Isoleucine patch superfamily), *Fischerella thermalis/Mastigocladus laminosus* JSC-11
- carboxysome assembly protein CcmM, *Thermosynechococcus vestitus* BP-1/(*Thermosynechococcus elongatus* BP-1) carboxysome assembly protein CcmM, *Methanothrix thermoacetophila* carbonate dehydratase, *Thermosyntrropha lipolytica* carbonic anhydrase or acetyltransferase, isoleucine patch superfamily, Desulfovibrio thermobenzoicus transferase, *Archaeoglobus veneficus* carbonate dehydratase, Suberites domuncula carbonic anhydrase.
7. The method of claim 1, wherein the enzyme having silicase activity has an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9%, or more sequence identity to an amino acid sequence of any one of SEQ ID NOS: 1-402.
8. The method of claim 1, wherein the reaction conditions comprise a temperature from about 23 to about 85 degrees Celsius (C).
9. The method of claim 1, wherein the reaction conditions comprise a pH from about 4 to about 11.
10. The method of claim 1, wherein the reaction conditions comprise contacting the enzyme having silicase activity with a co-factor.
11. The method of claim 10, wherein the co-factor is selected from the group consisting of: iron, zinc, copper, nickel, and cobalt.
12. The method of claim 1, wherein the metal is selected from the group consisting of: lithium, aluminum, iron, nickel, cobalt, strontium, and a rare earth element.
13. The method of claim 1, wherein the metal is released into a solution.
14. The method of claim 13, further comprising extracting the metal from the solution.
15. The method of claim 13, further comprising purifying the metal from the solution, thereby generating a purified metal.
16. The method of claim 15, wherein the purified metal has a purity of at least about 80%.
17. The method of claim 1, wherein the method is performed in situ or ex situ.

18. The method of claim 1, wherein the reaction conditions comprise a rock to liquid ratio from about 1-40% (w/v).

19. The method of claim 1, wherein the reaction conditions comprise a buffer.

20. The method of claim 19, wherein the buffer is selected from the group consisting of: TRIS, PBS, citrate, monosodium glutamate, and any combination thereof.

* * * *