



(51) International Patent Classification:

CI2N 9/22 (2006.01) CI2N 15/63 (2006.01)

CI2N 15/113 (2010.01) CI2N 9/78 (2006.01)

CI2N 15/10 (2006.01)

(21) International Application Number:

PCT/US2021/024945

(22) International Filing Date:

30 March 2021 (30.03.2021)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

63/003,159 31 March 2020 (31.03.2020) US

63/116,149 19 November 2020 (19.11.2020) US

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ,

(54) Title: CLASS II, TYPE II CRISPR SYSTEMS

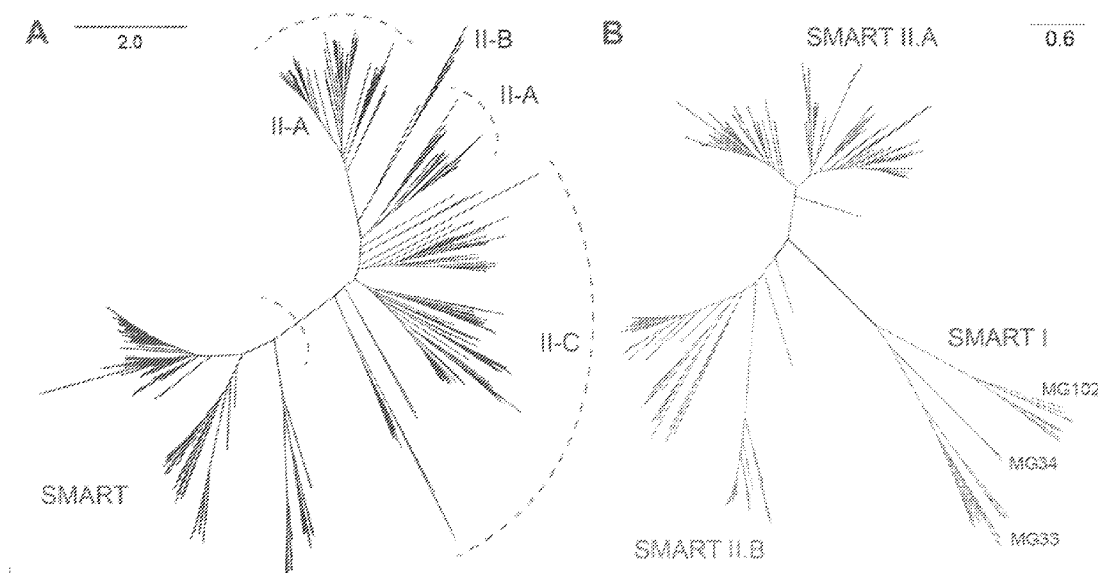


FIGURE 1

(57) Abstract: The present disclosure provides for endonuclease enzymes as well as methods of using such enzymes or variants thereof.



TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- *with international search report (Art. 21(3))*
- *with sequence listing part of description (Rule 5.2(a))*

CLASS II, TYPE II CRISPR SYSTEMS**CROSS-REFERENCE**

[0001] This application claims the benefit of U.S. Provisional Application No. 63/116,149, entitled "CLASS II, TYPE II CRISPR SYSTEMS", filed on November 19, 2020, and U.S. Provisional Application No. 63/003,159, entitled "CLASS II, TYPE II CRISPR SYSTEMS", filed on March 31, 2020, both of which are incorporated in their entireties herein.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on March 27, 2021, is named 55921-711_601_SL.txt and is 2,235,526 bytes in size.

BACKGROUND

[0003] Cas enzymes along with their associated Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) guide ribonucleic acids (RNAs) appear to be a pervasive (~45% of bacteria, ~84% of archaea) component of prokaryotic immune systems, serving to protect such microorganisms against non-self nucleic acids, such as infectious viruses and plasmids by CRISPR-RNA guided nucleic acid cleavage. While the deoxyribonucleic acid (DNA) elements encoding CRISPR RNA elements may be relatively conserved in structure and length, their CRISPR-associated (Cas) proteins are highly diverse, containing a wide variety of nucleic acid-interacting domains. While CRISPR DNA elements have been observed as early as 1987, the programmable endonuclease cleavage ability of CRISPR/Cas complexes has only been recognized relatively recently, leading to the use of recombinant CRISPR/Cas systems in diverse DNA manipulation and gene editing applications. Owing to the utility of these enzymes, they are being repurposed for a wide variety of biotechnology, gene editing, and therapeutic applications. Due to their single-effector architecture, the majority of systems currently being repurposed for genome engineering belong to the CRISPR Class 2, Type II and Class 2, Type V categories.

SUMMARY

[0004] The large size (greater than ca. 1200 amino acids) of many class 2 Cas effectors makes delivery for therapeutic applications challenging. Accordingly, described herein are methods, compositions, and systems relating to novel putative guided dsDNA nucleases referred to as SMART (SMall ARchaeal-associaTed) nuclease systems. These endonuclease effectors are defined by their small size (400 aa - 1050 aa), the presence of RuvC and HNH catalytic domains, and other predicted protein features that together suggest novel biochemical mechanisms.

[0005] In some aspects, the present disclosure provides for an engineered nuclease system, comprising: (a) an endonuclease comprising a RuvC domain and an HNH domain, wherein said endonuclease is derived from an uncultivated microorganism; and (b) an engineered guide ribonucleic acid structure configured to form a complex with said endonuclease comprising: (i) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and (ii) a tracr ribonucleic acid sequence configured to bind to said endonuclease; wherein said endonuclease has a molecular weight of about 96kDa or less. In some embodiments, said endonuclease is an archaeal endonuclease. In some embodiments, said endonuclease is a Class 2, Type II Cas endonuclease. In some embodiments, said endonuclease comprises a sequence with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease further comprises an arginine-rich region comprising an RRxRR motif or a domain with PF14239 homology. In some embodiments, said arginine rich region or said domain with PF14239 homology has at least 85%, at least 90%, or at least 95% identity to an arginine rich region or a domain with PF14239 homology of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease further comprises a REC (recognition) domain. In some embodiments, said REC domain has at least 85%, at least 90%, or at least 95% identity to a REC domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease further comprises a BH (bridge helix) domain, a WED (wedge) domain, and a PI (PAM interacting) domain. In some embodiments, said BH domain, said WED domain, or said PI domain has at least 85%, at least 90%, or at least 95% identity to a BH domain, a WED domain, and/or a PI domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

[0006] In some aspects, the present disclosure provides for an engineered nuclease system comprising: (a) an endonuclease comprising a RuvC-I domain and an HNH domain; and (b) an engineered guide ribonucleic acid structure configured to form a complex with said endonuclease comprising: (i) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and (ii) a ribonucleic acid sequence configured to bind to said endonuclease, wherein said endonuclease comprises a sequence with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease is an archaeal endonuclease. In some embodiments, said endonuclease is a class 2, type II Cas endonuclease. In some embodiments, said endonuclease further comprises an arginine-rich region comprising an RRxRR motif or a domain with PF14239 homology. In some embodiments, said arginine rich region or said domain with PF14239 homology has at least 85%, at least 90%, or at least 95% identity to an

arginine rich region of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease further comprises a REC (recognition) domain. In some embodiments, said REC domain having at least 85%, at least 90%, or at least 95% identity to a REC domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease further comprises a BH domain, a WED domain, and a PI domain. In some embodiments, said BH domain, said WED domain, or said PI domain has at least 85%, at least 90%, or at least 95% identity to a BH domain, a WED domain, and/or a PI domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease is derived from an uncultivated microorganism. In some embodiments, said ribonucleic acid sequence configured to bind said endonuclease comprises a sequence with at least 80% sequence identity to any one of SEQ ID NOs: 199-200, 460-461, or 669-673, or a sequence with at least 80% sequence identity to the non-degenerate nucleotides of any one of SEQ ID NOs: 201-203 or 613-616. In some embodiments, said guide nucleic acid structure comprises a sequence with at least 80% identity to the non-degenerate nucleotides of any one of SEQ ID NOs: 201-203, 613-616..

[0007] In some aspects, the present disclosure provides for an engineered nuclease system comprising: (a) an engineered guide ribonucleic acid structure comprising: (i) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and (ii) a ribonucleic acid sequence configured to bind to an endonuclease, wherein said ribonucleic acid sequence comprises a sequence with at least 80% sequence identity to any one of SEQ ID NOs: 199-200, 460-461, or 669-673, or a sequence with at least 80% sequence identity to nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616; and (b) an RNA-guided endonuclease configured to bind to said engineered guide ribonucleic acid. In some embodiments, said RNA-guided endonuclease is an archaeal endonuclease. In some embodiments, said endonuclease has a molecular weight of about 120 kDa or less, 100kDa or less, 90 kDa or less, or 60 kDa or less. In some embodiments, said engineered guide ribonucleic acid structure comprises at least two ribonucleic acid polynucleotides. In some embodiments, said engineered guide ribonucleic acid structure comprises a single ribonucleic acid polynucleotide comprising said guide ribonucleic acid sequence and said tracr ribonucleic acid sequence. In some embodiments, said guide ribonucleic acid sequence is complementary to a prokaryotic, bacterial, archaeal, eukaryotic, fungal, plant, mammalian, or human genomic sequence. In some embodiments, said guide ribonucleic acid sequence is 15-24 nucleotides in length. In some embodiments, said endonuclease comprises one or more nuclear localization sequences (NLSs) proximal to an N- or C-terminus of said endonuclease. In some embodiments, said NLS comprises a sequence selected from SEQ ID NOs: 205-220. In some embodiments, the

system further comprises a single- or double-stranded DNA repair template comprising from 5' to 3': a first homology arm comprising a sequence of at least 20 nucleotides 5' to said target deoxyribonucleic acid sequence, a synthetic DNA sequence of at least 10 nucleotides, and a second homology arm comprising a sequence of at least 20 nucleotides 3' to said target sequence. In some embodiments, said first or second homology arm comprises a sequence of at least 40, 80, 120, 150, 200, 300, 500, or 1,000 nucleotides. In some embodiments, said system further comprises a source of Mg^{2+} . In some embodiments, said endonuclease and said tracr ribonucleic acid sequence are derived from distinct bacterial species within a same phylum. In some embodiments, said endonuclease comprises a sequence with at least 70% sequence identity to any one of SEQ ID NOs: 2-24 and said guide RNA structure comprises an RNA sequence predicted to comprise a hairpin comprising a stem and a loop, wherein said stem comprises at least 12 pairs of ribonucleotides. In some embodiments, said guide RNA structure further comprises a second stem and a second loop, wherein the second stem comprises at least 5 pairs of ribonucleotides. In some embodiments, said guide RNA structure further comprises an RNA structure comprising at least two hairpins. In some embodiments, said endonuclease comprises a sequence with at least 70% sequence identity to SEQ ID NO: 1 and said guide RNA structure comprises an RNA sequence predicted to comprise at least four hairpins comprising a stem and a loop. In some embodiments: a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 1, 2, 10, 17, or 613-616; and b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 199-200 or 669-673 or the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616. In some embodiments: a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 1-24, 462-488, or 501-612; and b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 199-200 or 669-673 or the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616. In some embodiments: a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 2, 10, or 17; and b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to the nonvariable nucleotides of any one of SEQ ID NOs: 202-203 or 613-614. In some embodiments: a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 25-198, 221-459, or 489-580; and b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to a class 2, type II sgRNA or tracr sequence. In some embodiments, said sequence identity is determined by a BLASTP, CLUSTALW, MUSCLE, MAFFT, or CLUSTALW with parameters of the Smith-Waterman homology search algorithm. In some

embodiments, said sequence identity is determined by said BLASTP homology search algorithm using parameters of a wordlength (W) of 3, an expectation (E) of 10, and a BLOSUM62 scoring matrix setting gap costs at existence of 11, extension of 1, and using a conditional compositional score matrix adjustment. In some embodiments, said endonuclease is not a Cas9 endonuclease, a Cas14 endonuclease, a Cas12a endonuclease, a Cas12b endonuclease, a Cas 12c endonuclease, a Cas12d endonuclease, a Cas12e endonuclease, a Cas13a endonuclease, a Cas13b endonuclease, a Cas13c endonuclease, or a Cas 13d endonuclease. In some embodiments, said endonuclease has less than 80% identity to a Cas9 endonuclease.

[0008] In some aspects, the present disclosure provides for an engineered single guide ribonucleic acid polynucleotide comprising: a) a DNA-targeting segment comprising a nucleotide sequence that is complementary to a target sequence in a target DNA molecule; and b) a protein-binding segment comprising two complementary stretches of nucleotides that hybridize to form a double-stranded RNA (dsRNA) duplex, wherein said two complementary stretches of nucleotides are covalently linked to one another with intervening nucleotides, and wherein said engineered guide ribonucleic acid polynucleotide is configured to form a complex with an endonuclease comprising a variant having at least 75% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said DNA-targeting segment is positioned 5' of both of said two complementary stretches of nucleotides. In some embodiments: a) said protein binding segment comprises a sequence having at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 199-200 or 669-673; b) said protein binding segment comprises a sequence having at least 70%, at least 80%, or at least 90% identical to the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616. In some embodiments: a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 2, 10, or 17; and b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to at least one of SEQ ID NO: 200 or the nonvariable nucleotides of SEQ ID NO: 202-203 or 613-614. In some embodiments: a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 25-198, 221-459, or 489-580; and b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to a class 2, type II sgRNA. In some embodiments, said endonuclease further comprises a base editor or a histone editor coupled to said endonuclease. In some embodiments, said base editor is an adenosine deaminase. In some embodiments, said adenosine deaminase comprises ADAR1 or ADAR2. In some embodiments, said base editor is a cytosine deaminase. In some embodiments, said cytosine deaminase comprises APOBEC1, APOBEC2, APOBEC3A,

APOBEC3B, APOBEC3C, APOBEC3D, APOBEC3F, APOBEC3G, APOBEC3H, or APOBEC4. .

[0009] In some aspects, the present disclosure provides for a deoxyribonucleic acid polynucleotide encoding any of the engineered guide ribonucleic acid polynucleotides described herein.

[0010] In some aspects, the present disclosure provides for a nucleic acid comprising an engineered nucleic acid sequence optimized for expression in an organism, wherein said nucleic acid encodes a class 2, type II Cas endonuclease comprising a RuvC domain and an HNH domain, wherein said endonuclease is derived from an uncultivated microorganism, and wherein said endonuclease has a molecular weight of about 120 kDa or less, 100kDa or less, 90 kDa or less, 60 kDa or less, or 30 kDa or less. In some embodiments, said endonuclease comprises SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668 or a variant thereof having at least 70% sequence identity thereto. In some embodiments, said endonuclease further comprises a sequence encoding one or more nuclear localization sequences (NLSs) proximal to an N- or C-terminus of said endonuclease. In some embodiments, said NLS comprises a sequence selected from SEQ ID NOs: 205-220. In some embodiments, said organism is prokaryotic, bacterial, eukaryotic, fungal, plant, mammalian, rodent, or human. In some embodiments, said organism is prokaryotic or bacterial, and said organism is a different organism from an organism from which said endonuclease is derived. In some embodiments, said organism is not said uncultivated microorganism.

[0011] In some aspects, the present disclosure provides for a vector comprising a nucleic acid sequence encoding an RNA-guided endonuclease comprising a RuvC-I domain and an HNH domain, wherein said endonuclease is derived from an uncultivated microorganism, and wherein said endonuclease has a molecular weight of about 120 kDa or less, 100kDa or less, 90 kDa or less, or 60 kDa or less, wherein the RNA-guided endonuclease is optionally archaeal. In some embodiments, said endonuclease further comprises an arginine-rich region comprising an RRxRR motif or a domain with PF14239 homology. In some embodiments, said endonuclease further comprises a REC (recognition) domain. In some embodiments, said endonuclease further comprises a BH domain, a WED domain, and a PI domain.

[0012] In some aspects, the present disclosure provides for a vector comprising any of the nucleic acids described herein. In some embodiments, the vector further comprising a nucleic acid encoding an engineered guide ribonucleic acid structure configured to form a complex with said endonuclease, said engineered guide ribonucleic acid structure comprising: a) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and b) a tracr ribonucleic acid sequence configured to binding to said endonuclease. In some

embodiments, the vector is a plasmid, a minicircle, a CELiD, an adeno-associated virus (AAV) derived virion, or a lentivirus.

[0013] In some aspects, the present disclosure provides for a cell comprising any of the vectors described herein. In some embodiments, said cell is a bacterial, archaeal, fungal, eukaryotic, mammalian, or plant cell. In some embodiments, said cell is a bacterial cell.

[0014] In some aspects, the present disclosure provides for a method of manufacturing an endonuclease, comprising cultivating any of the cells described herein.

[0015] In some aspects, the present disclosure provides for a method for binding, cleaving, marking, or modifying a double-stranded deoxyribonucleic acid polynucleotide, comprising: (a) contacting said double-stranded deoxyribonucleic acid polynucleotide with a class 2, type II Cas endonuclease in complex with an engineered guide ribonucleic acid structure configured to bind to said endonuclease and said double-stranded deoxyribonucleic acid polynucleotide; (b) wherein said double-stranded deoxyribonucleic acid polynucleotide comprises a protospacer adjacent motif (PAM); wherein said endonuclease has a molecular weight of about 120 kDa or less, 100 kDa or less, 90 kDa or less, or 60 kDa or less. In some embodiments, said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide, wherein said PAM comprises NGG. In some embodiments, said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide 6-8 nucleotides or 7 nucleotides from said PAM. In some embodiments, said endonuclease comprises a variant with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

[0016] In some aspects, the present disclosure provides for a method for binding, cleaving, marking, or modifying a double-stranded deoxyribonucleic acid polynucleotide, comprising: (a) contacting said double-stranded deoxyribonucleic acid polynucleotide with an RNA-guided archaeal endonuclease in complex with an engineered guide ribonucleic acid structure configured to bind to said endonuclease and said double-stranded deoxyribonucleic acid polynucleotide; wherein said double-stranded deoxyribonucleic acid polynucleotide comprises a protospacer adjacent motif (PAM); and wherein said endonuclease comprises a variant with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. In some embodiments, said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide, wherein said PAM comprises NGG. In some embodiments, said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide 6-8 or 7 nucleotides from said PAM. In some embodiments, said class 2, type II Cas endonuclease is not a Cas9 endonuclease, a Cas14 endonuclease, a Cas12a endonuclease, a Cas12b endonuclease, a Cas 12c endonuclease, a Cas12d endonuclease, a Cas12e endonuclease, a Cas13a endonuclease, a Cas13b endonuclease, a Cas13c endonuclease, or a Cas 13d

endonuclease. In some embodiments, said class 2, type II Cas endonuclease is derived from an uncultivated microorganism. In some embodiments, said double-stranded deoxyribonucleic acid polynucleotide is a prokaryotic, archaeal, bacterial, eukaryotic, plant, fungal, mammalian, rodent, or human double-stranded deoxyribonucleic acid polynucleotide. In some embodiments, said double-stranded deoxyribonucleic acid polynucleotide is a prokaryotic, archaeal, or bacterial double-stranded deoxyribonucleic acid polynucleotide from a species other than a species from which said endonuclease was derived.

[0017] In some aspects, the present disclosure provides for a method of modifying a target nucleic acid locus, said method comprising delivering to said target nucleic acid locus any of the engineered nuclease systems described herein, wherein said endonuclease is configured to form a complex with said engineered guide ribonucleic acid structure, and wherein said complex is configured such that upon binding of said complex to said target nucleic acid locus, said complex modifies said target nucleic acid locus. In some embodiments, modifying said target nucleic acid locus comprises binding, nicking, cleaving, or marking said target nucleic acid locus. In some embodiments, said target nucleic acid locus comprises deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). In some embodiments, said target nucleic acid comprises genomic eukaryotic DNA, archaeal DNA, viral DNA, or bacterial DNA. In some embodiments, said target nucleic acid comprises bacterial DNA wherein said bacterial DNA is derived from a bacterial or archaeal species different from a species from which said endonuclease was derived. In some embodiments, said target nucleic acid locus is *in vitro*. In some embodiments, said target nucleic acid locus is within a cell. In some embodiments, said endonuclease and said engineered guide nucleic acid structure are encoded by separate nucleic acid molecules. In some embodiments, said cell is a prokaryotic cell, a bacterial cell, an archaeal cell, a eukaryotic cell, a fungal cell, a plant cell, an animal cell, a mammalian cell, a rodent cell, a primate cell, or a human cell. In some embodiments, said cell is derived from a species different from a species from which said endonuclease was derived. In some embodiments, delivering said engineered nuclease system to said target nucleic acid locus comprises delivering any of the nucleic acids described herein or any of the vectors described herein. In some embodiments, delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a nucleic acid comprising an open reading frame encoding said endonuclease. In some embodiments, said nucleic acid comprises a promoter to which said open reading frame encoding said endonuclease is operably linked. In some embodiments, delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a capped mRNA containing said open reading frame encoding said endonuclease. In some embodiments, delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a translated polypeptide. In some

embodiments, delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a deoxyribonucleic acid (DNA) encoding said engineered guide ribonucleic acid structure operably linked to a ribonucleic acid (RNA) pol III promoter. In some embodiments, said endonuclease induces a single-stranded break or a double-stranded break at or proximal to said target locus. In some embodiments, said endonuclease induces a double stranded break proximal to said target locus 5' from a protospacer adjacent motif (PAM). In some embodiments, said endonuclease induces a double-stranded break 6-8 nucleotides or 7 nucleotides 5' from said PAM. In some embodiments, said engineered nuclease system induces a chemical modification of a nucleotide base within or proximal to said target locus or a chemical modification of a histone within or proximal to said target locus. In some embodiments, said chemical modification is deamination of an adenosine or a cytosine nucleotide. In some embodiments, said endonuclease further comprises a base editor coupled to said endonuclease. In some embodiments, said base editor is an adenosine deaminase. In some embodiments, said adenosine deaminase comprises ADAR1 or ADAR2. In some embodiments, said base editor is a cytosine deaminase. In some embodiments, said cytosine deaminase comprises APOBEC1, APOBEC2, APOBEC3A, APOBEC3B, APOBEC3C, APOBEC3D, APOBEC3F, APOBEC3G, APOBEC3H, or APOBEC4.

[0018] Additional aspects and advantages of the present disclosure will become readily apparent to those skilled in this art from the following detailed description, wherein only illustrative embodiments of the present disclosure are shown and described. As will be realized, the present disclosure is capable of other and different embodiments, and its several details are capable of modifications in various obvious respects, all without departing from the disclosure.

Accordingly, the drawings and description are to be regarded as illustrative in nature, and not as restrictive.

INCORPORATION BY REFERENCE

[0019] 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

[0020] 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 (also "Figure"

and “FIG.” herein), of which:

[0021] FIG. 1 depicts a dendrogram showing homology relationships of CRISPR/Cas loci of different classes and types. Shown are SMART I and II Cas enzyme classes described herein relative to Class 2, Type II-A, II-B, and II-C Cas systems, demonstrating that these systems group into separate classes than II-A, II-B, and II-C. (A) shows a SMART phylogenetic tree in context of Cas9 reference sequences, where SMART effectors are distantly clustered away from Cas9 reference sequences (Type II-A, II-B, and II-C); (B) shows a SMART phylogenetic tree illustrating subgroups of SMART enzymes.

[0022] FIG. 2 shows length distribution for SMART effectors described herein, showing that SMART I and II enzymes are clustered at a lower molecular weight than Cas9-like enzymes. SMART nucleases show a bimodal distribution with one peak around 400 aa (SMART II) and a second peak around 750 aa (SMART I). Cas9 nucleases also show a bimodal distribution with peaks around 1,100 aa (e.g. SaCas9) and 1,300 aa (e.g. SpCas9).

[0023] FIG. 3 depicts the genomic context of ‘small’ Type II nucleases MG33-1, MG35-236. SMART nucleases and CRISPR accessory proteins are shown as dark grey arrows, other genes are depicted as light grey arrows. Domains predicted for all genes in a genomic fragment are shown as grey boxes under the arrows.. Shown are: (A) genomic context of the SMART I MG33-1 nuclease and CRISPR loci encoded upstream from a SMART II nuclease MG35-236, showing downstream from the SMART II a predicted insertion sequence carrying transposases TnpA and TnpB; (B): genomic context of the SMART I nuclease MG34-1, where environmental expression sequencing reads are shown aligned under the CRISPR array and the predicted tracrRNA, and the transcriptomic coverage for the regions is illustrated above the contig sequence; (C) genomic context of the SMART I nuclease MG34-16, wherein environmental expression sequencing reads are shown aligned under the CRISPR array and the predicted tracrRNA, and the transcriptomic coverage for the regions is illustrated above the contig sequence; and (D) a genomic fragment targeted by spacer 7 from the MG34-16 CRISPR array in (D), where the genomic fragment was identified as being derived from phage based on virus-specific gene annotations terminase and portal; the inset shows the location of the MG34-16 spacer 7 targeting the C-terminus of a viral gene of unknown function--the putative NGG PAM for MG34-16 is highlighted by a grey box downstream from the spacer match.

[0024] FIG. 4 shows a multiple sequence alignment of example SMART endonucleases (MG33-1 (SEQ ID NO: 1), MG33-2 (SEQ ID NO: 463), MG33-3 (SEQ ID NO: 464), MG34-1 (SEQ ID NO: 2), MG 34-9 (SEQ ID NO: 10), MG34-16 (SEQ ID NO: 17), MG 102-1 (SEQ ID NO: 581), MG102-2 (SEQ ID NO: 582), MG35-1 (SEQ ID NO: 25), MG 35-2 (SEQ ID NO: 26), MG 35-3 (SEQ ID NO: 27), MG 35-102 (SEQ ID NO: 126), MG35-236 (SEQ ID NO: 284), MG35-419

(SEQ ID NO: 222), MG35-420 (SEQ ID NO: 223), and MG 35-421 (SEQ ID NO: 224)), where the sequence of SaCas9 was used as reference domains are shown as a rectangles below the reference sequence, and catalytic residues are shown as squares above each sequence.. Shown are: (A) an alignment of the endonuclease region containing the RuvC-I and bridge helix domains; (B) an alignment of the region containing the RuvC-III domain; and (C) an alignment of the region containing the RuvC-II and HNH domains

[0025] FIG. 5 depicts an example domain organization for SMART I endonucleases, using MG34-1 as an example. Shown are (A) a diagram showing the predicted domain architecture of SMART I nucleases consisting of three RuvC domains, a bridge helix (“BH”), a domain with homology to a Pfam PF14239 which interrupts a recognition domain (“REC”), an HNH endonuclease domain (“HNH”), a wedge domain (“WED”), and a PAM interacting domain (PI); and (B) a multiple sequence alignment overview of two SMART I nucleases relative to reference Cas9 nuclease sequences, wherein RuvC and HNH catalytic residues are shown as black bars above each sequence, regions that align in 3D space with the crystal structure of SaCas are represented by rounded boxes, and dashed lines represent regions with poor or no alignment in 3D space between the 3D structure prediction of the SMART and SaCas9.

[0026] FIG. 6 depicts an example domain organization for SMART II endonucleases, using MG35 family enzymes (MG35-3, MG35-4) as an example. Shown are (A) a diagram showing the predicted domain architecture of SMART II nucleases consist of three RuvC domains, a domain with homology to a Pfam PF14239, an HNH endonuclease domain, an unknown domain, and a recognition domain (REC); and (B) a multiple sequence alignment overview of two SMART II nucleases relative to reference Cas9 nuclease sequences, where RuvC and HNH catalytic residues are shown as black bars above each sequence, regions that align in 3D space with the crystal structure of SaCas are represented by rounded boxes, and residues identified from 3D structure prediction which may be involved in recognizing a guide/target/PAM sequence are represented by dark grey boxes above the MG35-419 sequence (within the RRXRR and REC domains).

[0027] FIG. 7 illustrates various features of SMART enzymes. Shown are (A) a dot plot showing identity of SMART I domains of various enzymes depicted herein versus those of spCas9 showing that these have a maximum of about 35% sequence identity; (B) a dot plot of length of individual SMART I domains of enzymes described herein.

[0028] FIG. 8 illustrates count distribution of various SMART-specific motifs versus motifs predicted in Cas9 nuclease sequences showing that these motifs occur more commonly in SMART enzymes; motifs were predicted on 803 reference Cas9 sequences (Type II-A, II-B, and II-C), 84 SMART I sequences, and 471 SMART II sequences. Shown are (A) a box plot of

count frequency of Zn-binding ribbon motifs (CX_[2-4]C and CX_[2-4]H) in various types of class 2 Cas enzymes; and (B) a histogram of count frequency of RRXRR motifs in various types of class 2 Cas enzymes. In (A) and (B) lines track the mean count value, while outliers are represented by dots.

[0029] FIG. 9 illustrates predicted guide RNA structures of designed single-guide RNAs (sgRNAs) for cleavage activity with SMART I endonucleases. Shown are (A) MG34-1 sgRNA 1; (B) MG34-1 sgRNA 2; (C) MG34-9 sgRNA 1, and (D) MG34-16 sgRNA 1.

[0030] FIG. 10 depicts cleavage characterization of SMART I nucleases as described in Example 1. (A) shows an Agilent TapeStation gel of the ligation products of a cleavage assay for MG34-1 with two sgRNA designs vs. the negative control. Lane L3: ladder. Lane A4: Apo, no sgRNA. Lanes B4 and C4: MG34-1 sgRNAs tested (sg1: SEQ ID No. 612, sg2: 613). Cleavage product bands are labeled with arrows. Lanes G3 and H3: greyed out, not relevant to this experiment. (B) shows a PCR gel of the ligation products show activity of MG34-1, 34-9 and 34-16. Lane 1: ladder. Lanes 2-7: sgRNA designs with six spacer lengths for MG34-1. Lanes 8 and 9: sgRNA design for 34-9 and 34-16, respectively. Arrows indicate cleavage confirmation bands.

[0031] FIG. 11 illustrates sequence cutting preference for MG34 nucleases. (A) shows a SeqLogo representation of a consensus PAM sequence (NGGN) for MG34-1 with sgRNA 1 (top, SEQ ID NO: 612) and sgRNA 2 (bottom, SEQ ID NO: 613). (B) shows a histogram showing the location of the cut site for MG34-1, demonstrating that MG34-1 prefers to cleave at about position 7 from the PAM. (C) shows a sanger sequencing chromatogram shows a preferred NGG PAM for MG34-9 (highlighted with a box). The arrow indicates the cut site at position 7 from the PAM.

[0032] FIG. 12 illustrates the results of plasmid targeting experiments in *E. coli* for MG 34-1. (A) shows replica plating of *E. coli* strains demonstrating plasmid cutting; *E. coli* expressing MG34-1 and a sgRNA were transformed with a kanamycin resistance plasmid containing a target for the sgRNA (+sp). Plate quadrants that show growth impairment (+sp) vs. the negative control (without the target and PAM (-sp)) indicate successful targeting and cleavage by the enzyme. The experiment was replicated twice and performed in triplicate. (B) Shows graphs of colony forming unit (cfu) measurements from the replica plating experiments in A showing growth repression in the target condition (+sp) vs. the non-target control (-sp), demonstrating the plasmid was cut.

[0033] FIG. 13 shows an example genomic context of a SMART system for MG35-419. SMART nucleases are shown as dark grey arrows, other genes are depicted as lighter grey arrows. Domains predicted for all genes in a genomic fragment are shown as grey boxes under

the arrows. Environmental expression sequencing reads are shown aligned under the CRISPR arrays in (A) and upstream from the effector in (B). Transcriptomic coverage for the regions showing expression is illustrated above the contig sequence. (A) Shows the genomic context of the SMART II MG35-419 effector and CRISPR loci encoded in the vicinity. (B) Shows the genomic context of the SMART II effector MG35-3 showing a transcribed 5' UTR.

[0034] FIG. 14 shows a 3D structural prediction for SMART II MG35-419. This 3D model aligns well with regions of the SaCas9 crystal structure, despite being less than half its size. Regions that aligned with the SaCas9 template include the catalytic lobe (RuvC-I, HNH and RuvC-III domains) and a short region of the recognition (REC) lobe. SMART II-specific domains include a domain containing an RRXRR motif and homology to a Pfam PF14239, and a domain of unknown function.

[0035] FIG. 15 depicts results of preliminary cleavage assays for SMART II effectors. MG35-420 (SEQ ID NO:223) protein preps were tested for cleavage activity in TXTL extracts where the entire locus was expressed. Experiments incubated the protein prep with a PAM library (dsDNA target), a repetitive region predicted in the locus (cr1) in both forward and reverse orientations (fw and rv), and with intergenic regions potentially encoding needed cofactors. Lanes 2-9 (no cr array): control experiments without a repetitive region. Apo: only protein prep with a target PAM library. Labels 1 - 2.5 represent seven different intergenic regions. -IG: no intergenic region included as control. PCR gel of the ligation products shows putative cleavage bands (arrows) suggesting dsDNA cleavage.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

[0036] The Sequence Listing filed herewith provides exemplary polynucleotide and polypeptide sequences for use in methods, compositions and systems according to the disclosure. Below are exemplary descriptions of sequences therein.

[0037] MG33 nucleases

[0038] SEQ ID NOs: 1 and 463-486 shows the full-length peptide sequence of a MG33 nuclease.

[0039] SEQ ID NOs : 199 and 669-670 show the nucleotide sequence of a tracrRNA predicted to function with an MG33 nuclease.

[0040] SEQ ID NO: 201 shows the nucleotide sequence of a predicted single-guide RNA (sgRNA) sequence predicted to function with an MG33 nuclease. "N"s denote variable residues and non-N-residues represent the scaffold sequence.

[0041] MG34 nucleases

[0042] SEQ ID NOs: 2-24 and 487-488 show the full-length peptide sequences of MG34 nucleases.

[0043] SEQ ID NO: 200 shows the nucleotide sequence of a tracrRNA predicted to function with an MG34 nuclease.

[0044] SEQ ID NOs: 202,203, and 613-616 show the nucleotide sequences of predicted single-guide RNA (sgRNA) sequences predicted to function with an MG34 nuclease. “N”s denote variable residues and non-N-residues represent the scaffold sequence.

[0045] MG35 nucleases

[0046] SEQ ID NOs: 25-198,221-459, 489-580, and 617-668 show the full-length peptide sequences of MG35 nucleases.

[0047] SEQ ID NOs: 460-461 show the nucleotide sequences of MG35 tracrRNAs derived from the same loci as MG35 nucleases.

[0048] SEQ ID NO: 462 shows a repeat of MG35 nucleases described herein.

[0049] MG102 nucleases

[0050] SEQ ID NOs: 581-612 show the full-length peptide sequences of MG102 nucleases.

[0051] SEQ ID NOs: 672-673 show the nucleotide sequences of MG102 tracrRNAs derived from the same loci as MG102 nucleases

[0052] SEQ ID NOs: 205-220 show the sequences of example nuclear localization sequences (NLSs) that can be appended to nucleases according to the disclosure.

DETAILED DESCRIPTION

[0053] While various embodiments of the 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 may 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.

[0054] The practice of some methods disclosed herein employ, unless otherwise indicated, techniques of immunology, biochemistry, chemistry, molecular biology, microbiology, cell biology, genomics and recombinant DNA. See for example Sambrook and Green, Molecular Cloning: A Laboratory Manual, 4th Edition (2012); the series Current Protocols in Molecular Biology (F. M. Ausubel, et al. eds.); the series Methods In Enzymology (Academic Press, Inc.), PCR 2: A Practical Approach (M.J. MacPherson, B.D. Hames and G.R. Taylor eds. (1995)), Harlow and Lane, eds. (1988) Antibodies, A Laboratory Manual, and Culture of Animal Cells: A Manual of Basic Technique and Specialized Applications, 6th Edition (R.I. Freshney, ed. (2010)) (which is entirely incorporated by reference herein).

[0055] As used herein, the singular forms “a”, “an” and “the” are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the

terms “including”, “includes”, “having”, “has”, “with”, or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term “comprising”.

[0056] The term “about” or “approximately” 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 one or more than one standard deviation, per the practice in the art. Alternatively, “about” can mean a range of up to 20%, up to 15%, up to 10%, up to 5%, or up to 1% of a given value.

[0057] As used herein, a “cell” generally refers to a biological cell. A cell may be the basic structural, functional and/or biological unit of a living organism. A cell may originate from any organism having one or more cells. Some non-limiting examples include: a prokaryotic cell, eukaryotic cell, a bacterial cell, an archaeal cell, a cell of a single-cell eukaryotic organism, a protozoa cell, a cell from a plant (e.g., cells from plant crops, fruits, vegetables, grains, soy bean, corn, maize, wheat, seeds, tomatoes, rice, cassava, sugarcane, pumpkin, hay, potatoes, cotton, cannabis, tobacco, flowering plants, conifers, gymnosperms, ferns, clubmosses, hornworts, liverworts, mosses), an algal cell, (e.g., *Botryococcus braunii*, *Chlamydomonas reinhardtii*, *Nannochloropsis gaditana*, *Chlorella pyrenoidosa*, *Sargassum patens* C. Agardh, and the like), seaweeds (e.g., kelp), a fungal cell (e.g., a yeast cell, a cell from a mushroom), an animal cell, a cell from an invertebrate animal (e.g., fruit fly, cnidarian, echinoderm, nematode, etc.), a cell from a vertebrate animal (e.g., fish, amphibian, reptile, bird, mammal), a cell from a mammal (e.g., a pig, a cow, a goat, a sheep, a rodent, a rat, a mouse, a non-human primate, a human, etc.), and etcetera. Sometimes a cell is not originating from a natural organism (e.g., a cell can be synthetically made, sometimes termed an artificial cell).

[0058] The term “nucleotide,” as used herein, generally refers to a base-sugar-phosphate combination. A nucleotide may comprise a synthetic nucleotide. A nucleotide may comprise a synthetic nucleotide analog. Nucleotides may be monomeric units of a nucleic acid sequence (e.g., deoxyribonucleic acid (DNA) and ribonucleic acid (RNA)). The term nucleotide may include ribonucleoside triphosphates adenosine triphosphate (ATP), uridine triphosphate (UTP), cytosine triphosphate (CTP), guanosine triphosphate (GTP) and deoxyribonucleoside triphosphates such as dATP, dCTP, dITP, dUTP, dGTP, dTTP, or derivatives thereof. Such derivatives may include, for example, [α S]dATP, 7-deaza-dGTP and 7-deaza-dATP, and nucleotide derivatives that confer nuclease resistance on the nucleic acid molecule containing them. The term nucleotide as used herein may refer to dideoxyribonucleoside triphosphates (ddNTPs) and their derivatives. Illustrative examples of dideoxyribonucleoside triphosphates

may include, but are not limited to, ddATP, ddCTP, ddGTP, ddITP, and ddTTP. A nucleotide may be unlabeled or detectably labeled, such as using moieties comprising optically detectable moieties (e.g., fluorophores). Labeling may also be carried out with quantum dots. Detectable labels may include, for example, radioactive isotopes, fluorescent labels, chemiluminescent labels, bioluminescent labels and enzyme labels. Fluorescent labels of nucleotides may include but are not limited fluorescein, 5-carboxyfluorescein (FAM), 2'7'-dimethoxy-4'5-dichloro-6-carboxyfluorescein (JOE), rhodamine, 6-carboxyrhodamine (R6G), N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), 6-carboxy-X-rhodamine (ROX), 4-(4'dimethylaminophenylazo) benzoic acid (DABCYL), Cascade Blue, Oregon Green, Texas Red, Cyanine and 5-(2'-aminoethyl)aminonaphthalene-1-sulfonic acid (EDANS). Specific examples of fluorescently labeled nucleotides can include [R6G]dUTP, [TAMRA]dUTP, [R110]dCTP, [R6G]dCTP, [TAMRA]dCTP, [JOE]ddATP, [R6G]ddATP, [FAM]ddCTP, [R110]ddCTP, [TAMRA]ddGTP, [ROX]ddTTP, [dR6G]ddATP, [dR110]ddCTP, [dTAMRA]ddGTP, and [dROX]ddTTP available from Perkin Elmer, Foster City, Calif; FluoroLink DeoxyNucleotides, FluoroLink Cy3-dCTP, FluoroLink Cy5-dCTP, FluoroLink Fluor X-dCTP, FluoroLink Cy3-dUTP, and FluoroLink Cy5-dUTP available from Amersham, Arlington Heights, Ill.; Fluorescein-15-dATP, Fluorescein-12-dUTP, Tetramethyl-rhodamine-6-dUTP, IR770-9-dATP, Fluorescein-12-ddUTP, Fluorescein-12-UTP, and Fluorescein-15-2'-dATP available from Boehringer Mannheim, Indianapolis, Ind.; and Chromosome Labeled Nucleotides, BODIPY-FL-14-UTP, BODIPY-FL-4-UTP, BODIPY-TMR-14-UTP, BODIPY-TMR-14-dUTP, BODIPY-TR-14-UTP, BODIPY-TR-14-dUTP, Cascade Blue-7-UTP, Cascade Blue-7-dUTP, fluorescein-12-UTP, fluorescein-12-dUTP, Oregon Green 488-5-dUTP, Rhodamine Green-5-UTP, Rhodamine Green-5-dUTP, tetramethylrhodamine-6-UTP, tetramethylrhodamine-6-dUTP, Texas Red-5-UTP, Texas Red-5-dUTP, and Texas Red-12-dUTP available from Molecular Probes, Eugene, Oreg. Nucleotides can also be labeled or marked by chemical modification. A chemically-modified single nucleotide can be biotin-dNTP. Some non-limiting examples of biotinylated dNTPs can include, biotin-dATP (e.g., bio-N6-ddATP, biotin-14-dATP), biotin-dCTP (e.g., biotin-11-dCTP, biotin-14-dCTP), and biotin-dUTP (e.g., biotin-11-dUTP, biotin-16-dUTP, biotin-20-dUTP). A nucleotide may comprise a nucleotide analog. In some embodiments, nucleotide analogs may comprise structures of natural nucleotides that are modified at any position so as to alter certain chemical properties of the nucleotide yet retain the ability of the nucleotide analog to perform its intended function (e.g. hybridization to other nucleotides in RNA or DNA). Examples of positions of the nucleotide which may be derivatized include the 5 position, e.g., 5-(2-amino)propyl uridine, 5-bromo uridine, 5-propyne uridine, 5-propenyl uridine, etc.; the 6 position, e.g., 6-(2-amino)propyl uridine; the 8-position for adenosine and/or guanosines, e.g., 8-bromo guanosine, 8-chloro

guanosine, 8-fluoroguanosine, etc. Nucleotide analogs also include deaza nucleotides, e.g., 7-deaza-adenosine: O- and N-modified (e.g., alkylated, e.g., N6-methyl adenosine, or as otherwise known in the art) nucleotides; and other heterocyclically modified nucleotide analogs such as those described in Herdewijn, *Antisense Nucleic Acid Drug Dev.*, 2000 Aug. 10(4):297-310. Nucleotide analogs may also comprise modifications to the sugar portion of the nucleotides. For example the 2' OH-group may be replaced by a group selected from H, OR, R, F, Cl, Br, I, SH, SR, NH₂, NHR, NR₂, COOR, or OR, wherein R is substituted or unsubstituted C1-C6 alkyl, alkenyl, alkynyl, aryl, etc. Other possible modifications include those described in U.S. Pat. Nos. 5,858,988, and 6,291,438. Examples of positions of the nucleotide which may be derivatized include the 5 position, e.g., 5-(2-amino)propyl uridine, 5-bromo uridine, 5-propyne uridine, 5-propenyl uridine, etc.; the 6 position, e.g., 6-(2-amino)propyl uridine; the 8-position for adenosine and/or guanosines, e.g., 8-bromo guanosine, 8-chloro guanosine, 8-fluoroguanosine, etc. Nucleotide analogs also include deaza nucleotides, e.g., 7-deaza-adenosine: O- and N-modified (e.g., alkylated, e.g., N6-methyl adenosine, or as otherwise known in the art) nucleotides; and other heterocyclically modified nucleotide analogs such as those described in Herdewijn, *Antisense Nucleic Acid Drug Dev.*, 2000 Aug. 10(4):297-310.

Nucleotide analogs may also comprise modifications to the sugar portion of the nucleotides. For example the 2' OH-group may be replaced by a group selected from H, OR, R, F, Cl, Br, I, SH, SR, NH₂, NHR, NR₂, COOR, or OR, wherein R is substituted or unsubstituted C1-C6 alkyl, alkenyl, alkynyl, aryl, etc. Other possible modifications include those described in U.S. Pat. Nos. 5,858,988, and 6,291,438.

[0059] The terms “polynucleotide,” “oligonucleotide,” and “nucleic acid” are used interchangeably to generally refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof, either in single-, double-, or multi-stranded form. A polynucleotide may be exogenous or endogenous to a cell. A polynucleotide may exist in a cell-free environment. A polynucleotide may be a gene or fragment thereof. A polynucleotide may be DNA. A polynucleotide may be RNA. A polynucleotide may have any three-dimensional structure and may perform any function. A polynucleotide may comprise one or more analogs (e.g., altered backbone, sugar, or nucleobase). If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. Some non-limiting examples of analogs include: 5-bromouracil, peptide nucleic acid, xeno nucleic acid, morpholinos, locked nucleic acids, glycol nucleic acids, threose nucleic acids, dideoxynucleotides, cordycepin, 7-deaza-GTP, fluorophores (e.g., rhodamine or fluorescein linked to the sugar), thiol containing nucleotides, biotin linked nucleotides, fluorescent base analogs, CpG islands, methyl-7-guanosine, methylated nucleotides, inosine, thiouridine,

pseudouridine, dihydrouridine, queuosine, and wyosine. Non-limiting examples of polynucleotides include coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, cell-free polynucleotides including cell-free DNA (cfDNA) and cell-free RNA (cfRNA), nucleic acid probes, and primers. The sequence of nucleotides may be interrupted by non-nucleotide components.

[0060] The terms “transfection” or “transfected” generally refer to introduction of a nucleic acid into a cell by non-viral or viral-based methods. The nucleic acid molecules may be gene sequences encoding complete proteins or functional portions thereof. See, e.g., Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*, 18.1-18.88 (which is entirely incorporated by reference herein).

[0061] The terms “peptide,” “polypeptide,” and “protein” are used interchangeably herein to generally refer to a polymer of at least two amino acid residues joined by peptide bond(s). This term does not connote a specific length of polymer, nor is it intended to imply or distinguish whether the peptide is produced using recombinant techniques, chemical or enzymatic synthesis, or is naturally occurring. The terms apply to naturally occurring amino acid polymers as well as amino acid polymers comprising at least one modified amino acid. In some cases, the polymer may be interrupted by non-amino acids. The terms include amino acid chains of any length, including full length proteins, and proteins with or without secondary and/or tertiary structure (e.g., domains). The terms also encompass an amino acid polymer that has been modified, for example, by disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, oxidation, and any other manipulation such as conjugation with a labeling component. The terms “amino acid” and “amino acids,” as used herein, generally refer to natural and non-natural amino acids, including, but not limited to, modified amino acids and amino acid analogues. Modified amino acids may include natural amino acids and non-natural amino acids, which have been chemically modified to include a group or a chemical moiety not naturally present on the amino acid. Amino acid analogues may refer to amino acid derivatives. The term “amino acid” includes both D-amino acids and L-amino acids.

[0062] As used herein, the term “non-native” can generally refer to a nucleic acid or polypeptide sequence that is not found in a native nucleic acid or protein. Non-native may refer to affinity tags. Non-native may refer to fusions. Non-native may refer to a naturally occurring nucleic acid or polypeptide sequence that comprises mutations, insertions and/or deletions. A non-native

sequence may exhibit and/or encode for an activity (e.g., enzymatic activity, methyltransferase activity, acetyltransferase activity, kinase activity, ubiquitinating activity, etc.) that may also be exhibited by the nucleic acid and/or polypeptide sequence to which the non-native sequence is fused. A non-native nucleic acid or polypeptide sequence may be linked to a naturally-occurring nucleic acid or polypeptide sequence (or a variant thereof) by genetic engineering to generate a chimeric nucleic acid and/or polypeptide sequence encoding a chimeric nucleic acid and/or polypeptide.

[0063] The term “promoter”, as used herein, generally refers to the regulatory DNA region which controls transcription or expression of a gene and which may be located adjacent to or overlapping a nucleotide or region of nucleotides at which RNA transcription is initiated. A promoter may contain specific DNA sequences which bind protein factors, often referred to as transcription factors, which facilitate binding of RNA polymerase to the DNA leading to gene transcription. A ‘basal promoter’, also referred to as a ‘core promoter’, may generally refer to a promoter that contains all the basic necessary elements to promote transcriptional expression of an operably linked polynucleotide. Eukaryotic basal promoters typically, though not necessarily, contain a TATA-box and/or a CAAT box.

[0064] The term “expression”, as used herein, generally refers to the process by which a nucleic acid sequence or a polynucleotide is transcribed from a DNA template (such as into mRNA or other RNA transcript) and/or the process by which a transcribed mRNA is subsequently translated into peptides, polypeptides, or proteins. Transcripts and encoded polypeptides may be collectively referred to as “gene product.” If the polynucleotide is derived from genomic DNA, expression may include splicing of the mRNA in a eukaryotic cell.

[0065] As used herein, “operably linked”, “operable linkage”, “operatively linked”, or grammatical equivalents thereof generally refer to juxtaposition of genetic elements, e.g., a promoter, an enhancer, a polyadenylation sequence, etc., wherein the elements are in a relationship permitting them to operate in the expected manner. For instance, a regulatory element, which may comprise promoter and/or enhancer sequences, is operatively linked to a coding region if the regulatory element helps initiate transcription of the coding sequence. There may be intervening residues between the regulatory element and coding region so long as this functional relationship is maintained.

[0066] A “vector” as used herein, generally refers to a macromolecule or association of macromolecules that comprises or associates with a polynucleotide and which may be used to mediate delivery of the polynucleotide to a cell. Examples of vectors include plasmids, viral vectors, liposomes, and other gene delivery vehicles. The vector generally comprises genetic elements, e.g., regulatory elements, operatively linked to a gene to facilitate expression of the

gene in a target.

[0067] As used herein, “an expression cassette” and “a nucleic acid cassette” are used interchangeably generally to refer to a combination of nucleic acid sequences or elements that are expressed together or are operably linked for expression. In some cases, an expression cassette refers to the combination of regulatory elements and a gene or genes to which they are operably linked for expression.

[0068] A “functional fragment” of a DNA or protein sequence generally refers to a fragment that retains a biological activity (either functional or structural) that is substantially similar to a biological activity of the full-length DNA or protein sequence. A biological activity of a DNA sequence may be its ability to influence expression in a manner known to be attributed to the full-length sequence.

[0069] As used herein, an “engineered” object generally indicates that the object has been modified by human intervention. According to non-limiting examples: a nucleic acid may be modified by changing its sequence to a sequence that does not occur in nature; a nucleic acid may be modified by ligating it to a nucleic acid that it does not associate with in nature such that the ligated product possesses a function not present in the original nucleic acid; an engineered nucleic acid may be synthesized *in vitro* with a sequence that does not exist in nature; a protein may be modified by changing its amino acid sequence to a sequence that does not exist in nature; an engineered protein may acquire a new function or property. An “engineered” system comprises at least one engineered component.

[0070] As used herein, the term “optimally aligned” generally refers to an alignment of two amino acid sequences that give the highest percent identity score or maximizes the number of matched residues.

[0071] As used herein, “synthetic” and “artificial” are used interchangeably to refer to a protein or a domain thereof that has low sequence identity (e.g., less than 50% sequence identity, less than 25% sequence identity, less than 10% sequence identity, less than 5% sequence identity, less than 1% sequence identity) to a naturally occurring human protein. For example, VPR and VP64 domains are synthetic transactivation domains.

[0072] The term “tracrRNA” or “tracr sequence”, as used herein, can generally refer to a nucleic acid with at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100% sequence identity and/or sequence similarity to a wild type exemplary tracrRNA sequence (e.g., a tracrRNA from *S. pyogenes* *S. aureus*, etc. or SEQ ID NOs: 199-203). tracrRNA can refer to a nucleic acid with at most about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% sequence identity and/or sequence similarity to a wild type exemplary tracrRNA sequence (e.g., a tracrRNA from *S. pyogenes* *S. aureus*, etc). tracrRNA may refer to a modified form of a

tracrRNA that can comprise a nucleotide change such as a deletion, insertion, or substitution, variant, mutation, or chimera. A tracrRNA may refer to a nucleic acid that can be at least about 60% identical to a wild type exemplary tracrRNA (e.g., a tracrRNA from *S. pyogenes* *S. aureus*, etc.) sequence over a stretch of at least 6 contiguous nucleotides. For example, a tracrRNA sequence can be at least about 60% identical, at least about 65% identical, at least about 70% identical, at least about 75% identical, at least about 80% identical, at least about 85% identical, at least about 90% identical, at least about 95% identical, at least about 98% identical, at least about 99% identical, or 100 % identical to a wild type exemplary tracrRNA (e.g., a tracrRNA from *S. pyogenes* *S. aureus*, etc.) sequence over a stretch of at least 6 contiguous nucleotides. Type II tracrRNA sequences can be predicted on a genome sequence by identifying regions with complementarity to part of the repeat sequence in an adjacent CRISPR array.

[0073] As used herein, a “guide nucleic acid” can generally refer to a nucleic acid that may hybridize to another nucleic acid. A guide nucleic acid may be RNA. A guide nucleic acid may be DNA. The guide nucleic acid may be programmed to bind to a sequence of nucleic acid site-specifically. The nucleic acid to be targeted, or the target nucleic acid, may comprise nucleotides. The guide nucleic acid may comprise nucleotides. A portion of the target nucleic acid may be complementary to a portion of the guide nucleic acid. The strand of a double-stranded target polynucleotide that is complementary to and hybridizes with the guide nucleic acid may be called the complementary strand. The strand of the double-stranded target polynucleotide that is complementary to the complementary strand, and therefore may not be complementary to the guide nucleic acid may be called noncomplementary strand. A guide nucleic acid may comprise a polynucleotide chain and can be called a “single guide nucleic acid.” A guide nucleic acid may comprise two polynucleotide chains and may be called a “double guide nucleic acid.” If not otherwise specified, the term “guide nucleic acid” may be inclusive, referring to both single guide nucleic acids and double guide nucleic acids. A guide nucleic acid may comprise a segment that can be referred to as a “nucleic acid-targeting segment” or a “nucleic acid-targeting sequence.” A nucleic acid-targeting segment may comprise a sub-segment that may be referred to as a “protein binding segment” or “protein binding sequence” or “Cas protein binding segment”.

[0074] The term “sequence identity” or “percent identity” in the context of two or more nucleic acids or polypeptide sequences, generally refers to two (e.g., in a pairwise alignment) or more (e.g., in a multiple sequence alignment) sequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence over a local or global comparison window, as measured using a sequence comparison algorithm. Suitable sequence comparison algorithms for polypeptide

sequences include, e.g., BLASTP using parameters of a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix setting gap costs at existence of 11, extension of 1, and using a conditional compositional score matrix adjustment for polypeptide sequences longer than 30 residues; BLASTP using parameters of a wordlength (W) of 2, an expectation (E) of 1000000, and the PAM30 scoring matrix setting gap costs at 9 to open gaps and 1 to extend gaps for sequences of less than 30 residues (these are the default parameters for BLASTP in the BLAST suite available at <https://blast.ncbi.nlm.nih.gov>); or CLUSTALW with parameters of the Smith-Waterman homology search algorithm with parameters of a match of 2, a mismatch of -1, and a gap of -1; MUSCLE with default parameters; MAFFT with parameters retree of 2 and maxiterations of 1000; Novafold with default parameters; HMMER hmalign with default parameters.

[0075] As used herein, the term “RuvC_III domain” generally refers to a third discontinuous segment of a RuvC endonuclease domain (the RuvC nuclease domain being comprised of three discontinuous segments, RuvC_I, RuvC_II, and RuvC_III). A RuvC domain or segments thereof (e.g. RuvC_I, RuvC_II, or RuvC_III) can generally be identified by alignment to known domain sequences, structural alignment to proteins with annotated domains, or by comparison to Hidden Markov Models (HMMs) built based on known domain sequences (e.g., Pfam HMM PF18541 for RuvC_III).

[0076] As used herein, the term “HNH domain” generally refers to an endonuclease domain having characteristic histidine and asparagine residues. An HNH domain can generally be identified by alignment to known domain sequences, structural alignment to proteins with annotated domains, or by comparison to Hidden Markov Models (HMMs) built based on known domain sequences (e.g., Pfam HMM PF01844 for domain HNH).

[0077] As used herein, the term “bridge helix domain” or “BH domain” generally refers to an arginine-rich helix domain present in Cas enzymes that plays an important role in initiating cleavage activity upon binding of target DNA.

[0078] As used herein, the term “recognition domain” or “REC domain” generally refers to a domain thought to interact with the repeat:anti-repeat duplex of the gRNA and to mediate the formation of a Cas endonuclease/gRNA complex.

[0079] As used herein, the term “wedge domain” or “WED domain” generally refers to a fold comprising a twisted five-stranded beta sheet flanked by four alpha helices, which is generally responsible for the recognition of the distorted repeat: anti-repeat duplex for Cas enzymes. WED domains can be responsible for the recognition of single-guide RNA scaffolds.

[0080] As used herein, the term “PAM interacting domain” or “PI domain” generally refers to a domain found in Cas enzymes positioned in the endonuclease-DNA-complex to recognize the

PAM sequence on the non-complementary DNA strand of the guide RNA.

[0081] *Overview*

[0082] The discovery of new Cas enzymes with unique functionality and structure may offer the potential to further disrupt deoxyribonucleic acid (DNA) editing technologies, improving speed, specificity, functionality, and ease of use. Relative to the predicted prevalence of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) systems in microbes and the sheer diversity of microbial species, relatively few functionally characterized CRISPR/Cas enzymes exist in the literature. This is partly because a huge number of microbial species may not be readily cultivated in laboratory conditions. Metagenomic sequencing from natural environmental niches that represent large numbers of microbial species may offer the potential to drastically increase the number of new CRISPR/Cas systems known and speed the discovery of new oligonucleotide editing functionalities. A recent example of the fruitfulness of such an approach is demonstrated by the 2016 discovery of CasX/CasY CRISPR systems from metagenomic analysis of natural microbial communities.

[0083] CRISPR/Cas systems are RNA-directed nuclease complexes that have been described to function as an adaptive immune system in microbes. In their natural context, CRISPR/Cas systems occur in CRISPR (clustered regularly interspaced short palindromic repeats) operons or loci, which generally comprise two parts: (i) an array of short repetitive sequences (30-40bp) separated by equally short spacer sequences, which encode the RNA-based targeting element; and (ii) ORFs encoding the Cas encoding the nuclease polypeptide directed by the RNA-based targeting element alongside accessory proteins/enzymes. Efficient nuclease targeting of a particular target nucleic acid sequence generally requires both (i) complementary hybridization between the first 6-8 nucleic acids of the target (the target seed) and the crRNA guide; and (ii) the presence of a protospacer-adjacent motif (PAM) sequence within a defined vicinity of the target seed (the PAM usually being a sequence not commonly represented within the host genome). Depending on the exact function and organization of the system, CRISPR-Cas systems are commonly organized into 2 classes, 5 types and 16 subtypes based on shared functional characteristics and evolutionary similarity.

[0084] Class I CRISPR-Cas systems have large, multisubunit effector complexes, and comprise Types I, III, and IV.

[0085] Type I CRISPR-Cas systems are considered of moderate complexity in terms of components. In Type I CRISPR-Cas systems, the array of RNA-targeting elements is transcribed as a long precursor crRNA (pre-crRNA) that is processed at repeat elements to liberate short, mature crRNAs that direct the nuclease complex to nucleic acid targets when they are followed by a suitable short consensus sequence called a protospacer-adjacent motif (PAM). This

processing occurs via an endoribonuclease subunit (Cas6) of a large endonuclease complex called Cascade, which also comprises a nuclease (Cas3) protein component of the crRNA-directed nuclease complex. Cas I nucleases function primarily as DNA nucleases.

[0086] Type III CRISPR systems may be characterized by the presence of a central nuclease, known as Cas10, alongside a repeat-associated mysterious protein (RAMP) that comprises Csm or Cmr protein subunits. Like in Type I systems, the mature crRNA is processed from a pre-crRNA using a Cas6-like enzyme. Unlike type I and II systems, type III systems appear to target and cleave DNA-RNA duplexes (such as DNA strands being used as templates for an RNA polymerase).

[0087] Type IV CRISPR-Cas systems possess an effector complex that consists of a highly reduced large subunit nuclease (csf1), two genes for RAMP proteins of the Cas5 (csf3) and Cas7 (csf2) groups, and, in some cases, a gene for a predicted small subunit; such systems are commonly found on endogenous plasmids.

[0088] Class II CRISPR-Cas systems generally have single-polypeptide multidomain nuclease effectors, and comprise Types II, V and VI.

[0089] Type II CRISPR-Cas systems are considered the simplest in terms of components. In Type II CRISPR-Cas systems, the processing of the CRISPR array into mature crRNAs does not require the presence of a special endonuclease subunit, but rather a small trans-encoded crRNA (tracrRNA) with a region complementary to the array repeat sequence; the tracrRNA interacts with both its corresponding effector nuclease (e.g. Cas9) and the repeat sequence to form a precursor dsRNA structure, which is cleaved by endogenous RNase III to generate a mature effector enzyme loaded with both tracrRNA and crRNA. Cas II nucleases are known as DNA nucleases. Type II effectors generally exhibit a structure consisting of a RuvC-like endonuclease domain that adopts the RNase H fold with an unrelated HNH nuclease domain inserted within the folds of the RuvC-like nuclease domain. The RuvC-like domain is responsible for the cleavage of the target (e.g., crRNA complementary) DNA strand, while the HNH domain is responsible for cleavage of the displaced DNA strand.

[0090] Type V CRISPR-Cas systems are characterized by a nuclease effector (e.g. Cas12) structure similar to that of Type II effectors, comprising a RuvC-like domain. Similar to Type II, most (but not all) Type V CRISPR systems use a tracrRNA to process pre-crRNAs into mature crRNAs; however, unlike Type II systems which requires RNase III to cleave the pre-crRNA into multiple crRNAs, type V systems are capable of using the effector nuclease itself to cleave pre-crRNAs. Like Type-II CRISPR-Cas systems, Type V CRISPR-Cas systems are again known as DNA nucleases. Unlike Type II CRISPR-Cas systems, some Type V enzymes (e.g., Cas12a)

appear to have a robust single-stranded nonspecific deoxyribonuclease activity that is activated by the first crRNA directed cleavage of a double-stranded target sequence.

[0091] Type VI CRISPR-Cas systems have RNA-guided RNA endonucleases. Instead of RuvC-like domains, the single polypeptide effector of Type VI systems (e.g. Cas13) comprises two HEPN ribonuclease domains. Differing from both Type II and V systems, Type VI systems also appear to not need a tracrRNA for processing of pre-crRNA into crRNA. Similar to type V systems, however, some Type VI systems (e.g., C2C2) appear to possess robust single-stranded nonspecific nuclease (ribonuclease) activity activated by the first crRNA directed cleavage of a target RNA.

[0092] Because of their simpler architecture, Class II CRISPR-Cas have been most widely adopted for engineering and development as designer nuclease/genome editing applications.

[0093] One of the early adaptations of such a system for *in vitro* use can be found in Jinek et al. (Science. 2012 Aug 17;337(6096):816-21, which is entirely incorporated herein by reference). The Jinek study first described a system that involved (i) recombinantly-expressed, purified full-length Cas9 (e.g., a Class II, Type II Cas enzyme) isolated from *S. pyogenes* SF370, (ii) purified mature ~42 nt crRNA bearing a ~20 nt 5' sequence complementary to the target DNA sequence desired to be cleaved followed by a 3' tracr-binding sequence (the whole crRNA being *in vitro* transcribed from a synthetic DNA template carrying a T7 promoter sequence); (iii) purified tracrRNA *in vitro* transcribed from a synthetic DNA template carrying a T7 promoter sequence, and (iv) Mg²⁺. Jinek later described an improved, engineered system wherein the crRNA of (ii) is joined to the 5' end of (iii) by a linker (e.g., GAAA) to form a single fused synthetic guide RNA (sgRNA) capable of directing Cas9 to a target by itself (compare top and bottom panel of FIG. 2).

[0094] Mali et al. (Science. 2013 Feb 15; 339(6121): 823–826.), which is entirely incorporated herein by reference, later adapted this system for use in mammalian cells by providing DNA vectors encoding (i) an ORF encoding codon-optimized Cas9 (e.g., a Class II, Type II Cas enzyme) under a suitable mammalian promoter with a C-terminal nuclear localization sequence (e.g., SV40 NLS) and a suitable polyadenylation signal (e.g., TK pA signal); and (ii) an ORF encoding an sgRNA (having a 5' sequence beginning with G followed by 20 nt of a complementary targeting nucleic acid sequence joined to a 3' tracr-binding sequence, a linker, and the tracrRNA sequence) under a suitable Polymerase III promoter (e.g., the U6 promoter).

[0095] *MG Enzymes*

[0096] In one aspect, the present disclosure provides for an engineered nuclease system. The engineered nuclease system may comprise (a) an endonuclease. In some cases, the endonuclease comprises a RuvC domain and an HNH domain. The endonuclease may be from an uncultivated

microorganism. The endonuclease may be a Cas endonuclease. The endonuclease may be a class 2 endonuclease. The endonuclease may be a class 2, type II Cas endonuclease. The engineered nuclease system may comprise (b) an engineered guide ribonucleic acid structure. The engineered guide ribonucleic acid structure may be configured to form a complex with the endonuclease. In some cases, the engineered guide ribonucleic acid structure configured to form a complex with the endonuclease comprises a guide ribonucleic acid sequence. The guide ribonucleic acid sequence may be configured to hybridize to a target deoxyribonucleic acid sequence. In some cases, the engineered guide ribonucleic acid structure configured to form a complex with the endonuclease comprises a tracr ribonucleic acid sequence. The tracr ribonucleic acid sequence may be configured to bind to the endonuclease. In some cases, the endonuclease has a molecular weight of about 120 kDa or less, about 110 kDa or less, about 100 kDa or less, about 90 kDa or less, about 80 kDa or less, about 70 kDa or less, about 60 kDa or less, about 50 kDa or less, about 40 kDa or less, about 30 kDa or less, about 20 kDa or less, or about 10 kDa or less.

[0097] In some cases, the endonuclease comprises a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

[0098] In one aspect, the present disclosure provides an engineered nuclease system. The engineered nuclease system may comprise (a) an endonuclease. The endonuclease may comprise a RuvC-1 domain or a RuvC domain. The endonuclease may comprise an HNH domain. The endonuclease may comprise a RuvC-1 domain and an HNH domain. The endonuclease may be a Cas endonuclease. The endonuclease may be a class 2 endonuclease. The endonuclease may be a class 2, type II Cas endonuclease. The engineered nuclease system may comprise (b) an engineered guide ribonucleic acid. The engineered guide ribonucleic acid structure may be configured to form a complex with the endonuclease. The guide ribonucleic acid structure configured to form a complex with the endonuclease may comprise a guide ribonucleic acid sequence. The guide ribonucleic acid sequence may be configured to hybridize to a target deoxyribonucleic acid sequence. The engineered guide ribonucleic acid structure configured to form a complex with the endonuclease may comprise a tracr ribonucleic acid sequence. The tracr ribonucleic acid sequence may be configured to bind to the endonuclease. The endonuclease may comprise a sequence with at least 50%, at least 55%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99% sequence identity to any one of 1-198, 221-459, 463-612, or 617-668. The endonuclease may be an archaeal endonuclease. The endonuclease may be a Class 2, Type II Cas endonuclease. The endonuclease may comprise an arginine rich region comprising an RRxRR motif or a domain with PF14239 homology. The arginine-rich region or domain with PF14239 homology can comprise a sequence with at least 50%, at least 55%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99% sequence identity to an arginine rich region or a domain with PF14239 homology of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. The domain boundaries of the arginine rich domain or the domain with PF14239 homology can be identified by optimal alignment to MG34-1 or MG34-9. The endonuclease may comprise REC domain. The REC domain can comprise a sequence with at least 50%, at least 55%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99% sequence identity to a REC domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. The domain boundaries of the REC domain can be identified by optimal alignment to MG34-1 or MG34-9. The endonuclease may comprise BH (Bridge Helix) domain. The BH domain can comprise a sequence with at least 50%, at least 55%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99% sequence identity to a BH domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. The domain boundaries of the BH domain can be identified by optimal alignment to MG34-1 or MG34-9.

[0099] The endonuclease may comprise WED (wedge) domain. The WED domain can comprise a sequence with at least 50%, at least 55%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99% sequence identity to a WED domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. The domain boundaries of the WED domain can be identified by optimal

alignment to MG34-1 or MG34-9. The endonuclease may comprise PI (PAM interacting) domain. The PI domain can comprise a sequence with at least 50%, at least 55%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99% sequence identity to a PI domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668. The domain boundaries of the PI domain can be identified by optimal alignment to MG34-1 or MG34-9.

[00100] In some cases, the endonuclease is derived from an uncultivated microorganism. In some cases, the tracr ribonucleic acid sequence comprises a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to at least 50, at least 60, at least 70, at least 80 consecutive nucleotides from any one of SEQ ID NOs: 199-200, 460-461, or 669-673 or a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to at least 50, at least 60, at least 70, at least 80 consecutive nucleotides of the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

[00101] In some cases, the guide nucleic acid structure comprises SEQ ID NO: 201. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 202. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 203. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 201-203. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 613. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 614. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 615. In some cases, the guide nucleic acid structure comprises SEQ ID NO: 616.

[00102] In one aspect, the present disclosure provides an engineered nuclease system. The engineered nuclease system may comprise (a) an engineered guide ribonucleic acid structure. The engineered guide ribonucleic acid structure may comprise a guide ribonucleic acid sequence. The guide ribonucleic acid sequence may be configured to hybridize to a target deoxyribonucleic acid sequence. The engineered guide ribonucleic acid structure may comprise a tracr ribonucleic acid sequence. The tracr ribonucleic acid sequence may be configured to bind to an endonuclease. In some cases, the tracr ribonucleic acid sequence comprises a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to at least 50, at least 60, at least 70, at least 80 consecutive nucleotides from any one of SEQ ID NOs: 199-200, 460-461, or 669-673 or a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80 consecutive nucleotides of the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

[00103] In some cases, the engineered nuclease system comprises an endonuclease. The endonuclease may be a class 2 endonuclease. The endonuclease may be a Cas endonuclease. The endonuclease may be a class 2, Type II Cas endonuclease.

[00104] In some cases, the endonuclease has a particular molecular weight range. In some embodiments the endonuclease has a molecular weight of about 120 kDa or less, about 110 kDa or less, about 105 kDa or less, about 100 kDa or less, about 95 kDa or less, about 90 kDa or less, about 85 kDa or less, about 80 kDa or less, about 75 kDa or less, about 70 kDa or less, about 65 kDa or less, about 60 kDa or less, about 55 kDa or less, about 50 kDa or less, about 45 kDa or less, about 40 kDa or less, about 35 kDa or less, about 30 kDa or less, about 25 kDa or less, about 20 kDa or less, about 15 kDa or less, or about 10 kDa or less. In some cases, the engineered guide ribonucleic acid structure comprises at least two ribonucleic acid polynucleotides. In some cases, the endonuclease comprises a particular number of residues. The endonuclease can comprise equal to or fewer than about 1,100 residues, equal to or fewer than about 1,000 residues, equal to or fewer than about 950 residues, equal to or fewer than about 900 residues, equal to or fewer than about 850 residues, equal to or fewer than about 800 residues, equal to or fewer than about 750 residues, equal to or fewer than about 700 residues, equal to or fewer than about 650 residues, equal to or fewer than about 600 residues, equal to or fewer than about 550 residues, equal to or fewer than about 500 residues, equal to or fewer than about 450 residues, equal to or fewer than about 400 residues, or equal to or fewer than about 350 residues. The endonuclease can comprise about 700 to about 1,100 residues. The endonuclease can comprise about 400 to about 600 residues. In some cases, the engineered guide ribonucleic acid structure comprises a single ribonucleic acid polynucleotide. The single ribonucleic acid polynucleotide may comprise the guide ribonucleic acid sequence and the tracr ribonucleic acid sequence.

[00105] In some cases, the guide ribonucleic acid sequence is complementary to a prokaryotic, bacterial, archaeal, eukaryotic, fungal, plant, mammalian, or human genomic sequence. In some

cases, the guide ribonucleic acid sequence is complementary to a prokaryotic genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to a bacterial genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to an archaeal genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to a eukaryotic genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to a fungal genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to a plant genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to a mammalian genomic sequence. In some cases, the guide ribonucleic acid sequence is complementary to a human genomic sequence.

[00106] In some cases, the guide ribonucleic acid targeting sequence or spacer is 10-30 nucleotides in length, or 12-28 nucleotides in length, or 15-24 nucleotides in length. In some cases, the endonuclease comprises one or more nuclear localization sequences (NLSs) proximal to an N- or C-terminus of the endonuclease. In some cases, the NLS comprises a sequence selected from SEQ ID NOs: 205-220.

Table 1: Examples NLS Sequences that may be used with Cas effectors according to the present disclosure.

Source	NLS amino acid sequence	SEQ ID NO:
SV40 NLS	PKKKRKV	205
nucleoplasmin bipartite	KRPAATKKAGQAKKKK	206
c-myc	PAAKRVKLD	207
c-myc	RQRRNELKRSP	208
hnRNPA1 M9	NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGY	209
Importin-alpha IBB domain	RMRIZFKNKGKDTAELRRRRVEVSVELRKAKKDEQILKRRNV	210
Myoma T protein	VSRKRPRP	211
Myoma T protein	PPKKARED	212
p53	PQPKKKPL	213
mouse c-abl IV	SALIKKKKKMAP	214
influenza virus NS1	DRLRR	215
influenza virus NS1	PKQKKRK	216
Hepatitis virus delta antigen	RKLKKKIKKL	217
mouse Mx1 protein	REKKKFLKRR	218
human poly(ADP-	KRKGDEV DGVDEVAKKKSKK	219

ribose) polymerase		
steroid hormone receptors glucocorticoid	RKCLQAGMNLEARKTKK	220

[00107] Included in the current disclosure are variants of any of the enzymes described herein with one or more conservative amino acid substitutions. Such conservative substitutions can be made in the amino acid sequence of a polypeptide without disrupting the three-dimensional structure or function of the polypeptide. Conservative substitutions can be accomplished by substituting amino acids with similar hydrophobicity, polarity, and R chain length for one another. Additionally, or alternatively, by comparing aligned sequences of homologous proteins from different species, conservative substitutions can be identified by locating amino acid residues that have been mutated between species (e.g., non-conserved residues) without altering the basic functions of the encoded proteins. Such conservatively substituted variants may include variants with 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 86%, at least about 87%, at least about 88%, at least about 89%, 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% identity to any one of the endonuclease protein sequences described herein. In some embodiments, such conservatively substituted variants are functional variants. Such functional variants can encompass sequences with substitutions such that the activity of one or more critical active site residues or guide RNA binding residues of the endonuclease are not disrupted. In some embodiments, a functional variant of any of the proteins described herein lacks substitution of at least one of the conserved or functional residues called out in FIGURE 4. In some embodiments, a functional variant of any of the proteins described herein lacks substitution of all of the conserved or functional residues called out in FIGURE 4. Also provided for by the disclosure herein are altered activity variants of any of the nucleases described herein. Such altered activity variants may comprise an inactivating mutation in one or more catalytic residues identified herein (e.g. in FIGURE 4) or generally described for RuvC domains. Such altered activity variants may comprise a change-switch mutation in a catalytic residue of a RuvCI, RuvCII, or RuvCIII domain.

[00108] Conservative substitution tables providing functionally similar amino acids are available from a variety of references (see, for e.g., Creighton, *Proteins: Structures and Molecular Properties* (W H Freeman & Co.; 2nd edition (December 1993)). The following eight groups

each contain amino acids that are conservative substitutions for one another:

- 1) Alanine (A), Glycine (G);
- 2) Aspartic acid (D), Glutamic acid (E);
- 3) Asparagine (N), Glutamine (Q);
- 4) Arginine (R), Lysine (K);
- 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V);
- 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W);
- 7) Serine (S), Threonine (T); and
- 8) Cysteine (C), Methionine (M)

[00109] Included in the current disclosure are variants of any of the endonucleases described herein with sequence identity to particular domains. The domain can be an arginine rich domain (e.g. a domain with PF14239 homology), a REC (recognition) domain, a BH (bridge helix) domain, a WED (wedge) domain, a PI (PAM-interacting) domain, a PF14239 homology domain, or any other domain described herein. In some embodiments, residues encompassing one or more of these domains is identified in a protein by alignment to one of the proteins below (e.g. when one of the proteins below and the protein of interest are optimally aligned), wherein the residue boundaries for example domains are described.

Table 2: Example domain boundaries for endonucleases described herein

	RuvC -I	BH	REC	Domain w/ PF14239 homology	RuvC -II	HNH	RuvC -III	WED and PI
MG34 -1 effect or	1-41	42-76	77- 281	4-65; 123-339	282- 323	324- 459	460- 551	552- 747
MG34 -9 effect or	1-41	42-76	77- 280	4-65; 123-338	281- 322	323- 490	491- 582	583- 778

[00110] In some cases, the engineered nuclease system further comprises a single-stranded DNA repair template. In some cases, the engineered nuclease system further comprises a double-stranded DNA repair template. In some cases, the single- or double-stranded DNA repair template comprises from 5' to 3' a first homology arm comprising a sequence of at least 20 nucleotides 5' to the target deoxyribonucleic acid sequence. In some cases, the single- or double-stranded DNA repair template comprises from 5' to 3' a synthetic DNA sequence of at least 10 nucleotides. In some cases, the single- or double-stranded DNA repair template comprises from 5' to 3' a second homology arm comprising a sequence of at least 20 nucleotides 3' to the target

sequence. In some cases, the single- or double-stranded DNA repair template comprises from 5' to 3': a first homology arm comprising a sequence of at least 20 nucleotides 5' to the target deoxyribonucleic acid sequence, a synthetic DNA sequence of at least 10 nucleotides, or a second homology arm comprising a sequence of at least 20 nucleotides 3' to the target sequence.

[00111] In some cases, the first homology arm comprises a sequence of at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 175, at least 200, at least 250, at least 300, at least 400, at least 500, at least 750, or at least 1000 nucleotides. In some cases, the engineered nuclease system further comprises a source of Mg^{2+} . In some cases, the endonuclease and the tract ribonucleic acid sequence are derived from distinct bacterial species. In some cases, the endonuclease and the tract ribonucleic acid sequence are derived from distinct bacterial species within a same phylum.

[00112] In some cases, the endonuclease comprises a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to any one of SEQ ID NOs: 1-24 or 462-488. In some cases, the guide RNA structure comprises an RNA sequence predicted to comprise a hairpin. In some cases, the hair pin comprises a stem and a loop. In some cases, the stem comprises at least 12 pairs, at least 14 pairs, at least 16 pairs or at least 18 pairs or ribonucleotides.

[00113] In some cases, the guide RNA structure further comprises a second stem and a second loop. In some cases, the second stem comprises at least 5 pairs, at least 6 pairs, at least 7 pairs, at least 8 pairs, at least 9 pairs or at least 10 pairs of ribonucleotides. In some cases, the guide RNA structure further comprises an RNA structure and this RNA structure comprises at least two hairpins. In some cases, the endonuclease comprises a sequence with at least 50%, at least 55%, 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%, or at least 99% sequence identity to SEQ ID NO: 1 and the guide RNA structure comprises an RNA sequence predicted to comprise at least four hairpins. In some cases, each of these four hairpins comprises a stem and a loop.

[00114] In some cases, the engineered nuclease system comprises a sequence at least 50%, at least 55%, 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%, or at least 99% identical to SEQ ID NO: 1. In some cases, the engineered nuclease system comprises the guide RNA structure which comprises

a sequence at least 50%, at least 55%, 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%, or at least 99% identical to at least one of SEQ ID NO: 199 or the nonvariable nucleotides of SEQ ID NO: 201.

[00115] In some cases, the engineered nuclease system comprises a sequence at least 50%, at least 55%, 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%, or at least 99% identical to any one of SEQ ID NOs: 1-24 or 462-488. In some cases, the engineered nuclease system comprises a sequence at least 50%, at least 55%, 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%, or at least 99% identical to any one of SEQ ID NOs: 199-200 or 669-673 or the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

[00116] In some cases, the sequence identity is determined by a BLASTP, CLUSTALW, MUSCLE, MAFFT, or CLUSTALW with the Smith-Waterman homology search algorithm parameters. In some cases, the sequence identity is determined by said BLASTP homology search algorithm using parameters of a wordlength (W) of 3, an expectation (E) of 10, and a BLOSUM62 scoring matrix setting gap costs at existence of 11, extension of 1, and using a conditional compositional score matrix adjustment.

[00117] In some cases, the endonuclease is not a Cas9 endonuclease, a Cas14 endonuclease, a Cas12a endonuclease, a Cas12b endonuclease, a Cas 12c endonuclease, a Cas12d endonuclease, a Cas12e endonuclease, a Cas13a endonuclease, a Cas13b endonuclease, a Cas13c endonuclease, or a Cas 13d endonuclease. In some cases, the endonuclease has less than less than 80% identity, less than 75% identity, less than 70% identity, less than 65% identity, less than 60% identity, less than 55% identity, or less than 50% identity to a Cas9 endonuclease.

[00118] In one aspect, the present disclosure provides an engineered guide RNA comprising (a) a DNA-targeting segment. In some cases, the DNA-targeting segment comprises a nucleotide sequence that is complementary to a target sequence in a target DNA molecule. In some cases, the engineered single guide ribonucleic acid polynucleotide comprises a protein-binding segment. The protein-binding segment comprises two complementary stretches of nucleotides that hybridize to form a double-stranded RNA (dsRNA) duplex. In some cases, the two complementary stretches of nucleotides are covalently linked to one another with intervening nucleotides. In some cases, the engineered guide ribonucleic acid polynucleotide is configured to form a complex with an endonuclease comprising a variant having at least 50%, at least 55%, 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%, or at least 99% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

[00119] In some cases, the DNA-targeting segment is positioned 5' of both of the two complementary stretches of nucleotides. In some cases, the protein binding segment comprises a sequence at least 50%, at least 55%, 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%, or at least 99% identical to any one of SEQ ID NOs: 199-200 or 669-673 or the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616. In some cases, a deoxyribonucleic acid polynucleotide encodes the engineered guide ribonucleic acid polynucleotide described herein.

[00120] In one aspect, the present disclosure provides a nucleic acid comprising an engineered nucleic acid sequence. In some cases, the engineered nucleic acid sequence is optimized for expression in an organism. In some cases, the nucleic acid encodes an endonuclease. The endonuclease may be a Cas endonuclease. The endonuclease may be a class 2 endonuclease. The endonuclease may be a class 2, type II Cas endonuclease. In some cases, the endonuclease comprises a RuvC domain and an HNH domain. In some cases, the endonuclease is derived from an uncultivated microorganism. In some cases, the endonuclease has a particular molecular weight range. In some embodiments the endonuclease has a molecular weight of about 120 kDa or less, about 110 kDa or less, about 105 kDa or less, about 100 kDa or less, about 95 kDa or less, about 90 kDa or less, about 85 kDa or less, about 80 kDa or less, about 75 kDa or less, about 70 kDa or less, about 65 kDa or less, about 60 kDa or less, about 55 kDa or less, about 50 kDa or less, about 45 kDa or less, about 40 kDa or less, about 35 kDa or less, about 30 kDa or less, about 25 kDa or less, about 20 kDa or less, about 15 kDa or less, or about 10 kDa or less. In some cases, the engineered guide ribonucleic acid structure comprises at least two ribonucleic acid polynucleotides. In some cases, the endonuclease comprises a particular number of residues. The endonuclease can comprise equal to or fewer than about 1,100 residues, equal to or fewer than about 1,000 residues, equal to or fewer than about 950 residues, equal to or fewer than about 900 residues, equal to or fewer than about 850 residues, equal to or fewer than about 800 residues, equal to or fewer than about 750 residues, equal to or fewer than about 700 residues, equal to or fewer than about 650 residues, equal to or fewer than about 600 residues, equal to or fewer than about 550 residues, equal to or fewer than about 500 residues, equal to or fewer than about 450 residues, equal to or fewer than about 400 residues, or equal to or fewer than about 350 residues. The endonuclease can comprise about 700 to about 1,100 residues. The endonuclease

can comprise about 400 to about 600 residues. In some cases, the endonuclease comprises SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668 or a variant thereof 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%, or at least 99% sequence identity thereto. In some cases, the endonuclease further comprises a sequence encoding one or more nuclear localization sequences (NLSs) proximal to an N- or C-terminus of said endonuclease. In some cases, the NLS comprises a sequence selected from SEQ ID NOs: 205-220.

[00121] In some cases, the organism is prokaryotic, bacterial, eukaryotic, fungal, plant, mammalian, rodent, or human. In some cases, the organism is prokaryotic. In some cases, the organism is bacterial. In some cases, the organism is eukaryotic. In some cases, the organism is fungal. In some cases, the organism is plant. In some cases, the organism is mammalian. In some cases, the organism is rodent. In some cases, the organism is human. Where the organism is prokaryotic or bacterial, then the organism may be a different organism from an organism from which the endonuclease is derived. In some cases, the organism is not the uncultivated microorganism.

[00122] In one aspect, the present disclosure provides a vector which comprises a nucleic acid sequence. In some cases, the nucleic acid sequence encodes an endonuclease. In some cases, the endonuclease is a Cas endonuclease. In some cases, the endonuclease is a class 2 endonuclease. In some cases, the endonuclease is a class 2, type II Cas endonuclease. The endonuclease may comprise a RuvC-I domain and an HNH domain. In some cases, the endonuclease is derived from an uncultivated microorganism. In some cases, the endonuclease has a particular molecular weight range. In some embodiments the endonuclease has a molecular weight of about 120 kDa or less, about 110 kDa or less, about 105 kDa or less, about 100 kDa or less, about 95 kDa or less, about 90 kDa or less, about 85 kDa or less, about 80 kDa or less, about 75 kDa or less, about 70 kDa or less, about 65 kDa or less, about 60 kDa or less, about 55 kDa or less, about 50 kDa or less, about 45 kDa or less, about 40 kDa or less, about 35 kDa or less, about 30 kDa or less, about 25 kDa or less, about 20 kDa or less, about 15 kDa or less, or about 10 kDa or less. In some cases, the engineered guide ribonucleic acid structure comprises at least two ribonucleic acid polynucleotides. In some cases, the endonuclease comprises a particular number of residues. The endonuclease can comprise equal to or fewer than about 1,100 residues, equal to or fewer than about 1,000 residues, equal to or fewer than about 950 residues, equal to or fewer than about 900 residues, equal to or fewer than about 850 residues, equal to or fewer than about 800 residues, equal to or fewer than about 750 residues, equal to or fewer than about 700 residues, equal to or fewer than about 650 residues, equal to or fewer than about 600 residues, equal to or

fewer than about 550 residues, equal to or fewer than about 500 residues, equal to or fewer than about 450 residues, equal to or fewer than about 400 residues, or equal to or fewer than about 350 residues. The endonuclease can comprise about 700 to about 1,100 residues. The endonuclease can comprise about 400 to about 600 residues.

[00123] In some aspects, the present disclosure provides for an endonuclease described herein configured to induce a double stranded break proximal to said target locus 5' to a protospacer adjacent motif (PAM). The endonuclease can induce a double-stranded break 6-8 nucleotides from the PAM or 7 nucleotides from the PAM. In some aspects, the present disclosure provides for an endonuclease described herein configured to induce a single-stranded break proximal to said target locus 5' to a protospacer adjacent motif (PAM). The endonuclease can induce a single-stranded break 6-8 nucleotides from the PAM or 7 nucleotides from the PAM. In some cases, an endonuclease configured to induce a single-stranded break comprises an inactivating mutation in one or more catalytic residues of an endonuclease described herein.

[00124] In some aspects, the present disclosure provides for an endonuclease system described herein configured to cause a chemical modification of a nucleotide base within or proximal to a target locus targeted by the endonuclease system. In this case, chemical modification of a nucleotide base generally refers to modification of the chemical moiety involved in base-pairing rather than modification of the sugar or phosphate portion of the nucleotide. The chemical modification can comprise deamination of an adenosine or a cytosine nucleotide. In some cases, endonuclease systems configured to cause a chemical modification comprises an endonuclease having a base editor coupled or fused in frame to said endonuclease. The endonuclease to which the base editor is fused or coupled can comprise a deactivating mutation in at least one catalytic residue of the endonuclease (e.g. in the RuvC domain). The base editor can be fused N- or C-terminally to said endonuclease, or linked via chemical conjugation. Base editors can include any adenosine or cytosine deaminases, including but not limited to Adenosine Deaminase RNA Specific 1 (ADAR1), Adenosine Deaminase RNA Specific 2 (ADAR2), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 1 (APOBEC1), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 2 (APOBEC2), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3A (APOBEC3A), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3B (APOBEC3B), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3C (APOBEC3C), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3D (APOBEC3D), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3F (APOBEC3F), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3G (APOBEC3G), Apolipoprotein B mRNA Editing Enzyme Catalytic Subunit 3H (APOBEC3H), or Apolipoprotein B mRNA Editing Enzyme Catalytic

Subunit 4 (APOBEC4), or a functional fragment thereof. The base editor can comprise a yeast, eukaryotic, mammalian, or human base editor.

[00125] In some aspects, the present disclosure provides for an endonuclease system described herein configured to cause a chemical modification of histone within or proximal to a target locus targeted by the endonuclease system. . In some cases, endonuclease systems configured to cause a chemical modification of a histone comprise an endonuclease having a histone editor coupled or fused in frame to said endonuclease. The histone editor can be coupled or fused N- or C-terminally to the endonuclease. In some embodiments, the chemical modification can comprise methylation, acetylation, demethylation, or deacetylation. The endonuclease to which the histone editor is fused or coupled can comprise a deactivating mutation in at least one catalytic residue of the endonuclease (e.g. in the RuvC domain). The histone editor can comprise a histone methyltransferase (e.g. ASH1L, DOT1L, EHMT1, EHMT2, EZH1, EZH2, MLL, MLL2, MLL3, MLL4, MLL5, NSD1, PRDM2, SET, SETBP1, SETD1A, SETD1B, SETD2, SETD3, SETD4, SETD5, SETD6, SETD7, SETD8, SETD9, SETDB1, SETDB2, SETMAR, SMYD1, SMYD2, SMYD3, SMYD4, SMYD5, SUV39H1, SUV39H2, SUV420H1, or SUV420H2), a histone demethylase (e.g. the KDM1, KDM2, KDM3, KDM4, KDM5, or KDM6 families), a histone acetyltransferase (e.g. GNATs or HAT family acetyltransferases), or a histone deacetylase (e.g. HDAC1, HDAC2, HDAC 3, HDAC4, HDAC5, HDAC6, HDAC7, HDAC8, HDAC9, HDAC10, HDAC11, SIRT1, SIRT2, SIRT3, SIRT4, SIRT5, SIRT6, or SIRT7). The histone editor can comprise a yeast, eukaryotic, mammalian, or human histone editor.

[00126] In one aspect, the present disclosure provides a vector comprising the nucleic acid described herein. In some cases, the vector further comprises a nucleic acid encoding an engineered guide ribonucleic acid structure. The engineered guide ribonucleic acid structure may be configured to form a complex with the endonuclease. In some cases, the engineered guide ribonucleic acid structure comprises a guide ribonucleic acid sequence. In some cases, the guide ribonucleic acid sequence is configured to hybridize to a target deoxyribonucleic acid sequence. In some cases, the engineered guide ribonucleic acid structure comprises a tracr ribonucleic acid sequence. In some cases, the tracr ribonucleic acid sequence is configured to bind to the endonuclease. In some cases, the vector is a plasmid, a minicircle, a CELiD, an adeno-associated virus (AAV) derived virion, or a lentivirus.

[00127] In one aspect, the present disclosure provides a cell comprising any of the vectors described herein.

[00128] In one aspect, the present disclosure provides a method of manufacturing an endonuclease. The method can comprise cultivating any of the cells described herein.

[00129] In one aspect, the present disclosure provides a method for binding, cleaving, marking, or modifying a double-stranded deoxyribonucleic acid polynucleotide. The method may comprise contacting the double-stranded deoxyribonucleic acid polynucleotide with an endonuclease. In some cases, the endonuclease is a Cas endonuclease. In some cases, the endonuclease is a class 2 endonuclease. In some cases, the endonuclease is a class 2, type II Cas endonuclease. The endonuclease may complex with an engineered guide ribonucleic acid structure. In some cases, the engineered guide ribonucleic acid structure is configured to bind to the endonuclease and the double-stranded deoxyribonucleic acid polynucleotide. In some cases, the double-stranded deoxyribonucleic acid polynucleotide comprises a protospacer adjacent motif (PAM). In some cases, the endonuclease has a molecular weight of about 120 kDa or less, about 110 kDa or less, about 100 kDa or less, about 90 kDa or less, about 80 kDa or less, about 70 kDa or less, about 60 kDa or less, about 50 kDa or less, about 40 kDa or less, about 30 kDa or less, about 20 kDa or less, or about 10 kDa or less. In some cases, the endonuclease comprises a variant with at least 50%, at least 55%, 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%, or at least 99% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

[00130] In one aspect, the present disclosure provides a method for binding, cleaving, marking, or modifying a double-stranded deoxyribonucleic acid polynucleotide. The method may comprise contacting the double-stranded deoxyribonucleic acid polynucleotide with an endonuclease. In some cases, the endonuclease is a Cas endonuclease. In some cases, the endonuclease is a class 2 endonuclease. In some cases, the endonuclease is a class 2, type II Cas endonuclease. The endonuclease may complex with an engineered guide ribonucleic acid structure. In some cases, the engineered guide ribonucleic acid structure may be configured to bind to the endonuclease and the double-stranded deoxyribonucleic acid polynucleotide. In some cases, the double-stranded deoxyribonucleic acid polynucleotide comprises a protospacer adjacent motif (PAM). In some cases, the PAM is NGG. In some cases, the endonuclease comprises a variant with at least 50%, at least 55%, 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%, or at least 99% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

[00131] In some cases, the endonuclease is not a Cas9 endonuclease, a Cas14 endonuclease, a Cas12a endonuclease, a Cas12b endonuclease, a Cas 12c endonuclease, a Cas12d endonuclease, a Cas12e endonuclease, a Cas13a endonuclease, a Cas13b endonuclease, a Cas13c endonuclease, or a Cas 13d endonuclease. In some cases, the endonuclease is derived from an

uncultivated microorganism. In some cases, the double-stranded deoxyribonucleic acid polynucleotide is a prokaryotic, archaeal, bacterial, eukaryotic, plant, fungal, mammalian, rodent, or human double-stranded deoxyribonucleic acid polynucleotide. In some cases, the double-stranded deoxyribonucleic acid polynucleotide is a prokaryotic, archaeal, or bacterial double-stranded deoxyribonucleic acid polynucleotide from a species other than a species from which the endonuclease is derived.

[00132] In one aspect, the present disclosure provides a method of modifying a target nucleic acid locus. The method may comprise delivering to the target nucleic acid locus the engineered nuclease system described herein. In some cases, the endonuclease is configured to form a complex with the engineered guide ribonucleic acid structure. In some cases, the complex is configured such that upon binding of the complex to the target nucleic acid locus, the complex modifies the target nucleic locus. In some cases, modifying the target nucleic acid locus comprises binding, nicking, cleaving, or marking the target nucleic acid locus.

[00133] In some cases, the target nucleic acid locus comprises deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). In some cases, the target nucleic acid comprises genomic eukaryotic DNA, viral DNA, or bacterial DNA. In some cases, the target nucleic acid comprises bacterial DNA. The bacterial DNA may be derived from a bacterial species different to a species from which the endonuclease was derived. In some cases, the target nucleic acid locus is *in vitro*. In some cases, the nucleic acid locus is within a cell. In some cases, the endonuclease and the engineered guide nucleic acid structure are provided encoded on separate nucleic acid molecules. In some cases, the cell is a prokaryotic cell, a bacterial cell, a eukaryotic cell, a fungal cell, a plant cell, an animal cell, a mammalian cell, a rodent cell, a primate cell, or a human cell. In some cases, the cell is derived from a species different to a species from which the endonuclease is derived.

[00134] In some cases, delivering the engineered nuclease system to the target nucleic acid locus comprises delivering the nucleic acid described herein or the vector described herein. In some cases, delivering the engineered nuclease system to the target nucleic acid locus comprises delivering a nucleic acid comprising an open reading frame encoding the endonuclease. In some cases, the nucleic acid comprises a promoter to which the open reading frame encoding the endonuclease is operably linked. In some cases, delivering the engineered nuclease system to the target nucleic acid locus comprises delivering a capped mRNA containing the open reading frame encoding said endonuclease. In some cases, delivering the engineered nuclease system to said target nucleic acid locus comprises delivering a translated polypeptide.

[00135] In some cases, delivering the engineered nuclease system to the target nucleic acid locus comprises delivering a deoxyribonucleic acid (DNA) encoding the engineered guide ribonucleic

acid structure operably linked to a ribonucleic acid (RNA) pol III promoter. In some cases, the endonuclease induces a single-stranded break or a double-stranded break at or proximal to the target locus.

[00136] Systems of the present disclosure may be used for various applications, such as, for example, nucleic acid editing (e.g., gene editing), binding to a nucleic acid molecule (e.g., sequence-specific binding). Such systems may be used, for example, for addressing (e.g., removing or replacing) a genetically inherited mutation that may cause a disease in a subject, inactivating a gene in order to ascertain its function in a cell, as a diagnostic tool to detect disease-causing genetic elements (e.g. via cleavage of reverse-transcribed viral RNA or an amplified DNA sequence encoding a disease-causing mutation), as deactivated enzymes in combination with a probe to target and detect a specific nucleotide sequence (e.g. sequence encoding antibiotic resistance in bacteria), to render viruses inactive or incapable of infecting host cells by targeting viral genomes, to add genes or amend metabolic pathways to engineer organisms to produce valuable small molecules, macromolecules, or secondary metabolites, to establish a gene drive element for evolutionary selection, to detect cell perturbations by foreign small molecules and **nucleotides as a biosensor**.

EXAMPLES

Example 1. – Discovery of New Cas Effectors by Metagenomics

Metagenomic Mining

[00137] Metagenomic samples were collected from sediment, soil and animal. Deoxyribonucleic acid (DNA) was extracted with a Zymobiomics DNA mini-prep kit and sequenced on an Illumina HiSeq[®] 2500. Samples were collected with consent of property owners. DNA was extracted from samples using either the Qiagen DNeasy PowerSoil Kit or the ZymoBIOMICS DNA Miniprep Kit. DNA was sent for sequencing library preparation (Illumina TruSeq) and sequencing on an Illumina HiSeq 4000 or Novaseq to the Vincent J. Coates Genomics Sequencing Laboratory at UC Berkeley (paired 150 base pair (bp) reads with a 400-800 bp target insert size). Additionally, publicly available high temperature, as well as soil and ocean metagenomic sequencing data were downloaded from the NCBI SRA. Sequencing reads were trimmed using BBDuk (Bushnell B., sourceforge.net/projects/bbmap/) and assembled with Megahit (<https://paperpile.com/c/QSZG6K/clMrh>). Protein sequences were predicted with Prodigal (<https://paperpile.com/c/QSZG6K/BJ6oW>). HMM profiles of known Type II CRISPR nucleases were built and searched against all predicted proteins using HMMER3 (hmmer.org). CRISPR arrays were predicted on assembled contigs with Minced (<https://github.com/ctSkennerton/minced> or <https://paperpile.com/c/QSZG6K/OPC44>).

Taxonomy was assigned to proteins with Kaiju <https://paperpile.com/c/QSZG6K/nMi6k> and contig taxonomy was determined by finding the consensus of all encoded proteins.

[00138] Predicted and reference (e.g. SpCas9, SaCas9, and AsCas9) Type II effector proteins were aligned with MAFFT (<https://paperpile.com/c/QSZG6K/sVHNH>) and phylogenetic trees were inferred using FastTree2 (<https://paperpile.com/c/QSZG6K/osZNM>). Novel families were identified from clades composed of sequences recovered from this study. From within families, candidates were selected if they contained all necessary components for laboratory analysis (i.e. they were found on a well-assembled and annotated contig with a CRISPR array). Selected representative and reference sequences were aligned using MUSCLE (<https://paperpile.com/c/QSZG6K/ITOlA>) to identify catalytic and PAM interacting residues.

[00139] This metagenomic workflow resulted in the delineation of the SMART (SMall ARchaeal-associaTed) endonuclease systems described herein.

Discovery of SMART Endonucleases containing active residue signatures

[00140] Mining of tens of thousands of high quality CRISPR Cas systems assembled from metagenomic data uncovered novel effectors containing both RuvC and HNH domains, but that

were of unusually small size (<900 aa). These effector nucleases showed only low sequence similarity (<20 % amino acid identity) to archaeal Cas9 endonucleases as a reference point. Phylogenetic analysis of effector protein sequences indicated that the SMART systems are a divergent group relative to well-studied Type II systems from subtype A, B, or C (**FIG. 1A**). **[00141]** These compact “SMART” effectors (~400 - 1000 amino acids, **FIG. 2**) appeared in loci in the genome adjacent to CRISPR arrays. Some of these adjacent SMART loci also included sequences predicted to encode tracrRNAs and the CRISPR adaptation genes (e.g. genes involved in spacer acquisition) cas1, cas2, and/or cas4 within the same operon (**FIG. 3**). Despite their compact size, SMART effectors contain six putative HNH and RuvC catalytic residues when aligned with a reference SaCas9 sequence (**FIG. 4**). In addition, 3D structure predictions identified residues involved in guide and target binding, as well as in recognition of a PAM, suggesting that the SMART effectors are active dsDNA endonucleases.

Multiple groups of SMART endonucleases

[00142] Based on the location of important catalytic and binding residues, SMART nucleases comprise three RuvC domains, an arginine rich region usually containing an RRxRR motif (e.g. a domain with PF14239 homology), an HNH endonuclease domain, and a putative recognition domain (**FIG. 5** and **FIG. 6**). These domains share low sequence similarity with reference sequences (**FIG. 7**). In addition, SMART effectors, as well as reference archaeal sequences, contain RRxRR and zinc-binding ribbon motifs (CX[2-4]C or CX[2-4]H) significantly more frequently than Cas9 nucleases (**FIG. 8**). In addition, unlike Cas9 effector sequences, most SMART effectors contain significant hits to the Pfam domain PF14239, which is often associated with diverse endonucleases. Based upon differences in SMART effector size, phylogenetic relationship, and both operon and domain architecture, we classified these systems into two primary groups: SMART I and SMART II. The salient features of these groups are outlined in Table 3 below, which also illustrates differences compared to Class 2, Type II A/B/C Cas enzymes.

Table 3: Attributes of SMART I and II group enzymes described herein

Attribute	SMART I	SMART II	Type II: A, B, C
Zn-binding residues	yes	yes	no
Bridge helix	yes	no	yes
PAM interacting and WED domain	yes	no	yes
RRxRR motif	yes	yes	no
REC domain	Novel domain w/ homology to PF14239	Novel domain at C-terminus	Cas9 REC domain
Domain w/ PF14239 homology	yes	yes	no
Monophyletic clade	yes	no	yes
Related to TnpB	yes	yes	yes
Operon contains IS605 Tns repeats	no	sometimes	no
<900 aa	sometimes	yes	no
CRISPR-associated	yes	sometimes	yes
Contains RuvC and HNH	yes	yes	yes

SMART I Endonucleases

[00143] SMART I effectors range between approximately 700 amino acids and 1,050 amino acids in size. Common features in their genomic context were adaptation module genes (e.g. genes involved in spacer acquisition) and predicted tracrRNAs near the CRISPR array, the organization of which resembled Type II and Type V CRISPR systems (**FIG. 3A, 3B and 3C**). The RRXRR motif-containing region in SMART I effectors is unique but may play a similar functional role as the arginine-rich bridge helix in Cas9 nucleases. When modeled against the SaCas9 crystal structure, predicted 3D structures of SMART I effectors showed unaligned regions within the recognition lobe (which often contains the Pfam domain PF14239) and RuvC-II domains (**FIG. 5**). The results indicated that these domains have different origins relative to other Type II effectors. Taken together with their divergent placement in a Type II effector phylogenetic tree and their low sequence similarity to known Type II effectors (**FIG. 1A**), these results indicate that SMART I endonucleases belong to a new group of Type II CRISPR

systems. Following the accepted classification of CRISPR systems, these SMART I systems were classified as Type II-D.

[00144] Putative single guide RNAs (sgRNAs) were engineered using environmental RNA expression data for the SMART I MG34-1 system. In addition, multiple sgRNAs designed from SMART I repeat and tracrRNA predictions were tested *in vitro* in PAM enrichment assays. In the case of SMART I enzymes, optimal identification of PAM sequences was performed using end repair and blunt-end ligation at this step, suggesting that these enzymes can produce staggered double-stranded DNA breaks. Assays confirmed dsDNA cleavage for MG34-1 (SEQ ID NO: 2), MG34-9 (SEQ ID NO: 9), and MG34-16 (SEQ ID NO: 17) with multiple sgRNA designs (FIG. 7, depicting use of SEQ ID NOs: 612-615). MG34-1 demonstrated a preference for an NGGN PAM for target recognition and cleavage (**FIG. 8A**). Analysis of the cut site indicated preferential cleavage at position 7 (**FIG. 8B**). These results suggest a novel biochemical mechanism compared with cleavage mechanisms from other Type II enzymes, which preferentially cleave at positions 2-3 from the PAM, supporting a new classification for SMART I CRISPR systems.

[00145] Environmental expression data for some SMART I systems confirmed *in situ* transcription of the CRISPR array and intergenic region encoding the predicted tracrRNA (**FIGs. 3B** and **3C**). Additionally, cases of active CRISPR targeting were evaluated by searching spacer sequences that match other genomic sequences assembled from the same, or related metagenomes. Along these lines, a phage genome being targeted by one of the spacers encoded in a SMART I CRISPR array (**FIGs. 3C** and **3D**) was identified. Analysis of the region adjacent to the target sequence suggests a 3' PAM sequence containing a GG motif (**FIG. 3D**). These results indicate that SMART I CRISPR systems are active in their natural environments as RNA guided effectors involved in phage defense, likely functioning as nucleases that cut or degrade targeted DNA or RNA.

SMART I effectors are active, RNA guided dsDNA CRISPR endonucleases

[00146] Putative single guide RNA (sgRNA) were engineered using the environmental RNA expression data for SMART I MG34-1 and MG34-16 systems (**FIGs. 3B** and **3C**, and **FIG. 9**). In addition, multiple sgRNAs designed from SMART I repeat and tracrRNA predictions were tested *in vitro* in PAM enrichment assays (FIG. 10). Assays confirmed programmable dsDNA cleavage for MG34-1, MG34-9, and MG34-16 with multiple sgRNA designs (**FIG. 10**). MG34-1 and MG34-9 require an NGGN PAM for target recognition and cleavage (**FIGs. 11A** and **11C**). Analysis of the cut site indicates preferential cleavage at position 7 (**FIG. 11B** and **11C**). These results suggest a novel biochemical cleavage mechanism compared with Cas9 enzymes,

which preferentially cleave at position 3 from the PAM, and provide further support for a new classification for SMART I CRISPR systems.

[00147] PAM enrichment assays without an end repair step did not show activity for SMART I nucleases. The requirement for end repair to create blunt-end fragments prior to ligation in the PAM enrichment protocol indicates that these enzymes create a staggered double strand DNA break.

[00148] Experiments conducted in *E. coli* showed that the system has the required activity to function as a nuclease in cells. *E. coli* strains expressing MG34-1 and sgRNAs were transformed with a kanamycin resistance plasmid containing a target for the sgRNA. In the presence of the antibiotic, successful targeting and cutting of the antibiotic resistance plasmid will result in a growth defect. The assay showed an approximately 2-fold growth repression compared with control experiments conducted with a kanamycin resistance plasmid that did not contain a target for the sgRNA (**FIG. 12**).

SMART II Endonucleases

[00149] SMART II effectors have a size distribution that skews smaller (~400 amino acids - 600 amino acids) vs. SMART I effectors. Their genomic context suggested unusual repetitive regions or CRISPR arrays. The non-CRISPR repetitive regions contain direct repeats that range in size from about 10 to over 30 bp. In some cases, these include multiple distinct repeating units. Sometimes, common CRISPR identification algorithms will flag these regions as CRISPR systems; however, closer inspection will reveal that the regions identified as spacer sequences are repeated in the array. The arrays are not immediately adjacent to the effectors, but they are in the same genomic region (**FIG. 3A**, MG35-236 and **FIG. 13A**, e.g., >20kb from the effector gene). SMART II system operons were generally devoid of adaptation module genes (e.g. genes involved in spacer acquisition).

[00150] Structural predictions identified characteristic residues of Cas enzymes involved in guide RNA binding, target cleavage, and recognition of and interaction with a PAM, in addition to all six RuvC and HNH nuclease catalytic residues (**FIG. 6**) often found in class 2, type II Cas effectors. In addition, SMART II effectors contained multiple RRXRR and zinc binding ribbon motifs (CX_[2-4]C or CX_[2-4]H), which are possibly involved in recognition and binding of a target nucleic acid motif. Based on the location of important residues, the predicted domain architecture of SMART II nucleases consisted of three RuvC subdomains, an arginine-rich region containing an RRxRR motif (e.g. a domain with PF14239 homology), an HNH endonuclease domain, an unknown domain, and a recognition domain (REC) (**FIG. 6**). The

domain architecture of SMART II effectors differed from the known domain architecture for Type II Cas9 nucleases (**FIG. 6** and **FIG. 14**).

[00151] Environmental transcriptomic data for some SMART II systems confirmed *in situ* expression of CRISPR arrays and other repetitive regions in the natural environment (**FIG. 13A**). Transcription of the 5' untranslated region (UTR) of some SMART II effectors was also observed from environmental expression data (**FIG. 13B**), suggesting that this region may be important for either nuclease activity or regulation of the SMART system.

[00152] Preliminary *in vitro* experiments conducted with SMART II effector proteins, repetitive regions, and associated intergenic regions show that these enzymes may have the ability to cleave dsDNA, possibly in a programmable manner (**FIG. 15**). Results suggest that SMART II nuclease activity may be RNA and/or DNA guided, which may require using a repetitive region such as a CRISPR array, or via recognition of features encoded within the loci such as TIR or 5' UTR.

[00153] Some SMART II effectors were observed next to a putative insertion sequence (IS) encoding transposases TnpA and TnpB (**FIG. 3A**). The ends of the IS were identified as containing terminal inverted repeats (TIR) with predicted hairpin structures, and the target site duplication at which the IS most likely integrated into was also identified). In addition, some SMART II loci encoded putative TIRs flanking the SMART II effector (e.g. **FIG. 3**).

Example 2.- PAM Sequence identification/confirmation for the endonucleases described herein

[00154] Putative SMART endonucleases were expressed in an *E. coli* lysate-based expression system (PURExpress, New England Biolabs). In this system, the endonuclease was codon optimized for *E. coli* and cloned into a vector with a T7 promoter and C-terminal His tag. The gene was PCR amplified with primer binding sites 150 bp upstream and downstream from the T7 promoter and terminator sequences, respectively. This PCR product was added to NEB PURExpress at 5 nM final concentration and expressed for 2 hr at 37° to produce the endonucleases for the PAM assays.

[00155] The putative sgRNAs compatible with each SMART Cas enzyme described herein were identified from RNAseq reads assembled to the contig CRISPR locus assembled from sequencing data: secondary structure was determined for the tracr region from RNAseq data along with the repeat sequence from the CRISPR array in the Geneious software package (<https://www.geneious.com>), and the resulting helix was trimmed and concatenated with a GAAA tetra-loop. Multiple lengths of repeat-anti-repeat helix trimming were tested, as well as different spacer lengths and different tracr termination points (FIG. 12, which demonstrates SEQ

ID NOs: 612-615). Each sgRNA was then assembled via assembly PCR, purified with SPRI beads, and *in vitro* transcribed (IVT) following manufacturer's recommended protocol for short RNA transcripts (HiScribe T7 kit, NEB). RNA transcription reactions were cleaned with the Monarch RNA kit and checked for purity via Tapestation (Agilent).

[00156] PAM sequences were determined by sequencing plasmids containing randomly-generated potential PAM sequences that can be cleaved by the putative nucleases. In this system, an *E. coli* codon optimized nucleotide sequence encoding the putative nuclease was transcribed and translated *in vitro* from a PCR fragment under control of a T7 promoter. A second PCR fragment with a minimal CRISPR array composed of a T7 promoter followed by a repeat-spacer-repeat sequence was transcribed in the same reaction. Successful expression of the endonuclease and repeat-spacer-repeat sequence in the TXTL system followed by CRISPR array processing provides active *in vitro* CRISPR nuclease complexes.

[00157] A library of target plasmids containing a spacer sequence matching that in the minimal array preceded by 8N mixed degenerate bases (potential PAM sequences) were incubated with the output of the TXTL reaction (10 mM Tris pH 7.5, 100 mM NaCl, and 10 mM MgCl₂ with a 5-fold dilution of translated Cas enzyme, 5 nM of an 8N PAM plasmid library, and 50 nM of sgRNA targeting the PAM library). After 1-3 hr, the reaction was stopped, and the DNA was recovered via a DNA clean-up kit. Adapter sequences were blunt-end ligated to DNA with active PAM sequences that had been cleaved by the endonuclease, whereas DNA that had not been cleaved was inaccessible for ligation. DNA segments comprising active PAM sequences were then amplified by PCR with primers specific to the library and the adapter sequence. The PCR amplification products were resolved on a gel to identify amplicons that correspond to cleavage events. The amplified segments of the cleavage reaction were also used as a template for preparation of an NGS library or as a substrate for Sanger sequencing. Sequencing this resulting library, which was a subset of the starting 8N library, revealed sequences with PAM activity compatible with the CRISPR complex. For PAM testing with a processed RNA construct, the same procedure was repeated except that an *in vitro* transcribed RNA was added along with the plasmid library and the minimal CRISPR array/tracr template was omitted. The following spacer sequence was used as a target in these assays (5'-CGUGAGCCACCACGUCGCAAGCCUCGAC-3').

[00158] Having obtained raw sequencing reads from the PAM assays, reads were filtered by Phred quality score > 20. The 24 bp representing the known DNA sequence from the backbone adjacent to the PAM was used as a reference to find the PAM-proximal region and the 8 bp adjacent were identified as the putative PAM. The distance between the PAM and the ligated adapter was also measured for each read. Reads that did not have an exact match to the reference

sequence or adapter sequence were excluded. PAM sequences were filtered by cut site frequency such that only PAMs with the most frequent cut site ± 2 bp were included in the analysis. The filtered list of PAMs was used to generate a sequence logo using Logomaker (Tareen A, Kinney JB. Logomaker: beautiful sequence logos in Python. *Bioinformatics*. 2020;36(7):2272-2274, which is incorporated by reference herein).

Example 3. – Protocol for predicted RNA folding

[00159] Predicted RNA folding of the active single RNA sequence is computed at 37° using the method of Andronescu 2007. The color of the bases corresponds to the probability of base pairing of that base, where red is high probability and blue is low probability.

Example 4. – *In vitro* cleavage efficiency

[00160] Endonucleases are expressed as His-tagged fusion proteins from an inducible T7 promoter in a protease deficient *E. coli* B strain. The endonuclease was fused to two nuclear localization signals (N-term NLS nucleoplasmin bipartite and C-term simian virus 40 T-antigen NLS PPKKKRK), a maltose binding protein (MBP) tag, a tobacco etch virus (TEV) protease cleavage site, and a 6XHis tag in the following order from N to C termini: 6XHis-MBP-TEV-NLS-gene-NLS-STOP. This protein was expressed under a pTac promoter in NEB Iq *E. coli* by autoinduction media (MagicMedia ThermoFisher), grown at 30°C, and induced at 16°C.

[00161] Cells expressing the His-tagged proteins were lysed by sonication and the His-tagged proteins purified by Ni-NTA affinity chromatography on a HisTrap FF column (GE Lifescience) on an AKTA Avant FPLC (GE Lifescience). The eluate was resolved by SDS-PAGE on acrylamide gels (Bio-Rad) and stained with InstantBlue Ultrafast Coomassie (Sigma-Aldrich). Purity was determined using densitometry of the protein band with ImageLab software (Bio-Rad). Purified endonucleases were dialyzed into a storage buffer composed of 50 mM Tris-HCl, 300 mM NaCl, 1 mM TCEP, 5% glycerol; pH 7.5 and stored at -80°C.

[00162] Target DNAs containing spacer sequences and PAM sequences (determined e.g., as in Example 2) were constructed by DNA synthesis. A single representative PAM is chosen for testing when the PAM has degenerate bases. The target DNAs are comprised of 2200 bp of linear DNA derived from a plasmid via PCR amplification with a PAM and spacer located 700 bp from one end. Successful cleavage results in fragments of 700 and 1500 bp. The target DNA, *in vitro* transcribed single RNA, and purified recombinant protein are combined in cleavage buffer (10 mM Tris, 100 mM NaCl, 10 mM MgCl₂) with an excess of protein and RNA and are incubated for 5 minutes to 3 hours, usually 1 hr. The reaction is stopped via addition of

RNAse A and incubation at 60 minutes. The reaction is then resolved on a 1.2% TAE agarose gel and the fraction of cleaved target DNA is quantified in ImageLab software.

Example 5. – Activity in *E. coli*

[00163] *E. coli* lacks the capacity to efficiently repair double-stranded DNA breaks. Thus, cleavage of genomic DNA can be a lethal event. Exploiting this phenomenon, endonuclease activity is tested in *E. coli* by recombinantly expressing an endonuclease and a guide RNA in a target strain with spacer/target and PAM sequences integrated into its genomic DNA.

[00164] For testing of nuclease activity in bacterial cells, BL21 (DE3) strains (NEB) were transformed with plasmids containing T7-driven effector and sgRNA (10 ng each plasmid), plated and grown overnight. The resulting colonies were cultured overnight in triplicate, then subcultured in SOB and grown to OD 0.4-0.6. 0.5 OD equivalent of cell culture was made chemocompetent according to standard kit protocol (Zymo Mix and Go kit) and transformed with 130 ng of a kanamycin plasmid either with or without a spacer and PAM in the backbone. After heat shock, transformations were recovered in SOC for 1 hr at 37°C, and nuclease efficiency was determined by a 5-fold dilution series grown on induction media (LB agar plates with antibiotics and 0.05 mM IPTG). Colonies were quantified from the dilution series to measure overall repression due to nuclease-driven plasmid cleavage.

[00165] The results for such an assay are shown in **FIG. 12**. In **FIG. 12**, panel (A) shows replica plating of *E. coli* strains demonstrating plasmid cutting; *E. coli* expressing MG34-1 and a sgRNA were transformed with a kanamycin resistance plasmid containing a target for the sgRNA (+sp). Plate quadrants that show growth impairment (+sp) vs. the negative control (without the target and PAM (-sp)) indicate successful targeting and cleavage by the enzyme. The experiment was replicated twice and performed in triplicate. In **FIG. 12**, panel B shows graphs of colony forming unit (cfu) measurements from the replica plating experiments in A showing growth repression in the target condition (+sp) vs. the non-target control (-sp), demonstrating the plasmid was cut.

[00166] Engineered strains with PAM sequences (determined e.g. as in Example 2) integrated into their genomic DNA are transformed with DNA encoding the endonuclease. Transformants are then made chemocompetent and are transformed with 50 ng of guide RNAs (e.g., crRNAs) either specific to the target sequence (“on target”), or non-specific to the target (“non target”). After heat shock, transformations are recovered in SOC for 2 hrs at 37°C. Nuclease efficiency is then determined by a 5-fold dilution series grown on induction media. Colonies are quantified from the dilution series in triplicate.

Example 6. –Testing Genome Cleavage Activity of MG CRISPR Complexes in Mammalian Cells

[00167] To show targeting and cleavage activity in mammalian cells, the MG Cas effector protein sequences are tested in two mammalian expression vectors: (a) one with a C-terminal SV40 NLS and a 2A-GFP tag, and (b) one with no GFP tag and two SV40 NLS sequences, one on the N-terminus and one on the C-terminus. The NLS sequences comprise any of the NLS sequences described herein. In some instances, nucleotide sequences encoding the endonucleases are codon-optimized for expression in mammalian cells.

The corresponding crRNA sequence with targeting sequence attached is cloned into a second mammalian expression vector. The two plasmids are cotransfected into HEK293T cells. 72 hr after co-transfection of the expression plasmid and a gRNA targeting plasmid into HEK293T cells, the DNA is extracted and used for the preparation of an NGS-library. Percent NHEJ is measured via indels in the sequencing of the target site to demonstrate the targeting efficiency of the enzyme in mammalian cells. At least 10 different target sites are chosen to test each protein's activity.

Example 7. – Predicted activity of MG families described herein

[00168] *In situ* expression and protein sequence analyses indicate that these enzymes are active nucleases. They contain predicted endonuclease-associated domains (matching RRXRR and HNH_endonuclease Pfam domains; FIG. 2, 3A and 3B), and contain predicted HNH and RuvC catalytic residues (e.g. FIG. 2, 3A and 3B, rectangles). Furthermore, the presence of an RRXRR motif, found in Ribonuclease H-like protein families, indicates potential RNA targeting and/or nuclease activity (See FIG. 2).

[00169] Expression data confirms *in situ* natural activity for candidate MG34-1 nuclease, tracrRNA and CRISPR array (FIG. 4).

Example 8. –Activity in Mammalian Cells with mRNA Delivery

[00170] For genome editing using cell transfection/transformation with mRNA, the coding sequence is mouse or human codon optimized using algorithms from Twist Bioscience or Thermo Fisher Scientific (GeneArt). A cassette is constructed with two nuclear localization signals appended to the coding endonuclease sequence: SV40 and nucleoplasmin at the N and C terminal respectively. Additionally, untranslated regions from human complement 3 (C3) are appended to both the 5' and 3' to the coding sequence within the cassette.

[00171] This cassette is then cloned into a mRNA production vector upstream of a long poly A stretch. The mRNA construct organization can be as follows: 5' UTR from C3 – SV40 NLS –

codon optimized SMART gene – nucleoplasmin NLS – 3' UTR from C3 – 107 polyA tail. Run-of transcription of the mRNA is then driven by a T7 promoter using an engineered T7 RNA polymerase (Hi-T7: New England Biolabs). 5' capping of the mRNA occurs co-transcriptionally using CleanCap AG (Trilink Biolabs). mRNA is then purified using MEGAclear Transcription Clean-Up kit (Thermo Fisher Scientific).

[00172] Mammalian cells are co-transfected with transcribed mRNA and a set of at least 10 guides targeting a genomic region of interest using Lipofectamine Messenger Max (Thermo Fisher Scientific). Cells are incubated for a period of time (e.g. 48 hours) followed by genomic DNA isolation using a Purelink Genomic DNA extraction kit (Fisher Scientific). The region of interest is amplified using specific primers. Editing is then assessed by Sanger sequencing using Inference of CRISPR Edits and NGS for a thorough analysis of edit outcomes.

[00173] 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. It is not intended that the invention be limited by the specific examples provided within the specification. While the invention has been described with reference to the aforementioned specification, the descriptions and illustrations of the embodiments herein are not meant to be construed in a limiting sense. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. Furthermore, it shall be understood that all aspects of the invention are not limited to the specific depictions, configurations or relative proportions set forth herein which depend upon a variety of conditions and variables. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is therefore contemplated that the invention shall also cover any such alternatives, modifications, variations or equivalents. 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.

CLAIMS

WHAT IS CLAIMED IS:

1. An engineered nuclease system, comprising:
 - (a) an endonuclease comprising a RuvC domain and an HNH domain, wherein said endonuclease is derived from an uncultivated microorganism; and
 - (b) an engineered guide ribonucleic acid structure configured to form a complex with said endonuclease comprising:
 - (i) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and
 - (ii) a tracr ribonucleic acid sequence configured to bind to said endonuclease;wherein said endonuclease has a molecular weight of about 96kDa or less.
2. The engineered nuclease system of claim 1, wherein said endonuclease is an Archaeal endonuclease.
3. The engineered nuclease system of claim 1 or claim 2, wherein said endonuclease is a Class 2, Type II Cas endonuclease.
4. The engineered nuclease system of any one of claims 1-3, wherein said endonuclease comprises a sequence with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.
5. The engineered nuclease system of any one of claims 1-4, wherein said endonuclease further comprises an arginine-rich region comprising an RRxRR motif or a domain with PF14239 homology.
6. The engineered nuclease system of claim 5, wherein said arginine rich region or said domain with PF14239 homology has at least 85%, at least 90%, or at least 95% identity to said arginine rich region or said domain with PF14239 homology of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.
7. The engineered nuclease system of any one of claims 1-6, wherein said endonuclease further comprises a REC (recognition) domain.

8. The engineered nuclease system of claim 7, wherein said REC domain has at least 85%, at least 90%, or at least 95% identity to a REC domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

9. The engineered nuclease system of any one of claims 1-8, wherein said endonuclease further comprises a BH (bridge helix) domain, a WED (wedge) domain, and a PI (PAM interacting) domain.

10. The engineered nuclease system of claim 9, wherein said BH domain, said WED domain, or said PI domain has at least 85%, at least 90%, or at least 95% identity to a BH domain, a WED domain, and/or a PI domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

11. An engineered nuclease system comprising:

- (a) an endonuclease comprising a RuvC-I domain and an HNH domain; and
- (b) an engineered guide ribonucleic acid structure configured to form a complex with said endonuclease comprising:
 - (i) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and
 - (ii) a ribonucleic acid sequence configured to bind to said endonuclease,

wherein said endonuclease comprises a sequence with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

12. The engineered nuclease system of claim 11, wherein said endonuclease is an archaeal endonuclease.

13. The engineered nuclease system of claim 11 or 12, wherein said endonuclease is a class 2, type II Cas endonuclease.

14. The engineered nuclease system of any one of claim 11-13, wherein said endonuclease further comprises an arginine-rich region comprising an RRxRR motif or a domain with PF14239 homology.

15. The engineered nuclease system of claim 14, wherein said arginine rich region or said domain with PF14239 homology has at least 85%, at least 90%, or at least 95% identity to an arginine rich region of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

16. The engineered nuclease system of any one of claims 11-15, wherein said endonuclease further comprises a REC (recognition) domain.

17. The engineered nuclease system of claim 16, wherein said REC domain having at least 85%, at least 90%, or at least 95% identity to a REC domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

18. The engineered nuclease system of any one of claims 11-17, wherein said endonuclease further comprises a BH domain, a WED domain, and a PI domain.

19. The engineered nuclease system of claim 18, wherein said BH domain, said WED domain, or said PI domain has at least 85%, at least 90%, or at least 95% identity to a BH domain, a WED domain, and/or a PI domain of any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

20. The engineered nuclease system of any one of claims 11-19, wherein said endonuclease is derived from an uncultivated microorganism.

21. The engineered nuclease system of any one of claims 1-20, wherein said ribonucleic acid sequence configured to bind said endonuclease comprises a sequence with at least 80% sequence identity to any one of SEQ ID NOs: 199-200, 460-461, or 669-673, or a sequence with at least 80% sequence identity to the non-degenerate nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

22. The engineered nuclease system of claim 21, wherein said guide nucleic acid structure comprises a sequence with at least 80% identity to the non-degenerate nucleotides of any one of SEQ ID NOs: 201-203, 613-616.

23. An engineered nuclease system comprising,
(c) an engineered guide ribonucleic acid structure comprising:

- (i) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and
- (ii) a ribonucleic acid sequence configured to bind to an endonuclease, wherein said ribonucleic acid sequence comprises a sequence with at least 80% sequence identity to any one of SEQ ID NOs: 199-200, 460-461, or 669-673, or a sequence with at least 80% sequence identity to nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616; and
- (d) an RNA-guided endonuclease configured to bind to said engineered guide ribonucleic acid.

24. The engineered nuclease system of claim 23, wherein said RNA-guided endonuclease is an Archaeal endonuclease.

25. The engineered nuclease system of claim 23 or 24, wherein said endonuclease has a molecular weight of about 120 kDa or less, 100kDa or less, 90 kDa or less, or 60 kDa or less.

26. The engineered nuclease system of any one of claims 1-25, wherein said engineered guide ribonucleic acid structure comprises at least two ribonucleic acid polynucleotides.

27. The engineered nuclease system of any one of claims 1-26, wherein said engineered guide ribonucleic acid structure comprises a single ribonucleic acid polynucleotide comprising said guide ribonucleic acid sequence and said tracr ribonucleic acid sequence.

28. The engineered nuclease system of any one of claims 1-27, wherein said guide ribonucleic acid sequence is complementary to a prokaryotic, bacterial, archaeal, eukaryotic, fungal, plant, mammalian, or human genomic sequence.

29. The engineered nuclease system of any one of claims 1-28, wherein said guide ribonucleic acid sequence is 15-24 nucleotides in length.

30. The engineered nuclease system of any one of claims 1-29, wherein said endonuclease comprises one or more nuclear localization sequences (NLSs) proximal to an N- or C-terminus of said endonuclease.

31. The engineered nuclease system of any one of claims 1-30, wherein said NLS comprises a sequence selected from SEQ ID NOs: 205-220.

32. The engineered nuclease system of any one of claims 1-31, further comprising a single- or double-stranded DNA repair template comprising from 5' to 3': a first homology arm comprising a sequence of at least 20 nucleotides 5' to said target deoxyribonucleic acid sequence, a synthetic DNA sequence of at least 10 nucleotides, and a second homology arm comprising a sequence of at least 20 nucleotides 3' to said target sequence.

33. The engineered nuclease system of claim 32, wherein said first or second homology arm comprises a sequence of at least 40, 80, 120, 150, 200, 300, 500, or 1,000 nucleotides.

34. The engineered nuclease system of any one of claims 1-33, wherein said system further comprises a source of Mg^{2+} .

35. The engineered nuclease system of any one of claims 1-34, wherein said endonuclease and said target ribonucleic acid sequence are derived from distinct bacterial species within a same phylum.

36. The engineered nuclease system of any one of claims 1-35, wherein said endonuclease comprises a sequence with at least 70% sequence identity to any one of SEQ ID NOs: 2-24 and said guide RNA structure comprises an RNA sequence predicted to comprise a hairpin comprising a stem and a loop, wherein said stem comprises at least 12 pairs of ribonucleotides.

37. The engineered endonuclease system of claim 36, wherein said guide RNA structure further comprises a second stem and a second loop, wherein the second stem comprises at least 5 pairs of ribonucleotides.

38. The engineered endonuclease system of claim 36, wherein said guide RNA structure further comprises an RNA structure comprising at least two hairpins.

39. The engineered nuclease system of any one of claims 1-38, wherein said endonuclease comprises a sequence with at least 70% sequence identity to SEQ ID NO: 1 and

said guide RNA structure comprises an RNA sequence predicted to comprise at least four hairpins comprising a stem and a loop.

40. The engineered nuclease system of any one of claims 1-39, wherein:

- a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 1, 2, 10, 17, or 613-616; and
- b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 199-200 or 669-673 or the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

41. The engineered nuclease system of any one of claims 1-39, wherein:

- a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 1-24, 462-488, or 501-612; and
- b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 199-200 or 669-673 or the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

42. The engineered nuclease system of any one of claims 1-39, wherein:

- a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 2, 10, or 17; and
- b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to the nonvariable nucleotides of any one of SEQ ID NOs: 202-203 or 613-614.

43. The engineered nuclease system of any one of claims 1-39, wherein:

- a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 25-198, 221-459, or 489-580; and
- b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to a class 2, type II sgRNA or tracr sequence.

44. The engineered nuclease system of any one of claims 1-43, wherein said sequence identity is determined by a BLASTP, CLUSTALW, MUSCLE, MAFFT, or CLUSTALW with parameters of the Smith-Waterman homology search algorithm.

45. The engineered nuclease system of claim 44, wherein said sequence identity is determined by said BLASTP homology search algorithm using parameters of a wordlength (W) of 3, an expectation (E) of 10, and a BLOSUM62 scoring matrix setting gap costs at existence of 11, extension of 1, and using a conditional compositional score matrix adjustment.

46. The engineered nuclease system of any one of claims 1-45, wherein said endonuclease is not a Cas9 endonuclease, a Cas14 endonuclease, a Cas12a endonuclease, a Cas12b endonuclease, a Cas 12c endonuclease, a Cas12d endonuclease, a Cas12e endonuclease, a Cas13a endonuclease, a Cas13b endonuclease, a Cas13c endonuclease, or a Cas 13d endonuclease.

47. The engineered nuclease system of claim 46, wherein said endonuclease has less than 80% identity to a Cas9 endonuclease.

48. An engineered single guide ribonucleic acid polynucleotide comprising:

- a) a DNA-targeting segment comprising a nucleotide sequence that is complementary to a target sequence in a target DNA molecule; and
- b) a protein-binding segment comprising two complementary stretches of nucleotides that hybridize to form a double-stranded RNA (dsRNA) duplex,

wherein said two complementary stretches of nucleotides are covalently linked to one another with intervening nucleotides, and

wherein said engineered guide ribonucleic acid polynucleotide is configured to form a complex with an endonuclease comprising a variant having at least 75% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

49. The engineered guide ribonucleic acid polynucleotide of claim 48, wherein said DNA-targeting segment is positioned 5' of both of said two complementary stretches of nucleotides.

50. The engineered guide ribonucleic acid polynucleotide of any of claims 48-49, wherein:

- a) said protein binding segment comprises a sequence having at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 199-200 or 669-673;
- b) said protein binding segment comprises a sequence having at least 70%, at least 80%, or at least 90% identical to the nonvariable nucleotides of any one of SEQ ID NOs: 201-203 or 613-616.

51. The engineered nuclease system of any one of claims 48-49, wherein:

- a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 2, 10, or 17; and
- b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to at least one of SEQ ID NO: 200 or the nonvariable nucleotides of SEQ ID NO: 202-203 or 613-614.

52. The engineered nuclease system of any one of claims 48-49, wherein:

- a) said endonuclease comprises a sequence at least 70%, at least 80%, or at least 90% identical to any one of SEQ ID NOs: 25-198, 221-459, or 489-580; and
- b) said guide RNA structure comprises a sequence at least 70%, at least 80%, or at least 90% identical to a class 2, type II sgRNA.

53. The engineered nuclease system of any one of claims 1-52, wherein said endonuclease further comprises a base editor or a histone editor coupled to said endonuclease.

54. The engineered nuclease system of claim 53, wherein said base editor is an adenosine deaminase.

55. The engineered nuclease system of claim 54, wherein said adenosine deaminase comprises ADAR1 or ADAR2.

56. The engineered nuclease system of claim 53, wherein said base editor is a cytosine deaminase.

57. The engineered nuclease system of claim 56, wherein said cytosine deaminase comprises APOBEC1, APOBEC2, APOBEC3A, APOBEC3B, APOBEC3C, APOBEC3D, APOBEC3F, APOBEC3G, APOBEC3H, or APOBEC4.

58. A deoxyribonucleic acid polynucleotide encoding the engineered guide ribonucleic acid polynucleotide of any one of claims 48-57.

59. A nucleic acid comprising an engineered nucleic acid sequence optimized for expression in an organism, wherein said nucleic acid encodes a class 2, type II Cas endonuclease comprising a RuvC domain and an HNH domain, wherein said endonuclease is derived from an uncultivated microorganism, and wherein said endonuclease has a molecular weight of about 120 kDa or less, 100kDa or less, 90 kDa or less, 60 kDa or less, or 30 kDa or less.

60. The nucleic acid of claim 59, wherein said endonuclease comprises SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668 or a variant thereof having at least 70% sequence identity thereto.

61. The nucleic acid of any one of claims 59-60, wherein said endonuclease further comprises a sequence encoding one or more nuclear localization sequences (NLSs) proximal to an N- or C-terminus of said endonuclease.

62. The nucleic acid of claim 61, wherein said NLS comprises a sequence selected from SEQ ID NOs: 205-220.

63. The nucleic acid of any one of claims 59-62, wherein said organism is prokaryotic, bacterial, eukaryotic, fungal, plant, mammalian, rodent, or human.

64. The nucleic acid of claim 63, wherein said organism is prokaryotic or bacterial, and said organism is a different organism from an organism from which said endonuclease is derived.

65. The nucleic acid of claim 63, wherein said organism is not said uncultivated microorganism.

66. A vector comprising a nucleic acid sequence encoding an RNA-guided endonuclease comprising a RuvC-I domain and an HNH domain, wherein said endonuclease is derived from an uncultivated microorganism, and wherein said endonuclease has a molecular weight of about 120 kDa or less, 100kDa or less, 90 kDa or less, or 60 kDa or less, wherein the RNA-guided endonuclease is optionally archaeal.

67. The vector of claim 66, wherein said endonuclease further comprises an arginine-rich region comprising an RRxRR motif or a domain with PF14239 homology.

68. The vector of claim 66 or claim 67, wherein said endonuclease further comprises a REC (recognition) domain.

69. The vector of claim 67 or claim 68, wherein said endonuclease further comprises a BH domain, a WED domain, and a PI domain.

70. A vector comprising the nucleic acid of any of claims 59-69.

71. The vector of claim any one of claims 67-70, further comprising a nucleic acid encoding an engineered guide ribonucleic acid structure configured to form a complex with said endonuclease, said engineered guide ribonucleic acid structure comprising:

- a) a guide ribonucleic acid sequence configured to hybridize to a target deoxyribonucleic acid sequence; and
- b) a tracr ribonucleic acid sequence configured to binding to said endonuclease.

72. The vector of any of claims 66-71, wherein the vector is a plasmid, a minicircle, a CELiD, an adeno-associated virus (AAV) derived virion, or a lentivirus.

73. A cell comprising the vector of any of claims 66-72.

74. The cell of claim 73, wherein said cell is a bacterial, archaeal, fungal, eukaryotic, mammalian, or plant cell.

75. The cell of claim 74, wherein said cell is a bacterial cell.

76. A method of manufacturing an endonuclease, comprising cultivating said cell of any one of claims 73-75.

77. A method for binding, cleaving, marking, or modifying a double-stranded deoxyribonucleic acid polynucleotide, comprising:

(e) contacting said double-stranded deoxyribonucleic acid polynucleotide with a class 2, type II Cas endonuclease in complex with an engineered guide ribonucleic acid structure configured to bind to said endonuclease and said double-stranded deoxyribonucleic acid polynucleotide;

(f) wherein said double-stranded deoxyribonucleic acid polynucleotide comprises a protospacer adjacent motif (PAM);

wherein said endonuclease has a molecular weight of about 120 kDa or less, 100 kDa or less, 90 kDa or less, or 60 kDa or less.

78. The method of claim 77, wherein said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide, wherein said PAM comprises NGG.

79. The method of claim 77 or claim 78, wherein said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide 6-8 nucleotides or 7 nucleotides from said PAM.

80. The method of claim 77, wherein said endonuclease comprises a variant with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

81. A method for binding, cleaving, marking, or modifying a double-stranded deoxyribonucleic acid polynucleotide, comprising:

(g) contacting said double-stranded deoxyribonucleic acid polynucleotide with an RNA-guided archaeal endonuclease in complex with an engineered guide ribonucleic acid structure configured to bind to said endonuclease and said double-stranded deoxyribonucleic acid polynucleotide;

(h) wherein said double-stranded deoxyribonucleic acid polynucleotide comprises a protospacer adjacent motif (PAM); and

wherein said endonuclease comprises a variant with at least 70%, at least 75%, at least 80% or at least 90% sequence identity to any one of SEQ ID NOs: 1-198, 221-459, 463-612, or 617-668.

82. The method of claim 81, wherein said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide, wherein said PAM comprises NGG.

83. The method of claim 81 or claim 82, wherein said endonuclease cleaves said double-stranded deoxyribonucleic acid polynucleotide 6-8 or 7 nucleotides from said PAM.

84. The method of any one of claims 77-83, wherein said class 2, type II Cas endonuclease is not a Cas9 endonuclease, a Cas14 endonuclease, a Cas12a endonuclease, a Cas12b endonuclease, a Cas 12c endonuclease, a Cas12d endonuclease, a Cas12e endonuclease, a Cas13a endonuclease, a Cas13b endonuclease, a Cas13c endonuclease, or a Cas 13d endonuclease.

85. The method of any one of claims 77-84, wherein said class 2, type II Cas endonuclease is derived from an uncultivated microorganism.

86. The method of any one of claims 77-85, wherein said double-stranded deoxyribonucleic acid polynucleotide is a prokaryotic, archaeal, bacterial, eukaryotic, plant, fungal, mammalian, rodent, or human double-stranded deoxyribonucleic acid polynucleotide.

87. The method of claim 86, wherein said double-stranded deoxyribonucleic acid polynucleotide is a prokaryotic, archaeal, or bacterial double-stranded deoxyribonucleic acid polynucleotide from a species other than a species from which said endonuclease was derived.

88. A method of modifying a target nucleic acid locus, said method comprising delivering to said target nucleic acid locus said engineered nuclease system of any one of claims 1-47, wherein said endonuclease is configured to form a complex with said engineered guide ribonucleic acid structure, and wherein said complex is configured such that upon binding of said complex to said target nucleic acid locus, said complex modifies said target nucleic locus.

89. The method of claim 88, wherein modifying said target nucleic acid locus comprises binding, nicking, cleaving, or marking said target nucleic acid locus.

90. The method of claim 88 or claim 89, wherein said target nucleic acid locus comprises deoxyribonucleic acid (DNA) or ribonucleic acid (RNA).

91. The method of claim 90, wherein said target nucleic acid comprises genomic eukaryotic DNA, archaeal DNA, viral DNA, or bacterial DNA.

92. The method of claim 91, wherein said target nucleic acid comprises bacterial DNA wherein said bacterial DNA is derived from a bacterial or archaeal species different from a species from which said endonuclease was derived.

93. The method of any one of claims 88-92, wherein said target nucleic acid locus is *in vitro*.

94. The method of any one of claims 88-92, wherein said target nucleic acid locus is within a cell.

95. The method of claim 94, wherein said endonuclease and said engineered guide nucleic acid structure are encoded by separate nucleic acid molecules.

96. The method of claim 94 or 95, wherein said cell is a prokaryotic cell, a bacterial cell, an archaeal cell, a eukaryotic cell, a fungal cell, a plant cell, an animal cell, a mammalian cell, a rodent cell, a primate cell, or a human cell.

97. The method of claim 94 or 95, wherein said cell is derived from a species different from a species from which said endonuclease was derived.

98. The method of any one of claims 94-97, wherein delivering said engineered nuclease system to said target nucleic acid locus comprises delivering the nucleic acid of any of claims 59-64 or the vector of any of claims 65-72.

99. The method of any one of claims 88-98, wherein delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a nucleic acid comprising an open reading frame encoding said endonuclease.

100. The method of claim 99, wherein said nucleic acid comprises a promoter to which said open reading frame encoding said endonuclease is operably linked.

101. The method of any one of claims 97-100, wherein delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a capped mRNA containing said open reading frame encoding said endonuclease.

102. The method of any one of claims 88-95, wherein delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a translated polypeptide.

103. The method of any one of claims 88-101, wherein delivering said engineered nuclease system to said target nucleic acid locus comprises delivering a deoxyribonucleic acid (DNA) encoding said engineered guide ribonucleic acid structure operably linked to a ribonucleic acid (RNA) pol III promoter.

104. The method of any one of claims 88-103, wherein said endonuclease induces a single-stranded break or a double-stranded break at or proximal to said target locus.

105. The method of claim 104, wherein said endonuclease induces a double stranded break proximal to said target locus 5' from a protospacer adjacent motif (PAM).

106. The method of claim 105, wherein said endonuclease induces a double-stranded break 6-8 nucleotides or 7 nucleotides 5' from said PAM.

107. The method of any one of claims 88-103, wherein said engineered nuclease system induces a chemical modification of a nucleotide base within or proximal to said target locus.

108. The method of claim 107, wherein said chemical modification is deamination of an adenosine or a cytosine nucleotide.

109. The engineered nuclease system of any one of claims 88-103, wherein said endonuclease further comprises a base editor coupled to said endonuclease.

110. The engineered nuclease system of claim 109, wherein said base editor is an adenosine deaminase.

111. The engineered nuclease system of claim 110, wherein said adenosine deaminase comprises ADAR1 or ADAR2.

112. The engineered nuclease system of claim 109, wherein said base editor is a cytosine deaminase.

113. The engineered nuclease system of claim 112, wherein said cytosine deaminase comprises APOBEC1, APOBEC2, APOBEC3A, APOBEC3B, APOBEC3C, APOBEC3D, APOBEC3F, APOBEC3G, APOBEC3H, or APOBEC4.

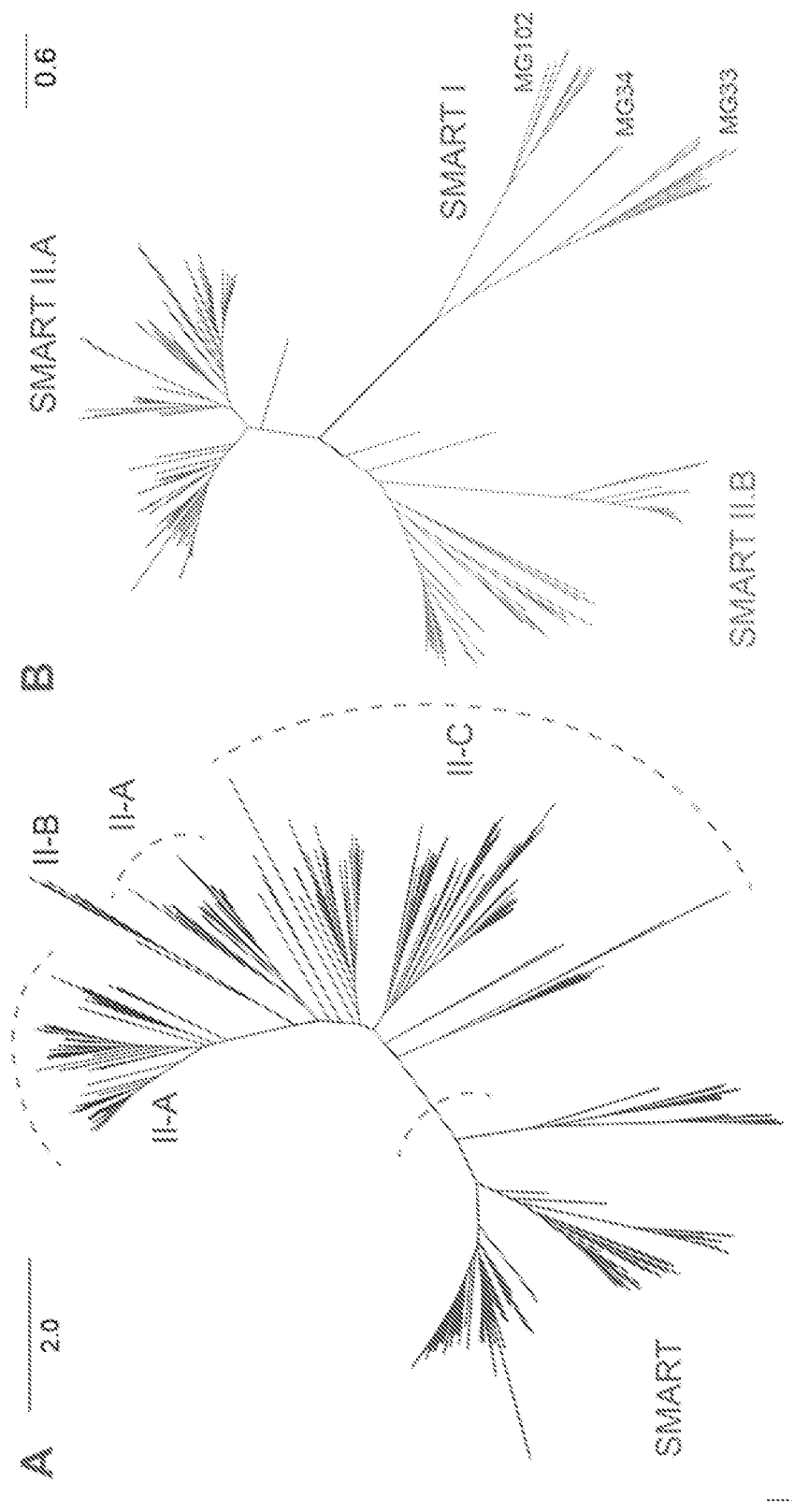


FIGURE 1

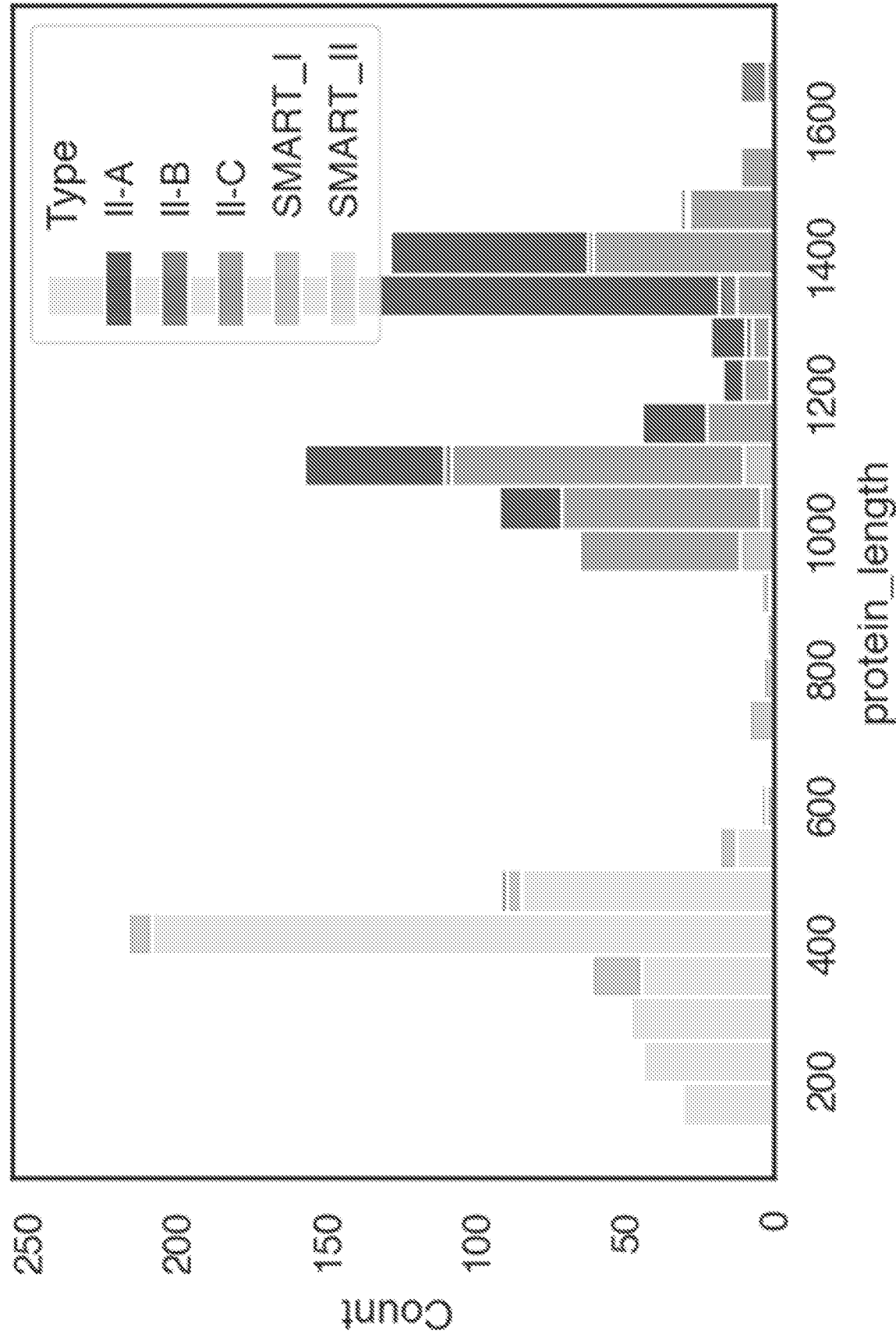


FIGURE 2

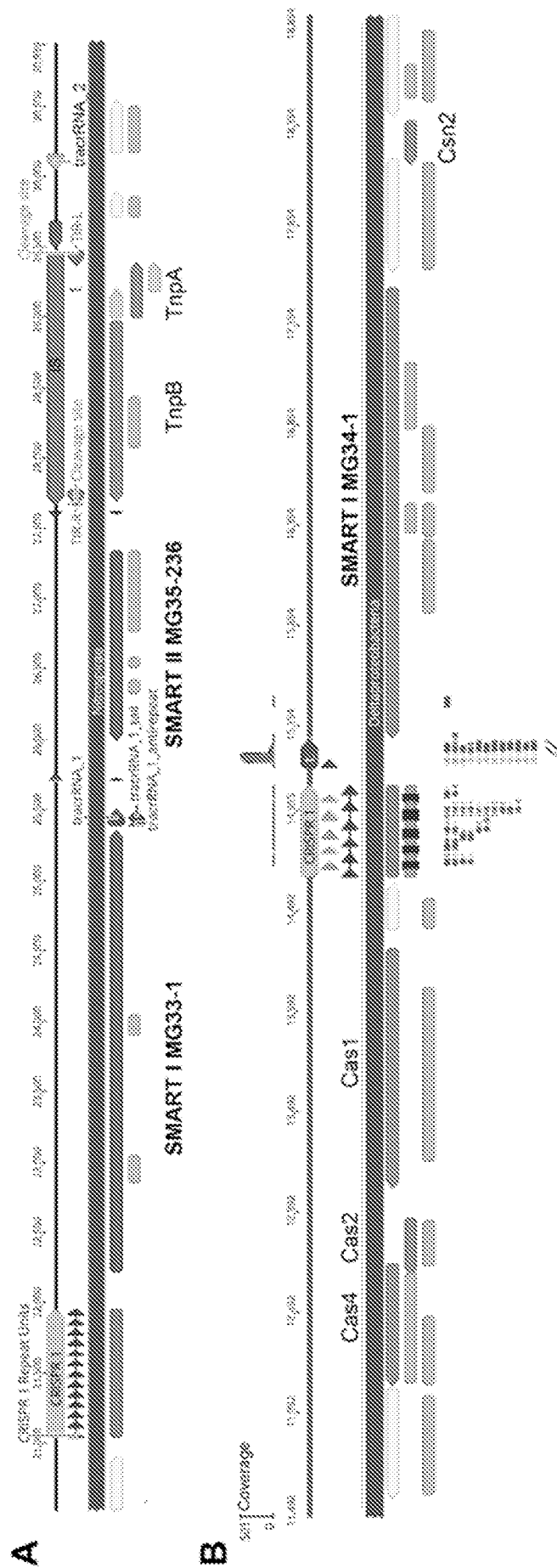


FIGURE 3

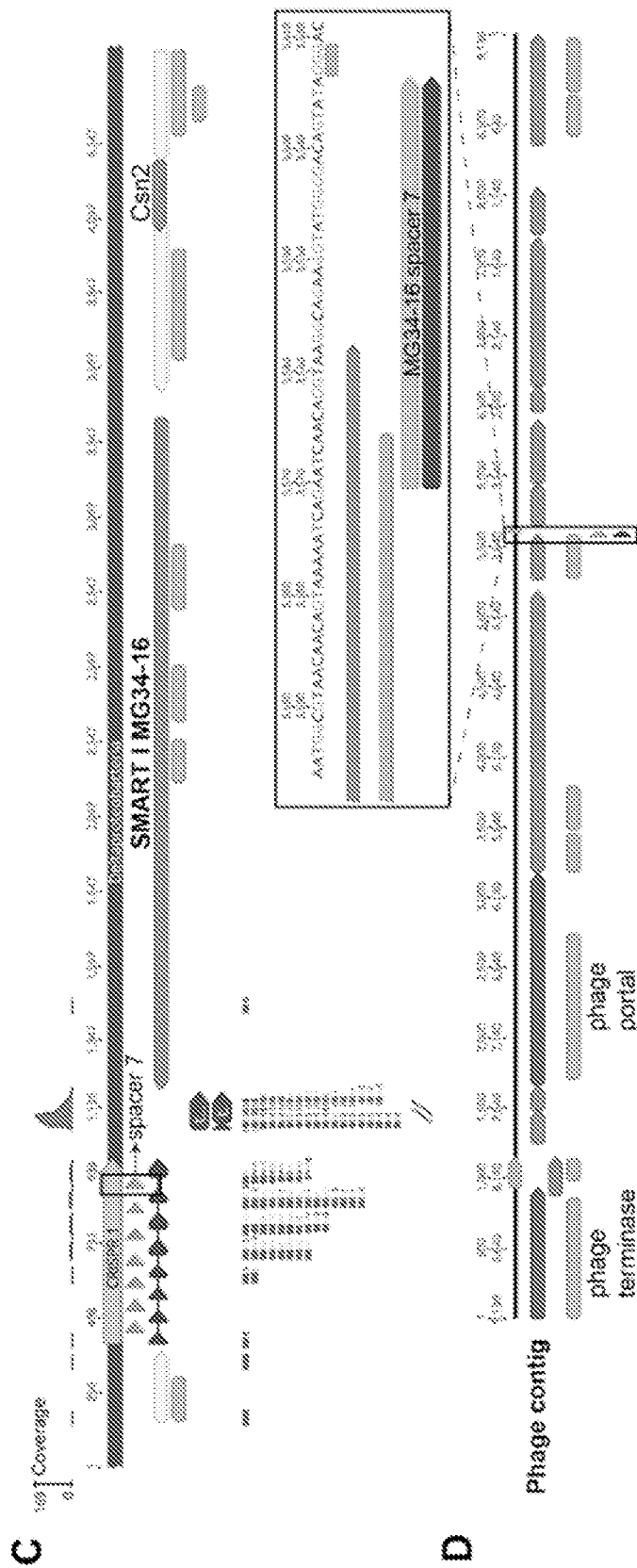


FIGURE 3 CONT'D

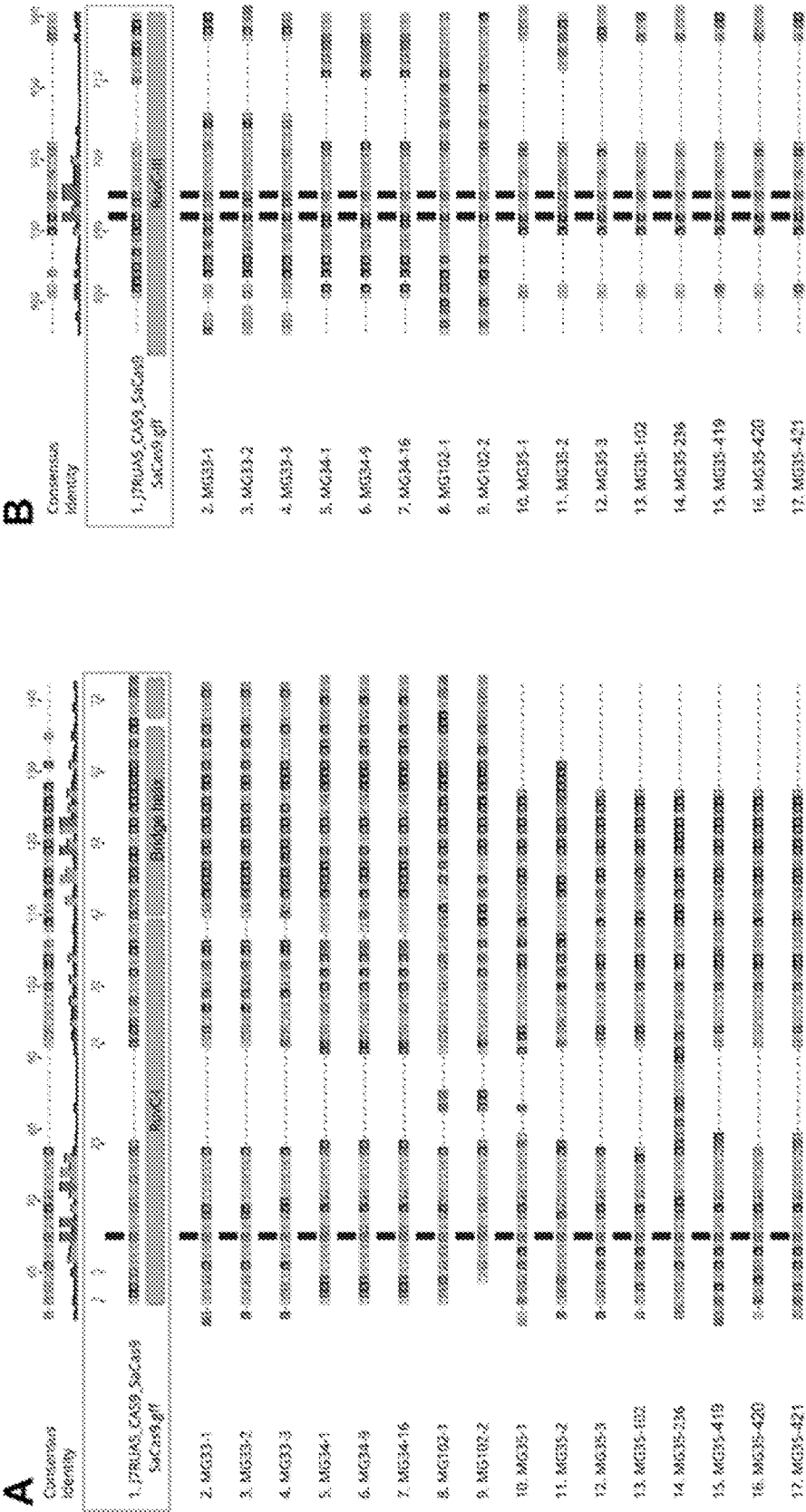


FIGURE 4

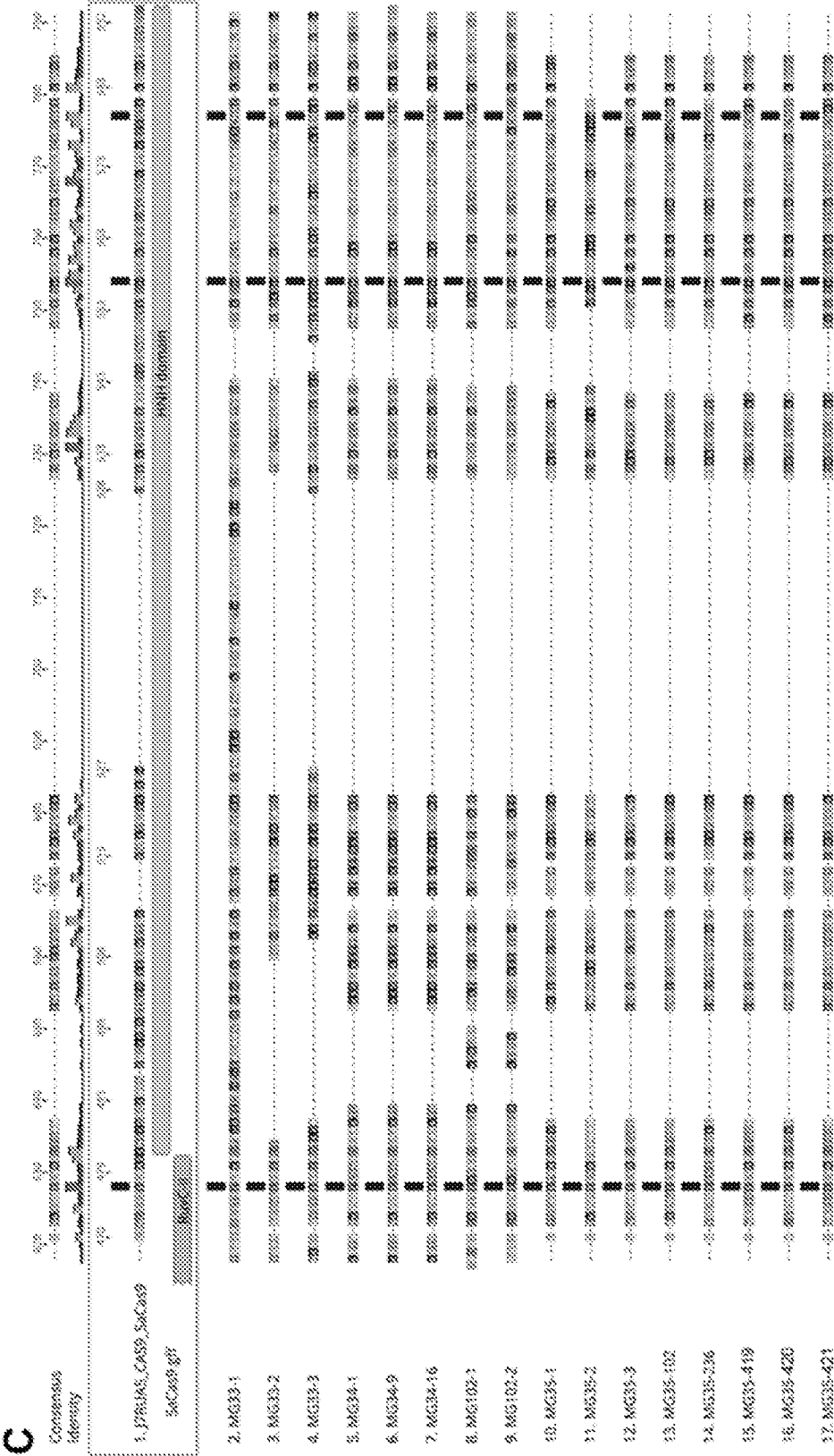


FIGURE 4 CONT'D

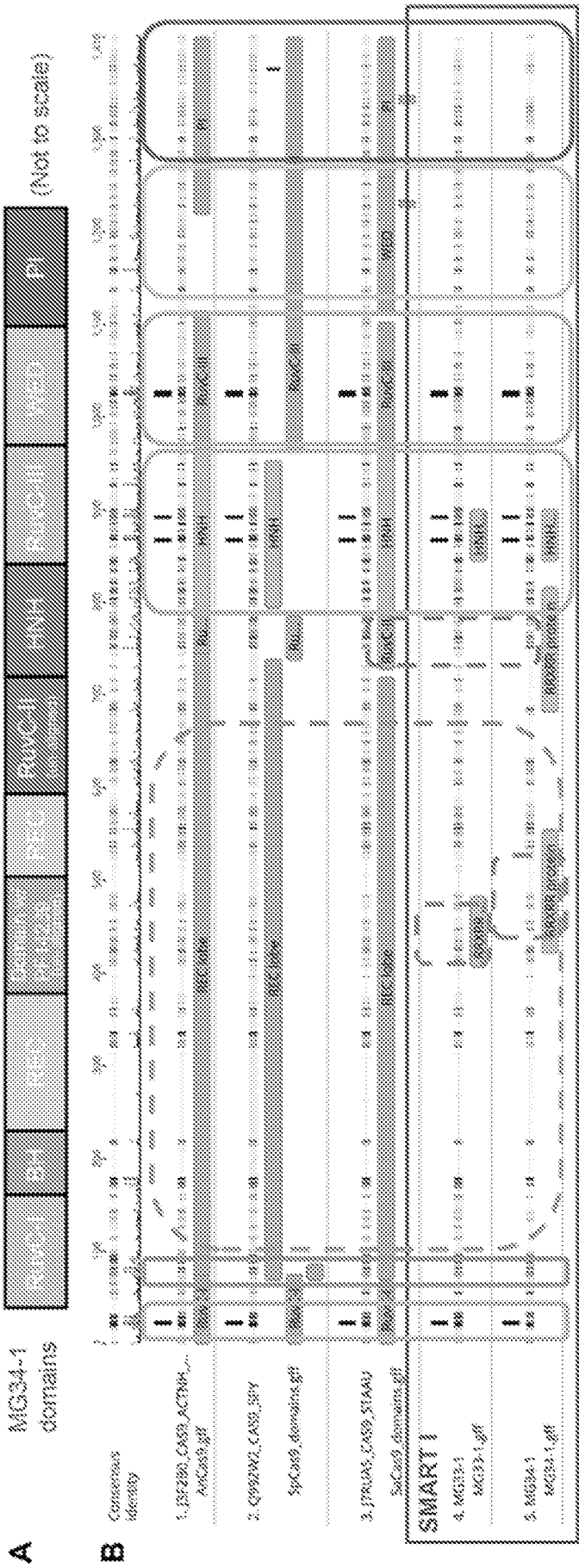


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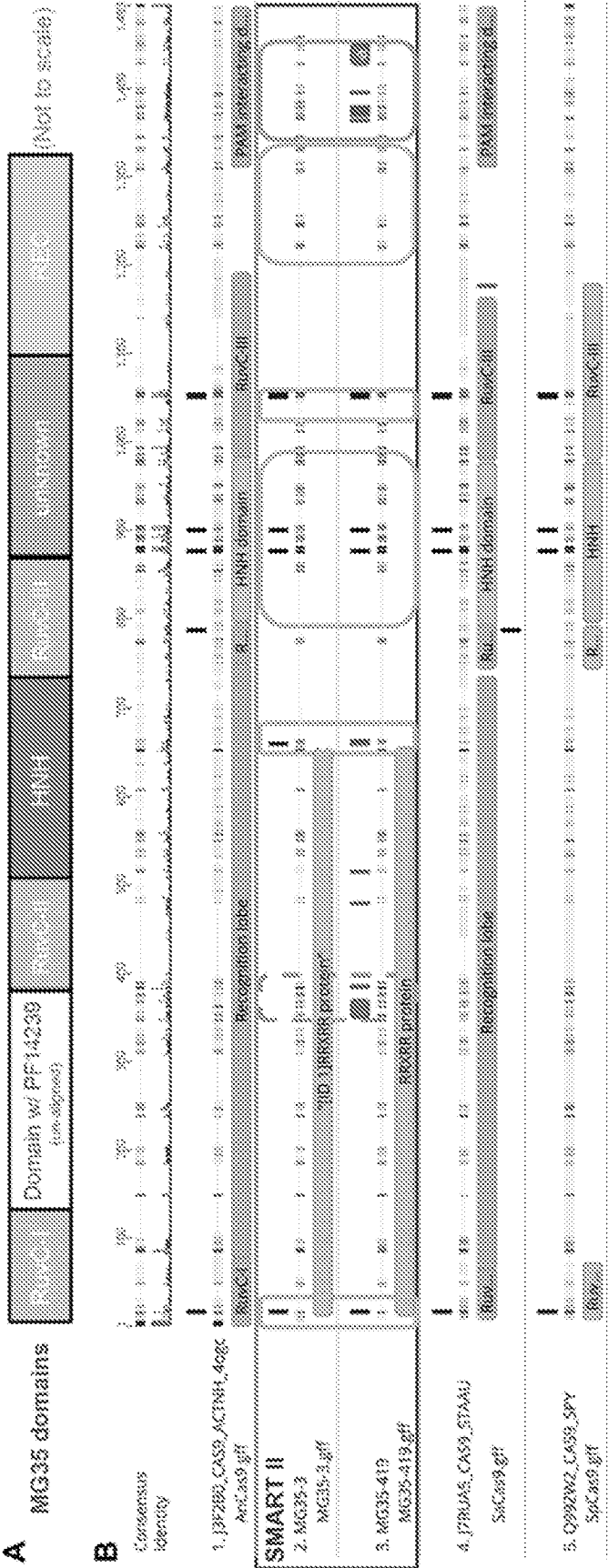


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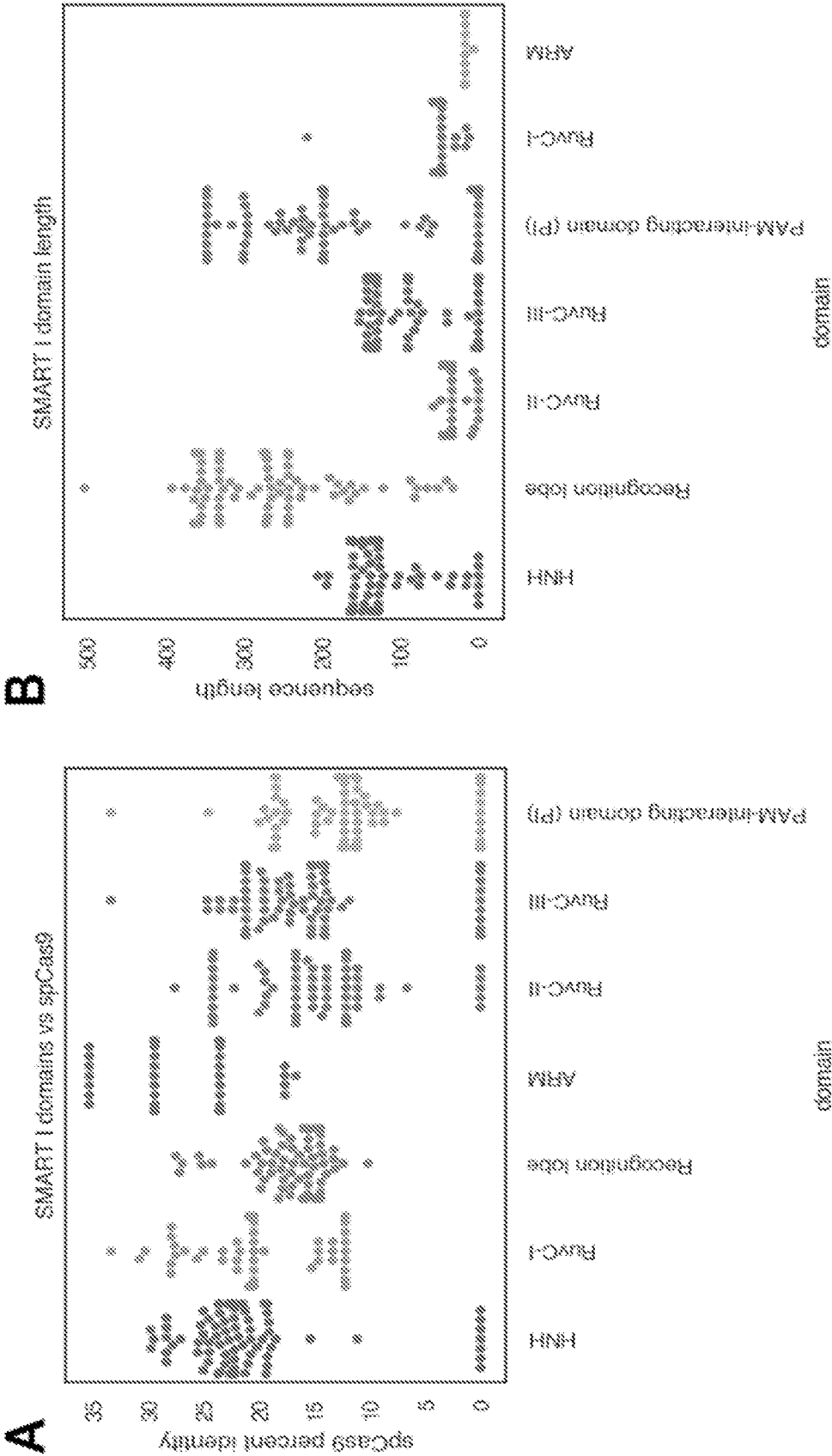


FIGURE 7

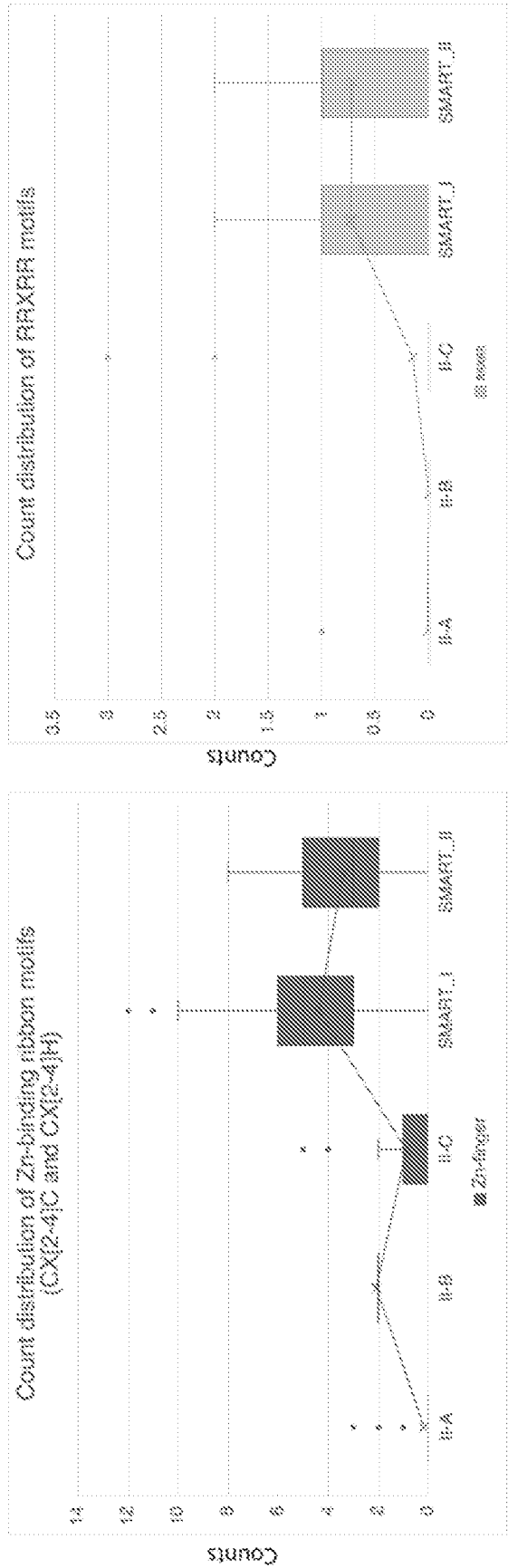


FIGURE 8

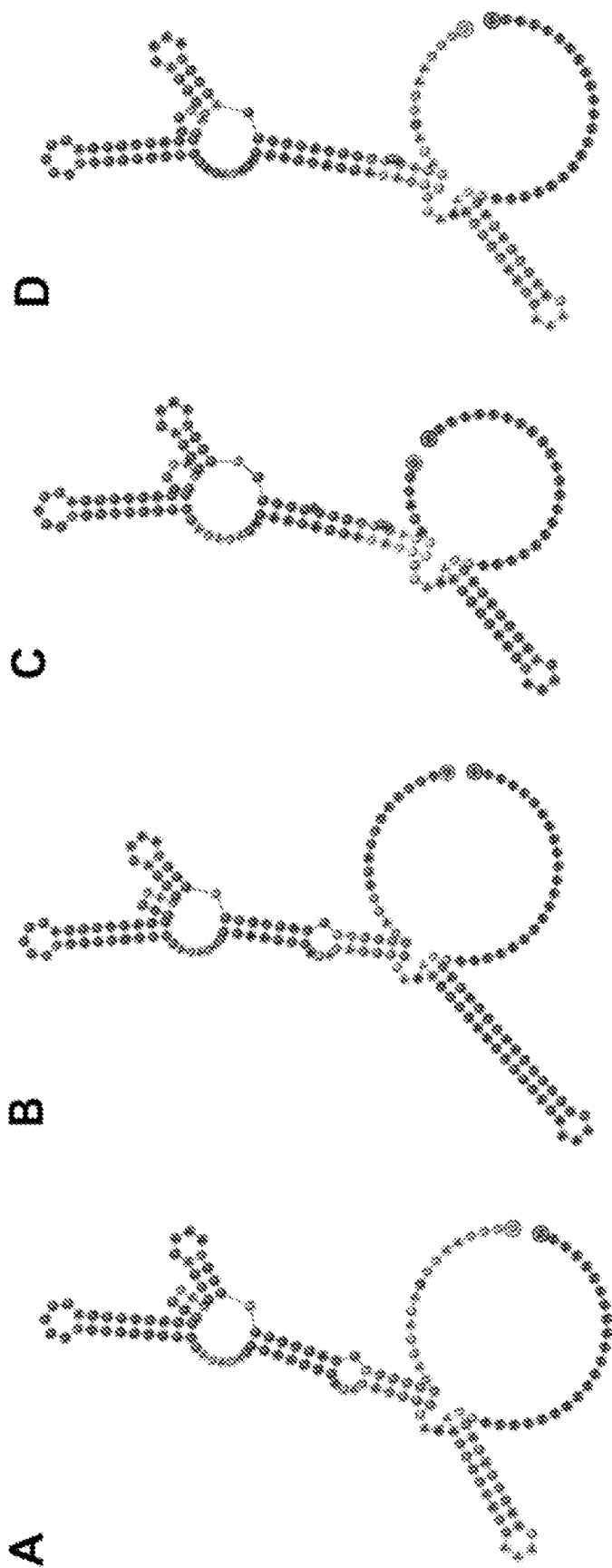


FIGURE 9

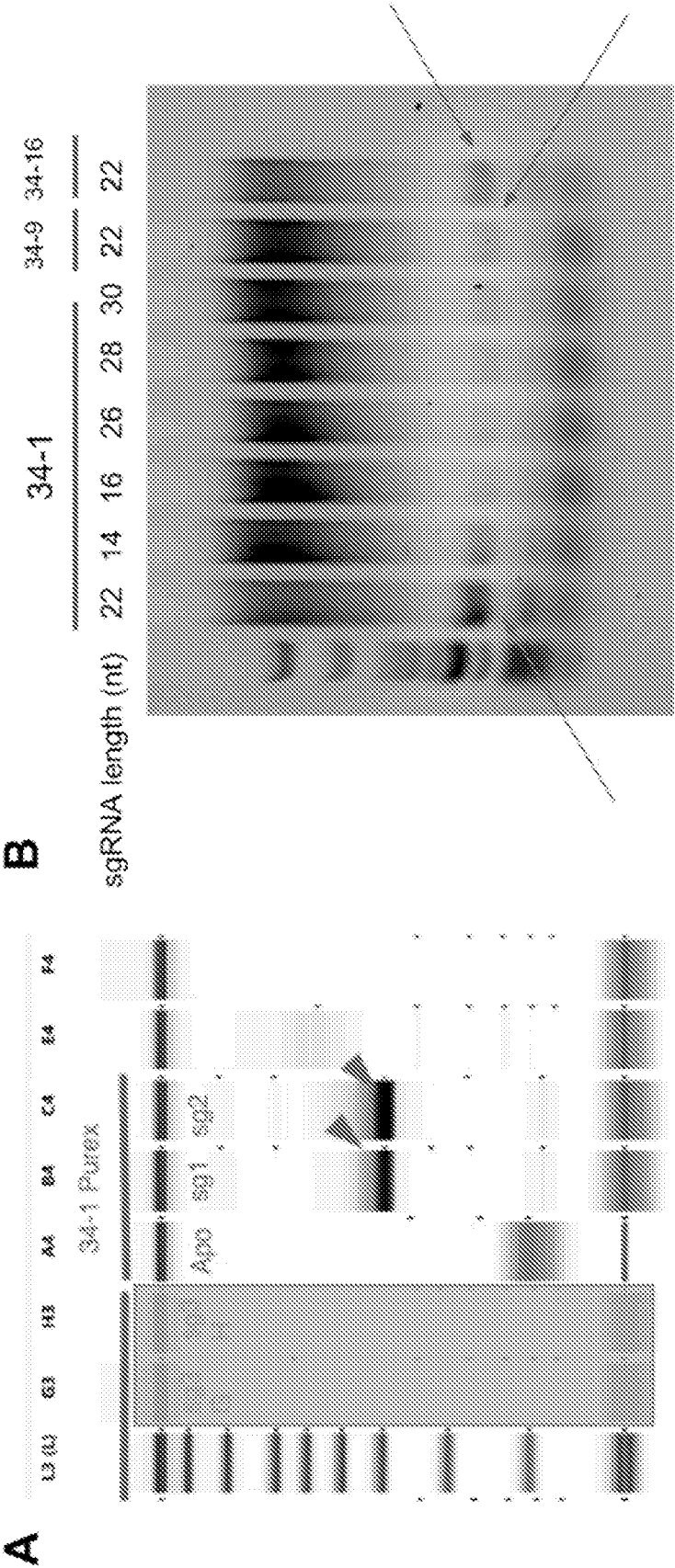


FIGURE 10

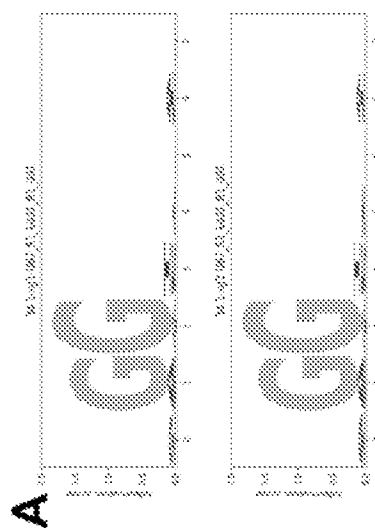
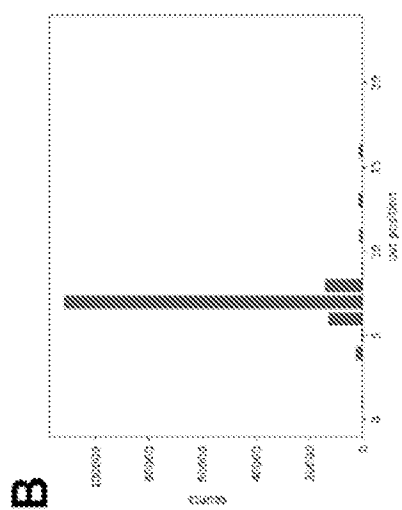
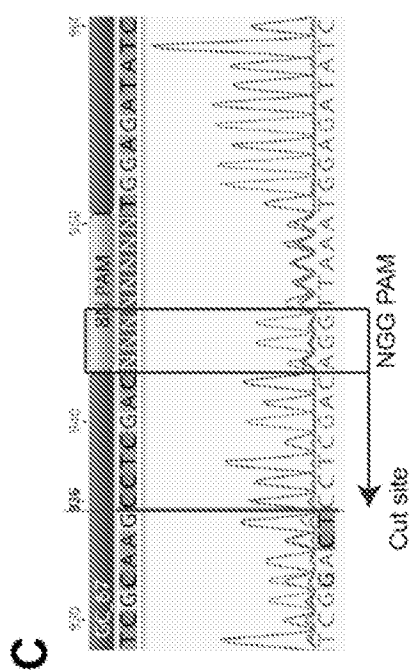


FIGURE 11

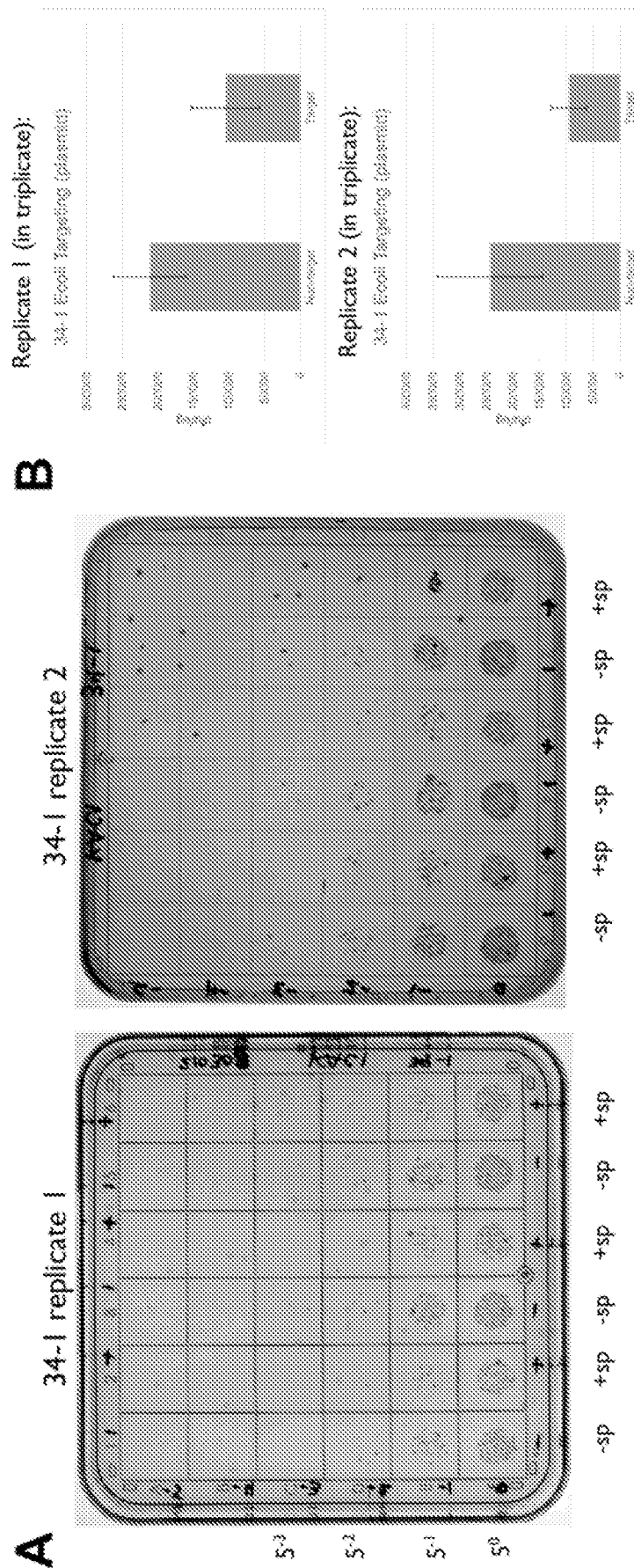


FIGURE 12

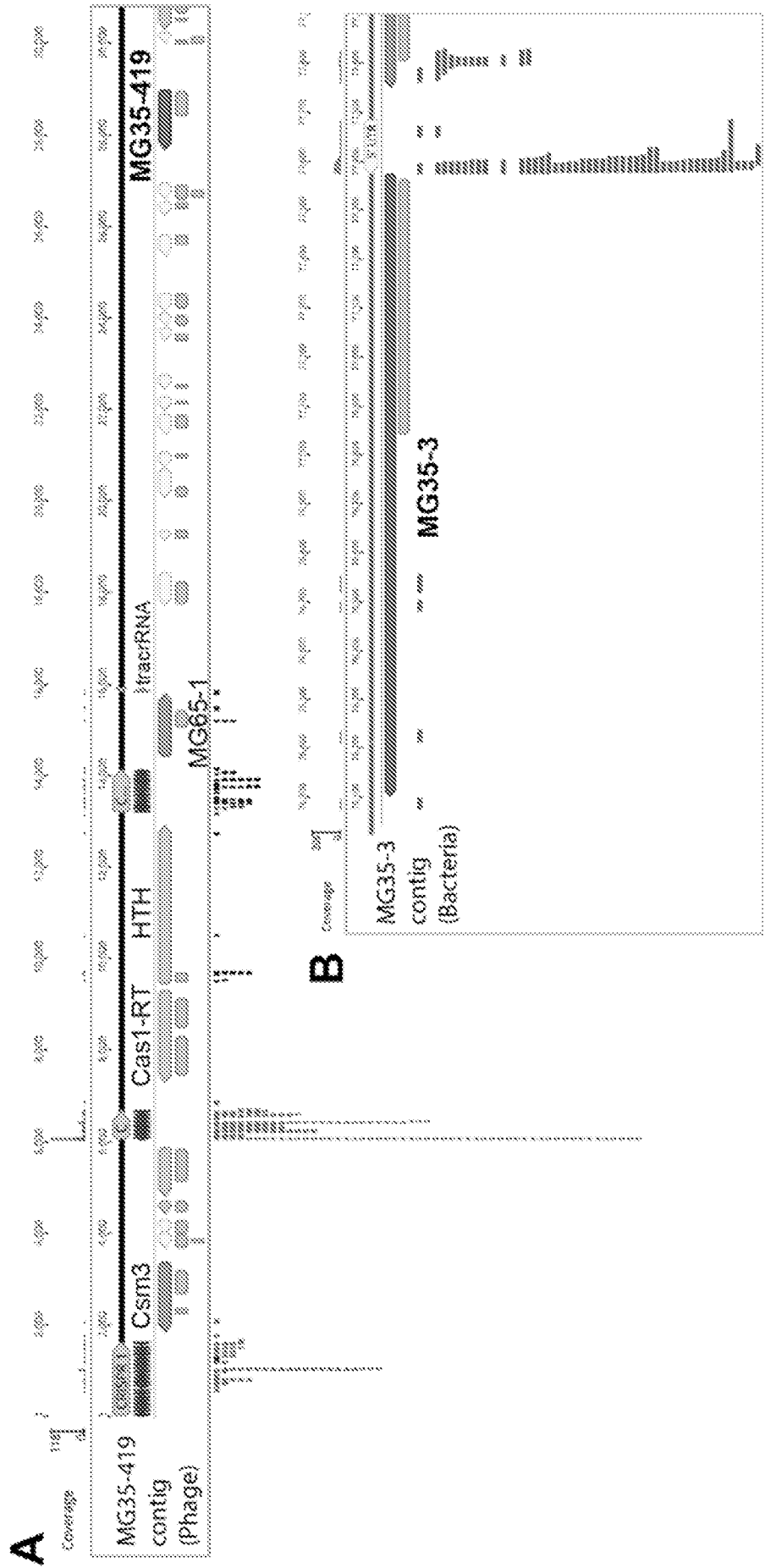


FIGURE 13

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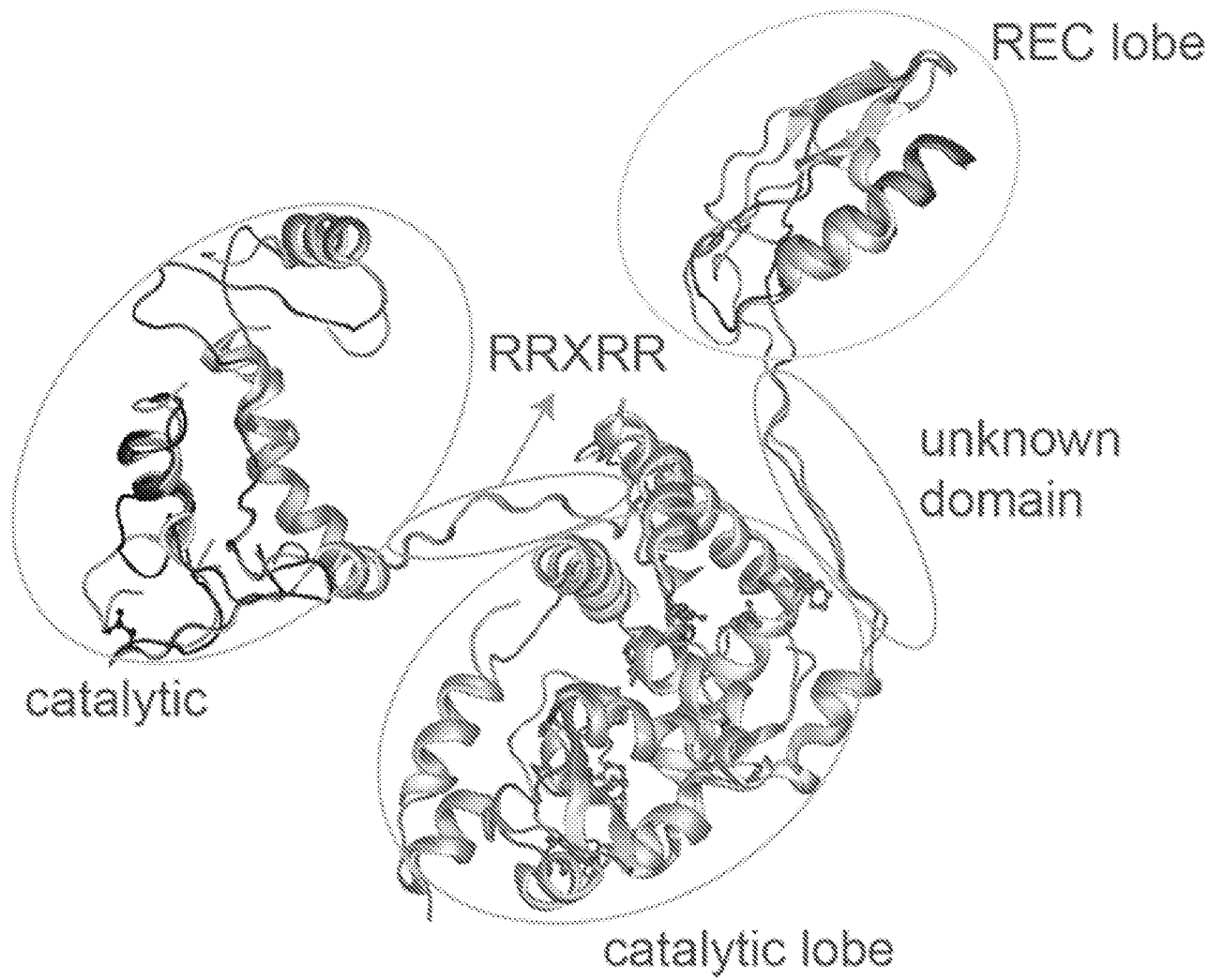


FIGURE 14

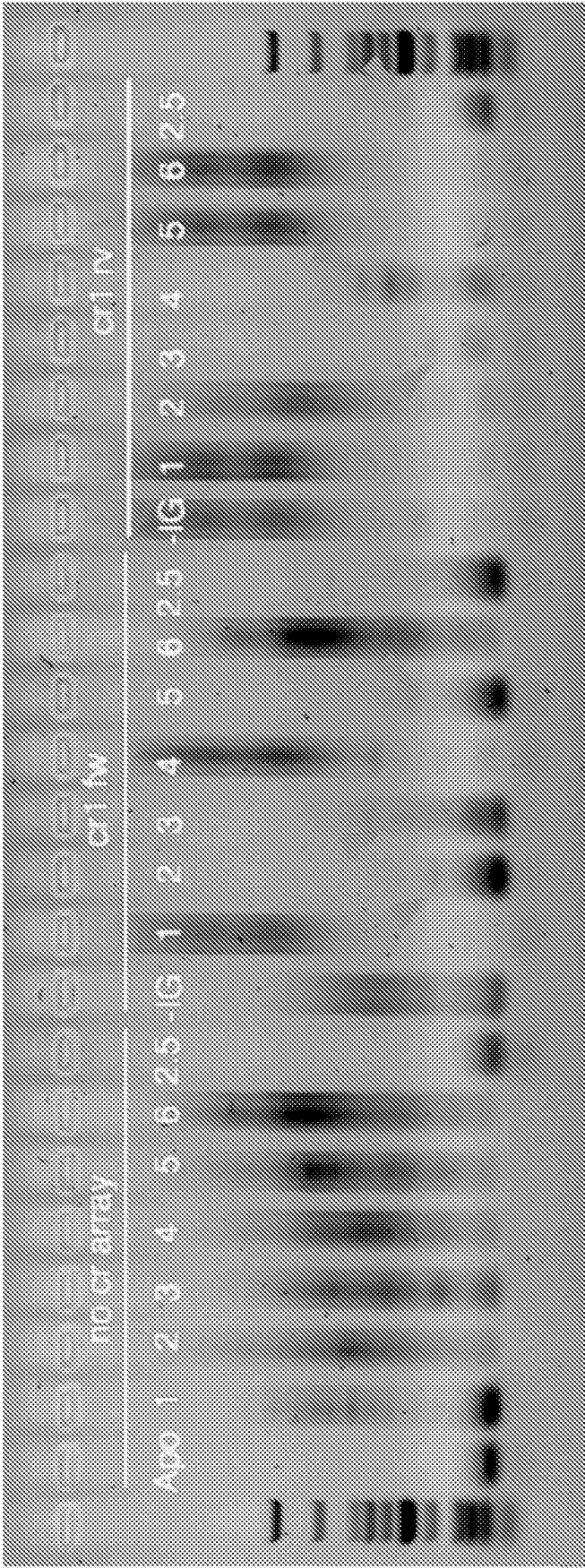


FIGURE 15

SEQUENCE LISTING

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Thr	Arg	Arg	Ala	Lys	Lys	Ser	Arg	Ile	Ala	Arg	Leu	Arg	Ser	Trp	Ile

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935

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Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys

245

250

255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
 260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
 275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
 290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
 305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
 325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
 340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
 355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
 370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Ala Val Cys Asn Glu Asn
 385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Ser Pro Lys Pro Glu
 405 410 415

Ile Ile Ala Phe Met Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
 420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
 435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly
 450 455 460

Asn Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr
465 470 475 480

Phe Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His
485 490 495

His Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp
500 505 510

Asp Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly
515 520 525

Glu Phe Asp Pro Glu Lys His Leu Pro Glu Pro Ile Glu Phe Lys Met
530 535 540

Asp Lys Gly Ser Arg Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser
545 550 555 560

Tyr Lys Lys Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu
565 570 575

Cys Gly Lys Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu
580 585 590

Lys Glu Ala Phe Lys Arg Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr
595 600 605

Asp Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys Asn Glu Leu
610 615 620

Val Met Ser Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met
625 630 635 640

Ile Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly
645 650 655

Val Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Ala Tyr Glu Arg
660 665 670

Lys Asn Pro Arg Leu Ser Lys His Phe Ile Glu Pro Pro Pro Gln Pro

675

680

685

Asn Gly Arg Val Ser Phe Thr Leu Lys Arg Arg Asp Met Val Thr Val
 690 695 700

Glu Gly Glu Asp Ala Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro
 705 710 715 720

Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser
 725 730 735

Ala Thr Lys Leu Thr Lys Ala Asn Ser Ala Glu
 740 745

<210> 3

<211> 145

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-2 effector

<400> 3

Ala Gly Phe Val Val Arg Lys Ser Gly Gln Met Met Ser Leu Lys Cys
 1 5 10 15

Tyr Ala Asp Ile Arg Thr Asp Glu Thr Gly Lys Lys Gln Ser Leu Gly
 20 25 30

Thr Gly Trp Ala Gln Ile Val Asn Ile Lys Asn Asn Ala Phe Lys Thr
 35 40 45

Asn Val His Asn Ile Gly Val Ala Val Tyr Leu Asp Glu Lys Gly Lys
 50 55 60

Lys Lys Ala Tyr Lys Leu Lys Asn Pro Arg Met Ser Lys His Phe Val
 65 70 75 80

Glu Arg Gln Glu Gln Ile Lys Ser Lys Ile Leu Phe Thr Leu Lys Arg
85 90 95

Gly Asp Met Val Ser Val Glu Gly Glu Asp Thr Ile Tyr Arg Ile Lys
100 105 110

Lys Leu Gly Thr Ser Pro Val Ile Glu Lys Val Val Gly Ser Asp Gly
115 120 125

Lys Thr Arg Pro Val Ser Ala Thr Lys Leu Thr Lys Ala Asn Asn Ala
130 135 140

Glu
145

<210> 4
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-3 effector

<400> 4
Cys Asn Glu Gly Lys Arg Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu
1 5 10 15

Pro Lys Pro Glu Ile Val Ser Phe Ile Thr Asn Asp Leu Lys Lys Lys
20 25 30

Ile Leu Glu Asp Ala Gln Tyr Ile Asn Thr Leu Asp Phe Asn Lys Tyr
35 40 45

Met Ser His Ala Ser Ile Gly Trp Arg His Met Arg Asp Arg Leu Arg
50 55 60

Glu Leu Thr Gly Asn Lys Glu Leu Leu Ile Lys Arg Gln Ser Gly Ile

65	70					75					80				
Tyr	Thr	Ala	Tyr	Phe	Arg	Lys	Trp	Trp	Gly	Phe	Ile	Lys	Glu	Arg	Gly
				85					90					95	
Asn	His	Gly	His	His	Ala	Leu	Asp	Ala	Val	Ile	Leu	Ala	Ser	Lys	Lys
			100					105					110		
Ser	Tyr	Ala	Glu	Asp	Gly	Lys	Val	Asp	Met	Thr	Ile	Lys	Pro	Cys	Gly
		115					120					125			
Glu	Asp	Gly	Lys	Glu	Phe	Asp	Ile	Glu	Arg	His	Leu	Ser	Glu	Met	Lys
	130					135					140				
Glu	Phe	Arg	Arg	Asp	Lys	Gly	Gly	Lys	Ser	Ala	Pro	Leu	His	Asp	Arg
145					150					155					160
Asn	Pro	Leu	Ser	Phe	Lys	Asn	Asp	Ile	Ile	Thr	Arg	Arg	Phe	Met	Val
				165					170					175	
Thr	Glu	Ile	Glu	Cys	Gly	Lys	Glu	Ala	Val	Ile	Ile	Ser	Glu	Glu	Tyr
			180					185					190		
Arg	Lys	Lys	Leu	Thr	Glu	Ala	Phe	Lys	Arg	Phe	Gly	Ile	Ala	Lys	Gly
		195					200					205			
Lys	Tyr	Leu	Thr	Asp	Glu	Gln	Ala	Lys	Asp	Ala	Gly	Phe	Tyr	Leu	Arg
	210					215					220				
Lys	Asn	Gly	Glu	Gly	Val	Met	Ser	Leu	Lys	Cys	Glu	Val	Lys	Gly	Thr
225					230					235					240
Gly	Tyr	Asn	Gln	Met	Ile	Arg	Ile	Lys	Asn	Asn	Ile	Phe	Lys	Thr	Asn
				245					250					255	
Val	His	Asn	Val	Gly	Val	Ala	Val	Phe	Leu	Asp	Glu	Lys	Gly	Lys	Lys
			260					265					270		
Arg	Ala	Cys	Glu	Leu	Lys	Asn	Pro	Arg	Leu	Ser	Lys	His	Phe	Val	Lys
		275					280					285			

Pro Ala Glu Gln Val Lys Gly Lys Val Ile Phe Ile Leu Lys Arg Gly
290 295 300

Asn Met Val Thr Val Glu Gly Glu Glu Met Ile Tyr Arg Val Lys Lys
305 310 315 320

Leu Gly Thr Ser Pro Val Ile Glu Ala Ile Val Gly Ser Asp Gly Lys
325 330 335

Thr Arg Thr Val Ser Ala Thr Lys Leu Leu Lys Ile Asn His Thr Lys
340 345 350

Lys Val

<210> 5
<211> 110
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-4 effector

<400> 5
Gly Gln Met Ile Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His
1 5 10 15

Asn Val Gly Val Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Ala
20 25 30

Tyr Glu Arg Lys His Pro Arg Leu Ser Lys His Phe Ile Glu Pro Pro
35 40 45

Pro Gln Pro Asn Gly Arg Val Ser Phe Thr Leu Lys Arg Arg Asp Met
50 55 60

Val Thr Val Glu Gly Glu Asp Ala Ile Tyr Arg Ile Lys Lys Leu Gly

65

70

75

80

Thr Ser Pro Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg
 85 90 95

Thr Val Ser Ala Thr Lys Leu Thr Lys Ala Asn Ser Ala Glu
 100 105 110

<210> 6

<211> 372

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-5 effector

<400> 6

Ile Phe Pro Arg Lys Ala Gly Gly Leu Asn Ile Phe Ala Asn Leu Val
 1 5 10 15

Ala Cys Cys Ala Val Cys Asn Glu Asn Lys Lys Gly Arg Thr Pro Leu
 20 25 30

Glu Ser Gly Ile Ser Pro Lys Pro Glu Ile Ile Ala Phe Met Lys Asn
 35 40 45

Asp Leu Lys Lys Lys Ile Leu Glu Asp Ala Arg Asn Ile Asn Thr Val
 50 55 60

Asp Phe Asn Lys Tyr Met Ser His Ala Ser Ile Gly Trp Arg Tyr Met
 65 70 75 80

Arg Asp Arg Leu Arg Glu Ser Ala Gly Asn Lys Lys Leu Ser Ile Glu
 85 90 95

Arg Gln Ser Gly Ile Tyr Thr Ala Tyr Phe Arg Arg Trp Trp Gly Phe
 100 105 110

Lys Lys Glu Arg Gly Asn Thr Leu His His Ala Leu Asp Ala Val Ile
115 120 125

Leu Ala Ser Arg Lys Gly Tyr Ser Asp Asp Gly Leu Val Asp Met Thr
130 135 140

Leu Lys Pro Lys Tyr Asn Lys Gly Gly Gly Phe Asp Ser Glu Lys His
145 150 155 160

Leu Pro Glu Pro Ile Glu Phe Lys Arg Asp Lys Gly Ser Lys Gly Ser
165 170 175

Ala Leu His Asp Arg Asn Pro Leu Ser Tyr Lys Lys Gly Ile Ile Thr
180 185 190

Arg Arg Phe Met Val Thr Glu Ile Glu Cys Gly Lys Glu Asp Asp Val
195 200 205

Ile Ser Glu Thr Tyr Arg Glu Lys Leu Lys Glu Ala Phe Lys Arg Phe
210 215 220

Asp Thr Lys Lys Gly Lys Cys Leu Thr Asp Lys Glu Ala Lys Glu Ala
225 230 235 240

Gly Phe Cys Ile Lys Lys Asn Glu Leu Val Met Ser Leu Lys Cys Ser
245 250 255

Ile Lys Gly Thr Gly Pro Gly Gln Met Ile Arg Ile Asn Asn Asn Val
260 265 270

Phe Lys Thr Asn Val His Asn Val Gly Val Asp Val Tyr Leu Asp Glu
275 280 285

Lys Gly Lys Lys Lys Ala Tyr Glu Arg Lys Asn Pro Arg Leu Ser Lys
290 295 300

His Phe Ile Glu Pro Pro Pro Gln Pro Asn Gly Arg Val Ser Phe Thr
305 310 315 320

Leu Lys Arg Arg Asp Met Val Thr Val Glu Gly Glu Asp Thr Ile Tyr

325

330

335

Arg Ile Lys Lys Leu Gly Thr Ser Pro Thr Ile Glu Ala Val Val Gly
 340 345 350

Ser Asp Gly Lys Thr Arg Thr Val Ser Ala Thr Lys Leu Thr Lys Ala
 355 360 365

Asn Asn Ala Glu
 370

<210> 7

<211> 119

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-6 effector

<400> 7

Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met Ile Arg Ile Asn
 1 5 10 15

Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly Val Asp Val Tyr
 20 25 30

Leu Asp Glu Lys Gly Lys Lys Lys Val Tyr Glu Arg Lys Asn Pro Arg
 35 40 45

Leu Ser Lys His Phe Ile Glu Pro Leu Pro Gln Pro Asn Gly Arg Ala
 50 55 60

Ser Phe Thr Leu Lys Arg Gly Asn Met Val Thr Val Glu Gly Glu Asp
 65 70 75 80

Thr Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro Thr Ile Glu Ala
 85 90 95

Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser Ala Thr Lys Leu
100 105 110

Thr Lys Ala Asn Asn Ala Glu
115

<210> 8
<211> 400
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-7 effector

<400> 8
Lys Glu Ala Leu Leu Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly
1 5 10 15

Lys Ser Ile Asp Ile Ser Asn Ala His Asp Asp His Ile Phe Pro Arg
20 25 30

Lys Ala Gly Gly Leu Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Ala
35 40 45

Val Cys Asn Glu Asn Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile
50 55 60

Ser Pro Lys Pro Glu Ile Ile Ala Phe Met Lys Asn Asp Leu Lys Lys
65 70 75 80

Lys Ile Leu Glu Asp Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys
85 90 95

Tyr Met Ser His Ala Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu
100 105 110

Arg Glu Ser Ala Gly Asn Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly

115

120

125

Ile Tyr Thr Ala Tyr Phe Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg
 130 135 140

Gly Asn Thr Leu His His Ala Leu Asp Ala Val Ile Leu Ala Ser Arg
 145 150 155 160

Lys Gly Tyr Ser Asp Asp Gly Leu Val Asp Met Thr Leu Lys Pro Lys
 165 170 175

Tyr Asn Lys Gly Gly Gly Phe Asp Ser Glu Lys His Leu Pro Glu Pro
 180 185 190

Ile Glu Phe Lys Arg Asp Lys Gly Ser Lys Gly Ser Ala Leu His Asp
 195 200 205

Arg Asn Pro Leu Ser Tyr Lys Lys Gly Ile Ile Thr Arg Arg Phe Met
 210 215 220

Val Thr Glu Ile Glu Cys Gly Lys Glu Asp Asp Val Ile Ser Glu Thr
 225 230 235 240

Tyr Arg Glu Lys Leu Lys Glu Ala Phe Lys Arg Phe Asp Thr Lys Lys
 245 250 255

Gly Lys Cys Leu Thr Asp Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile
 260 265 270

Lys Lys Asn Glu Leu Val Met Ser Leu Lys Cys Ser Ile Lys Gly Thr
 275 280 285

Gly Pro Gly Gln Met Ile Arg Ile Asn Asn Asn Val Phe Lys Thr Asn
 290 295 300

Val His Asn Val Gly Val Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys
 305 310 315 320

Lys Ala Tyr Glu Arg Lys Asn Pro Arg Leu Ser Lys His Phe Ile Glu
 325 330 335

Pro Pro Pro Gln Pro Asn Gly Arg Val Ser Phe Thr Leu Lys Arg Arg
340 345 350

Asp Met Val Ala Val Glu Gly Glu Asp Ala Ile Tyr Arg Ile Lys Lys
355 360 365

Leu Gly Thr Ser Pro Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys
370 375 380

Thr Arg Thr Val Ser Ala Thr Lys Leu Thr Lys Ala Asn Ser Ala Glu
385 390 395 400

<210> 9

<211> 402

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-8 effector

<400> 9

Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr Ala Thr Phe
1 5 10 15

Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp Tyr Ala Asp
20 25 30

Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met Asp Val Glu
35 40 45

Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu Glu Thr Lys
50 55 60

Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val His Lys Ala
65 70 75 80

Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg Val Glu Arg

85

90

95

Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn Arg Ile Leu
 100 105 110

Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro Leu Arg Lys
 115 120 125

Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe Phe Pro Ile
 130 135 140

Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu Asp Lys Asn
 145 150 155 160

Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys Thr Asp Glu
 165 170 175

His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys Leu Ser Gly
 180 185 190

Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr Glu His Ser
 195 200 205

Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu Lys Thr Lys
 210 215 220

Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu Pro Lys Phe
 225 230 235 240

Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp Ile Ala Ala
 245 250 255

Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr Gly Lys Gly
 260 265 270

Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu Arg Glu Thr
 275 280 285

Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile Ser Asn Ala
 290 295 300

His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu Asn Ile Phe
305 310 315 320

Ala Asn Leu Val Ala Cys Cys Thr Val Cys Asn Glu Asn Lys Lys Gly
325 330 335

Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Glu Ile Ile Ala
340 345 350

Ile Ile Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp Ala Arg Asn
355 360 365

Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala Ser Ile Gly
370 375 380

Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly Asn Lys Lys
385 390 395 400

Leu Ser

<210> 10

<211> 778

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-9 effector

<400> 10

Met Glu Arg Glu Ile Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Val Lys Met Arg Asp Asp Val Ala Asp Ile Leu Lys Gly Arg Arg

35

40

45

Glu Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
 50 55 60

Arg Glu Leu Arg Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
 65 70 75 80

Ala Thr Phe Lys Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
 85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Lys Ile Glu Ala Met
 100 105 110

Asp Glu Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Glu Glu Val Leu Lys Asp Val
 130 135 140

Arg Lys Ala Met Thr Glu Gly Arg Ala Ala Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Ser Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Cys Gly Lys Asn Thr Pro Leu Arg
 180 185 190

Arg Lys Val Arg Glu Leu Leu Leu Glu Asn Ile Val Arg Phe Leu Pro
 195 200 205

Leu Glu Ser Glu Met Lys Glu Thr Leu Lys Gln Thr Ile Leu Glu Gly
 210 215 220

Gln Gln Glu Asn Ile Asn Lys Ile Phe Arg Lys Leu Lys Phe Asn Gln
 225 230 235 240

Lys Asp Trp Pro Gly Lys Asn Leu Thr Asp Ile Ala Lys Asn Lys Leu
 245 250 255

Pro Gly Arg Leu Pro Phe Cys Lys Glu His Phe Ser Glu Asn Glu Lys
260 265 270

Phe Thr Met Ile Glu Lys Ser Thr Phe Arg Leu Ala Pro Ser Leu Lys
275 280 285

Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu Pro
290 295 300

Lys Phe Thr Ile Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp Ile
305 310 315 320

Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr Gly
325 330 335

Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu Arg
340 345 350

Glu Thr Asn Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile Ser
355 360 365

Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ser Gly Gly Leu Asn
370 375 380

Ile Phe Ala Asn Leu Val Ala Cys Cys Ala Val Cys Asn Glu Asn Lys
385 390 395 400

Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Asp Val
405 410 415

Ile Arg Phe Met Glu Asp Glu Phe Asn Arg Leu Lys Ile Lys Met Trp
420 425 430

Lys Ile Arg Arg Lys Gln Ser Leu Thr Thr Glu Glu Ile Met Asp Lys
435 440 445

Ala Lys Arg Asn Lys Leu Glu Leu Lys Leu Lys Ile Leu Glu Asp Ala
450 455 460

Gln Gln Val Asn Glu Leu Asp Phe Asn Lys Tyr Met Ser His Ala Ser

465		470		475		480
Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly Asn						
		485		490		495
Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr Phe						
		500		505		510
Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His His						
		515		520		525
Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp Asp						
		530		535		540
Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly Glu						
545		550		555		560
Phe Asp Pro Glu Lys His Ile Pro Glu Pro Ile Glu Phe Lys Arg Asp						
		565		570		575
Lys Gly Ser Lys Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser Tyr						
		580		585		590
Lys Lys Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu Cys						
		595		600		605
Gly Lys Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu Lys						
		610		615		620
Glu Ala Phe Lys Leu Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr Asp						
625		630		635		640
Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys His Glu Leu Val						
		645		650		655
Met Ser Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met Ile						
		660		665		670
Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly Val						
		675		680		685

Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Ala Tyr Glu Arg Lys
690 695 700

Asn Pro Arg Leu Ser Lys His Phe Ile Glu Pro Pro Pro Gln Pro Asn
705 710 715 720

Gly Arg Val Ser Phe Thr Leu Lys Arg Arg Asp Met Val Thr Val Glu
725 730 735

Gly Glu Asp Ala Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro Thr
740 745 750

Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser Ala
755 760 765

Thr Lys Leu Thr Lys Ala Asn Asn Ala Glu
770 775

<210> 11
<211> 754
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-10 effector

<400> 11
Met Glu Arg Glu Ile Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Val Lys Met Arg Asp Asp Val Ala Asp Ile Leu Lys Gly Arg Arg
35 40 45

Glu Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu

50

55

60

Arg Glu Leu Arg Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Lys Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Lys Ile Glu Ala Met
100 105 110

Asp Glu Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Glu Glu Val Leu Lys Asp Val
130 135 140

Arg Lys Ala Met Thr Glu Gly Arg Ala Ala Glu Glu Gln Ile Lys Arg
145 150 155 160

Val Glu Ser Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Cys Gly Lys Asn Thr Pro Leu Arg
180 185 190

Arg Lys Val Arg Glu Leu Leu Leu Glu Asn Ile Val Arg Phe Leu Pro
195 200 205

Leu Glu Ser Glu Met Lys Glu Thr Leu Lys Gln Thr Ile Leu Glu Gly
210 215 220

Gln Gln Glu Asn Ile Asn Lys Ile Phe Arg Lys Leu Lys Phe Asn Gln
225 230 235 240

Lys Asp Trp Pro Gly Lys Asn Leu Thr Asp Ile Ala Lys Asn Lys Leu
245 250 255

Pro Gly Arg Leu Pro Phe Cys Lys Glu His Phe Ser Glu Asn Glu Lys
260 265 270

Phe Thr Met Ile Glu Lys Ser Thr Phe Arg Leu Ala Pro Ser Leu Lys
275 280 285

Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu Pro
290 295 300

Lys Phe Thr Ile Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp Ile
305 310 315 320

Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr Gly
325 330 335

Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu Arg
340 345 350

Glu Thr Asn Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile Ser
355 360 365

Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ser Gly Gly Leu Asn
370 375 380

Ile Phe Ala Asn Leu Val Ala Cys Cys Ala Val Cys Asn Glu Asn Lys
385 390 395 400

Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Asp Val
405 410 415

Ile Arg Phe Met Glu Asp Glu Phe Asn Arg Leu Lys Ile Lys Met Trp
420 425 430

Lys Ile Arg Arg Lys Gln Ser Leu Thr Thr Glu Glu Ile Met Asp Lys
435 440 445

Ala Lys Arg Asn Lys Leu Glu Leu Lys Leu Lys Ile Leu Glu Asp Ala
450 455 460

Gln Gln Val Asn Glu Leu Asp Phe Asn Lys Tyr Met Ser His Ala Ser
465 470 475 480

Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly Asn

485

490

495

Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr Phe
500 505 510

Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His His
515 520 525

Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp Asp
530 535 540

Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly Glu
545 550 555 560

Phe Asp Pro Glu Lys His Ile Pro Glu Pro Ile Glu Phe Lys Arg Asp
565 570 575

Lys Gly Ser Lys Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser Tyr
580 585 590

Lys Lys Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu Cys
595 600 605

Gly Lys Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu Lys
610 615 620

Glu Ala Phe Lys Leu Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr Asp
625 630 635 640

Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys His Glu Leu Val
645 650 655

Met Ser Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met Ile
660 665 670

Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly Val
675 680 685

Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Val Tyr Glu Arg Lys
690 695 700

Asn Pro Arg Leu Ser Lys His Phe Ile Glu Pro Pro Pro Gln Pro Asn
705 710 715 720

Gly Arg Val Ser Phe Thr Leu Lys Arg Arg Asp Met Val Thr Val Glu
725 730 735

Gly Glu Asp Ala Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro Thr
740 745 750

Ile Glu

<210> 12
<211> 269
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-11 effector

<400> 12
Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp

85

90

95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
 100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Glu Glu Val Leu Lys Asp Val
 130 135 140

Arg Lys Ala Met Thr Glu Gly Arg Ala Ala Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Phe Lys Glu His Ile Leu
 260 265

<210> 13

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-12 effector

<400> 13

Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro

180

185

190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
 260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
 275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
 290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
 305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Ala Glu Tyr
 325 330 335

Val

<210> 14

<211> 530

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-13 effector

<400> 14

Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe

195

200

205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
 260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
 275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
 290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
 305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
 325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
 340 345 350

Arg Glu Thr Asp Asp Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
 355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
 370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Ala Val Cys Asn Glu Asn
 385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Ser Pro Lys Pro Glu
 405 410 415

Ile Ile Ala Phe Met Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly
450 455 460

Asn Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr
465 470 475 480

Phe Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His
485 490 495

His Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp
500 505 510

Asp Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly
515 520 525

Glu Phe
530

<210> 15
<211> 747
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-14 effector

<400> 15
Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn

20

25

30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
 35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
 50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
 65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
 85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
 100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
 130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
340 345 350

Arg Glu Thr Asp Asp Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Thr Val Cys Asn Glu Asn
385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Glu
405 410 415

Ile Ile Ala Ile Ile Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly

450

455

460

Asn Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr
 465 470 475 480

Phe Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His
 485 490 495

His Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp
 500 505 510

Asp Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly
 515 520 525

Gly Phe Asp Ser Glu Lys His Leu Pro Glu Pro Ile Glu Phe Lys Arg
 530 535 540

Asp Lys Gly Ser Lys Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser
 545 550 555 560

Tyr Lys Lys Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu
 565 570 575

Cys Gly Lys Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu
 580 585 590

Lys Glu Ala Phe Lys Arg Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr
 595 600 605

Asp Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys Asn Glu Leu
 610 615 620

Val Met Ser Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met
 625 630 635 640

Ile Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly
 645 650 655

Val Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Val Tyr Glu Arg
 660 665 670

Lys Asn Pro Arg Leu Ser Lys His Phe Ile Glu Pro Leu Pro Gln Pro
675 680 685

Asn Gly Arg Ala Ser Phe Thr Leu Lys Arg Arg Asp Met Val Thr Val
690 695 700

Glu Gly Glu Asp Thr Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro
705 710 715 720

Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser
725 730 735

Ala Thr Lys Leu Thr Lys Ala Asn Asn Ala Glu
740 745

<210> 16
<211> 394
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-15 effector

<400> 16
Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr

65	70					75					80				
Ala	Thr	Phe	Glu	Thr	Val	Tyr	Ser	Leu	Ala	His	Lys	Arg	Gly	Tyr	Asp
				85					90					95	
Tyr	Ala	Asp	Met	Pro	Glu	Glu	Lys	Thr	Ser	Glu	Glu	Ile	Glu	Ala	Met
			100					105					110		
Asp	Val	Glu	Glu	Arg	Lys	Gln	Trp	Glu	Lys	Glu	Lys	Gln	Glu	Trp	Glu
		115					120					125			
Glu	Thr	Lys	Arg	Asn	Ser	Arg	His	Arg	Lys	Glu	Val	Val	Lys	Asp	Val
	130					135					140				
His	Lys	Ala	Met	Ile	Glu	Gly	Arg	Ala	Thr	Glu	Glu	Gln	Ile	Lys	Arg
145					150					155					160
Val	Glu	Arg	Ile	Phe	Asn	Lys	Gln	Tyr	Arg	Pro	Lys	Arg	Phe	Asn	Asn
				165					170					175	
Arg	Ile	Leu	Thr	Lys	Cys	Lys	Val	Glu	Asp	Cys	Gly	Val	Asn	Thr	Pro
			180					185					190		
Leu	Arg	Lys	Asn	Val	Arg	Asp	Leu	Leu	Ile	Glu	Asn	Ile	Val	Arg	Phe
		195					200					205			
Phe	Pro	Ile	Glu	Gln	Ser	Glu	Lys	Asp	Asn	Leu	Lys	Asp	Ala	Val	Leu
	210					215					220				
Asp	Lys	Asn	Arg	Arg	Glu	Glu	Val	Lys	Ser	Phe	Phe	Arg	Lys	His	Lys
225					230					235					240
Thr	Asp	Glu	His	Ile	Arg	Lys	Gln	Val	Tyr	Asp	Ile	Ala	Asp	Asn	Lys
				245					250					255	
Leu	Ser	Gly	Arg	Thr	Val	Phe	Cys	Lys	Glu	His	Ile	Leu	Glu	His	Thr
			260					265					270		
Glu	His	Ser	Lys	Glu	Glu	Arg	Lys	Val	Phe	Arg	Leu	Ala	Pro	Ser	Leu
		275					280					285			

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys
385 390

<210> 17
<211> 747
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-16 effector

<400> 17
Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg

35

40

45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
 50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
 65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
 85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
 100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
 130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Ala Val Cys Asn Glu Asn
385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Ser Pro Lys Pro Glu
405 410 415

Ile Ile Ala Phe Met Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly
450 455 460

Asn Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr

465		470		475		480									
Phe	Arg	Arg	Trp	Trp	Gly	Phe	Lys	Lys	Glu	Arg	Gly	Asn	Thr	Leu	His
			485						490					495	
His	Ala	Leu	Asp	Ala	Val	Ile	Leu	Ala	Ser	Arg	Lys	Gly	Tyr	Ser	Asp
			500					505					510		
Asp	Gly	Leu	Val	Asp	Met	Thr	Leu	Lys	Pro	Lys	Tyr	Asn	Lys	Gly	Gly
		515						520				525			
Gly	Phe	Asp	Ser	Glu	Lys	His	Leu	Pro	Glu	Pro	Ile	Glu	Phe	Lys	Arg
	530					535					540				
Asp	Lys	Gly	Ser	Lys	Gly	Ser	Ala	Leu	His	Asp	Arg	Asn	Pro	Leu	Ser
545					550					555					560
Tyr	Lys	Lys	Gly	Ile	Ile	Thr	Arg	Arg	Phe	Met	Val	Thr	Glu	Ile	Glu
				565					570					575	
Cys	Gly	Lys	Glu	Asp	Asp	Val	Ile	Ser	Glu	Thr	Tyr	Arg	Glu	Lys	Leu
			580					585					590		
Lys	Glu	Ala	Phe	Lys	Arg	Phe	Asp	Thr	Lys	Lys	Gly	Lys	Cys	Leu	Thr
		595						600				605			
Asp	Lys	Glu	Ala	Lys	Glu	Ala	Gly	Phe	Cys	Ile	Lys	Lys	Asn	Glu	Leu
		610				615					620				
Val	Met	Ser	Leu	Lys	Cys	Ser	Ile	Lys	Gly	Thr	Gly	Pro	Gly	Gln	Met
625					630					635					640
Ile	Arg	Ile	Asn	Asn	Asn	Val	Phe	Lys	Thr	Asn	Val	His	Asn	Val	Gly
			645						650					655	
Val	Asp	Val	Tyr	Leu	Asp	Glu	Lys	Gly	Lys	Lys	Lys	Val	Tyr	Glu	Arg
			660					665					670		
Lys	Asn	Pro	Arg	Leu	Ser	Lys	His	Phe	Ile	Glu	Pro	Leu	Pro	Gln	Pro
		675						680				685			

Asn Gly Arg Ala Ser Phe Thr Leu Lys Arg Gly Asn Met Val Thr Val
690 695 700

Glu Gly Glu Asp Thr Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro
705 710 715 720

Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser
725 730 735

Ala Thr Lys Leu Thr Lys Ala Asn Asn Ala Glu
740 745

<210> 18

<211> 747

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-17 effector

<400> 18

Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp

85

90

95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
 100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
 130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
 260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
 275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
 290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Ala Val Cys Asn Glu Asn
385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Ser Pro Lys Pro Glu
405 410 415

Ile Ile Ala Phe Met Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly
450 455 460

Asn Lys Lys Leu Ser Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr
465 470 475 480

Phe Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His
485 490 495

His Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp
500 505 510

Asp Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly

515

520

525

Gly Phe Asp Ser Glu Lys His Leu Pro Glu Pro Ile Glu Phe Lys Arg
 530 535 540

Asp Lys Gly Ser Lys Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser
 545 550 555 560

Tyr Lys Lys Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu
 565 570 575

Cys Gly Lys Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu
 580 585 590

Lys Glu Ala Phe Lys Arg Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr
 595 600 605

Asp Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys Asn Glu Leu
 610 615 620

Val Met Ser Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met
 625 630 635 640

Ile Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly
 645 650 655

Val Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Ala Tyr Glu Arg
 660 665 670

Lys Asn Pro Arg Leu Ser Lys His Phe Ile Glu Pro Pro Pro Gln Pro
 675 680 685

Asn Gly Arg Val Ser Phe Thr Leu Lys Arg Arg Asp Met Val Thr Val
 690 695 700

Glu Gly Glu Asp Ala Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro
 705 710 715 720

Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser
 725 730 735

Ala Thr Lys Leu Thr Lys Ala Asn Ser Ala Glu
740 745

<210> 19
<211> 457
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-18 effector

<400> 19
Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val

130

135

140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
 260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
 275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
 290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
 305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
 325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
 340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Thr Val Cys Asn Glu Asn
385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Glu
405 410 415

Ile Ile Ala Ile Ile Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp
450 455

<210> 20

<211> 747

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-19 effector

<400> 20

Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg

35

40

45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
 50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
 65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp
 85 90 95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
 100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
 130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Thr Val Cys Asn Glu Asn
385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Glu
405 410 415

Ile Ile Ala Ile Ile Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly
450 455 460

Asn Lys Lys Leu Pro Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr

465		470		475		480									
Phe	Arg	Arg	Trp	Trp	Gly	Phe	Lys	Lys	Glu	Arg	Gly	Asn	Thr	Leu	His
			485						490					495	
His	Ala	Leu	Asp	Ala	Val	Ile	Leu	Ala	Ser	Arg	Lys	Gly	Tyr	Ser	Asp
			500					505					510		
Asp	Gly	Leu	Val	Asp	Met	Thr	Leu	Lys	Pro	Lys	Tyr	Asn	Lys	Gly	Gly
		515					520					525			
Glu	Phe	Asp	Pro	Glu	Lys	His	Leu	Pro	Glu	Pro	Ile	Glu	Phe	Lys	Met
	530					535					540				
Asp	Lys	Gly	Ser	Arg	Gly	Ser	Ala	Leu	His	Asp	Arg	Asn	Pro	Leu	Ser
545					550					555					560
Tyr	Lys	Lys	Gly	Ile	Ile	Thr	Arg	Arg	Phe	Met	Val	Thr	Glu	Ile	Glu
				565					570					575	
Cys	Gly	Lys	Glu	Asp	Asp	Val	Ile	Ser	Glu	Thr	Tyr	Arg	Glu	Lys	Leu
			580					585					590		
Lys	Glu	Ala	Phe	Lys	Arg	Phe	Asp	Thr	Lys	Lys	Gly	Lys	Cys	Leu	Thr
		595					600					605			
Asp	Lys	Glu	Ala	Lys	Glu	Ala	Gly	Phe	Cys	Ile	Lys	Lys	Asn	Glu	Leu
	610					615					620				
Val	Met	Ser	Leu	Lys	Cys	Ser	Ile	Lys	Gly	Thr	Gly	Pro	Gly	Gln	Met
625					630					635					640
Ile	Arg	Ile	Asn	Asn	Asn	Val	Phe	Lys	Thr	Asn	Val	His	Asn	Val	Gly
			645						650					655	
Val	Asp	Val	Tyr	Leu	Asp	Glu	Lys	Gly	Lys	Lys	Lys	Val	Tyr	Glu	Arg
		660						665					670		
Lys	Asn	Pro	Arg	Leu	Ser	Lys	His	Phe	Ile	Glu	Pro	Leu	Pro	Gln	Pro
		675						680				685			

Asn Gly Arg Ala Ser Phe Thr Leu Lys Arg Gly Asn Met Val Thr Val
690 695 700

Glu Gly Glu Asp Thr Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro
705 710 715 720

Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser
725 730 735

Ala Thr Lys Leu Thr Lys Ala Asn Asn Ala Glu
740 745

<210> 21

<211> 747

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-20 effector

<400> 21

Met Glu Arg Glu Leu Val Leu Gly Ile Asp Tyr Gly Gly Lys Tyr Thr
1 5 10 15

Gly Leu Ala Val Val Asp Arg Arg His Asn Gln Val Leu Tyr Ala Asn
20 25 30

Arg Leu Lys Met Arg Asp Asp Val Ala Gly Ile Leu Lys Asp Arg Arg
35 40 45

Lys Gln Arg Gly Ile Arg Arg Thr Ala Gln Thr Lys Lys Lys Arg Leu
50 55 60

Arg Glu Leu Lys Asn Tyr Leu Lys Ser Ile Gly Tyr Asn Glu Ser Thr
65 70 75 80

Ala Thr Phe Glu Thr Val Tyr Ser Leu Ala His Lys Arg Gly Tyr Asp

85

90

95

Tyr Ala Asp Met Pro Glu Glu Lys Thr Ser Glu Glu Ile Glu Ala Met
 100 105 110

Asp Val Glu Glu Arg Lys Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu
 115 120 125

Glu Thr Lys Arg Asn Ser Arg His Arg Lys Glu Val Val Lys Asp Val
 130 135 140

His Lys Ala Met Ile Glu Gly Arg Ala Thr Glu Glu Gln Ile Lys Arg
 145 150 155 160

Val Glu Arg Ile Phe Asn Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn
 165 170 175

Arg Ile Leu Thr Lys Cys Lys Val Glu Asp Cys Gly Val Asn Thr Pro
 180 185 190

Leu Arg Lys Asn Val Arg Asp Leu Leu Ile Glu Asn Ile Val Arg Phe
 195 200 205

Phe Pro Ile Glu Gln Ser Glu Lys Asp Asn Leu Lys Asp Ala Val Leu
 210 215 220

Asp Lys Asn Arg Arg Glu Glu Val Lys Ser Phe Phe Arg Lys His Lys
 225 230 235 240

Thr Asp Glu His Ile Arg Lys Gln Val Tyr Asp Ile Ala Asp Asn Lys
 245 250 255

Leu Ser Gly Arg Thr Val Phe Cys Lys Glu His Ile Leu Glu His Thr
 260 265 270

Glu His Ser Lys Glu Glu Arg Lys Val Phe Arg Leu Ala Pro Ser Leu
 275 280 285

Lys Thr Lys Ile Glu Asn Val Leu Ala Val Ile Lys Asp Glu Ile Leu
 290 295 300

Pro Lys Phe Thr Val Asn Lys Val Val Met Glu Ser Asn Asn Phe Asp
305 310 315 320

Ile Ala Ala Lys Thr Gln Gly Lys Lys Arg Leu Ala Lys Glu Glu Tyr
325 330 335

Gly Lys Gly Pro Arg Glu Gly Lys Glu Thr Arg Lys Glu Ala Leu Leu
340 345 350

Arg Glu Thr Asp Gly Arg Cys Ile Tyr Cys Gly Lys Ser Ile Asp Ile
355 360 365

Ser Asn Ala His Asp Asp His Ile Phe Pro Arg Lys Ala Gly Gly Leu
370 375 380

Asn Ile Phe Ala Asn Leu Val Ala Cys Cys Thr Val Cys Asn Glu Asn
385 390 395 400

Lys Lys Gly Arg Thr Pro Leu Glu Ser Gly Ile Leu Pro Lys Pro Glu
405 410 415

Ile Ile Ala Ile Ile Lys Asn Asp Leu Lys Lys Lys Ile Leu Glu Asp
420 425 430

Ala Arg Asn Ile Asn Thr Val Asp Phe Asn Lys Tyr Met Ser His Ala
435 440 445

Ser Ile Gly Trp Arg Tyr Met Arg Asp Arg Leu Arg Glu Ser Ala Gly
450 455 460

Asn Lys Lys Leu Ser Ile Glu Arg Gln Ser Gly Ile Tyr Thr Ala Tyr
465 470 475 480

Phe Arg Arg Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His
485 490 495

His Ala Leu Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp
500 505 510

Asp Gly Leu Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly

515

520

525

Glu Phe Asp Pro Glu Lys His Leu Pro Glu Pro Ile Glu Phe Lys Arg
 530 535 540

Asp Lys Gly Ser Lys Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser
 545 550 555 560

Tyr Lys Lys Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu
 565 570 575

Cys Gly Lys Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu
 580 585 590

Lys Glu Ala Phe Lys Arg Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr
 595 600 605

Asp Lys Glu Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys Asn Glu Leu
 610 615 620

Val Met Ser Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met
 625 630 635 640

Ile Arg Ile Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly
 645 650 655

Val Asp Val Tyr Leu Asp Glu Lys Gly Lys Lys Lys Val Tyr Glu Arg
 660 665 670

Lys Asn Pro Arg Leu Ser Lys His Phe Ile Glu Pro Leu Pro Gln Pro
 675 680 685

Asn Gly Arg Ala Ser Phe Thr Leu Lys Arg Gly Asn Met Val Thr Val
 690 695 700

Glu Gly Glu Asp Thr Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro
 705 710 715 720

Thr Ile Glu Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser
 725 730 735

Ala Thr Lys Leu Thr Lys Ala Asn Asn Ala Glu
740 745

<210> 22
<211> 434
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-21 effector

<400> 22
Met Glu Ser Asn Asn Phe Asp Ile Ala Ala Lys Thr Gln Gly Lys Lys
1 5 10 15

Arg Leu Ala Lys Glu Glu Tyr Gly Lys Gly Pro Arg Glu Gly Lys Glu
20 25 30

Thr Arg Lys Glu Ala Leu Leu Arg Glu Thr Asp Gly Arg Cys Ile Tyr
35 40 45

Cys Gly Lys Ser Ile Asp Ile Ser Asn Ala His Asp Asp His Ile Phe
50 55 60

Pro Arg Lys Ala Gly Gly Leu Asn Ile Phe Ala Asn Leu Val Ala Cys
65 70 75 80

Cys Thr Val Cys Asn Glu Asn Lys Lys Gly Arg Thr Pro Leu Glu Ser
85 90 95

Gly Ile Leu Pro Lys Pro Glu Ile Ile Ala Ile Ile Lys Asn Asp Leu
100 105 110

Lys Lys Lys Ile Leu Glu Asp Ala Arg Asn Ile Asn Thr Val Asp Phe
115 120 125

Asn Lys Tyr Met Ser His Ala Ser Ile Gly Trp Arg Tyr Met Arg Asp

130

135

140

Arg Leu Arg Glu Ser Ala Gly Asn Lys Lys Leu Ser Ile Glu Arg Gln
 145 150 155 160

Ser Gly Ile Tyr Thr Ala Tyr Phe Arg Arg Trp Trp Gly Phe Lys Lys
 165 170 175

Glu Arg Gly Asn Thr Leu His His Ala Leu Asp Ala Val Ile Leu Ala
 180 185 190

Ser Arg Lys Gly Tyr Ser Asp Asp Gly Leu Val Asp Met Thr Leu Lys
 195 200 205

Pro Lys Tyr Asn Lys Gly Gly Glu Phe Asp Pro Glu Lys His Ile Pro
 210 215 220

Glu Pro Ile Glu Phe Lys Arg Asp Lys Gly Ser Lys Gly Ser Ala Leu
 225 230 235 240

His Asp Arg Asn Pro Leu Ser Tyr Lys Lys Gly Ile Ile Thr Arg Arg
 245 250 255

Phe Met Val Thr Glu Ile Glu Cys Gly Lys Glu Asp Asp Val Ile Ser
 260 265 270

Glu Thr Tyr Arg Glu Lys Leu Lys Glu Ala Phe Lys Leu Phe Asp Thr
 275 280 285

Lys Lys Gly Lys Cys Leu Thr Asp Lys Glu Ala Lys Glu Ala Gly Phe
 290 295 300

Cys Ile Lys Lys Asn Glu Leu Val Met Ser Leu Lys Cys Ser Ile Lys
 305 310 315 320

Gly Thr Gly Pro Gly Gln Met Ile Arg Ile Asn Asn Asn Val Phe Lys
 325 330 335

Thr Asn Val His Asn Val Gly Val Asp Val Tyr Leu Asp Glu Lys Gly
 340 345 350

Lys Lys Lys Ala Tyr Glu Arg Lys Asn Pro Arg Leu Ser Lys His Phe
355 360 365

Ile Glu Pro Pro Pro Gln Pro Asn Gly Arg Val Ser Phe Thr Leu Lys
370 375 380

Arg Arg Asp Met Val Thr Val Glu Gly Glu Asp Ala Ile Tyr Arg Ile
385 390 395 400

Lys Lys Leu Gly Thr Ser Pro Thr Ile Glu Ala Val Val Gly Ser Asp
405 410 415

Gly Lys Thr Arg Thr Val Ser Ala Thr Lys Leu Thr Lys Ala Asn Asn
420 425 430

Ala Glu

<210> 23
<211> 443
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG34 effectors

<220>
<223> Description: MG34-22 effector

<400> 23
Gln Trp Glu Lys Glu Lys Gln Glu Trp Glu Glu Thr Lys Arg Asn Ser
1 5 10 15

Arg His Arg Glu Glu Val Leu Lys Asp Val Arg Lys Ala Met Thr Glu
20 25 30

Gly Arg Ala Ala Glu Glu Gln Ile Lys Arg Val Glu Ser Ile Phe Asn
35 40 45

Lys Gln Tyr Arg Pro Lys Arg Phe Asn Asn Arg Ile Leu Thr Lys Cys

50

55

60

Lys Val Cys Gly Lys Asn Thr Pro Leu Arg Arg Lys Val Arg Glu Leu
65 70 75 80

Leu Leu Glu Asn Ile Val Arg Phe Leu Pro Leu Glu Ser Glu Met Lys
85 90 95

Glu Thr Leu Lys Gln Thr Ile Leu Glu Gly Gln Gln Glu Asn Ile Asn
100 105 110

Lys Ile Phe Arg Lys Leu Lys Phe Asn Gln Lys Asp Trp Pro Gly Lys
115 120 125

Asn Leu Thr Asp Ile Ala Lys Asn Lys Leu Pro Gly Arg Leu Pro Phe
130 135 140

Cys Lys Glu His Phe Ser Glu Asn Glu Lys Phe Thr Met Ile Glu Lys
145 150 155 160

Ser Thr Phe Arg Leu Ala Pro Ser Leu Lys Thr Lys Ile Glu Asn Val
165 170 175

Leu Ala Val Ile Lys Asp Glu Ile Leu Pro Lys Phe Thr Ile Asn Lys
180 185 190

Val Val Met Glu Ser Asn Asn Phe Asp Ile Ala Ala Lys Thr Gln Gly
195 200 205

Lys Lys Arg Leu Ala Lys Glu Glu Tyr Gly Lys Gly Pro Arg Glu Gly
210 215 220

Lys Glu Thr Arg Lys Glu Ala Leu Leu Arg Glu Thr Asn Gly Arg Cys
225 230 235 240

Ile Tyr Cys Gly Lys Ser Ile Asp Ile Ser Asn Ala His Asp Asp His
245 250 255

Ile Phe Pro Arg Lys Ser Gly Gly Leu Asn Ile Phe Ala Asn Leu Val
260 265 270

Ala Cys Cys Ala Val Cys Asn Glu Asn Lys Lys Gly Arg Thr Pro Leu
275 280 285

Glu Ser Gly Ile Leu Pro Lys Pro Asp Val Ile Arg Phe Met Glu Asp
290 295 300

Glu Phe Asn Arg Leu Lys Ile Lys Met Trp Lys Ile Arg Arg Lys Gln
305 310 315 320

Ser Leu Thr Thr Glu Glu Ile Met Asp Lys Ala Lys Arg Asn Lys Leu
325 330 335

Glu Leu Lys Leu Lys Ile Leu Glu Asp Ala Gln Gln Val Asn Glu Leu
340 345 350

Asp Phe Asn Lys Tyr Met Ser His Ala Ser Ile Gly Trp Arg Tyr Met
355 360 365

Arg Asp Arg Leu Arg Glu Ser Ala Gly Asn Lys Lys Leu Pro Ile Glu
370 375 380

Arg Gln Ser Gly Ile Tyr Thr Ala Tyr Phe Arg Arg Trp Trp Gly Phe
385 390 395 400

Lys Lys Glu Arg Gly Asn Thr Leu His His Ala Leu Asp Ala Val Ile
405 410 415

Leu Ala Ser Arg Lys Gly Tyr Ser Asp Asp Gly Leu Val Asp Met Thr
420 425 430

Leu Lys Pro Lys Tyr Asn Lys Gly Gly Glu Phe
435 440

<210> 24

<211> 264

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG34 effectors

<220>

<223> Description: MG34-23 effector

<400> 24

Trp Trp Gly Phe Lys Lys Glu Arg Gly Asn Thr Leu His His Ala Leu
1 5 10 15

Asp Ala Val Ile Leu Ala Ser Arg Lys Gly Tyr Ser Asp Asp Gly Leu
20 25 30

Val Asp Met Thr Leu Lys Pro Lys Tyr Asn Lys Gly Gly Glu Phe Asp
35 40 45

Pro Glu Lys His Ile Pro Glu Pro Ile Glu Phe Lys Arg Asp Lys Gly
50 55 60

Ser Lys Gly Ser Ala Leu His Asp Arg Asn Pro Leu Ser Tyr Lys Lys
65 70 75 80

Gly Ile Ile Thr Arg Arg Phe Met Val Thr Glu Ile Glu Cys Gly Lys
85 90 95

Glu Asp Asp Val Ile Ser Glu Thr Tyr Arg Glu Lys Leu Lys Glu Ala
100 105 110

Phe Lys Arg Phe Asp Thr Lys Lys Gly Lys Cys Leu Thr Asp Lys Glu
115 120 125

Ala Lys Glu Ala Gly Phe Cys Ile Lys Lys Asn Glu Leu Val Met Ser
130 135 140

Leu Lys Cys Ser Ile Lys Gly Thr Gly Pro Gly Gln Met Ile Arg Ile
145 150 155 160

Asn Asn Asn Val Phe Lys Thr Asn Val His Asn Val Gly Val Asp Val
165 170 175

Tyr Leu Asp Glu Lys Gly Lys Lys Lys Ala Tyr Glu Arg Lys Asn Pro
180 185 190

Arg Leu Ser Lys His Phe Ile Glu Pro Leu Pro Gln Pro Asn Gly Arg
195 200 205

Ala Ser Phe Thr Leu Lys Arg Gly Asn Met Val Thr Val Glu Gly Glu
210 215 220

Asp Thr Ile Tyr Arg Ile Lys Lys Leu Gly Thr Ser Pro Thr Ile Glu
225 230 235 240

Ala Val Val Gly Ser Asp Gly Lys Thr Arg Thr Val Ser Ala Thr Lys
245 250 255

Leu Thr Lys Ala Asn Ser Ala Glu
260

<210> 25

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-1 effector

<400> 25

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Ala Ile Ile Met Thr His Arg Val Gly
35 40 45

Gly Asp Leu Gln Thr Val Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly Asp Phe Asp Arg Gly Lys Glu Val Ile

65		70		75		80									
Trp	Ala	Gly	Asn	Leu	Asn	His	Arg	Gly	His	Gln	Ile	Lys	Ser	Asn	Leu
			85						90					95	
Asn	Ser	Arg	Arg	Ala	Ile	Arg	Arg	Ala	Arg	Arg	Asn	Arg	Lys	Thr	Arg
			100					105					110		
Tyr	Arg	Gln	Ala	Arg	Phe	Asn	Asn	Arg	Arg	Arg	Pro	Lys	Gly	Trp	Leu
		115					120					125			
Pro	Pro	Ser	Leu	Arg	Ser	Arg	Val	Asp	Asn	Thr	Lys	Asn	Trp	Met	His
	130					135					140				
Lys	Leu	Ala	Arg	Leu	Ala	Pro	Leu	Thr	Gln	Ile	Ala	Val	Glu	Thr	Val
145					150					155					160
Arg	Phe	Asp	Thr	Gln	Lys	Leu	Gln	Lys	Pro	Glu	Ile	Ser	Gly	Val	Glu
				165					170					175	
Tyr	Gln	Gln	Gly	Glu	Leu	Ala	Gly	Tyr	Glu	Leu	Arg	Glu	Tyr	Leu	Leu
			180					185					190		
Glu	Lys	Trp	Gly	Arg	Glu	Cys	Ala	Tyr	Cys	Gly	Ala	Lys	Asn	Ile	Pro
		195					200					205			
Leu	Glu	Ile	Glu	His	Ile	Gln	Ala	Arg	Ser	Lys	Gly	Gly	Ser	Asp	Arg
	210					215					220				
Val	Ser	Asn	Leu	Thr	Leu	Ala	Cys	Thr	Pro	Cys	Asn	Ile	Asp	Lys	Gly
225					230					235					240
Asn	Lys	Asp	Ile	Lys	Glu	Phe	Leu	Ser	Leu	Lys	Pro	Lys	Arg	Leu	Lys
				245					250					255	
Lys	Ile	Gln	Ala	Thr	Ala	Thr	Ala	Pro	Leu	Lys	Asp	Ala	Ala	Ala	Val
			260					265					270		
Asn	Ala	Thr	Arg	Tyr	Ala	Thr	Gly	Asn	Val	Leu	Lys	Cys	Phe	Ser	Leu
		275					280					285			

Pro Ile Thr Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Val Lys
290 295 300

Leu Gly Tyr Leu Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
305 310 315 320

Ser Gly Ser Gln Val Val Ile Pro Lys Ala Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ser Lys Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Gly Pro Lys Lys Gln Lys Gln Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Ile Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Thr Tyr Ile Gly Arg Val Val Val Arg Ser Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ser Gly Glu Lys Lys Val Gly Ser Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Leu Gln Arg Ala Asp Gly Tyr Glu Tyr Thr
420 425

<210> 26

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-2 effector

<400> 26

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala

1		5		10		15											
Thr	Thr	Arg	Gly	Gly	Arg	Val	Arg	Tyr	Leu	Leu	Lys	Glu	Lys	Lys	Ala		
			20					25					30				
Arg	Val	Val	Ser	Ser	Thr	Pro	Phe	Thr	Ile	Gln	Leu	Asn	Tyr	Asp	Thr		
		35					40					45					
Pro	Asp	Ala	Thr	Gln	Asp	Leu	Ile	Leu	Gly	Ile	Asp	Pro	Gly	Arg	Thr		
	50					55					60						
Asn	Ile	Gly	Val	Ala	Val	Val	Lys	Glu	Asp	Gly	Gln	Cys	Val	Phe	Ser		
65					70					75					80		
Ala	His	Leu	Glu	Thr	Arg	Asn	Lys	Glu	Val	Pro	Leu	Leu	Met	Lys	Lys		
				85					90					95			
Arg	Ala	Ala	Phe	Arg	Arg	Gln	His	Arg	Thr	Gln	Asp	Arg	Arg	Arg	Lys		
			100					105					110				
Arg	Gln	Arg	Arg	Ala	Ile	Ala	Ala	Gly	Thr	Thr	Val	Glu	Ser	Asn	Thr		
		115					120					125					
Ile	Glu	Arg	Leu	Leu	Pro	Gly	Tyr	Glu	Lys	Pro	Ile	Val	Cys	His	His		
	130					135					140						
Ile	Arg	Asn	Lys	Glu	Ala	Arg	Phe	Asn	Asn	Arg	Ser	Arg	Pro	Ala	Gly		
145					150					155					160		
Trp	Leu	Thr	Pro	Thr	Ala	Asn	His	Leu	Leu	Gln	Ala	His	Ile	Asn	Leu		
				165					170					175			
Ile	Ala	Lys	Ala	Ala	Lys	Phe	Leu	Pro	Ile	Thr	Lys	Val	Val	Val	Glu		
			180					185					190				
Leu	Asn	Arg	Phe	Ala	Phe	Met	Ala	Met	Asp	Asn	Pro	Asn	Ile	Arg	Arg		
		195					200					205					
Trp	Glu	Tyr	Gln	Gln	Gly	Pro	Leu	Tyr	Gly	Leu	Gly	Ser	Val	Lys	Asp		
	210					215					220						

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Ile Gly Ser Glu Thr Leu Tyr Asp Ala Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Ala Asp Thr Lys Val Ser Thr Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu His Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala His Gly
405 410 415

Asn Ala Ala Val Ser Gln Leu Thr Val Lys Pro His His Ser Gln Cys
420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Met Met Asp Phe Asp Gly

435

440

445

Ile Val Gly Val Phe Lys Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro
 450 455 460

Asn Tyr Tyr Asn Ser Thr Lys Gly Glu Arg Phe Leu Thr Arg Ser Cys
 465 470 475 480

Val Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 27

<211> 423

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-3 effector

<400> 27

Met Gln Asn Tyr Thr Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Phe
 1 5 10 15

Pro Val His Pro Ala Val Ala Arg Lys Met Leu Ser Asn Ala Glu Ala
 20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys His Gly Ala
 35 40 45

Asp Arg Pro Thr Gln Ser Ile Glu Ile Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Thr Thr Gly Ile Ala Leu Leu Lys Gly Glu Arg Leu Ile Phe Ala Ala
 65 70 75 80

Glu Leu Ser His Arg Gly Gln Ala Ile Lys Ala Ser Leu Asp Ala Arg
 85 90 95

Arg Ala Ile Arg Arg Asn Arg Arg Thr Arg His Thr Arg Tyr Arg Pro
100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg Ser Lys Gly Trp Leu Thr Pro Ser
115 120 125

Leu Lys His Arg Val Cys Thr Thr Leu Thr Trp Val Asn Lys Phe Ile
130 135 140

Arg Phe Ala Pro Val Asn Ser Ile Ala Met Glu Leu Val Arg Phe Asp
145 150 155 160

Leu Gln Gln Leu Glu Asn Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln
165 170 175

Gly Glu Leu Leu Gly Tyr Glu Ile Arg Glu Tyr Leu Leu Asn Lys Trp
180 185 190

Asp Arg Lys Cys Thr Tyr Cys Gly Ala Glu Asn Ile Pro Leu Gln Val
195 200 205

Glu His Ile His Pro Arg Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn
210 215 220

Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu Lys Lys Gly Thr Gln Asp
225 230 235 240

Ile Lys Asp Phe Leu Ser Lys Lys Thr Asp Leu Leu Lys Gln Ile Met
245 250 255

Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ser Ala Val Asn Ser Thr
260 265 270

Arg Trp Ala Leu Phe Asn Gln Leu Lys Leu Thr Gly Leu Pro Val Thr
275 280 285

Thr Gly Ser Gly Gly Gln Thr Lys Tyr Asn Arg Thr Arg Leu Glu Leu
290 295 300

Pro Lys Thr His Tyr Phe Asp Ala Ala Cys Val Gly Lys Val Asp Lys

305 310 315 320

Leu Val Val Leu Thr Thr Gln Pro Leu Leu Ile Lys Ala Asn Gly His
325 330 335

Gly Thr Arg Gln Met Cys Arg Thr Asp Lys Phe Gly Phe Pro Ser Arg
340 345 350

His Ala Pro Arg Asn Lys Phe Val Lys Gly Phe Gln Thr Gly Asp Ile
355 360 365

Val Lys Ala Ile Val Thr Ser Gly Lys Lys Ile Gly Glu Tyr Val Gly
370 375 380

Arg Ala Ala Val Arg Ser Ser Gly Ser Phe Asn Ile Ser Ala Lys Glu
385 390 395 400

Leu Val Gln Gly Ile Gly His Lys Tyr Cys Glu Ile Leu His Arg Lys
405 410 415

Asp Gly Tyr Ser Tyr Gln Phe
420

<210> 28

<211> 229

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-4 effector

<400> 28

Ala Lys His His Asp Leu Val His Lys Asp Lys Ala Trp Thr Glu Lys
1 5 10 15

Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys Tyr His Ala Leu Ser
20 25 30

Val Leu Asn Gln Ile Ile Pro His Leu Met Glu His Ile Gly Ser Glu
35 40 45

Thr Pro Tyr Asp Ser Tyr Ala Thr Asp Gly Lys Ser Thr Lys Gly Phe
50 55 60

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys
65 70 75 80

Ile Ala Cys Ser Ile Leu Asp Thr Asp Ile Glu Val Ser Met Pro Val
85 90 95

Lys Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys
100 105 110

Ile Arg Gln Met Val Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val Val
115 120 125

Ala Thr Asn Arg His Lys Ser Ile Glu Gln Lys Ser Asp Ser Leu Glu
130 135 140

Glu Phe Arg Glu Ala Tyr Gly Asp Ala Ala Val Ser Gln Leu Thr Val
145 150 155 160

Arg Leu His Ser Pro Gln Tyr Lys Asp Met Ala Arg Ile Met Pro Gly
165 170 175

Ala Val Met Ala Phe Lys Gly Thr Ile Gly Val Met Gln Cys Ser Gly
180 185 190

Gly Arg Asn Asn Gly Lys Val Glu Phe Phe Lys Ser Thr Lys Gly Asn
195 200 205

Lys Thr Thr Pro Lys Lys Cys Val Leu Leu Ala Gln Asn Ala Gly Met
210 215 220

Val Phe Ile Pro Ala
225

<210> 29

<211> 229
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-5 effector

<400> 29

Ala Lys His His Asp Leu Val His Lys Asp Lys Ala Trp Thr Glu Lys
1 5 10 15

Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys Tyr His Ala Leu Ser
20 25 30

Val Leu Asn Gln Ile Ile Pro His Leu Met Glu Tyr Leu Gly Glu Glu
35 40 45

Thr Ser Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser Thr Lys Gly Phe
50 55 60

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys
65 70 75 80

Ile Ala Cys Ser Ile Leu Asp Thr Asn Ile Lys Val Ser Ala Pro Val
85 90 95

Glu Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys
100 105 110

His Gln Gln Arg Val Asp Arg Lys Tyr Tyr Leu Asp Gly Lys Gln Val
115 120 125

Ala Thr Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asn Ser Leu Glu
130 135 140

Glu Phe His Glu Thr Tyr Gly Asp Ala Ala Val Ser Gln Leu Thr Val
145 150 155 160

Lys Pro His Pro Pro Gln Tyr Lys Asp Met Thr Arg Ile Met Pro Gly
165 170 175

Ala Val Met Asn Phe Cys Gly Ala Val Gly Ile Leu Leu Gly Ser Asp
180 185 190

Gly Phe His Asn Gly Lys Pro Asp Tyr Tyr Lys Ser Thr Lys Glu Glu
195 200 205

Lys Val Arg Met Arg Arg Cys Ala Leu Leu Ala Gln Asn Ala Gly Met
210 215 220

Val Phe Ile Pro Ala
225

<210> 30
<211> 371
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-6 effector

<400> 30
Ala Leu Leu Val His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala
1 5 10 15

His Val Glu His Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg
20 25 30

Ala Ile Arg Arg Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala
35 40 45

Arg Phe Leu Asn Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu
50 55 60

Val Ser Lys Ala Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys

65					70					75				80	
Leu	Thr	Pro	Phe	Thr	Lys	Phe	Ala	Leu	Glu	Thr	Ala	Lys	Phe	Asp	Met
				85					90					95	
Gln	Lys	Leu	Glu	Asn	Pro	Asp	Thr	Gln	Gly	Val	Gly	Tyr	Gln	Gln	Gly
			100					105					110		
Arg	Met	Phe	Gly	Tyr	Ala	Asp	Lys	Lys	Ala	Tyr	Leu	Leu	Glu	Arg	Glu
		115					120					125			
Asn	Tyr	Thr	Cys	Ile	Tyr	Cys	Gly	Ile	His	Ala	Ser	Lys	Ala	Lys	Met
	130					135					140				
Glu	Ile	Glu	His	Val	Ile	Pro	Arg	Ser	Arg	Gly	Gly	Thr	Asp	Ser	Leu
145					150					155					160
Asn	Asn	Leu	Val	Leu	Ser	Cys	Arg	Ala	Cys	Asn	Glu	Ala	Lys	Gly	Ser
				165					170					175	
Gln	Asp	Val	Gln	Thr	Tyr	Leu	Lys	Gly	Asn	Pro	Ser	Val	Leu	Arg	Arg
			180					185					190		
Val	Lys	Ala	Arg	Leu	Asn	Thr	Asn	Tyr	Arg	Asp	Ala	Ala	His	Thr	Asn
		195					200					205			
Ser	Ile	Arg	Leu	Phe	Val	Leu	Asn	Lys	Leu	Gln	Thr	Met	Ala	Asp	Ala
	210					215					220				
Ile	Gly	Thr	Asn	Leu	Asn	Val	Gly	Phe	Gly	Tyr	Thr	Thr	Lys	Gln	Asn
225					230					235					240
Arg	Leu	Leu	Leu	Asn	Leu	Pro	Lys	Asp	His	Trp	Ile	Asp	Ala	Ala	Val
				245					250					255	
Cys	Thr	Ser	Asp	Gly	Ser	Ala	Val	Lys	Val	Asp	Pro	Ser	Leu	Lys	Pro
			260					265					270		
Leu	Thr	Ile	Lys	Ala	Ile	Gly	Arg	Gly	Ser	Arg	Gln	Phe	Cys	Arg	Met
		275					280					285			

Asn Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn
290 295 300

Phe Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu
305 310 315 320

Gly Ser Lys Thr Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala
325 330 335

Val Arg Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu
340 345 350

Gly Ile Tyr His Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr
355 360 365

Ser Tyr Ala
370

<210> 31
<211> 333
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-7 effector

<400> 31
Ala Ser Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser Arg Arg Ala Arg
1 5 10 15

His Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg Ile Arg Pro Lys
20 25 30

Gly Trp Leu Ala Pro Ser Leu Lys His Arg Val Asp Thr Thr Leu Thr
35 40 45

Trp Val Asn Lys Phe Ile Arg Phe Ala Pro Val Asn Ser Ile Val Met

50

55

60

Glu Leu Val Arg Phe Asp Leu Gln Gln Leu Glu Lys Pro Glu Ile Ser
65 70 75 80

Gly Ile Glu Tyr Gln Gln Gly Glu Leu Leu Gly Tyr Glu Leu Arg Glu
85 90 95

Tyr Leu Leu Asn Lys Trp Glu Arg Lys Cys Thr Tyr Cys Lys Ile Glu
100 105 110

Asn Val Pro Leu Gln Val Glu His Ile His Pro Lys Ala Lys Gly Gly
115 120 125

Ser Asn Arg Ile Ser Asn Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu
130 135 140

Lys Lys Gly Thr Gln Asp Ile Asn Asp Phe Leu Ile Arg Lys Pro Asp
145 150 155 160

Leu Leu Lys Gln Ile Met Ala Gln Val Lys Arg Pro Leu Lys Asp Ala
165 170 175

Thr Ala Val Asn Ser Thr Arg Trp Ala Leu Phe Asn Gln Leu Lys Leu
180 185 190

Thr Arg Leu Ser Val Thr Thr Gly Ser Gly Gly Gln Thr Lys Tyr Asn
195 200 205

Arg Thr Arg Leu Glu Leu Pro Lys Thr His Tyr Phe Asp Ala Ala Cys
210 215 220

Val Gly Lys Val Asn Lys Leu Val Val Leu Thr Thr Gln Pro Leu Leu
225 230 235 240

Ile Lys Ala Asn Gly Gln Gly Thr Arg Gln Met Cys Arg Thr Asp Arg
245 250 255

Phe Arg Phe Pro Ser Arg Asn Val Pro Arg Asn Lys Ser Val Lys Gly
260 265 270

Phe Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys
275 280 285

Ile Gly Glu Tyr Ile Gly Arg Val Ala Val Arg Ser Ser Gly Ser Phe
290 295 300

Asn Ile Ser Ala Lys Glu Leu Val Gln Gly Ile Ser His Lys Tyr Cys
305 310 315 320

Gln Thr Leu Gln Arg Lys Asp Gly Tyr Ser Tyr Gln Phe
325 330

<210> 32

<211> 71

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-8 effector

<400> 32

Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys
1 5 10 15

Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro His Leu Ile Glu
20 25 30

His Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala Thr Asp Gly Arg
35 40 45

Ser Thr Lys Gly Phe Arg Ile Ala Lys His Val Leu Lys Glu His Tyr
50 55 60

Thr Asp Ala Tyr Cys Val Ala
65 70

<210> 33

<211> 150
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-9 effector

<400> 33

Cys Ile Ala Cys Ser Ile Leu Asp Ala Asp Thr Lys Val Ser Ala Pro
1 5 10 15

Ala Glu Pro Phe Lys Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ser
20 25 30

Cys Ile Arg Gln Met Ala Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val
35 40 45

Val Ala Thr Asn Arg His Lys Ala Ile Glu Gln Arg Ser Asp Ser Leu
50 55 60

Glu Glu Phe Arg Glu Ala Tyr Gly Asp Ala Ala Val Ser Gln Leu Thr
65 70 75 80

Val Arg Pro His Ser Pro Gln Tyr Lys Asp Met Asn Arg Ile Met Pro
85 90 95

Gly Ala Val Met Asp Phe Asn Gly Thr Ile Gly Val Met Gln Cys Ser
100 105 110

Gly Gly Arg Asn Asn Gly Lys Val Glu Phe Phe Lys Ser Thr Lys Gly
115 120 125

Asn Lys Thr Thr Pro Lys Lys Cys Val Leu Leu Ala Gln Asn Ala Gly
130 135 140

Met Val Phe Ile Pro Ala
145 150

<210> 34
<211> 182
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-10 effector

<400> 34
Asp Phe Leu Phe Gly Lys Pro Glu Leu Val Gln Arg Ile Leu Thr Gln
1 5 10 15

Ala Lys Ala Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp
20 25 30

Ala Leu Phe Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Thr Thr Gly
35 40 45

Thr Gly Gly Gln Thr Lys Phe Asn Arg Thr Arg Leu Asn Leu Pro Lys
50 55 60

Ala His Trp Leu Asp Ala Val Cys Val Gly Gln Val Gly Ala Leu Lys
65 70 75 80

Val Leu Thr Ser Lys Pro Leu Leu Ile Ile Ala Lys Gly His Gly Thr
85 90 95

Arg Gln Met Cys Arg Thr Asp Lys Phe Gly Phe Pro Thr Arg His Lys
100 105 110

Ser Arg Val Gln Ile His Lys Gly Phe Gln Thr Gly Asp Ile Val Arg
115 120 125

Ala Thr Val Thr Ala Gly Lys Lys Ile Gly Phe Tyr Val Gly Arg Val
130 135 140

Ile Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala Thr Ala Thr Gly Lys

Pro Arg Thr Gly Pro Lys Lys Lys Lys Arg Val Lys Gly Phe Gln Thr
115 120 125

Gly Asp Ile Val Lys Ala Ile Val Thr Ser Gly Lys Lys Ile Gly Thr
130 135 140

Tyr Val Gly Arg Val Met Val Arg Lys Thr Gly Cys Phe Asp Ile Tyr
145 150 155 160

Thr Gly Phe Gly Arg Ile Ser Ser Leu Ser Tyr Arg Phe Cys Arg Leu
165 170 175

Ile Gln Arg Thr Asp Gly Tyr Glu Tyr Ser Thr Asp Leu Cys Pro Ile
180 185 190

Lys Lys Gly Ser Gly Lys Tyr Phe Asn Ser
195 200

<210> 36

<211> 441

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-12 effector

<400> 36

Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr Asn Ile Gly Val Ala
1 5 10 15

Val Val Lys Glu Asp Arg Pro Cys Val Phe Ser Ala His Leu Glu Thr
20 25 30

Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys Arg Ala Gly Phe Arg
35 40 45

Lys Gln His Arg Thr Leu Asp Arg Arg Arg Lys Arg Gln Arg Arg Ala

50

55

60

Lys Val Ala Gly Thr Thr Val Glu Gly Glu Thr Ile Glu Arg Leu Leu
65 70 75 80

Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr Ile Arg Asn Lys Glu
85 90 95

Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly Trp Leu Thr Pro Thr
100 105 110

Ala Asn His Leu Leu Gln Thr His Ile Asn Leu Ile Ala Lys Val Gly
115 120 125

Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu Leu Asn Arg Phe Ala
130 135 140

Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg Trp Glu Tyr Gln Gln
145 150 155 160

Gly Ser Leu Tyr Gly Leu Gly Phe Val Glu Asp Ala Val Tyr Ala Gln
165 170 175

Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro Ile Asp His Tyr His
180 185 190

His Val Val Pro Arg Arg Lys Asn Gly Ser Glu Thr Leu Ala Asn Arg
195 200 205

Cys Gly Leu Cys Ala Lys His His Ala Leu Val His Thr Asp Lys Ala
210 215 220

Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys Tyr
225 230 235 240

His Ala Leu Ser Val Leu Asn Gln Ile Ile Ser Phe Leu Met Glu Tyr
245 250 255

Leu Gly Arg Glu Thr Pro Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser
260 265 270

Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr
275 280 285

Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp Thr Asn Ile Lys Val
290 295 300

Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp
305 310 315 320

Arg Gln Ala Cys His Gln Gln Arg Val Asp Arg Lys Tyr Tyr Leu Asp
325 330 335

Gly Lys Gln Val Ala Thr Asn Arg His Lys Ala Ile Glu Gln Lys Ser
340 345 350

Asn Ser Leu Glu Glu Phe Arg Glu Thr Tyr Gly Asp Ala Ala Val Ser
355 360 365

Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr Lys Asp Met Thr Arg
370 375 380

Ile Met Pro Gly Ala Val Met Asn Phe Cys Gly Ala Val Gly Ile Leu
385 390 395 400

Leu Gly Ser Asp Gly Phe His Asn Gly Lys Pro Asp Tyr Tyr Lys Ser
405 410 415

Thr Lys Glu Glu Lys Val Arg Met Arg Arg Cys Ala Leu Leu Ala Gln
420 425 430

Asn Ala Gly Met Val Phe Ile Pro Ala
435 440

<210> 37

<211> 218

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-13 effector

<400> 37

Glu His Ile Gln Pro Arg Ser Lys Glu Gly Ser Asn Arg Val Ser Asn
1 5 10 15

Leu Thr Leu Ala Cys Thr Lys Cys Asn Gln Lys Lys Gly Asn Lys Asp
20 25 30

Val Lys Asp Phe Leu Lys Gly Lys Pro Asp Arg Leu Lys Lys Ile Gln
35 40 45

Ala Gln Ala Lys Ala Ser Leu Arg Asp Thr Ala Ala Val Asn Ala Thr
50 55 60

Arg Tyr Ala Ile Gly Glu Ala Leu Lys Thr Phe Gly Phe Val Ile Ser
65 70 75 80

Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Thr Gln Gln Gly Tyr
85 90 95

Pro Lys Glu His Trp Val Asp Ala Ala Cys Val Gly Glu Asn Gly Asn
100 105 110

Pro Val Ala Ile Pro Lys Ala Ile Thr Pro Leu Ile Ile Thr Ala Lys
115 120 125

Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Lys Tyr Gly Phe Pro
130 135 140

Arg Thr Gly Pro Lys Lys His Lys Arg Val Lys Gly Phe Gln Thr Gly
145 150 155 160

Asp Ile Val Lys Ala Ile Val Thr Lys Gly Lys Lys Ile Gly Thr Tyr
165 170 175

Val Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asp Ile Gly Ser
180 185 190

Gly Ile Glu Ala Val Gly Ser Ile Ser Tyr Lys Tyr Cys Gln Leu Leu
195 200 205

Gln Arg Ser Asp Gly Tyr Asp Tyr Leu Lys
210 215

<210> 38
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-14 effector

<400> 38
Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
1 5 10 15

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
20 25 30

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
35 40 45

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
50 55 60

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
65 70 75 80

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
85 90 95

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
100 105 110

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg

115

120

125

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 130 135 140

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
 145 150 155 160

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu
 165 170 175

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
 180 185 190

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
 195 200 205

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
 210 215 220

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
 225 230 235 240

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
 245 250 255

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser
 260 265 270

Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His
 275 280 285

Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 290 295 300

<210> 39

<211> 242

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-15 effector

<400> 39

Glu Val Arg Glu Tyr Leu Leu Thr Lys Trp Asn Arg Lys Cys Ala Tyr
1 5 10 15

Cys Ser Val Glu Asn Val Pro Phe Glu Ile Glu His Ile Gln Pro Lys
20 25 30

Ser Lys Gly Gly Ser Asp Arg Val Ser Asn Leu Thr Ile Ala Cys His
35 40 45

Asp Cys Asn Gln Lys Lys Gly Asn Gln Asp Val Gln Ala Phe Leu Ala
50 55 60

Thr Lys Pro Asp Leu Leu Asn Cys Ile Leu Lys Gln Ala Lys Leu Pro
65 70 75 80

Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Phe Asn
85 90 95

Ala Leu Lys Glu Thr Gly Leu Ser Val Thr Thr Gly Thr Gly Gly Gln
100 105 110

Thr Lys Phe Asn Arg Asn Arg Leu Gly Leu Pro Lys Ser His Trp Leu
115 120 125

Asp Ala Ala Cys Val Gly Asn Val Glu Thr Leu Glu Ile Leu Thr Ser
130 135 140

Lys Pro Leu Leu Ile Ala Ala Lys Gly His Gly Thr Arg Gln Met Cys
145 150 155 160

Gly Thr Asn Lys Tyr Gly Phe Pro Ile Arg His Lys Ser Arg Val His
165 170 175

Ile His Lys Gly Phe Gln Thr Gly Asp Ile Val Asn Ala Thr Val Thr

180

185

190

Ala Gly Lys Lys Val Gly Ser Tyr Val Gly Arg Val Leu Cys Arg Ala
 195 200 205

Ser Gly Ser Phe Asp Ile Val Thr Lys Thr Gly Arg Val Ala Gly Ile
 210 215 220

Ser His Lys Tyr Cys Lys Ala Ile His Lys Lys Asp Gly Tyr Ser Tyr
 225 230 235 240

Gly Phe

<210> 40

<211> 257

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-16 effector

<400> 40

Phe Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr
 1 5 10 15

Thr Cys Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile
 20 25 30

Glu His Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn
 35 40 45

Leu Val Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp
 50 55 60

Val Gln Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys
 65 70 75 80

Ala Arg Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile
85 90 95

Arg Leu Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly
100 105 110

Thr Asn Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu
115 120 125

Leu Leu Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr
130 135 140

Ser Asp Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr
145 150 155 160

Ile Lys Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys
165 170 175

Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe
180 185 190

Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser
195 200 205

Lys Thr Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg
210 215 220

Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val
225 230 235 240

Ser His Lys Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr
245 250 255

Ala

<210> 41

<211> 135

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-17 effector

<400> 41

Gly Leu Gly Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly Arg
1 5 10 15

Cys Leu Phe Cys Lys Lys Pro Ile Asp His Tyr His His Val Val Pro
20 25 30

Arg His Lys Gly Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys
35 40 45

Arg Glu His His Ala Leu Val His Thr Asp Lys Val Trp Ala Asp Lys
50 55 60

Leu Val Thr Arg Lys Glu Gly Val Asn Lys Lys Tyr His Ala Leu Ser
65 70 75 80

Val Leu Asn Gln Ile Ile Pro His Leu Met Glu Tyr Leu Gly Ser Glu
85 90 95

Thr Arg Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser Thr Lys Gly Phe
100 105 110

Arg Val Ala Lys Asn Val Pro Lys Asp Leu Thr Thr Glu Lys Arg Pro
115 120 125

Tyr Gly Arg Phe Ser Phe Ala
130 135

<210> 42

<211> 433

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-18 effector

<400> 42

Gly Arg Thr Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys
1 5 10 15

Val Phe Ser Ala His Leu Glu Thr Arg Asn Asn Glu Val Pro Phe Leu
20 25 30

Met Lys Lys Arg Ala Ala Phe Arg Arg Ser His Arg Thr Leu Asp Arg
35 40 45

Arg Arg Lys Arg Gln Arg Arg Ala Lys Val Ala Gly Thr Thr Ile Ala
50 55 60

Glu Gly Ser Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val
65 70 75 80

Cys Arg Tyr Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg
85 90 95

Pro Ala Gly Trp Leu Thr Pro Thr Val Asn His Leu Leu Arg Thr His
100 105 110

Ile Asn Leu Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val
115 120 125

Val Val Glu Leu Asn Leu Phe Ala Phe Ile Ala Met Asp Asn Pro Asn
130 135 140

Ile Arg Arg Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser
145 150 155 160

Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys
165 170 175

Lys Lys Pro Ile Asp His Tyr His His Val Ile Pro Arg Arg Lys Asn

180

185

190

Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His
 195 200 205

Asp Leu Val His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg
 210 215 220

Lys Gly Gly Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln
 225 230 235 240

Ile Ile Pro His Leu Leu Glu Tyr Leu Gly Asp Glu Thr Leu Tyr Asp
 245 250 255

Ile Tyr Ala Thr Asn Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys
 260 265 270

Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser
 275 280 285

Ile Leu Asp Thr Asp Ile Lys Val Ser Ala Pro Val Glu Pro Phe Glu
 290 295 300

Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met
 305 310 315 320

Val Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg
 325 330 335

His Lys Ala Ile Glu Gln Lys Ser Asp Ser Leu Ala Glu Phe Arg Glu
 340 345 350

Ala Tyr Gly Glu Ala Ala Val Ser Gln Leu Thr Val Lys Pro His Pro
 355 360 365

Pro Gln Tyr Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Asp
 370 375 380

Phe Gly Gly Ala Val Gly Ile Leu Gln Gly Ser Glu Gly Phe His Asn
 385 390 395 400

Gly Lys Pro Asp Tyr Tyr Arg Ser Thr Lys Gly Glu Lys Val Arg Pro
405 410 415

Arg Arg Cys Glu Leu Ile Ala Gln Asn Ala Gly Met Val Phe Ile Pro
420 425 430

Ala

<210> 43
<211> 124
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-19 effector

<400> 43
Gly Tyr Ser Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu Ser
1 5 10 15

Gly Ser His Val Val Ile Pro Lys Thr Ile Thr Pro Leu Ile Ile Thr
20 25 30

Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr Gly
35 40 45

Phe Pro Arg Thr Gly Pro Lys Lys Gln Lys Arg Val Lys Gly Phe Gln
50 55 60

Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Lys Ile Gly
65 70 75 80

Thr Tyr Ile Gly Arg Val Val Val Arg Ala Lys Gly Ser Phe Asp Ile
85 90 95

Gly Ser Gly Glu Glu Lys Val Gly Gly Ile Ser Tyr Lys Tyr Cys Gln

100

105

110

Leu Leu Gln Arg Ser Asp Gly Tyr Glu Tyr Leu Lys
 115 120

<210> 44

<211> 137

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-20 effector

<400> 44

His Asp Cys Asn Gln Lys Lys Gly Asn Gln Asp Val Arg Glu Phe Leu
 1 5 10 15

Ala Thr Lys Pro Asp Leu Leu Asn Arg Ile Leu Gln Gln Ala Lys Leu
 20 25 30

Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Phe
 35 40 45

Arg Ala Leu Lys Glu Thr Gly Leu Pro Val Thr Asp Gly Thr Gly Gly
 50 55 60

Gln Thr Lys Phe Asn Arg Asn Arg Leu Gly Leu Pro Lys Ser His Trp
 65 70 75 80

Leu Asp Ala Ala Cys Val Gly Asn Val Glu Thr Leu Lys Val Leu Thr
 85 90 95

Ser Lys Pro Leu Leu Ile Ala Ala Thr Gly His Gly Arg Arg Gln Met
 100 105 110

Cys Gly Thr Asn Lys Tyr Gly Phe Pro Thr Arg His Lys Ser Arg Val
 115 120 125

Gln Ile His Lys Gly Phe Leu Ala Trp
130 135

<210> 45
<211> 41
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-21 effector

<400> 45
Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp Ile Gly Ile
1 5 10 15

Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys Gln Leu Ile
20 25 30

Gln Arg Val Asp Gly Tyr Glu Tyr Ile
35 40

<210> 46
<211> 309
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-22 effector

<400> 46
Ile Thr Lys Val Val Val Glu Leu Asn Arg Phe Ala Phe Met Ala Met
1 5 10 15

Asp Asn Pro Asn Ile Arg Arg Trp Glu Tyr Gln Gln Gly Pro Leu Cys

20

25

30

Gly Leu Gly Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His
 35 40 45

Cys Leu Phe Cys Lys Lys Pro Ile Asp His Tyr His His Val Val Pro
 50 55 60

Arg His Lys Gly Gly Ser Glu Thr Leu Val Asn Arg Cys Gly Leu Cys
 65 70 75 80

Thr Glu His His Ser Leu Val His Thr Asp Lys Val Trp Ala Asp Lys
 85 90 95

Leu Val Thr Arg Lys Glu Gly Met Asn Lys Lys Tyr His Ala Leu Ser
 100 105 110

Val Leu Asn Gln Ile Ile Pro His Leu Met Glu Tyr Leu Gly Asn Glu
 115 120 125

Thr Leu Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser Thr Lys Gly Phe
 130 135 140

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys
 145 150 155 160

Ile Ala Cys Ser Ile Leu Asp Thr Asp Ile Glu Val Ser Ala Pro Val
 165 170 175

Glu Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys
 180 185 190

Ile Arg Gln Met Ala Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val Val
 195 200 205

Ala Ala Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asp Cys Leu Ala
 210 215 220

Glu Phe Arg Glu Ala Cys Gly Ala Ala Val Ile Ser Gln Leu Thr Val
 225 230 235 240

Lys Pro His Pro Pro Gln Tyr Lys Asp Met Ala Arg Ile Met Pro Gly
245 250 255

Ala Val Met Asp Phe Asn Gly Thr Ile Gly Val Met Gln Cys Ser Ser
260 265 270

Gly Arg Asn Asn Gly Gly Val Asp Tyr Phe Lys Ser Thr Lys Gly His
275 280 285

Lys Ala Thr Pro Lys Arg Cys Val Leu Leu Thr Gln Ile Ala Gly Met
290 295 300

Val Phe Ile Pro Thr
305

<210> 47
<211> 47
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-23 effector

<400> 47
Lys Lys Ile Gly Thr His Ile Gly Arg Val Val Val Arg Ala Arg Gly
1 5 10 15

Ser Phe Asp Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr
20 25 30

Lys Tyr Cys Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr Thr
35 40 45

<210> 48
<211> 209
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-24 effector

<400> 48

Lys	Leu	Val	Thr	Arg	Lys	Glu	Gly	Met	Asn	Lys	Lys	Tyr	His	Ala	Leu
1				5					10					15	

Ser	Val	Leu	Asn	Gln	Ile	Ile	Pro	Phe	Leu	Met	Glu	Tyr	Leu	Gly	Ser
			20					25					30		

Glu	Thr	Leu	Tyr	Asp	Val	Tyr	Ala	Ile	Asp	Gly	Arg	Ser	Ile	Lys	Gly
		35					40					45			

Phe	Arg	Ile	Ala	Lys	Asn	Val	Pro	Lys	Glu	His	Tyr	Thr	Asp	Ala	Tyr
	50					55					60				

Cys	Ile	Ala	Cys	Ser	Ile	Leu	Asp	Thr	Asp	Asn	Lys	Val	Ser	Ala	Pro
65					70					75					80

Val	Glu	Pro	Phe	Glu	Leu	Lys	Gln	Phe	Arg	Arg	His	Asp	Arg	Gln	Ala
				85					90					95	

Cys	Ile	Arg	Gln	Met	Val	Asp	Arg	Lys	Tyr	Leu	Leu	His	Gly	Lys	Val
			100					105					110		

Val	Ala	Ala	Asn	Arg	His	Lys	Ala	Phe	Glu	Gln	Lys	Ser	Asp	Ser	Leu
		115					120					125			

Gln	Glu	Phe	Arg	Glu	Ala	Tyr	Ser	Asp	Val	Ala	Val	Ser	Gln	Leu	Thr
	130					135					140				

Val	Lys	Pro	His	Pro	Pro	Gln	Tyr	Lys	Asp	Met	Ser	Arg	Ile	Met	Pro
145					150					155					160

Gly	Ala	Val	Met	Asp	Phe	Asp	Gly	Ile	Val	Gly	Val	Met	Gln	Ser	Ser
				165					170					175	

Ile Val Gly Gln Phe Tyr Lys Ser Thr Lys Gly His Lys Ala Thr Pro
180 185 190

Lys Arg Cys Val Leu Leu Ser Gln Asn Ala Gly Met Val Phe Ile Pro
195 200 205

Thr

<210> 49
<211> 214
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-25 effector

<400> 49
Lys Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys Tyr His Ala Leu
1 5 10 15

Ser Val Leu Asn Gln Ile Ile Pro His Leu Met Glu Tyr Leu Gly Arg
20 25 30

Glu Thr Pro Tyr Asp Val Tyr Ala Thr Asp Gly Lys Ser Thr Lys Gly
35 40 45

Phe Arg Val Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr
50 55 60

Cys Ile Ala Cys Ser Ile Leu Asp Ala Asp Thr Thr Val Ser Thr Pro
65 70 75 80

Val Glu Pro Phe Arg Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ser
85 90 95

Cys Ile Arg Gln Met Val Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val

100

105

110

Val Ala Thr Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asp Ser Leu
 115 120 125

Glu Glu Phe Arg Glu Ala Tyr Gly Asp Ala Ala Val Ser Gln Leu Ile
 130 135 140

Val Lys Pro His Gln Pro Gln His Lys Asp Met Thr Arg Ile Met Pro
 145 150 155 160

Gly Ala Val Met Asp Phe Cys Gly Thr Ala Gly Ile Leu Gln Gly Ser
 165 170 175

Glu Gly Phe His Asn Gly Lys Pro Asp Tyr Tyr Lys Ser Thr Lys Gly
 180 185 190

Ala Lys Gly Leu Thr Lys Arg Cys Val Leu Leu Ala Arg Asn Ala Gly
 195 200 205

Met Val Phe Ile Pro Ala
 210

<210> 50

<211> 87

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-26 effector

<400> 50

Leu Ala Cys Thr Pro Cys Asn Ile Asp Pro Gly Asn Arg Asp Ile Lys
 1 5 10 15

Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys Lys Ile Gln Thr Gln
 20 25 30

Ser Lys Ala Pro Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr
35 40 45

Ala Thr Gly Asn Ala Leu Lys Ser Phe Gly Leu Pro Ile Ala Phe Ser
50 55 60

Ser Gly Gly Arg Thr Lys Phe Asn Arg Ile Lys Leu Gly Tyr Ser Lys
65 70 75 80

Asp His Trp Ile Asp Ala Ala
85

<210> 51

<211> 88

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-27 effector

<400> 51

Leu Ala Cys Thr Pro Cys Asn Ile Asp Pro Gly Asn Arg Asp Ile Lys
1 5 10 15

Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys Lys Ile Gln Thr Gln
20 25 30

Ser Lys Ala Pro Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr
35 40 45

Ala Thr Gly Asn Ala Leu Lys Ser Phe Gly Leu Pro Ile Ala Phe Ser
50 55 60

Ser Gly Gly Arg Thr Lys Phe Asn Arg Ile Lys Leu Gly Tyr Ser Lys
65 70 75 80

Asp His Trp Ile Asp Ala Ala Trp

<210> 52
 <211> 423
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-28 effector

<400> 52
 Leu Ala His Asn Lys Gln Pro Leu Met Pro Cys His Pro Ala Arg Ala
 1 5 10 15

Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala Val Tyr Arg Arg Tyr Pro
 20 25 30

Phe Thr Ile Ile Met Thr His Arg Leu Cys Gly Asp Leu Gln Pro Ile
 35 40 45

Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr Thr Gly Ile Ala Leu Val
 50 55 60

Gly His Phe Asp Arg Gly Ser Glu Val Ile Trp Ala Gly Asn Leu Asn
 65 70 75 80

His Arg Gly Leu Gln Val Lys Ser Asn Leu Val Ser Arg Arg Ala Ile
 85 90 95

Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Pro Ala Arg Phe
 100 105 110

Leu Asn Arg Arg Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Arg Ser
 115 120 125

Arg Val Leu Asn Val Lys Asn Trp Met Leu Lys Leu Ser Arg Leu Ala
 130 135 140

Pro Leu Thr Gln Ile Ala Ile Glu Thr Val Arg Phe Asp Thr Gln Lys
145 150 155 160

Met Gln Lys Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Glu Leu
165 170 175

Val Gly Tyr Glu Leu Arg Glu Tyr Leu Leu Glu Lys Trp Asp Arg Gln
180 185 190

Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro Leu Glu Ile Glu His Ile
195 200 205

Gln Ala Ser Ser Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu
210 215 220

Ala Cys Ser Pro Cys Asn Phe Asp Lys Gly Asn Lys Asp Ile Lys Glu
225 230 235 240

Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys Lys Ile Gln Ala Gln Ala
245 250 255

Lys Ala Ser Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr Ala
260 265 270

Thr Gly Asn Ile Leu Lys Cys Phe Gly Leu Pro Ile Thr Phe Ser Ser
275 280 285

Gly Gly Arg Thr Lys Phe Asn Arg Leu Lys Leu Gly Tyr Ser Lys Asp
290 295 300

His Trp Ile Asp Ala Ala Cys Val Gly Glu Ser Gly Ser His Val Val
305 310 315 320

Ile Pro Lys Thr Ile Thr Pro Leu Ile Ile Thr Ala Lys Gly Arg Gly
325 330 335

Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr Gly Phe Pro Arg Thr Gly
340 345 350

Pro Lys Lys Gln Lys Arg Val Lys Gly Phe Gln Thr Gly Asp Ile Val

355

360

365

Lys Ala Val Val Thr Lys Gly Lys Lys Ile Gly Thr Tyr Ile Gly Arg
 370 375 380

Val Val Val Arg Ala Lys Gly Ser Phe Asp Ile Gly Ser Gly Glu Glu
 385 390 395 400

Lys Val Gly Gly Ile Ser Tyr Lys Tyr Cys Gln Leu Leu Gln Arg Ser
 405 410 415

Asp Gly Tyr Glu Tyr Leu Lys
 420

<210> 53

<211> 441

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-29 effector

<400> 53

Leu Ala Arg Arg Ala Leu Pro Thr Gln Val Glu Leu Gly Asn Glu Pro
 1 5 10 15

Cys Lys Glu Lys Lys Pro Leu Met Pro Cys His Pro Ala Arg Ala Arg
 20 25 30

Lys Leu Leu Lys Asn Gly Lys Ala Ala Val Asp Arg Thr Tyr Pro Phe
 35 40 45

Thr Ile Ile Leu Lys Tyr Cys Val Lys Glu Gly Leu Gln Pro Ile Glu
 50 55 60

Val Lys Phe Asp Pro Gly Ser Arg Thr Thr Gly Leu Ala Leu Val Gly
 65 70 75 80

Asn Phe Glu Arg Gly Lys Glu Val Ile Phe Ala Gly Asn Leu Ile His
85 90 95

Arg Gly Gly Gln Ile Lys Ser Asn Leu Asn Ser Arg Arg Ala Ile Arg
100 105 110

Arg Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg Pro Ala Arg Phe Asn
115 120 125

Asn Arg Arg Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Arg Ser Arg
130 135 140

Val Leu Asn Val Glu Asn Trp Met Leu Lys Leu Ala Arg Leu Ala Pro
145 150 155 160

Leu Thr Gln Ile Ala Val Glu Thr Val Arg Phe Asp Thr Gln Lys Leu
165 170 175

Gln Lys Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu Ala
180 185 190

Gly Tyr Glu Leu Arg Glu Tyr Leu Leu Glu Lys Trp Glu Arg Gln Cys
195 200 205

Ala Tyr Cys Gly Ala Lys Asn Val Pro Leu Glu Val Glu His Ile Gln
210 215 220

Ala Arg Ser Lys Gly Gly Thr Asn Arg Val Ser Asn Leu Thr Leu Ala
225 230 235 240

Cys Thr Glu Cys Asn Gln Lys Lys Gly Asn Gln Asp Val Lys Asp Phe
245 250 255

Leu Lys Arg Lys Pro Ser Arg Leu Lys Lys Val Leu Ala Gln Ala Lys
260 265 270

Lys Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr Ala Ile
275 280 285

Gly Val Ala Leu Lys Thr Phe Gly Leu Pro Ile Val Phe Ala Thr Gly

290

295

300

Gly Arg Thr Lys Phe Asn Arg Thr Ser Gly His Tyr Pro Lys Asp His
 305 310 315 320

Trp Ile Asp Ala Ala Cys Val Gly Glu Ser Gly Ser Asp Val Ile Ile
 325 330 335

Pro Lys Ala Val Thr Pro Leu Ile Ile Lys Ala Lys Gly Arg Gly Ser
 340 345 350

Arg Gln Lys Cys Arg Val Asn Gln Tyr Gly Phe Pro Arg Thr Ser Ala
 355 360 365

Lys Lys Gln Lys Arg Val Asn Gly Phe Gln Thr Gly Asp Phe Val Lys
 370 375 380

Ala Ile Val Thr Lys Gly Lys Lys Ile Gly Thr Tyr Lys Gly Arg Val
 385 390 395 400

Leu Val Gln Ala Ala Gly Asn Phe Asp Ile Val Thr Lys Lys Gly Arg
 405 410 415

Val Ser Gly Ile Ser His Lys Tyr Cys Gln Leu Phe Gln Arg Ile Asp
 420 425 430

Gly Tyr Glu Tyr Ser Leu Thr Ser Asn
 435 440

<210> 54

<211> 104

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-30 effector

<400> 54

Leu Glu Val Leu Thr Gly Lys Pro Leu Leu Ile Lys Ala Thr Gly His
1 5 10 15

Gly Ser Arg Gln Met Cys Gly Thr Asp Lys Phe Gly Phe Pro Ser Arg
20 25 30

His Arg Thr Arg Lys Gln Ile His Gln Gly Phe Gln Thr Gly Asp Ile
35 40 45

Val Lys Ala Leu Val Thr Ser Gly Lys Lys Ile Gly Ser Tyr Val Gly
50 55 60

Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Gln Val Lys Ser
65 70 75 80

Gly Arg Val Gln Gly Leu Ser His Lys Phe Cys Arg Ser Val His Arg
85 90 95

Lys Asp Gly Tyr Gly Tyr Gly Phe
100

<210> 55

<211> 149

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-31 effector

<400> 55

Leu Phe Asn Ala Leu Arg Ala Thr Gly Leu Pro Val Thr Thr Gly Thr
1 5 10 15

Gly Gly Gln Thr Lys Phe Asn Arg Thr Arg Leu Gly Leu Pro Lys Ala
20 25 30

His Trp Leu Asp Ala Ala Cys Val Gly Gln Val Gly Ala Leu Glu Val

35

40

45

Leu Thr Ser Lys Pro Leu Leu Ile Thr Ala Lys Gly Asn Gly Thr Arg
 50 55 60

Gln Met Cys Gly Thr Asn Lys Phe Gly Phe Pro Thr Arg His Arg Ser
 65 70 75 80

Arg Val Gln Ile His Arg Gly Phe Gln Thr Gly Asp Ile Val Arg Ala
 85 90 95

Thr Val Thr Ala Gly Lys Lys Val Gly Val Tyr Val Gly Arg Val Leu
 100 105 110

Cys Arg Ala Ser Gly Ser Phe Asp Ile Val Thr Ala Thr Gly Arg Val
 115 120 125

Ser Ser Ile Asn His Lys Tyr Cys Lys Thr Ile His Lys Lys Asp Gly
 130 135 140

Tyr Ala Tyr Val Val
 145

<210> 56

<211> 509

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-32 effector

<400> 56

Leu Lys Leu Arg Ser Glu Gly His Asp Thr His Gly Cys Val Pro Val
 1 5 10 15

Arg Gly Ser Ile Val Arg Val His Ala Ala Leu Val Gly Asp Gly Ala
 20 25 30

Lys Asp Ala Gly Ala Thr Ser Pro Arg Asp Met Ser Glu Ala Asn Val
35 40 45

Thr Ala Arg Glu Pro Lys Gly Ser Glu Ala Arg Thr Arg Arg Ser Ala
50 55 60

Gly Ala Val Val Pro Arg Arg His Ser Gly His Val Phe Val Leu Gly
65 70 75 80

Ala Asp Arg Gln Pro Leu Asn Pro Cys Ser Ser Ala Tyr Ala Arg Arg
85 90 95

Leu Leu Arg Asn Gly Lys Ala Ala Val Phe Arg Arg Phe Pro Phe Thr
100 105 110

Ile Ile Leu Lys Glu Arg Thr Arg Asp Leu Ser Lys Val Ser Asp His
115 120 125

Arg Leu Lys Leu Asp Pro Gly Ser Lys Thr Thr Gly Ile Ala Val Leu
130 135 140

Ser Gly Lys Asn Val Val Phe Ala Ala Glu Leu Lys His Arg Gly Gln
145 150 155 160

Glu Ile Thr Thr Arg Leu Met Glu Arg Arg Gln Phe Arg Arg Cys Arg
165 170 175

Arg Asn Arg Thr Thr Arg Tyr Arg Lys Pro Arg Phe Asn Asn Arg Arg
180 185 190

Arg Pro Asp Gly Trp Leu Ala Pro Ser Leu Glu His Arg Val Ala Asn
195 200 205

Leu Met Thr Trp Val Arg Arg Leu Arg Lys Val Cys Pro Ile Ser Ser
210 215 220

Ile Ser Val Glu Leu Ala Lys Phe Asp Thr Gln Leu Met Glu Asn Pro
225 230 235 240

Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Thr Leu Lys Gly Tyr Glu

245

250

255

Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Arg Cys Ala Tyr Cys
 260 265 270

Gly Thr Glu Asn Ala Gln Leu Glu Val Glu His Ile Val Pro Lys Ser
 275 280 285

Arg Gly Gly Ser Asn Arg Val Asp Asn Leu Thr Leu Ala Cys His Pro
 290 295 300

Cys Asn Glu Lys Lys Gly Ala Arg Thr Ala Ala Glu Phe Gly Tyr Pro
 305 310 315 320

Glu Ile Gln Lys Lys Ala Lys Gln Pro Ile Lys Asp Ala Ala Ala Met
 325 330 335

Asn Ala Thr Arg Trp Ile Ile Phe Glu Arg Leu Lys Glu Thr Gly Leu
 340 345 350

Pro Val Glu Cys Gly Thr Gly Ser Arg Thr Lys Phe Asn Arg Lys Arg
 355 360 365

Leu Gly Leu Pro Lys Thr His Trp Gly Asp Ala Val Cys Val Gly Val
 370 375 380

Ser Val Pro Asn Arg Ile Ile Gly Pro Ser Ser Val Leu Asn Ile Thr
 385 390 395 400

Ala Thr Gly His Gly Asn Arg Gln Met Cys Gly Thr Asp Arg Cys Gly
 405 410 415

Phe Pro Ile Arg His Arg Thr Arg Leu Lys Arg His Phe Gly Phe Gln
 420 425 430

Thr Gly Asp Met Val Arg Ala Thr Val Pro Ser Gly Lys Arg Ala Gly
 435 440 445

Thr His Val Gly Arg Val Leu Cys Arg Ser Thr Gly Asn Phe Asp Ile
 450 455 460

Gln Thr Arg Met Gly Arg Val Thr Gly Ile Ser His Arg Tyr Cys Arg
465 470 475 480

Thr Ile His Arg Gln Asp Gly Tyr Arg Tyr Ser Ile Glu Gly Gly Gly
485 490 495

Ala Ser Ser Pro Arg Leu Lys Pro Gly Ala Ser Ala Pro
500 505

<210> 57
<211> 469
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-33 effector

<400> 57
Leu Leu Lys Glu Lys Lys Ala Arg Val Val Cys Thr Thr Pro Phe Thr
1 5 10 15

Ile Gln Leu Asn Tyr Asp Thr Pro Asp Ile Thr Gln Asp Leu Ile Leu
20 25 30

Gly Ile Asp Pro Gly Arg Thr Asn Ile Gly Val Ala Val Val Lys Glu
35 40 45

Asp Gly Gln Cys Val Phe Ser Ala His Leu Glu Thr Arg Asn Lys Asp
50 55 60

Val Pro Leu Leu Met Lys Lys Arg Ala Gly Phe Arg Lys Gln His Arg
65 70 75 80

Thr Leu Asp Arg Arg Arg Lys Arg Gln Arg Arg Ala Lys Ala Thr Gly
85 90 95

Asn Thr Val Lys Asn Glu Thr Ile Glu Arg Leu Leu Pro Cys Tyr Gln

100

105

110

Arg Pro Ile Val Cys His Tyr Ile Arg Asn Lys Glu Ala Arg Phe Asn
 115 120 125

Asn Arg Ser Arg Pro Ala Gly Trp Leu Thr Pro Thr Ala Asn His Leu
 130 135 140

Leu Gln Thr His Ile Asn Leu Ile Ala Lys Val Gly Lys Phe Leu Pro
 145 150 155 160

Ile Thr Lys Val Val Val Glu Leu Asn Arg Phe Ala Phe Met Ala Met
 165 170 175

Asp Asn Pro Asn Ile Arg Arg Trp Glu Tyr Gln Gln Gly Pro Leu Tyr
 180 185 190

Gly Leu Gly Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His
 195 200 205

Cys Leu Phe Cys Asp Lys Pro Ile Asp His Tyr His His Val Val Pro
 210 215 220

Arg His Lys Gly Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys
 225 230 235 240

Ala Glu His His Asp Leu Val His Lys Asp Lys Ala Trp Ala Glu Lys
 245 250 255

Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys Tyr His Ala Gln Ser
 260 265 270

Val Leu Asn Gln Ile Ile Ser Phe Leu Met Glu Tyr Leu Gly Arg Glu
 275 280 285

Thr Pro Tyr Asp Val Tyr Ala Thr Asp Gly Lys Ser Thr Lys Gly Phe
 290 295 300

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys
 305 310 315 320

Ile Ala Cys Ser Ile Leu Asp Ala Asn Thr Lys Val Ser Thr Pro Ala
325 330 335

Glu Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ser Cys
340 345 350

Ile Arg Gln Met Val Asp Arg Lys Tyr Ile Leu Asp Ser Lys Val Val
355 360 365

Ala Thr Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asp Ser Leu Gln
370 375 380

Glu Phe Arg Glu Val Tyr Gly Asp Ala Ala Val Ser Gln Leu Thr Val
385 390 395 400

Arg Pro His Ser Pro Gln Tyr Lys Asp Met Thr Arg Ile Met Pro Gly
405 410 415

Ala Val Met Asp Phe Asn Gly Thr Ile Gly Val Met Gln Cys Ser Gly
420 425 430

Gly Arg Asn Asn Gly Lys Val Glu Phe Phe Lys Ser Thr Lys Gly Asn
435 440 445

Lys Thr Pro Pro Lys Lys Cys Val Leu Leu Ala Gln Asn Ala Gly Met
450 455 460

Val Phe Ile Pro Ala
465

<210> 58

<211> 130

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-34 effector

<400> 58

Leu Leu Leu Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys
1 5 10 15

Thr Ser Asp Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu
20 25 30

Thr Ile Lys Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn
35 40 45

Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe
50 55 60

Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly
65 70 75 80

Ser Lys Thr Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val
85 90 95

Arg Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly
100 105 110

Ile Tyr His Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser
115 120 125

Tyr Ala
130

<210> 59

<211> 416

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-35 effector

<400> 59

Leu Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Leu Pro Phe Thr
1 5 10 15

Ile Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Met
20 25 30

Glu Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Val Met Leu
35 40 45

Val His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu
50 55 60

His Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg
65 70 75 80

Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu
85 90 95

Asn Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Cys Lys
100 105 110

Ala Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro
115 120 125

Phe Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu
130 135 140

Val Asn Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe
145 150 155 160

Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys
165 170 175

Cys Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu
180 185 190

His Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu
195 200 205

Val Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu

210

215

220

Ser Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala
 225 230 235 240

His Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg
 245 250 255

Leu Tyr Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala
 260 265 270

Lys Leu Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu
 275 280 285

Leu Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys
 290 295 300

Asp Gly Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile
 305 310 315 320

Lys Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys His
 325 330 335

Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly
 340 345 350

Phe Lys Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys
 355 360 365

Thr Lys Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser
 370 375 380

Lys Gly Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser
 385 390 395 400

His Lys Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 405 410 415

<210> 60

<211> 436

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-36 effector

<400> 60

Leu Val Leu Asp Thr Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala
1 5 10 15

Arg Ala Lys Lys Leu Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg
20 25 30

Phe Pro Phe Thr Ile Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu
35 40 45

Leu Gln Asp Thr Glu Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly
50 55 60

Val Ala Leu Leu Val His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala
65 70 75 80

Ala His Val Glu His Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg
85 90 95

Arg Ala Ile Arg Arg Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln
100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser
115 120 125

Leu Val Ser Lys Ala Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr
130 135 140

Lys Leu Thr Pro Phe Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp
145 150 155 160

Met Gln Lys Leu Glu Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln

165

170

175

Gly Arg Met Phe Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg
 180 185 190

Glu Asn Tyr Thr Cys Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys
 195 200 205

Met Glu Ile Glu His Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser
 210 215 220

Leu Asn Asn Leu Val Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly
 225 230 235 240

Ser Gln Asp Val Gln Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg
 245 250 255

Arg Val Lys Ala Arg Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr
 260 265 270

Asn Ser Ile Arg Leu Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp
 275 280 285

Ala Ile Gly Thr Asn Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln
 290 295 300

Asn Arg Leu Leu Leu Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala
 305 310 315 320

Val Cys Thr Ser Asp Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys
 325 330 335

Pro Leu Thr Ile Lys Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg
 340 345 350

Met Asn Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys
 355 360 365

Asn Phe Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro
 370 375 380

Leu Gly Ser Lys Thr Lys Val Pro Val Gly Thr His Thr Gly Arg Val
385 390 395 400

Ala Val Arg Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys
405 410 415

Leu Gly Ile Tyr His Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly
420 425 430

Tyr Ser Tyr Ala
435

<210> 61
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-37 effector

<400> 61
Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Phe Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp

<210> 62
 <211> 494
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-38 effector

<400> 62
 Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Lys Glu Lys Lys Ala
 20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Phe Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Lys Lys
 85 90 95

Arg Ala Ala Phe Arg Arg Ser His Arg Thr Leu Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Met Ala Ala Gly Thr Thr Val Glu Asn Glu Thr
 115 120 125

Ile Glu Arg Leu Leu Pro Cys Tyr Lys Lys Pro Val Val Cys His Tyr
 130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Lys Arg Pro Lys Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Val Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Lys Asp Lys Ala Trp Thr Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu His Ile Gly Ser Glu Thr Pro Tyr Asp Ser Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Ile Glu Val Ser Met Pro Val Lys Pro Phe Glu Leu Lys Gln

355

360

365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ser
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
 405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Arg Leu His Ser Pro Gln Tyr
 420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Ala Phe Lys Gly
 435 440 445

Thr Ile Gly Val Met Gln Cys Ser Gly Gly Arg Asn Asn Gly Lys Val
 450 455 460

Glu Phe Phe Lys Ser Thr Lys Gly Asn Lys Thr Thr Pro Lys Lys Cys
 465 470 475 480

Val Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 63

<211> 353

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-39 effector

<400> 63

Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Phe Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Ser His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Met Ala Ala Gly Thr Thr Val Glu Asn Glu Thr
115 120 125

Ile Glu Arg Leu Leu Pro Cys Tyr Lys Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Lys Arg Pro Lys Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Val Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro

225		230		235		240									
Ile	Asp	His	Tyr	His	His	Val	Val	Thr	Arg	His	Lys	Gly	Gly	Ser	Glu
				245					250					255	
Thr	Leu	Ala	Asn	Arg	Cys	Gly	Leu	Cys	Ala	Lys	His	His	Asp	Leu	Val
			260					265					270		
His	Lys	Asp	Lys	Ala	Trp	Thr	Glu	Lys	Leu	Val	Thr	Arg	Lys	Gly	Gly
		275					280					285			
Met	Asn	Lys	Lys	Tyr	His	Ala	Leu	Ser	Val	Leu	Asn	Gln	Ile	Ile	Pro
	290					295					300				
His	Leu	Met	Glu	His	Ile	Gly	Ser	Glu	Thr	Pro	Tyr	Asp	Ser	Tyr	Ala
305					310					315					320
Thr	Asp	Gly	Lys	Ser	Thr	Lys	Gly	Phe	Arg	Ile	Ala	Lys	Asn	Val	Pro
				325					330					335	
Lys	Glu	His	Tyr	Thr	Asp	Ala	Tyr	Cys	Ile	Ala	Cys	Ser	Ile	Leu	Asp
			340					345					350		

Thr

<210> 64
 <211> 489
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-40 effector

<400> 64
 Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Arg Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Ala Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro

225		230		235		240									
Ile	Asp	His	Tyr	His	His	Val	Ile	Pro	Arg	His	Lys	Gly	Gly	Ser	Glu
				245					250					255	
Thr	Leu	Ala	Asn	Arg	Cys	Gly	Leu	Cys	Ala	Lys	His	His	Ala	Leu	Val
			260				265						270		
His	Lys	Asp	Lys	Ala	Trp	Ala	Asp	Lys	Leu	Val	Thr	Arg	Lys	Glu	Gly
		275					280					285			
Met	Asn	Lys	Lys	Tyr	His	Ala	Leu	Ser	Val	Leu	Asn	Gln	Ile	Ile	Pro
	290					295					300				
Phe	Leu	Met	Glu	Tyr	Leu	Gly	Ser	Glu	Thr	Leu	Tyr	Asp	Val	Tyr	Ala
305					310					315					320
Ile	Asp	Gly	Arg	Ser	Ile	Lys	Gly	Phe	Arg	Ile	Ala	Lys	Asn	Val	Pro
				325					330					335	
Lys	Glu	His	Tyr	Thr	Asp	Ala	Tyr	Cys	Ile	Ala	Cys	Ser	Ile	Leu	Asp
			340					345					350		
Thr	Asp	Asn	Lys	Val	Ser	Ala	Pro	Val	Glu	Pro	Phe	Glu	Leu	Lys	Gln
		355					360					365			
Phe	Arg	Arg	His	Asp	Arg	Gln	Ala	Cys	Ile	Arg	Gln	Met	Val	Asp	Arg
	370					375					380				
Lys	Tyr	Leu	Leu	His	Gly	Lys	Val	Val	Ala	Ala	Asn	Arg	His	Lys	Ala
385					390					395					400
Phe	Glu	Gln	Lys	Ser	Asp	Ser	Leu	Gln	Glu	Phe	Arg	Glu	Ala	Tyr	Ser
				405					410					415	
Asp	Val	Ala	Val	Ser	Gln	Leu	Thr	Val	Lys	Pro	His	Pro	Pro	Gln	Tyr
			420					425					430		
Lys	Asp	Met	Ser	Arg	Ile	Met	Pro	Gly	Ala	Val	Met	Asp	Phe	Asp	Gly
		435					440					445			

Ile Val Gly Val Met Gln Ser Ser Ile Val Gly Gln Phe Tyr Lys Ser
450 455 460

Thr Lys Gly His Lys Ala Thr Pro Lys Arg Cys Val Leu Leu Ser Gln
465 470 475 480

Asn Ala Gly Met Val Phe Ile Pro Thr
485

<210> 65
<211> 489
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-41 effector

<400> 65
Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys

100	105	110
Arg Gln Arg Arg Ala Arg Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser		
115	120	125
Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr		
130	135	140
Ile Arg Asn Lys Ala Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly		
145	150	155
Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu		
	165	170
Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu		
	180	185
Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg		
	195	200
Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp		
	210	215
Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro		
225	230	235
Ile Asp His Tyr His His Val Ile Pro Arg His Lys Gly Gly Ser Glu		
	245	250
Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val		
	260	265
His Lys Asp Lys Ala Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly		
	275	280
Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro		
	290	295
Phe Leu Met Glu Tyr Leu Gly Ser Glu Thr Leu Tyr Asp Val Tyr Ala		
305	310	315
		320

Ile Asp Gly Arg Ser Ile Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Asn Lys Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu His Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Phe Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Ser
405 410 415

Asp Val Ala Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr
420 425 430

Lys Asp Met Ser Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
435 440 445

Ile Val Gly Val Met Gln Ser Ser Ile Val Gly Gln Phe Tyr Lys Ser
450 455 460

Thr Lys Gly Tyr Lys Ala Thr Pro Lys Arg Cys Val Leu Leu Ser Gln
465 470 475 480

Asn Ala Gly Met Val Phe Ile Pro Thr
485

<210> 66

<211> 168

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-42 effector

<400> 66

Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Arg Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys Pro Ser
130 135 140

Pro Pro Asn Gly Gly Gly Arg Leu Asn Thr Arg Gly Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His
165

<210> 67

<211> 489

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-43 effector

<400> 67

Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Arg Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Ala Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu

165

170

175

Ile Ala Lys Ile Ala Lys Val Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Cys Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Ile Pro Arg His Lys Gly Gly Ser Glu
 245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
 260 265 270

His Lys Asp Lys Ala Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
 275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
 290 295 300

Phe Leu Met Glu Tyr Leu Gly Ser Glu Thr Leu Tyr Asp Val Tyr Ala
 305 310 315 320

Ile Asp Gly Arg Ser Ile Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
 325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Thr Asp Asn Lys Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu His Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Phe Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Ser
405 410 415

Asp Val Ala Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr
420 425 430

Lys Asp Met Ser Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
435 440 445

Ile Val Gly Val Met Gln Ser Ser Ile Val Gly Gln Phe Tyr Lys Ser
450 455 460

Thr Lys Gly His Lys Ala Thr Pro Lys Arg Cys Val Leu Leu Ser Gln
465 470 475 480

Asn Ala Gly Met Val Phe Ile Pro Thr
485

<210> 68
<211> 489
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-44 effector

<400> 68
Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Asn Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr

35

40

45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
 85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Arg Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
 115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
 130 135 140

Ile Arg Asn Lys Ala Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
 165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Cys Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Ile Pro Arg His Lys Gly Gly Ser Glu
 245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

Phe Leu Met Glu Tyr Leu Gly Ser Glu Thr Leu Tyr Asp Val Tyr Ala
305 310 315 320

Ile Asp Gly Arg Ser Ile Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Asn Lys Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu His Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Phe Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Ser
405 410 415

Asp Val Ala Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr
420 425 430

Lys Asp Met Ser Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
435 440 445

Ile Val Gly Val Met Gln Ser Ser Ile Val Gly Gln Phe Tyr Lys Ser
450 455 460

Thr Lys Gly His Lys Ala Thr Pro Lys Arg Cys Val Leu Leu Ser Gln

465

470

475

480

Asn Ala Gly Met Val Phe Ile Pro Thr
485

<210> 69

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-45 effector

<400> 69

Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Asn Lys Ala
20 25 30

Arg Val Val Ser Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
85 90 95

Arg Ala Gly Phe Arg Lys Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Val Ala Gly Thr Thr Val Glu Gly Glu Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly Arg Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Arg Glu His His Ala Leu Val
260 265 270

His Thr Asp Lys Val Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Val Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Arg Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Val Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp

340

345

350

Thr Asp Ile Glu Val Ser Thr Pro Val Glu Pro Phe Glu Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys His Gln Gln Arg Val Asp Arg
 370 375 380

Lys Tyr Tyr Leu Asn Gly Lys Gln Val Ala Thr Asn Arg His Lys Ala
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ser Tyr Gly
 405 410 415

Asp Thr Ala Val Ser Gln Leu Ala Val Lys Pro His Ser Pro Gln Tyr
 420 425 430

Lys Asp Met Thr Arg Ile Met Gln Gly Ala Val Met Asp Phe Gly Gly
 435 440 445

Thr Val Gly Val Phe Gln Gly Ser Asp Gly Phe His Asn Gly Lys Pro
 450 455 460

Asp Tyr Tyr Lys Ser Ala Lys Gly Ala Arg Val Leu Thr Lys Arg Cys
 465 470 475 480

Val Leu Leu Ala Gln Asn Thr Gly Ile Val Phe Ile Pro Ala
 485 490

<210> 70

<211> 403

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-46 effector

<400> 70

Met Ala Arg Lys Leu Leu Asn Ala Gly Lys Ala Ala Val Phe Arg Arg
1 5 10 15

Phe Pro Phe Thr Ile Ile Leu Lys Lys Glu Val Glu Val Thr Pro Lys
20 25 30

Ser Ile Thr Leu Lys Leu Asp Pro Gly Ser Lys Thr Thr Gly Ile Ala
35 40 45

Leu Lys Gln Gly Asp Lys Ile Ile Phe Gly Ala Glu Leu Thr His Arg
50 55 60

Gly Gln Ala Ile Lys Ala Ser Leu Glu Ser Arg Arg Ser Leu Arg Arg
65 70 75 80

Ser Arg Arg Asn Arg His Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
85 90 95

Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val
100 105 110

Glu Thr Thr Leu Thr Trp Val Asn Lys Leu Ile Arg Leu Val Pro Ile
115 120 125

Gly Ser Ile Val Gln Glu Leu Val Arg Phe Asp Leu Gln Gln Ile Glu
130 135 140

Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Glu Leu Ala Gly
145 150 155 160

Tyr Glu Val Arg Glu Tyr Leu Leu Asn Lys Trp Asp Arg Lys Cys Ala
165 170 175

Tyr Cys Ser Ala Glu Asn Ile Pro Leu Gln Val Glu His Ile His Ser
180 185 190

Lys Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ala Cys
195 200 205

Glu Lys Cys Asn Leu Lys Lys Gly Thr Gln Asp Ile Asn Val Phe Leu

210

215

220

Ala Lys Lys Pro Asp Leu Leu Lys Arg Ile Leu Ser Gln Ala Lys Arg
 225 230 235 240

Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Leu
 245 250 255

Asn Arg Leu Gln Glu Thr Gly Leu Pro Val Leu Thr Gly Ser Gly Gly
 260 265 270

Gln Thr Lys Phe Asn Arg Thr Arg Leu Asp Leu Pro Lys Thr His Trp
 275 280 285

Leu Asp Ala Ala Cys Val Gly His Val Asp Gln Leu Glu Val Leu Thr
 290 295 300

Gly Lys Pro Leu Leu Ile Lys Ala Thr Gly His Gly Ser Arg Gln Met
 305 310 315 320

Cys Gly Thr Asp Lys Phe Gly Phe Pro Ser Arg His Arg Thr Arg Lys
 325 330 335

Gln Ile His Gln Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Leu Val
 340 345 350

Thr Ser Gly Lys Lys Ile Gly Ser Tyr Gly Gly Arg Val Leu Cys Arg
 355 360 365

Ala Ser Gly Ser Phe Asp Ile Gln Val Lys Ser Gly Arg Val Gln Gly
 370 375 380

Leu Ser His Lys Phe Cys Arg Ser Val His Arg Lys Asp Gly Tyr Gly
 385 390 395 400

Tyr Gly Phe

<210> 71

<211> 153

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-47 effector

<400> 71

Met Ala Trp Val Asn Arg Leu Arg Arg Trp Ala Pro Val Thr Ala Leu
1 5 10 15

Ser Gln Glu Leu Val Lys Phe Asp Thr Gln Ala Leu Gln Ser Pro Glu
20 25 30

Ile Arg Gly Val Glu Tyr Gln Gln Gly Thr Leu Phe Gly Tyr Glu Val
35 40 45

Arg Glu Tyr Leu Leu Glu Lys Trp His Arg Arg Cys Ala Tyr Cys Ala
50 55 60

Ala Thr Asp Val Pro Leu Gln Val Glu His Ile Val Pro Lys Ser Lys
65 70 75 80

Gly Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ser Cys Ala Asp Cys
85 90 95

Asn Gln Lys Lys Gly Val Leu Pro Val Glu Gly Phe Leu Ala Ser Gln
100 105 110

Pro Asp Arg Leu Lys Arg Ile Leu Ala Gln Ala Thr Pro Gln Ala Gly
115 120 125

Cys Gly Cys Arg Ala Val Val Pro Gly Gly Ala Gly Trp Arg Arg Ala
130 135 140

Gly Asp Gly Glu Thr Arg Pro Ala Ala
145 150

<210> 72

<211> 358
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-48 effector

<400> 72

Met Cys Lys Val Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys Ser Gln Arg Arg Ala Lys Ile Leu Leu Arg Arg Gly Lys Ala Ala
20 25 30

Val Phe Arg Arg Phe Pro Phe Ala Ile Ile Leu Lys Arg Ser Val Ala
35 40 45

Asp Arg Ser Val Leu Arg Leu Lys Ala Gln Pro Leu Arg Leu Lys Ile
50 55 60

Asp Pro Gly Ser Lys Thr Thr Gly Leu Ala Ile Val Asn Asp Ser Ser
65 70 75 80

Gly Glu Val Leu Phe Gly Ala Glu Leu Glu His Arg Gly Asn Leu Ile
85 90 95

Lys Ala Ala Leu Glu Gly Arg Arg Ala Leu Arg Arg Ser Arg Arg Gln
100 105 110

Arg Lys Thr Arg Tyr Arg Lys Ala Arg Phe Ser Asn Arg Arg Arg Gln
115 120 125

Gln Gly Lys Gly Ile Thr Leu Ser Trp Leu Pro Pro Ser Leu Glu Ser
130 135 140

Arg Val Ala Asn Thr Val Thr Trp Val Asn Arg Leu Arg Arg Leu Cys
145 150 155 160

Ser Ile Arg Ala Ile Ser Gln Glu Leu Ala Arg Phe Asp Thr Gln Leu
165 170 175

Met Gln Asn Gly Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu
180 185 190

Ala Gly Tyr Glu Ile Arg Glu Tyr Leu Leu Glu Lys Phe Asn Arg Lys
195 200 205

Cys Ala Tyr Cys Lys Ser Glu Asn Leu Pro Leu Glu Ile Asp His Ile
210 215 220

Ile Pro Lys Ser Arg Gly Gly Thr Asn Arg Val Ser Asn Leu Thr Thr
225 230 235 240

Ala Cys Arg Ala Cys Asn Cys Lys Lys Gly Asn Leu Thr Ala Glu Glu
245 250 255

Phe Gly Tyr Arg Gln Val Gln Ala Ser Ala Lys Ala Pro Leu Lys Asp
260 265 270

Ala Ala Ala Val Asn Thr Thr Arg Trp Glu Leu Tyr Arg Arg Leu Gln
275 280 285

Ala Thr Gly Leu Pro Leu Glu Val Gly Thr Gly Gly Thr Thr Lys Phe
290 295 300

Asn Arg Thr Arg Gln Ala Leu Ala Lys Ala His Trp Ile Asp Ala Ala
305 310 315 320

Cys Val Gly Ala Ser Thr Pro Gln Lys Leu Ile Ile Ile Gly Val Asn
325 330 335

Pro Leu Thr Ile Lys Ala Thr Gly His Gly Arg Arg Gln Arg Cys Arg
340 345 350

Pro Ser Lys Tyr Gly Phe
355

<210> 73

<211> 321
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-49 effector

<400> 73

Met Cys Lys Val Phe Val Leu Asn Ile Asn Lys Gln Pro Leu Thr Pro
1 5 10 15

Cys Ser Pro Arg Arg Ala Lys Ile Leu Leu Gly Lys Gly Lys Ala Ala
20 25 30

Val Phe Arg Arg Phe Pro Phe Thr Ile Ile Leu Lys Arg Ser Val Ala
35 40 45

Asp Ala Ser Val Leu Arg Leu Lys Ala Gln Pro Leu Arg Leu Lys Ile
50 55 60

Asp Pro Gly Ser Lys Thr Thr Gly Leu Ala Ile Val Asn Asp Ser Ser
65 70 75 80

Gly Glu Val Leu Phe Gly Ala Glu Leu Glu His Arg Ser Asn Leu Ile
85 90 95

Lys Ala Ala Leu Glu Gly Arg Arg Ala Leu Arg Arg Cys Arg Arg Gln
100 105 110

Arg Lys Thr Arg Tyr Arg Lys Ala Arg Phe Ser Asn Arg Arg Arg Gln
115 120 125

Gln Gly Lys Gly Ile Thr Leu Ser Trp Leu Pro Pro Ser Leu Glu Ser
130 135 140

Arg Val Ala Asn Thr Val Thr Trp Val Asn Arg Leu Arg Arg Leu Cys
145 150 155 160

Pro Ile Arg Ala Ile Ser Gln Glu Leu Val Cys Phe Asp Thr Gln Leu
165 170 175

Met His Asn Ala Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu
180 185 190

Ala Gly Tyr Glu Ile Arg Glu Tyr Leu Leu Glu Lys Phe Asn Arg Lys
195 200 205

Cys Ala Tyr Cys Lys Ser Glu Asn Leu Pro Leu Glu Ile Asp His Ile
210 215 220

Ile Pro Lys Ser Arg Gly Gly Thr Asn Arg Val Ser Asn Leu Thr Thr
225 230 235 240

Ala Cys Arg Val Cys Asn Arg Lys Lys Gly Asn Leu Thr Ala Gln Glu
245 250 255

Phe Gly Tyr Pro Gln Val Gln Ala Ser Ala Lys Ala Pro Leu Lys Asp
260 265 270

Ala Ala Ala Val Asn Thr Thr Arg Trp Glu Leu Tyr Arg Arg Leu Gln
275 280 285

Ala Thr Gly Leu Pro Leu Glu Val Ala Thr Gly Gly Arg Thr Lys Phe
290 295 300

Asn Arg Thr Arg Gln Ala Leu Ala Lys Ala His Trp Ile Asp Ala Ala
305 310 315 320

Cys

<210> 74

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-50 effector

<400> 74

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ala Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His His
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Ala His Ile Asn Leu
165 170 175

Ile Ala Lys Ala Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Lys Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Ile Gly Ser Glu Thr Leu Tyr Asp Ala Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Ala Asp Thr Lys Val Ser Thr Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu His Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala His Gly

405

410

415

Asn Ala Ala Val Ser Gln Leu Thr Val Lys Pro His His Ser Gln Cys
 420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Met Met Asp Phe Asp Gly
 435 440 445

Ile Val Gly Val Phe Lys Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro
 450 455 460

Asn Tyr Tyr Asn Ser Thr Lys Gly Glu Arg Phe Leu Thr Arg Ser Cys
 465 470 475 480

Val Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 75

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-51 effector

<400> 75

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
 1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
 20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Ala Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Asn His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Met Cys His His
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Cys Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Ile Pro Arg His Lys Arg Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Thr Asp Lys Ala Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly

275

280

285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
 290 295 300

His Leu Met Glu Tyr Ile Gly Ser Glu Thr Leu Tyr Asp Ala Tyr Ala
 305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
 325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Thr Asp Ile Glu Val Ser Ala Pro Val Glu Pro Phe Glu Met Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Ile Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ala
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala His Gly
 405 410 415

Asn Ala Ala Val Ser Gln Leu Thr Val Lys Pro His His Pro Gln Cys
 420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Val Phe Asp Gly
 435 440 445

Ala Val Gly Val Phe Gln Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro
 450 455 460

Asn Tyr Tyr Asn Ser Thr Lys Gly Glu Arg Phe Leu Thr Arg Ser Cys
 465 470 475 480

Val Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 76
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-52 effector

<400> 76
Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Phe Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp
85

<210> 77
<211> 494
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>

<223> Description: MG35-53 effector

<400> 77

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Val Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His His
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Cys Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Val Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Val Asn Arg Cys Gly Leu Cys Thr Glu His His Ser Leu Val
260 265 270

His Thr Asp Lys Val Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Asn Glu Thr Leu Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Ile Glu Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Ala Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Cys Leu Ala Glu Phe Arg Glu Ala Cys Gly
405 410 415

Ala Ala Val Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr

420

425

430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Asp Phe Asn Gly
 435 440 445

Thr Ile Gly Val Met Gln Cys Ser Ser Gly Arg Asn Asn Gly Gly Val
 450 455 460

Asp Tyr Phe Lys Ser Thr Lys Gly His Lys Ala Thr Pro Lys Arg Cys
 465 470 475 480

Val Leu Leu Thr Gln Asn Ala Gly Met Val Phe Ile Pro Thr
 485 490

<210> 78

<211> 489

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-54 effector

<400> 78

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
 1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
 20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Ile Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Val Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Cys Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Asn Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Lys Asp Lys Ala Trp Glu Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro

290

295

300

Phe Leu Met Glu Tyr Leu Gly Ser Glu Thr Leu Tyr Asp Val Tyr Ala
 305 310 315 320

Ile Asp Gly Arg Ser Ile Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
 325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Thr Asp Asn Lys Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu His Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
 385 390 395 400

Phe Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Ser
 405 410 415

Asp Val Ala Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr
 420 425 430

Lys Asp Met Ser Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
 435 440 445

Ile Val Gly Val Met Gln Ser Ser Ile Val Gly Gln Phe Tyr Lys Ser
 450 455 460

Thr Lys Gly His Lys Ala Thr Pro Lys Arg Cys Ala Leu Leu Ser Gln
 465 470 475 480

Asn Ala Gly Met Val Phe Ile Pro Thr
 485

<210> 79

<211> 97

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-55 effector

<400> 79

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
85 90 95

Arg

<210> 80

<211> 343

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-56 effector

<400> 80

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His His
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Ile Ala Lys Val Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Ser Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

Phe Leu Met Glu Tyr Leu Gly Glu Glu Thr Pro Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala
340

<210> 81
<211> 149
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-57 effector

<400> 81
Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala

1	5	10	15
Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala	20	25	30
Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr	35	40	45
Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Val Asp Pro Gly Arg Thr	50	55	60
Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser	65	70	75
Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Lys Lys	85	90	95
Arg Ala Ala Phe Arg Arg Asn His Arg Thr Leu Asp Arg Arg Arg Lys	100	105	110
Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser	115	120	125
Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Met Cys His His	130	135	140
Ile Arg Asn Lys Glu	145		

<210> 82
 <211> 260
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-58 effector

<400> 82

Met Glu Asn Pro Asp Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu
1 5 10 15

Gln Gly Tyr Asp Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Thr
20 25 30

Cys Ala Tyr Cys Gly Val Gln Asn Val Pro Leu Asp Val Glu His Ile
35 40 45

Gln Pro Arg Ser Lys Gly Gly Ser Asp Arg Val Ser Asn Leu Thr Ile
50 55 60

Ala Cys Arg Ser Cys Asn Gln Ala Lys Gly Asn Glu Asp Ile Arg Asp
65 70 75 80

Phe Leu Ser Gly Gln Pro Asp Val Leu Ser Arg Leu Leu Arg Gln Ala
85 90 95

Lys Ser Pro Leu Asn Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala
100 105 110

Leu Phe Lys Ala Leu Lys Ala Thr Gly Val Pro Val Thr Thr Gly Thr
115 120 125

Gly Gly Gln Thr Lys Phe Asn Arg Leu Arg Phe Asn Leu Pro Lys Ala
130 135 140

His Trp Leu Asp Ala Ala Cys Val Gly Asp Val Glu Ser Leu Asp Ile
145 150 155 160

Val Thr Ser Ile Pro Leu Met Ile Arg Ala Lys Gly His Gly Thr Arg
165 170 175

Arg Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Thr Arg His Arg Ser
180 185 190

Arg Arg Gln Ile His Asn Gly Phe Gln Thr Gly Asp Ile Val Thr Ala
195 200 205

Thr Val Thr Ala Gly Lys Lys Ile Gly Ser Tyr Val Gly Arg Val Leu

210

215

220

Cys Arg Ala Ser Gly Ser Phe Asp Ile Thr Thr Ala Ser Gly Arg Val
 225 230 235 240

Thr Gly Ile Asn His Lys Tyr Cys Lys Pro Ile His Arg Lys Asp Gly
 245 250 255

Tyr Ala Tyr Ala
 260

<210> 83

<211> 260

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-59 effector

<400> 83

Met Glu Asn Pro Asp Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu
 1 5 10 15

Gln Gly Tyr Asp Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Thr
 20 25 30

Cys Ala Tyr Cys Gly Val Gln Asn Val Pro Leu Asp Val Glu His Ile
 35 40 45

Gln Pro Arg Ser Lys Gly Gly Ser Asp Arg Val Ser Asn Leu Thr Ile
 50 55 60

Ala Cys Arg Ser Cys Asn Gln Ala Lys Gly Asn Glu Asp Ile Arg Asp
 65 70 75 80

Phe Leu Ser Gly Gln Pro Asp Val Leu Ser Arg Leu Leu Arg Gln Ala
 85 90 95

Lys Ser Pro Leu Asn Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala
100 105 110

Leu Phe Lys Ala Leu Lys Ala Thr Gly Val Pro Val Thr Thr Gly Thr
115 120 125

Gly Gly Gln Thr Lys Phe Asn Arg Leu Arg Phe Asn Leu Pro Lys Ala
130 135 140

His Trp Leu Asp Ala Ala Cys Val Gly Asp Val Glu Ser Leu Asp Ile
145 150 155 160

Val Thr Ser Lys Pro Leu Met Ile Arg Ala Lys Gly His Gly Thr Arg
165 170 175

Arg Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Thr Arg His Arg Ser
180 185 190

Arg Arg Gln Ile His Asn Gly Phe Gln Thr Gly Asp Ile Val Thr Ala
195 200 205

Thr Val Thr Ala Gly Lys Lys Ile Gly Ser Tyr Val Gly Arg Val Leu
210 215 220

Cys Arg Ala Ser Gly Ser Phe Asp Ile Thr Thr Ala Ser Gly Arg Val
225 230 235 240

Thr Gly Ile Asn His Lys Tyr Cys Lys Pro Ile His Arg Lys Asp Gly
245 250 255

Tyr Ala Tyr Ala
260

<210> 84

<211> 429

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-60 effector

<400> 84

Met Glu Thr Phe Lys Cys Pro Ile Leu Tyr Leu Phe Ser Thr Arg Thr
1 5 10 15

Ser Asp Pro Leu Thr Ser Val His Pro Gly Thr Ala Arg His Leu Leu
20 25 30

Asn Ser Gly Glu Ala Ala Val Leu Arg Arg Phe Pro Phe Ser Ile Ile
35 40 45

Leu Lys Glu Ala Arg Pro Glu Ala Thr Val Gln Asp Leu Glu Leu Lys
50 55 60

Leu Asp Pro Gly Ser Lys Val Thr Gly Ile Ala Ile Lys Gln Gly Asn
65 70 75 80

Lys Ile Ile Phe Gly Ala Gln Leu Gln His Arg Gly Gln Gln Ile Gln
85 90 95

Asn Ala Leu Leu Ser Arg Arg Gln Leu Arg Arg Gly Arg Arg Asn Arg
100 105 110

Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp
115 120 125

Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Leu Thr Thr Met Thr
130 135 140

Trp Val Gln Lys Phe Ile Arg Leu Ala Pro Ile Thr Cys Leu Ala Gln
145 150 155 160

Glu Leu Val Arg Phe Asp Leu Gln Leu Met Gln Asn Ser Glu Ile Ser
165 170 175

Gly Val Gln Tyr Gln Gln Gly Glu Leu Lys Gly Tyr Glu Val Arg Glu
180 185 190

Tyr Leu Leu Glu Lys Trp Asn Arg Arg Cys Ala Tyr Cys Ser Val Glu
195 200 205

Asn Val Pro Leu Glu Val Glu His Ile Gln Ala Lys Ser Lys Gly Gly
210 215 220

Ser Asp Arg Val Ser Asn Leu Thr Ile Ala Cys His Gly Cys Asn Gln
225 230 235 240

Gly Lys Gly Asn Gln Asp Ile Arg Asp Phe Leu Ser Ser Gln Pro Asp
245 250 255

Leu Leu Asn Arg Ile Leu Lys Gln Ala Lys Ser Pro Leu Lys Asp Ala
260 265 270

Thr Ala Val Asn Ser Thr Arg Trp Val Leu Phe Asn Tyr Leu Lys Glu
275 280 285

Thr Gly Leu Pro Val Thr Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn
290 295 300

Arg Thr Arg Leu Glu Leu Ser Lys Ser His Trp Leu Asp Ala Ala Cys
305 310 315 320

Val Gly Arg Ile Asp Gly Leu Glu Val Leu Thr Ser Lys Pro Leu Leu
325 330 335

Ile Val Ala Lys Gly His Gly Thr Arg Gln Met Cys Gly Thr Asp Lys
340 345 350

Tyr Gly Phe Pro Thr Arg His Arg Cys Arg Thr Gln Ile His Lys Gly
355 360 365

Phe Gln Thr Gly Asp Ile Val Lys Ala Thr Val Thr Ala Gly Gln Lys
370 375 380

Ile Gly Ser Tyr Arg Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe
385 390 395 400

Asp Ile Val Thr Thr Ala Ala Arg Val Ser Gly Ile Ser His Lys Tyr

405

410

415

Cys Gln Pro Ile His Lys Lys Asp Gly Tyr Ser Tyr Gly
 420 425

<210> 85

<211> 258

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-61 effector

<400> 85

Met Phe Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn
 1 5 10 15

Tyr Thr Cys Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu
 20 25 30

Ile Glu His Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn
 35 40 45

Asn Leu Val Leu Ser Cys His Glu Cys Asn Gln Ala Lys Gly Lys Leu
 50 55 60

Ser Leu Ser Glu Tyr Leu Lys Gly Lys Pro Asn Val Leu Arg Arg Val
 65 70 75 80

Lys Ala Arg Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser
 85 90 95

Ile Arg Leu Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile
 100 105 110

Gly Thr Asn Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg
 115 120 125

Leu Leu Leu Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys
130 135 140

Thr Lys Asp Gly Asn Ala Val Lys Val Glu Pro Ser Leu Lys Pro Leu
145 150 155 160

Thr Ile Lys Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn
165 170 175

Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe
180 185 190

Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly
195 200 205

Ser Lys Thr Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val
210 215 220

Arg Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly
225 230 235 240

Ile Tyr His Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser
245 250 255

Tyr Ala

<210> 86
<211> 446
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-62 effector

<400> 86
Met Phe Lys Gln Pro Asn Phe Asn Lys Ala Leu Val Leu Asp Thr Asn

1	5	10	15
Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu	20	25	30
Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile	35	40	45
Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile	50	55	60
Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His	65	70	75
Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg	85	90	95
Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser	100	105	110
Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg	115	120	125
Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu	130	135	140
Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr	145	150	155
Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn	165	170	175
Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly Tyr	180	185	190
Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys Ile	195	200	205
Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val	210	215	220

Ile Gln Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu Gly
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys His Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys
420 425 430

Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala

435

440

445

<210> 87

<211> 301

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-63 effector

<400> 87

Met	Phe	Lys	Gln	Pro	Asn	Phe	Asn	Lys	Val	Leu	Val	Leu	Asp	Thr	Asn
1				5					10					15	

Arg	Lys	Pro	Leu	Met	Pro	Cys	Tyr	Pro	Ala	Arg	Ala	Lys	Lys	Leu	Leu
			20					25					30		

Ala	Ser	Gly	Arg	Ala	Ser	Val	Phe	Arg	Arg	Phe	Pro	Phe	Thr	Ile	Ile
		35					40					45			

Leu	His	Asp	Arg	Thr	Val	Glu	Glu	Ser	Glu	Leu	Gln	Asp	Thr	Glu	Ile
	50					55					60				

Lys	Ile	Asp	Gln	Gly	Ser	Lys	Thr	Thr	Gly	Val	Ala	Leu	Leu	Val	His
65					70					75					80

Gly	Gln	Asp	Gly	Asp	Thr	Val	Ala	Phe	Ala	Ala	His	Val	Glu	His	Arg
				85					90					95	

Thr	Asn	Val	Lys	Ser	Gly	Leu	Asp	Ser	Arg	Arg	Ile	Ile	Arg	Arg	Ser
			100					105					110		

Arg	Arg	Asn	Arg	Lys	Thr	Arg	Tyr	Arg	Gln	Ala	Arg	Phe	Leu	Asn	Arg
		115					120					125			

Thr	Lys	Pro	Lys	Gly	Trp	Leu	Pro	Pro	Ser	Leu	Met	Ser	Lys	Ala	Glu
	130					135					140				

Asn Ile Leu Asn Trp Val Thr Arg Phe Ala Lys Leu Thr Ser Ile Thr
145 150 155 160

Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu Ser
165 170 175

Pro Asp Ile Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys Ile
195 200 205

Tyr Cys Gly Thr His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Val Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ser His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly
290 295 300

<210> 88

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-64 effector

<400> 88

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Ser
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn
165 170 175

Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu Gly
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Pro Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys His Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys

420

425

430

Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 435 440 445

<210> 89

<211> 224

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-65 effector

<400> 89

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
 1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
 20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
 35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile
 50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
 65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
 85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
 100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
 115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Ala Asn
165 170 175

Pro Asn Ile Glu Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

<210> 90

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-66 effector

<400> 90

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile

50

55

60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Ala Asn
165 170 175

Pro Asn Ile Glu Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu His Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu Gly
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys His Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys
420 425 430

Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 91

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-67 effector

<400> 91

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn
165 170 175

Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Lys Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Trp Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu Gly
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys Tyr Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Thr Lys Thr Lys
385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Ser Gly

405

410

415

Tyr Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Thr Val Ser His Lys
 420 425 430

Tyr Cys Gln Pro Ile Tyr Leu Met Asp Gly Tyr Asn Tyr Val
 435 440 445

<210> 92

<211> 229

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-68 effector

<400> 92

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
 1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
 20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
 35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile
 50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
 65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
 85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
 100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn
165 170 175

Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg
225

<210> 93

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-69 effector

<400> 93

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu

20

25

30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
 35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile
 50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
 65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
 85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
 100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
 115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
 130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr
 145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn
 165 170 175

Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly Tyr
 180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys Ile
 195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
 210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
 225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu Gly
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys His Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys
420 425 430

Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<211> 446
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-70 effector

<400> 94

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln Asp Met Glu Ile
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn
165 170 175

Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu Gly
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys Tyr Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys

370

375

380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
 385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
 405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys
 420 425 430

Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 435 440 445

<210> 95

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-71 effector

<400> 95

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
 1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
 20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
 35 40 45

Leu His Asp Arg Thr Leu Glu Lys Ser Lys Leu Gln Asp Met Glu Ile
 50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Ile Val His
 65 70 75 80

Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Asp
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Leu Thr
145 150 155 160

Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val Asn
165 170 175

Pro Asp Ile Lys Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser Glu
245 250 255

Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ala His Leu
260 265 270

Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu

290

295

300

Val Val Gly Phe Gly Ser Thr Thr
305 310

<210> 96

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-72 effector

<400> 96

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu Ile
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val His
65 70 75 80

Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His Arg
85 90 95

Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Ala Pro Phe Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu Asn
165 170 175

Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln Thr
245 250 255

Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg Leu
260 265 270

Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Phe
275 280 285

Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn Leu
290 295 300

Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu Asn
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp Gly
325 330 335

Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys Ala

340

345

350

Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly Phe
 355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
 370 375 380

Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr Lys
 385 390 395 400

Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser Gly
 405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His Lys
 420 425 430

Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 435 440 445

<210> 97

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-73 effector

<400> 97

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
 1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
 20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile
 35 40 45

Leu His Asp Arg Thr Val Glu Glu Ser Val Leu Gln Glu Val Glu Val
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val His
65 70 75 80

Gly Gln Asp Gly Ala Thr Val Ala Phe Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Ile Lys Leu Thr Pro Phe Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu Asn
165 170 175

Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr
180 185 190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys Ile
195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
225 230 235 240

Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln Thr
245 250 255

Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg Leu

260

265

270

Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Glu Asn Arg Leu Leu Leu Asn
305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys Tyr Gly Phe
355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys
420 425 430

Cys Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 98

<211> 360

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-74 effector

<400> 98

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Val Glu Glu Ser Val Leu Gln Glu Val Glu Val
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val His
65 70 75 80

Gly Gln Asp Gly Ala Thr Val Ala Phe Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu Asn
165 170 175

Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr

180

185

190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys Ile
 195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
 210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
 225 230 235 240

Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln Thr
 245 250 255

Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg Leu
 260 265 270

Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
 275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
 290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Glu Asn Arg Leu Leu Leu Asn
 305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
 325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
 340 345 350

Val Gly Arg Gly Ser Arg Gln Phe
 355 360

<210> 99

<211> 446

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-75 effector

<400> 99

Met Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr Asn
1 5 10 15

Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu Leu
20 25 30

Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile
35 40 45

Leu His Asp Arg Thr Val Glu Glu Ser Val Leu Gln Glu Val Glu Val
50 55 60

Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val His
65 70 75 80

Gly Gln Asp Gly Ala Thr Val Ala Phe Ala Ala His Ile Glu His Arg
85 90 95

Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser
100 105 110

Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg
115 120 125

Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu
130 135 140

Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe Thr
145 150 155 160

Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu Asn
165 170 175

Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr

180

185

190

Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys Ile
 195 200 205

Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val
 210 215 220

Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu
 225 230 235 240

Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln Thr
 245 250 255

Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg Leu
 260 265 270

Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr
 275 280 285

Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys Leu
 290 295 300

Val Val Gly Phe Gly Ser Thr Thr Lys Glu Asn Arg Leu Leu Leu Asn
 305 310 315 320

Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp Gly
 325 330 335

Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys Ala
 340 345 350

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys Tyr Gly Phe
 355 360 365

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
 370 375 380

Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr Lys
 385 390 395 400

Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys Gly
405 410 415

Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His Lys
420 425 430

Cys Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 100

<211> 160

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-76 effector

<400> 100

Met Gly Tyr His Asp Tyr Pro Ile Leu Thr Gly Ile Leu Phe Ile Arg
1 5 10 15

Glu Ser Leu Thr Leu Ala Cys His Asp Cys Asn Gln Lys Lys Gly Asn
20 25 30

Gln Asp Val Arg Glu Phe Leu Ala Thr Lys Pro Asp Leu Leu Asn Arg
35 40 45

Ile Leu Gln Gln Ala Lys Leu Pro Leu Lys Asp Ala Ala Ala Val Asn
50 55 60

Ser Thr Arg Trp Ala Leu Phe Arg Ala Leu Lys Glu Thr Gly Leu Pro
65 70 75 80

Val Thr Asp Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Asn Arg Leu
85 90 95

Gly Leu Pro Lys Ser His Trp Leu Asp Ala Ala Cys Val Gly Asn Val

100

105

110

Glu Thr Leu Lys Val Leu Thr Ser Lys Pro Leu Leu Ile Ala Ala Thr
 115 120 125

Gly His Gly Arg Arg Gln Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro
 130 135 140

Thr Arg His Lys Ser Arg Val Gln Ile His Lys Gly Phe Leu Ala Trp
 145 150 155 160

<210> 101

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-77 effector

<400> 101

Met His Leu Arg Val Phe Pro Ala Arg Ser Ser Ala Lys His Thr Pro
 1 5 10 15

Arg Gln Gly Lys His Tyr Arg Pro Ser Gly Val Cys Leu Ile Gly Lys
 20 25 30

Lys Leu Arg Lys Glu Ile Thr Leu Asn Met Asp Met Val Tyr Val Leu
 35 40 45

Asn Lys Asp Gly Lys Pro Leu Met Ala Thr Thr Arg Gly Gly Arg Val
 50 55 60

Arg Tyr Leu Leu Lys Glu Lys Lys Ala Arg Val Val Ser Ser Thr Pro
 65 70 75 80

Phe Thr Ile Gln Leu Asn Tyr Asp Thr Pro Asp Val Thr Gln Asp Leu
 85 90 95

Ile Leu Gly Ile Asp Pro Gly Arg Thr Asn Ile Gly Val Ala Val Val
100 105 110

Lys Glu Asp Gly Ser Cys Val Phe Ser Ala His Leu Glu Thr Arg Asn
115 120 125

Lys Asp Val Pro Leu Leu Met Gln Lys Arg Ala Gly Phe Arg Lys Gln
130 135 140

His Arg Asn Leu Asp Arg Arg Arg Lys Arg Gln Arg Arg Ala Lys Ala
145 150 155 160

Ala Gly Thr Ala Ile Ala Glu Gly Ser Val Glu Arg Leu Leu Pro Gly
165 170 175

Tyr Lys Lys Pro Ile Val Cys His His Ile Arg Asn Lys Glu Ala Arg
180 185 190

Phe Asn Asn Arg Ser Arg
195

<210> 102
<211> 253
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-78 effector

<400> 102
Met Asn Arg Val Phe Val Leu Asp Thr Gln Arg Arg Pro Leu Asp Pro
1 5 10 15

Val His Pro Gly Lys Ala Arg Leu Leu Leu Asn Gln Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Glu Ala His Pro

35

40

45

Asp Val Pro Val Gln Asp Leu Glu Leu Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Val Thr Gly Ile Ala Ile Lys Gln Gly Asn Lys Ile Ile Phe Gly Ala
 65 70 75 80

Glu Leu Arg His Arg Gly Gln Gln Ile Arg Asp Ala Leu Leu Ser Arg
 85 90 95

Arg Gln Leu Arg His Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln
 100 105 110

Pro Arg Phe Leu Asn Arg Lys Arg Pro Asp Gly Trp Leu Ala Pro Ser
 115 120 125

Leu Lys His Arg Val Asp Thr Val Leu Thr Trp Val Asn Arg Phe Arg
 130 135 140

Lys Leu Ala Pro Leu Gly Ser Ile Ala Gln Glu Leu Val Arg Phe Asp
 145 150 155 160

Leu Gln Lys Leu Gln Asn Pro Glu Val Ser Gly Ile Glu Tyr Gln Gln
 165 170 175

Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp
 180 185 190

Gly Arg Lys Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu Glu Val
 195 200 205

Glu His Ile His Pro Arg Ser Lys Gly Gly Thr Asp Arg Val Ser Asn
 210 215 220

Leu Ala Ile Ala Cys His Ala Cys Asn Gln Arg Lys Gly Asn Arg Asp
 225 230 235 240

Ile Arg Asp Phe Leu Phe Gly Lys Pro Glu Leu Leu Gln
 245 250

<210> 103
<211> 216
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-79 effector

<400> 103
Met Pro Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys
1 5 10 15

Ala Ala Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Glu Arg
20 25 30

Val Asp Gly Gln Leu Gln Pro Val Glu Ile Lys Phe Asp Pro Gly Ser
35 40 45

Arg Thr Thr Gly Ile Ala Leu Val Gly His Phe Glu Arg Gly Ser Glu
50 55 60

Val Ile Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Ser
65 70 75 80

Asn Leu Val Ser Arg Arg Ala Ile Arg Arg Ser Arg Arg Asn Arg Lys
85 90 95

Thr Arg Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Lys Ser
100 105 110

Trp Leu Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp
115 120 125

Ala Leu Lys Leu Ser Arg Leu Ala Pro Ile Thr Gln Ile Ala Val Glu
130 135 140

Thr Val Arg Phe Asp Thr Gln Lys Met Gln Asn Pro Glu Val Ser Gly

145		150		155		160									
Met	Glu	Tyr	Gln	Gln	Gly	Glu	Leu	Ala	Gly	Tyr	Glu	Phe	Arg	Glu	Tyr
				165					170					175	
Leu	Leu	Glu	Lys	Trp	Gly	Arg	Gln	Cys	Ala	Tyr	Cys	Gly	Val	Gln	Asn
			180					185					190		
Val	Pro	Leu	Glu	Val	Asp	Val	Leu	Met	Glu	Asp	Val	Glu	Leu	Glu	Glu
		195					200					205			
Leu	Leu	His	Gln	Phe	Arg	Tyr	Arg								
	210					215									

<210> 104
 <211> 274
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-80 effector

<400> 104
Met Pro Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Arg Lys
1 5 10 15

Ala Ala Val Leu Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys His Arg
20 25 30

Val Gly Gly Asp Leu Gln Pro Val Glu Ile Lys Phe Asp Pro Gly Ser
35 40 45

Arg Thr Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Ser Glu
50 55 60

Val Ile Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Ser
65 70 75 80

Asn Leu Asp Ser Arg Arg Ser Ile Arg Arg Ser Arg Arg Asn Arg Lys
85 90 95

Thr Arg Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Lys Gly
100 105 110

Trp Leu Pro Pro Ser Leu Trp Ser Arg Val Asp Asn Val Lys Asn Leu
115 120 125

Met Leu Lys Leu Ser Arg Leu Ala Pro Ile Thr Gln Ile Ala Val Glu
130 135 140

Thr Val Arg Phe Asp Thr Gln Gln Met Gln Asn Pro Glu Ile Ser Gly
145 150 155 160

Val Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr
165 170 175

Leu Leu Glu Lys Trp Gly Arg Gln Cys Ala Tyr Cys Gly Ala Lys Asn
180 185 190

Val Pro Leu Glu Val Glu His Ile Gln Ala Arg Ser Gln Gly Gly Thr
195 200 205

Asp Arg Val Ser Asn Leu Thr Leu Ala Cys Thr Ser Cys Asn Leu Gln
210 215 220

Lys Gly Asn Lys Asp Ile Lys Glu Phe Leu Lys His Lys Pro Lys Arg
225 230 235 240

Leu Lys Thr Ile Gln Thr Phe Ala Lys Ala Pro Leu Lys Asp Ala Ala
245 250 255

Ala Met Asn Ala Thr Arg Asn Ala Ile Gly Asn Val Leu Lys Gly Phe
260 265 270

Gly Leu

<210> 105

<211> 430
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-81 effector

<400> 105

Met Pro Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Arg Lys
1 5 10 15

Ala Ala Val Leu Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys His Arg
20 25 30

Val Gly Gly Asp Leu Gln Pro Val Glu Ile Lys Phe Asp Pro Gly Ser
35 40 45

Arg Thr Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Ser Glu
50 55 60

Val Ile Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Ser
65 70 75 80

Asn Leu Asp Ser Arg Arg Ser Ile Arg Arg Ser Arg Arg Asn Arg Lys
85 90 95

Thr Arg Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Lys Gly
100 105 110

Trp Leu Pro Pro Ser Leu Trp Ser Arg Val Asp Asn Val Lys Asn Leu
115 120 125

Met Leu Lys Leu Ser Arg Leu Ala Pro Ile Thr Gln Ile Ala Val Glu
130 135 140

Thr Val Arg Phe Asp Thr Gln Gln Met Gln Asn Pro Glu Ile Ser Gly
145 150 155 160

Val Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr
165 170 175

Leu Leu Glu Lys Trp Gly Arg Gln Cys Ala Tyr Cys Gly Ala Lys Asn
180 185 190

Val Pro Leu Glu Val Glu His Ile Gln Ala Arg Ser Gln Gly Gly Thr
195 200 205

Asp Arg Val Ser Asn Leu Thr Leu Ala Cys Thr Ser Cys Asn Leu Gln
210 215 220

Lys Gly Asn Lys Asp Ile Lys Glu Phe Leu Lys His Lys Pro Lys Arg
225 230 235 240

Leu Lys Thr Ile Gln Thr Phe Ala Lys Ala Pro Leu Lys Asp Ala Ala
245 250 255

Ala Met Asn Ala Thr Arg Asn Ala Ile Gly Asn Val Leu Lys Gly Phe
260 265 270

Gly Leu Pro Ile Thr Ile Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg
275 280 285

Thr Gln Gln Gly Tyr Pro Lys Asp His Trp Ile Asp Ala Ala Cys Val
290 295 300

Gly Glu Ser Gly Asn Asn Val Ile Ile Pro Lys Ala Ile Thr Pro Leu
305 310 315 320

Ile Ile Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn
325 330 335

Gln Tyr Gly Phe Pro Arg Thr Gly Pro Lys Lys Lys Lys Arg Val Lys
340 345 350

Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Ile Val Thr Ser Gly Lys
355 360 365

Lys Ile Gly Thr Tyr Val Gly Arg Val Met Val Arg Lys Thr Gly Cys

370

375

380

Phe Asp Ile Tyr Thr Gly Phe Gly Arg Ile Ser Ser Leu Ser Tyr Arg
 385 390 395 400

Phe Cys Arg Leu Ile Gln Arg Thr Asp Gly Tyr Glu Tyr Ser Thr Asp
 405 410 415

Leu Cys Pro Ile Lys Lys Gly Ser Gly Lys Tyr Phe Asn Ser
 420 425 430

<210> 106

<211> 413

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-82 effector

<400> 106

Met Pro Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Asn Gly Lys
 1 5 10 15

Ala Ala Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Lys Cys Arg
 20 25 30

Val Gly Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser
 35 40 45

Arg Thr Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Ser Glu
 50 55 60

Val Ile Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Arg
 65 70 75 80

Asn Leu Asp Ser Arg Arg Ala Val Arg Arg Ser Arg Arg Asn Arg Lys
 85 90 95

Thr Arg Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Arg Gly
100 105 110

Trp Leu Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp
115 120 125

Met Ile Lys Leu Ser Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu
130 135 140

Thr Val Lys Phe Asp Thr Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly
145 150 155 160

Val Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr
165 170 175

Leu Leu Glu Lys Trp Gly Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn
180 185 190

Val Pro Leu Glu Ile Glu His Ile Gln Ala Cys Ser Lys Gly Gly Ser
195 200 205

Asp Arg Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp
210 215 220

Lys Gly Asn Lys Asp Ile Lys Glu Phe Met Lys Arg Lys Thr Glu Arg
225 230 235 240

Leu Lys Lys Ile Gln Ala Gln Gly Lys Ala Pro Leu Lys Asp Thr Ala
245 250 255

Ala Val Asn Ala Thr Arg Tyr Ala Thr Gly Asn Ala Leu Lys Gly Leu
260 265 270

Gly Leu Pro Ile Thr Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg
275 280 285

Val Lys Leu Gly Tyr Ser Lys Asp His Trp Ile Asp Ala Ala Cys Val
290 295 300

Gly Glu Ser Gly Ala Gln Val Val Ile Pro Pro Ala Ile Thr Pro Leu

305 310 315 320

Ile Ile Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn
325 330 335

Gln Tyr Gly Phe Pro Arg Thr Gly Pro Lys Lys His Lys Arg Val Lys
340 345 350

Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys
355 360 365

Lys Ile Gly Thr His Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser
370 375 380

Phe Asp Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys
385 390 395 400

Tyr Cys Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr
405 410

<210> 107
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-83 effector

<400> 107
Met Pro Val Lys Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg
1 5 10 15

Gln Ala Cys Ile Arg Gln Met Val Asp Arg Lys Tyr Leu Leu Asp Gly
20 25 30

Lys Val Val Ala Thr Asn Arg His Lys Ser Ile Glu Gln Lys Ser Asp
35 40 45

Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly Asp Ala Ala Val Ser Gln
50 55 60

Leu Thr Val Arg Leu His Ser Pro Gln Tyr Lys Asp Met Ala Arg Ile
65 70 75 80

Met Pro Gly Ala Val Met Ala Phe Lys Gly Thr Ile Gly Val Met Gln
85 90 95

Cys Ser Gly Gly Arg Asn Asn Gly Lys Val Glu Phe Phe Lys Ser Thr
100 105 110

Lys Gly Asn Lys Thr Thr Pro Lys Lys Cys Val Leu Leu Ala Gln Asn
115 120 125

Ala Gly Met Val Phe Ile Pro Ala
130 135

<210> 108

<211> 113

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-84 effector

<400> 108

Met Gln Leu Gly Asp Arg Ser Ser His Val Val Ile Pro Gln Thr Ile
1 5 10 15

Thr Pro Leu Ile Ile Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys
20 25 30

Ser Met Asn Gln Tyr Gly Phe Pro Arg Thr Ser Pro Lys Lys Tyr Lys
35 40 45

Arg Val Lys Gly Phe Gln Ser Gly Asp Ile Val Lys Ala Ile Val Thr

50

55

60

Lys Gly Lys Lys Ile Gly Thr Tyr Val Gly Cys Val Ala Val Arg Ala
65 70 75 80

Asn Gly Ser Phe Asp Ile Gly Asn Gly Glu Glu Arg Val Gly Ser Ile
85 90 95

Ser Tyr Lys Tyr Cys Gln Leu Leu Gln Arg Ala Asp Gly Tyr Glu Tyr
100 105 110

Thr

<210> 109

<211> 423

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-85 effector

<400> 109

Met Gln Asn Tyr Thr Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Phe
1 5 10 15

Pro Val His Pro Ala Val Ala Arg Lys Met Leu Ser Asn Ala Glu Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys His Gly Ala
35 40 45

Asp Arg Pro Thr Gln Ser Ile Glu Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Ile Ala Leu Leu Lys Gly Glu Arg Leu Ile Phe Ala Ala
65 70 75 80

Glu Leu Ser His Arg Gly Gln Ala Ile Lys Ala Ser Leu Asp Ala Arg
85 90 95

Arg Ala Ile Arg Arg Asn Arg Arg Thr Arg His Thr Arg Tyr Arg Pro
100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg Ser Lys Gly Trp Leu Thr Pro Ser
115 120 125

Leu Lys His Arg Val Cys Thr Thr Leu Thr Trp Val Asn Lys Phe Ile
130 135 140

Arg Phe Ala Pro Val Asn Ser Ile Ala Met Glu Leu Val Arg Phe Asp
145 150 155 160

Leu Gln Gln Leu Glu Asn Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln
165 170 175

Gly Glu Leu Leu Gly Tyr Glu Ile Arg Glu Tyr Leu Leu Asn Lys Trp
180 185 190

Asp Arg Lys Cys Thr Tyr Cys Gly Ala Glu Asn Ile Pro Leu Gln Val
195 200 205

Glu His Ile His Pro Arg Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn
210 215 220

Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu Lys Lys Gly Thr Gln Asp
225 230 235 240

Ile Lys Asp Phe Leu Ser Lys Lys Thr Asp Leu Leu Lys Gln Ile Met
245 250 255

Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ser Ala Val Asn Ser Thr
260 265 270

Arg Trp Ala Leu Phe Asn Gln Leu Lys Leu Thr Gly Leu Pro Val Thr
275 280 285

Thr Gly Ser Gly Gly Gln Thr Lys Tyr Asn Arg Thr Arg Leu Glu Leu

290

295

300

Pro Lys Thr His Tyr Phe Asp Ala Ala Cys Val Gly Lys Val Asp Lys
 305 310 315 320

Leu Val Val Leu Thr Thr Gln Pro Leu Leu Ile Lys Ala Asn Gly His
 325 330 335

Gly Thr Arg Gln Met Cys Arg Thr Asp Lys Phe Gly Phe Pro Ser Arg
 340 345 350

His Ala Pro Arg Asn Lys Phe Val Lys Gly Phe Gln Thr Gly Asp Ile
 355 360 365

Val Lys Ala Ile Val Thr Ser Gly Lys Lys Ile Gly Glu Tyr Val Gly
 370 375 380

Arg Ala Ala Val Arg Ser Ser Gly Ser Phe Asn Ile Ser Ala Lys Glu
 385 390 395 400

Leu Val Gln Gly Ile Gly His Lys Tyr Cys Glu Ile Leu His Arg Lys
 405 410 415

Asp Gly Tyr Ser Tyr Gln Phe
 420

<210> 110

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-86 effector

<400> 110

Met Gln Arg Ile Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
 1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Thr Tyr Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Thr Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Val Lys Asn Asn Leu
85 90 95

Asn Ser Arg Arg Ser Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Gln Gly Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Ser Ile Trp Met Ile
130 135 140

Lys Leu Ser Trp Leu Ala Pro Ile Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Met Gln Lys Pro Glu Ile Ser Gly Val Glu
165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Gly Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro
195 200 205

Phe Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp Lys Gly

225		230		235		240									
Asn	Lys	Asp	Ile	Lys	Glu	Phe	Met	Lys	Arg	Lys	Pro	Lys	Arg	Leu	Lys
				245					250					255	
Lys	Ile	Gln	Ala	Gln	Ser	Lys	Ala	Pro	Leu	Lys	Asp	Ala	Ala	Ala	Val
			260					265					270		
Asn	Ala	Thr	Arg	Tyr	Val	Ile	Gly	Asn	Ala	Leu	Lys	Ser	Phe	Gly	Leu
		275					280					285			
Pro	Ile	Thr	Phe	Ser	Ser	Gly	Gly	Arg	Thr	Lys	Phe	Asn	Arg	Ile	Lys
	290					295					300				
Gln	Gly	Tyr	Lys	Lys	Asp	His	Trp	Ile	Asp	Ala	Ala	Cys	Val	Ser	Glu
305					310					315					320
Ser	Gly	Gly	His	Val	Val	Ile	Pro	Gln	Ala	Ile	Thr	Pro	Leu	Ile	Ile
				325					330					335	
Thr	Ala	Lys	Gly	Arg	Gly	Ser	Arg	Gln	Lys	Cys	Ser	Met	Asn	Gln	Tyr
			340					345					350		
Gly	Phe	Pro	Arg	Thr	Gly	Pro	Lys	Lys	Tyr	Lys	Arg	Val	Lys	Gly	Phe
		355					360					365			
Gln	Thr	Gly	Asp	Ile	Val	Lys	Ala	Ile	Val	Thr	Lys	Gly	Lys	Lys	Ile
	370					375					380				
Gly	Thr	Tyr	Val	Gly	Arg	Val	Ala	Val	Arg	Ala	Ser	Gly	Ser	Phe	Asp
385					390					395					400
Ile	Gly	Ser	Gly	Glu	Glu	Arg	Val	Gly	Ser	Ile	Ser	Tyr	Lys	Tyr	Cys
				405					410					415	
Arg	Leu	Leu	Gln	Lys	Ser	Asp	Gly	Tyr	Glu	Tyr	Thr				
			420					425							

<210> 111
 <211> 414
 <212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-87 effector

<400> 111

Met Gln Arg Val Phe Ile Leu Asp His Asn Lys Lys Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Asn Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Ile Ile Ile Met Lys Cys Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Pro Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly His Gln Ile Lys Arg Asn Leu
85 90 95

Asp Ser Arg Arg Ala Val Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Pro Ala Arg Phe Asn Asn Arg Gln Arg Pro Lys Ser Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp Met Ile
130 135 140

Lys Leu Ser Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Val Glu

165

170

175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
 180 185 190

Glu Lys Trp Asp Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro
 195 200 205

Leu Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
 210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Gln Lys Lys Gly
 225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys
 245 250 255

Lys Ile Gln Ala Gln Ala Lys Val Pro Leu Lys Asp Ala Ala Ala Val
 260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Val Leu Lys Asp Phe Gly Leu
 275 280 285

Pro Ile Thr Phe Ser Thr Gly Gly Arg Thr Lys Phe Asn Arg Thr Thr
 290 295 300

Arg Gly Tyr Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Glu
 305 310 315 320

Ser Gly Ala Lys Val Val Ile Pro Pro Ala Ile Thr Pro Leu Ile Ile
 325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn Gln Tyr
 340 345 350

Gly Phe Pro Arg Thr Ser Pro Lys Lys His Lys Arg Val Lys Gly Phe
 355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Asn Ile
 370 375 380

Gly Thr Tyr Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys
405 410

<210> 112
<211> 427
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-88 effector

<400> 112
Met Gln Arg Val Phe Ile Leu Asp His Asn Lys Lys Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Asn Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Ile Ile Ile Met Lys Cys Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Pro Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly His Gln Ile Lys Arg Asn Leu
85 90 95

Asp Ser Arg Arg Ala Val Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Pro Ala Arg Phe Asn Asn Arg Gln Arg Pro Lys Ser Trp Leu

115

120

125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp Met Ile
 130 135 140

Lys Leu Ser Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
 145 150 155 160

Arg Phe Asp Thr Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Val Glu
 165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
 180 185 190

Glu Lys Trp Asp Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro
 195 200 205

Leu Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
 210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Gln Lys Lys Gly
 225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys
 245 250 255

Lys Ile Gln Ala Gln Ala Lys Val Pro Leu Lys Asp Ala Ala Ala Val
 260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Val Leu Lys Asp Phe Gly Leu
 275 280 285

Pro Ile Thr Phe Ser Thr Gly Gly Arg Thr Lys Phe Asn Arg Thr Thr
 290 295 300

Arg Gly Tyr Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Glu
 305 310 315 320

Ser Gly Ala Lys Val Val Ile Pro Pro Ala Ile Thr Pro Leu Ile Ile
 325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Ser Pro Lys Lys His Lys Arg Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Asn Ile
370 375 380

Gly Thr Tyr Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr
420 425

<210> 113

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-89 effector

<400> 113

Met Gln Arg Val Phe Ile Leu Asp His Asn Lys Lys Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Asn Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Ile Ile Ile Met Lys Cys Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr

50

55

60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Pro Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly His Gln Ile Lys Arg Asn Leu
85 90 95

Asp Ser Arg Arg Ala Val Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Pro Ala Arg Phe Asn Asn Arg Gln Arg Pro Lys Ser Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp Met Ile
130 135 140

Lys Leu Ser Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Val Glu
165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Asp Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro
195 200 205

Leu Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Gln Lys Lys Gly
225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys
245 250 255

Lys Ile Gln Ala Gln Ala Lys Val Pro Leu Lys Asp Ala Ala Ala Val
260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Val Leu Lys Asp Phe Gly Leu
275 280 285

Pro Ile Thr Phe Ser Thr Gly Gly Arg Thr Lys Phe Asn Arg Thr Thr
290 295 300

Arg Gly Tyr Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Glu
305 310 315 320

Ser Gly Ala Lys Val Val Ile Pro Pro Ala Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Ser Pro Lys Lys His Lys Arg Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Asn Ile
370 375 380

Gly Thr Tyr Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr Thr
420 425

<210> 114

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-90 effector

<400> 114

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Ala Ile Ile Met Thr His Arg Val Gly
35 40 45

Gly Asp Leu Gln Thr Val Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly Asp Phe Asp Arg Gly Lys Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly His Gln Ile Lys Ser Asn Leu
85 90 95

Asn Ser Arg Arg Ala Ile Arg Arg Ala Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Gln Ala Arg Phe Asn Asn Arg Arg Arg Pro Lys Gly Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Thr Lys Asn Trp Met His
130 135 140

Lys Leu Ala Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Leu Gln Lys Pro Glu Ile Ser Gly Val Glu
165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Gly Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Ile Pro
195 200 205

Leu Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp Lys Gly
225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Leu Ser Leu Lys Pro Lys Arg Leu Lys
245 250 255

Lys Ile Gln Ala Thr Ala Thr Ala Pro Leu Lys Asp Ala Ala Ala Val
260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Val Leu Lys Cys Phe Ser Leu
275 280 285

Pro Ile Thr Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Val Lys
290 295 300

Leu Gly Tyr Leu Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
305 310 315 320

Ser Gly Ser Gln Val Val Ile Pro Lys Ala Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ser Lys Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Gly Pro Lys Lys Gln Lys Gln Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Ile Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Thr Tyr Ile Gly Arg Val Val Val Arg Ser Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ser Gly Glu Lys Lys Val Gly Ser Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Leu Gln Arg Ala Asp Gly Tyr Glu Tyr Thr

420

425

<210> 115

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-91 effector

<400> 115

Met	Gln	Arg	Val	Phe	Val	Leu	Asp	His	Asn	Lys	Gln	Pro	Leu	Met	Pro
1				5					10					15	

Cys	His	Pro	Ala	Arg	Ala	Arg	Lys	Leu	Leu	Lys	Lys	Gly	Lys	Ala	Ala
			20				25						30		

Val	Tyr	Arg	Arg	Tyr	Pro	Phe	Thr	Ile	Ile	Met	Thr	His	Arg	Leu	Cys
		35					40					45			

Gly	Asp	Leu	Gln	Pro	Ile	Glu	Ile	Lys	Phe	Asp	Leu	Gly	Ser	Arg	Thr
	50					55					60				

Thr	Gly	Ile	Ala	Leu	Val	Gly	His	Phe	Asp	Arg	Gly	Ser	Glu	Val	Ile
65					70					75					80

Trp	Ala	Gly	Asn	Leu	Asn	His	Arg	Gly	Tyr	Gln	Ile	Lys	Lys	Asp	Leu
				85					90					95	

Asn	Ser	Arg	Arg	Ala	Ile	Arg	Arg	Thr	Arg	Arg	Asn	Arg	Lys	Thr	Arg
			100					105					110		

Tyr	Arg	Pro	Ala	Arg	Phe	Leu	Asn	Arg	Arg	Arg	Pro	Thr	Gly	Trp	Leu
		115					120					125			

Pro	Pro	Ser	Leu	Arg	Ser	Arg	Val	Leu	Asn	Val	Asn	Asn	Trp	Met	Leu
	130					135					140				

Lys Leu Ser Gln Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Ile Gln Lys Pro Glu Ile Ser Gly Val Glu
165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Gly Arg Glu Cys Val Tyr Cys Gly Ala Lys Asn Val Pro
195 200 205

Leu Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp Lys Gly
225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys
245 250 255

Lys Ile Gln Thr Ile Ala Thr Ala Ser Leu Lys Asp Ala Ala Ala Ile
260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Ala Leu Lys Gly Phe Gly Leu
275 280 285

Pro Ile Ala Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Thr Ser
290 295 300

Cys Gly Tyr Pro Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
305 310 315 320

Ser Gly Ser Asp Val Phe Ile Pro Lys Met Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Arg Pro Lys Lys His Lys Arg Val Lys Gly Phe

355

360

365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Lys Ile
 370 375 380

Gly Thr Tyr Val Gly Arg Val Val Val Arg Ala Ser Gly Ser Phe Asp
 385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
 405 410 415

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr Thr
 420 425

<210> 116

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-92 effector

<400> 116

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
 1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
 20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Thr His Arg Leu Cys
 35 40 45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
 50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Ser Glu Val Ile
 65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Tyr Gln Ile Lys Lys Asp Leu
85 90 95

Asn Ser Arg Arg Ala Ile Arg Arg Thr Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Thr Gly Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Leu Asn Val Asn Asn Trp Met Leu
130 135 140

Lys Leu Ser Gln Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Ile Gln Lys Pro Glu Ile Ser Gly Val Glu
165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Gly Arg Glu Cys Val Tyr Cys Gly Ala Lys Asn Val Pro
195 200 205

Leu Glu Ile Glu His Ile Gln Ala Arg Ser Lys Gly Gly Ser Asp Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp Lys Gly
225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys
245 250 255

Lys Ile Gln Thr Ile Ala Thr Ala Ser Leu Lys Asp Ala Ala Ala Ile
260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Ala Leu Lys Gly Phe Gly Leu
275 280 285

Pro Ile Ala Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Thr Ser

290

295

300

Cys Gly Tyr Pro Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
305 310 315 320

Ser Gly Ser Asp Val Phe Ile Pro Lys Met Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Arg Pro Lys Lys His Lys Arg Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Thr Tyr Val Gly Arg Val Val Val Arg Ala Ser Gly Ser Phe Asp
385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr Thr
420 425

<210> 117

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-93 effector

<400> 117

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Thr His Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Val Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asn Arg Gly Leu Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Ile Gln Ile Lys Ser His Leu
85 90 95

Glu Ser Arg Arg Ala Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Gln Ala Arg Phe Leu Asn Arg Met Arg Pro Ala Gly Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Gly Met Leu
130 135 140

Lys Leu Ser Ser Leu Thr Pro Val Ser Gln Ile Ala Val Glu Thr Val
145 150 155 160

Lys Phe Asp Met Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Leu Glu
165 170 175

Tyr Gln His Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Gln Asn Val Pro
195 200 205

Leu Glu Ile Glu His Ile Arg Ala Ser Ser Lys Gly Gly Ser Asn Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Asn Lys Cys Asn Gln Lys Lys Gly

225		230		235		240									
Asn	Gln	Asp	Ile	Lys	Glu	Phe	Leu	Lys	Ser	Gln	Pro	Asp	Arg	Leu	Arg
				245					250					255	
Lys	Ile	Gln	Ser	Gln	Ala	Leu	Lys	Pro	Leu	Lys	Asp	Ala	Ala	Ala	Val
			260					265					270		
Asn	Ala	Thr	Arg	Tyr	Ala	Ile	Ser	Asn	Val	Leu	Lys	Ser	Phe	Gly	Leu
		275					280					285			
Pro	Ile	Val	Phe	Ser	Thr	Gly	Gly	Arg	Thr	Lys	Phe	Asn	Arg	Leu	Lys
	290					295					300				
Leu	Gly	Tyr	Gln	Lys	Asp	His	Trp	Ile	Asp	Ala	Ala	Cys	Val	Gly	Glu
305					310					315					320
Ser	Gly	Ser	Gln	Ile	Val	Ile	Pro	Lys	Thr	Ile	Thr	Pro	Leu	Thr	Ile
			325						330					335	
Thr	Ala	Lys	Gly	Arg	Gly	Ser	Arg	Gln	Lys	Cys	Ser	Met	Asn	Lys	Tyr
			340					345					350		
Gly	Phe	Pro	Arg	Thr	Gly	Pro	Lys	Lys	Ala	Lys	Arg	Val	Lys	Gly	Phe
		355					360					365			
Gln	Thr	Gly	Asp	Ile	Val	Lys	Ala	Val	Val	Thr	Lys	Gly	Lys	Lys	Ile
	370					375					380				
Gly	Thr	Tyr	Phe	Gly	Arg	Val	Ala	Val	Arg	Ala	Ser	Gly	Ser	Phe	Asp
385					390					395					400
Ile	Gly	Ser	Gly	Glu	Glu	Arg	Val	Gly	Ser	Ile	Ser	Tyr	Lys	Tyr	Cys
				405					410					415	
Cys	Leu	Leu	Gln	Arg	Ser	Asp	Gly	Tyr	Glu	Tyr	Thr				
			420					425							

<210> 118
 <211> 428
 <212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-94 effector

<400> 118

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Thr His Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Val Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asn Arg Gly Leu Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Ile Gln Ile Lys Ser His Leu
85 90 95

Glu Ser Arg Arg Ala Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Gln Ala Arg Phe Leu Asn Arg Met Arg Pro Ala Gly Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Gly Met Leu
130 135 140

Lys Leu Ser Ser Leu Thr Pro Val Ser Gln Ile Ala Val Glu Thr Val
145 150 155 160

Lys Phe Asp Met Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Leu Glu

165

170

175

Tyr Gln His Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu
 180 185 190

Glu Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Gln Asn Val Ser
 195 200 205

Leu Glu Ile Glu His Ile Arg Ala Ser Ser Lys Gly Gly Ser Asn Arg
 210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Asn Lys Cys Asn Gln Lys Lys Gly
 225 230 235 240

Asn Gln Asp Ile Lys Glu Phe Leu Lys Ser Gln Pro Asp Arg Leu Arg
 245 250 255

Lys Ile Gln Ser Gln Ala Leu Lys Pro Leu Lys Asp Ala Ala Ala Val
 260 265 270

Asn Ala Thr Arg Tyr Ala Ile Ser Asn Val Leu Lys Ser Phe Gly Leu
 275 280 285

Pro Ile Val Phe Ser Thr Gly Gly Arg Thr Lys Phe Asn Arg Leu Lys
 290 295 300

Leu Gly Tyr Gln Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
 305 310 315 320

Ser Gly Ser Gln Ile Val Ile Pro Lys Thr Ile Thr Pro Leu Thr Ile
 325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn Lys Tyr
 340 345 350

Gly Phe Pro Arg Thr Gly Pro Lys Lys Ala Lys Arg Val Lys Gly Phe
 355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Lys Ile
 370 375 380

Gly Thr Tyr Phe Gly Arg Val Ala Val Arg Ala Ser Gly Ser Phe Asp
385 390 395 400

Ile Gly Ser Gly Glu Glu Arg Val Gly Ser Ile Ser Tyr Lys Tyr Cys
405 410 415

Cys Leu Leu Gln Arg Ser Asp Gly Tyr Glu Tyr Thr
420 425

<210> 119

<211> 427

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-95 effector

<400> 119

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Asn Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Lys Cys Arg Val Gly
35 40 45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Ser Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Arg Asn Leu
85 90 95

Asp Ser Arg Arg Ala Val Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg

100

105

110

Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Arg Gly Trp Leu
 115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp Met Ile
 130 135 140

Lys Leu Ser Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
 145 150 155 160

Lys Phe Asp Thr Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Val Glu
 165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
 180 185 190

Glu Lys Trp Gly Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro
 195 200 205

Leu Glu Ile Glu His Ile Gln Ala Cys Ser Lys Gly Gly Ser Asp Arg
 210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp Lys Gly
 225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Met Lys Arg Lys Thr Glu Arg Leu Lys
 245 250 255

Lys Ile Gln Ala Gln Gly Lys Ala Pro Leu Lys Asp Thr Ala Ala Val
 260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Ala Leu Lys Gly Leu Gly Leu
 275 280 285

Pro Ile Thr Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Val Lys
 290 295 300

Leu Gly Tyr Ser Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
 305 310 315 320

Ser Gly Ala Gln Val Val Ile Pro Pro Ala Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Gly Pro Lys Lys His Lys Arg Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Thr His Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr
420 425

<210> 120

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-96 effector

<400> 120

Met Gln Arg Val Phe Val Leu Asp His Asn Lys Gln Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Asn Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Met Lys Cys Arg Val Gly

35

40

45

Gly Asp Leu Gln Pro Ile Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
 50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Asp Arg Gly Ser Glu Val Ile
 65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Arg Asn Leu
 85 90 95

Asp Ser Arg Arg Ala Val Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
 100 105 110

Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Arg Gly Trp Leu
 115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp Met Ile
 130 135 140

Lys Leu Ser Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu Thr Val
 145 150 155 160

Lys Phe Asp Thr Gln Lys Ile Gln Asn Pro Glu Ile Ser Gly Val Glu
 165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu
 180 185 190

Glu Lys Trp Gly Arg Glu Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro
 195 200 205

Leu Glu Ile Glu His Ile Gln Ala Cys Ser Lys Gly Gly Ser Asp Arg
 210 215 220

Val Ser Asn Leu Thr Leu Ala Cys Thr Pro Cys Asn Ile Asp Lys Gly
 225 230 235 240

Asn Lys Asp Ile Lys Glu Phe Met Lys Arg Lys Thr Glu Arg Leu Lys
 245 250 255

Lys Ile Gln Ala Gln Gly Lys Ala Pro Leu Lys Asp Thr Ala Ala Val
260 265 270

Asn Ala Thr Arg Tyr Ala Thr Gly Asn Ala Leu Lys Gly Leu Gly Leu
275 280 285

Pro Ile Thr Phe Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Val Lys
290 295 300

Leu Gly Tyr Ser Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu
305 310 315 320

Ser Gly Ala Gln Val Val Ile Pro Pro Ala Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Ser Met Asn Gln Tyr
340 345 350

Gly Phe Pro Arg Thr Gly Pro Lys Lys His Lys Arg Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Thr His Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp
385 390 395 400

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr Thr
420 425

<210> 121

<211> 231

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-97 effector

<400> 121

Met Gln Arg Val Phe Val Leu Asp Thr Lys Lys Lys Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Glu Arg Val Asp
35 40 45

Gly Gln Leu Gln Pro Val Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Glu Arg Gly Ser Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Ser Asn Leu
85 90 95

Val Ser Arg Arg Ala Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg
100 105 110

Tyr Arg Pro Ala Arg Phe Leu Asn Arg Arg Arg Pro Lys Ser Trp Leu
115 120 125

Pro Pro Ser Leu Arg Ser Arg Val Asp Asn Val Lys Asn Trp Ala Leu
130 135 140

Lys Leu Ser Arg Leu Ala Pro Ile Thr Gln Ile Ala Val Glu Thr Val
145 150 155 160

Arg Phe Asp Thr Gln Lys Met Gln Asn Pro Glu Val Ser Gly Met Glu
165 170 175

Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Phe Arg Glu Tyr Leu Leu
180 185 190

Glu Lys Trp Gly Arg Gln Cys Ala Tyr Cys Gly Val Gln Asn Val Pro
195 200 205

Leu Glu Val Glu His Ile Gln Pro Arg Ser Lys Glu Gly Ser Asn Arg
210 215 220

Val Ser Asn Leu Thr Leu Ala
225 230

<210> 122

<211> 429

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-98 effector

<400> 122

Met Gln Arg Val Phe Val Leu Asp Thr Lys Lys Lys Pro Leu Met Pro
1 5 10 15

Cys His Pro Ala Arg Ala Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala
20 25 30

Val Tyr Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Glu Arg Val Asp
35 40 45

Gly Gln Leu Gln Pro Val Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr
50 55 60

Thr Gly Ile Ala Leu Val Gly His Phe Glu Arg Gly Ser Glu Val Ile
65 70 75 80

Trp Ala Gly Asn Leu Asn His Arg Gly Leu Gln Ile Lys Ser Asn Leu
85 90 95

Val Ser Arg Arg Ala Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg

			100					105						110					
Tyr	Arg	Pro	Ala	Arg	Phe	Leu	Asn	Arg	Arg	Arg	Pro	Lys	Ser	Trp	Leu				
		115					120					125							
Pro	Pro	Ser	Leu	Arg	Ser	Arg	Val	Asp	Asn	Val	Lys	Asn	Trp	Ala	Leu				
		130				135					140								
Lys	Leu	Ser	Arg	Leu	Ala	Pro	Ile	Thr	Gln	Ile	Ala	Val	Glu	Thr	Val				
145					150					155					160				
Arg	Phe	Asp	Thr	Gln	Lys	Met	Gln	Asn	Pro	Glu	Val	Ser	Gly	Met	Glu				
				165					170					175					
Tyr	Gln	Gln	Gly	Glu	Leu	Ala	Gly	Tyr	Glu	Phe	Arg	Glu	Tyr	Leu	Leu				
			180					185					190						
Glu	Lys	Trp	Gly	Arg	Gln	Cys	Ala	Tyr	Cys	Gly	Val	Gln	Asn	Val	Pro				
		195					200					205							
Leu	Glu	Val	Glu	His	Ile	Gln	Pro	Arg	Ser	Lys	Glu	Gly	Ser	Asn	Arg				
		210				215					220								
Val	Ser	Asn	Leu	Thr	Leu	Ala	Cys	Thr	Lys	Cys	Asn	Gln	Lys	Lys	Gly				
225					230					235					240				
Asn	Lys	Asp	Val	Lys	Asp	Phe	Leu	Lys	Gly	Lys	Pro	Asp	Arg	Leu	Lys				
				245					250					255					
Lys	Ile	Gln	Ala	Gln	Ala	Lys	Ala	Ser	Leu	Arg	Asp	Thr	Ala	Ala	Val				
			260					265					270						
Asn	Ala	Thr	Arg	Tyr	Ala	Ile	Gly	Glu	Ala	Leu	Lys	Thr	Phe	Gly	Phe				
		275					280					285							
Val	Ile	Ser	Phe	Ser	Ser	Gly	Gly	Arg	Thr	Lys	Phe	Asn	Arg	Thr	Gln				
		290				295					300								
Gln	Gly	Tyr	Pro	Lys	Glu	His	Trp	Val	Asp	Ala	Ala	Cys	Val	Gly	Glu				
305					310					315					320				

Asn Gly Asn Pro Val Ala Ile Pro Lys Ala Ile Thr Pro Leu Ile Ile
325 330 335

Thr Ala Lys Gly Arg Gly Ser Arg Gln Lys Cys Arg Met Asn Lys Tyr
340 345 350

Gly Phe Pro Arg Thr Gly Pro Lys Lys His Lys Arg Val Lys Gly Phe
355 360 365

Gln Thr Gly Asp Ile Val Lys Ala Ile Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Thr Tyr Val Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asp
385 390 395 400

Ile Gly Ser Gly Ile Glu Ala Val Gly Ser Ile Ser Tyr Lys Tyr Cys
405 410 415

Gln Leu Leu Gln Arg Ser Asp Gly Tyr Asp Tyr Leu Lys
420 425

<210> 123

<211> 424

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-99 effector

<400> 123

Met Ser Asn Phe Ile Phe Val Leu Asp Thr Lys Arg Arg Pro Leu Ser
1 5 10 15

Pro Cys Lys Pro Gly Val Gly Arg Ser Leu Leu Lys Val Gly Lys Ala
20 25 30

Ser Val Phe Arg Arg Phe Pro Phe Thr Val Ile Leu Asn Lys Glu Val

35

40

45

Asp Ala Ser Pro Glu Pro Leu Glu Leu Lys Phe Asp Pro Gly Ser Lys
 50 55 60

Thr Thr Gly Ile Val Ile Asn Gln Gly Gly Lys Ile Ile Phe Gly Ala
 65 70 75 80

Glu Leu Gln His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser Arg
 85 90 95

His Gln Leu Arg Leu Arg Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln
 100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg His Asp Gly Trp Leu Ala Pro Ser
 115 120 125

Leu Gln His Arg Ile Glu Thr Thr Leu Thr Trp Val Arg Lys Leu Ile
 130 135 140

Arg Phe Ala Pro Ile Ile Ser Ile Ala Gln Glu Leu Val Arg Phe Asp
 145 150 155 160

Ser Gln Leu Met Gln Asn Pro Glu Ile Ser Gly Val Ile Tyr Gln Gln
 165 170 175

Gly Gln Leu His Gly Tyr Glu Val Arg Glu Tyr Leu Leu Thr Lys Trp
 180 185 190

Asn Arg Lys Cys Ala Tyr Cys Ser Val Glu Asn Val Pro Phe Glu Ile
 195 200 205

Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Ser Asn
 210 215 220

Leu Thr Ile Ala Cys His Asp Cys Asn Gln Lys Lys Gly Asn Gln Asp
 225 230 235 240

Val Gln Ala Phe Leu Ala Thr Lys Pro Asp Leu Leu Asn Cys Ile Leu
 245 250 255

Lys Gln Ala Lys Leu Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr
260 265 270

Arg Trp Ala Leu Phe Asn Ala Leu Lys Glu Thr Gly Leu Ser Val Thr
275 280 285

Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Asn Arg Leu Gly Leu
290 295 300

Pro Lys Ser His Trp Leu Asp Ala Ala Cys Val Gly Asn Val Glu Thr
305 310 315 320

Leu Glu Ile Leu Thr Ser Lys Pro Leu Leu Ile Ala Ala Lys Gly His
325 330 335

Gly Thr Arg Gln Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Ile Arg
340 345 350

His Lys Ser Arg Val His Ile His Lys Gly Phe Gln Thr Gly Asp Ile
355 360 365

Val Asn Ala Thr Val Thr Ala Gly Lys Lys Val Gly Ser Tyr Val Gly
370 375 380

Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Val Thr Lys Thr
385 390 395 400

Gly Arg Val Ala Gly Ile Ser His Lys Tyr Cys Lys Ala Ile His Lys
405 410 415

Lys Asp Gly Tyr Ser Tyr Gly Phe
420

<210> 124

<211> 424

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-100 effector

<400> 124

Met Ser Asn Phe Ile Phe Val Leu Asp Thr Lys Arg Arg Pro Leu Ser
1 5 10 15

Pro Cys Lys Pro Gly Val Gly Arg Ser Leu Leu Lys Val Gly Lys Ala
20 25 30

Ser Val Phe Arg Arg Phe Pro Phe Thr Val Ile Leu Asn Lys Glu Val
35 40 45

Asp Ala Ser Pro Glu Pro Leu Glu Leu Lys Phe Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Ile Val Ile Asn Gln Gly Gly Lys Ile Ile Phe Gly Ala
65 70 75 80

Glu Leu Gln His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser Arg
85 90 95

His Gln Leu Arg Leu Arg Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln
100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro Ser
115 120 125

Leu Gln His Arg Ile Glu Thr Thr Leu Thr Trp Val Arg Lys Leu Ile
130 135 140

Arg Phe Ala Pro Ile Ile Ser Ile Ala Gln Glu Leu Val Arg Phe Asp
145 150 155 160

Ser Gln Leu Met Gln Asn Pro Glu Ile Ser Gly Val Ile Tyr Gln Gln
165 170 175

Gly Gln Leu His Gly Tyr Glu Val Arg Glu Tyr Leu Leu Thr Lys Trp
180 185 190

Asn Arg Lys Cys Ala Tyr Cys Ser Val Glu Asn Val Pro Phe Glu Ile
195 200 205

Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Ser Asn
210 215 220

Leu Thr Ile Ala Cys His Asp Cys Asn Gln Lys Lys Gly Asn Gln Asp
225 230 235 240

Val Gln Ala Phe Leu Ala Thr Lys Pro Asp Leu Leu Asn Cys Ile Leu
245 250 255

Lys Gln Ala Lys Leu Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr
260 265 270

Arg Trp Ala Leu Phe Asn Ala Leu Lys Glu Thr Gly Leu Ser Val Thr
275 280 285

Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Asn Arg Leu Gly Leu
290 295 300

Pro Lys Ser His Trp Leu Asp Ala Ala Cys Val Gly Asn Val Glu Thr
305 310 315 320

Leu Glu Ile Leu Thr Ser Lys Pro Leu Leu Ile Ala Ala Lys Gly His
325 330 335

Gly Thr Arg Gln Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Ile Arg
340 345 350

His Lys Ser Arg Val His Ile His Lys Gly Phe Gln Thr Gly Asp Ile
355 360 365

Val Asn Ala Thr Val Thr Ala Gly Lys Lys Val Gly Ser Tyr Val Gly
370 375 380

Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Val Thr Lys Thr
385 390 395 400

Gly Arg Val Ala Gly Ile Ser His Lys Tyr Cys Lys Ala Ile His Lys

405

410

415

Lys Asp Gly Tyr Ser Tyr Gly Phe
420

<210> 125

<211> 429

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-101 effector

<400> 125

Met Ser Asn Phe Ile Phe Val Leu Asp Thr Asn Lys Gly Pro Leu Asp
1 5 10 15

Arg Val His Pro Gly Lys Ala Arg Arg Leu Leu Ser Thr Gly Asn Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Gln Ala Tyr
35 40 45

Pro Glu Ile Pro Val Gln Asp Leu Glu Leu Lys Leu Asp Pro Gly Ser
50 55 60

Gln Val Thr Gly Ile Ala Val Val Gln Gly Thr Lys Val Ile Phe Gly
65 70 75 80

Ala Glu Leu Glu His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser
85 90 95

Arg Arg Gln Leu Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg
100 105 110

Gln Ala Arg Phe Leu Asn Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro
115 120 125

Ser Leu Gln His Arg Val Asp Thr Thr Met Thr Trp Val Asn Arg Phe
130 135 140

Arg Arg Leu Ala Pro Ile Ala Arg Ile Ala Gln Glu Leu Val Arg Phe
145 150 155 160

Asp Leu Gln Leu Ile Gln Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln
165 170 175

Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys
180 185 190

Trp Asn Arg Lys Cys Ala Tyr Cys Gly Ala Glu Asn Leu Pro Leu Glu
195 200 205

Leu Glu His Ile His Pro Arg Ser Lys Gly Gly Thr Asp Arg Val Ser
210 215 220

Asn Leu Thr Leu Ala Cys His Ser Cys Asn Gln Ser Lys Ser Asn Arg
225 230 235 240

Asp Ile Arg Asp Phe Leu Ser Gly Lys Pro Ser Leu Leu Asn Arg Ile
245 250 255

Leu Lys Gln Ser Gln Ser Pro Leu Lys Asp Ala Ala Ala Val Asn Leu
260 265 270

Thr Arg Trp Ala Leu Phe Asn Ala Leu Lys Gln Thr Gly Leu Pro Val
275 280 285

Ala Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Thr Arg Leu Asn
290 295 300

Leu Pro Lys Thr His Trp Leu Asp Ala Ala Ser Val Gly Lys Ile Asp
305 310 315 320

Ser Leu Lys Val Leu Thr Thr Asn Pro Leu Leu Ile Ala Ala Lys Gly
325 330 335

His Gly Thr Arg Gln Met Cys Gly Thr Asp Lys Phe Gly Phe Pro Lys

340

345

350

Arg His Arg Ser Arg Val Gln Ile His Gln Gly Phe Arg Thr Gly Asp
 355 360 365

Ile Val Thr Ala Ile Val Thr Lys Gly Lys Lys Ile Gly Ser Tyr Val
 370 375 380

Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Thr Thr Gln
 385 390 395 400

Ser Gly Arg Val Ser Gly Ile Ser His Arg Tyr Cys Gln Pro Ile His
 405 410 415

Lys Arg Asp Gly Tyr Ala Tyr Ala Phe Ala His Thr Leu
 420 425

<210> 126

<211> 424

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-102 effector

<400> 126

Met Ser Asn Phe Val Phe Val Ile Asp Thr Asn His Lys Pro Leu Ser
 1 5 10 15

Pro Cys Lys Pro Gly Met Ala Arg Ser Leu Leu Lys Ala Gly Lys Ala
 20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Lys Ala Val
 35 40 45

Glu Thr Asn Pro Glu Pro Leu Glu Leu Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Val Thr Gly Ile Ala Ile Lys Gln Gly Asp Lys Ile Ile Phe Gly Ala
65 70 75 80

Glu Leu Gln His Arg Gly Gln Gln Ile Lys Glu Ala Leu Leu Ser Cys
85 90 95

Arg Gln Leu Arg Arg Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln
100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro Ser
115 120 125

Leu Gln His Arg Ile Glu Thr Ala Leu Thr Trp Val Arg Lys Leu Ile
130 135 140

Arg Phe Ala Pro Ile Ala Arg Ile Val Gln Glu Leu Val Arg Phe Asp
145 150 155 160

Thr Gln Leu Ile Gln Asn Pro Glu Ile Ser Gly Val Leu Tyr Gln Gln
165 170 175

Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp
180 185 190

Asn Arg Gln Cys Ala Tyr Cys Ser Ala Gln Asn Val Pro Phe Glu Val
195 200 205

Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Pro Asn
210 215 220

Leu Thr Leu Ala Cys His Asp Cys Asn Gln Lys Lys Gly Asn Gln Asp
225 230 235 240

Val Arg Ala Phe Leu Ala Thr Lys Pro Asp Leu Leu Asn Arg Ile Leu
245 250 255

Lys Gln Ala Lys Leu Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr
260 265 270

Arg Trp Ala Leu Phe Asn Ala Leu Lys Glu Thr Gly Leu Pro Val Thr

275

280

285

Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Asn Arg Leu Gly Leu
 290 295 300

Pro Lys Ser His Trp Leu Asp Ala Ala Cys Val Gly Asn Phe Glu Ala
 305 310 315 320

Leu Glu Val Leu Thr Ser Lys Pro Leu Leu Ile Ala Ala Lys Gly His
 325 330 335

Gly Thr Arg Gln Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Thr Arg
 340 345 350

His Lys Ser Arg Val Gln Ile His Lys Gly Tyr Gln Thr Gly Asp Ile
 355 360 365

Val Ser Ala Thr Val Thr Ala Gly Lys Lys Val Gly Ser Tyr Ile Gly
 370 375 380

Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala Thr Lys Thr
 385 390 395 400

Gly Arg Ile Thr Gly Ile Ser His Lys Tyr Cys Asn Pro Ile His Lys
 405 410 415

Lys Asp Gly Tyr Ser Tyr Ala Phe
 420

<210> 127

<211> 224

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-103 effector

<400> 127

Met Ser Asn Phe Val Phe Val Leu Asp Thr Asp Lys Arg Ser Leu Asp
1 5 10 15

Pro Ile His Pro Gly Thr Ala Arg His Leu Leu Asn Gln Gly Lys Ala
20 25 30

Ala Val Leu Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Glu Ala Arg
35 40 45

Pro Asp Ile Pro Val Gln Asp Leu Glu Leu Lys Ile Asp Pro Gly Ser
50 55 60

Lys Val Thr Gly Ile Ala Ile Lys Gln Gly Asn Lys Val Ile Phe Gly
65 70 75 80

Ala Glu Leu Gln His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser
85 90 95

Arg Cys Gln Leu Arg Arg Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg
100 105 110

Pro Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro
115 120 125

Ser Leu Gln His Arg Val Leu Thr Ile Met Thr Trp Val Arg Lys Phe
130 135 140

Ile Arg Leu Ala Pro Ile Ser Ser Ile Ala Gln Glu Leu Val Arg Phe
145 150 155 160

Asp Thr Gln Leu Met Gln Asn Ala Glu Val Ser Gly Val Leu Tyr Gln
165 170 175

Arg Gly Thr Leu Ala Gly Tyr Glu Thr Arg Glu Tyr Leu Leu Glu Lys
180 185 190

Trp Asn Arg Arg Cys Ala Tyr Cys Ser Ala Leu Asn Val Pro Phe Glu
195 200 205

Val Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Ser

210

215

220

<210> 128

<211> 425

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-104 effector

<400> 128

Met	Ser	Asn	Phe	Val	Phe	Val	Leu	Asp	Thr	Asp	Lys	Arg	Ser	Leu	Asp
1				5					10					15	

Pro	Ile	His	Pro	Gly	Thr	Ala	Arg	His	Leu	Leu	Asn	Gln	Gly	Lys	Ala
			20					25					30		

Ala	Val	Leu	Arg	Arg	Tyr	Pro	Phe	Thr	Ile	Ile	Leu	Lys	Glu	Ala	Arg
		35					40					45			

Pro	Asp	Ile	Pro	Val	Gln	Asp	Leu	Glu	Leu	Lys	Ile	Asp	Pro	Gly	Ser
	50					55					60				

Lys	Val	Thr	Gly	Ile	Ala	Ile	Lys	Gln	Gly	Asn	Lys	Val	Ile	Phe	Gly
65					70					75					80

Ala	Glu	Leu	Gln	His	Arg	Gly	Gln	Gln	Ile	Lys	Asp	Ala	Leu	Leu	Ser
				85					90					95	

Arg	Cys	Gln	Leu	Arg	Arg	Gly	Arg	Arg	Asn	Arg	Lys	Thr	Arg	Tyr	Arg
			100					105						110	

Pro	Ala	Arg	Phe	Leu	Asn	Arg	Thr	Arg	Pro	Asp	Gly	Trp	Leu	Ala	Pro
		115					120					125			

Ser	Leu	Gln	His	Arg	Val	Leu	Thr	Ile	Met	Thr	Trp	Val	Arg	Lys	Phe
	130					135					140				

Ile Arg Leu Ala Pro Ile Ser Ser Ile Ala Gln Glu Leu Val Arg Phe
145 150 155 160

Asp Thr Gln Leu Met Gln Asn Ala Glu Val Ser Gly Val Leu Tyr Gln
165 170 175

Arg Gly Thr Leu Ala Gly Tyr Glu Thr Arg Glu Tyr Leu Leu Glu Lys
180 185 190

Trp Asn Arg Arg Cys Ala Tyr Cys Ser Ala Leu Asn Val Pro Phe Glu
195 200 205

Val Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Ser
210 215 220

Asn Leu Thr Leu Ala Cys His Pro Cys Asn Gln Ser Lys Gly Asn Gln
225 230 235 240

Asp Val Arg Asp Phe Leu Ser Asn Lys Pro Asp Leu Leu Asn Arg Ile
245 250 255

Leu Lys Gln Ala Lys Ser Pro Leu Lys Asp Ala Ala Ala Val Asn Ser
260 265 270

Thr Arg Trp Ala Leu Phe Asn Ala Leu Lys Ala Thr Ser Leu Pro Val
275 280 285

Ser Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Glu Arg Leu Asp
290 295 300

Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly Ser Val Asp
305 310 315 320

Glu Leu Lys Val Leu Thr Ser Lys Pro Leu Leu Ile Ala Ala Lys Gly
325 330 335

His Gly Thr Arg Gln Met Cys Arg Thr Asp Lys Tyr Gly Phe Pro Ser
340 345 350

Arg Tyr Met Pro Arg Ser Lys Phe Val Arg Ser Phe Gln Thr Gly Asp

355

360

365

Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys Val Gly Thr His Ile
 370 375 380

Gly Arg Val Ala Val Arg Ser Thr Gly Ser Phe Asn Ile Ser Thr Ala
 385 390 395 400

Gln Gln Leu Val Gln Gly Ile Ser His Lys Tyr Cys Lys His Ile His
 405 410 415

Lys Lys Asp Gly Phe Ala Tyr Glu Phe
 420 425

<210> 129

<211> 425

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-105 effector

<400> 129

Met Ser Asn Phe Val Phe Val Leu Asp Thr Asn Lys Arg Pro Leu Asp
 1 5 10 15

Pro Val His Pro Gly Ala Ala Arg His Leu Leu Asn Ala Gly Lys Ala
 20 25 30

Ala Val Phe Arg Lys Tyr Pro Phe Thr Ile Ile Leu Lys Glu Ala Cys
 35 40 45

Pro Asp Val Pro Val Gln Asp Leu Glu Leu Lys Leu Asp Pro Gly Ser
 50 55 60

Lys Val Thr Gly Ile Ala Ile Lys Gln Gly Asn Lys Leu Ile Phe Gly
 65 70 75 80

Ala Glu Leu Gln His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser
85 90 95

Arg Arg Gln Leu Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg
100 105 110

Lys Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro
115 120 125

Ser Leu Gln His Arg Val Leu Thr Thr Leu Thr Trp Val Arg Lys Phe
130 135 140

Met Arg Leu Ala Pro Ile Ala Ser Ile Ala Gln Glu Leu Val Arg Phe
145 150 155 160

Asp Val Gln Leu Ile Ser Asn Pro Glu Ile Ser Gly Val Glu Tyr Gln
165 170 175

Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys
180 185 190

Trp Asn Arg Lys Cys Ala Tyr Cys Ser Val Glu Asn Val Ser Leu Glu
195 200 205

Ile Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Ser
210 215 220

Asn Leu Ala Leu Ala Cys His Pro Cys Asn Gln Ser Lys Gly Asn Gln
225 230 235 240

Asp Ile Arg Asp Phe Leu Ala Asp Lys Pro Asp Leu Leu Ser Arg Ile
245 250 255

Leu Lys Gln Ala Lys Ser Pro Leu Lys Asp Ala Ala Ala Val Asn Ser
260 265 270

Thr Arg Trp Ala Leu Phe Asn Ala Leu Lys Ile Thr Gly Leu Pro Val
275 280 285

Thr Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Thr Arg Leu Asn

290

295

300

Leu Pro Lys Ser His Trp Phe Asp Ala Ala Cys Val Gly Asn Val Gly
 305 310 315 320

Thr Leu Lys Val Leu Ala Ser Lys Pro Leu Leu Ile Ala Ala Lys Gly
 325 330 335

His Gly Ser Arg Gln Met Cys Gly Thr Asp Lys Tyr Gly Phe Pro Thr
 340 345 350

Arg His Lys Ser Arg Val Gln Ile His Lys Gly Phe Gln Thr Gly Asp
 355 360 365

Ile Val Thr Ala Thr Val Thr Ala Gly Lys Lys Ile Gly Ser Tyr Val
 370 375 380

Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Asn Thr Thr
 385 390 395 400

Ala Gly Arg Val Ala Gly Ile Ser His Lys Tyr Cys Lys Pro Ile His
 405 410 415

Lys Lys Asp Gly Tyr Ser Tyr Gly Phe
 420 425

<210> 130

<211> 180

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-106 effector

<400> 130

Met Ser Asn His Val Phe Val Ile Asp Thr Asn Lys Lys Pro Val Gly
 1 5 10 15

Thr Val His Pro Ala Tyr Ala Arg Lys Leu Leu Ser Ser Gln Gln Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Thr Ser Val
35 40 45

Pro Glu Gly Phe Gln Pro Arg Ala Leu Arg Val Lys Ile Asp Pro Gly
50 55 60

Ala Lys Thr Thr Gly Ile Val Val Leu Asp Gly Asn Lys Val Val Trp
65 70 75 80

Ala Ala Glu Leu Thr His Arg Gly Glu Gln Ile Arg Asn Arg Leu Thr
85 90 95

Ser Arg Arg Gln Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr
100 105 110

Arg Pro Ala Arg Phe Leu Asn Arg Thr Arg Asp Lys Glu Trp Leu Ala
115 120 125

Pro Ser Leu Lys Ser Arg Val Glu Asn Ile Leu Thr Trp Val Asn Arg
130 135 140

Leu Arg Arg Val Ser Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr
165 170 175

Gln Gln Gly Thr
180

<210> 131

<211> 347

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-107 effector

<400> 131

Met Ser Asn His Val Phe Val Ile Asp Thr Asn Lys Lys Pro Val Gly
1 5 10 15

Thr Val His Pro Ala Tyr Ala Arg Lys Leu Leu Ser Ser Gln Gln Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Thr Ser Val
35 40 45

Pro Glu Gly Phe Gln Pro Arg Ala Leu Arg Val Lys Ile Asp Pro Gly
50 55 60

Ala Lys Thr Thr Gly Ile Val Val Leu Asp Gly Asn Lys Val Val Trp
65 70 75 80

Ala Ala Glu Leu Thr His Arg Gly Glu Gln Ile Arg Asn Arg Leu Thr
85 90 95

Ser Arg Arg Gln Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr
100 105 110

Arg Pro Ala Arg Phe Leu Asn Arg Thr Arg Asp Lys Glu Trp Leu Ala
115 120 125

Pro Ser Leu Lys Ser Arg Val Glu Asn Ile Leu Thr Trp Val Asn Arg
130 135 140

Leu Arg Arg Val Ser Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr
165 170 175

Gln Gln Gly Thr Leu Tyr Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu
180 185 190

Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu
195 200 205

Gln Val Glu His Ile Val Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
210 215 220

Ser Asn Leu Thr Leu Ala Cys Val Ser Cys Asn Gln Ala Lys Gly Asn
225 230 235 240

Gln Asp Ile Arg Glu Phe Leu Lys His Lys Pro Glu Leu Leu Ser Arg
245 250 255

Ile Leu Gln Gln Thr Lys Gln Pro Leu Val Val Ala Ala Val Val Asn
260 265 270

Thr Ala Arg Trp Val Leu Phe Asn Arg Leu Lys Glu Thr Gly Leu Pro
275 280 285

Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Arg Gln
290 295 300

Gln Leu Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Ala Ser
305 310 315 320

Thr Pro Asn Leu Val Phe Val Thr Lys Gln Pro Leu Gln Ile Lys Ala
325 330 335

Lys Gly His Gly Thr Arg Gln Met Cys Ile Thr
340 345

<210> 132

<211> 424

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-108 effector

<400> 132

Met Ser Asn His Val Phe Val Leu Asp Thr Asn His Lys Gln Leu Thr
1 5 10 15

Pro Cys Lys Pro Gly Val Ala Arg Ser Leu Leu Asn Thr Gly Lys Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Lys Glu Val
35 40 45

Asn Ala His Pro Glu Pro Ile Glu Leu Lys Leu Asp Pro Gly Ser Arg
50 55 60

Val Thr Gly Ile Ala Leu Lys Gln Gly Asn Gln Ile Ile Phe Gly Ala
65 70 75 80

Glu Leu Gln His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser Arg
85 90 95

Arg Gln Leu Arg Arg Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln
100 105 110

Ala Arg Phe Leu Asn Arg Thr Arg Gln Ser Gly Trp Leu Ala Pro Ser
115 120 125

Leu Gln His Arg Val Ala Thr Val Leu Thr Trp Gly Asn Arg Phe Arg
130 135 140

Lys Ile Ala Pro Ile Ala Ser Ile Ala Gln Glu Leu Val Arg Phe Asp
145 150 155 160

Leu Gln Leu Met Gln Asn Pro Glu Met Ser Gly Val Glu Tyr Gln Gln
165 170 175

Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp
180 185 190

Asn Arg Lys Cys Ala Tyr Cys Gly Ala Glu Asn Val Pro Leu Glu Val
195 200 205

Glu His Ile Gln Pro Arg Ser Lys Gly Gly Ser Asp Arg Val Ser Asn
210 215 220

Leu Ala Leu Ala Cys Asn Pro Cys Asn Gln Ser Lys Gly Ser Gln Asp
225 230 235 240

Ile Arg Asp Phe Leu Ser Gly Lys Pro Asp Leu Leu Asn Arg Ile Leu
245 250 255

Lys Gln Ser Lys Ser Pro Leu Arg Asp Ala Ala Ala Val Asn Ser Thr
260 265 270

Arg Trp Ala Leu Asn Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Thr
275 280 285

Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Thr Arg Leu Asn Leu
290 295 300

Pro Lys Ala His Trp Leu Asp Ala Ala Cys Val Gly Gln Val Glu Thr
305 310 315 320

Leu Lys Ile Leu Thr Ser Lys Pro Leu Leu Ile Ala Ala Lys Gly His
325 330 335

Gly Thr Arg Gln Met Cys Gly Thr Asp Lys Phe Gly Phe Pro Asn Arg
340 345 350

His Arg Ser Arg Val Gln Val His Lys Gly Phe Gln Thr Gly Asp Ile
355 360 365

Val Ile Ala Thr Val Thr Ala Gly Lys Lys Ile Gly Ser Tyr Val Gly
370 375 380

Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala Thr Lys Thr
385 390 395 400

Gly Arg Val Ala Gly Ile Ser His Lys Tyr Cys Lys Pro Ile His Lys
405 410 415

Lys Asp Gly Tyr Ala Tyr Thr Phe

<210> 133

<211> 427

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-109 effector

<400> 133

Met	Ser	Asn	Tyr	Val	Phe	Val	Ile	Asp	Thr	Asn	Lys	Lys	Pro	Val	Gly
1				5					10					15	

Thr	Val	His	Pro	Ala	Cys	Ala	Arg	Lys	Leu	Leu	Ser	Ser	Gln	Gln	Ala
			20					25					30		

Ala	Val	Phe	Arg	Arg	Tyr	Pro	Phe	Thr	Ile	Ile	Leu	Lys	Thr	Ser	Val
		35					40					45			

Leu	Glu	Gly	Phe	Gln	Ala	Arg	Ser	Leu	Arg	Ile	Lys	Ile	Asp	Pro	Gly
	50					55					60				

Ala	Lys	Thr	Thr	Gly	Ile	Ala	Val	Leu	Asp	Gly	Asn	Lys	Val	Val	Trp
65					70					75					80

Ala	Ala	Glu	Leu	Thr	His	Arg	Gly	Glu	Gln	Ile	Arg	Asn	Arg	Leu	Thr
				85					90					95	

Ser	Arg	Arg	Gln	Ile	Arg	Arg	Ser	Arg	Arg	Asn	Arg	Lys	Thr	Arg	Tyr
			100					105					110		

Arg	Pro	Ala	Arg	Phe	Leu	Asn	Arg	Thr	Arg	Asp	Lys	Gly	Trp	Leu	Ala
		115					120					125			

Pro	Ser	Leu	Lys	Ser	Arg	Val	Glu	Asn	Ile	Leu	Thr	Trp	Val	Asn	Arg
		130				135					140				

Leu Arg Arg Val Ser Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr
165 170 175

Gln Gln Gly Thr Leu Tyr Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu
180 185 190

Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Thr Asn Val Pro Leu
195 200 205

Gln Val Glu His Ile Val Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
210 215 220

Ser Asn Leu Thr Leu Ala Cys Val Ser Cys Asn Gln Thr Lys Gly Asn
225 230 235 240

Gln Asp Ile Arg Glu Phe Leu Lys His Lys Pro Glu Leu Leu Ser Arg
245 250 255

Ile Leu Gln Gln Thr Lys Gln Pro Leu Val Ala Ala Ala Val Val Asn
260 265 270

Thr Thr Arg Trp Ala Leu Phe Asn Arg Leu Lys Glu Thr Gly Leu Pro
275 280 285

Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Arg Gln
290 295 300

Gln Leu Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Ala Ser
305 310 315 320

Thr Pro Asn Leu Val Phe Val Thr Lys Gln Pro Leu Gln Ile Lys Ala
325 330 335

Lys Gly His Gly Thr Arg Gln Met Cys Ile Thr Asp Lys Tyr Gly Phe
340 345 350

Pro Lys Gln His Arg Thr Arg Val Gln Ile His Lys Gly Phe Arg Thr

355

360

365

Gly Asp Ile Val Arg Ala Val Val Thr Lys Gly Lys Lys Ile Gly Thr
 370 375 380

Tyr Ile Gly Arg Val Val Cys Arg Ala Ser Gly Ser Phe Asp Ile Thr
 385 390 395 400

Thr Lys Gln Gly Lys Ile Ala Ser Ile Asn Tyr Lys Tyr Cys Thr Val
 405 410 415

Ile Asn Lys Lys Asp Gly Tyr Glu Tyr Ala Phe
 420 425

<210> 134

<211> 427

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-110 effector

<400> 134

Met Ser Asn Tyr Val Phe Val Ile Asp Thr Asn Lys Lys Pro Val Gly
 1 5 10 15

Thr Val His Pro Ala Cys Ala Arg Lys Leu Leu Ser Ser Gln Gln Ala
 20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Thr Ser Val
 35 40 45

Pro Glu Gly Phe Gln Ala Arg Ser Leu Arg Ile Lys Ile Asp Pro Gly
 50 55 60

Ala Lys Thr Thr Gly Ile Ala Val Leu Asp Gly Asn Lys Val Val Trp
 65 70 75 80

Ala Ala Glu Leu Thr His Arg Gly Glu Gln Ile Arg Asn Arg Leu Thr
85 90 95

Ser Arg Arg Gln Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr
100 105 110

Arg Pro Ala Arg Phe Leu Asn Arg Thr Arg Asp Lys Gly Trp Leu Ala
115 120 125

Pro Ser Leu Lys Ser Arg Val Glu Asn Ile Leu Thr Trp Val Asn Arg
130 135 140

Leu Arg Arg Val Ser Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr
165 170 175

Gln Gln Gly Thr Leu Tyr Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu
180 185 190

Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Thr Asn Val Pro Leu
195 200 205

Gln Val Glu His Ile Val Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
210 215 220

Ser Asn Leu Thr Leu Ala Cys Met Ser Cys Asn Gln Ala Lys Gly Asn
225 230 235 240

Gln Asp Ile Arg Glu Phe Leu Lys His Lys Pro Glu Leu Leu Ser Arg
245 250 255

Ile Leu Gln Gln Thr Lys Gln Pro Leu Val Ala Ala Ala Val Val Asn
260 265 270

Thr Ala Arg Trp Val Leu Phe Asn Arg Leu Lys Glu Thr Gly Leu Pro
275 280 285

Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Arg Gln

290

295

300

Gln Leu Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Ala Ser
 305 310 315 320

Thr Pro Asn Leu Val Phe Val Thr Lys Gln Pro Leu Gln Ile Lys Val
 325 330 335

Lys Gly His Gly Thr Arg Gln Met Cys Ile Thr Asp Lys Tyr Gly Phe
 340 345 350

Pro Arg Gln His Arg Thr Arg Val Gln Ile His Lys Gly Phe Arg Thr
 355 360 365

Gly Asp Ile Val Arg Ala Val Val Thr Arg Gly Lys Lys Val Gly Lys
 370 375 380

Tyr Ile Gly Arg Val Val Cys Arg Ala Ser Gly Ser Phe Asp Ile Thr
 385 390 395 400

Thr Lys Gln Gly Arg Ile Thr Gly Ile Ser Tyr Lys Tyr Cys Lys Thr
 405 410 415

Val His Lys Lys Asp Gly Tyr Glu Tyr Ala Phe
 420 425

<210> 135

<211> 427

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-111 effector

<400> 135

Met Ser Asn Tyr Val Phe Val Ile Asp Thr Asn Lys Lys Pro Val Gly
 1 5 10 15

Thr Val His Pro Ala Cys Ala Arg Lys Leu Leu Ser Ser Gln Gln Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Thr Ser Val
35 40 45

Pro Glu Gly Phe Gln Ala Arg Ser Leu Arg Ile Lys Ile Asp Pro Gly
50 55 60

Ala Lys Thr Thr Gly Ile Ala Val Leu Asp Gly Asn Lys Val Val Trp
65 70 75 80

Ala Ala Glu Leu Thr His Arg Gly Glu Gln Ile Arg Asn Arg Leu Thr
85 90 95

Ser Arg Arg Gln Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr
100 105 110

Arg Pro Ala Arg Phe Leu Asn Arg Thr Arg Asp Lys Gly Trp Leu Ala
115 120 125

Pro Ser Leu Lys Ser Arg Val Glu Asn Ile Leu Thr Trp Val Asn Arg
130 135 140

Leu Arg Arg Val Ser Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr
165 170 175

Gln Gln Gly Thr Leu Tyr Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu
180 185 190

Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Thr Asn Val Pro Leu
195 200 205

Gln Val Glu His Ile Val Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
210 215 220

Ser Asn Leu Thr Leu Ala Cys Val Ser Cys Asn Gln Thr Lys Gly Asn

225		230		235		240
Gln Asp Ile Arg	Glu Phe Leu Lys His	Lys Pro Glu Leu Leu Ser Arg				
	245	250	255			
Ile Leu Gln Gln Thr Lys Gln Pro Leu Val Ala Ala Ala Val Val Asn						
	260	265	270			
Thr Thr Arg Trp Ala Leu Phe Asn Arg Leu Lys Glu Thr Gly Leu Pro						
	275	280	285			
Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Arg Gln						
	290	295	300			
Gln Leu Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Ala Ser						
305	310	315	320			
Thr Pro Asn Leu Val Phe Val Thr Lys Gln Pro Leu Gln Ile Lys Ala						
	325	330	335			
Lys Gly His Gly Thr Arg Gln Met Cys Ile Thr Asp Lys Tyr Gly Phe						
	340	345	350			
Pro Lys Gln His Arg Thr Arg Val Gln Ile His Lys Gly Phe Arg Thr						
	355	360	365			
Gly Asp Ile Val Arg Ala Val Val Thr Lys Gly Lys Lys Ile Gly Thr						
	370	375	380			
Tyr Ile Gly Arg Val Val Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala						
385	390	395	400			
Thr Lys Gln Gly Arg Ile Thr Gly Ile Ser Tyr Lys Tyr Cys Lys Thr						
	405	410	415			
Val His Lys Lys Asp Gly Tyr Glu Tyr Ala Phe						
	420	425				

<210> 136
 <211> 427
 <212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-112 effector

<400> 136

Met Ser Asn Tyr Val Phe Val Ile Asp Thr Asn Lys Lys Pro Val Gly
1 5 10 15

Thr Val His Pro Ala Cys Ala Arg Lys Leu Leu Ser Ser Gln Gln Ala
20 25 30

Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Ile Leu Lys Thr Ser Val
35 40 45

Pro Glu Gly Phe Gln Ala Arg Ser Leu Arg Ile Lys Ile Asp Pro Gly
50 55 60

Ala Lys Thr Thr Gly Ile Ala Val Leu Asp Gly Asn Lys Val Val Trp
65 70 75 80

Ala Ala Glu Leu Thr His Arg Gly Glu Gln Ile Arg Asn Arg Leu Thr
85 90 95

Ser Arg Arg Gln Ile Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr
100 105 110

Arg Pro Ala Arg Phe Leu Asn Arg Thr Arg Asp Lys Gly Trp Leu Ala
115 120 125

Pro Ser Leu Arg Ser Arg Val Glu Asn Ile Leu Thr Trp Val Asn Arg
130 135 140

Leu Arg Arg Val Ser Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr

165

170

175

Gln Gln Gly Thr Leu Tyr Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu
 180 185 190

Lys Trp Gly Arg Lys Cys Ala Tyr Cys Gly Ala Thr Asn Val Pro Leu
 195 200 205

Gln Val Glu His Ile Val Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
 210 215 220

Ser Asn Leu Thr Leu Ala Cys Val Ser Cys Asn Gln Thr Lys Gly Asn
 225 230 235 240

Lys Asp Ile Arg Glu Phe Leu Lys His Lys Pro Glu Leu Leu Ser Arg
 245 250 255

Ile Leu Gln Gln Thr Lys Gln Pro Leu Val Ala Ala Ala Val Val Asn
 260 265 270

Thr Thr Arg Trp Ala Leu Phe Asn Arg Leu Lys Glu Thr Gly Leu Pro
 275 280 285

Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser His Gln
 290 295 300

Gln Leu Pro Lys Ala His Trp Ile Asp Ala Ala Cys Val Gly Ala Ser
 305 310 315 320

Thr Pro Asn Leu Val Phe Val Thr Lys Gln Pro Leu Gln Ile Lys Ala
 325 330 335

Lys Gly His Gly Thr Arg Gln Met Cys Ile Thr Asp Lys Tyr Gly Phe
 340 345 350

Pro Lys Gln His Arg Thr Arg Val Gln Ile His Lys Gly Phe Arg Thr
 355 360 365

Gly Asp Ile Val Arg Ala Val Val Thr Lys Gly Lys Lys Ile Gly Thr
 370 375 380

Tyr Ile Gly Arg Val Val Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala
385 390 395 400

Thr Lys Gln Gly Lys Ile Thr Gly Ile Asn Tyr Lys Tyr Cys Lys Thr
405 410 415

Val His Lys Lys Asp Gly Tyr Glu Tyr Ala Phe
420 425

<210> 137

<211> 425

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-113 effector

<400> 137

Met Ser Asn Tyr Val Leu Val Leu Asp Ala Glu Lys Arg Pro Leu Asp
1 5 10 15

Pro Ile His Pro Gly Ala Ala Arg His Leu Leu Asn Glu Gly Lys Ala
20 25 30

Ala Val Phe Arg Arg Phe Pro Phe Thr Ile Ile Leu Lys Glu Ser Arg
35 40 45

Pro Asp Ala Pro Val Gln Asp Leu Glu Leu Lys Leu Asp Pro Gly Ser
50 55 60

Lys Val Thr Gly Ile Ala Ile Lys Gln Gly Asn Lys Val Ile Phe Gly
65 70 75 80

Ala Glu Leu Gln His Arg Gly Gln Gln Ile Lys Asp Ala Leu Leu Ser
85 90 95

Arg Arg Gln Leu Arg Arg Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg

100

105

110

Gln Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro
 115 120 125

Ser Leu Gln His Arg Val Leu Thr Thr Leu Thr Trp Val Arg Lys Phe
 130 135 140

Met Arg Leu Ala Pro Ile Thr Asn Ile Thr Gln Glu Leu Val Arg Phe
 145 150 155 160

Asp Leu Gln Leu Met Gln Asn Pro Glu Ile Ser Gly Ile Gln Tyr Gln
 165 170 175

Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys
 180 185 190

Trp Asn Arg Lys Cys Ala Tyr Cys Ser Val Glu Asn Val Pro Leu Glu
 195 200 205

Val Glu His Ile Gln Pro Arg Ser Lys Gly Gly Ser Asp Arg Val Ser
 210 215 220

Asn Leu Thr Ile Ala Cys His Ala Cys Asn Gln Ser Lys Gly Asn Gln
 225 230 235 240

Asp Ile Arg Asp Phe Leu Ala Gly Lys His Asp Leu Leu Asn Arg Ile
 245 250 255

Leu Lys Gln Ala Lys Ser Pro Leu Lys Asp Ala Ala Ala Val Asn Ser
 260 265 270

Thr Arg Trp Ala Leu Phe Asn Ala Leu Lys Glu Thr Gly Leu Pro Val
 275 280 285

Ala Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Thr Arg Leu Gly
 290 295 300

Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly Asn Val Glu
 305 310 315 320

Ser Leu Glu Ile Leu Thr Ser Lys Pro Leu Ile Ile Ala Ala Lys Gly
325 330 335

His Gly Thr Arg Gln Met Cys Gly Thr Asn Lys Phe Gly Phe Pro Thr
340 345 350

Arg His Lys Ser Arg Val Gln Ile His Lys Gly Phe Gln Thr Gly Asp
355 360 365

Ile Val Arg Ala Thr Val Thr Ala Gly Lys Lys Ile Gly Ser Tyr Val
370 375 380

Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala Thr Thr
385 390 395 400

Asp Gly Arg Val Ala Gly Ile Ser His Lys Tyr Cys Lys Pro Ile His
405 410 415

Lys Lys Asp Gly Tyr Leu Tyr Gly Phe
420 425

<210> 138

<211> 490

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-114 effector

<400> 138

Met Ser Thr Thr Arg Arg Lys Ala Lys Ala Arg His Pro Gly Val Leu
1 5 10 15

His Gln Pro Gln Ala Leu Ser Pro Thr Thr Lys Lys Arg Ala Thr Thr
20 25 30

Arg Leu Pro Thr Ser Arg Leu Asn Asp Leu Arg Ala Pro Gly Glu Val

35

40

45

Thr Ile Thr Cys Ala Ser Arg Arg Gly Arg Leu Leu Ala Tyr Ser Arg
 50 55 60

Pro Lys Thr Pro Arg Val Phe Val Leu Ser Asn Thr Leu Lys Pro Leu
 65 70 75 80

Met Pro Cys Arg Pro Ala Arg Ala Gln Asp Leu Leu Ala Cys Gly Arg
 85 90 95

Ala Ala Val Tyr Arg Leu Gln Pro Phe Thr Ile Val Leu Lys Asp Arg
 100 105 110

Ala Asp Gly Asn Val Gln Pro Val Glu Phe Lys Val Asp Pro Gly Ser
 115 120 125

Lys Val Thr Gly Leu Ala Leu Val Ala Glu Phe Glu Lys Arg Gly Arg
 130 135 140

Thr Val Val Trp Ala Ala Asn Leu Ala His Arg Gly Tyr Arg Val Lys
 145 150 155 160

Ala Ser Ile Thr Asp Arg Ala Met Phe Arg Arg Gly Arg Arg Gly Arg
 165 170 175

Lys Thr Arg Tyr Arg Ala Ala Arg Phe Glu Asn Arg Thr Arg Pro Thr
 180 185 190

Asn Trp Leu Ala Pro Ser Leu Gln Ser Arg Val Leu Asn Val Lys Ser
 195 200 205

Trp Tyr Ser Arg Leu Leu Ser Arg Ala Pro Ile Ser Val Ala Gln Val
 210 215 220

Glu Thr Ser Ser Phe Asp Thr Gln Leu Met Glu Asn Ala Asp Ile Ser
 225 230 235 240

Gly Val Glu Tyr Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Gln
 245 250 255

Tyr Val Leu Glu Arg Gly Gly His Thr Cys Ser Tyr Cys Asp Ala Lys
260 265 270

Asp Val Ala Leu His Leu Asp His Val Leu Pro Arg Ser Arg Gly Gly
275 280 285

Ser Asn Arg Val Ser Asn Leu Val Pro Ala Cys Lys Pro Cys Asn Asp
290 295 300

Ala Lys Ser Asn Arg Ala Val Glu Asp Tyr Leu Val Asp Arg Pro Glu
305 310 315 320

Val Leu Arg Gln Val Lys Ala Gln Leu Arg Ser Pro Leu Arg Asp Ala
325 330 335

Ala Val Met Asn Ala Thr Arg Phe Ala Ile Val Asp Ala Leu Arg Glu
340 345 350

Phe Gly Leu Glu Val Arg Met Trp Ser Gly Gly Arg Thr Lys Trp Asn
355 360 365

Arg Thr Asn Leu Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Cys
370 375 380

Val Gly Glu Ser Gly Ala Ala Val Arg Val Pro Val Leu Arg Pro Leu
385 390 395 400

Thr Ile Ser Ala Met Gly Arg Gly His Arg Arg Val His Gly Asn Asp
405 410 415

Arg Tyr Gly Phe Pro Arg Gly Thr Ala Arg Arg Ala Lys Arg Val Ala
420 425 430

Gly Phe Gln Thr Gly Asp Leu Val Arg Leu Val Cys Leu Arg Gly Lys
435 440 445

Cys Ala Gly Val His Thr Gly Arg Leu Ser Ser Ile Arg Thr Arg Gly
450 455 460

Gln Phe Val Leu Gly Lys His Asp Arg Pro Ala Arg Glu Phe Thr Leu

465

470

475

480

Leu Gln Arg Ser Asp Gly Tyr Ala Tyr Gly
 485 490

<210> 139

<211> 489

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-115 effector

<400> 139

Met Thr Ile Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
 20 25 30

Arg Val Val Ser Lys Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Val Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Lys Asp Gly Ser Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Lys Lys
 85 90 95

Arg Ala Ala Phe Arg Lys Asn His Arg Thr Leu Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Ile Val Glu Ser Asn Thr
 115 120 125

Ile Glu Lys Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Thr Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Val Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Ala Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp

340

345

350

Ala Asp Thr Lys Val Ser Ala Pro Ala Glu Pro Phe Lys Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ala
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
 405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Arg Pro His Leu Pro Gln Tyr
 420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Ala Phe Asn Gly
 435 440 445

Ser Val Gly Val Met Gln Ser Ser Ile Val Gly Ser Phe Tyr Lys Ser
 450 455 460

Thr Lys Gly His Lys Ala Thr Pro Arg Arg Cys Val Leu Leu Ala Gln
 465 470 475 480

Asn Ala Gly Met Val Phe Asn Pro Ala
 485

<210> 140

<211> 41

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-116 effector

<400> 140

Met Thr Lys Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr
35 40

<210> 141

<211> 241

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-117 effector

<400> 141

Met Thr Lys Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys

100

105

110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Asn Ile Ala Ala Gly Ser
 115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His Tyr
 130 135 140

Ile Arg Asn Lys Lys Ala Arg Phe Asn Asn Arg Lys Arg Pro Gln Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
 165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly Arg Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile

<210> 142

<211> 263

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-118 effector

<400> 142

Met Thr Lys Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Asn Ile Ala Ala Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Lys Ala Arg Phe Asn Asn Arg Lys Arg Pro Gln Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp

210

215

220

Ala Val Tyr Ala Gln Gln Asp Gly Arg Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
 245 250 255

Thr Leu Ala Asn Arg Cys Gly
 260

<210> 143

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-119 effector

<400> 143

Met Thr Lys Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
 20 25 30

Arg Val Val Ser Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
 85 90 95

Arg Ala Gly Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Asn Ile Ala Ala Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Lys Ala Arg Phe Asn Asn Arg Lys Arg Pro Gln Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly Arg Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Arg Glu His His Ala Leu Val
260 265 270

His Thr Asp Lys Val Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Val Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Arg Tyr Asp Val Tyr Ala

305		310		315		320									
Thr	Asp	Gly	Arg	Ser	Thr	Lys	Gly	Phe	Arg	Val	Ala	Lys	Asn	Val	Pro
				325					330					335	
Lys	Glu	His	Tyr	Thr	Asp	Ala	Tyr	Cys	Ile	Ala	Cys	Ser	Ile	Leu	Asp
			340					345					350		
Thr	Asp	Ile	Glu	Val	Ser	Thr	Pro	Val	Glu	Pro	Phe	Glu	Leu	Lys	Gln
		355					360					365			
Phe	Arg	Arg	His	Asp	Arg	Gln	Ala	Cys	His	Gln	Gln	Arg	Val	Asp	Arg
	370					375					380				
Lys	Tyr	Tyr	Leu	Asn	Gly	Lys	Gln	Val	Ala	Thr	Asn	Arg	His	Lys	Ala
385					390					395					400
Ile	Glu	Gln	Lys	Ser	Asp	Ser	Leu	Gln	Glu	Phe	Arg	Glu	Ser	Tyr	Gly
				405					410					415	
Asp	Thr	Ala	Val	Ser	Gln	Leu	Ala	Val	Lys	Pro	His	Ser	Pro	Gln	Tyr
			420					425					430		
Lys	Asp	Met	Thr	Arg	Ile	Met	Gln	Gly	Ala	Val	Met	Asp	Phe	Gly	Gly
		435					440					445			
Thr	Val	Gly	Val	Phe	Gln	Gly	Ser	Asp	Gly	Phe	His	Asn	Gly	Lys	Pro
	450					455					460				
Asp	Tyr	Tyr	Lys	Ser	Ala	Lys	Gly	Ala	Arg	Val	Leu	Thr	Lys	Arg	Cys
465					470					475					480
Val	Leu	Leu	Ala	Gln	Asn	Thr	Gly	Ile	Val	Phe	Ile	Pro	Ala		
				485					490						

<210> 144
 <211> 23
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-120 effector

<400> 144

Met	Thr	Met	Val	Tyr	Val	Gln	Asn	Lys	Asp	Gly	Lys	Pro	Leu	Met	Pro
1				5					10					15	

Thr	Thr	Arg	Tyr	Cys	Tyr	Val
			20			

<210> 145

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-121 effector

<400> 145

Met	Thr	Met	Val	Tyr	Val	Gln	Asn	Lys	Asp	Gly	Lys	Pro	Leu	Met	Pro
1				5					10					15	

Thr	Thr	Arg	Tyr	Cys	Tyr	Val	Arg	Leu	Leu	Leu	Lys	Glu	Lys	Lys	Ala
			20					25					30		

Arg	Val	Val	Cys	Thr	Thr	Pro	Phe	Thr	Ile	Gln	Leu	Asn	Tyr	Asp	Thr
		35					40					45			

Pro	Asp	Ile	Thr	Gln	Asp	Leu	Ile	Leu	Gly	Ile	Asp	Pro	Gly	Arg	Thr
	50					55					60				

Asn	Ile	Gly	Val	Ala	Val	Val	Lys	Glu	Asp	Gly	Gln	Cys	Val	Phe	Ser
65					70					75					80

Ala	His	Leu	Glu	Thr	Arg	Asn	Lys	Asp	Val	Pro	Leu	Leu	Met	Gln	Lys

85

90

95

Arg Ala Gly Phe Arg Lys Gln His Arg Thr Leu Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Thr Asp Gly Ser
 115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His His
 130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Cys Arg Pro Val Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
 165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
 245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
 260 265 270

His Thr Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
 275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
 290 295 300

His Leu Met Glu Tyr Leu Gly Asn Glu Thr Leu Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Ile Glu Val Ser Thr Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Ile Leu Asp Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Phe Glu Gln Glu Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Gly
405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Lys Pro His Ser Pro Gln Tyr
420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Asp Phe Gly Gly
435 440 445

Ala Val Gly Ile Phe Gln Gly Ser Glu Gly Phe His Asn Gly Lys Pro
450 455 460

Asp Tyr Tyr Lys Ser Thr Lys Gly Glu Arg Val Leu Thr Arg Arg Cys
465 470 475 480

Ala Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
485 490

<210> 146

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-122 effector

<400> 146

Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
85 90 95

Arg Ala Ala Phe Arg Arg Asn His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Ser Gly Tyr Glu Lys Pro Ile Val Cys His His
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Ile Ala Lys Val Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Pro Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Thr Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Val Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Trp Asp
340 345 350

Ala Asp Thr Lys Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ser

385 390 395 400
 Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
 405 410 415
 Asp Pro Ala Val Ser Gln Leu Thr Val Arg Pro His Leu Pro Gln Tyr
 420 425 430
 Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
 435 440 445
 Ile Val Gly Val Phe Gln Gly Ser Glu Gly Phe His Asn Gly Lys Pro
 450 455 460
 Asp Tyr Tyr Lys Ser Thr Lys Gly Ala Lys Val Ser Thr Lys Arg Cys
 465 470 475 480
 Ala Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

 <210> 147
 <211> 489
 <212> PRT
 <213> Unknown

 <220>
 <223> Description of Unknown:
 uncultivated organism

 <220>
 <223> Category: MG35 effectors

 <220>
 <223> Description: MG35-123 effector

 <400> 147
 Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

 Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
 20 25 30

 Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Ile Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Val Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Ile Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Arg His His Ala Leu Val

260

265

270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
 275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
 290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala
 305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
 325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Thr Asp Ile Glu Val Ser Ala Pro Thr Ser Pro Phe Gly Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Thr Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Ile Ala Thr Asn Arg His Lys Ala
 385 390 395 400

Ile Glu Gln Lys Ser Asn Ser Leu Gln Glu Leu Arg Glu Ala Tyr Gly
 405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr
 420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Asp Phe Asn Gly
 435 440 445

Thr Ile Gly Val Met Gln Ser Ser Ile Val Gly Arg Phe Tyr Lys Ser
 450 455 460

Thr Lys Gly Tyr Lys Ala Thr Pro Arg Arg Cys Val Leu Leu Ala Gln
 465 470 475 480

Asn Ala Gly Met Val Phe Leu Pro Ala
485

<210> 148

<211> 489

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-124 effector

<400> 148

Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr

130

135

140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Val Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
 165 170 175

Ile Ala Lys Ile Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
 245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Arg His His Ala Leu Val
 260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
 275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
 290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala
 305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
 325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Thr Asp Ile Glu Val Ser Ala Pro Thr Ser Pro Phe Gly Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Thr Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Ile Ala Thr Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asn Ser Leu Gln Glu Leu Arg Glu Ala Tyr Gly
405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr
420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Asp Phe Asn Gly
435 440 445

Thr Ile Gly Val Met Gln Ser Ser Ile Val Gly Arg Phe Tyr Lys Ser
450 455 460

Thr Lys Gly Tyr Lys Ala Thr Pro Arg Arg Cys Val Leu Leu Ala Gln
465 470 475 480

Asn Ala Gly Met Val Phe Leu Pro Ala
485

<210> 149
<211> 137
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-125 effector

<400> 149
Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro

1	5	10	15
Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala	20	25	30
Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr	35	40	45
Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Val Asp Pro Gly Arg Thr	50	55	60
Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser	65	70	75
Ala His Leu Glu Thr Arg Asn Asn Glu Val Pro Phe Leu Met Lys Lys	85	90	95
Arg Ala Gly Phe Arg Lys Gln His Arg Thr Leu Asp Arg Arg Arg Lys	100	105	110
Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser	115	120	125
Val Glu Arg Leu Phe Pro Gly Tyr Lys	130	135	

<210> 150
 <211> 141
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-126 effector

<400> 150
Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Ser Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asn Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Asn His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Ser Thr Pro Ile Val
130 135 140

<210> 151

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-127 effector

<400> 151

Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala

20

25

30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Arg Leu Asn Tyr Asp Thr
 35 40 45

Pro Asn Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
 85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
 115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His His
 130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Ala His Ile Asn Leu
 165 170 175

Ile Ala Lys Ala Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Lys Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Ala Asp Thr Lys Val Ser Ala Pro Ala Glu Pro Phe Lys Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ser
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Arg Pro His Ser Pro Gln Tyr
420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
435 440 445

Ile Val Gly Val Phe Lys Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro

450

455

460

Asn Tyr Tyr Asn Ser Thr Lys Gly Ala Arg Val Leu Thr Lys Arg Cys
 465 470 475 480

Ala Leu Leu Ala Lys Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 152

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-128 effector

<400> 152

Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
 20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Arg Leu Asn Tyr Asp Thr
 35 40 45

Pro Asn Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
 85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His His
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Ala His Ile Asn Leu
165 170 175

Ile Ala Lys Ala Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Lys Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro

325

330

335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Ala Asp Thr Lys Val Ser Ala Pro Ala Glu Pro Phe Lys Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ser
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
 405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Arg Pro His Ser Pro Gln Tyr
 420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Val Phe Asp Gly
 435 440 445

Ala Val Gly Val Phe Lys Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro
 450 455 460

Asn Tyr Tyr Asn Ser Thr Lys Gly Ala Arg Val Leu Thr Lys Arg Cys
 465 470 475 480

Ala Leu Leu Ala Lys Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 153

<211> 484

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-129 effector

<400> 153

Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Ser Arg Thr Pro Phe Thr Ile Arg Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Asn His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Val Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Cys Arg Pro Gln Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Ile Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile His Arg

195

200

205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
 245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
 260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
 275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
 290 295 300

His Leu Met Glu Tyr Leu Gly Arg Glu Thr Pro Tyr Asp Val Tyr Ala
 305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
 325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Ala Asp Thr Lys Val Ser Thr Pro Val Glu Pro Phe Glu Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
 370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Ala Asn Arg His Lys Ser
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Cys Glu Ala Tyr Gly
 405 410 415

Asp Ala Ala Val Ser Gln Ile Thr Val Arg Pro His Ser Pro Gln Tyr
420 425 430

Lys Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Asp Phe Asp Gly
435 440 445

Ile Val Gly Val Phe Lys Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro
450 455 460

Asn Tyr Tyr Asn Ser Thr Lys Gly Ala Ser Val Leu Thr Asn Arg Cys
465 470 475 480

Ala Leu Leu Ala

<210> 154

<211> 489

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-130 effector

<400> 154

Met Thr Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Asn Lys Ala
20 25 30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser

65					70					75					80
Ala	His	Leu	Glu	Thr	Arg	Asn	Lys	Asp	Val	Pro	Leu	Leu	Met	Lys	Lys
				85					90					95	
Arg	Ala	Ala	Phe	Arg	Arg	Asn	His	Arg	Thr	Leu	Gly	Arg	Arg	Arg	Lys
			100					105					110		
Arg	Gln	Arg	Arg	Ala	Lys	Ala	Ala	Gly	Thr	Thr	Val	Glu	Asn	Glu	Ser
		115					120					125			
Ile	Lys	Arg	Leu	Leu	Pro	Gly	Tyr	Glu	Lys	Pro	Val	Ile	Cys	His	His
	130					135					140				
Ile	Arg	Asn	Arg	Lys	Ala	Arg	Phe	Asn	Asn	Arg	Cys	Arg	Pro	Gln	Gly
145					150					155					160
Trp	Leu	Thr	Pro	Thr	Ala	Asn	His	Leu	Leu	Gln	Thr	His	Ile	Asn	Leu
				165					170					175	
Ile	Ala	Lys	Val	Glu	Lys	Phe	Leu	Pro	Ile	Thr	Thr	Val	Val	Val	Glu
			180					185					190		
Leu	Asn	Arg	Phe	Ala	Phe	Met	Ala	Met	Asp	Asn	Pro	Asn	Ile	Arg	Arg
		195					200					205			
Trp	Glu	Cys	Gln	Gln	Gly	Pro	Leu	Tyr	Gly	Leu	Gly	Ser	Val	Glu	Asp
	210					215					220				
Ala	Val	Tyr	Ser	Gln	Gln	Asp	Gly	His	Cys	Leu	Phe	Cys	Lys	Lys	Pro
225					230					235					240
Ile	Asp	His	Tyr	His	His	Val	Val	Pro	Arg	His	Lys	Gly	Gly	Ser	Glu
				245					250					255	
Thr	Leu	Ala	Asn	Arg	Cys	Gly	Leu	Cys	Val	Lys	His	His	Asp	Leu	Val
			260					265					270		
His	Lys	Asp	Lys	Ala	Trp	Ala	Asp	Lys	Leu	Val	Thr	Arg	Lys	Glu	Gly
		275					280					285			

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Leu Glu Tyr Leu Gly Asp Glu Thr His Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Ser Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Ile Glu Val Ser Val Pro Val Glu Pro Phe Glu Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Ile Ala Val Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Gly
405 410 415

Asp Ala Val Val Ser Gln Leu Ala Val Lys Pro His Leu Pro Gln Tyr
420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Met Met Asp Phe Asn Gly
435 440 445

Thr Ile Gly Val Met Gln Ser Ser Ile Val Gly Ser Phe Tyr Lys Ser
450 455 460

Thr Lys Gly His Lys Ala Thr Pro Lys Asn Cys Val Leu Leu Ala Gln
465 470 475 480

Asn Ala Gly Met Val Phe Ile Pro Ala
485

<210> 155

<211> 124
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-131 effector

<400> 155
Met Val Gln Ala Ser Ala Ala Gly Asn Lys Pro Phe His Asn Met Gly
1 5 10 15

Glu Gly Asp Ala Asp Lys Arg Pro Asn Thr Arg Ala Ser Gly Asp Tyr
20 25 30

Asp Thr Gly Leu Thr Arg Pro Ala Arg Ala Lys Ala Gly Arg Val Gln
35 40 45

Tyr Gly Phe Gln Thr Gly Asp Ile Val Arg Ala Ala Val Ser Thr Gly
50 55 60

Lys Lys Ala Gly Thr Tyr Ser Gly Arg Val Ala Val Arg Ser Ser Gly
65 70 75 80

Arg Phe Asp Ile Thr Thr Cys Thr Gly Lys Ala Gly Ser Asn Tyr Arg
85 90 95

Tyr Cys Thr His Leu His Lys Ser Asp Gly Tyr Ser Tyr Glu Lys Gly
100 105 110

Glu Ala Ala Ala Asn Phe Trp Phe Asp Ser Thr Arg
115 120

<210> 156
<211> 320
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-132 effector

<400> 156

Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg Thr Arg
1 5 10 15

Pro Asp Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Glu Thr Thr
20 25 30

Leu Thr Trp Val His Lys Leu Ile Arg Phe Ala Pro Ile Ala Ser Ile
35 40 45

Val Gln Glu Leu Val Gln Phe Asp Leu Gln Leu Met Gln Asn Ala Glu
50 55 60

Ile Ser Gly Val Leu Tyr Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val
65 70 75 80

Ser Glu Tyr Leu Leu Thr Lys Trp His Arg Gln Cys Ala Tyr Cys Ser
85 90 95

Val Glu Asn Val Pro Phe Glu Ile Glu His Val Gln Pro Lys Ser Arg
100 105 110

Gly Gly Ser Asp Arg Val Ser Asn Leu Thr Leu Ala Cys His Asp Cys
115 120 125

Asn Gln Lys Lys Gly Asn Gln Asp Val Arg Glu Phe Leu Ala Thr Lys
130 135 140

Pro His Leu Leu Asn Arg Ile Leu Lys Gln Ala Lys Leu Pro Leu Lys
145 150 155 160

Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Phe Asn Ala Leu
165 170 175

Lys Glu Thr Gly Leu Pro Val Thr Thr Gly Thr Gly Gly Gln Thr Lys

180

185

190

Phe Asn Arg Asn Arg Leu Glu Leu Pro Lys Ser His Trp Leu Asp Ala
 195 200 205

Ala Cys Val Gly Asn Phe Glu Ala Leu Glu Val Leu Thr Ser Lys Pro
 210 215 220

Leu Leu Ile Ala Ala Lys Gly His Gly Thr Arg Gln Met Cys Gly Thr
 225 230 235 240

Asn Lys Tyr Gly Phe Ala Thr Arg His Lys Ser Arg Val Gln Ile His
 245 250 255

Asn Gly Phe Gln Thr Gly Asp Ile Val Ser Ala Thr Val Thr Ala Gly
 260 265 270

Lys Lys Ile Gly Ser Tyr Val Gly Arg Val Leu Cys Arg Ala Ser Gly
 275 280 285

Ser Phe Asp Ile Ala Thr Lys Ser Gly Arg Val Ala Gly Ile Ser His
 290 295 300

Lys Tyr Cys Ser Pro Ile His Lys Lys Asp Gly Tyr Ser Tyr Ala Phe
 305 310 315 320

<210> 157

<211> 341

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-133 effector

<400> 157

Asn Arg Ser Arg Pro Ala Gly Trp Leu Thr Pro Thr Ala Asn His Leu
 1 5 10 15

Leu Gln Thr His Ile Ile Leu Ile Ala Lys Val Ala Lys Phe Leu Pro
20 25 30

Ile Thr Lys Val Val Val Glu Leu Asn Arg Phe Ala Phe Met Ala Met
35 40 45

Glu Asn Pro Asn Ile His Arg Trp Glu Tyr Gln Gln Gly Pro Leu Tyr
50 55 60

Gly Leu Gly Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His
65 70 75 80

Cys Leu Phe Cys Lys Glu Pro Ile Asp His Tyr His His Val Val Pro
85 90 95

Arg His Lys Gly Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys
100 105 110

Ala Lys His His Asp Leu Val His Lys Asp Lys Ala Trp Ala Glu Lys
115 120 125

Leu Val Thr Arg Lys Gly Gly Met Asn Lys Lys Tyr His Ala Leu Ser
130 135 140

Val Leu Asn Gln Ile Ile Pro His Leu Met Glu His Leu Gly Ser Glu
145 150 155 160

Thr Pro Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser Thr Lys Gly Phe
165 170 175

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Ala Asp Ala Tyr Cys
180 185 190

Ile Ala Cys Ser Ile Leu Asp Ser Asp Ile Glu Thr Ser Ala Pro Val
195 200 205

Glu Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys
210 215 220

Ile Arg Gln Met Val Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val Val

Phe Asp Met Gln Lys Leu Glu Asn Pro Asp Thr Gln Gly Val Gly Tyr
35 40 45

Gln Gln Gly Arg Met Phe Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu
50 55 60

Glu Arg Glu Asn Tyr Thr Cys Ile Tyr Cys Gly Ile His Ala Ser Lys
65 70 75 80

Ala Lys Met Glu Ile Glu His Val Ile Pro Arg Ser Arg Gly Gly Thr
85 90 95

Asp Ser Leu Asn Asn Leu Val Leu Ser Cys Arg Ala Cys Asn Glu Ala
100 105 110

Lys Gly Ser Gln Asp Val Gln Thr Tyr Leu Lys Gly Asn Pro Ser Val
115 120 125

Leu Arg Arg Val Lys Ala Arg Leu Asn Thr Asn Tyr Arg Asp Ala Ala
130 135 140

His Thr Asn Ser Ile Arg Leu Phe Val Leu Asn Lys Leu Gln Thr Met
145 150 155 160

Ala Asp Ala Ile Gly Thr Asn Leu Asn Val Gly Phe Gly Tyr Thr Thr
165 170 175

Lys Gln Asn Arg Leu Leu Leu Asn Leu Pro Lys Asp His Trp Ile Asp
180 185 190

Ala Ala Val Cys Thr Ser Asp Gly Ser Ala Val Lys Val Asp Pro Ser
195 200 205

Leu Lys Pro Phe Thr Ile Lys Ala Ile Gly Arg Gly Ser Arg Gln Phe
210 215 220

Cys Arg Met Asn Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg
225 230 235 240

Ser Lys Asn Phe Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val

245

250

255

Val Pro Leu Gly Ser Lys Thr Lys Val Pro Val Gly Thr His Thr Gly
 260 265 270

Arg Val Ala Val Arg Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp
 275 280 285

Ala Lys Leu Gly Ile Tyr His Lys Tyr Cys Gln Gln Ile His Leu Met
 290 295 300

Asp Gly Tyr Ser Tyr Ala
 305 310

<210> 159

<211> 278

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-135 effector

<400> 159

Gln Glu Leu Val Lys Phe Asp Thr Gln Ala Leu Gln Ser Pro Glu Ile
 1 5 10 15

Arg Gly Val Glu Tyr Gln Gln Gly Thr Leu Phe Gly Tyr Glu Val Arg
 20 25 30

Glu Tyr Leu Leu Glu Lys Trp His Arg Arg Cys Ala Tyr Cys Ala Ala
 35 40 45

Thr Asp Val Pro Leu Gln Val Glu His Ile Val Pro Lys Ser Lys Gly
 50 55 60

Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ser Cys Ala Asp Cys Asn
 65 70 75 80

Gln Lys Lys Gly Val Leu Pro Val Glu Val Phe Leu Ala Ser Gln Pro
85 90 95

Asp Arg Leu Asn Arg Ile Leu Ala Gln Ala Lys Ala Pro Leu Lys Asp
100 105 110

Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Phe Gln Arg Leu Lys
115 120 125

Ala Thr Gly Leu Pro Val Glu Val Gly Thr Gly Gly Arg Thr Lys Phe
130 135 140

Asn Arg Thr Arg Leu Ser Leu Pro Lys Thr His Ala Leu Asp Ala Ala
145 150 155 160

Cys Val Gly Asp Val Asp Ala Ile Glu Gly Trp Gln Val Pro Thr Leu
165 170 175

Arg Val Lys Ala Thr Gly Arg Gly Thr Tyr Gln Arg Thr Arg Leu Thr
180 185 190

Ala Gln Gly Phe Pro Arg Gly Ser Leu Thr Arg Ala Lys Arg His Phe
195 200 205

Gly Phe Gln Thr Gly Asp Gln Val Lys Ala Val Val Pro Ala Gly Lys
210 215 220

Lys Ala Gly Thr His Val Gly Arg Val Ala Val Arg Ala Ser Gly Ser
225 230 235 240

Phe Asn Ile Gln Thr Pro His Gly Val Val Gln Gly Ile His His Arg
245 250 255

His Cys His Leu Leu Gln Arg Gly Asp Gly Tyr Gly Tyr Ala Ile Ser
260 265 270

Thr Phe Asp Ser Thr His
275

<210> 160

<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-136 effector

<400> 160
Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Asn Ile
1 5 10 15

Gly Thr Tyr Ile Gly Arg Val Val Val Arg Ala Arg Gly Ser Phe Asp
20 25 30

Ile Gly Ile Gly Lys Lys Lys Val Ser Gly Ile Ser Tyr Lys Tyr Cys
35 40 45

Gln Leu Ile Gln Arg Val Asp Gly Tyr Glu Tyr Thr
50 55 60

<210> 161
<211> 217
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-137 effector

<400> 161
Gln Val Glu His Ile His Pro Lys Ala Lys Gly Gly Ser Asn Arg Ile
1 5 10 15

Ser Asn Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu Lys Lys Gly Thr
20 25 30

Gln Asp Ile Lys Asn Phe Leu Ser Lys Lys Pro Asp Leu Leu Lys Gln
35 40 45

Ile Met Gly Gln Val Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn
50 55 60

Ser Thr Arg Trp Ala Leu Phe Asn Gln Leu Lys Leu Thr Gly Leu Pro
65 70 75 80

Val Thr Thr Gly Ser Gly Gly Gln Thr Lys Tyr Asn Arg Thr Arg Leu
85 90 95

Lys Leu Pro Lys Thr His Tyr Phe Asp Ala Ala Cys Val Gly Arg Val
100 105 110

Asp Gln Leu Ile Val Leu Thr Thr Gln Pro Leu Leu Ile Lys Ser Arg
115 120 125

Gly His Gly Thr Arg Gln Met Cys Arg Thr Asp Lys Phe Gly Phe Pro
130 135 140

Ser Arg His Val Pro Arg Asn Lys Leu Val Lys Gly Phe Gln Thr Gly
145 150 155 160

Asp Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys Val Gly Glu Tyr
165 170 175

Val Gly Arg Val Ala Val Arg Ser Asn Gly Ser Phe Asn Ile Ser Ala
180 185 190

Lys Glu Leu Val Gln Ser Ile Ser His Lys Tyr Cys Gln Thr Leu Gln
195 200 205

Arg Lys Asp Gly Tyr Ser Tyr Gln Phe
210 215

<210> 162

<211> 124

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-138 effector

<400> 162

Arg Leu Asp Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly
1 5 10 15

His Val Asp Gln Leu Glu Val Leu Thr Gly Lys Pro Leu Leu Ile Lys
20 25 30

Ala Thr Gly His Gly Ser Arg Gln Met Cys Gly Thr Asp Lys Phe Gly
35 40 45

Phe Pro Ser Arg His Arg Thr Arg Lys Gln Ile His Gln Gly Phe Gln
50 55 60

Thr Gly Asp Ile Val Lys Ala Leu Val Thr Ser Gly Lys Lys Ile Gly
65 70 75 80

Ser Tyr Gly Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile
85 90 95

Gln Val Lys Ser Gly Arg Val Gln Gly Leu Ser His Lys Phe Cys Arg
100 105 110

Ser Val His Arg Lys Asp Gly Tyr Gly Tyr Gly Phe
115 120

<210> 163

<211> 125

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-139 effector

<400> 163

Arg Leu Arg Phe Asn Leu Pro Lys Ala His Trp Leu Asp Ala Ala Cys
1 5 10 15

Val Gly Asp Val Glu Ser Leu Asp Ile Val Thr Ser Lys Pro Leu Met
20 25 30

Ile Arg Ala Lys Gly His Gly Thr Arg Arg Met Cys Gly Thr Asn Lys
35 40 45

Tyr Gly Phe Pro Thr Arg His Arg Ser Arg Arg Gln Ile His Asn Gly
50 55 60

Phe Gln Thr Gly Asp Ile Val Thr Ala Thr Val Thr Ala Gly Lys Lys
65 70 75 80

Ile Gly Ser Tyr Val Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe
85 90 95

Asp Ile Thr Thr Ala Ser Gly Arg Val Thr Gly Ile Asn His Lys Tyr
100 105 110

Cys Lys Pro Ile His Arg Lys Asp Gly Tyr Ala Tyr Ala
115 120 125

<210> 164

<211> 171

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-140 effector

<400> 164

Arg Thr Arg Asp Lys Gly Trp Leu Ala Pro Ser Leu Lys Ser Arg Val

1	5	10	15
Glu Asn Ile Leu Thr Trp Val Asn Arg Leu Arg Arg Val Ser Asn Ile	20	25	30
Thr Ala Ile Ser Gln Glu Leu Val Arg Phe Asp Thr Gln Lys Leu Gln	35	40	45
Asn Pro Glu Ile Ser Gly Glu Glu Tyr Gln Gln Gly Thr Leu Tyr Gln	50	55	60
Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Lys Cys Ala	65	70	75
Tyr Cys Gly Ala Lys Asp Val Pro Leu Gln Val Glu His Ile Val Pro	85	90	95
Arg Ser Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu Ala Cys	100	105	110
Val Ser Cys Asn Gln Ala Lys Gly Asn Gln Asp Ile Arg Glu Phe Leu	115	120	125
Lys His Lys Pro Asp Leu Leu Ser Arg Ile Leu Gln Gln Thr Lys Gln	130	135	140
Pro Leu Val Ala Ala Ala Val Val Asn Thr Thr Arg Trp Ala Leu Phe	145	150	155
Asn Arg Leu Lys Glu Thr Gly Leu Pro Val Asp	165	170	

<210> 165

<211> 294

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-141 effector

<400> 165

Arg Val Glu Asn Ile Leu Thr Trp Val Asn Arg Leu Arg Arg Val Ser
1 5 10 15

Asn Ile Thr Ala Ile Ser Gln Glu Leu Val Arg Phe Asp Thr Gln Lys
20 25 30

Leu Gln Asn Pro Glu Ile Ser Gly Glu Glu Tyr Gln Gln Gly Thr Leu
35 40 45

Tyr Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Lys
50 55 60

Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu Gln Val Glu His Ile
65 70 75 80

Val Pro Arg Ser Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu
85 90 95

Ala Cys Val Ser Cys Asn Gln Ala Lys Gly Asn Gln Asp Ile Arg Glu
100 105 110

Phe Leu Lys His Lys Pro Glu Leu Leu Ser Arg Ile Leu Gln Gln Thr
115 120 125

Lys Gln Pro Leu Val Val Ala Ala Val Val Asn Thr Ala Arg Trp Val
130 135 140

Leu Phe Asn Arg Leu Lys Glu Thr Gly Leu Pro Val Glu Thr Gly Thr
145 150 155 160

Gly Gly Gln Thr Lys Phe Asn Arg Ser Arg Gln Gln Leu Pro Lys Ala
165 170 175

His Trp Ile Asp Ala Ala Cys Val Gly Ala Ser Thr Pro Asn Leu Val
180 185 190

Phe Val Thr Lys Gln Pro Leu Gln Ile Lys Ala Lys Gly His Gly Thr

195

200

205

Arg Gln Met Cys Ile Thr Asp Lys Tyr Gly Phe Pro Lys Gln His Arg
 210 215 220

Thr His Val Gln Ile His Lys Gly Phe Arg Thr Gly Asp Ile Val Arg
 225 230 235 240

Ala Val Val Thr Arg Gly Lys Lys Val Gly Lys Tyr Ile Gly Arg Val
 245 250 255

Val Cys Arg Ala Ser Gly Ser Phe Asp Ile Thr Thr Lys Gln Gly Arg
 260 265 270

Ile Thr Gly Ile Ser Tyr Lys Tyr Cys Lys Thr Val His Lys Lys Asp
 275 280 285

Gly Tyr Glu Tyr Ala Phe
 290

<210> 166

<211> 110

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-142 effector

<400> 166

Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Ile Ile Lys Ala
 1 5 10 15

Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys Tyr Gly Phe
 20 25 30

Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys
 35 40 45

Thr Gly Asp Met Ile Lys Val Val Ile Pro Val Gly Thr Lys Thr Lys
50 55 60

Val Ser Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Ser Gly
65 70 75 80

Phe Phe Tyr Val Lys Ala Gly Val Ala Lys Leu Asn Val Ser His Lys
85 90 95

Tyr Cys Gln Gln Ile Tyr Leu Met Asp Gly Tyr Ser Tyr Glu
100 105 110

<210> 167

<211> 413

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-143 effector

<400> 167

Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile Leu
1 5 10 15

His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu Ile Lys
20 25 30

Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val His Gly
35 40 45

Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His Arg Thr
50 55 60

Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg Ser Arg
65 70 75 80

Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn Arg Thr

85

90

95

Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala Glu Asn
 100 105 110

Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe Thr Lys
 115 120 125

Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu Asn Pro
 130 135 140

Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr Ala
 145 150 155 160

Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys Ile Tyr
 165 170 175

Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His Val Ile
 180 185 190

Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu Ser
 195 200 205

Cys His Glu Cys Asn Gln Ala Lys Ser Ser Gln Asp Val Gln Thr Tyr
 210 215 220

Leu Lys Gly Arg Pro Ser Val Leu Gln Arg Val Lys Ala Arg Leu Asn
 225 230 235 240

Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu Tyr Met
 245 250 255

Ile Asp Lys Leu Ser Ala Ile Ala Thr Thr Ile Gly Ala Thr Leu Lys
 260 265 270

Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Ser Leu Gly Leu
 275 280 285

Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp Gly Ser
 290 295 300

Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Ile Ile Lys Ala Val
305 310 315 320

Gly Arg Gly Ser Arg Gln Phe Cys Arg Val Asp Lys Tyr Gly Phe Pro
325 330 335

Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys Thr
340 345 350

Gly Asp Met Val Lys Val Val Ile Pro Asp Asn Ala Lys Thr Lys Val
355 360 365

Pro Ala Gly Thr Tyr Ile Gly Arg Val Ala Val Arg Ser Ser Gly Ser
370 375 380

Phe Asp Val Lys Thr Gly Asp Ala Lys Ile Thr Val Ser His Lys Tyr
385 390 395 400

Cys Gln Pro Ile Tyr Leu Met Asp Gly Tyr Asn Tyr Val
405 410

<210> 168
<211> 43
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-144 effector

<400> 168
Ser Thr Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Pro Thr
1 5 10 15

Thr Arg Cys Gly His Val Arg His Leu Leu Glu Glu Gln Lys Ala Arg
20 25 30

Val Val Arg Asn Glu Pro Phe Thr Ile Glu Asp

<210> 169
 <211> 114
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-146 effector

<400> 169
 Thr Lys Asp Gly Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu
 1 5 10 15

Val Ile Lys Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn
 20 25 30

Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe
 35 40 45

Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly
 50 55 60

Ser Lys Thr Lys Val Leu Val Gly Thr His Thr Gly Arg Val Ala Val
 65 70 75 80

Arg Ser Ser Gly Ile Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Thr
 85 90 95

Val Ser His Lys Tyr Cys Gln Pro Ile His Leu Met Asp Gly Tyr Ser
 100 105 110

Tyr Ala

<210> 170
 <211> 317
 <212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-147 effector

<400> 170

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Gly Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu

165

170

175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
 180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
 195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
 210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
 245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
 260 265 270

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
 290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg
 305 310 315

<210> 171

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-148 effector

<400> 171

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Lys
100 105 110

Ser Arg Arg Ser Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His

210

215

220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
 245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
 260 265 270

Leu Ser Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
 290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu
 305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
 325 330 335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
 340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
 355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
 370 375 380

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
 385 390 395 400

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser
 405 410 415

Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His
 420 425 430

Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 172
<211> 361
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-149 effector

<400> 172
Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala

130

135

140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu
 145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Val
 165 170 175

Asn Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg Met Phe Gly
 180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys
 195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
 210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys His Glu Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
 245 250 255

Glu Tyr Leu Lys Asp Lys Pro Ser Val Leu Lys Arg Val Lys Ala His
 260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Tyr Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys
 290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys Glu Asn Arg Leu Leu Leu
 305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
 325 330 335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
 340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe
355 360

<210> 173

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-150 effector

<400> 173

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Pro Leu Val Ser Lys Ala

130

135

140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Ala Pro Phe
 145 150 155 160

Thr Lys Phe Ala Leu Asp Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
 165 170 175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
 180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
 195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
 210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
 245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
 260 265 270

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
 290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu
 305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
 325 330 335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
 340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
385 390 395 400

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser
405 410 415

Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His
420 425 430

Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 174
<211> 447
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-151 effector

<400> 174
Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu

50

55

60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu Thr Pro Leu
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Ala
165 170 175

Asn Pro Asn Ile Glu Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Gly Cys Cys
195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys Tyr Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
245 250 255

Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Glu His
260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Tyr Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile Gly Ala Lys
290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg Leu Leu Leu
305 310 315 320

Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp
325 330 335

Gly Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu Val Ile Lys
340 345 350

Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp Lys His Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Ala Lys Thr
385 390 395 400

Lys Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Lys
405 410 415

Gly Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His
420 425 430

Lys Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 175

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-152 effector

<400> 175

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Ala Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
260 265 270

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu
305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
325 330 335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
385 390 395 400

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser

405

410

415

Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His
 420 425 430

Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 435 440 445

<210> 176

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-153 effector

<400> 176

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
 1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
 20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
 35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
 50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
 65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
 85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
 100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
260 265 270

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu
305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp

325

330

335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
 340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
 355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
 370 375 380

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
 385 390 395 400

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser
 405 410 415

Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His
 420 425 430

Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 435 440 445

<210> 177

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-154 effector

<400> 177

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
 1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
 20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Asn Pro Glu Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asn Val Gln

245

250

255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
260 265 270

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu
305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
325 330 335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
385 390 395 400

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser
405 410 415

Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu Gly Ile Tyr His
420 425 430

Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 178

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-155 effector

<400> 178

Val Gly Phe Lys Gln Pro Asn Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Lys Lys Leu
20 25 30

Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Val
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Thr Thr Val Ala Leu Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu

165

170

175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
 180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
 195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
 210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser Gln Asp Val Gln
 245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
 260 265 270

Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Val Val Gly Thr Thr
 290 295 300

Leu Lys Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Ser Leu Leu Leu
 305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Ser Asp
 325 330 335

Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro Leu Thr Ile Lys
 340 345 350

Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly
 355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
 370 375 380

Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu Gly Ser Lys Thr
385 390 395 400

Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala Val Arg Ser Ser
405 410 415

Gly Ser Phe Asp Val Lys Thr Arg Asp Thr Lys Leu Thr Val Ser His
420 425 430

Lys Tyr Cys Lys Gln Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 179

<211> 314

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-156 effector

<400> 179

Val Gly Phe Lys Gln Pro Gln Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Arg Lys Leu
20 25 30

Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Asp Thr Val Ala Phe Ala Ala His Val Glu His

85

90

95

Arg Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ile Ile Arg Arg
 100 105 110

Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
 115 120 125

Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Met Ser Lys Ala
 130 135 140

Glu Asn Ile Leu Asn Trp Val Thr Arg Phe Ala Lys Leu Thr Ser Ile
 145 150 155 160

Thr Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
 165 170 175

Ser Pro Asp Ile Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
 180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys
 195 200 205

Ile Tyr Cys Gly Thr His Ala Ser Lys Ala Lys Met Glu Ile Glu His
 210 215 220

Val Val Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
 245 250 255

Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ser His
 260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Tyr Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly Ala Lys
 290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys
305 310

<210> 180
<211> 425
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-157 effector

<400> 180
Val Gly Phe Lys Gln Pro Gln Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Arg Lys Leu
20 25 30

Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Asp Thr Val Ala Phe Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ile Ile Arg Arg
100 105 110

Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Met Ser Lys Ala

130

135

140

Glu Asn Ile Leu Asn Trp Val Thr Arg Phe Ala Lys Leu Thr Ser Ile
 145 150 155 160

Thr Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
 165 170 175

Ser Pro Asp Ile Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
 180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys
 195 200 205

Ile Tyr Cys Gly Thr His Ala Ser Lys Ala Lys Met Glu Ile Glu His
 210 215 220

Val Val Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
 225 230 235 240

Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
 245 250 255

Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ser His
 260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
 275 280 285

Tyr Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly Ala Lys
 290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys Glu Asn Arg Leu Leu Leu
 305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp
 325 330 335

Gly Ala Ser Ala Arg Val Val Pro Ser Leu Lys Pro Leu Val Ile Lys
 340 345 350

Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Val Asp Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Thr Lys Thr
385 390 395 400

Lys Val Leu Val Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Ser
405 410 415

Gly Tyr Phe Asp Val Lys Thr Lys Asp
420 425

<210> 181
<211> 447
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-158 effector

<400> 181
Val Gly Phe Lys Gln Pro Gln Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Arg Lys Leu
20 25 30

Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val

65					70					75					80
His	Gly	Gln	Asp	Gly	Asp	Thr	Val	Ala	Phe	Ala	Ala	His	Val	Glu	His
				85					90					95	
Arg	Thr	Asn	Val	Lys	Ser	Gly	Leu	Asp	Ser	Arg	Arg	Ile	Ile	Arg	Arg
			100					105					110		
Ser	Arg	Arg	Asn	Arg	Lys	Thr	Arg	Tyr	Arg	Gln	Ala	Arg	Phe	Leu	Asn
			115				120					125			
Arg	Thr	Lys	Pro	Lys	Gly	Trp	Leu	Pro	Pro	Ser	Leu	Met	Ser	Lys	Ala
			130			135					140				
Glu	Asn	Ile	Leu	Asn	Trp	Val	Thr	Arg	Phe	Ala	Lys	Leu	Thr	Ser	Ile
145					150					155					160
Thr	Lys	Phe	Ala	Ile	Glu	Thr	Ala	Lys	Phe	Asp	Met	Gln	Lys	Leu	Glu
				165					170					175	
Ser	Pro	Asp	Ile	Gln	Gly	Val	Gly	Tyr	Gln	Gln	Gly	Arg	Met	Phe	Gly
			180					185					190		
Tyr	Ala	Asp	Lys	Lys	Ala	Tyr	Leu	Leu	Glu	Arg	Glu	Gln	Arg	Cys	Cys
		195					200					205			
Ile	Tyr	Cys	Gly	Thr	His	Ala	Ser	Lys	Ala	Lys	Met	Glu	Ile	Glu	His
		210				215					220				
Val	Val	Pro	Arg	Ser	Arg	Gly	Gly	Thr	Asp	Ser	Leu	Asn	Asn	Leu	Val
225					230					235				240	
Leu	Ser	Cys	His	Ala	Cys	Asn	Gln	Ala	Lys	Gly	Asn	Leu	Ser	Leu	Ser
				245					250					255	
Glu	Tyr	Leu	Lys	Gly	Lys	Pro	Ser	Val	Leu	Lys	Arg	Val	Lys	Ser	His
			260					265					270		
Leu	Gly	Ile	Asn	Tyr	Arg	Asp	Ala	Ala	His	Thr	Asn	Ser	Ile	Arg	Leu
		275					280					285			

Tyr Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly Ala Lys
290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys Glu Asn Arg Leu Leu Leu
305 310 315 320

Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp
325 330 335

Gly Ala Ser Ala Arg Val Val Pro Ser Leu Lys Pro Leu Val Ile Lys
340 345 350

Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Val Asp Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly Thr Lys Thr
385 390 395 400

Lys Val Leu Val Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Ser
405 410 415

Gly Tyr Phe Asp Val Lys Thr Lys Asp Ala Lys Leu Asn Val Ser His
420 425 430

Lys His Cys Gln Gln Ile Tyr Leu Met Asp Gly Tyr Ser Tyr Ala
435 440 445

<210> 182

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-159 effector

<400> 182

Val Gly Phe Lys Gln Pro Gln Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Arg Lys Leu
20 25 30

Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Asp Thr Val Ala Phe Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ile Ile Arg Arg
100 105 110

Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Met Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Thr Arg Phe Ala Lys Leu Thr Ser Ile
145 150 155 160

Thr Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Ser Pro Asp Ile Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys
195 200 205

Ile Tyr Cys Gly Thr His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Val Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
245 250 255

Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ser His
260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Tyr Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly Ala Lys
290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys Lys Asn Arg Leu Ser Leu
305 310 315 320

Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp
325 330 335

Gly Ala Ser Ala Arg Val Val Pro Ser Leu Lys Pro Leu Val Ile Lys
340 345 350

Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Ser Val Asp Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Thr Ile Pro Asp Asn Ala Lys Thr
385 390 395 400

Lys Val Leu Thr Gly Thr Tyr Thr Gly Arg Val Ala Val Arg Ser Ser
405 410 415

Gly Tyr Phe Asp Val Lys Thr Lys Asp Thr Lys Leu Thr Val Ser His

420

425

430

Lys Tyr Cys Lys Pro Ile His Leu Met Asp Gly Tyr Ser Tyr Ala
 435 440 445

<210> 183

<211> 314

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-160 effector

<400> 183

Val Gly Phe Lys Gln Pro Gln Phe Asn Lys Val Leu Val Leu Asp Thr
 1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Arg Lys Leu
 20 25 30

Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
 35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
 50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
 65 70 75 80

His Gly Gln Asp Gly Asp Thr Val Ala Phe Ala Ala His Val Glu His
 85 90 95

Arg Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ile Ile Arg Arg
 100 105 110

Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
 115 120 125

Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Met Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Thr Arg Phe Ala Lys Leu Thr Ser Ile
145 150 155 160

Thr Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Ser Pro Asp Ile Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys
195 200 205

Ile Tyr Cys Gly Thr His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Val Pro Arg Ser Arg Gly Gly Thr Asn Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
245 250 255

Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ser His
260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Tyr Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly Ala Lys
290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys
305 310

<210> 184

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-161 effector

<400> 184

Val Gly Phe Lys Gln Pro Gln Phe Asn Lys Val Leu Val Leu Asp Thr
1 5 10 15

Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala Arg Lys Leu
20 25 30

Leu Ser Gly Gly Arg Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile
35 40 45

Ile Leu His Asp Arg Thr Val Glu Glu Ser Glu Leu Gln Asp Thr Glu
50 55 60

Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala Leu Leu Val
65 70 75 80

His Gly Gln Asp Gly Asp Thr Val Ala Phe Ala Ala His Val Glu His
85 90 95

Arg Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ile Ile Arg Arg
100 105 110

Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Met Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Thr Arg Phe Ala Lys Leu Thr Ser Ile
145 150 155 160

Thr Lys Phe Ala Ile Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Ser Pro Asp Ile Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln Arg Cys Cys
195 200 205

Ile Tyr Cys Gly Thr His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Val Pro Arg Ser Arg Gly Gly Thr Asn Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu Ser Leu Ser
245 250 255

Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val Lys Ser His
260 265 270

Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Tyr Val Met Asn Lys Leu Arg Val Met Ala Glu Ala Ile Gly Ala Lys
290 295 300

Leu Val Val Gly Phe Gly Ser Thr Thr Lys Lys Asn Arg Leu Ser Leu
305 310 315 320

Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys Thr Lys Asp
325 330 335

Gly Ala Ser Ala Arg Val Val Pro Ser Leu Lys Pro Leu Val Ile Lys
340 345 350

Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Val Asp Lys Tyr Gly
355 360 365

Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe
370 375 380

Lys Thr Gly Asp Met Val Lys Val Thr Ile Pro Asp Asn Ala Lys Thr

385					390					395					400
Lys	Val	Leu	Thr	Gly	Thr	Tyr	Thr	Gly	Arg	Val	Ala	Val	Arg	Ser	Ser
				405					410					415	
Gly	Tyr	Phe	Asp	Val	Lys	Thr	Lys	Asp	Thr	Lys	Leu	Thr	Val	Ser	His
			420					425					430		
Lys	Tyr	Cys	Lys	Pro	Ile	His	Leu	Met	Asp	Gly	Tyr	Ser	Tyr	Ala	
		435					440					445			
<210> 185															
<211> 351															
<212> PRT															
<213> Unknown															
<220>															
<223> Description of Unknown: uncultivated organism															
<220>															
<223> Category: MG35 effectors															
<220>															
<223> Description: MG35-162 effector															
<400> 185															
Val	Gly	Phe	Lys	Gln	Pro	Gln	Phe	Asn	Lys	Val	Leu	Val	Leu	Asp	Thr
1				5					10					15	
Asn	Arg	Lys	Pro	Leu	Met	Pro	Cys	Tyr	Pro	Ala	Arg	Ala	Arg	Lys	Leu
			20					25					30		
Leu	Ser	Gly	Gly	Arg	Ala	Ser	Val	Phe	Arg	Arg	Phe	Pro	Phe	Thr	Ile
		35					40					45			
Ile	Leu	His	Asp	Arg	Thr	Val	Glu	Glu	Ser	Glu	Leu	Gln	Asp	Thr	Glu
	50					55					60				
Ile	Lys	Ile	Asp	Gln	Gly	Ser	Lys	Thr	Thr	Gly	Val	Ala	Leu	Leu	Val
65					70					75					80
His	Gly	Gln	Asp	Gly	Thr	Thr	Val	Ala	Leu	Ala	Ala	His	Val	Glu	His
				85					90					95	

Arg Thr Asn Ile Lys Ser Asn Leu Asp Ser Arg Arg Ala Ile Arg Arg
100 105 110

Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
115 120 125

Arg Thr Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Val Ser Lys Ala
130 135 140

Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Thr Lys Leu Thr Pro Phe
145 150 155 160

Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln Lys Leu Glu
165 170 175

Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly Arg Met Phe Gly
180 185 190

Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Asn Tyr Thr Cys
195 200 205

Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu Ile Glu His
210 215 220

Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn Asn Leu Val
225 230 235 240

Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Asn Gln Asp Val Gln
245 250 255

Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg Val Lys Ala Arg
260 265 270

Leu Ser Thr Asn Tyr Arg Asp Ala Ala His Thr Asn Ser Ile Arg Leu
275 280 285

Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala Ile Gly Thr Asn
290 295 300

Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu

305		310		315		320									
Asn	Leu	Pro	Lys	Asp	His	Trp	Ile	Asp	Ala	Ala	Val	Cys	Thr	Lys	Asp
				325					330					335	
Gly	Ala	Ser	Val	Arg	Val	Glu	Pro	Ala	Leu	Lys	Pro	Leu	Val	Ile	
			340					345					350		

<210> 186
 <211> 265
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-163 effector

<400> 186
 Val Gly Tyr Gln Gln Gly Arg Met Phe Gly Tyr Ala Asp Lys Asn Ala
 1 5 10 15

Tyr Leu Leu Glu Arg Lys Asn Tyr Thr Cys Ile Tyr Cys Gly Ile His
 20 25 30

Ala Ser Lys Ala Lys Met Glu Ile Glu His Val Ile Pro Arg Ser Arg
 35 40 45

Gly Gly Thr Asp Ser Leu Asn Asn Leu Val Leu Ser Cys Arg Ala Cys
 50 55 60

Asn Glu Ala Lys Gly Ser Gln Asp Val Gln Thr Tyr Leu Lys Gly Asn
 65 70 75 80

Pro Ser Val Leu Arg Arg Val Lys Ala Arg Leu Asn Thr Asn Tyr Arg
 85 90 95

Asp Ala Ala His Thr Asn Ser Ile Arg Leu Phe Val Leu Asn Lys Leu
 100 105 110

Gln Thr Met Ala Asp Ala Ile Gly Thr Asn Leu Asn Val Gly Phe Gly
115 120 125

Tyr Thr Thr Lys Gln Asn Arg Leu Leu Leu Asn Leu Pro Lys Asp His
130 135 140

Trp Ile Asp Ala Ala Val Cys Thr Ser Asp Gly Ser Ala Val Lys Val
145 150 155 160

Asp Pro Ser Leu Lys Pro Phe Thr Ile Lys Ala Ile Gly Arg Gly Ser
165 170 175

Arg Gln Phe Cys Arg Met Asn Lys Tyr Gly Phe Pro Arg Thr Ser Pro
180 185 190

Lys Pro Arg Ser Lys Asn Phe Phe Gly Phe Lys Thr Gly Asp Met Val
195 200 205

Lys Val Val Val Pro Leu Gly Ser Lys Thr Lys Val Pro Val Gly Thr
210 215 220

His Thr Gly Arg Val Ala Val Arg Ser Ser Gly Ser Phe Asp Val Lys
225 230 235 240

Thr Arg Asp Ala Lys Leu Gly Ile Tyr His Lys Tyr Cys Gln Gln Ile
245 250 255

His Leu Met Asp Gly Tyr Ser Tyr Ala
260 265

<210> 187

<211> 56

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-164 effector

<400> 187

Val Ile Val Pro Thr Gly Ala Lys Thr Lys Val Ala Thr Gly Thr Tyr
1 5 10 15

Thr Gly Arg Val Ala Val Arg Ser Lys Gly Ser Phe Asp Val Lys Thr
20 25 30

Arg Asp Thr Lys Leu Thr Val Ser His Lys Tyr Cys Lys Gln Ile His
35 40 45

Leu Met Asp Gly Tyr Ser Tyr Ala
50 55

<210> 188

<211> 233

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-165 effector

<400> 188

Val Leu Asp Ile Thr Ser His Ala Asn Leu Val Glu Val Thr Ile Thr
1 5 10 15

Arg Ala Ile Gly Glu Glu Ile Thr Met Ser Asn Ala Val Phe Val Leu
20 25 30

Asp His Ala Gln Arg Pro Leu Arg Pro Val His Pro Ala Val Ala Arg
35 40 45

Arg Met Leu Asn Ala Lys Gln Ala Ala Val Phe Arg Arg Tyr Pro Phe
50 55 60

Thr Ile Ile Cys His Ala Gly Val Ser Thr Gly Ala Pro Leu Pro Leu
65 70 75 80

Arg Leu Lys Ile Asp Pro Gly Ser Lys Thr Thr Gly Leu Ala Leu Leu
85 90 95

Asp Gly Phe Arg Leu Leu Trp Ala Ala Glu Leu Gln His Arg Gly Gln
100 105 110

Arg Leu Lys Ala Ala Leu Asp Ala Arg Arg Ala Val Arg Arg Ser Arg
115 120 125

Arg Gln Arg Asn Thr Arg Tyr Arg Gln Pro Arg Phe Ala Asn Arg Thr
130 135 140

Arg Pro Ala Gly Trp Leu Pro Pro Ser Leu Trp Ser Arg Val Cys Asn
145 150 155 160

Val Met Thr Trp Val Glu Arg Leu Thr Arg Tyr Cys His Ile Thr Ala
165 170 175

Leu Ser Gln Glu Leu Val Arg Phe Asp Met Gln Leu Met Gln Asp Ala
180 185 190

Val Val Ser Gly Ile Ala Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu
195 200 205

Val Arg Glu Tyr Leu Leu Glu Lys Trp His Arg Thr Cys Ala Tyr Cys
210 215 220

Gly Ala Lys Asn Val Pro Ile Gln Val
225 230

<210> 189

<211> 418

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-166 effector

<400> 189

Val Leu Gly Thr Thr Ser His Ala Asn Leu Val Glu Val Thr Ile Thr
1 5 10 15

Arg Ala Ile Gly Glu Glu Ile Thr Met Ser Asn Ala Val Phe Val Leu
20 25 30

Asp His Ala Gln Arg Pro Leu Arg Pro Val His Pro Ala Val Ala Arg
35 40 45

Arg Met Leu His Ala Lys Gln Ala Ala Val Phe Arg His Tyr Pro Phe
50 55 60

Thr Ile Ile Cys His Ala Gly Met Ser Thr Gly Ala Pro Leu Pro Leu
65 70 75 80

Arg Leu Lys Ile Asp Pro Gly Ser Lys Thr Thr Gly Leu Ala Leu Leu
85 90 95

Asp Gly Phe Arg Leu Leu Trp Ala Ala Glu Leu Gln His Arg Gly Gln
100 105 110

Arg Leu Lys Ala Ala Leu Asp Ala Arg Arg Ala Val Arg Arg Ser Arg
115 120 125

Arg Gln Arg His Thr Arg Tyr Arg Gln Pro Arg Phe Asp Asn Arg Thr
130 135 140

Arg Pro Ala Gly Trp Leu Pro Pro Ser Leu Trp Ser Arg Val Cys Asn
145 150 155 160

Val Met Thr Trp Val Glu Arg Leu Thr Arg Ser Cys His Ile Thr Ala
165 170 175

Leu Ser Gln Glu Leu Val Arg Phe Asp Met Gln Arg Met Gln Asp Ala
180 185 190

Val Val Ser Gly Ile Ala Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu
195 200 205

Val Arg Glu Tyr Leu Leu Glu Lys Trp His Arg Thr Cys Ala Tyr Cys
210 215 220

Gly Ala Lys Asn Val Pro Ile Gln Val Glu His Ile Ile Pro Thr Ala
225 230 235 240

Arg Gly Gly Ser Asp Arg Val Ser Asn Leu Thr Leu Ala Cys Ala Pro
245 250 255

Cys Asn Gln Lys Lys Gly Ala Gln Thr Ala Ala Glu Phe Gly Phe Pro
260 265 270

Gln Val Gln Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val
275 280 285

Asn Ala Thr Arg Trp Ala Leu Tyr Ala Gln Leu Cys Ala Thr Gly Leu
290 295 300

Pro Val Glu Cys Gly Thr Gly Gly Arg Thr Lys Tyr Asn Arg Thr Arg
305 310 315 320

Leu Gly Ile Pro Lys Ser His Trp Gly Asp Ala Ala Cys Val Gly Ala
325 330 335

Ser Thr Pro Glu Ala Leu Asp Val Pro Arg Gly Ala Ala Ala Gly His
340 345 350

Pro Arg Pro Arg Ala Arg Met Pro Pro Glu Val Ser His Arg Cys Pro
355 360 365

Arg Leu Ser His Thr Thr Ser Gly Ser Gln Glu Ala Ala Phe Trp Leu
370 375 380

Ser Asp Gly Arg Tyr Cys Ala Arg Tyr Gly Ala Ser Trp Gln Ile Cys
385 390 395 400

Trp His Ala Arg Gly Ala Cys His Arg Ala Arg Ser Trp Val Val Gln
405 410 415

Pro Gln

<210> 190
<211> 197
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-167 effector

<400> 190
Val Leu Asn Gln Ile Ile Pro His Leu Met Glu Tyr Leu Gly Asn Glu
1 5 10 15

Thr Leu Tyr Asp Val Tyr Ala Thr Asp Gly Cys Ser Thr Lys Gly Phe
20 25 30

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys
35 40 45

Ile Ala Cys Ser Ile Leu Asp Thr Asp Ile Glu Val Ser Ala Pro Thr
50 55 60

Arg Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys
65 70 75 80

Ile Arg Gln Met Val Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val Val
85 90 95

Ala Thr Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asp Ser Leu Glu
100 105 110

Glu Phe Arg Glu Ala His Gly Asn Ala Ala Val Ser Gln Leu Thr Val
115 120 125

Lys Pro His His Pro Gln Cys Lys Asp Met Ala Arg Ile Met Pro Gly
130 135 140

Ala Val Met Val Phe Asp Gly Ala Val Gly Val Phe Gln Gly Ser Ser
145 150 155 160

Gly Gln Asn Asn Gly Thr Pro Asn Tyr Tyr Asn Ser Thr Lys Gly Glu
165 170 175

Arg Phe Leu Met Arg Ser Cys Val Leu Leu Ala Gln Asn Ala Gly Met
180 185 190

Val Phe Ile Pro Ala
195

<210> 191
<211> 271
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-168 effector

<400> 191
Val Met Glu Leu Val Arg Phe Asp Leu Gln Gln Leu Glu Lys Pro Glu
1 5 10 15

Ile Ser Glu Ile Glu Tyr Gln Gln Gly Glu Leu Leu Gly Tyr Glu Ile
20 25 30

Arg Glu Tyr Leu Leu Asn Lys Trp Asp Arg Lys Cys Thr Tyr Cys Lys
35 40 45

Val Glu Asn Ile Pro Leu Gln Val Glu His Ile His Pro Arg Ala Lys
50 55 60

Gly Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ala Cys Glu Lys Cys
65 70 75 80

Asn Leu Lys Lys Gly Thr Gln Asp Ile Asn Asp Phe Leu Ile Arg Lys

85

90

95

Pro Asp Leu Leu Lys Gln Ile Met Ala Gln Val Lys Arg Pro Leu Lys
 100 105 110

Asp Ala Thr Ala Val Asn Ser Thr Arg Trp Ala Leu Phe Asn Gln Leu
 115 120 125

Lys Leu Thr Arg Leu Ser Val Thr Thr Gly Ser Gly Gly Gln Thr Lys
 130 135 140

Tyr Asn Arg Thr Arg Leu Glu Leu Pro Lys Thr His Tyr Phe Asp Ala
 145 150 155 160

Ala Cys Val Gly Lys Val Asn Lys Leu Val Val Leu Thr Thr Gln Pro
 165 170 175

Leu Phe Ile Lys Ala Asn Gly Gln Gly Thr Arg Gln Ile Cys Arg Thr
 180 185 190

Asp Arg Phe Gly Phe Pro Ser Arg His Val Pro Arg Asn Lys Ser Val
 195 200 205

Lys Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Ser Gly
 210 215 220

Lys Lys Ile Gly Glu Tyr Val Gly Arg Val Ala Val Arg Ser Ser Gly
 225 230 235 240

Ser Phe Asn Ile Ser Ala Lys Glu Leu Val Gln Gly Ile Ser His Lys
 245 250 255

Tyr Cys Gln Thr Leu Gln Arg Lys Asp Gly Tyr Ser Tyr Gln Phe
 260 265 270

<210> 192

<211> 339

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-169 effector

<400> 192

Val Gln Pro Val Glu Phe Lys Val Asp Pro Gly Ser Lys Val Thr Gly
1 5 10 15

Leu Ala Leu Val Ala Glu Phe Glu Lys Arg Gly Arg Thr Val Val Trp
20 25 30

Ala Ala Asn Leu Ala His Arg Gly Tyr Arg Val Lys Ala Ser Ile Thr
35 40 45

Asp Arg Ala Met Phe Arg Arg Gly Arg Arg Gly Arg Lys Thr Arg Tyr
50 55 60

Arg Ala Ala Arg Phe Glu Asn Arg Thr Arg Pro Thr His Trp Leu Ala
65 70 75 80

Pro Ser Leu Gln Ser Arg Val Leu Asn Val Lys Ser Trp Tyr Ser Arg
85 90 95

Leu Leu Ser Arg Ala Pro Ile Ser Val Ala Gln Val Glu Thr Ser Ser
100 105 110

Phe Asp Thr Gln Leu Met Glu Asn Ala Asp Ile Ser Gly Val Glu Tyr
115 120 125

Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Gln Tyr Val Leu Glu
130 135 140

Arg Gly Gly His Thr Cys Ser Tyr Cys Asp Ala Lys Asp Val Ala Leu
145 150 155 160

His Leu Asp His Val Leu Pro Arg Ser Arg Gly Gly Ser Asn Arg Val
165 170 175

Ser Asn Leu Val Pro Ala Cys Lys Pro Cys Asn Asp Ala Lys Ser Asn

180

185

190

Arg Ala Val Glu Asp Tyr Leu Val Asp Arg Pro Glu Val Leu Arg Gln
 195 200 205

Val Lys Ala Gln Leu Arg Ser Pro Leu Lys Asp Ala Ala Val Met Asn
 210 215 220

Ala Thr Arg Phe Ala Ile Val Asp Ala Leu Arg Glu Phe Gly Leu Glu
 225 230 235 240

Val Arg Met Trp Ser Gly Gly Arg Thr Lys Trp Asn Arg Thr Asn Leu
 245 250 255

Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Cys Val Gly Glu Ser
 260 265 270

Gly Ala Ala Val Arg Val Pro Val Leu Arg Pro Leu Thr Ile Thr Ala
 275 280 285

Met Gly Arg Gly His Arg Arg Val His Gly Asn Asp Arg Tyr Gly Phe
 290 295 300

Pro Arg Gly Thr Ala Arg Arg Ala Lys Arg Val Ala Gly Phe Gln Thr
 305 310 315 320

Gly Asp Leu Val Arg Leu Val Cys Leu Arg Gly Lys Cys Ala Gly Val
 325 330 335

His Thr Gly

<210> 193

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-170 effector

<400> 193

Val Arg Lys Tyr Met Val Lys Gln Pro Asn Phe Asn Lys Val Leu Val
1 5 10 15

Leu Asp Thr Asn Arg Lys Pro Leu Met Pro Cys Tyr Pro Ala Arg Ala
20 25 30

Lys Lys Leu Leu Asn Ser Gly Arg Ala Ser Val Phe Arg Arg Phe Pro
35 40 45

Phe Thr Ile Ile Leu His Asp Arg Thr Leu Glu Glu Ser Lys Leu Gln
50 55 60

Asp Met Glu Ile Lys Ile Asp Gln Gly Ser Lys Thr Thr Gly Val Ala
65 70 75 80

Leu Ile Val His Gly Lys Lys Ser Ser Thr Val Thr Leu Ala Ala His
85 90 95

Ile Glu His Arg Thr Asn Val Lys Ser Gly Leu Asp Ser Arg Arg Ala
100 105 110

Ile Arg Arg Ser Arg Arg His Arg Lys Thr Arg Tyr Arg Gln Ala Arg
115 120 125

Phe Leu Asn Arg Thr Lys Pro Lys Gly Trp Leu Pro Pro Ser Leu Val
130 135 140

Ser Lys Ala Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys Leu
145 150 155 160

Thr Pro Leu Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met Gln
165 170 175

Lys Leu Val Asn Pro Asn Ile Gln Gly Val Val Tyr Gln Gln Gly Arg
180 185 190

Met Phe Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu Gln

195

200

205

Arg Cys Ser Ile Asp Cys Gly Ile His Ala Ser Lys Ala Lys Met Glu
 210 215 220

Ile Glu His Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu Asn
 225 230 235 240

Asn Leu Val Leu Ser Cys His Ala Cys Asn Gln Ala Lys Gly Asn Leu
 245 250 255

Ser Leu Ser Glu Tyr Leu Lys Gly Lys Pro Ser Val Leu Lys Arg Val
 260 265 270

Lys Ala His Leu Gly Ile Asn Tyr Arg Asp Ala Ala His Thr Asn Ser
 275 280 285

Ile Arg Leu Tyr Val Met Asn Lys Leu Arg Ala Met Ala Glu Ala Ile
 290 295 300

Gly Ala Lys Leu Val Val Gly Phe Gly Ser Thr Thr Lys Gln Asn Arg
 305 310 315 320

Leu Leu Leu Gly Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val Cys
 325 330 335

Thr Lys Asp Gly Ala Ser Val Arg Val Glu Pro Ala Leu Lys Pro Leu
 340 345 350

Val Ile Lys Ala Val Gly Arg Gly Ser Arg Gln Phe Cys Arg Met Asp
 355 360 365

Lys His Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn Phe
 370 375 380

Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Ile Val Pro Thr Gly
 385 390 395 400

Ala Lys Thr Lys Val Pro Thr Gly Thr Tyr Thr Gly Arg Val Ala Val
 405 410 415

Arg Ser Lys Gly Ser Phe Asp Val Lys Thr Arg Asp
420 425

<210> 194

<211> 307

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-171 effector

<400> 194

Val Ser Lys Ala Glu Asn Ile Leu Asn Trp Val Ile Arg Phe Ala Lys
1 5 10 15

Leu Thr Pro Leu Thr Lys Phe Ala Leu Glu Thr Ala Lys Phe Asp Met
20 25 30

Gln Lys Leu Glu Asn Pro Asp Thr Gln Gly Val Gly Tyr Gln Gln Gly
35 40 45

Arg Met Phe Gly Tyr Ala Asp Lys Lys Ala Tyr Leu Leu Glu Arg Glu
50 55 60

Asn Tyr Thr Cys Ile Tyr Cys Gly Ile His Ala Ser Lys Ala Lys Met
65 70 75 80

Glu Ile Glu His Val Ile Pro Arg Ser Arg Gly Gly Thr Asp Ser Leu
85 90 95

Asn Asn Leu Val Leu Ser Cys Arg Ala Cys Asn Glu Ala Lys Gly Ser
100 105 110

Gln Asp Val Gln Thr Tyr Leu Lys Gly Asn Pro Ser Val Leu Arg Arg
115 120 125

Val Lys Ala Arg Leu Asn Thr Asn Tyr Arg Asp Ala Ala His Thr Asn

130

135

140

Ser Ile Arg Leu Phe Val Leu Asn Lys Leu Gln Thr Met Ala Asp Ala
 145 150 155 160

Ile Gly Thr Asn Leu Asn Val Gly Phe Gly Tyr Thr Thr Lys Gln Asn
 165 170 175

Arg Leu Leu Leu Asn Leu Pro Lys Asp His Trp Ile Asp Ala Ala Val
 180 185 190

Cys Thr Ser Asp Gly Ser Ala Val Lys Val Asp Pro Ser Leu Lys Pro
 195 200 205

Leu Thr Ile Lys Ala Ile Gly Arg Gly Ser Arg Gln Phe Cys Arg Met
 210 215 220

Asn Lys Tyr Gly Phe Pro Arg Thr Ser Pro Lys Pro Arg Ser Lys Asn
 225 230 235 240

Phe Phe Gly Phe Lys Thr Gly Asp Met Val Lys Val Val Val Pro Leu
 245 250 255

Gly Ser Lys Thr Lys Val Pro Val Gly Thr His Thr Gly Arg Val Ala
 260 265 270

Val Arg Ser Ser Gly Ser Phe Asp Val Lys Thr Arg Asp Ala Lys Leu
 275 280 285

Gly Ile Tyr His Lys Tyr Cys Gln Gln Ile His Leu Met Asp Gly Tyr
 290 295 300

Ser Tyr Ala
 305

<210> 195

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-172 effector

<400> 195

Val Val Arg Ala Arg Gly Ser Phe Asp Ile Gly Ile Gly Lys Lys Lys
1 5 10 15

Val Ser Gly Ile Ser Tyr Lys Tyr Cys Gln Leu Ile Gln Arg Val Asp
20 25 30

Gly Tyr Glu Tyr Thr
35

<210> 196

<211> 306

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-173 effector

<400> 196

Val Val Val Glu Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro
1 5 10 15

Asn Ile Arg Arg Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly
20 25 30

Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe
35 40 45

Cys Lys Lys Pro Ile Asp His Tyr His His Val Val Pro Arg His Lys
50 55 60

Gly Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Arg His

65					70					75					80
His	Ala	Leu	Val	His	Lys	Asp	Lys	Ala	Trp	Ala	Glu	Lys	Leu	Val	Thr
				85					90					95	
Arg	Lys	Gly	Gly	Met	Asn	Lys	Lys	Tyr	His	Ala	Leu	Ser	Val	Leu	Asn
			100					105					110		
Gln	Ile	Ile	Pro	Phe	Leu	Met	Glu	Tyr	Leu	Gly	Glu	Glu	Thr	Pro	Tyr
		115					120					125			
Asp	Val	Tyr	Ala	Thr	Asp	Gly	Arg	Ser	Thr	Lys	Gly	Phe	Arg	Val	Ala
	130					135					140				
Lys	Asn	Val	Pro	Lys	Glu	His	Tyr	Thr	Asp	Ala	Tyr	Cys	Val	Ala	Cys
145					150					155					160
Ser	Ile	Leu	Gly	Thr	Asp	Ile	Asp	Val	Ser	Ala	Pro	Val	Glu	Pro	Phe
				165					170					175	
Glu	Leu	Lys	Gln	Phe	Arg	Arg	His	Asp	Arg	Gln	Ala	Cys	Ile	Arg	Gln
			180					185					190		
Met	Val	Asp	Arg	Lys	Tyr	Leu	Leu	Asp	Gly	Lys	Val	Val	Ala	Ala	Asn
		195					200					205			
Arg	His	Lys	Ala	Ile	Glu	Gln	Lys	Ser	Asp	Ser	Leu	Glu	Glu	Phe	Arg
	210					215					220				
Glu	Ala	Tyr	Gly	Glu	Ala	Ala	Val	Ser	Gln	Leu	Thr	Val	Arg	Pro	His
225					230					235					240
Leu	Pro	Gln	Tyr	Lys	Asp	Met	Thr	Arg	Ile	Met	Pro	Gly	Ala	Val	Met
				245					250					255	
Asp	Phe	Asp	Gly	Thr	Ile	Gly	Val	Phe	Gln	Gly	Ser	Glu	Gly	Phe	His
			260					265					270		
Asn	Gly	Lys	Ser	Asn	Tyr	Tyr	Lys	Ser	Thr	Lys	Gly	Thr	Lys	Val	Leu
		275					280					285			

Thr Arg Arg Cys Ala Leu Leu Ala Lys Asn Val Gly Met Val Phe Ile
290 295 300

Pro Ala
305

<210> 197
<211> 269
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-174 effector

<400> 197
Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro Ile
1 5 10 15

Asp His Tyr His His Val Ile Pro Arg His Lys Arg Gly Ser Glu Thr
20 25 30

Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Ala Leu Val His
35 40 45

Lys Asp Lys Ala Trp Glu Glu Lys Met Val Thr Arg Lys Gly Gly Met
50 55 60

Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro His
65 70 75 80

Leu Met Glu His Leu Gly Ser Glu Thr Pro Tyr Asp Val Tyr Ala Thr
85 90 95

Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro Lys
100 105 110

Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp Thr

115

120

125

Asp Ile Glu Val Ser Ala Pro Val Glu Pro Phe Glu Leu Lys Gln Phe
 130 135 140

Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg Lys
 145 150 155 160

Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ala Ile
 165 170 175

Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala His Gly Asn
 180 185 190

Ala Ala Val Ser Gln Leu Thr Val Lys Pro His His Pro Gln Cys Lys
 195 200 205

Asp Met Ala Arg Ile Met Pro Gly Ala Val Met Val Phe Asp Gly Ala
 210 215 220

Val Gly Val Phe Gln Gly Ser Ser Gly Arg Asn Asn Gly Thr Pro Asn
 225 230 235 240

Tyr Tyr Asn Ser Thr Lys Gly Glu Arg Phe Leu Met Arg Ser Cys Val
 245 250 255

Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 260 265

<210> 198

<211> 470

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-175 effector

<400> 198

Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala Arg Val Val
1 5 10 15

Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr Pro Asp Val
20 25 30

Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr Asn Ile Gly
35 40 45

Val Ala Val Val Lys Glu Asp Gly Ser Cys Val Phe Ser Ala His Leu
50 55 60

Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys Arg Ala Ala
65 70 75 80

Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys Arg Gln Arg
85 90 95

Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr Ile Glu Arg
100 105 110

Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr Ile Arg Asn
115 120 125

Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly Trp Leu Thr
130 135 140

Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu Ile Ala Lys
145 150 155 160

Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Ile Glu Leu Asn Arg
165 170 175

Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg Trp Glu Tyr
180 185 190

Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp Ala Val Tyr
195 200 205

Ala Gln Gln Asp Gly His Cys Leu Phe Cys Glu Lys Pro Met Asp His

210

215

220

Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu Thr Leu Ala
 225 230 235 240

Asn Arg Cys Gly Leu Cys Ala Arg His His Asp Leu Val His Thr Asp
 245 250 255

Lys Ser Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly Met Asn Lys
 260 265 270

Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro His Leu Ile
 275 280 285

Glu His Leu Gly Ser Glu Thr Pro Tyr Glu Ala Tyr Ala Thr Asp Gly
 290 295 300

Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro Lys Glu His
 305 310 315 320

Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp Thr Asp Ile
 325 330 335

Glu Val Ser Ala Pro Thr Ser Pro Phe Glu Leu Lys Gln Phe Arg Arg
 340 345 350

His Asp Arg Gln Ala Cys Ile Arg Gln Met Val Asp Arg Lys Tyr Leu
 355 360 365

Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ala Ile Glu Gln
 370 375 380

Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ala Tyr Gly Gly Ala Ala
 385 390 395 400

Val Ser Gln Leu Thr Val Lys Pro His Pro Pro Gln Tyr Lys Asp Met
 405 410 415

Thr Arg Ile Met Pro Gly Ala Val Met Asp Phe Asn Gly Thr Ile Gly
 420 425 430

Val Met Gln Ser Ser Ile Val Gly Arg Phe Tyr Lys Ser Thr Lys Gly
435 440 445

Tyr Lys Ala Ala Pro Arg Arg Cys Val Leu Leu Ala Gln Asn Ala Gly
450 455 460

Met Val Phe Leu Pro Ala
465 470

<210> 199
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> Category: MG33 active effectors tracrRNA sequence

<220>
<223> Description: MG33-1 tracrRNA sequence

<400> 199
cuuucagaau acucucuuuu uugguagcgg augaaacucc agggcacuuu gaugugcccg 60
ugauccuucg gaugcccgag ccucggggcc aaugggucag cuggcuacga ggg 113

<210> 200
<211> 127
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> Category: MG34 active effectors tracrRNA sequence

<220>
<223> Description: MG34-1 tracrRNA sequence

<400> 200
gcgaaauuuu aaaagagccu uaauguuaaa acgccuauac agugaaggga uauacgcuug 60
gguuuugucca gccugagccu cuaugccaga aauggcgccu ucaucguggg uuaggacauu 120

uaauuuuu

127

<210> 201

<211> 128

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> Category: putative sgRNA

<220>

<223> Description: putative MG33-1 sgRNA

<220>

<221> modified_base

<222> (1)..(22)

<223> a, c, u, g, unknown or other

<400> 201

nnnnnnnnnn nnnnnnnnnn nnguucaca cgcuagaaau agcggaugaa acuccagggc 60

acuuugaugu gcccgugauc cuucggaugc ccgagccucg gggccaauagg gucagcuggc 120

uacgagggg 128

<210> 202

<211> 93

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>

<223> Category: putative sgRNA

<220>

<223> Description: putative MG34-1 sgRNA

<220>

<221> modified_base

<222> (1)..(22)

<223> a, c, u, g, unknown or other

<400> 202

nnnnnnnnnnnn nnnnnnnnnnn nnguacagu uaaggcucug aaaagagccu uauuuguaaa	60
acgccuauac agugaaggga uauacgcuug ggu	93

<210> 203
 <211> 157
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> Category: putative sgRNA

<220>
 <223> Description: putative MG34-1 sgRNA

<220>
 <221> modified_base
 <222> (1)..(22)
 <223> a, c, u, g, unknown or other

<400> 203	
nnnnnnnnnnnn nnnnnnnnnnn nnguacagu uaaggcucug aaaagagccu uauuuguaaa	60
acgccuauac agugaaggga uauacgcuug gguuugucca gccugagccu cuauugccaga	120
aauggcgccu ucaucguggg uuaggacauu uauuuuu	157

<210> 204
 <211> 28
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
 <223> Category: target

<220>
 <223> Description: test target sequence

<400> 204	
cgugagccac cacgucgcaa gccucgac	28

<210> 205

<211> 7
<212> PRT
<213> Simian virus 40

<220>
<223> Category: NLS

<220>
<223> Description: SV40 NLS

<400> 205
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 206
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> Category: NLS

<220>
<223> Description: nucleoplasmin bipartite NLS

<400> 206
Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1 5 10 15

<210> 207
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> Category: NLS

<220>
<223> Description: c-myc NLS

<400> 207
Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

<210> 208
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> Category: NLS

<220>

<223> Description: c-myc NLS

<400> 208

Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Pro
1 5 10

<210> 209

<211> 38

<212> PRT

<213> Mus sp.

<220>

<223> Category: NLS

<220>

<223> Description: hnRNPA1 M9 NLS

<400> 209

Asn Gln Ser Ser Asn Phe Gly Pro Met Lys Gly Gly Asn Phe Gly Gly
1 5 10 15

Arg Ser Ser Gly Pro Tyr Gly Gly Gly Gly Gln Tyr Phe Ala Lys Pro
20 25 30

Arg Asn Gln Gly Gly Tyr
35

<210> 210

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<223> Category: NLS

<220>

<223> Description: Importin-alpha IBB domain NLS

<400> 210

Arg Met Arg Ile Glx Phe Lys Asn Lys Gly Lys Asp Thr Ala Glu Leu
1 5 10 15

Arg Arg Arg Arg Val Glu Val Ser Val Glu Leu Arg Lys Ala Lys Lys
20 25 30

Asp Glu Gln Ile Leu Lys Arg Arg Asn Val

<210> 211
 <211> 8
 <212> PRT
 <213> Mus musculus polyomavirus 1

<220>
 <223> Category: NLS

<220>
 <223> Description: Myoma T protein NLS

<400> 211
 Val Ser Arg Lys Arg Pro Arg Pro
 1 5

<210> 212
 <211> 8
 <212> PRT
 <213> Mus musculus polyomavirus 1

<220>
 <223> Category: NLS

<220>
 <223> Description: Myoma T protein NLS

<400> 212
 Pro Pro Lys Lys Ala Arg Glu Asp
 1 5

<210> 213
 <211> 8
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Category: NLS

<220>
 <223> Description: p53 NLS

<400> 213
 Pro Gln Pro Lys Lys Lys Pro Leu
 1 5

<210> 214
 <211> 12
 <212> PRT

<213> Mus sp.

<220>

<223> Category: NLS

<220>

<223> Description: mouse c-abl IV NLS

<400> 214

Ser	Ala	Leu	Ile	Lys	Lys	Lys	Lys	Lys	Met	Ala	Pro
1				5					10		

<210> 215

<211> 5

<212> PRT

<213> Influenza virus

<220>

<223> Category: NLS

<220>

<223> Description: influenza virus NS1 NLS

<400> 215

Asp	Arg	Leu	Arg	Arg
1			5	

<210> 216

<211> 7

<212> PRT

<213> Influenza virus

<220>

<223> Category: NLS

<220>

<223> Description: influenza virus NS1 NLS

<400> 216

Pro	Lys	Gln	Lys	Lys	Arg	Lys
1			5			

<210> 217

<211> 10

<212> PRT

<213> Hepatitis delta virus

<220>

<223> Category: NLS

<220>

<223> Description: Hepatitis virus delta antigen NLS

<400> 217

Arg Lys Leu Lys Lys Lys Ile Lys Lys Leu
1 5 10

<210> 218

<211> 10

<212> PRT

<213> Mus sp.

<220>

<223> Category: NLS

<220>

<223> Description: mouse Mx1 protein NLS

<400> 218

Arg Glu Lys Lys Lys Phe Leu Lys Arg Arg
1 5 10

<210> 219

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<223> Category: NLS

<220>

<223> Description: human poly(ADP-ribose) polymerase NLS

<400> 219

Lys Arg Lys Gly Asp Glu Val Asp Gly Val Asp Glu Val Ala Lys Lys
1 5 10 15

Lys Ser Lys Lys
20

<210> 220

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<223> Category: NLS

<220>

<223> Description: steroid hormone receptors glucocorticoid NLS

<400> 220

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
1 5 10 15

Lys

<210> 221

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-4 effector

<400> 221

Val Ser Lys Val Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Asn Pro
1 5 10 15

Ile His Ser Gly Arg Ala Arg Met Leu Leu Ser Gln Gly Lys Ala Ala
20 25 30

Val Phe Arg Gly Phe Pro Phe Thr Leu Ile Leu Lys Glu Glu Val Ser
35 40 45

Ser Pro Asp Val Lys Pro Leu Arg Ile Lys Ile Asp Pro Gly Ala Lys
50 55 60

Thr Thr Gly Leu Ala Leu Val Asn Asp Lys Thr Gly Glu Val Val Trp
65 70 75 80

Val Ala Glu Leu Gln His Arg Asp Phe Gln Ile Arg Asp Ala Leu Thr
85 90 95

Ser Arg Arg Gln Leu Arg Arg Phe Arg Arg Ser Arg Lys Thr Arg Tyr
100 105 110

Arg Lys Pro Arg Phe Leu Asn Arg Thr Arg Pro Lys Gly Trp Leu Pro

115

120

125

Pro Ser Leu Asn Ser Arg Val Ala Asn Ile Leu Thr Trp Val Lys Arg
 130 135 140

Leu Ser Ser Leu Cys Gln Ile Asn Ala Ile Ser Gln Glu Leu Val Arg
 145 150 155 160

Phe Asp Thr Gln Gln Met Glu Asn Pro Glu Ile Ser Gly Thr Gly Tyr
 165 170 175

Gln Gln Gly Thr Leu Ala Gly Tyr Glu Ile Arg Glu Phe Leu Leu Glu
 180 185 190

Lys Trp Asn Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp Thr Lys Leu
 195 200 205

Glu Ile Glu His Ile Gln Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
 210 215 220

Ser Asn Leu Cys Leu Ala Cys Val Pro Cys Asn Arg Glu Lys Gly Asn
 225 230 235 240

Gln Asp Ile Lys Asp Phe Leu Lys Gly Lys Pro Asp Leu Leu Lys Arg
 245 250 255

Ile Leu Gly Gln Ala Lys Arg Pro Leu Ala Asp Thr Ser Ala Val Asn
 260 265 270

Ala Thr Arg Trp Asn Leu Tyr Asp Asn Leu Arg Gln Thr Ser Leu Pro
 275 280 285

Val Glu Val Gly Thr Gly Gly Leu Thr Lys Tyr Asn Arg Thr Ile Arg
 290 295 300

Gly Leu Asp Lys Thr His Tyr Trp Asp Ala Ala Cys Val Gly Ala Ser
 305 310 315 320

Thr Pro Glu Arg Leu Ile Thr Ser Gly Ile Lys Pro Leu Leu Ile Ser
 325 330 335

Ala Lys Gly His Gly Thr Arg Gln Gln Cys Arg Thr Asn Lys Leu Gly
340 345 350

Phe Pro Val Arg Tyr Cys Ser Arg Thr Lys Phe His Lys Gly Phe Gln
355 360 365

Thr Gly Asp Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys Val Gly
370 375 380

Thr Tyr Val Gly Arg Val Ala Thr Arg Ala Thr Leu Arg Phe Asn Ile
385 390 395 400

Ser Thr Lys Asp Gly Leu Val Gln Gly Ile Ser His Lys Tyr Cys Lys
405 410 415

His Ile His Lys Lys Asp Gly Tyr Ala Tyr Ala Tyr
420 425

<210> 222

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-419 effector

<400> 222

Met Ser Lys Val Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Asn Pro
1 5 10 15

Ile His Ser Gly Arg Ala Arg Met Leu Leu Ser Gln Gly Lys Ala Ala
20 25 30

Val Phe Arg Gly Phe Pro Phe Thr Leu Ile Leu Lys Glu Glu Val Ser
35 40 45

Ser Pro Asp Val Lys Pro Leu Arg Ile Lys Ile Asp Pro Gly Ala Lys

50

55

60

Thr Thr Gly Leu Ala Leu Val Asn Asp Lys Thr Gly Glu Val Val Trp
65 70 75 80

Val Ala Glu Leu Gln His Arg Asp Phe Gln Ile Arg Asp Ala Leu Thr
85 90 95

Ser Arg Arg Gln Leu Arg Arg Phe Arg Arg Ser Arg Lys Thr Arg Tyr
100 105 110

Arg Lys Pro Arg Phe Leu Asn Arg Thr Arg Pro Lys Gly Trp Leu Pro
115 120 125

Pro Ser Leu Asn Ser Arg Val Ala Asn Ile Leu Thr Trp Val Lys Arg
130 135 140

Leu Ser Ser Leu Cys Gln Ile Asn Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Gln Met Glu Asn Pro Glu Ile Ser Gly Thr Gly Tyr
165 170 175

Gln Gln Gly Thr Leu Ala Gly Tyr Glu Ile Arg Glu Phe Leu Leu Glu
180 185 190

Lys Trp Asn Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp Thr Lys Leu
195 200 205

Glu Ile Glu His Ile Gln Pro Arg Ser Lys Gly Gly Ser Asn Arg Val
210 215 220

Ser Asn Leu Cys Leu Ala Cys Val Pro Cys Asn Arg Glu Lys Gly Asn
225 230 235 240

Gln Asp Ile Lys Asp Phe Leu Lys Gly Lys Pro Asp Leu Leu Lys Arg
245 250 255

Ile Leu Gly Gln Ala Lys Arg Pro Leu Ala Asp Thr Ser Ala Val Asn
260 265 270

Ala Thr Arg Trp Asn Leu Tyr Asp Asn Leu Arg Gln Thr Ser Leu Pro
275 280 285

Val Glu Val Gly Thr Gly Gly Leu Thr Lys Tyr Asn Arg Thr Ile Arg
290 295 300

Gly Leu Asp Lys Thr His Tyr Trp Asp Ala Ala Cys Val Gly Ala Ser
305 310 315 320

Thr Pro Glu Arg Leu Ile Thr Ser Gly Ile Lys Pro Leu Leu Ile Ser
325 330 335

Ala Lys Gly His Gly Thr Arg Gln Gln Cys Arg Thr Asn Lys Leu Gly
340 345 350

Phe Pro Val Arg Tyr Cys Ser Arg Thr Lys Phe His Lys Gly Phe Gln
355 360 365

Thr Gly Asp Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys Val Gly
370 375 380

Thr Tyr Val Gly Arg Val Ala Thr Arg Ala Thr Leu Arg Phe Asn Ile
385 390 395 400

Ser Thr Lys Asp Gly Leu Val Gln Gly Ile Ser His Lys Tyr Cys Lys
405 410 415

His Ile His Lys Lys Asp Gly Tyr Ala Tyr Ala Tyr
420 425

<210> 223

<211> 493

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-420 effector

<400> 223

Met Ser Lys Thr Asn Tyr Val Leu Val Val Asp Thr Asn Lys His Pro
1 5 10 15

Leu Ser Pro Cys Lys Pro Gly Val Ala Arg Ser Leu Leu Lys Ala Gly
20 25 30

Lys Ala Ala Val Phe Arg Arg Tyr Thr Phe Thr Ile Ile Leu Lys Lys
35 40 45

Glu Val Glu Gly Asp Ile Leu Lys Ser Gln Ile Lys Ile Asp Pro Gly
50 55 60

Ser Lys Thr Thr Gly Leu Ala Leu Val Gln Asn Gly Val Val Ile Trp
65 70 75 80

Ala Ala Glu Leu Gln His Arg Gly Gln Leu Ile Lys Gln Ser Leu Asp
85 90 95

Asn Arg Arg Ser Leu Arg Arg Asn Arg Arg Asn Arg Lys Thr Arg Tyr
100 105 110

Arg Gln Pro Arg Phe Leu Asn Arg Val Lys Ser Lys Pro Lys Gly Trp
115 120 125

Leu Ala Pro Ser Leu Met His Arg Val Glu Asn Val Ser Thr Trp Val
130 135 140

Asn Lys Leu Ile Lys Phe Ser Ala Val Asp Ser Val Met Met Glu Leu
145 150 155 160

Val Arg Phe Asp Thr Gln Lys Met Thr Asn Pro Asp Val Ser Gly Val
165 170 175

Gln Tyr Gln Gln Gly Glu Leu Thr Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Phe Asp Arg Thr Cys Val Tyr Cys Gln Ala Lys Asn Val
195 200 205

Pro Leu Glu Val Glu His Ile Gln Pro Lys Ser Lys Gly Gly Ser Asn
210 215 220

Arg Ile Ser Asn Leu Thr Leu Ala Cys Arg Pro Cys Asn Gln Ser Lys
225 230 235 240

Gly Asn Gln Asp Ile Gln Asp Phe Leu Ser Gly Lys Pro Ser Leu Leu
245 250 255

Lys Arg Ile Leu Asn Gln Thr Lys Gln Pro Leu Lys Asp Ala Ala Ala
260 265 270

Val Asn Ser Thr Arg Trp Lys Leu Lys Glu Ser Leu Glu Leu Thr Gly
275 280 285

Leu Pro Val Phe Thr Gly Asn Gly Ala Leu Thr Lys Tyr Asn Arg Cys
290 295 300

Arg Leu Gly Leu Pro Lys Thr His Trp Leu Asp Ala Ala Ser Val Gly
305 310 315 320

Glu Ile Asp Asn Leu Val Ile Ala Thr His Gln Pro Leu Leu Ile Lys
325 330 335

Ser Phe Gly Phe Gly Ser Arg Gln Met Cys Arg Thr Asp Lys Tyr Gly
340 345 350

Phe Pro Thr Arg His Cys Ser Arg Gln Lys Val His Phe Gly Phe Thr
355 360 365

Thr Gly Asp Ile Val Lys Ala Asp Ile Pro Lys Gly Lys Tyr Ala Gly
370 375 380

Lys Tyr Thr Ala Arg Val Thr Val Arg Ser Thr Gly Ser Phe Ala Ile
385 390 395 400

Lys Ser Leu Thr His Gly Lys Gln Ile Asp Val Asn His Lys Tyr Cys
405 410 415

Lys Ala Ile His Lys Leu Asp Gly Tyr Gly Tyr Gly Phe Gly Glu Leu

420

425

430

Ile Asn Ile Asn Pro Thr Lys Leu Asn Pro Val Glu Thr Gln Ile Val
 435 440 445

Lys Gly Arg Thr Ala Ala Asn Pro Thr Gln Leu Asn Leu Phe Asp Ser
 450 455 460

Ser Ile Phe Ala Val Glu Ser Ser Glu Ser Lys Ile His Lys Lys Gln
 465 470 475 480

Lys Val Lys Gly Asp Asp Tyr Glu Gln Leu Ser Leu Phe
 485 490

<210> 224

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-421 effector

<400> 224

Met Ser Lys Val Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Asn Pro
 1 5 10 15

Ile His Pro Gly Arg Ala Arg Met Leu Leu Ser Gln Arg Lys Ala Ala
 20 25 30

Val Phe Arg Arg Tyr Pro Leu Thr Leu Ile Leu Lys Glu Glu Val Leu
 35 40 45

Asn Pro Asp Ile Glu Pro Leu Arg Ile Lys Ile Asp Pro Gly Ala Lys
 50 55 60

Thr Thr Gly Leu Ala Leu Val Asn Asp Ser Thr Gly Glu Val Val Trp
 65 70 75 80

Ile Ala Glu Leu Gln His Arg Gly Phe Gln Ile Arg Asp Ala Leu Thr
85 90 95

Ser Arg Arg Gln Leu Arg Lys Ser Arg Arg Ser Arg Lys Thr Arg Tyr
100 105 110

Arg Lys Pro Arg Gly Leu Asn Arg Thr Arg Pro Thr Gly Trp Leu Pro
115 120 125

Pro Ser Leu Asn Ser Arg Val Ala Asn Ile Leu Thr Trp Val Lys Arg
130 135 140

Leu Ser Ser Leu Cys Gln Ile Asn Ala Ile Ser Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Thr Gln Gln Met Glu Asn Pro Glu Ile Ser Gly Ile Ala Tyr
165 170 175

Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Phe Leu Leu Phe
180 185 190

Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp Thr Lys Leu
195 200 205

Glu Val Glu His Ile Gln Ser Arg Ser Lys Gly Gly Ser Asn Arg Val
210 215 220

Ser Asn Leu Cys Leu Ala Cys Val Pro Cys Asn Arg Glu Lys Gly Asn
225 230 235 240

Gln Asp Ile Lys Asp Phe Leu Lys Gly Lys Pro Asp Leu Arg Lys Gln
245 250 255

Ile Leu Ala Gln Ala Lys Arg Pro Leu Ala Asp Ala Ala Ala Val Asn
260 265 270

Val Thr Arg Trp Asn Leu Tyr Phe Asn Leu Lys Lys Met Gly Leu Pro
275 280 285

Val Glu Ile Gly Thr Gly Gly Arg Thr Lys Tyr Asn Arg Thr Lys Leu

290

295

300

Leu Leu Glu Lys Thr His Tyr Trp Asp Ala Ala Cys Val Gly Glu Ser
 305 310 315 320

Thr Pro Glu Arg Leu Ile Thr Ala Gly Ile Lys Pro Leu Leu Ile Asn
 325 330 335

Ala Lys Gly His Gly Thr Arg Gln Gln Cys Arg Pro Asn Lys Phe Gly
 340 345 350

Phe Pro Val Arg Tyr Cys Ser Arg Thr Lys Phe His Lys Gly Phe Gln
 355 360 365

Thr Gly Asp Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys Val Gly
 370 375 380

Thr His Gln Gly Arg Val Ala Thr Arg Ala Thr Gly Arg Phe Asn Ile
 385 390 395 400

Ser Thr Thr Asp Gly Leu Val Gln Gly Ile Ser His Lys Tyr Cys Lys
 405 410 415

His Ile His Lys Lys Asp Gly Tyr Ala Tyr Val Ala
 420 425

<210> 225

<211> 159

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-176 effector

<400> 225

Ala Ala Val Asn Ala Thr Arg Trp Ala Leu Phe Asn Arg Leu Lys Glu
 1 5 10 15

Phe Gly Leu Asp Leu Asp Val Gly Thr Gly Gly Arg Thr Gln Phe Asn
20 25 30

Arg Thr Gln Gln Gly Leu Pro Lys Thr His Trp Ile Asp Ala Ala Cys
35 40 45

Val Gly Glu Ser Thr Pro Lys Leu Val Leu Cys Thr Asn Gln Pro Leu
50 55 60

Leu Ile Ala Ala Lys Gly His Gly Thr Arg Gln Met Cys Gly Thr Asp
65 70 75 80

Lys Tyr Gly Phe Pro Thr Arg His Arg Ser Arg Val Gln Ile His Lys
85 90 95

Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Thr Val Thr Ala Gly Arg
100 105 110

Lys Thr Gly Ser Tyr Ala Gly Arg Val Leu Cys Arg Ala Ser Gly Ser
115 120 125

Phe Asp Val Ala Thr Pro Ser Ala Arg Val Ala Gly Ile Ser His Lys
130 135 140

Tyr Cys Lys Ala Ile His Lys Lys Asp Gly Tyr Ala Tyr Ala Phe
145 150 155

<210> 226

<211> 197

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-177 effector

<400> 226

Ala Cys His Asp Cys Asn Gln Lys Lys Gly Asn Gln Asp Val Arg Ala

1	5	10	15
Phe	Leu	Ala	Thr
	20		
Lys	Pro	Asp	Leu
			25
Leu	Asn	Arg	Ile
			30
Lys	Gln	Ala	
Lys	Leu	Pro	Leu
	35		
Lys	Asp	Ala	Ala
		40	
Ala	Val	Asn	Ser
			45
Thr	Arg	Trp	Ala
Leu	Phe	Asn	Ala
	50		
Lys	Glu	Thr	Gly
	55		
Leu	Pro	Val	Thr
		60	
Thr	Gly	Thr	
Gly	Gly	Gln	Thr
65			
Lys	Phe	Asn	Arg
	70		
Asn	Arg	Leu	Gly
		75	
Leu	Pro	Lys	Ser
			80
His	Trp	Leu	Asp
			85
Ala	Ala	Cys	Val
Gly	Asn	Phe	Glu
	90		
Ala	Leu	Glu	Val
		95	
Leu	Thr	Ser	Lys
		100	
Pro	Leu	Leu	Ile
Ala	Ala	Lys	Gly
	105		
His	Gly	Thr	Arg
		110	
Gln	Met	Cys	Gly
	115		
Thr	Asn	Lys	Tyr
			120
Gly	Phe	Pro	Thr
Arg	His	Lys	Ser
			125
Arg	Val	Gln	Ile
	130		
His	Lys	Gly	Tyr
		135	
Gln	Thr	Gly	Asp
			140
Ile	Val	Ser	Ala
Thr	Val	Thr	Ala
145			
Gly	Lys	Lys	Leu
	150		
Gly	Ser	Tyr	Ile
		155	
Gly	Arg	Val	Leu
			160
Cys	Arg	Ala	Ser
			165
Gly	Ser	Phe	Asp
Ile	Ala	Thr	Lys
	170		
Thr	Gly	Arg	Ile
		175	
Thr	Gly	Ile	Ser
			180
His	Lys	Tyr	Cys
Asn	Pro	Ile	His
	185		
Lys	Lys	Asp	Gly
			190
Tyr	Ser	Tyr	Ala
			Phe
	195		

<210> 227
 <211> 309
 <212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-178 effector

<400> 227

Ala Glu Ile Ala Gly Val Gly Tyr Gln Gln Gly Thr Leu Ala Gly Tyr
1 5 10 15

Glu Leu Arg Glu Tyr Leu Leu Glu Lys Phe Asn Arg Thr Cys Cys Tyr
20 25 30

Cys Asp Ala Gln Asp Val Pro Leu Asn Ile Glu His Ile His Pro Lys
35 40 45

Ala Gln Gly Gly Thr Asn Arg Val Ser Asn Leu Ala Ile Ala Cys Ile
50 55 60

Pro Cys Asn Thr Lys Lys Gly Ala Arg Ser Ile Glu Ala Phe Leu Ala
65 70 75 80

Lys Asp Pro Ala Arg Leu Ala Arg Ile Arg Ala Gln Leu Lys Arg Pro
85 90 95

Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Trp Ala Leu Phe Glu
100 105 110

Ala Leu Ala Arg Gly Arg Cys Arg Val His Gln Pro Glu Ala Thr Met
115 120 125

Leu Pro Val Glu Ile Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Thr
130 135 140

Arg Leu Gln Ile Pro Lys Ser His Ala Leu Asp Ala Ala Cys Val Gly
145 150 155 160

Gln Ile Asp Ala Ile His Ala Trp Ser Arg Pro Thr Leu Gln Ile Lys

165

170

175

Cys Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Thr Gln Tyr Gly
 180 185 190

Phe Ala Arg Gly Tyr Leu Met Arg Thr Lys Ser Val Lys Gly Phe Arg
 195 200 205

Thr Gly Asp Leu Val Arg Ala Ser Val Thr Ser Gly Lys Lys Ile Gly
 210 215 220

Glu Tyr Ile Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn Ile
 225 230 235 240

Gln Thr Val Gly Ala Val Val Gln Gly Val Ser His Lys Tyr Cys Arg
 245 250 255

Ile Val Gln Arg Gly Asp Gly Tyr Gly Tyr Ala Trp Ser Ile Thr Pro
 260 265 270

Phe Asn Thr Gly Lys Asn Asn Phe Pro Val Ser Ser His Pro Leu Ala
 275 280 285

Ser Arg Ser Ala Leu Met Ser Leu Arg Asp Ser Ala Pro Lys Gly Gly
 290 295 300

Tyr Pro Pro Glu Leu
 305

<210> 228

<211> 345

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-179 effector

<400> 228

Ala Glu Leu Thr His Arg Gly Gln Ala Ile Lys Ala Ser Leu Glu Ser
1 5 10 15

Arg Arg Ser Leu Arg Arg Ser Arg Arg Asn Arg His Thr Arg Tyr Arg
20 25 30

Gln Ala Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro
35 40 45

Ser Leu Gln His Arg Val Glu Thr Thr Leu Thr Trp Val Asn Lys Phe
50 55 60

Ile Gln Leu Ala Pro Ile Gly Ser Ile Val Gln Glu Leu Val Arg Phe
65 70 75 80

Asp Leu Gln Gln Ile Glu Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln
85 90 95

Gln Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Asn Lys
100 105 110

Trp Asp Arg Lys Cys Ala Tyr Cys Ser Ala Glu Asn Ile Pro Leu Gln
115 120 125

Val Glu His Ile His Ser Lys Ala Lys Gly Gly Ser Asn Arg Ile Ser
130 135 140

Asn Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu Lys Lys Gly Thr Gln
145 150 155 160

Asp Ile Glu Val Phe Leu Ala Lys Lys Pro Asp Leu Leu Lys Arg Ile
165 170 175

Leu Ser Gln Ala Lys Arg Pro Leu Arg Asp Ala Ala Ala Val Asn Ser
180 185 190

Thr Arg Trp Ala Leu Leu Asn Arg Leu Gln Glu Thr Gly Leu Pro Val
195 200 205

Leu Thr Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Thr Arg Leu Asp

210

215

220

Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly His Val Asp
 225 230 235 240

Gln Leu Glu Val Leu Thr Gly Lys Pro Leu Leu Ile Lys Ala Thr Gly
 245 250 255

His Gly Ser Arg Gln Met Cys Gly Thr Asp Lys Phe Gly Phe Pro Ser
 260 265 270

Arg His Arg Thr Arg Lys Gln Ile His Gln Gly Phe Gln Thr Gly Asp
 275 280 285

Ile Val Lys Ala Leu Val Thr Ser Gly Lys Lys Ile Gly Ser Tyr Gly
 290 295 300

Gly Arg Val Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Gln Val Lys
 305 310 315 320

Ser Gly Arg Val Gln Gly Leu Ser His Lys Phe Cys Arg Ser Val His
 325 330 335

Arg Lys Asp Gly Tyr Gly Tyr Gly Phe
 340 345

<210> 229

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-180 effector

<400> 229

Ala Asn Leu Arg Tyr Arg Gly Pro Arg Ile Leu Asn Arg Lys Asn Lys
 1 5 10 15

Gly Lys Gly Trp Leu Ala Pro Ser Leu Gln His Arg Ile Asp Thr Thr
20 25 30

Leu Ser Trp Val Ala Arg Leu Arg Asn Val Ala Pro Val Thr His Leu
35 40 45

Ala Gln Glu Leu Val Arg Phe Asp Met Gln Gln Leu Glu Asn Pro Glu
50 55 60

Ile Ala Gly Val Glu Tyr Gln Gln Gly Glu Leu Val Gly Tyr Glu Val
65 70 75 80

Arg Glu Tyr Leu Leu Glu Lys Trp Arg Arg Gln Cys Ala Tyr Cys Asp
85 90 95

Ala Ser Thr Val Pro Leu Gln Ile Asp His Ile His Pro Lys Ala Arg
100 105 110

Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu Ala Cys Ala Pro Cys
115 120 125

Asn Leu Arg Lys Ala Ala Gln Asp Val Thr Gln Phe Leu Glu Lys Asp
130 135 140

Pro Lys Arg Leu Ala Lys Ile Gln Ala Gln Ala Lys Arg Pro Leu Arg
145 150 155 160

Asp Ala Ala Val Val Asn Ala Thr Arg Trp Lys Leu Leu Asn Ala Leu
165 170 175

Lys Ala Thr Gly Leu Thr Val Arg Thr Gly Ser Gly Gly Leu Thr Lys
180 185 190

Cys Asn Arg Ser Lys Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala
195 200 205

Val Cys Ile Gly Glu Val Asp Gln Val Glu Gln Trp Gln Thr Pro Thr
210 215 220

Leu Glu Ile Lys Ala Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu

225 230 235 240
 Asn Arg Phe Gly Phe Pro Arg Gly Tyr Leu Ile Arg Gln Lys Arg Ile
 245 250 255
 His Gly Phe Gln Thr Gly Asp Arg Val Lys Ala Ile Val Thr Lys Gly
 260 265 270
 Lys Lys Val Gly Thr Tyr Met Gly Arg Val Ala Val Arg Asp Ser Gly
 275 280 285
 Ser Phe Asn Ile Gln Thr Ala Glu Gly Leu Val Gln Gly Ile Ser His
 290 295 300
 Arg Tyr Cys Thr Leu Ile Gln Arg Ser Asp Gly Tyr Gly Tyr Ser Leu
 305 310 315 320
 Arg Ser Asp Ser Asn
 325

<210> 230
 <211> 312
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-181 effector

<400> 230
 Ala Pro Glu Thr Ala Ile Ser Thr Glu Leu Val Arg Phe Asp Met Gln
 1 5 10 15

Ala Met Glu Asn Pro Glu Ile Glu Gly Ile Gln Tyr Gln Gln Gly Thr
 20 25 30

Met Ala Gly Tyr Glu Val Arg Glu Tyr Leu Phe Glu Lys Trp Lys Arg
 35 40 45

Thr Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu Gln Val Glu His
50 55 60

Ile Gln Pro Lys Ala Lys Gly Gly Ser Asn Arg Ile Asn Asn Leu Thr
65 70 75 80

Leu Ala Cys Gln Cys Cys Asn Gln Lys Lys Ala Ala Leu Pro Val Glu
85 90 95

Met Phe Leu Ala Lys Lys Pro Glu Leu Leu Lys Arg Ile Leu Ala Gln
100 105 110

Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp
115 120 125

Ala Leu Val Asn Thr Leu Lys Thr Thr Gly Leu Val Val Glu Thr Gly
130 135 140

Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro Lys
145 150 155 160

Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Gly Ser Ile Thr
165 170 175

Asp Trp Gln Lys Pro Thr Leu Ala Ile Lys Ala Met Gly Arg Gly Ser
180 185 190

Tyr Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu
195 200 205

Thr Arg Ser Lys Ser Ile Lys Gly Phe Gln Thr Gly Asp Met Val Lys
210 215 220

Ala Glu Val Thr Thr Gly Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val
225 230 235 240

Ala Val Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr Ser Thr Gly Leu
245 250 255

Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly Asn

260

265

270

Gly Tyr Gly Tyr Ser Leu Val Ala Lys Met Asp Val Thr Gly Thr Pro
 275 280 285

Pro Gln His Arg Asp Ala Ser His Pro Ala Leu Tyr Leu Pro Gly Leu
 290 295 300

Lys Ala Glu Val Ser Arg Ala Asn
 305 310

<210> 231

<211> 228

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-183 effector

<400> 231

Ala Ser Asn Phe Thr Leu Ala Cys Ile Pro Cys Asn Gln Lys Lys Gly
 1 5 10 15

Ala Gln Asp Ile Arg Val Phe Leu Ala Lys Asp Pro Arg Arg Leu Glu
 20 25 30

Arg Ile Leu Ala Gln Ala Lys Lys Ser Leu Lys Asp Ala Ala Ala Val
 35 40 45

Asn Ser Thr Arg Trp Ala Leu Leu Asn Ala Leu Lys Ala Thr Gly Leu
 50 55 60

Pro Val Thr Thr Gly Ser Gly Gly Arg Thr Lys His Asn Arg Ser Arg
 65 70 75 80

Leu Glu Leu Pro Lys Thr His Ala Leu Asp Ala Val Cys Val Gly Thr
 85 90 95

Thr Asp Ala Val Ala Gly Trp Gln Lys Pro Thr Met Val Ile Lys Ala
100 105 110

Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Tyr Gly Phe
115 120 125

Pro Arg Gly Tyr Leu Thr Arg Gln Lys Arg Ile Lys Gly Phe Gln Thr
130 135 140

Gly Asp Met Val Lys Ala His Val Thr Lys Gly Lys Lys Phe Gly Arg
145 150 155 160

Tyr Ser Gly Arg Val Ala Val Arg Ala Ser Gly Ser Phe Asn Ile Gln
165 170 175

Thr Ala Asp Ser Val Val Gln Gly Ile Gly Tyr Arg Tyr Cys Thr Val
180 185 190

Ile Gln Arg Ala Asp Gly Tyr Gly Tyr Ser Trp Gln Ala Lys Ala Ser
195 200 205

Thr Ala Met Leu Ser Leu Leu His Leu Pro Ala Leu Asn Gly Gly Val
210 215 220

Ser Arg Arg Ile
225

<210> 232
<211> 406
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-184 effector

<400> 232
Ala Val Phe Val Ile Asp Arg Arg Gln Ala Pro Leu Met Pro Cys Ser

1	5	10	15
Glu Lys Arg Ala Arg Leu Leu Leu Ala Arg Gly Arg Ala Arg Val His	20	25	30
Arg Leu Ile Pro Phe Thr Ile Arg Leu Ile Asp Arg Ala Val Ala Gln	35	40	45
Ser Glu Leu Gln Pro Leu Glu Leu Lys Ile Asp Pro Gly Ser Lys Thr	50	55	60
Ser Gly Leu Ala Leu Val Arg Asn Arg Asp Thr Val Asn Ala Glu Thr	65	70	75
Gly Glu Ile Thr Ala Thr Ala His Val Leu Asn Leu Phe Glu Leu Ile	85	90	95
His Arg Gly Val Gln Ile Ser His Ala Leu Thr Ala Arg Arg Gln Met	100	105	110
Arg Arg Arg Arg Arg Ser Ala Asn Leu Arg Tyr Arg Ala Pro Arg Phe	115	120	125
Leu Asn Arg Lys Asn Lys Gly Lys Gly Trp Leu Ala Pro Ser Leu Gln	130	135	140
His Arg Ile Asp Thr Thr Leu Ser Trp Val Ala Arg Leu Arg Asn Val	145	150	155
Ala Pro Ile Thr His Leu Ala Gln Glu Leu Val Arg Phe Asp Met Gln	165	170	175
Gln Leu Glu Asn Pro Glu Ile Ala Gly Val Glu Tyr Gln Gln Gly Glu	180	185	190
Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Cys Arg Arg	195	200	205
Gln Cys Ala Tyr Cys Asp Ala Ser Thr Val Pro Leu Gln Ile Glu His	210	215	220

Ile His Pro Lys Ala Arg Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala
225 230 235 240

Leu Ala Cys Ala Pro Cys Asn Leu Lys Lys Ala Ala Gln Asp Ile Ala
245 250 255

Leu Phe Leu Ala Lys Asp Pro Lys Arg Leu Ala Lys Ile Gln Ala Gln
260 265 270

Ala Lys Arg Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg Trp
275 280 285

Lys Leu Leu Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Arg Thr Gly
290 295 300

Ser Gly Gly Leu Thr Lys Cys Asn Arg Ser Arg Leu Val Ile Pro Lys
305 310 315 320

Thr His Ala Leu Asp Ala Val Cys Val Gly Glu Val Asp Phe Val Glu
325 330 335

His Trp Gln Lys Pro Thr Leu Val Ile Lys Ala Thr Gly Arg Gly Ser
340 345 350

Tyr Gln Arg Thr Arg Leu Asn Arg Phe Gly Phe Pro Arg Gly Tyr Leu
355 360 365

Thr Arg Gln Lys Gln Ile His Gly Phe Gln Thr Gly Asp Met Val Lys
370 375 380

Ala Ile Val Thr Lys Gly Lys Lys Val Gly Thr Tyr Val Gly Arg Val
385 390 395 400

Ala Val Arg Ala Ser Gly
405

<210> 233

<211> 384

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-185 effector

<400> 233

Ala Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser
1 5 10 15

Glu Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys
20 25 30

Leu Arg Tyr Arg Pro Pro Arg Phe Gly Asn Arg Gly Asn Gln Lys Lys
35 40 45

Gly Trp Leu Pro Pro Ser Leu Gln His Arg Val Asp Thr Gly Met Ala
50 55 60

Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr
65 70 75 80

Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu
85 90 95

Gly Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu
100 105 110

Tyr Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys
115 120 125

Asp Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly
130 135 140

Ser Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln
145 150 155 160

Lys Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu
165 170 175

Leu Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala
180 185 190

Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr
195 200 205

Thr Gly Leu Val Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn
210 215 220

Arg Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys
225 230 235 240

Val Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala
245 250 255

Ile Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys
260 265 270

Phe Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly
275 280 285

Phe Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys
290 295 300

Ile Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe
305 310 315 320

Asn Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr
325 330 335

Cys Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala
340 345 350

Lys Thr Asp Val Arg Gly Thr Pro Pro Gln His Arg Ala Ala Lys His
355 360 365

Pro Ala Leu Tyr Leu Pro Gly Leu Lys Ala Glu Val Ser Arg Ala Asn
370 375 380

<210> 234

<211> 281
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-186 effector

<400> 234

Cys Ala Tyr Cys Pro Ala Thr Asn Val Pro Leu Gln Val Glu His Ile
1 5 10 15

Val Pro Arg Ala Lys Gly Gly Ser His Arg Val Ser Asn Leu Thr Leu
20 25 30

Ala Cys Gly Pro Cys Asn Thr Ala Lys Gly Thr Gln Asp Val Arg Ala
35 40 45

Phe Leu Ala Gln Asp Pro Lys Arg Leu Ala Arg Val Leu Ala Gln Ala
50 55 60

Lys Ala Pro Leu Arg Asp Ala Ala Ala Met Lys Leu Phe Thr Gln Ala
65 70 75 80

Glu Phe Asp Asn Leu Pro Val Ile Asp Gly Val Lys Gln Cys Pro Thr
85 90 95

Gly Asp Tyr Ser Ser Val Arg Asn Phe Gly Glu Arg Cys Val Phe Gly
100 105 110

Ala Glu Ser Ile Phe Cys Arg Asp Ser Arg Phe Ala Asp Ser Cys Ile
115 120 125

Phe Gly Glu Lys Ser Arg Phe Gly Val Gly Cys Ser Phe Cys Asp Arg
130 135 140

Cys Val Phe Gly Ile Gly Ile Arg Phe Glu Ile Trp Cys Lys Phe Gly
145 150 155 160

Leu Gly Cys Ile Phe Gly Ser Glu Thr Arg Phe Gly Asp Trp Cys Gly
165 170 175

Phe Gly Ala Glu Cys Val Phe Gly Asp Arg Cys Ala Phe Gly Val Gln
180 185 190

Asn Arg Phe Gly Glu Arg Cys Ile Phe Ala Gly Arg Arg Ala Leu Pro
195 200 205

Glu Asn Pro Leu Leu Val Phe Pro Gly Ala Gly Thr Asp Asp Arg Ile
210 215 220

Val Tyr Ala Ile Asn Val Glu Gly Gly Pro Trp Ile Glu Gly Trp Ser
225 230 235 240

Phe Ser Gly Gly Ile Asp Glu Phe Arg Ala Lys Val Arg Val Asn Gly
245 250 255

Gly Gly Leu Lys Ser Arg Tyr Leu Ser Val Ala Tyr Glu Val Ala Ala
260 265 270

Lys Trp Cys Pro Glu Lys Val Glu Ser
275 280

<210> 235
<211> 371
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-187 effector

<400> 235
Glu Glu Gly Glu Thr His His Val Leu His Leu Ala Glu Val His His
1 5 10 15

Arg Gly Ala Pro Ile Arg Lys Ala Leu Gln Gln Arg Ala Gly Tyr Arg

20

25

30

Arg Gly Arg Arg Ser Arg Lys Leu Arg His Arg Ala Pro Arg Phe Leu
 35 40 45

Asn Arg Arg Arg Asp Asp Gly Trp Leu Ala Pro Ser Leu Gln His Arg
 50 55 60

Val Leu Thr Thr Gln Thr Trp Val Lys Arg Tyr Arg Ala Leu Ala Pro
 65 70 75 80

Ile Val Ala Leu Thr Val Glu Arg Val Arg Phe Asp Met Gln Gln Met
 85 90 95

Val Thr Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Thr Leu Ala
 100 105 110

Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Thr Cys
 115 120 125

Val Tyr Cys Asp His Thr Asp Arg Pro Leu Gln Val Glu His Leu Thr
 130 135 140

Pro Pro Gly Ser Gly Gly Ser Asp Gln Gly Ser Asn Leu Ala Leu Ala
 145 150 155 160

Cys Glu Ser Cys Asn Ala Ala Lys Gly Asn Gln Thr Val Glu Val Tyr
 165 170 175

Leu Ala Asp Asp Pro Val Arg Arg Asp Arg Ile Leu Arg Gln Ala Gln
 180 185 190

Gln Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg Trp Ala Ile
 195 200 205

Trp Glu Ile Leu Thr Lys Thr Gly Leu Pro Val Glu Ser Thr Thr Gly
 210 215 220

Gly Arg Thr Lys Trp Asn Arg Thr Arg Met Gly Ile Pro Lys Arg Asp
 225 230 235 240

Ala Trp Asp Ala Ala Cys Ala Gly Thr Val Asp Gln Val Leu Gly Trp
245 250 255

Asp Arg Pro Ile Gln Arg Val Asp Cys Leu Gly Arg Gly Ser His Gln
260 265 270

Arg Thr Arg Val Thr Lys Asp Gly Phe Pro Arg Gly Tyr Leu Pro Arg
275 280 285

Thr Lys Met Val Gln Trp Phe Arg Thr Trp Asp His Val Arg Ala Ile
290 295 300

Val Glu Thr Gly Ala His Arg Gly Thr Trp Thr Gly Arg Val Ala Val
305 310 315 320

Arg Ser Thr Gly Ser Phe Asn Ile Gln Thr Gly Ala Ala Thr Ile Gln
325 330 335

Gly Ile Ala Ala Arg Trp Cys Val Leu Leu Gln Arg Gly Asp Gly Tyr
340 345 350

Arg Tyr Ser Leu Ala Leu Pro Arg Thr Glu His Ala Ile Arg Pro Ser
355 360 365

Ser Val Ala
370

<210> 236
<211> 416
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-188 effector

<400> 236
Glu Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser

1		5		10		15											
Lys	Ala	Thr	Gly	Ile	Ala	Leu	Val	Arg	Glu	Thr	Glu	Gly	Lys	Cys	Val		
			20					25					30				
Ala	Val	Val	Asn	Leu	Phe	Glu	Leu	Val	His	Arg	Gly	Arg	Gln	Ile	Ser		
		35					40					45					
Glu	Ala	Leu	Thr	Ala	Arg	Arg	Gly	His	Arg	Arg	Leu	Arg	Arg	Ser	Lys		
	50					55					60						
Leu	Arg	Tyr	Arg	Pro	Pro	Arg	Phe	Asp	Asn	Arg	Gly	Asn	Gln	Lys	Lys		
65					70				75						80		
Gly	Trp	Leu	Pro	Pro	Ser	Leu	Gln	His	Arg	Val	Asp	Thr	Ser	Met	Ala		
				85					90					95			
Trp	Val	Ser	Arg	Ile	Gln	Arg	Leu	Ala	Pro	Val	Ser	Ala	Ile	Ser	Thr		
			100					105					110				
Glu	Leu	Val	Arg	Phe	Asp	Met	Gln	Ala	Leu	Glu	Asn	Pro	Glu	Ile	Lys		
		115					120					125					
Gly	Ala	Gln	Tyr	Gln	Gln	Gly	Thr	Leu	Val	Gly	Tyr	Glu	Val	Arg	Glu		
	130					135					140						
Tyr	Leu	Leu	Glu	Lys	Trp	Asp	Arg	Thr	Cys	Ala	Tyr	Cys	Gly	Ala	Lys		
145					150					155					160		
Asp	Val	Pro	Leu	Gln	Val	Glu	His	Ile	Gln	Pro	Lys	Ala	Lys	Gly	Gly		
				165					170					175			
Ser	Asn	Arg	Ile	Ser	Asn	Leu	Ala	Leu	Ala	Cys	Gln	Cys	Cys	Asn	Gln		
			180					185					190				
Lys	Lys	Ala	Ala	Leu	Pro	Val	Glu	Met	Phe	Leu	Ala	Lys	Lys	Pro	Glu		
		195					200					205					
Leu	Leu	Lys	Arg	Ile	Leu	Ala	Gln	Ala	Lys	Arg	Pro	Leu	Lys	Asp	Ala		
	210					215					220						

Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu Lys Ala
225 230 235 240

Thr Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Gln Thr Lys Phe Asn
245 250 255

Arg Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys
260 265 270

Val Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala
275 280 285

Ile Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys
290 295 300

Phe Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly
305 310 315 320

Phe Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys
325 330 335

Ile Gly Ser Tyr Thr Gly Arg Val Ser Val Arg Ala Thr Gly Ser Phe
340 345 350

Asn Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr
355 360 365

Cys Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala
370 375 380

Lys Thr Asp Val Thr Gly Thr Pro Pro Gln His Arg Asp Ala Ser His
385 390 395 400

Pro Ala Leu Tyr Leu Pro Gly Leu Lys Ala Glu Val Ser Arg Glu Lys
405 410 415

<210> 237

<211> 438

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-189 effector

<400> 237

Glu Arg Gly Arg Ala Cys Val His Leu Val Met Pro Phe Thr Ile Arg
1 5 10 15

Ile Val Asp Leu Lys Ala Glu Asn Cys Ala Phe Gln Ala Leu Arg Val
20 25 30

Lys Leu Asp Pro Gly Ser Lys Ala Thr Gly Ile Ala Leu Val Arg Glu
35 40 45

Thr Glu Gly Lys Gly Val Ala Val Val Asn Leu Phe Glu Leu Val His
50 55 60

Arg Gly Arg Gln Ile Ser Glu Ala Leu Thr Ala Arg Arg Gly Asn Arg
65 70 75 80

Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg Pro Pro Arg Phe Asn Asn
85 90 95

Arg Gly Asn Lys Gln Arg Gly Trp Leu Ala Pro Ser Leu Gln His Arg
100 105 110

Val Asp Thr Ser Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro
115 120 125

Val Ser Ala Ser Ser Ser Glu Leu Val Arg Phe Asp Ala Gln Ala Leu
130 135 140

Glu Asn Pro Glu Ile Glu Gly Ala Gln Tyr Gln Gln Gly Thr Leu Ala
145 150 155 160

Val Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Asp Arg Thr Cys
165 170 175

Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu Gln Ile Glu His Ile Arg
180 185 190

Gln Lys Ser Lys Asn Gly Ser Asp Arg Ile Asn Asn Leu Thr Leu Ala
195 200 205

Cys Gln Cys Cys Asn Gln Lys Lys Ala Ala Leu Pro Val Glu Met Phe
210 215 220

Leu Ala Lys Lys Pro Glu Leu Leu Lys Arg Ile Leu Ala Gln Ala Lys
225 230 235 240

Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu
245 250 255

Val Asn Thr Leu Lys Thr Thr Gly Leu Val Val Glu Thr Gly Thr Gly
260 265 270

Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro Lys Thr His
275 280 285

Ala Leu Asp Ala Ala Cys Val Gly Glu Val Gly Ser Ile Thr Asp Trp
290 295 300

Gln Lys Pro Thr Leu Ala Ile Lys Ala Met Gly Arg Gly Arg Tyr Gln
305 310 315 320

Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu Ile Arg
325 330 335

Ser Lys Ser Ile Lys Gly Phe Gln Thr Gly Asp Met Val Lys Ala Glu
340 345 350

Val Thr Thr Gly Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val Ala Val
355 360 365

Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr Ser Ala Gly Leu Val Gln
370 375 380

Gly Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly Asn Gly Tyr

Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
85 90 95

Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Met Leu Thr Arg Thr Gly
100 105 110

Val Pro Val Glu Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Thr
115 120 125

Arg Met Gly Ile Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys Ala Gly
130 135 140

Thr Val Asp Gln Val Leu Gly Trp Asp Arg Pro Ile Gln Arg Val Asp
145 150 155 160

Cys Leu Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Lys Asp Gly
165 170 175

Phe Pro Arg Gly Tyr Leu Pro Arg Thr Lys Met Val Gln Gly Phe Arg
180 185 190

Thr Gly Asp His Val Arg Ala Ile Val Glu Thr Gly Ala His Arg Gly
195 200 205

Thr Trp Thr Gly Arg Val Ala Val Arg Ser Thr Gly Ser Phe Asn Ile
210 215 220

Gln Thr Gly Ala Ala Thr Ile Gln Gly Ile Ala Ala Arg Trp Cys Val
225 230 235 240

Leu Leu Gln Arg Gly Asp Gly Tyr Arg Tyr Ser Leu Ala Leu Pro Arg
245 250 255

Thr Glu His Ala Ile Arg Pro Ser Ser Val Ala
260 265

<210> 239

<211> 346

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-191 effector

<400> 239

Phe Asp Asn Arg Gly Asn Lys Gln Arg Gly Trp Leu Ala Pro Ser Leu
1 5 10 15

Gln His Arg Val Asp Thr Ser Met Ala Trp Val Ser Arg Ile Gln Arg
20 25 30

Leu Ala Pro Val Ser Ala Ile Ser Thr Glu Leu Val Arg Phe Asp Met
35 40 45

Gln Ala Met Glu Asn Pro Glu Ile Glu Gly Ala Gln Tyr Gln Gln Gly
50 55 60

Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Asp
65 70 75 80

Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu Gln Ile Glu
85 90 95

His Ile His Pro Lys Ser Lys Asn Gly Ser Asp Arg Ile Asn Asn Leu
100 105 110

Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys Lys Ala Ala Leu Pro Val
115 120 125

Glu Met Phe Leu Ala Lys Lys Pro Glu Leu Leu Lys Arg Ile Leu Ala
130 135 140

Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg
145 150 155 160

Trp Ala Leu Val Asn Thr Leu Lys Thr Thr Gly Leu Val Val Glu Thr
165 170 175

Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro
180 185 190

Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Phe Gly Ser Ile
195 200 205

Thr Asp Trp Gln Lys Pro Thr Leu Ser Ile Lys Ala Met Gly Arg Gly
210 215 220

Ser Cys Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr
225 230 235 240

Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe Gln Thr Gly Asp Met Val
245 250 255

Lys Ala Glu Val Thr Thr Gly Lys Lys Ile Gly Ser Tyr Thr Gly Arg
260 265 270

Val Ala Val Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr Ser Thr Gly
275 280 285

Leu Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly
290 295 300

Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys Thr Asp Val Arg Gly Thr
305 310 315 320

Pro Pro Gln His Arg Asp Ala Ser His Pro Ala Leu Tyr Leu Pro Gly
325 330 335

Leu Lys Ala Glu Val Ser Arg Ala Asn Arg
340 345

<210> 240

<211> 346

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-192 effector

<400> 240

Phe Gly Ala Glu Leu Thr His Arg Gly Gln Thr Ile Lys Ala Ser Leu
1 5 10 15

Glu Ser Arg Arg Ser Leu Arg Arg Gly Arg Arg Asn Arg His Thr Arg
 20 25 30

Tyr Arg Gln Ala Arg Phe Leu Asn Arg Thr Arg Lys Lys Gly Trp Leu
 35 40 45

Ala Pro Ser Leu Gln His Arg Val Glu Thr Thr Leu Thr Trp Val Glu
 50 55 60

Lys Leu Arg Arg Leu Ala Pro Ile Gly Leu Ile Val Gln Glu Leu Val
65 70 75 80

Arg Phe Asp Leu Gln Gln Leu Glu Asn Pro Glu Ile Ser Ala Ile Glu
 85 90 95

Tyr His Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Gln Tyr Leu Leu
 100 105 110

Asn Lys Trp Asn Arg Lys Cys Ala Tyr Cys Asp Ala Glu Asn Val Pro
 115 120 125

Leu Gln Val Glu His Ile His Pro Lys Ser Gln Gly Gly Ser Asn Arg
 130 135 140

Ile Ser Asn Leu Cys Leu Ala Cys Gln Lys Cys Asn Gln Lys Lys Gly
145 150 155 160

Thr Gln Asn Ile Glu Gln Phe Leu Ala Lys Lys Pro Asp Ile Leu Ser
 165 170 175

Arg Ile Leu Thr Gln Ser Lys Arg Pro Leu Lys Asp Ala Ala Ala Val
 180 185 190

Asn Ser Thr Arg Trp Thr Leu Phe Gly Arg Leu Lys Glu Thr Gly Leu
 195 200 205

Pro Val Leu Thr Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Ser Arg
210 215 220

Leu Gln Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly Gln
225 230 235 240

Val Glu Ala Leu Glu Leu Leu Thr Asn Lys Pro Leu Leu Ile Lys Ala
245 250 255

Thr Gly His Gly Thr Arg Gln Met Cys Arg Thr Asp Lys Phe Gly Phe
260 265 270

Pro Ser Arg Tyr Val Pro Arg Asn Lys Phe Val Lys Gly Phe Gln Thr
275 280 285

Gly Asp Ile Val Lys Ala Ile Val Ile Ser Gly Lys Lys Ile Gly Glu
290 295 300

Tyr Val Gly Arg Val Ala Val Arg Thr Thr Gly Ser Phe Asn Ile Ser
305 310 315 320

Ala Ser Glu Leu Val Gln Gly Ile Ser His Lys Tyr Cys Lys Ile Val
325 330 335

His Lys Lys Asp Gly Tyr Ser Tyr Ala Tyr
340 345

<210> 241

<211> 82

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-193 effector

<400> 241

Phe Thr Ile Ile Leu Thr Glu Arg Glu Asp Gly Glu Thr Gln Glu Val

1	5	10	15												
Glu	Leu	Lys	Val	Asp	Pro	Gly	Ser	Lys	Thr	Ser	Gly	Met	Ala	Leu	Val
		20						25					30		
Ala	Thr	Cys	Lys	Arg	Gly	Lys	Lys	Val	Ile	Phe	Ala	Ala	Asn	Leu	Glu
		35					40					45			
His	Arg	Gly	His	Thr	Ile	Lys	Lys	Val	Ala	Arg	Phe	Gln	Thr	Arg	Cys
	50					55					60				
Lys	Thr	Ser	Lys	Lys	Val	Gln	Lys	Asn	Thr	Leu	Gln	Gly	Ala	Ser	Val
65					70					75					80

Phe Lys

<210> 242
 <211> 407
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-194 effector

<400>	242														
Phe	Thr	Ile	Arg	Leu	Ile	Asp	Arg	Ala	Val	Ala	Gln	Ser	Glu	Leu	Gln
1				5					10					15	

Pro	Leu	Glu	Leu	Lys	Ile	Asp	Pro	Gly	Arg	Lys	Thr	Ser	Gly	Leu	Ala
		20						25					30		

Leu	Val	Arg	Asn	Arg	Asn	Thr	Val	Asn	Ala	Glu	Thr	Gly	Glu	Ile	Thr
		35					40					45			

Ala	Thr	Thr	His	Val	Leu	Asn	Leu	Phe	Glu	Leu	Ile	His	Arg	Gly	Val
	50					55					60				

Gln Ile Ser His Ala Leu Thr Ala Arg Arg Gln Met Arg Arg Arg Arg
65 70 75 80

Arg Ser Ala Asn Leu Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Lys
85 90 95

Asn Lys Gly Lys Gly Trp Leu Ala Pro Ser Leu Gln His Arg Ile Asp
100 105 110

Thr Thr Leu Ser Trp Val Ala Arg Leu Arg Asn Val Ala Pro Ile Thr
115 120 125

His Leu Ala Gln Glu Leu Val Arg Phe Asp Met Gln Gln Leu Glu Asn
130 135 140

Pro Glu Ile Ala Gly Val Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr
145 150 155 160

Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Arg Arg Gln Cys Ala Tyr
165 170 175

Cys Asp Ala Ser Thr Val Pro Leu Gln Ile Asp His Ile His Pro Lys
180 185 190

Ala Arg Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu Ala Cys Ala
195 200 205

Pro Cys Asn Leu Arg Lys Ala Ala Gln Asp Val Thr Gln Phe Leu Glu
210 215 220

Lys Asp Pro Lys Arg Leu Ala Lys Ile Gln Ala Gln Ala Lys Arg Pro
225 230 235 240

Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg Trp Lys Leu Leu Asn
245 250 255

Ala Leu Lys Ala Thr Gly Leu Thr Asn Arg Thr Gly Ser Gly Gly Leu
260 265 270

Thr Lys Phe Asn Arg Ser Arg Leu Val Ile Pro Lys Thr His Ala Leu

275

280

285

Asp Ala Val Cys Val Gly Glu Val Asp Phe Val Glu Gln Trp Gln Lys
 290 295 300

Pro Thr Leu Glu Ile Lys Ala Thr Gly Arg Gly Ser Tyr Gln Arg Thr
 305 310 315 320

Arg Leu Asn Arg Phe Gly Phe Pro Arg Gly Tyr Leu Thr Arg Gln Lys
 325 330 335

Arg Thr Gln Gly Phe Gln Thr Gly Asp Met Val Lys Ala Ile Val Thr
 340 345 350

Lys Gly Lys Lys Val Gly Thr Tyr Val Gly Arg Val Ala Val Arg Ala
 355 360 365

Ser Gly Ser Phe Asn Ile Gln Ser Ala Glu Gly Leu Val Gln Gly Ile
 370 375 380

Ser His Arg Tyr Cys Thr Leu Ile Gln Arg Ser Asp Gly Tyr Gly Tyr
 385 390 395 400

Ser Thr Arg Ile Asp Ser Phe
 405

<210> 243

<211> 134

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-195 effector

<400> 243

Gly Gln Thr Lys Phe Asn Arg Asn Arg Leu Gly Leu Pro Lys Ser His
 1 5 10 15

Trp Leu Asp Ala Ala Cys Val Gly Asn Ile Glu Ala Glu Ala Leu Phe
20 25 30

Val Leu Ile Ser Lys Pro Leu Leu Ile Val Ala Thr Gly His Gly Arg
35 40 45

Arg Gln Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Thr Arg His Lys
50 55 60

Ser Arg Val Gln Ile His Lys Gly Phe Gly Thr Gly Asp Ile Val Ser
65 70 75 80

Pro Thr Val Thr Ala Gly Lys Lys Val Gly Tyr Tyr Val Gly Arg Val
85 90 95

Leu Cys Arg Ala Ser Gly Ser Phe Asp Ile Ala Thr Lys Thr Gly Arg
100 105 110

Val Ala Gly Ile Ser His Lys Tyr Cys Ser Pro Ile His Lys Lys Asp
115 120 125

Gly Tyr Ser Tyr Ala Phe
130

<210> 244

<211> 79

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-196 effector

<400> 244

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
1 5 10 15

Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys

20

25

30

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Gln Val Ala Lys
 35 40 45

Met Asp Val Thr Gly Thr Pro Pro Gln His Arg Asp Ala Ser His Pro
 50 55 60

Ala Leu Tyr Leu Pro Gly Leu Lys Ala Glu Val Ser Arg Ala Asn
 65 70 75

<210> 245

<211> 269

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-197 effector

<400> 245

Gly Val Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu
 1 5 10 15

Tyr Leu Leu Glu Lys Trp Gly Arg Thr Cys Val Tyr Cys Asp His Thr
 20 25 30

Asp Arg Pro Leu Gln Val Glu His Leu Thr Pro Thr Gly Ser Gly Gly
 35 40 45

Ser Asp Gln Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala
 50 55 60

Ala Lys Gly Asn Gln Thr Val Glu Val Tyr Leu Ala Asp Asp Pro Val
 65 70 75 80

Arg Arg Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala
 85 90 95

Ala Ala Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Met Leu Thr Arg
100 105 110

Thr Gly Val Pro Val Glu Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn
115 120 125

Arg Thr Arg Met Gly Ile Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys
130 135 140

Ala Gly Thr Val Asp Gln Val Leu Gly Trp Asp Arg Pro Ile Gln Arg
145 150 155 160

Val Asp Cys Leu Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Lys
165 170 175

Asp Gly Phe Pro Arg Gly Tyr Leu Pro Arg Thr Lys Met Val Gln Gly
180 185 190

Phe Arg Thr Gly Asp His Val Arg Ala Ile Val Glu Thr Gly Ala His
195 200 205

Arg Gly Thr Trp Thr Gly Arg Val Ala Val Arg Ser Thr Gly Ser Phe
210 215 220

Asn Ile Gln Thr Gly Ala Ala Thr Ile Gln Gly Ile Ala Ala Arg Trp
225 230 235 240

Cys Val Leu Leu Gln Arg Gly Asp Gly Tyr Arg Tyr Ser Leu Ala Leu
245 250 255

Pro Arg Thr Glu His Ala Ile Arg Pro Ser Ser Val Ala
260 265

<210> 246

<211> 387

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-198 effector

<400> 246

Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala Val Val Asn
1 5 10 15

Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu Ala Leu Thr
20 25 30

Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg
35 40 45

Pro Pro Arg Phe Asp Asn Arg Gly Asn Lys Gln Arg Gly Trp Leu Ala
50 55 60

Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp Val Ser Arg
65 70 75 80

Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu Leu Val Arg
85 90 95

Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly Ala Gln Tyr
100 105 110

Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu
115 120 125

Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu
130 135 140

Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser Asp Arg Ile
145 150 155 160

Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys Lys Ala Ala
165 170 175

Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu Leu Lys Arg
180 185 190

Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn
195 200 205

Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr Gly Leu Val
210 215 220

Val Glu Thr Ala Ser Gly Gly Gln Thr Lys Phe Asn Arg Asn Gln Leu
225 230 235 240

Gly Ile Pro Lys Thr His Ala Leu Asp Ala Val Cys Val Gly Glu Val
245 250 255

Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile Lys Ala Met
260 265 270

Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val
275 280 285

Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe Gln Thr Gly
290 295 300

Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile Gly Ser Tyr
305 310 315 320

Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr
325 330 335

Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val
340 345 350

Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys Met Asp Val
355 360 365

Thr Gly Thr Pro Pro Gln Arg Arg Asp Ala Ser Ser Arg Ala Leu Pro
370 375 380

Pro Pro Asp
385

<210> 247

<211> 382
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-199 effector

<400> 247

Ile Asp Pro Gly Ser Lys Thr Ser Gly Leu Ala Leu Val Arg Asn Asn
1 5 10 15

Asn Thr Val Asn Ala Glu Thr Gly Glu Ile Thr Ala Thr Ala His Val
20 25 30

Leu Asn Leu Phe Glu Leu Ile His Arg Gly Ala Gln Ile Ser His Ala
35 40 45

Leu Thr Ala Arg Arg Gln Met Arg Arg Arg Arg Arg Ser Ala Asn Leu
50 55 60

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Lys Asn Lys Gly Lys Gly
65 70 75 80

Trp Leu Ala Pro Ser Leu Gln His Arg Ile Asp Thr Thr Leu Ser Trp
85 90 95

Val Ala Arg Ile Arg Asn Val Ala Pro Val Thr His Leu Thr Gln Glu
100 105 110

Leu Val Arg Phe Asp Met Gln Gln Leu Glu Asn Pro Glu Ile Ala Gly
115 120 125

Val Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr
130 135 140

Leu Leu Glu Lys Trp Gln Arg Gln Cys Ala Tyr Cys Asp Val Ser Glu
145 150 155 160

Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ala Cys Gly Gly Ser
165 170 175

Asn Arg Val Ser Asn Leu Ala Leu Ala Cys Ala Pro Cys Asn Leu Lys
180 185 190

Lys Ala Ala Gln Asp Ile Ala Leu Phe Leu Ala Lys Asp Pro Lys Arg
195 200 205

Leu Ala Thr Ile Gln Ala Gln Ala Lys Arg Pro Leu Arg Asp Ala Ala
210 215 220

Ala Val Asn Ala Thr Arg Trp Lys Leu Leu Asn Ala Leu Lys Ala Thr
225 230 235 240

Gly Leu Thr Asn Arg Thr Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg
245 250 255

Ser Arg Leu Val Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
260 265 270

Gly Glu Val Asp Phe Val Glu Gln Trp Gln Lys Pro Thr Leu Glu Ile
275 280 285

Lys Ala Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Thr Arg Phe
290 295 300

Gly Phe Pro Arg Gly Tyr Leu Thr Arg Gln Lys Arg Ile His Gly Phe
305 310 315 320

Gln Thr Gly Asp Met Val Lys Ala Ile Val Thr Lys Gly Lys Lys Ile
325 330 335

Gly Thr Tyr Val Gly Arg Val Ala Val Arg Ala Ser Gly Ser Phe Asn
340 345 350

Ile Gln Ser Ala Glu Gly Leu Val Gln Gly Ile Ser His Arg Tyr Cys
355 360 365

Thr Leu Ile Gln Arg Ser Asp Gly Tyr Gly Tyr Ser Thr Arg

370

375

380

<210> 248

<211> 94

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-200 effector

<400> 248

Ile	Glu	Gln	Lys	Ser	Asp	Ser	Leu	Glu	Glu	Phe	Arg	Glu	Ala	Tyr	Gly
1				5				10						15	

Asp	Ala	Ala	Val	Ser	Gln	Leu	Thr	Val	Arg	Pro	His	Leu	Pro	Gln	Tyr
			20					25					30		

Lys	Asp	Met	Asn	Arg	Ile	Met	Pro	Gly	Ala	Val	Met	Asp	Phe	Asp	Gly
		35					40					45			

Ala	Val	Gly	Val	Phe	Gln	Gly	Ser	Ser	Gly	Arg	Asn	Asn	Gly	Thr	Pro
	50					55					60				

Asn	Tyr	Tyr	Asn	Ser	Thr	Lys	Gly	Ala	Arg	Val	Leu	Thr	Lys	Arg	Cys
65					70					75					80

Ala	Leu	Leu	Ala	Lys	Asn	Ile	Gly	Met	Val	Phe	Ile	Pro	Ala
				85					90				

<210> 249

<211> 410

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-201 effector

<400> 249

Ile Leu Thr Pro Cys Lys Pro Ser Met Ala His Lys Leu Leu Thr Ala
1 5 10 15

Gly Lys Ala Ile Val Phe Arg Arg Phe Pro Phe Thr Ile Ile Leu Lys
20 25 30

Lys Thr Val Thr Ala Thr Pro Glu Ser Ile Thr Leu Lys Met Asp Pro
35 40 45

Gly Ser Lys Thr Thr Gly Leu Ala Leu Leu Glu Gly Glu Lys Val Ile
50 55 60

Phe Gly Ala Glu Leu Thr His Arg Gly Gln Thr Ile Lys Ala Ser Leu
65 70 75 80

Asp Ser Arg Arg Ala Leu Arg Arg Gly Arg Arg Ser Arg His Thr Arg
85 90 95

Tyr Arg Gln Ala Arg Phe Leu Asn Arg Thr Arg Lys Glu Gly Trp Leu
100 105 110

Val Pro Ser Leu Gln His Arg Val Glu Thr Thr Leu Thr Trp Val Asn
115 120 125

Lys Leu Arg Arg Leu Ala Pro Ile Ser Leu Ile Val Gln Glu Leu Val
130 135 140

Arg Phe Asp Leu Gln Gln Leu Glu Asn Pro Glu Ile Ser Gly Ile Glu
145 150 155 160

Tyr Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu
165 170 175

Asn Lys Trp Asn Arg Lys Cys Ala Tyr Cys Asp Ala Glu His Val Pro
180 185 190

Leu Gln Val Glu His Ile His Pro Lys Ala Lys Gly Gly Ser Asn Arg

195

200

205

Ile Ser Asn Leu Cys Leu Ala Cys Glu Lys Cys Asn Ile Lys Lys Ser
 210 215 220

Thr Gln Asn Ile Glu Gln Phe Leu Thr Lys Lys Pro Asp Ile Leu Lys
 225 230 235 240

His Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val
 245 250 255

Asn Ser Thr Arg Trp Val Leu Phe Ser Arg Leu Lys Glu Thr Gly Leu
 260 265 270

Pro Val Leu Thr Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Thr Arg
 275 280 285

Leu Lys Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly Gln
 290 295 300

Ile Glu Ser Pro Glu Val Leu Thr Asn Lys Pro Leu Leu Ile Lys Ala
 305 310 315 320

Thr Gly His Gly Thr Arg Gln Met Cys Arg Thr Asp Lys Phe Gly Phe
 325 330 335

Pro Ser Arg Tyr Phe Pro Arg Asn Lys Phe Val Lys Gly Phe Gln Thr
 340 345 350

Gly Asp Ile Val Lys Ala Val Val Thr Ser Gly Lys Lys Ile Gly Glu
 355 360 365

Tyr Val Gly Arg Val Ala Val Arg Ser Thr Gly Ser Phe Asn Ile Ser
 370 375 380

Ala Ser Glu Leu Val Gln Gly Ile Ser His Lys Tyr Cys Lys Thr Val
 385 390 395 400

His His Lys Asp Gly Tyr Ser Tyr Ser Phe
 405 410

<210> 250
<211> 126
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-202 effector

<400> 250
Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Asp
1 5 10 15

Phe Val Glu Gln Trp Gln Lys Pro Thr Leu Ala Ile Lys Ala Thr Gly
20 25 30

Arg Gly Ser Tyr Gln Arg Thr Arg Leu Thr Arg Phe Gly Phe Pro Arg
35 40 45

Gly Ser Leu Thr Arg Gln Lys Arg Ile His Ala Phe Gln Thr Gly Asp
50 55 60

Met Val Lys Ala Ile Val Thr Lys Gly Lys Lys Val Gly Thr Tyr Val
65 70 75 80

Gly Arg Val Ala Val Arg Ala Ser Gly Ser Phe Asn Ile Gln Ser Ala
85 90 95

Glu Gly Leu Val Gln Gly Ile Ser His Arg Tyr Cys Thr Leu Ile Gln
100 105 110

Arg Ser Asp Gly Tyr Gly Tyr Ser Thr Arg Ile Asp Ser Phe
115 120 125

<210> 251
<211> 338
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-203 effector

<400> 251

Ile Arg Asp Ala Leu Thr Ser Arg Arg Gln Leu Arg Arg Ser Arg Arg
1 5 10 15

Asn Arg Lys Thr Arg Tyr Arg Lys Ser Arg Phe Leu Asn Arg Thr Arg
20 25 30

Pro Glu Gly Trp Leu Pro Pro Ser Leu Asn Ser Arg Val Ala Asn Ile
35 40 45

Leu Thr Trp Val Asn Arg Leu Ser Ser Ile Ser Gln Ile Thr Ala Ile
50 55 60

Ser Gln Glu Leu Val Arg Phe Asp Thr Gln Gln Met Glu Asp Ala Glu
65 70 75 80

Ile Ser Gly Ile Gly Tyr Gln Gln Gly Thr Leu Phe Gly Tyr Glu Ile
85 90 95

Arg Glu Phe Leu Leu Glu Lys Trp Asn Arg Thr Cys Ala Tyr Cys Gly
100 105 110

Glu Lys Asp Thr Gln Leu Glu Ile Glu His Ile Asn Ala Arg Ser Lys
115 120 125

Gly Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ala Cys Thr Ser Cys
130 135 140

Asn Gln Lys Lys Gly Asn Gln Asp Ile Lys Asp Phe Leu Lys Gly Lys
145 150 155 160

Pro Asp Leu Leu Lys Cys Ile Leu Ser Gln Ala Lys Arg Pro Leu Ala
165 170 175

Asp Thr Ala Ala Val Asn Ala Thr Arg Trp Asn Leu Tyr Tyr Asn Leu
180 185 190

Lys Lys Thr Gly Leu Pro Val Glu Val Gly Thr Gly Gly Arg Thr Lys
195 200 205

Tyr Asn Arg Thr Ile Arg Gly Leu Asp Lys Thr His Tyr Trp Asp Ala
210 215 220

Ala Cys Val Gly Ala Ser Thr Pro Glu Gln Leu Ile Thr Ser Glu Val
225 230 235 240

Lys Pro Leu Leu Ile Ala Ala Lys Gly His Gly Thr Arg Gln Gln Cys
245 250 255

Arg Thr Asp Arg Phe Gly Phe Pro Ser Arg Tyr Cys Lys Arg Thr Lys
260 265 270

Phe His Lys Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr
275 280 285

Ser Gly Lys Lys Ile Gly Thr Tyr Val Gly Arg Val Ala Thr Arg Ala
290 295 300

Thr Gly Ser Phe Asn Ile Ser Thr Thr Asp Gly Leu Val Gln Gly Ile
305 310 315 320

Ser His Lys Tyr Cys Leu Pro Leu His Lys Lys Asp Gly Tyr Ser Tyr
325 330 335

Ile Gln

<210> 252

<211> 467

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-204 effector

<400> 252

Lys Glu Lys Lys Ala Arg Val Val Ser Arg Thr Pro Phe Thr Ile Arg
1 5 10 15

Leu Asn Tyr Asp Thr Pro Asn Ile Thr Gln Asp Leu Ile Leu Gly Ile
20 25 30

Asp Pro Gly Arg Thr Asn Ile Gly Gly Ala Val Val Lys Glu Asp Gly
35 40 45

Ser Cys Val Phe Ser Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro
50 55 60

Leu Leu Met Lys Lys Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln
65 70 75 80

Asp Arg Arg Arg Lys Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr
85 90 95

Val Glu Ser Asn Thr Val Glu Arg Leu Leu Pro Ser Tyr Glu Lys Pro
100 105 110

Val Val Cys His Tyr Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg
115 120 125

Ser Arg Pro Ala Gly Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln
130 135 140

Thr His Ile Asn Leu Ile Ala Lys Ile Ala Lys Val Leu Pro Ile Thr
145 150 155 160

Lys Val Val Val Glu Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn
165 170 175

Pro Asn Ile Arg Arg Trp Glu Tyr Gln Gln Gly Pro Leu Cys Gly Leu
180 185 190

Gly Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu
195 200 205

Phe Cys Lys Lys Pro Ile Asp His Tyr His His Val Val Pro Arg Arg
210 215 220

Lys Asn Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys
225 230 235 240

His His Ala Leu Val His Thr Asp Lys Ala Trp Ala Asp Lys Leu Val
245 250 255

Thr Arg Lys Glu Gly Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu
260 265 270

Asn Gln Ile Val Pro His Leu Met Glu Tyr Leu Gly Asp Glu Thr Leu
275 280 285

Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile
290 295 300

Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala
305 310 315 320

Cys Ser Ile Leu Asp Thr Asp Thr Lys Val Ser Ala Pro Val Glu Pro
325 330 335

Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys His Gln
340 345 350

Gln Arg Val Asp Arg Lys Tyr Tyr Leu Asn Gly Lys Gln Val Ala Thr
355 360 365

Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe
370 375 380

Arg Glu Ser Tyr Gly Asp Thr Ala Val Ser Gln Leu Ala Val Lys Pro
385 390 395 400

His Ser Pro Gln Tyr Lys Asp Met Thr Arg Ile Met Gln Gly Ala Val

405

410

415

Met Asp Phe Gly Gly Thr Val Gly Val Phe Gln Gly Ser Asp Gly Phe
 420 425 430

His Asn Gly Lys Pro Asp Tyr Tyr Lys Ser Ala Lys Gly Ala Arg Val
 435 440 445

Leu Thr Lys Arg Cys Val Leu Leu Ala Gln Asn Thr Gly Ile Val Phe
 450 455 460

Ile Pro Ala
 465

<210> 253

<211> 467

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-205 effector

<400> 253

Lys Glu Lys Lys Ala Arg Val Val Ser Arg Thr Pro Phe Thr Ile Arg
 1 5 10 15

Leu Asn Tyr Asp Thr Pro Asn Ile Thr Gln Asp Leu Ile Leu Gly Ile
 20 25 30

Asp Pro Gly Arg Thr Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly
 35 40 45

Gln Cys Val Phe Ser Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro
 50 55 60

Leu Leu Met Lys Lys Arg Ala Ala Phe Arg Arg Asn His Arg Thr Leu
 65 70 75 80

Asp Arg Arg Arg Lys Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr
85 90 95

Val Glu Ser Asn Thr Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro
100 105 110

Val Val Cys His Tyr Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg
115 120 125

Ser Arg Pro Ala Gly Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln
130 135 140

Thr His Ile Asn Leu Ile Ala Lys Ile Ala Lys Phe Leu Pro Ile Thr
145 150 155 160

Lys Val Val Val Glu Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn
165 170 175

Pro Asn Ile Arg Arg Trp Glu Tyr Gln Gln Gly Ser Leu Tyr Gly Leu
180 185 190

Gly Ser Val Glu Asp Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu
195 200 205

Phe Cys Lys Glu Pro Ile Asp His Tyr His His Val Val Pro Arg His
210 215 220

Lys Gly Gly Ser Glu Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Arg
225 230 235 240

His His Ala Leu Val His Lys Asp Lys Ala Trp Ala Gly Lys Leu Val
245 250 255

Thr Gln Lys Glu Gly Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu
260 265 270

Asn Gln Ile Ile Pro Ser Leu Met Glu Tyr Leu Gly Asp Glu Met Leu
275 280 285

Tyr Asp Val Tyr Ala Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile

290

295

300

Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala
 305 310 315 320

Cys Ser Ile Leu Asp Thr Asn Ile Lys Val Ser Ala Pro Val Glu Pro
 325 330 335

Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys His Gln
 340 345 350

Gln Arg Val Asp Arg Lys Tyr Tyr Leu Asp Gly Lys Gln Val Ala Thr
 355 360 365

Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asn Ser Leu Glu Glu Phe
 370 375 380

Arg Glu Thr Tyr Gly Asp Ala Ala Val Ser Gln Leu Thr Val Lys Pro
 385 390 395 400

His Pro Pro Gln Tyr Lys Asp Ile Thr Arg Ile Met Pro Gly Ala Val
 405 410 415

Met Asn Phe Cys Gly Ala Val Gly Ile Leu Leu Gly Ser Asp Gly Phe
 420 425 430

His Asn Gly Lys Pro Asp Tyr Tyr Lys Ser Thr Lys Glu Glu Lys Val
 435 440 445

Arg Met Arg Arg Cys Ala Leu Leu Ala Gln Asn Ala Gly Met Val Phe
 450 455 460

Ile Pro Ala
 465

<210> 254

<211> 504

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-206 effector

<400> 254

Lys Gly Lys Gly Ser Lys Val Leu Val Ala Thr His Lys Ser Arg Ser
1 5 10 15

Arg Leu Leu Thr Phe Pro Arg Gly Asp Trp Ser Gln Gly Gln Arg Asn
20 25 30

Lys Ser Arg Lys Gly Glu Gly Phe Glu Met Thr Val Phe Val Leu Asp
35 40 45

Arg Ser Gly Arg Pro Leu Met Pro Cys Thr Glu Lys Arg Ala Arg Leu
50 55 60

Leu Leu Glu Arg Gly Arg Ala Cys Val His Leu Val Met Pro Phe Thr
65 70 75 80

Ile Arg Ile Val Asp Leu Lys Ala Glu Asn Cys Ala Phe Gln Ala Leu
85 90 95

Arg Val Lys Leu Asp Pro Gly Ser Lys Ala Thr Gly Ile Ala Leu Val
100 105 110

Arg Glu Thr Glu Gly Lys Gly Val Ala Val Val Asn Leu Phe Glu Leu
115 120 125

Val His Arg Gly Arg Gln Ile Ser Glu Ala Leu Thr Ala Arg Arg Gly
130 135 140

His Arg Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg Pro Pro Arg Phe
145 150 155 160

Asn Asn Arg Gly Asn Lys Gln Arg Gly Trp Leu Ala Pro Ser Leu Gln
165 170 175

His Arg Val Asp Thr Ser Met Ala Trp Val Ser Arg Ile Gln Arg Leu

180

185

190

Ala Pro Val Ser Ala Ile Ser Thr Glu Leu Val Arg Phe Asp Met Gln
 195 200 205

Ala Met Glu Asn Pro Glu Ile Glu Gly Met Gln Tyr Gln Gln Gly Thr
 210 215 220

Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Lys Arg
 225 230 235 240

Thr Cys Ala Tyr Cys Asp Ala Lys Asp Val Pro Leu Gln Val Glu His
 245 250 255

Ile Gln Pro Lys Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala
 260 265 270

Leu Ala Cys Pro Ser Cys Asn Ser Lys Lys Ala Ala Leu Pro Ile Glu
 275 280 285

Ser Phe Leu Ser Lys Gln Pro Glu Arg Leu Lys Arg Ile Gln Val Gln
 290 295 300

Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp
 305 310 315 320

Ala Leu Val Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Glu Thr Ala
 325 330 335

Ser Gly Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro Lys
 340 345 350

Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Gly Ser Ile Thr
 355 360 365

Asp Trp Gln Lys Pro Thr Leu Val Ile Lys Ala Met Gly Arg Gly Ser
 370 375 380

Tyr Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu
 385 390 395 400

Thr Arg Ser Lys Ser Ile Lys Gly Phe Gln Thr Gly Asp Met Val Gln
405 410 415

Ala Glu Val Thr Lys Gly Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val
420 425 430

Ala Val Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr Ser Thr Gly Leu
435 440 445

Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly Asn
450 455 460

Gly Tyr Gly Tyr Ser Leu Val Ala Lys Thr Asp Val Arg Gly Thr Pro
465 470 475 480

Pro Gln His Arg Asp Ala Ser His Pro Ala Leu Tyr Leu Pro Gly Leu
485 490 495

Lys Ala Glu Val Ser Arg Ala Asn
500

<210> 255

<211> 378

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-207 effector

<400> 255

Lys Ile Asp Pro Gly Ser Lys Thr Thr Gly Leu Ala Leu Val Asn Asp
1 5 10 15

Glu Ser Gly Ala Val Val Phe Ala Ala Asp Leu Ala His Arg Gly Gln
20 25 30

Gln Ile Lys Lys Gly Leu Asp Thr Arg Arg Gly Ala Arg Arg Gly Arg

35

40

45

Arg Gln Arg Lys Thr His Tyr Arg Ala Pro Arg Trp Arg Asn Arg Arg
 50 55 60

Arg Glu Gln Gly Trp Leu Pro Pro Ser Leu Leu Ser Arg Ile Cys Asn
 65 70 75 80

Val Val Thr Trp Val Glu Arg Leu Arg Arg Leu Ala Pro Ile Gln Ala
 85 90 95

Ile Ser Met Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro
 100 105 110

Glu Ile Ser Gly Leu Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu
 115 120 125

Thr Arg Glu Tyr Leu Leu Glu Lys Trp Gln Arg Lys Cys Ala Tyr Cys
 130 135 140

Gly Lys Glu Gly Val Pro Leu Gln Val Glu His Ile Val Pro Arg Ala
 145 150 155 160

Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu Ala Cys Glu Pro
 165 170 175

Cys Asn Thr Lys Lys Gly Thr Leu Asp Leu Pro Ala Phe Leu Lys Lys
 180 185 190

Lys Pro Asp Val Leu Lys Arg Ile Gln Ala Gln Ala Lys Ala Ser Leu
 195 200 205

Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Phe Ala Leu Leu Glu Arg
 210 215 220

Leu Lys Ala Val Gly Leu Pro Ile Glu Cys Gly Ser Gly Gly Arg Thr
 225 230 235 240

Lys Tyr Asn Arg Val Met Arg Asn Leu Pro Lys Thr His Trp Leu Asp
 245 250 255

Ala Ala Cys Val Gly Ala Ser Thr Pro Glu Val Leu Gln Val Ala Gly
260 265 270

Val His Pro Leu Leu Ile Glu Ala Cys Gly His Gly Cys Arg Arg Met
275 280 285

Arg Asn Val Asn Lys Ile Gly Leu Pro Cys Ser Ala Pro Lys Gly Pro
290 295 300

Lys Lys Val Gln Gly Phe Gln Thr Gly Asp Ile Thr Arg Ala Ile Val
305 310 315 320

Thr Thr Gly Lys Lys Gln Gly Ile Tyr Val Gly Arg Val Leu Val Arg
325 330 335

Ala Thr Gly Ser Phe Asp Ile Thr Thr Arg Arg Thr Arg Ile Ala Gly
340 345 350

Leu Asp Val Arg Phe Phe Ser His Leu His Arg Ser Asp Gly Tyr Ser
355 360 365

Tyr Ala Lys Gly Glu Gly Tyr Ala Asn Pro
370 375

<210> 256
<211> 444
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-208 effector

<400> 256
Leu Ala Leu Leu Leu Leu Glu Arg Gly Arg Ala Cys Val His Leu Val
1 5 10 15

Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu Asn Cys Ala

20

25

30

Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys Ala Thr Gly
 35 40 45

Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala Val Val Asn
 50 55 60

Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu Ala Leu Thr
 65 70 75 80

Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg
 85 90 95

Pro Pro Arg Phe Asn Asn Arg Gly Asn Lys Gln Arg Gly Trp Leu Ala
 100 105 110

Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp Val Ser Arg
 115 120 125

Ile Gln Arg Leu Thr Pro Val Ser Ala Ile Ser Thr Glu Leu Val Arg
 130 135 140

Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Asp Gly Ala Gln Tyr
 145 150 155 160

Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu
 165 170 175

Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp Val Pro Leu
 180 185 190

Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser Asp Arg Ile
 195 200 205

Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys Lys Ala Ala
 210 215 220

Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu Leu Lys Arg
 225 230 235 240

Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn
245 250 255

Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr Gly Leu Val
260 265 270

Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe
275 280 285

Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val
290 295 300

Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile Lys Ala Met
305 310 315 320

Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val
325 330 335

Arg Gly Tyr Leu Thr Arg Ser Lys Ile Ile Lys Gly Phe Gln Thr Gly
340 345 350

Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile Gly Ser Tyr
355 360 365

Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr
370 375 380

Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val
385 390 395 400

Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys Thr Asp Val
405 410 415

Arg Gly Thr Pro Pro Gln His Arg Asp Thr Ser His Pro Ala Leu Tyr
420 425 430

Leu Pro Gly Leu Lys Ala Glu Val Ser Arg Ala Asn
435 440

<210> 257

<211> 334
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-209 effector

<400> 257

Leu Arg Arg Ser Lys Leu Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg
1 5 10 15

Gly Asn Lys Gln Arg Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val
20 25 30

Asp Thr Ser Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val
35 40 45

Ser Ala Ile Ser Ile Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu
50 55 60

Asn Pro Glu Ile Glu Gly Ile Gln Tyr Gln Gln Gly Thr Leu Ala Gly
65 70 75 80

Tyr Glu Val Arg Glu Tyr Leu Phe Glu Lys Trp Lys Arg Thr Cys Ala
85 90 95

Tyr Cys Gly Ala Lys Asp Val Pro Leu Gln Val Glu His Ile Gln Pro
100 105 110

Lys Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys
115 120 125

Gln Cys Cys Asn Gln Lys Lys Ala Ala Leu Pro Val Glu Met Phe Leu
130 135 140

Ala Lys Lys Pro Glu Leu Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg
145 150 155 160

Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Val
165 170 175

Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Glu Thr Ala Ser Gly Gly
180 185 190

Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro Lys Thr His Ala
195 200 205

Leu Asp Ala Ala Cys Val Gly Glu Val Gly Ser Ile Thr Asp Trp Gln
210 215 220

Lys Pro Thr Leu Ala Ile Lys Ala Thr Gly Arg Gly Ser Tyr Gln Arg
225 230 235 240

Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser
245 250 255

Lys Ser Ile Lys Gly Phe Gln Thr Gly Asp Met Val Lys Ala Glu Val
260 265 270

Thr Thr Gly Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val Ala Val Arg
275 280 285

Ala Thr Gly Ser Phe Asn Ile Gln Thr Ser Ala Gly Leu Val Gln Gly
290 295 300

Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly Asn Gly Tyr Gly
305 310 315 320

Tyr Ser Leu Val Ala Lys Thr Asp Val Arg Gly Thr Pro Pro
325 330

<210> 258

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-210 effector

<400> 258

Leu Arg Tyr Arg Pro Ala His Phe Asp Asn Arg Thr Arg Lys Ala Gly
1 5 10 15

Trp Leu Pro Pro Ser Val Gln His Arg Leu Asp Thr Thr Phe Ala Leu
20 25 30

Val Gln Lys Leu Lys Arg Arg Cys Pro Ile Ser Ala Ile Val Phe Glu
35 40 45

Gln Val Lys Phe Asp Met Gln Lys Met Gln Asn Pro Asn Ile Gln Gly
50 55 60

Val Glu Tyr Gln His Gly Thr Leu Phe Gln Tyr Glu Val Arg Glu Tyr
65 70 75 80

Leu Leu Glu Lys His Arg His Thr Cys Ala Tyr Cys Gly Gly Glu Ser
85 90 95

Gln Asp Thr Ile Leu Glu Val Glu His Lys His Pro Arg Ala Gln Gly
100 105 110

Val Ser Asn Ser Ile Arg Asn Leu Val Met Ala Cys His Thr Cys Asn
115 120 125

Gln Thr Lys Gly Asn Arg Thr Leu Ser Glu Phe Leu Thr Val Leu Lys
130 135 140

Asn Thr Lys Leu Asp Lys Val Arg Lys Val Asn Ile Thr Gln Ile Leu
145 150 155 160

Ala Gly Lys Val Phe Arg Leu Lys Asp Ala Thr Ala Val Asn Ala Cys
165 170 175

Arg His Gln Leu Gly Lys Thr Leu Leu Thr Leu Ser Leu Pro Val Ser
180 185 190

Thr Gly Thr Gly Ala Gln Thr Lys Tyr Asn Arg Met His Tyr Gln Leu
195 200 205

Pro Lys Ser His Ala Leu Asp Ala Leu Met Thr Gly Asn Met Glu Lys
210 215 220

Pro Ile Glu Ala Trp Asn Lys Pro Thr Leu Ile Val Lys Ala Met Gly
225 230 235 240

Arg Gly Cys Tyr Gln Arg Thr Arg Leu Asn Gln Tyr Gly Phe Pro Arg
245 250 255

Gly Tyr Leu Gln Arg Lys Lys Thr Tyr Phe Gly Phe Gln Thr Gly Asp
260 265 270

Leu Val Val Ser Thr Val Leu Lys Gly Lys Lys Ile Gly Thr Tyr Ile
275 280 285

Gly Arg Leu Ala Val Arg Asp Ser Gly Tyr Phe Asn Ile Gln Thr Pro
290 295 300

Ala Gly Val Ile Gln Gly Ile Ser His Lys Thr Cys Arg Leu Ile Gln
305 310 315 320

Arg Asn Thr Gly Tyr His Tyr Tyr Phe Asn Gln Lys Ile Ala Asn
325 330 335

<210> 259

<211> 365

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-211 effector

<400> 259

Leu Thr Phe Pro Met Gly Asp Ser Pro Pro Leu Lys Ala Val Tyr Gly

1	5	10	15
Thr Arg Pro Val Arg Ala Glu Gly Phe Glu Met Gly Val Phe Val Leu	20	25	30
Asp Lys Arg Gly Lys Pro Leu Met Gln Cys Ser Glu Lys Arg Ala Arg	35	40	45
Leu Leu Leu Asp Arg Gly Arg Ala Arg Ile His Lys Met Leu Pro Phe	50	55	60
Thr Ile Arg Val Val Asp Arg Leu Val Glu Asp Ser Gln Leu Gln Pro	65	70	75
Leu Glu Ile Lys Leu Asp Pro Gly Ser Lys Thr Thr Gly Val Ala Val	85	90	95
Val Arg Ile Ser Val Ala Val Asp Ala Gln Thr Gly Glu Val Gln Lys	100	105	110
His Val His Val Leu Asn Leu Phe Glu Leu Ile His Arg Ser Arg Gln	115	120	125
Ile Thr Glu Ala Leu Ile Gly Arg Arg Gly His Arg Arg Leu Arg Arg	130	135	140
Ser Lys Leu Arg Tyr Arg Ala Pro Arg Phe Asp Asn Arg Gly Asn Gln	145	150	155
Lys Lys Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser	165	170	175
Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile	180	185	190
Ser Thr Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu	195	200	205
Ile Glu Gly Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val	210	215	220

Arg Glu Tyr Leu Leu Glu Lys Trp Lys Arg Thr Cys Ala Tyr Cys Asp
225 230 235 240

Ala Lys Asp Val Pro Leu Gln Val Glu His Ile Gln Pro Lys Ala Lys
245 250 255

Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys Pro Ser Cys
260 265 270

Asn Ser Lys Lys Ala Ala Leu Pro Ile Glu Ser Phe Leu Ser Lys Gln
275 280 285

Pro Glu Arg Leu Lys Arg Ile Gln Val Gln Ala Lys Arg Pro Leu Lys
290 295 300

Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu
305 310 315 320

Lys Ala Thr Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Gln Thr Lys
325 330 335

Phe Asn Arg Asn Lys Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala
340 345 350

Val Cys Val Gly Glu Val Gly Ser Ile Thr Asp Trp Gln
355 360 365

<210> 260

<211> 87

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-212 effector

<400> 260

Met Ala Cys Thr Pro Cys Asn Ile Asp Pro Gly Asn Arg Asp Ile Lys

1	5	10	15
Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys Lys Ile Gln Thr Gln	20	25	30
Ser Lys Ala Pro Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr	35	40	45
Ala Thr Gly Asn Ala Leu Lys Ser Phe Gly Leu Pro Ile Ala Phe Ser	50	55	60
Ser Gly Gly Arg Thr Lys Phe Asn Arg Ile Lys Leu Gly Tyr Ser Lys	65	70	75
Asp His Trp Ile Asp Ala Ala	85		

<210> 261
 <211> 88
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-213 effector

<400> 261
Met Ala Cys Thr Pro Cys Asn Ile Asp Pro Gly Asn Arg Asp Ile Lys
1 5 10 15

Glu Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys Lys Ile Gln Thr Gln	20	25	30

Ser Lys Ala Pro Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr	35	40	45

Ala Thr Gly Asn Ala Leu Lys Ser Phe Gly Leu Pro Ile Ala Phe Ser	50	55	60

Ser Gly Gly Arg Thr Lys Phe Asn Arg Ile Lys Leu Gly Tyr Ser Lys
65 70 75 80

Asp His Trp Ile Asp Ala Ala Trp
85

<210> 262
<211> 423
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-214 effector

<400> 262
Met Ala His Asn Lys Gln Pro Leu Met Pro Cys His Pro Ala Arg Ala
1 5 10 15

Arg Lys Leu Leu Lys Lys Gly Lys Ala Ala Val Tyr Arg Arg Tyr Pro
20 25 30

Phe Thr Ile Ile Met Thr His Arg Leu Cys Gly Asp Leu Gln Pro Ile
35 40 45

Glu Ile Lys Phe Asp Pro Gly Ser Arg Thr Thr Gly Ile Ala Leu Val
50 55 60

Gly His Phe Asp Arg Gly Ser Glu Val Ile Trp Ala Gly Asn Leu Asn
65 70 75 80

His Arg Gly Leu Gln Val Lys Ser Asn Leu Val Ser Arg Arg Ala Ile
85 90 95

Arg Arg Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Pro Ala Arg Phe
100 105 110

Leu Asn Arg Arg Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Arg Ser

115

120

125

Arg Val Leu Asn Val Lys Asn Trp Met Leu Lys Leu Ser Arg Leu Ala
 130 135 140

Pro Leu Thr Gln Ile Ala Ile Glu Thr Val Arg Phe Asp Thr Gln Lys
 145 150 155 160

Met Gln Lys Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Glu Leu
 165 170 175

Val Gly Tyr Glu Leu Arg Glu Tyr Leu Leu Glu Lys Trp Asp Arg Gln
 180 185 190

Cys Ala Tyr Cys Gly Ala Lys Asn Val Pro Leu Glu Ile Glu His Ile
 195 200 205

Gln Ala Ser Ser Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu
 210 215 220

Ala Cys Ser Pro Cys Asn Phe Asp Lys Gly Asn Lys Asp Ile Lys Glu
 225 230 235 240

Phe Leu Lys Arg Lys Pro Lys Arg Leu Lys Lys Ile Gln Ala Gln Ala
 245 250 255

Lys Ala Ser Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr Ala
 260 265 270

Thr Gly Asn Ile Leu Lys Cys Phe Gly Leu Pro Ile Thr Phe Ser Ser
 275 280 285

Gly Gly Arg Thr Lys Phe Asn Arg Leu Lys Leu Gly Tyr Ser Lys Asp
 290 295 300

His Trp Ile Asp Ala Ala Cys Val Gly Glu Ser Gly Ser His Val Val
 305 310 315 320

Ile Pro Lys Thr Ile Thr Pro Leu Ile Ile Thr Ala Lys Gly Arg Gly
 325 330 335

Ser Arg Gln Lys Cys Arg Met Asn Gln Tyr Gly Phe Pro Arg Thr Gly
340 345 350

Pro Lys Lys Gln Lys Arg Val Lys Gly Phe Gln Thr Gly Asp Ile Val
355 360 365

Lys Ala Val Val Thr Lys Gly Lys Lys Ile Gly Thr Tyr Ile Gly Arg
370 375 380

Val Val Val Arg Ala Lys Gly Ser Phe Asp Ile Gly Ser Gly Glu Glu
385 390 395 400

Lys Val Gly Gly Ile Ser Tyr Lys Tyr Cys Gln Leu Leu Gln Arg Ser
405 410 415

Asp Gly Tyr Glu Tyr Leu Lys
420

<210> 263

<211> 185

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-215 effector

<400> 263

Met Ala Lys Asp Pro Lys Arg Val Ala Thr Ile Arg Ala Gln Ala Lys
1 5 10 15

Arg Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg Trp Lys Leu
20 25 30

Leu Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Arg Thr Gly Ser Gly
35 40 45

Gly Leu Thr Lys Cys Asn Arg Ser Arg Leu Ala Ile Pro Lys Thr His

50

55

60

Ala Leu Asp Ala Val Cys Ile Gly Glu Val Asp Gln Val Glu Gln Trp
65 70 75 80

Gln Lys Pro Thr Leu Ala Ile Asn Ala Thr Gly Arg Gly Ser Tyr Gln
85 90 95

Arg Thr Arg Leu Asn Arg Phe Gly Phe Pro Arg Gly Tyr Leu Thr Arg
100 105 110

Gln Lys Arg Ile His Gly Phe Gln Thr Gly Asp Arg Val Lys Ala Met
115 120 125

Val Thr Lys Gly Lys Lys Leu Gly Ala Tyr Met Gly Arg Val Ala Val
130 135 140

Arg Ala Ser Gly Ser Phe Asn Ile Gln Ser Ala Glu Gly Leu Val Gln
145 150 155 160

Gly Ile Ser His Arg Tyr Cys Thr Leu Ile Gln Arg Ser Asp Gly Tyr
165 170 175

Gly Tyr Ser Leu Arg Ser Glu Ser Asn
180 185

<210> 264

<211> 185

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-216 effector

<400> 264

Met Ala Lys Lys Pro Glu Leu Leu Lys Arg Ile Leu Ala Gln Ala Lys
1 5 10 15

Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu
20 25 30

Val Asn Thr Leu Lys Thr Thr Gly Leu Val Val Glu Thr Gly Thr Gly
35 40 45

Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro Lys Thr His
50 55 60

Ala Leu Asp Ala Ala Cys Val Gly Glu Val Gly Ser Ile Thr Asp Trp
65 70 75 80

Gln Lys Pro Thr Leu Ala Ile Lys Ala Met Gly Arg Gly Ser Tyr Gln
85 90 95

Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu Thr Arg
100 105 110

Ser Lys Ser Ile Lys Gly Phe Gln Thr Gly Asp Met Val Lys Ala Ile
115 120 125

Val Leu Lys Gly Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val Ala Val
130 135 140

Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr Ser Thr Gly Leu Val Gln
145 150 155 160

Gly Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly Asn Gly Tyr
165 170 175

Gly Tyr Ser Leu Val Ala Lys Arg Thr
180 185

<210> 265

<211> 315

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-217 effector

<400> 265

Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Phe Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Lys Lys
85 90 95

Arg Ala Ala Phe Arg Arg Ser His Arg Thr Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Met Ala Ala Gly Thr Thr Val Glu Asn Glu Thr
115 120 125

Ile Glu Arg Leu Leu Pro Cys Tyr Lys Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Lys Arg Pro Lys Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Val Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Thr Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Lys Asp Lys Ala Trp Thr Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Pro Leu Ser Leu Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Val Glu His Ile Gly Ser Asp Pro Pro
305 310 315

<210> 266
<211> 494
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-218 effector

<400> 266
Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Lys Lys Ala

20

25

30

Arg Val Val Ser Arg Thr Pro Phe Thr Ile Arg Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Val Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Thr Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
 85 90 95

Arg Ala Asp Phe Arg Arg Gln His Arg Thr Leu Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Thr Ile Ala Glu Gly Ser
 115 120 125

Val Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
 130 135 140

Ile Arg Asn Lys Lys Ala Arg Phe Asn Asn Arg Cys Arg Pro Gln Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
 165 170 175

Ile Ala Lys Ile Ala Lys Phe Leu Pro Leu Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Val Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Glu Thr Pro
 225 230 235 240

Ile Glu Arg Tyr His His Val Ile Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Val Asn Arg Cys Gly Leu Cys Ala Lys His His Asp Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Thr Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Glu Lys Thr Ser Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Thr Asp Ile Glu Val Ser Ser Pro Val Gly Phe Phe Glu Met Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys His Gln Gln Arg Val Asp Arg
370 375 380

Lys Tyr Tyr Leu Asn Gly Lys Lys Val Ala Thr Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Ala Glu Phe Arg Val Thr Tyr Gly
405 410 415

Asp Thr Ala Val Ser Gln Leu Ser Val Lys Pro His Ser Pro Gln Tyr
420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Asp Phe Gly Gly
435 440 445

Thr Val Gly Val Phe Gln Gly Ser Tyr Gly Phe His Ser Gly Lys Pro

450

455

460

Asp Tyr Tyr Lys Ser Thr Lys Gly Ala Lys Asp Leu Thr Lys Arg Cys
 465 470 475 480

Ala Leu Leu Ala Gln Asn Ala Gly Met Val Phe Ile Pro Ala
 485 490

<210> 267

<211> 494

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-219 effector

<400> 267

Met Ala Met Val Tyr Val Gln Asn Lys Asp Gly Lys Pro Leu Met Pro
 1 5 10 15

Thr Thr Arg Tyr Cys Tyr Val Arg Leu Leu Leu Lys Glu Asn Lys Ala
 20 25 30

Arg Val Val Ser Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Gln Lys
 85 90 95

Arg Ala Gly Phe Arg Lys Gln His Arg Thr Leu Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Lys Val Ala Gly Thr Thr Val Glu Gly Glu Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
165 170 175

Ile Ala Lys Val Ala Lys Phe Leu Pro Ile Thr Lys Val Val Val Glu
180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
195 200 205

Trp Glu Tyr Gln Gln Gly Pro Leu Tyr Gly Leu Gly Ser Val Glu Asp
210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly Arg Cys Leu Phe Cys Lys Lys Pro
225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Arg Glu His His Ala Leu Val
260 265 270

His Thr Asp Lys Val Trp Ala Asp Lys Leu Val Thr Arg Lys Glu Gly
275 280 285

Val Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

His Leu Met Glu Tyr Leu Gly Ser Glu Thr Arg Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Arg Ser Thr Lys Gly Phe Arg Val Ala Lys Asn Val Pro

325

330

335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
 340 345 350

Thr Asp Ile Glu Val Ser Thr Pro Val Glu Pro Phe Glu Leu Lys Gln
 355 360 365

Phe Arg Arg His Asp Arg Gln Ala Cys His Gln Gln Arg Val Asp Arg
 370 375 380

Lys Tyr Tyr Leu Asn Gly Lys Gln Val Ala Thr Asn Arg His Lys Ala
 385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Gln Glu Phe Arg Glu Ser Tyr Gly
 405 410 415

Asp Thr Ala Val Ser Gln Leu Ala Val Lys Pro His Ser Pro Gln Tyr
 420 425 430

Lys Asp Met Thr Arg Ile Met Gln Gly Ser Val Met Asp Phe Gly Gly
 435 440 445

Thr Val Gly Val Phe Gln Gly Ser Asp Gly Phe His Asn Gly Lys Pro
 450 455 460

Asp Tyr Tyr Lys Ser Ala Lys Gly Ala Arg Val Leu Thr Lys Arg Cys
 465 470 475 480

Val Leu Leu Ala Gln Asn Thr Gly Ile Val Phe Ile Pro Ala
 485 490

<210> 268

<211> 83

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-220 effector

<400> 268

Met Ala Arg Lys Leu Leu Asn Ala Gly Lys Ala Ala Val Phe Arg Arg
1 5 10 15

Phe Pro Phe Thr Ile Ile Leu Lys Lys Glu Val Glu Val Thr Pro Lys
20 25 30

Ser Ile Thr Leu Lys Leu Asp Pro Gly Ser Lys Thr Thr Gly Ile Ala
35 40 45

Leu Lys Gln Gly Asp Lys Ile Ile Phe Gly Ala Glu Leu Thr His Arg
50 55 60

Gly Gln Ala Ile Lys Ala Ser Leu Glu Ser Arg Arg Ser Leu Arg Arg
65 70 75 80

Ser Arg Arg

<210> 269

<211> 402

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-221 effector

<400> 269

Met Ala Arg Lys Leu Leu Thr Ala Gly Lys Ala Ala Ile Phe Arg Arg
1 5 10 15

Phe Pro Cys Thr Ile Ile Leu Lys Lys Ala Val Thr Ala Thr Ile Glu
20 25 30

Ser Ile Thr Leu Lys Leu Asp Pro Gly Ser Lys Thr Thr Gly Ile Ala

35

40

45

Leu Leu Gln Gly Glu Lys Val Ile Phe Gly Ala Glu Leu Thr His Arg
 50 55 60

Gly Gln Thr Ile Lys Ala Ser Leu Glu Ser Arg Arg Ser Leu Arg Arg
 65 70 75 80

Gly Arg Arg Asn Arg His Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
 85 90 95

Arg Thr Arg Lys Lys Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val
 100 105 110

Glu Thr Thr Leu Thr Trp Val Glu Lys Leu Arg Arg Leu Ala Pro Ile
 115 120 125

Gly Leu Ile Val Gln Glu Leu Val Arg Phe Asp Leu Gln Gln Leu Glu
 130 135 140

Asn Pro Glu Ile Ser Ala Ile Glu Tyr His Gln Gly Glu Leu Gln Gly
 145 150 155 160

Tyr Glu Val Arg Gln Tyr Leu Leu Asn Lys Trp Asn Arg Lys Cys Ala
 165 170 175

Tyr Cys Asp Ala Glu Asn Val Pro Leu Gln Val Glu His Ile His Pro
 180 185 190

Lys Ser Gln Gly Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ala Cys
 195 200 205

Gln Lys Cys Asn Gln Lys Lys Gly Thr Gln Asn Ile Glu Gln Phe Leu
 210 215 220

Ala Lys Lys Pro Asp Ile Leu Ser Arg Ile Leu Thr Gln Ser Lys Arg
 225 230 235 240

Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Thr Leu Phe
 245 250 255

Gly Arg Leu Lys Glu Thr Gly Leu Pro Val Leu Thr Gly Ser Gly Gly
260 265 270

Leu Thr Lys Phe Asn Arg Ser Arg Leu Gln Leu Pro Lys Thr His Trp
275 280 285

Leu Asp Ala Ala Cys Val Gly Gln Val Glu Ala Leu Glu Leu Leu Thr
290 295 300

Asn Lys Pro Leu Leu Ile Lys Ala Thr Gly His Gly Thr Arg Gln Met
305 310 315 320

Cys Arg Thr Asp Lys Phe Gly Phe Pro Ser Arg Tyr Val Pro Arg Asn
325 330 335

Lys Phe Val Lys Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Ile Val
340 345 350

Ile Ser Gly Lys Lys Ile Gly Glu Tyr Val Gly Arg Val Ala Val Arg
355 360 365

Thr Thr Gly Ser Phe Asn Ile Ser Ala Ser Glu Leu Val Gln Gly Ile
370 375 380

Ser His Lys Tyr Cys Lys Ile Val His Lys Lys Asp Gly Tyr Ser Tyr
385 390 395 400

Ala Tyr

<210> 270

<211> 402

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-222 effector

<400> 270

Met Ala Arg Lys Leu Leu Thr Ala Gly Lys Ala Ala Ile Phe Arg Arg
1 5 10 15

Phe Pro Cys Thr Ile Ile Leu Lys Lys Ala Val Thr Ala Thr Ile Glu
20 25 30

Ser Ile Thr Leu Lys Leu Asp Pro Gly Ser Lys Thr Thr Gly Ile Ala
35 40 45

Leu Leu Gln Gly Glu Lys Val Ile Phe Gly Ala Glu Leu Thr His Arg
50 55 60

Gly Gln Thr Ile Lys Ala Ser Leu Glu Ser Arg Arg Ser Leu Arg Arg
65 70 75 80

Gly Arg Arg Asn Arg His Thr Arg Tyr Arg Gln Ala Arg Phe Leu Asn
85 90 95

Arg Thr Arg Lys Lys Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val
100 105 110

Glu Thr Thr Leu Thr Trp Val Glu Lys Leu Arg Arg Leu Ala Pro Ile
115 120 125

Gly Leu Ile Val Gln Glu Leu Val Arg Phe Asp Leu Gln Gln Leu Glu
130 135 140

Asn Pro Glu Ile Ser Ala Ile Glu Tyr His Gln Gly Glu Leu Gln Gly
145 150 155 160

Tyr Glu Val Arg Gln Tyr Leu Leu Asn Lys Trp Asn Arg Lys Cys Ala
165 170 175

Tyr Cys Asp Ala Glu Asn Val Pro Leu Gln Val Glu His Ile His Pro
180 185 190

Lys Ser Gln Gly Gly Ser Asn Arg Ile Ser Asn Leu Cys Leu Ala Cys
195 200 205

Gln Lys Cys Asn Gln Lys Lys Gly Thr Gln Asn Ile Glu Gln Phe Leu
210 215 220

Ala Lys Lys Pro Asp Ile Leu Ser Arg Ile Leu Thr Gln Ser Lys Arg
225 230 235 240

Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Thr Leu Phe
245 250 255

Gly Arg Leu Lys Glu Thr Gly Leu Pro Val Leu Thr Gly Ser Gly Gly
260 265 270

Leu Thr Lys Phe Asn Arg Ser Arg Leu Gln Leu Pro Lys Thr His Trp
275 280 285

Leu Asp Ala Ala Cys Val Gly Gln Val Glu Ala Leu Glu Leu Leu Thr
290 295 300

Asn Lys Pro Leu Leu Ile Lys Glu Thr Gly His Gly Thr Arg Gln Met
305 310 315 320

Cys Arg Thr Asp Lys Phe Gly Phe Pro Ser Arg Tyr Val Pro Arg Asn
325 330 335

Lys Phe Val Lys Gly Phe Gln Thr Gly Asp Ile Val Lys Ala Ile Val
340 345 350

Ile Ser Gly Lys Lys Ile Gly Glu Tyr Val Gly Arg Val Ala Val Arg
355 360 365

Thr Thr Gly Ser Phe Asn Ile Ser Ala Ser Glu Leu Val Gln Gly Ile
370 375 380

Ser His Lys Tyr Cys Lys Ile Val His Lys Lys Asp Gly Tyr Ser Tyr
385 390 395 400

Ala Tyr

<210> 271

<211> 441
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-223 effector

<400> 271

Met Ala Arg Arg Ala Leu Pro Thr Gln Val Glu Leu Gly Asn Glu Pro
1 5 10 15

Cys Lys Glu Lys Lys Pro Leu Met Pro Cys His Pro Ala Arg Ala Arg
20 25 30

Lys Leu Leu Lys Asn Gly Lys Ala Ala Val Asp Arg Thr Tyr Pro Phe
35 40 45

Thr Ile Ile Leu Lys Tyr Cys Val Lys Glu Gly Leu Gln Pro Ile Glu
50 55 60

Val Lys Phe Asp Pro Gly Ser Arg Thr Thr Gly Leu Ala Leu Val Gly
65 70 75 80

Asn Phe Glu Arg Gly Lys Glu Val Ile Phe Ala Gly Asn Leu Ile His
85 90 95

Arg Gly Gly Gln Ile Lys Ser Asn Leu Asn Ser Arg Arg Ala Ile Arg
100 105 110

Arg Gly Arg Arg Asn Arg Lys Thr Arg Tyr Arg Pro Ala Arg Phe Asn
115 120 125

Asn Arg Arg Arg Pro Lys Gly Trp Leu Pro Pro Ser Leu Arg Ser Arg
130 135 140

Val Leu Asn Val Glu Asn Trp Met Leu Lys Leu Ala Arg Leu Ala Pro
145 150 155 160

Leu Thr Gln Ile Ala Val Glu Thr Val Arg Phe Asp Thr Gln Lys Leu
165 170 175

Gln Lys Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu Ala
180 185 190

Gly Tyr Glu Leu Arg Glu Tyr Leu Leu Glu Lys Trp Glu Arg Gln Cys
195 200 205

Ala Tyr Cys Gly Ala Lys Asn Val Pro Leu Glu Val Glu His Ile Gln
210 215 220

Ala Arg Ser Lys Gly Gly Thr Asn Arg Val Ser Asn Leu Thr Leu Ala
225 230 235 240

Cys Thr Glu Cys Asn Gln Lys Lys Gly Asn Gln Asp Val Lys Asp Phe
245 250 255

Leu Lys Arg Lys Pro Ser Arg Leu Lys Lys Val Leu Ala Gln Ala Lys
260 265 270

Lys Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg Tyr Ala Ile
275 280 285

Gly Val Ala Leu Lys Thr Phe Gly Leu Pro Ile Val Phe Ala Thr Gly
290 295 300

Gly Arg Thr Lys Phe Asn Arg Thr Ser Gly His Tyr Pro Lys Asp His
305 310 315 320

Trp Ile Asp Ala Ala Cys Val Gly Glu Ser Gly Ser Asp Val Ile Ile
325 330 335

Pro Lys Ala Val Thr Pro Leu Ile Ile Lys Ala Lys Gly Arg Gly Ser
340 345 350

Arg Gln Lys Cys Arg Val Asn Gln Tyr Gly Phe Pro Arg Thr Ser Ala
355 360 365

Lys Lys Gln Lys Arg Val Asn Gly Phe Gln Thr Gly Asp Phe Val Lys

370

375

380

Ala Ile Val Thr Lys Gly Lys Lys Ile Gly Thr Tyr Lys Gly Arg Val
 385 390 395 400

Leu Val Gln Ala Ala Gly Asn Phe Asp Ile Val Thr Lys Lys Gly Arg
 405 410 415

Val Ser Gly Ile Ser His Lys Tyr Cys Gln Leu Phe Gln Arg Ile Asp
 420 425 430

Gly Tyr Glu Tyr Ser Leu Thr Ser Asn
 435 440

<210> 272

<211> 461

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-224 effector

<400> 272

Met Ala Val Cys Val Leu Asp Arg His Ser Lys Ala Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Met Pro Phe Val Ile Arg Leu Ile Asp Arg Glu Val Glu
 35 40 45

Glu Cys Glu Phe Gln Pro Leu Arg Leu Lys Cys Asp Pro Gly Ser Arg
 50 55 60

Thr Thr Gly Met Ala Leu Val Arg Ile Gln Glu Asp Gly Gly Thr Val
 65 70 75 80

Val Leu His Leu Phe Glu Leu Lys His Arg Gly Arg Ala Ile Ser Glu
85 90 95

Ala Leu Thr Gly Arg Arg Ala Lys Arg Arg Arg Arg Arg Asn Ala Asn
100 105 110

Leu Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Pro Gly
115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Thr Met Val Trp
130 135 140

Val His Arg Leu Gln Gln Trp Val Leu Leu Thr Gly Ile Ser Ile Glu
145 150 155 160

Leu Val Arg Phe Asp Thr Gln Ala Leu Asp Asn Pro Ala Ile Glu Gly
165 170 175

Ala Glu Tyr Gln Gln Gly Thr Leu Gln Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Gly Arg Lys Cys Ala Tyr Cys Asp Gly Ala Gly
195 200 205

Met Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Gln Gly Gly Ser
210 215 220

His Arg Ile Ser Asn Leu Thr Leu Ala Cys Ala Gly Cys Asn Leu Asn
225 230 235 240

Lys Gly Pro Gln Asp Ile Arg Leu Phe Leu Ala Pro His Pro Gln Arg
245 250 255

Leu Ala Arg Ile Leu Ala Gln Ala Lys Ala Pro Leu Gln Asp Ala Ala
260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Phe Lys Ala Leu Lys Gly Thr
275 280 285

Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Arg Thr Lys Trp Asn Arg

290

295

300

Ser Arg Phe Gly Ile Pro Lys Thr His Ala Leu Asp Ala Val Cys Val
 305 310 315 320

Gly Ser Val Ala Lys Val Ser Leu Trp Gln Arg Pro Thr Leu Ala Ile
 325 330 335

Lys Ala Thr Gly Arg Gly Ala Tyr Gln Arg Thr Arg Leu Ser Gly His
 340 345 350

Gly Phe Pro Arg Gly Tyr Leu Met Gly Gln Lys Gln Val Gln Gly Phe
 355 360 365

Gln Thr Gly Asp Arg Val Arg Ala Ile Val Leu Lys Gly Gln Arg Ala
 370 375 380

Gly Thr Tyr Leu Gly Arg Val Ala Val Arg Arg Ser Gly Ser Phe Asn
 385 390 395 400

Ile Gln Thr Asp Ser Gly Val Val Gln Gly Ile Ser Tyr Lys Tyr Cys
 405 410 415

Gln Leu Leu Gln Arg Asn Asp Gly Tyr Gly Tyr Gly Gln His His Asp
 420 425 430

Phe Lys Lys Gly Glu Ala Gly Arg Gly Gln Ala Ala Pro Asp Ala Leu
 435 440 445

Ser Leu Pro Gly Met Asn Ala Glu Val Ser Arg Ala Ile
 450 455 460

<210> 273

<211> 370

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-225 effector

<400> 273

Met Ala Val Phe Val Phe Asp Lys Arg Gly Lys Pro Leu Met Gln Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Gly Arg Gly Arg Ala Arg Ile
20 25 30

His Lys Met Leu Pro Phe Thr Ile Arg Val Val Asp Arg Leu Val Glu
35 40 45

Asp Ser Gln Leu Gln Pro Leu Glu Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Val Ala Val Val Arg Ile Ser Val Ala Val Asp Ala Gln
65 70 75 80

Thr Gly Glu Val Gln Lys His Val His Val Leu Asn Leu Phe Glu Leu
85 90 95

Ile His Arg Ser Arg Gln Ile Thr Glu Ala Leu Ile Gly Arg Arg Gly
100 105 110

His Arg Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg Ala Pro Arg Phe
115 120 125

Asn Asn Arg Gly Asn Gln Lys Lys Gly Trp Leu Pro Pro Ser Leu Gln
130 135 140

His Leu Val Asp Thr Ser Leu Glu Trp Val Lys Arg Ile Glu Lys Leu
145 150 155 160

Ala Pro Ile Ser Gly Ile Ser Thr Glu Leu Val Arg Phe Asp Met Gln
165 170 175

Ala Met Glu Asn Pro Glu Ile Glu Gly Met Gln Tyr Gln Gln Gly Thr
180 185 190

Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Lys Arg

195

200

205

Thr Cys Ala Tyr Cys Asp Ala Lys Asp Val Pro Leu Gln Ile Glu His
 210 215 220

Ile Gln Pro Lys Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala
 225 230 235 240

Leu Ala Cys Pro Ser Cys Asn Ser Lys Lys Ala Ala Leu Pro Ile Glu
 245 250 255

Ser Phe Leu Ser Lys Gln Pro Glu Arg Leu Lys Arg Ile Gln Val Gln
 260 265 270

Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp
 275 280 285

Ala Leu Val Asn Ala Leu Lys Ala Thr Gly Leu Pro Val Glu Thr Ala
 290 295 300

Ser Gly Gly Gln Thr Lys Phe Asn Arg Ser Gln Phe Asp Ile Pro Lys
 305 310 315 320

Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Gly Ser Ile Thr
 325 330 335

Asp Trp Gln Lys Pro Thr Leu Ala Ile Lys Ala Met Gly Arg Gly Ser
 340 345 350

Tyr Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu
 355 360 365

Thr Arg
 370

<210> 274

<211> 391

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-226 effector

<400> 274

Met Ala Val Phe Val Ile Asp Arg Arg Gln Ala Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Ile Pro Phe Thr Ile Arg Leu Ile Asp Arg Glu Val Ala
35 40 45

Gln Ser Glu Leu Gln Pro Leu Glu Leu Lys Ile Asp Pro Gly Ser Lys
50 55 60

Thr Ser Gly Leu Ala Leu Val Arg Asn Arg Asn Thr Val Asn Ala Glu
65 70 75 80

Thr Gly Glu Ile Thr Ala Thr Ala His Val Leu Asn Leu Phe Glu Leu
85 90 95

Ile His Arg Gly Val Gln Ile Ser His Ala Leu Thr Ala Arg Arg Gln
100 105 110

Met Arg Arg Arg Arg Arg Ser Ala Asn Leu Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Lys Asn Lys Gly Lys Gly Trp Leu Ala Pro Ser Leu
130 135 140

Gln His Arg Ile Asp Thr Thr Leu Ser Trp Val Ala Arg Leu Arg Asn
145 150 155 160

Val Ala Pro Ile Thr His Leu Ala Gln Glu Leu Val Arg Phe Asp Met
165 170 175

Gln Gln Leu Glu Asn Pro Glu Ile Ala Gly Val Glu Tyr Gln Gln Gly

180

185

190

Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Arg
 195 200 205

Arg Gln Cys Ala Tyr Cys Asp Ala Ser Thr Val Pro Leu Gln Ile Asp
 210 215 220

His Ile His Pro Lys Ala Arg Gly Gly Ser Asn Arg Val Ser Asn Leu
 225 230 235 240

Thr Leu Ala Cys Ala Pro Cys Asn Leu Arg Lys Ala Ala Gln Asp Val
 245 250 255

Thr Gln Phe Leu Glu Lys Asp Pro Lys Arg Leu Ala Lys Ile Gln Ala
 260 265 270

Gln Ala Lys Arg Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg
 275 280 285

Trp Lys Leu Leu Asn Ala Leu Lys Ala Thr Gly Leu Thr Asn Arg Thr
 290 295 300

Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Ser Arg Leu Val Ile Pro
 305 310 315 320

Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Asp Phe Val
 325 330 335

Glu Gln Trp Gln Lys Pro Thr Leu Glu Ile Lys Ala Thr Gly Arg Gly
 340 345 350

Ser Tyr Gln Arg Thr Arg Leu Thr Arg Phe Gly Phe Pro Arg Gly Tyr
 355 360 365

Leu Thr Arg Gln Lys Arg Ile His Gly Phe Gln Thr Gly Asp Met Val
 370 375 380

Lys Ala Ile Val Thr Lys Gly
 385 390

<210> 275
<211> 251
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-227 effector

<400> 275
Met Ala Val Phe Val Leu Asp Lys Arg Gly Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Asp Arg Gly Arg Ala Arg Ile
20 25 30

His Lys Met Leu Pro Phe Thr Ile Arg Val Val Asp Arg Leu Val Glu
35 40 45

Asp Ser Gln Leu Gln Pro Leu Glu Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Val Ala Val Ala Arg Ile Ser Val Ala Val Asp Ala Gln
65 70 75 80

Thr Gly Glu Val Gln Lys Arg Val His Val Leu Asn Leu Phe Asp Leu
85 90 95

Ile His Arg Ser Arg Gln Ile Thr Glu Ala Leu Thr Gly Arg Arg Gly
100 105 110

His Arg Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg Ala Pro Arg Phe
115 120 125

Asp Asn Arg Gly Asn Gln Lys Lys Gly Trp Leu Pro Pro Ser Leu Gln
130 135 140

His Arg Val Asp Thr Ser Met Ala Trp Val Ser Arg Ile Gln Arg Leu

Asp Ser Gln Leu Gln Pro Leu Glu Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Val Ala Val Val Arg Ile Ser Val Ala Val Asp Ala Gln
65 70 75 80

Thr Gly Glu Val Gln Lys His Val His Val Leu Asn Leu Phe Asp Leu
85 90 95

Ile His Arg Ser Arg Gln Ile Thr Glu Ala Leu Ile Gly Arg Arg Gly
100 105 110

His Arg Arg Leu Arg Arg Ser Lys Leu Arg Tyr Arg Ala Pro Arg Phe
115 120 125

Asn Asn Arg Gly Asn Gln Lys Lys Gly Trp Leu Pro Pro Ser Leu Gln
130 135 140

His Leu Val Asn Thr Ser Leu Glu Trp Val Lys Arg Ile Glu Lys Leu
145 150 155 160

Ala Pro Ile Ser Gly Ile Ser Thr Glu Leu Val Arg Phe Asp Met Gln
165 170 175

Ala Met Glu Asn Pro Lys Ile Glu Gly Met Gln Tyr Gln Gln Gly Thr
180 185 190

Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Lys Arg
195 200 205

Thr Cys Ala Tyr Cys Asp Ala Lys Asp Val Pro Leu Gln Val Glu His
210 215 220

Ile Gln Pro Lys Ala Lys Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala
225 230 235 240

Leu Ala Cys Pro Ser Cys Asn Ser Lys Lys Ala Ala Leu Pro Ile Glu
245 250 255

Ser Phe Leu Ser Lys Gln Pro Glu Arg Leu Lys Arg Ile Gln Val Gln

260

265

270

Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp
 275 280 285

Ala Leu Val Asn Ala Leu Lys Ala Thr Trp Leu Pro Val Glu Thr Ala
 290 295 300

Ser Gly Gly Lys Thr Lys Phe Asn Arg Asn Gln Leu Gly Ile Pro Lys
 305 310 315 320

Thr His Ala Leu Asp Ala Val Cys Val Gly Asn Ile Ser Thr Val Thr
 325 330 335

Asp Trp Gln Lys Pro Thr Leu Ser Ile Lys Ala Met Gly Arg Gly Ser
 340 345 350

Tyr Gln Arg Thr Arg Leu Asp Lys Phe Gly Cys Val Arg Gly Tyr Met
 355 360 365

Thr Arg Ser Lys Ser Ile His Gly Phe Gln Thr Gly Asp Met Val Lys
 370 375 380

Ala Ile Val Leu Lys Gly Lys Lys Ile Gly Thr Tyr Met Gly Arg Val
 385 390 395 400

Ala Val Arg Ala Ser Gly Ser Phe Asn Ile Gln Thr Gly Asn Gly Leu
 405 410 415

Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val Gln Arg Gly Asp
 420 425 430

Gly Tyr Gly Tyr Ser Leu Val Ala Lys Thr Asp Val Arg Gly Thr Pro
 435 440 445

Pro Gln His Arg Asp Ala Ser His Pro Ala Leu Tyr Leu Pro Gly Leu
 450 455 460

Lys Ala Glu Val Ser Arg Ala Asn
 465 470

<210> 277
<211> 26
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-229 effector

<400> 277
Met Ala Val Phe Val Leu Asp Lys Arg Lys Arg Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu
20 25

<210> 278
<211> 434
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-230 effector

<400> 278
Met Ala Val Phe Val Leu Asp Lys Arg Lys Arg Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Ile Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
35 40 45

Asp Ser Val Leu Gln Pro Val Arg Leu Lys Leu Asp Pro Gly Ser Lys

50

55

60

Thr Thr Gly Met Ala Leu Ala Arg Glu Lys Glu Thr Val Asp Asp Ser
65 70 75 80

Thr Gly Glu Ile Ile Arg Thr Leu Ser Val Leu Met Leu Leu Glu Leu
85 90 95

Thr His Arg Gly His Val Ile Arg Asp Ala Leu Thr Ser Arg Ser Gly
100 105 110

His Arg Arg Phe Arg Arg Ser Lys Leu Arg Tyr Arg Pro Ala Arg Phe
115 120 125

Asn Asn Arg Thr Lys Pro Lys Gly Trp Leu Ala Pro Ser Leu Gln His
130 135 140

Arg Val Asp Thr Val Leu Ser Trp Val Asn Arg Leu Thr Arg Trp Ala
145 150 155 160

Pro Val Thr Ala Leu Ser Gln Glu Leu Val Arg Phe Asp Thr Gln Ala
165 170 175

Met Gln Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Glu Leu
180 185 190

Leu Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Lys
195 200 205

Cys Ala Tyr Cys Gly Ala Glu Asn Thr Pro Leu Glu Ile Asp His Ile
210 215 220

His Pro Arg Ser Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Thr Leu
225 230 235 240

Ala Cys His Ala Cys Asn Lys Arg Lys Gly Ser Met Asp Val Lys Lys
245 250 255

Phe Leu Ala Lys Asn Pro Glu Arg Leu Arg Asn Ile Leu Ala Gln Ala
260 265 270

Lys Ala Pro Leu Arg Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala
275 280 285

Leu Phe Gln Arg Leu Lys Ala Thr Gly Leu Pro Val Glu Ile Gly Thr
290 295 300

Gly Gly Arg Thr Lys Trp Asn Arg Arg Arg Leu Asn Val Pro Lys Glu
305 310 315 320

His Cys Leu Asp Ala Val Cys Val Gly His Val Asp Leu Leu Glu Asn
325 330 335

Trp Lys Gln Pro Met Leu Phe Val Lys Ala Thr Gly Arg Gly Ser Tyr
340 345 350

Gln Arg Thr Gln Leu Thr Lys Tyr Gly Phe Pro Arg Gly Tyr Phe Met
355 360 365

Arg Ser Lys Lys Ala Phe Gly Phe Gln Thr Gly Asp Met Val Arg Ala
370 375 380

Val Val Thr Thr Gly Lys Lys Val Gly Thr Tyr Phe Gly Arg Val Thr
385 390 395 400

Val Arg Thr Lys Gly Ser Phe Asp Ile Lys Asn Val Ala Thr Ser Ile
405 410 415

Ser Tyr Arg Phe Cys Val Leu Leu Gln Arg Ala Asp Gly Tyr Ala Tyr
420 425 430

Ile Gln

<210> 279

<211> 465

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-231 effector

<400> 279

Met Ala Val Phe Val Leu Asp Gln Ala Gly His Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Val Val Pro Phe Val Ile Arg Leu Val Asp Arg Arg Ala Asp
35 40 45

Ser Cys Gln Phe Gln Pro Leu Arg Val Thr Ile Asp Pro Gly Ser Gln
50 55 60

Ile Thr Gly Leu Ala Leu Val Arg Glu Thr Ala Asp His Gly Arg Ala
65 70 75 80

Val Leu Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Ser Met Arg Arg Arg Arg Arg Gly Asn Leu
100 105 110

Arg Tyr Arg Ala Ser Arg Phe Leu Asn Arg Thr Arg Pro Thr Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Pro Leu Ser Trp Val
130 135 140

His Lys Ile Arg Arg Trp Ala Pro Val Ser Gly Leu Ser Ser Glu Arg
145 150 155 160

Val Arg Phe Asp Met Gln Gln Met Glu Asn Pro Glu Ile Ala Gly Val
165 170 175

Glu Tyr Gln Arg Gly Thr Leu Ala Gly Tyr Asp Leu Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Gln His Val
195 200 205

Pro Leu Asn Leu Asp Pro Ile Gln Ala Gln Ala Arg Asn Gly Ser Asn
210 215 220

Arg Ala Ser Asn Phe Thr Leu Ala Cys Leu Pro Cys Asn Gln Lys Lys
225 230 235 240

Ala Glu Arg Asp Ile Arg Glu Phe Leu Ala His Asn Pro Asn Lys Leu
245 250 255

Ala Leu Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Trp Ala Leu Val Asn Ala Leu Arg Ser Thr Gly
275 280 285

Leu Ala Val Glu Thr Gly Ser Gly Gly Arg Thr Lys Trp Asn Arg Ser
290 295 300

Thr Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly
305 310 315 320

Val Val Asp Ser Val Ser Gly Trp Gln Arg Pro Thr Leu Thr Ile Lys
325 330 335

Ala Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Ala Phe Gly
340 345 350

Phe Pro Arg Gly Asp Leu Met Lys Asn Lys Ser Val Lys Gly Phe Gln
355 360 365

Thr Gly Asp Gln Val Ile Ala Thr Val Pro Ala Gly Lys Lys Thr Gly
370 375 380

Val His Arg Gly Arg Val Ala Leu Arg Lys Thr Gly Arg Phe Asn Ile
385 390 395 400

Gln Thr Ala His Gly Val Ile Gln Gly Ile Ser His Ala His Cys Arg

405

410

415

Leu Ile Gln Arg Asn Asp Gly Tyr Gly Tyr Val Gln His Val Arg Ser
 420 425 430

Gly Gly Val Val His Ser Trp Lys Asp Lys Leu Pro Asp Phe Leu Pro
 435 440 445

Gln Pro His Arg Ala Ala Ser Pro Val Gly Arg Phe Ala Ser Ser Pro
 450 455 460

Val
 465

<210> 280
 <211> 465
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-232 effector

<400> 280
 Met Ala Val Phe Val Leu Asp Gln Ala Gly His Pro Leu Met Pro Cys
 1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Val Val Pro Phe Val Ile Arg Leu Val Asp Arg Arg Ala Asp
 35 40 45

Ser Cys Gln Phe Gln Pro Leu Arg Val Thr Ile Asp Pro Gly Ser Gln
 50 55 60

Ile Thr Gly Leu Ala Leu Val Arg Glu Thr Ala Asp His Gly Arg Ala
 65 70 75 80

Val Leu Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Ser Met Arg Arg Arg Arg Arg Gly Asn Leu
100 105 110

Arg Tyr Arg Ala Ser Arg Phe Leu Asn Arg Thr Arg Pro Thr Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Thr Leu Ser Trp Val
130 135 140

His Lys Ile Arg Arg Trp Ala Pro Val Ser Gly Leu Ser Ser Glu Arg
145 150 155 160

Val Arg Phe Asp Met Gln Gln Met Glu Asp Pro Glu Ile Ala Gly Val
165 170 175

Glu Tyr Gln Arg Gly Thr Leu Ala Gly Tyr Asp Leu Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Gln His Val
195 200 205

Pro Leu His Leu Asp Pro Ile Gln Ala Gln Ala Arg Asn Gly Ser Asn
210 215 220

Arg Ala Ser Asn Phe Thr Leu Ala Cys Leu Pro Cys Asn Gln Lys Lys
225 230 235 240

Ala Ala Arg Asp Ile Arg Glu Phe Leu Ala His Asn Pro Asn Lys Leu
245 250 255

Ala Leu Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Trp Ala Leu Val Asn Ala Leu Arg Ser Thr Gly
275 280 285

Leu Ala Val Glu Thr Gly Ser Gly Gly Arg Thr Lys Trp Asn Arg Ser

290

295

300

Thr Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly
 305 310 315 320

Val Val Asp Ser Val Ser Gly Trp Gln Arg Pro Thr Leu Thr Ile Lys
 325 330 335

Ala Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Ala Phe Gly
 340 345 350

Phe Arg Arg Gly Asp Leu Met Lys Asn Lys Ser Val Lys Gly Phe Gln
 355 360 365

Thr Gly Asp Gln Val Ile Ala Thr Val Pro Ala Gly Lys Lys Thr Gly
 370 375 380

Val His Arg Gly Arg Val Ala Ile Arg Lys Thr Gly Arg Phe Asn Ile
 385 390 395 400

Gln Thr Ala His Gly Val Ile Gln Gly Ile Ser His Ala His Cys Arg
 405 410 415

Leu Ile Gln Arg Asn Asp Gly Tyr Gly Tyr Val Gln His Val Arg Ser
 420 425 430

Gly Gly Val Val His Ser Trp Lys Asp Lys Leu Pro Asp Phe Leu Pro
 435 440 445

Gln Pro His Arg Ala Ala Ser Pro Val Gly Arg Phe Ala Ser Ser Pro
 450 455 460

Val
 465

<210> 281

<211> 465

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-233 effector

<400> 281

Met Ala Val Phe Val Leu Asp Gln Ala Gly His Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Val Val Pro Phe Val Ile Arg Leu Val Asp Arg Arg Val Asp
35 40 45

Ser Cys Gln Phe Gln Pro Leu Arg Val Thr Ile Asp Pro Gly Ser Gln
50 55 60

Ile Thr Gly Leu Ala Leu Val Arg Glu Thr Ala Asp His Gly Arg Ala
65 70 75 80

Val Leu Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Ser Met Arg Arg Arg Arg Arg Gly Asn Leu
100 105 110

Arg Tyr Arg Ala Ser Arg Leu Leu Asn Arg Thr Arg Pro Thr Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Pro Leu Ser Trp Val
130 135 140

His Lys Ile Arg Arg Trp Ala Pro Val Ser Gly Leu Ser Ser Glu Arg
145 150 155 160

Val Arg Phe Asp Met Gln Gln Met Glu Asp Pro Glu Ile Ala Gly Val
165 170 175

Glu Tyr Gln Arg Gly Thr Leu Ala Gly Tyr Asp Leu Arg Glu Tyr Leu

180

185

190

Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Gln His Val
 195 200 205

Pro Leu Asn Leu Asp Pro Ile Gln Ala Gln Ala Arg Asn Gly Ser Asn
 210 215 220

Arg Ala Ser Asn Phe Thr Leu Ala Cys Leu Pro Cys Asn Gln Lys Lys
 225 230 235 240

Ala Ala Arg Asp Ile Arg Glu Phe Leu Ala His Asn Pro Asn Lys Leu
 245 250 255

Ala Leu Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala
 260 265 270

Val Asn Ala Thr Arg Trp Ala Leu Val Asn Ala Leu Arg Ser Thr Gly
 275 280 285

Leu Ala Val Glu Thr Gly Ser Gly Gly Arg Thr Lys Trp Asn Arg Ser
 290 295 300

Thr Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly
 305 310 315 320

Val Val Asp Ser Val Ser Gly Trp Gln Arg Pro Thr Leu Thr Ile Lys
 325 330 335

Ala Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Ala Phe Gly
 340 345 350

Phe Pro Arg Gly Asp Leu Met Lys Asn Lys Ser Val Lys Gly Phe Gln
 355 360 365

Thr Gly Asp Gln Val Ile Ala Thr Val Pro Ala Gly Lys Lys Thr Gly
 370 375 380

Val His Arg Gly Arg Val Ala Leu Arg Lys Thr Gly Arg Phe Asn Ile
 385 390 395 400

Gln Thr Ala His Gly Val Ile Gln Gly Ile Ser His Ala His Cys Arg
405 410 415

Leu Ile Gln Arg Asn Asp Gly Tyr Gly Tyr Val Gln His Val Arg Ser
420 425 430

Gly Gly Val Val His Ser Gly Lys Asp Lys Leu Pro Asp Phe Leu Pro
435 440 445

Gln Pro His Arg Ala Ala Ser Pro Val Gly Arg Phe Ala Ser Ser Pro
450 455 460

Val
465

<210> 282
<211> 370
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-234 effector

<400> 282
Met Ala Val Phe Val Leu Asp Gln His Gln Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Ile Pro Phe Thr Ile Arg Val Val Asp Arg Arg Val Ala
35 40 45

Glu Ser Ala Leu Gln Pro Leu Ala Leu Lys Ile Asp Pro Gly Ser Lys
50 55 60

Thr Ser Gly Leu Ala Leu Val Arg Lys Ser Glu Ser Val Asp Val Thr

65					70						75					80
Thr	Gly	Glu	Val	Thr	Thr	Thr	Thr	His	Val	Leu	Asn	Leu	Phe	Glu	Leu	
				85					90					95		
Ile	His	Arg	Gly	Phe	Gln	Ile	Ser	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Gln	
			100					105					110			
Met	Arg	Arg	Arg	Arg	Arg	Ser	Ala	Asn	Leu	Arg	Tyr	Arg	Ala	Pro	Arg	
		115					120					125				
Phe	Leu	Asn	Arg	Lys	Asn	Lys	Gly	Lys	Gly	Trp	Leu	Ala	Pro	Ser	Leu	
	130					135					140					
Gln	His	Arg	Ile	Asp	Thr	Thr	Leu	Ser	Trp	Val	Thr	Arg	Ile	Ser	Asp	
145					150					155					160	
Val	Ala	Pro	Val	Thr	Leu	Leu	Thr	Gln	Glu	Leu	Val	Arg	Phe	Asp	Met	
				165					170					175		
Gln	Gln	Leu	Glu	Asn	Pro	Glu	Ile	Ala	Gly	Val	Glu	Tyr	Gln	Gln	Gly	
			180					185					190			
Glu	Leu	Ala	Gly	Tyr	Glu	Val	Arg	Glu	Tyr	Leu	Leu	Glu	Lys	Trp	Gln	
		195					200					205				
Arg	Gln	Cys	Ala	Tyr	Cys	Asp	Val	Ser	Glu	Val	Pro	Leu	Gln	Ile	Glu	
	210					215					220					
His	Ile	His	Pro	Lys	Ala	Cys	Gly	Gly	Ser	Asn	Arg	Val	Ser	Asn	Leu	
225					230					235					240	
Ala	Leu	Ala	Cys	Ala	Pro	Cys	Asn	Leu	Lys	Lys	Ala	Ala	Gln	Asp	Ile	
				245					250					255		
Ala	Leu	Phe	Leu	Ala	Lys	Asp	Pro	Lys	Arg	Leu	Ala	Thr	Ile	Gln	Ala	
			260					265					270			
Gln	Ala	Lys	Arg	Pro	Leu	Arg	Asp	Ala	Ala	Ala	Val	Asn	Ala	Thr	Arg	
		275					280					285				

Trp Lys Leu Leu Asn Ala Leu Lys Ala Thr Gly Leu Thr Asn Arg Thr
290 295 300

Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Ser Arg Leu Val Ile Pro
305 310 315 320

Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Asp Ser Val
325 330 335

Glu Gln Trp Gln Lys Pro Thr Leu Val Ile Asn Ala Thr Gly Arg Gly
340 345 350

Ser Tyr Gln Arg Thr Arg Leu Thr Arg Phe Gly Phe Pro Arg Gly Tyr
355 360 365

Leu Thr
370

<210> 283
<211> 239
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-235 effector

<400> 283
Met Ala Val Phe Val Leu Asp Arg Gly Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys

50

55

60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Lys Gln Arg Gly
115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Leu Glu Asn Pro Glu Ile Glu Gly
165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
195 200 205

Val Pro Leu Gln Val Glu His Ile Gln Pro Lys Ala Lys Gly Gly Ser
210 215 220

Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys Gln Cys Cys Asn Gln
225 230 235

<210> 284

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-236 effector

<400> 284

Met Ala Val Phe Val Leu Asp Arg His Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Arg Arg Ala Val Val
20 25 30

His Arg Cys Ile Pro Phe Thr Ile Arg Ile Lys Asp Arg Gln Val Glu
35 40 45

Ser Cys Ala Leu Gln Pro Leu Arg Leu Ser Phe Asp Pro Gly Ser Glu
50 55 60

Lys Thr Gly Leu Ala Leu Val Arg Glu Ser Gln Glu Ala Asp Arg Ile
65 70 75 80

Val Gly Gly Ser His Arg Ile Arg Thr Val Cys Phe Leu Leu Glu Ile
85 90 95

Trp His Arg Ala Ala Leu Ile Arg Lys Arg Leu Arg Gln Arg Lys Ala
100 105 110

Phe Arg Arg His Arg Arg Ala Arg Lys Thr Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Arg Arg Pro Ala Gly Trp Leu Pro Pro Ser Leu Glu
130 135 140

His Leu Val Ala Thr Thr Ile Thr Trp Val Arg Arg Ile Arg Arg Trp
145 150 155 160

Ala Pro Val Ser Gly Leu Ala Met Glu Ser Asn Ser Phe Asp Val Gln
165 170 175

Lys Leu Glu Asn Pro Asp Thr Thr Gly Thr Met Tyr Gln Arg Gly Thr

180

185

190

Leu Asn Gly Tyr Ala Val Arg Lys Tyr Leu Leu Asp Lys Trp Ala Arg
 195 200 205

Arg Cys Ala Tyr Cys Gly Thr Glu Gly Val Pro Leu Glu Ile Asp His
 210 215 220

Ile Val Pro Lys Ser Arg Gly Gly Ser Asp Arg Met Ser Asn Leu Ile
 225 230 235 240

Leu Ala Cys Arg Asn Cys Asn Gln Ala Lys Gly Asn Leu Asn Val Arg
 245 250 255

Ala Phe Met Ala His Asp Gln Lys Arg Leu Ala Arg Ile Leu Ala Gln
 260 265 270

Ala Arg Ala Ser Leu Arg Asp Ala Ala Ala Val Asn Ser Thr Cys Trp
 275 280 285

Arg Leu Met Thr Thr Leu Ala Lys Thr Gly Leu Pro Val Glu Thr Ser
 290 295 300

Thr Gly Glu Arg Thr Lys Trp Asn Arg Thr Arg Leu Gly Leu Pro Lys
 305 310 315 320

Thr His Ala Leu Asp Ala Ala Cys Val Gly Gln Val Asp Ala Ile Val
 325 330 335

Ala Trp Arg Val Pro Ile Leu Asn Ile Arg Cys Thr Gly Arg Gly Ser
 340 345 350

His Gln Arg Thr Arg Leu Asp Arg Tyr Gly Phe Pro Arg Gly Tyr Leu
 355 360 365

Met Arg Ser Lys Arg Val Gln Gly Phe Gln Thr Gly Asp Leu Val Lys
 370 375 380

Ala Val Val Leu Ser Gly Lys Asn Ala Ala Ile His Val Gly Arg Val
 385 390 395 400

Ala Ile Arg Ala Ser Gly Lys Phe Asn Ile Gln Thr Ser Thr Gly Val
405 410 415

Ile Gln Gly Val His Ala Arg Arg Cys Ser Ile Val Gln Arg Gly Asp
420 425 430

Gly Tyr Ala Tyr Ser Phe Arg Gln Ile Pro Gln Met Thr Ser Val
435 440 445

<210> 285

<211> 351

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-237 effector

<400> 285

Met Ala Val Phe Val Leu Asp Arg His Gln Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Lys Leu Leu Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Met Pro Phe Ser Ile Arg Leu Val Asp Arg Cys Val Asn
35 40 45

Asp Ser Val Leu Gln Pro Leu Lys Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Met Ala Leu Val Arg Glu Ser Ala Val Val Asp Glu Glu
65 70 75 80

Thr Gly Glu Leu Lys Ala Met Val His Val Leu Asn Leu Phe Glu Ile
85 90 95

Gln His Arg Gly Gln Gln Ile Ser Glu Thr Leu Thr Ala Arg Arg Gln

	100		105		110										
Met	Arg	Arg	Arg	Arg	Arg	Gly	Asn	Leu	Arg	Tyr	Arg	Ala	Pro	Gln	Phe
	115						120					125			
Leu	Asn	Arg	Gly	Asn	Lys	Lys	Lys	Gly	Trp	Ile	Ala	Pro	Ser	Leu	Gln
	130					135					140				
His	Arg	Val	Asp	Thr	Thr	Leu	Ala	Trp	Val	Asn	Arg	Leu	Thr	Gly	Leu
145					150					155					160
Ala	Pro	Val	Thr	Gly	Ile	Ala	Gln	Glu	Leu	Val	Arg	Phe	Asp	Leu	Gln
				165					170					175	
Gln	Met	Glu	Asn	Pro	Glu	Ile	Ser	Gly	Ile	Glu	Tyr	Gln	Gln	Gly	Thr
			180					185					190		
Leu	Ala	Gly	Tyr	Glu	Thr	Arg	Glu	Tyr	Leu	Leu	Asn	Gln	Trp	Gly	Arg
		195					200					205			
Glu	Cys	Ala	Tyr	Cys	Gly	Ala	Arg	Asn	Thr	Pro	Leu	Gln	Ile	Glu	His
	210					215					220				
Ile	His	Ser	Lys	Ala	Gln	Gly	Gly	Ser	Asp	Arg	Val	Ser	Asn	Leu	Thr
225					230					235					240
Leu	Ala	Cys	Arg	Pro	Cys	Asn	Gln	Gln	Lys	Gly	Ala	Gln	Asp	Leu	Lys
				245					250					255	
Val	Phe	Leu	Val	Lys	Asp	Pro	Lys	Arg	Leu	Ala	Arg	Ile	Gln	Ala	Gln
			260					265					270		
Ala	Lys	Lys	Pro	Leu	Lys	Asp	Ala	Ala	Ala	Val	Asn	Ser	Thr	Arg	Trp
		275					280					285			
Ala	Leu	Phe	Gln	Ala	Leu	His	Ala	Thr	Gly	Leu	Pro	Val	Thr	Thr	Gly
	290					295					300				
Ser	Gly	Gly	Leu	Thr	Lys	Phe	Asn	Arg	Met	Arg	Phe	Gly	Ile	Pro	Lys
305					310					315					320

Thr His Ala Leu Asp Ala Ala Cys Val Gly Phe Ile Ala Ala Leu Ser
325 330 335

Asp Trp Glu Lys Pro Thr Leu Val Ile Lys Ala Thr Gly Arg Gly
340 345 350

<210> 286
<211> 457
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-238 effector

<400> 286
Met Ala Val Phe Val Leu Asp Arg His Gln Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Lys Leu Leu Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Met Pro Phe Ser Ile Arg Leu Val Asp Arg Cys Val Asn
35 40 45

Asp Ser Val Leu Gln Pro Leu Lys Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Met Ala Leu Val Arg Glu Ser Ala Val Val Asp Glu Glu
65 70 75 80

Thr Gly Glu Leu Lys Ala Met Val His Val Leu Asn Leu Phe Glu Ile
85 90 95

Gln His Arg Gly Gln Gln Ile Ser Glu Thr Leu Thr Ala Arg Arg Gln
100 105 110

Met Arg Arg Arg Arg Arg Gly Asn Leu Arg Tyr Arg Ala Pro Gln Phe

115

120

125

Leu Asn Arg Gly Asn Lys Lys Lys Gly Trp Ile Ala Pro Ser Leu Gln
 130 135 140

His Arg Val Asp Thr Thr Leu Ala Trp Val Asn Arg Leu Thr Gly Leu
 145 150 155 160

Ala Pro Val Thr Gly Ile Ala Gln Glu Leu Val Arg Phe Asp Leu Gln
 165 170 175

Gln Met Glu Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Thr
 180 185 190

Leu Ala Gly Tyr Glu Thr Arg Glu Tyr Leu Leu Asn Gln Trp Gly Arg
 195 200 205

Glu Cys Ala Tyr Cys Gly Ala Arg Asn Thr Pro Leu Gln Ile Glu His
 210 215 220

Ile His Ser Lys Ala Gln Gly Gly Ser Asp Arg Val Ser Asn Leu Thr
 225 230 235 240

Leu Ala Cys Arg Pro Cys Asn Gln Gln Lys Gly Ala Gln Asp Leu Lys
 245 250 255

Val Phe Leu Val Lys Asp Pro Lys Arg Leu Ala Arg Ile Gln Ala Gln
 260 265 270

Ala Lys Lys Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp
 275 280 285

Ala Leu Phe Gln Ala Leu His Ala Thr Gly Leu Pro Val Thr Thr Gly
 290 295 300

Ser Gly Gly Leu Thr Lys Phe Asn Arg Met Arg Phe Gly Ile Pro Lys
 305 310 315 320

Thr His Ala Leu Asp Ala Ala Cys Val Gly Phe Ile Ala Ala Leu Ser
 325 330 335

Asp Trp Glu Lys Pro Thr Leu Val Ile Lys Ala Thr Gly Arg Gly Ser
340 345 350

Tyr Gln Arg Thr Arg Leu Asn Ala Phe Gly Phe Pro Arg Gly Tyr Leu
355 360 365

Thr Arg Gln Lys Arg Ile Lys Glu Phe Gln Thr Gly Asp Leu Ile Lys
370 375 380

Ala Asp Val Thr Lys Gly Lys Lys Met Gly Val Tyr Ile Gly Arg Val
385 390 395 400

Ala Val Arg Ala Ser Gly Ser Phe Asn Ile Gln Thr Ala Gln Gly Val
405 410 415

Val Gln Gly Ile Ser Asp Arg Tyr Cys Gln Ile Leu Gln Arg Ala Asp
420 425 430

Gly Tyr Gly Tyr Ser Gln Arg Gly Thr Pro Glu Lys Ala Ala Glu Leu
435 440 445

Cys Ser Ala Arg Tyr Pro Ser Pro Ala
450 455

<210> 287

<211> 52

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-239 effector

<400> 287

Met Ala Val Phe Val Leu Asp Arg His Gln Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Met Leu Leu Asp Arg Gly Arg Ala Arg Val

20

25

30

His Arg Leu Met Pro Phe Ser Ile Arg Leu Val Asp Arg Cys Val Asn
 35 40 45

Asp Ser Ala Leu
 50

<210> 288
 <211> 239
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-240 effector

<400> 288
 Met Ala Val Phe Val Leu Asp Arg His Gln Lys Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Met Leu Leu Asp Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Met Pro Phe Ser Ile Arg Leu Val Asp Arg Cys Val Asn
 35 40 45

Asp Ser Ala Leu Gln Pro Ile Lys Ile Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Thr Thr Gly Ile Ala Leu Val Arg Glu Ser Glu Thr Leu Asp Thr Glu
 65 70 75 80

Thr Gly Asp Val Thr Thr Thr Ala His Val Leu Ser Leu Phe Glu Leu
 85 90 95

Ala His Arg Gly His Gln Ile Ser Glu Ala Leu Thr Ala Arg Arg Gln
 100 105 110

Met Arg Arg Arg Arg Arg Gly Asn Leu Arg Asp Arg Lys Pro Arg Phe
115 120 125

Leu Asn Arg Lys Asn Arg Gly Gln Gly Trp Ile Ala Pro Ser Leu Gln
130 135 140

His Arg Val Asp Thr Val Gly Ala Trp Val Gln Arg Phe Gln Arg Leu
145 150 155 160

Ala Pro Ile Thr Gly Ile Val Gln Glu Leu Val Arg Phe Asp Leu Gln
165 170 175

Gln Met Glu Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Thr
180 185 190

Leu Ala Gly Tyr Glu Thr Arg Glu Tyr Leu Leu Asn Lys Trp Asp Arg
195 200 205

Glu Cys Ala Tyr Cys Gly Thr Gln Asn Val Pro Leu Gln Ile Glu His
210 215 220

Ile Gln Pro Lys Ala His Gly Gly Ser Arg Arg Ile Ala Asn Leu
225 230 235

<210> 289

<211> 89

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-241 effector

<400> 289

Met Ala Val Phe Val Leu Asp Arg His Gln Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Met Leu Leu Asp Arg Gly Arg Ala Arg Val

20

25

30

His Arg Leu Met Pro Phe Ser Ile Arg Leu Val Asp Arg Cys Val Asn
 35 40 45

Asp Ser Ala Leu Gln Pro Ile Lys Ile Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Thr Thr Gly Ile Ala Leu Val Arg Glu Ser Glu Thr Leu Asp Thr Glu
 65 70 75 80

Thr Gly Asp Val Thr Thr Thr Ala Gln
 85

<210> 290

<211> 47

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-242 effector

<400> 290

Met Ala Val Phe Val Leu Asp Arg Arg Gly Thr Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Asp Arg Gly Arg Ala Arg Ile
 20 25 30

His Lys Met Leu Pro Phe Thr Ile Arg Val Val Asp Arg Leu Val
 35 40 45

<210> 291

<211> 352

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-243 effector

<400> 291

Met Ala Val Phe Val Leu Asp Arg Arg Gly Thr Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Gln Lys Lys Gly
115 120 125

Trp Leu Pro Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly
165 170 175

Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr

180

185

190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
 195 200 205

Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser
 210 215 220

Asp Arg Ile Ser Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys
 225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
 245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Cys Pro Leu Lys Asp Ala Ala
 260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu Lys Ala Thr
 275 280 285

Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Gln Thr Lys Phe Asn Arg
 290 295 300

Asn Gln Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
 305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
 325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe
 340 345 350

<210> 292

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-244 effector

<400> 292

Met Ala Val Phe Val Leu Asp Arg Arg Gly Thr Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asn Asn Arg Gly Asn Lys Gln Arg Gly
115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly
165 170 175

Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp

195

200

205

Val Pro Leu Gln Val Glu His Ile Gln Pro Lys Ala Lys Gly Gly Ser
 210 215 220

Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys Gln Cys Cys Asn Gln Lys
 225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
 245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
 260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu Lys Ala Thr
 275 280 285

Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Lys Thr Lys Phe Asn Arg
 290 295 300

Asn Gln Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
 305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
 325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe
 340 345 350

Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe
 355 360 365

Gln Thr Gly Asp Met Val Lys Val Glu Val Thr Lys Gly Lys Lys Ile
 370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
 385 390 395 400

Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys
 405 410 415

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys
420 425 430

Met Asp Val Arg Gly Thr Leu Pro Gln His Arg Asp Ala Ser His Pro
435 440 445

Ala Leu Tyr Leu Pro Gly Leu Lys Ala Glu Val Ser Arg Ala Asn
450 455 460

<210> 293

<211> 47

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-245 effector

<400> 293

Met Ala Val Phe Val Leu Asp Arg Arg Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Arg Glu Thr Ser Arg Ile Ser Val Val Gln Leu Leu
35 40 45

<210> 294

<211> 77

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-246 effector

<400> 294

Met Ala Val Phe Val Leu Asp Arg Arg Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Ile Asp Arg Glu Gln Glu
35 40 45

Asp Cys Ala Leu Gln Pro Val Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Met Ala Leu Val Arg Glu Ser Gln Gln Val
65 70 75

<210> 295

<211> 506

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-247 effector

<400> 295

Met Ala Val Phe Val Leu Asp Arg Arg Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
35 40 45

Asp Ser Ser Leu Gln Gln Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Ile Ala Leu Val Arg Asp Ser Lys Asp Val Asp Ala Gln
65 70 75 80

Thr Gly Gln Ala Arg Lys Thr Ala His Val Leu Phe Leu Ala Glu Leu
85 90 95

His His Arg Gly His Ala Ile Arg Asp Ala Leu Arg Gln Arg Ala Ala
100 105 110

Phe Arg Arg Arg Arg Arg Cys Ala Asn Leu Arg His Arg Gln Pro Arg
115 120 125

Phe Asp Asn Arg Thr Arg Arg Asn Gly Trp Leu Ala Pro Ser Leu Gln
130 135 140

His Arg Val Asp Thr Ile Met Ala Trp Val Arg Arg Leu Ser Arg Trp
145 150 155 160

Ala Pro Ile Ser Ala Leu Ser Gln Glu Leu Val Arg Phe Asp Thr Gln
165 170 175

Ala Leu Gln Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Thr
180 185 190

Leu Ala Gly Cys Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg
195 200 205

Lys Cys Ala Tyr Cys Asp Ala Gln Asp Val Pro Leu Glu Ile Asp His
210 215 220

Ile His Pro Arg Ser Lys Gly Gly Ser His Arg Val Ser Asn Leu Val
225 230 235 240

Ile Ala Cys Arg Thr Cys Asn Gln Lys Lys Gly Asn Arg Asp Val Ala
245 250 255

Glu Phe Leu Ala Cys Asp Pro Gln Arg Leu Ala Arg Ile Glu Ala Gln
260 265 270

Ser Lys Ala Pro Leu Arg Asp Ala Ser Ala Val Asn Ser Thr Arg Trp

275

280

285

Ala Leu Tyr Ala Ala Leu Lys Gly Thr Gly Leu Pro Val Glu Val Gly
 290 295 300

Thr Gly Gly Arg Thr Lys Phe Asn Arg Ser Arg Leu Gly Ile Pro Lys
 305 310 315 320

Thr His Ala Leu Asp Ala Val Cys Val Gly Asp Val Ala Ala Val Arg
 325 330 335

Gly Trp Ser Val Pro Thr Leu Gly Ile Gln Cys Ala Gly Arg Gly Ser
 340 345 350

Tyr Gln Arg Thr Arg Leu Asn Arg His Gly Phe Pro Arg Gly Tyr Leu
 355 360 365

Thr Arg Ser Lys Arg His Phe Gly Phe Gln Thr Gly Asp Met Val Arg
 370 375 380

Ala Val Val Thr Thr Arg Arg Lys Val Val Thr Tyr Val Gly Arg Val
 385 390 395 400

Ala Ile Arg Ala Ser Gly Ser Phe Asn Leu Gln Thr Lys Asn Gly Leu
 405 410 415

Val Gln Gly Ile His His Arg Phe Cys Ala Leu Met Gln Arg Ala Asp
 420 425 430

Gly Tyr Gly Tyr Ala Trp Arg Arg Thr Ala Phe Val Lys Glu Glu Ala
 435 440 445

Gly Thr Gly Ile Ala Cys Ala Thr Ala Leu Tyr Pro Leu Arg Pro Glu
 450 455 460

Gly Arg Ser Leu Pro Arg Asn Leu Asp Glu Ile Arg Ser Gly Thr Asp
 465 470 475 480

Leu Thr Gly Tyr Ala Gly Arg Ala Ile Arg Thr Ala Leu Ala Ala Ile
 485 490 495

Gly Ser Asp Leu Ser Val Gln Pro Thr Asp
500 505

<210> 296
<211> 370
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-248 effector

<400> 296
Met Ala Val Phe Val Leu Asp Arg Arg Gln Ala Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Ile Pro Phe Thr Ile Arg Leu Ile Asp Arg Ala Val Ala
35 40 45

Gln Ser Glu Leu Gln Pro Leu Glu Leu Lys Ile Asp Pro Gly Ser Lys
50 55 60

Thr Ser Gly Leu Ala Leu Val Arg Asn Arg Asp Thr Val Asn Ala Glu
65 70 75 80

Thr Gly Glu Ile Thr Ala Thr Ala His Val Leu Asn Leu Phe Glu Leu
85 90 95

Ile His Arg Gly Ala Gln Ile Ser His Ala Leu Thr Ala Arg Arg Gln
100 105 110

Met Arg Arg Arg Arg Arg Ser Ala Asn Leu Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Lys Asn Lys Gly Lys Gly Trp Leu Ala Pro Ser Leu

130

135

140

Gln His Arg Ile Asp Thr Thr Leu Ser Trp Val Ala Arg Ile Arg Asn
 145 150 155 160

Val Ala Pro Val Thr Leu Leu Thr Gln Glu Leu Val Arg Phe Asp Met
 165 170 175

Gln Gln Leu Glu Asn Pro Glu Ile Ala Gly Val Gln Tyr Gln Gln Gly
 180 185 190

Glu Leu Arg Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly
 195 200 205

Arg Gln Cys Ala Tyr Cys Asp Val Ser Asn Val Pro Leu Gln Ile Glu
 210 215 220

His Ile His Pro Lys Ala Cys Gly Gly Ser Asn Arg Val Ser Asn Leu
 225 230 235 240

Ala Leu Ala Cys Ala Pro Cys Asn Leu Arg Lys Ala Ala Gln Asp Val
 245 250 255

Thr Gln Phe Leu Glu Lys Asp Pro Lys Arg Leu Ala Thr Ile Gln Ala
 260 265 270

Gln Ala Lys Arg Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg
 275 280 285

Trp Lys Leu Leu Asn Ala Leu Lys Ala Thr Gly Leu Thr Asn Arg Thr
 290 295 300

Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Ser Arg Leu Val Ile Pro
 305 310 315 320

Lys Thr His Ala Leu Asp Ala Val Cys Val Gly Glu Gly Asp Phe Val
 325 330 335

Glu Gln Trp Gln Lys Pro Thr Leu Val Ile Lys Ala Thr Gly Arg Gly
 340 345 350

Ser Tyr Gln Arg Thr Arg Leu Asn Arg Phe Gly Phe Pro Arg Gly Tyr
355 360 365

Leu Thr
370

<210> 297
<211> 222
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-249 effector

<400> 297
Met Ala Val Phe Val Leu Asp Arg Ser Ala Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Lys Val Met Pro Phe Thr Ile Arg Val Val Asp Leu Glu Ala Glu
35 40 45

Asp Cys Glu Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Ile Ala Leu Val Arg Glu Thr Ala Glu Lys Asn Gly Val
65 70 75 80

Ala Val Ile Asn Leu Phe Glu Leu Met His Arg Gly Lys Gln Ile Ser
85 90 95

Glu Ala Leu Thr Ala Arg Arg Gly His Arg Arg Met Arg Arg Ser His
100 105 110

Leu Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Gly Asn Lys Lys Ser

115

120

125

Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Thr Leu Ala
 130 135 140

Trp Val Asn Arg Leu Glu Arg Leu Ala Pro Val Ser Ala Ile Ser Thr
 145 150 155 160

Glu Leu Val Arg Phe Asp Met Gln Ala Leu Glu Asn Pro Asp Ile Glu
 165 170 175

Gly Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val His Glu
 180 185 190

Tyr Leu Leu Glu Asn Trp Gly Arg Thr Cys Ala Ser Cys Gly Ala Arg
 195 200 205

His Val Pro Leu His Asn Glu His Leu His Arg Asn Ser Lys
 210 215 220

<210> 298

<211> 480

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-250 effector

<400> 298

Met Ala Val Phe Val Leu Asp Arg Ser Gly Lys Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Lys Leu Leu Ala Ala Gly Arg Ala Arg Val
 20 25 30

His Arg Val Met Pro Phe Val Ile Arg Ile Val Asp Arg Arg Leu Gln
 35 40 45

Asp Ser Ala Leu Gln Pro Leu Arg Val Lys Ile Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Leu Ala Leu Val Arg Glu Ala Glu Ser Ile Asp Ala Ala
65 70 75 80

Ser Gly Glu Val Arg Arg Glu Leu Phe Val Leu Asn Leu Phe Asp Leu
85 90 95

Val His Arg Gly Arg Gln Ile Ser Glu Ala Leu Thr Gly Arg Arg Thr
100 105 110

Phe Arg Arg Arg Arg Arg Gly Ala Asn Leu Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Gly Lys Gly Arg Gly Trp Leu Ala Pro Ser Leu Arg
130 135 140

His Arg Ile Glu Thr Thr Leu Ala Trp Val Arg Arg Leu Gln Arg Trp
145 150 155 160

Ala Pro Val Thr Ala Leu Ser Gln Glu Leu Val Arg Phe Asp Met Gln
165 170 175

Lys Met Glu Asn Ala Glu Ile Ala Gly Val Glu Tyr Gln Gln Gly Thr
180 185 190

Leu Ala Gly Tyr Glu Leu Arg Glu Tyr Leu Leu Glu Lys Phe Asn Arg
195 200 205

Ser Cys Cys Tyr Cys Asp Ala Lys Asp Val Pro Leu Asn Ile Glu His
210 215 220

Ile His Pro Lys Ala Gln Gly Gly Thr Asn Arg Ala Ser Asn Leu Ala
225 230 235 240

Ile Ala Cys Val Pro Cys Asn Thr Lys Lys Gly Ala Arg Ser Ile Glu
245 250 255

Ala Phe Leu Ala Lys Asp Pro Ala Arg Leu Ala Arg Ile Arg Ala Gln

260

265

270

Leu Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn Ala Thr Arg Trp
 275 280 285

Ala Leu Phe Glu Ala Leu Lys Ser Lys Gly Leu Pro Val Glu Thr Gly
 290 295 300

Ser Gly Gly Leu Thr Lys Phe Asn Arg Thr Arg Leu Gly Val Pro Lys
 305 310 315 320

Ser His Ala Leu Asp Ala Ala Cys Val Gly Gln Val Asn Ala Ile His
 325 330 335

Ala Trp Ser Arg Gln Thr Leu Gln Ile Lys Cys Thr Gly Arg Gly Ser
 340 345 350

Tyr Gln Arg Thr Arg Leu Thr Gln Tyr Gly Phe Ala Arg Gly Tyr Leu
 355 360 365

Met Arg Thr Lys Ser Val Lys Gly Phe Arg Thr Gly Asp Leu Val Arg
 370 375 380

Ala Ser Val Thr Ala Gly Lys Lys Ile Gly Glu Tyr Ile Gly Arg Val
 385 390 395 400

Ala Val Arg Ala Thr Gly Ser Phe Asn Ile Gln Thr Val Asp Ala Val
 405 410 415

Val Gln Gly Val Ser His Lys Tyr Cys Arg Ile Val Gln Arg Gly Asp
 420 425 430

Gly Tyr Ser Tyr Ala Trp Ser Ile Thr Pro Ser Asn Thr Gly Lys Asn
 435 440 445

Asn Phe Pro Val Ser Ser Arg Leu Leu Thr Gly Arg Leu Arg Leu Asn
 450 455 460

Val Ala Thr Gln Gln Ala Ser Gln Gly Gly Gly Ile His Arg Ser Ile
 465 470 475 480

<210> 299
<211> 286
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-251 effector

<400> 299
Met Ala Val Phe Val Leu Asp Arg Ser Gly Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Lys Leu Leu Ala Ala Gly Arg Ala Arg Val
20 25 30

His Arg Val Met Pro Phe Val Ile Arg Leu Val Asp Arg Arg Leu Gln
35 40 45

Asp Ser Ala Leu Gln Pro Leu Arg Val Lys Ile Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Leu Ala Leu Val Arg Glu Ala Glu Ser Ile Asp Ala Ala
65 70 75 80

Ser Gly Glu Val Arg Arg Glu Leu Phe Val Leu Asn Leu Phe Asp Leu
85 90 95

Val His Arg Gly Arg Gln Ile Ser Glu Ala Leu Thr Gly Arg Arg Thr
100 105 110

Phe Arg Arg Arg Arg Arg Gly Ala Asn Leu Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Gly Lys Gly Arg Gly Trp Leu Ala Pro Ser Leu Arg
130 135 140

His Arg Ile Glu Thr Thr Leu Ala Trp Val Arg Arg Leu Gln Arg Trp

145		150		155		160									
Ala	Pro	Val	Thr	Ala	Leu	Gln	Glu	Leu	Val	Arg	Phe	Asp	Met	Gln	
				165				170					175		
Lys	Met	Glu	Asn	Ala	Glu	Ile	Ala	Gly	Val	Glu	Tyr	Gln	Gln	Gly	Thr
			180					185					190		
Leu	Ala	Gly	Tyr	Glu	Leu	Arg	Glu	Tyr	Leu	Leu	Glu	Lys	Phe	Asn	Arg
		195					200					205			
Ser	Cys	Cys	Tyr	Cys	Asp	Ala	Lys	Asp	Val	Pro	Leu	Asn	Ile	Glu	His
	210					215					220				
Ile	His	Pro	Lys	Ala	Gln	Gly	Gly	Thr	Asn	Arg	Ala	Ser	Asn	Leu	Ala
225					230					235					240
Ile	Ala	Cys	Val	Pro	Cys	Asn	Thr	Lys	Lys	Gly	Ala	Arg	Ser	Ile	Glu
				245					250					255	
Ala	Phe	Leu	Ala	Lys	Asp	Pro	Ala	Arg	Leu	Ala	Arg	Ile	Arg	Ala	Gln
			260					265					270		
Leu	Lys	Arg	Pro	Leu	Lys	Asp	Ala	Ala	Ala	Val	Asn	Ala	Thr		
		275					280					285			

<210> 300
 <211> 475
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-252 effector

<400> 300
 Met Ala Val Phe Val Leu Asp Arg Ser Gly Lys Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Asp Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Leu Ala Ile Arg Leu Leu Asp Arg Arg Val Ala
35 40 45

Asp Cys Thr Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Ile Ala Leu Val Arg Asp Thr Ala Thr Val Glu Thr Thr
65 70 75 80

Thr Gly Glu Ser Gly Pro Gly Ala Val Val Cys Asn Leu Phe Glu Leu
85 90 95

Met His Arg Gly Ala Ala Ile Arg Lys Ala Leu Arg Gln Arg Ala Ala
100 105 110

Phe Arg Arg Arg Arg Arg Ser Ala Asn Leu Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Thr Arg Thr Glu Ser Trp Leu Ala Pro Ser Leu Gln
130 135 140

His Arg Val Asp Thr Thr Leu Ala Trp Val Glu Arg Leu Arg Arg Leu
145 150 155 160

Ala Pro Val Thr Ala Leu Ala Ser Glu Leu Val Arg Phe Asp Leu Gln
165 170 175

Gln Val Gln Asn Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Thr
180 185 190

Leu Arg Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Phe Glu Arg
195 200 205

Thr Cys Ala Tyr Cys Asp Ala Gln Asn Val Pro Phe Asn Val Asp His
210 215 220

Val Arg Pro Gln Ala Gly Gly Gly Ser Asp Arg Val Ser Asn Leu Ala

225		230		235		240
Leu Ser Cys Val	Pro Cys Asn Glu Ala	Lys Asp Asp Ser	Pro Val Glu			
	245	250	255			
Met Phe Leu Ala	His Asp Pro Glu Arg	Leu Ala Arg Ile	Lys Gln Gln			
	260	265	270			
Leu Lys Thr Pro	Leu Arg Asp Ala Ala	Val Val Asn Ala	Thr Arg Trp			
	275	280	285			
Thr Leu Val Arg	Ala Leu Arg Ala Thr	Gly Leu Pro Leu	Glu Thr Gly			
	290	295	300			
Ser Gly Gly Arg	Thr Lys Trp Asn Arg	Val Arg Leu Gly	Ile Pro Lys			
305	310	315	320			
Thr His Ala Leu	Asp Ala Ala Cys Val	Gly Ala Val Glu	Gln Val Val			
	325	330	335			
Asp Trp Ser Arg	Pro Ala Leu Thr Ile	Lys Ala Thr Gly	Arg Gly Ala			
	340	345	350			
Tyr Gln Arg Thr	Leu Leu Thr Ala His	Gly Phe Pro Arg	Gly Tyr Leu			
	355	360	365			
Met Arg Gln Lys	Arg Ala His Gly Phe	Arg Thr Gly Asp	Leu Val Ala			
	370	375	380			
Ala Thr Ile Pro	Ala Gly Arg His Ala	Gly Gln His Arg	Gly Arg Val			
385	390	395	400			
Ala Ile Arg Thr	Arg Pro Ser Phe Ala	Leu Gln Thr Glu	Ser Gly Thr			
	405	410	415			
Phe Asp Val His	Ala Arg His Leu Arg	Leu Leu Gln Arg	Gly Asp Gly			
	420	425	430			
Tyr Gly Tyr Cys	Ser Gln Pro Leu Pro	Gln Pro Leu Arg	Gly Gly Leu			
	435	440	445			

Ser Ser Pro Arg Tyr Asp Gly Gly Ala Val Asp Gln Gln Ala Leu Trp
450 455 460

Ser Glu Arg Trp Val Arg Ala Lys Gln Asp Cys
465 470 475

<210> 301
<211> 293
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-253 effector

<400> 301
Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Cys Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asn Asn Arg Gly Asn Gln Lys Lys Gly

115

120

125

Trp Leu Pro Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
 130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
 145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly
 165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
 180 185 190

Leu Leu Glu Lys Trp Gly Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
 195 200 205

Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser
 210 215 220

Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys
 225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
 245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
 260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu Lys Ala Thr
 275 280 285

Arg Leu Pro Val Glu
 290

<210> 302

<211> 440

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-254 effector

<400> 302

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Lys Gln Arg Gly
115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Ala Gln Ala Leu Glu Asn Pro Glu Ile Glu Gly
165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr

180

185

190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
 195 200 205

Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser
 210 215 220

Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys
 225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Lys Leu
 245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
 260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr
 275 280 285

Gly Leu Val Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg
 290 295 300

Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
 305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
 325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe
 340 345 350

Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe
 355 360 365

Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile
 370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
 385 390 395 400

Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys
405 410 415

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys
420 425 430

Thr Asp Val Ile Gly Thr Pro Pro
435 440

<210> 303

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-255 effector

<400> 303

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu

100

105

110

Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Lys Gln Arg Gly
 115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
 130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
 145 150 155 160

Leu Val Arg Phe Asp Ala Gln Ala Leu Glu Asn Pro Glu Ile Glu Gly
 165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
 180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
 195 200 205

Val Pro Leu Gln Val Glu His Ile Gln Pro Lys Ala Lys Gly Gly Ser
 210 215 220

Asn Arg Ile Ile Asn Leu Ala Leu Ala Cys Gln Cys Cys Asn Gln Lys
 225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
 245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
 260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu Lys Ala Thr
 275 280 285

Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Gln Thr Lys Phe Asn Arg
 290 295 300

Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
 305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ser Ile
325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe
340 345 350

Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe
355 360 365

Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile
370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
385 390 395 400

Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys
405 410 415

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys
420 425 430

Thr Asp Val Thr Gly Thr Pro Pro Gln His Arg Asp Ala Ser His Pro
435 440 445

Ala Leu Tyr Leu Pro Gly Leu Lys Ala Glu Val Ser Arg Ala Asn
450 455 460

<210> 304

<211> 458

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-256 effector

<400> 304

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys

1	5	10	15												
Thr	Glu	Lys	Arg	Ala	Arg	Leu	Leu	Leu	Glu	Arg	Gly	Arg	Ala	Cys	Val
			20					25					30		
His	Leu	Val	Met	Pro	Phe	Thr	Ile	Arg	Ile	Val	Asp	Leu	Lys	Ala	Glu
		35					40				45				
Asn	Cys	Ala	Phe	Gln	Ala	Leu	Arg	Val	Lys	Leu	Asp	Pro	Gly	Ser	Lys
	50					55					60				
Ala	Thr	Gly	Ile	Ala	Leu	Val	Arg	Glu	Thr	Glu	Gly	Lys	Gly	Val	Ala
65					70					75					80
Val	Val	Asn	Leu	Phe	Glu	Leu	Val	His	Arg	Gly	Arg	Gln	Ile	Ser	Glu
				85					90					95	
Ala	Leu	Thr	Ala	Arg	Arg	Gly	His	Arg	Arg	Leu	Arg	Arg	Ser	Lys	Leu
			100					105					110		
Arg	Tyr	Arg	Pro	Pro	Arg	Phe	Asp	Asn	Arg	Gly	Asn	Gln	Lys	Lys	Gly
		115					120					125			
Trp	Leu	Pro	Pro	Ser	Leu	Gln	His	Arg	Val	Asp	Thr	Ser	Met	Ala	Trp
	130					135					140				
Val	Ser	Arg	Ile	Gln	Arg	Leu	Ala	Pro	Val	Ser	Ala	Ile	Ser	Thr	Glu
145					150					155					160
Leu	Val	Arg	Phe	Asp	Ala	Gln	Ala	Leu	Glu	Asn	Pro	Glu	Ile	Glu	Gly
				165					170					175	
Ala	Gln	Tyr	Gln	Gln	Gly	Thr	Leu	Ala	Gly	Tyr	Glu	Val	Arg	Glu	Tyr
			180					185					190		
Leu	Leu	Glu	Lys	Trp	Asp	Arg	Thr	Cys	Ala	Tyr	Cys	Asp	Ala	Lys	Asp
		195					200					205			
Val	Pro	Leu	Gln	Val	Glu	His	Ile	Gln	Pro	Lys	Ala	Lys	Gly	Gly	Ser
	210					215					220				

Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys Gln Cys Cys Asn Gln Lys
225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Lys Leu
245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Ala Leu Lys Ala Thr
275 280 285

Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Gln Thr Lys Phe Asn Arg
290 295 300

Asn Gln Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe
340 345 350

Gly Cys Val Arg Gly Tyr Met Thr Arg Ser Lys Ser Ile Lys Gly Phe
355 360 365

Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Lys Gly Lys Lys Ile
370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
385 390 395 400

Ile Gln Thr Ser Ala Gly Leu Val Gln Ser Val Ser His Arg Tyr Cys
405 410 415

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Arg Val Ala Lys
420 425 430

Met Asp Val Thr Gly Thr Pro Pro Gln His Arg Asp Ala Ser Ser Arg

435

440

445

Ala Leu Pro Pro Arg Pro Glu Gly Arg Gly
 450 455

<210> 305

<211> 884

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-257 effector

<400> 305

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
 1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
 20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
 35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
 65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
 85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
 100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Gln Lys Lys Gly
 115 120 125

Trp Leu Pro Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly
165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
195 200 205

Val Pro Leu Gln Val Glu His Ile Gln Pro Lys Ala Lys Gly Gly Ser
210 215 220

Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys Gln Cys Cys Asn Gln Lys
225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Lys Leu
245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr
275 280 285

Gly Leu Val Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg
290 295 300

Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Leu Leu Asp Lys Phe

340

345

350

Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe
 355 360 365

Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile
 370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
 385 390 395 400

Ile Gln Thr Ser Thr Gly Leu Val Gln Ser Val Ser His Arg Tyr Cys
 405 410 415

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys
 420 425 430

Met Asp Val Thr Gly Thr Pro Pro Gln His Arg Asp Ala Ser Ser Arg
 435 440 445

Ala Leu Pro Pro Arg Pro Glu Gly Arg Gly Phe Thr Arg Lys Leu Met
 450 455 460

Phe Asn Glu Gln Lys Leu Ala Glu Thr Val Gly Ser Thr Asn Gly Ser
 465 470 475 480

Ala Gln Phe Gly Gly Ala Gly Phe Glu Leu Ala Phe Lys Ala Val Ala
 485 490 495

Lys Leu Ser Pro Thr Asn Val Leu Val Phe Phe Asp Gly Glu Gly Ser
 500 505 510

Gly Trp Val Met His Ile Ala Pro Asp Val Ser Val Val Cys Ala Ala
 515 520 525

Arg Phe Pro Ala Glu Ser Ala Thr Ala Phe Ser Val Met Val Asp Val
 530 535 540

Leu Leu Ala Lys Arg Ile Lys Lys Thr His Val Ala Thr Leu Ser Leu
 545 550 555 560

Thr Ala Gly Arg Lys Leu Asp Leu Ser Leu Glu Pro Asp Thr Thr Lys
565 570 575

Lys Gly Lys Ala Thr Arg Ala Asn Val Ser Val Ala Ala Gln Asn Gly
580 585 590

Leu Ala Lys Val Val Ala Asp Arg Val Met His Asn Leu Ser Leu Ser
595 600 605

Ser Thr Asp Asn Leu Leu Leu Ser Asn Asp Cys Trp Gln Ala Ile Val
610 615 620

Ala Ser Ile Arg Arg Leu Asp Ile Leu Ala Phe Phe Thr Ala Arg Lys
625 630 635 640

Glu Arg Leu Asp Ile Tyr Ala Cys Ser Gln Pro Asp Gly Asn Leu Tyr
645 650 655

Val Tyr Cys Ala Asp Lys Ala Ser Leu Gly Ala Val Ala Cys Pro Ala
660 665 670

Pro Glu Gly Thr Gly Glu Phe Thr Thr Val Leu Thr Ala Asp Ala Leu
675 680 685

Ala Val Ile Gly Leu Leu Phe Asp Ile Asp Met Glu Glu Asp Gly Ala
690 695 700

Asp Ala Ala Asp Met Val Ala Asn Val Ser Leu Ala Leu Thr Asn Thr
705 710 715 720

Gly Phe Leu Val Tyr Asn Glu Ala Ala Leu Leu Tyr Met Pro Ser Pro
725 730 735

Arg Val Phe Pro Asp Gln Thr Asn Val Thr Leu Pro Lys Val Gln Ala
740 745 750

Met Tyr Gln His Ile Lys Glu Ser Tyr His Ser Asp Asp Asn Gly Gly
755 760 765

Glu Tyr Ser Thr Tyr Cys Asp Val Asp Glu Leu Asp Pro Gln Val Leu

770

775

780

Ala Ser Ser Val Lys Phe Gly Ala Asp Leu Ile Glu Asp Ala Ala Val
785 790 795 800

Arg Leu Leu Thr Gly Thr Glu Glu Tyr Leu Ile Val Glu Met Arg Glu
805 810 815

Asn Ala Ser Ser Ile Gln Ser Ala Ile Pro Ala Leu Ile Ser Ser Ser
820 825 830

Val Asn Val Val Leu Asp Pro Arg Leu Leu Gly Gln Ala Val Ile Asn
835 840 845

Phe Lys Gln Pro Val Arg Leu Lys Val Glu Ser Lys Phe Thr Val Leu
850 855 860

His Ala Phe Val Gln Glu Leu Asp Gly Glu His Phe Ile Leu Ile Gly
865 870 875 880

Asn Gln Arg Glu

<210> 306

<211> 213

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-258 effector

<400> 306

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Ser Lys Gln Arg Gly
115 120 125

Trp Leu Ala His Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly
165 170 175

Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
195 200 205

Val Pro Leu Gln Val
210

<210> 307

<211> 304

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-259 effector

<400> 307

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val
20 25 30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg Ser Lys Leu
100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asn Asn Arg Gly Asn Lys Gln Arg Gly
115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Ala Gln Ala Leu Glu Asn Pro Lys Ile Glu Gly
165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
195 200 205

Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser
210 215 220

Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys
225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr
275 280 285

Gly Leu Val Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg
290 295 300

<210> 308

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-260 effector

<400> 308

Met Ala Val Phe Val Leu Asp Arg Ser Gly Arg Pro Leu Met Pro Cys
1 5 10 15

Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Cys Val

20

25

30

His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu Lys Ala Glu
 35 40 45

Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys Gly Val Ala
 65 70 75 80

Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln Ile Ser Glu
 85 90 95

Ala Leu Thr Ala Arg Arg Gly Asn Arg Arg Leu Arg Arg Ser Lys Leu
 100 105 110

Arg Tyr Arg Pro Pro Arg Phe Asn Asn Leu Gly Asn Lys Gln Arg Gly
 115 120 125

Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser Met Ala Trp
 130 135 140

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
 145 150 155 160

Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu Ile Glu Gly
 165 170 175

Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
 180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
 195 200 205

Val Pro Leu Gln Ile Glu His Ile Arg Pro Lys Ser Lys Asn Gly Ser
 210 215 220

Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys
 225 230 235 240

Lys Ala Ala Leu Ser Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr
275 280 285

Gly Leu Val Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg
290 295 300

Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
325 330 335

Lys Ala Met Gly Arg Gly Arg Tyr Gln Arg Thr Arg Leu Asp Lys Phe
340 345 350

Gly Cys Val Arg Gly Tyr Leu Ile Arg Ser Lys Ser Ile Lys Gly Phe
355 360 365

Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile
370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
385 390 395 400

Ile Gln Thr Ser Ala Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys
405 410 415

Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys
420 425 430

Thr Asp Val Arg Gly Thr Pro Pro Gln His Arg Asp Ala Ser His Pro
435 440 445

Ala Leu Tyr Leu Pro Gly Met Asn Ala Glu Val Ser Arg Ala Ile

450

455

460

<210> 309

<211> 426

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-261 effector

<400> 309

Met	Ala	Val	Phe	Val	Leu	Asp	Arg	Ser	Gly	Arg	Pro	Leu	Met	Pro	Cys
1				5					10					15	

Thr	Glu	Lys	Arg	Ala	Arg	Leu	Leu	Leu	Glu	Arg	Gly	Arg	Ala	Cys	Val
			20					25					30		

His	Met	Val	Met	Pro	Phe	Thr	Ile	Arg	Ile	Val	Asp	Leu	Lys	Ala	Glu
		35					40					45			

Asn	Cys	Ala	Phe	Gln	Ala	Leu	Arg	Val	Lys	Leu	Asp	Pro	Gly	Ser	Lys
	50					55					60				

Ala	Thr	Gly	Ile	Ala	Leu	Val	Arg	Glu	Thr	Glu	Gly	Lys	Gly	Val	Ala
65					70					75					80

Val	Val	Asn	Leu	Phe	Glu	Leu	Val	His	Arg	Gly	Arg	Gln	Ile	Ser	Glu
				85					90					95	

Ala	Leu	Thr	Ala	Arg	Arg	Gly	Asn	Arg	Arg	Leu	Arg	Arg	Ser	Lys	Leu
			100					105						110	

Arg	Tyr	Arg	Pro	Pro	Arg	Phe	Asn	Asn	Arg	Gly	Asn	Lys	Gln	Arg	Gly
		115					120					125			

Trp	Leu	Ala	Pro	Ser	Leu	Gln	His	Arg	Val	Asp	Thr	Ser	Met	Ala	Trp
	130					135					140				

Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile Ser Thr Glu
145 150 155 160

Leu Val Arg Phe Asp Ala Gln Ala Leu Glu Asn Pro Glu Ile Glu Gly
165 170 175

Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr
180 185 190

Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly Ala Lys Asp
195 200 205

Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys Asn Gly Ser
210 215 220

Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Gln Lys
225 230 235 240

Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys Pro Glu Leu
245 250 255

Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala
260 265 270

Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu Lys Thr Thr
275 280 285

Gly Leu Val Val Glu Thr Gly Thr Gly Gly Gln Thr Lys Phe Asn Arg
290 295 300

Ser Gln Phe Asp Ile Pro Lys Thr His Ala Leu Asp Ala Ala Cys Val
305 310 315 320

Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr Leu Ala Ile
325 330 335

Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Asp Lys Phe
340 345 350

Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile Lys Gly Phe

355

360

365

Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly Lys Lys Ile
 370 375 380

Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe Asn
 385 390 395 400

Ile Gln Thr Ser Ala Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys
 405 410 415

Ala Val Val Gln Arg Gly Asn Gly Tyr Gly
 420 425

<210> 310

<211> 39

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-262 effector

<400> 310

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Val Pro Phe Thr
 35

<210> 311

<211> 245

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-263 effector

<400> 311

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
65 70 75 80

Leu His Leu Thr Glu Leu His His Arg Gly Ala Ser Ile Arg Lys Ala
85 90 95

Leu Gln Gln Arg Lys Asn Tyr Arg Arg Gly Arg Arg Ser Arg Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Ala Asp Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu

180

185

190

Leu Glu Lys Phe Gly Arg Gln Cys Val Tyr Cys Asp Arg Thr Asp Arg
 195 200 205

Pro Leu Gln Ile Glu His Leu Thr Pro Lys Gly Ser Gly Gly Ser Asp
 210 215 220

Arg Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
 225 230 235 240

Gly Asn Arg Thr Val
 245

<210> 312

<211> 319

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-264 effector

<400> 312

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
 35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
 65 70 75 80

Leu His Leu Thr Glu Leu His His Arg Gly Ala Ser Ile Arg Lys Ala
85 90 95

Leu Gln Gln Arg Lys Asn Tyr Arg Arg Gly Arg Arg Ser Arg Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Ala Asp Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Phe Gly Arg Gln Cys Val Tyr Cys Asp Arg Thr Asp Arg
195 200 205

Pro Leu Gln Ile Glu His Leu Thr Pro Lys Gly Ser Gly Gly Ser Asp
210 215 220

Arg Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
225 230 235 240

Gly Asn Arg Thr Val Glu His Tyr Leu Ala His Asp Pro Ile Arg Arg
245 250 255

Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Ile Leu Thr Lys Thr Gly
275 280 285

Leu Pro Val Glu Ser Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Ser

290

295

300

Arg Leu Gly Ile Pro Lys Arg Asp Ala Phe Asp Ala Ala Cys Ala
 305 310 315

<210> 313

<211> 373

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-265 effector

<400> 313

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
 35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
 65 70 75 80

Leu His Leu Thr Glu Leu His His Arg Gly Ala Ser Ile Arg Lys Ala
 85 90 95

Leu Gln Gln Arg Lys Asn Tyr Arg Arg Gly Arg Arg Ser Arg Asn Leu
 100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Ala Asp Gly Trp
 115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Phe Gly Arg Gln Cys Val Tyr Cys Asp Arg Thr Asp Arg
195 200 205

Pro Leu Gln Ile Glu His Leu Thr Pro Lys Gly Ser Gly Gly Ser Asp
210 215 220

Arg Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
225 230 235 240

Gly Asn Arg Thr Val Glu His Tyr Leu Ala His Asp Pro Ile Arg Arg
245 250 255

Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Val Arg Asp Ala Ala Ala
260 265 270

Val Asn Gly Thr Arg Trp Ala Ile Trp Glu Ile Leu Thr Lys Thr Gly
275 280 285

Leu Pro Val Glu Cys Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Ser
290 295 300

Arg Leu Gly Ile Pro Lys Arg Asp Ala Phe Asp Ala Ala Cys Ala Gly
305 310 315 320

Thr Val Asp Gln Val Leu Gly Trp Asp Arg Pro Ile Gln Arg Ile Asp
325 330 335

Cys Leu Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Lys Asp Gly

340

345

350

Val Pro Arg Gly Tyr Leu Pro Arg Thr Gln Ile Arg Gln Gly Val Arg
 355 360 365

Thr Gly His Gln Val
 370

<210> 314
 <211> 323
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-266 effector

<400> 314
 Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
 35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Val Thr Gly Val Ala Val Val Arg Glu Ala Gly Asp Thr His His Val
 65 70 75 80

Leu His Leu Ser Glu Leu His His Arg Gly Ala Ser Ile Arg Lys Thr
 85 90 95

Leu Gln Gln Arg Lys Asn Tyr Arg Arg Gly Arg Arg Thr Arg Asn Leu
 100 105 110

Arg His Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Glu Gly Trp
115 120 125

Leu Ala Pro Ser Leu Leu His Arg Val Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ala Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Met Gln Gln Met Val Ser Pro Glu Leu Ser Gly Leu
165 170 175

Ala Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Gly Arg Thr Cys Val Cys Cys Asp Arg Thr Asp Arg
195 200 205

Pro Leu Gln Val Glu His Leu Thr Pro Gln Gly Ser Gly Gly Ser Asp
210 215 220

Arg Ile Ser Asn Leu Ala Leu Ala Cys Gln Pro Cys Asn Glu Ala Lys
225 230 235 240

Gly Asn Gln Thr Val Glu Val Tyr Leu Ile Ser Asp Pro Ile Arg Arg
245 250 255

Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Met Leu Thr Arg Thr Gly
275 280 285

Leu Ala Val Glu Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Ala
290 295 300

Arg Met Gly Ile Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys Ala Gly
305 310 315 320

Thr Val Asp

<210> 315
<211> 259
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-267 effector

<400> 315
Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Arg Val Glu
35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Val Thr Gly Val Ala Val Val Arg Glu Ala Gly Asp Thr His His Val
65 70 75 80

Leu His Leu Thr Glu Leu His His Arg Gly Ala Ser Ile Arg Lys Thr
85 90 95

Leu Gln Gln Arg Lys Asn Tyr Arg Arg Gly Arg Arg Thr Arg Asn Leu
100 105 110

Arg His Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Glu Gly Trp
115 120 125

Leu Ala Pro Ser Leu Leu His Arg Val Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ala Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Met Gln Leu Met Val Ser Pro Glu Ile Ser Gly Ile
165 170 175

Ala Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Gly Arg Thr Cys Val Cys Cys Asp Arg Thr Asp Arg
195 200 205

Pro Leu Gln Val Glu His Leu Thr Pro Lys Gly Ser Gly Gly Ser Asp
210 215 220

Arg Ile Ser Asn Leu Ala Leu Ala Cys Gln Pro Cys Asn Glu Ala Lys
225 230 235 240

Gly Asn Gln Thr Val Glu Val Tyr Leu Ile Ser Asp Pro Ile Arg Arg
245 250 255

Asp Arg Ile

<210> 316

<211> 466

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-268 effector

<400> 316

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val

20

25

30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Ser Val Glu
 35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
 50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
 65 70 75 80

Leu His Leu Ala Glu Val His His Arg Gly Ala His Ile Arg Lys Val
 85 90 95

Leu Gln Gln Arg Ala Gly Tyr Arg Arg Gly Arg Arg Ser Arg Asn Leu
 100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Asp Gly Trp
 115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Ala Glu Thr Trp Val
 130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
 145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
 165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
 180 185 190

Leu Glu Lys Trp Gly Arg Thr Cys Val Tyr Cys Asp Trp Thr Asp Arg
 195 200 205

Pro Leu Gln Val Glu His Leu Ile Pro Lys Gly Ser Gly Gly Ser Asp
 210 215 220

Arg Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
 225 230 235 240

Gly Asn Gln Thr Val Glu Ala Tyr Leu Ala His Asp Pro Val Arg Arg
245 250 255

Asp Arg Ile Leu Gln Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Met Leu Thr Lys Thr Gly
275 280 285

Leu Asp Val Glu Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Ser
290 295 300

Arg Leu Gly Ile Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys Ala Gly
305 310 315 320

Thr Ile Glu Gln Val Val Gly Trp Asp Arg Pro Ile Gln Arg Ile Asp
325 330 335

Cys Leu Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Lys Asp Gly
340 345 350

Phe Pro Arg Gly Tyr Leu Pro Arg Thr Lys Met Val Arg Gly Phe Arg
355 360 365

Thr Gly Asp His Val Arg Ala Thr Val Pro Thr Gly Lys Lys Thr Gly
370 375 380

Thr Trp Ile Gly Arg Val Ala Val Arg Thr Thr Gly Ser Phe Asp Ile
385 390 395 400

Gln Thr Val Ala Lys Thr Val Gln Gly Ile Ser Ala Arg Trp Cys Val
405 410 415

Leu Leu Gln Arg Gly Asp Gly Tyr Arg Tyr Ser Arg Val Glu Ser Glu
420 425 430

Pro Pro Leu Ala Val Arg Pro Ser Ser Arg Arg Pro Lys Ala Thr Leu
435 440 445

Ser Gly Pro Arg Val Ser Leu Val Thr Thr Arg Ser Leu Glu Gly Ser

450

455

460

Gly Arg
465

<210> 317
<211> 185
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-269 effector

<400> 317
Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Ser Val Glu
35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
65 70 75 80

Leu His Leu Ala Glu Val His His Arg Gly Ala His Ile Arg Lys Val
85 90 95

Leu Gln Gln Arg Ala Gly Tyr Arg Arg Gly Arg Arg Ser Arg Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Asp Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly
180 185

<210> 318

<211> 466

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-270 effector

<400> 318

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Ser Val Glu
35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
65 70 75 80

Leu His Leu Ala Glu Val His His Arg Gly Ala His Ile Arg Lys Val

85

90

95

Leu Gln Gln Arg Ala Gly Tyr Arg Arg Gly Arg Arg Ser Arg Asn Leu
 100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Asp Gly Trp
 115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Thr Glu Thr Trp Val
 130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
 145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
 165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
 180 185 190

Leu Glu Lys Trp Gly Arg Thr Cys Val Tyr Cys Asp Trp Thr Asp Arg
 195 200 205

Pro Leu Gln Val Glu His Leu Ile Pro Lys Gly Ser Gly Gly Ser Asp
 210 215 220

Arg Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
 225 230 235 240

Gly Asn Gln Thr Val Glu Ala Tyr Leu Ala His Asp Pro Val Arg Arg
 245 250 255

Asp Arg Ile Leu Gln Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
 260 265 270

Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Met Leu Thr Lys Thr Gly
 275 280 285

Leu Asp Val Glu Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Ser
 290 295 300

Arg Leu Gly Ile Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys Ala Gly
305 310 315 320

Thr Ile Glu Gln Val Val Gly Trp Asp Arg Pro Ile Gln Arg Ile Asp
325 330 335

Cys Leu Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Lys Asp Gly
340 345 350

Phe Pro Arg Gly Tyr Leu Pro Arg Thr Lys Met Val Arg Gly Phe Arg
355 360 365

Thr Gly Asp His Val Arg Ala Thr Val Pro Thr Gly Lys Lys Thr Gly
370 375 380

Thr Trp Ile Gly Arg Val Ala Val Arg Thr Thr Gly Ser Phe Asp Ile
385 390 395 400

Gln Thr Val Ala Lys Thr Val Gln Gly Ile Ser Ala Arg Trp Cys Val
405 410 415

Leu Leu Gln Arg Gly Asp Gly Tyr Arg Tyr Ser Arg Val Glu Ser Glu
420 425 430

Pro Pro Leu Ala Val Arg Pro Ser Ser Arg Arg Pro Lys Ala Thr Leu
435 440 445

Ser Gly Pro Arg Val Ser Leu Val Thr Thr Arg Ser Leu Glu Gly Ser
450 455 460

Gly Arg
465

<210> 319

<211> 274

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-271 effector

<400> 319

Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Ser Val Glu
35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Val Thr Gly Leu Ala Ile Val Arg Glu Ala Gly Asp Thr His His Val
65 70 75 80

Leu His Leu Ala Glu Val His His Arg Gly Ala His Ile Arg Lys Val
85 90 95

Leu Gln Gln Arg Ala Gly Tyr Arg Arg Gly Arg Trp Ser Arg Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Pro Asp Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Met Val Thr Thr Glu Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ser Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Leu Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Phe Gly Arg Gln Cys Val Tyr Cys Asp Arg Thr Asp Arg
195 200 205

Pro Leu Gln Ile Glu His Leu Thr Pro Lys Gly Ser Gly Gly Ser Asp
210 215 220

Arg Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
225 230 235 240

Gly Asn Arg Thr Val Glu His Tyr Leu Ala His Asp Pro Ile Arg Arg
245 250 255

Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
260 265 270

Val Asn

<210> 320
<211> 443
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-272 effector

<400> 320
Met Ala Val Phe Val Leu Asp Arg Ser Lys His Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Val Pro Phe Thr Ile Arg Leu Val Asp Arg Thr Val Ala
35 40 45

Thr Ser Val Leu Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys

50

55

60

Val Thr Gly Leu Ala Ile Val Arg Glu Glu Gly Glu Thr His His Val
65 70 75 80

Leu His Leu Ala Glu Val His His Arg Gly Ala Pro Ile Arg Lys Ala
85 90 95

Leu Gln Gln Arg Ala Gly Tyr Arg Arg Gly Arg Arg Ser Arg Lys Leu
100 105 110

Arg His Arg Ala Pro Arg Phe Leu Asn Arg Arg Arg Asp Asp Gly Trp
115 120 125

Leu Ala Pro Ser Leu Gln His Arg Val Leu Thr Thr Gln Thr Trp Val
130 135 140

Lys Arg Tyr Arg Ala Leu Ala Pro Ile Val Ala Leu Thr Val Glu Arg
145 150 155 160

Val Arg Phe Asp Met Gln Gln Met Val Thr Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Gly Arg Thr Cys Val Tyr Cys Asp His Thr Asp Arg
195 200 205

Pro Leu Gln Val Glu His Leu Thr Pro Thr Gly Ser Gly Gly Ser Asp
210 215 220

Gln Val Ser Asn Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys
225 230 235 240

Gly Asn Gln Thr Val Glu Val Tyr Leu Ala Asp Asp Pro Val Arg Arg
245 250 255

Asp Arg Ile Leu Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Trp Ala Ile Trp Glu Met Leu Thr Arg Thr Gly
275 280 285

Val Pro Val Glu Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Thr
290 295 300

Arg Met Gly Ile Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys Ala Gly
305 310 315 320

Thr Val Asp Gln Val Leu Gly Trp Asp Arg Pro Ile Gln Arg Val Asp
325 330 335

Cys Leu Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Lys Asp Gly
340 345 350

Phe Pro Arg Gly Tyr Leu Pro Arg Thr Lys Met Val Gln Gly Phe Arg
355 360 365

Thr Gly Asp His Val Arg Ala Ile Val Glu Thr Gly Ala His Arg Gly
370 375 380

Thr Trp Thr Gly Arg Val Ala Val Arg Ser Thr Gly Ser Phe Asn Ile
385 390 395 400

Gln Thr Gly Ala Ala Thr Ile Gln Gly Ile Ala Ala Arg Trp Cys Val
405 410 415

Leu Leu Gln Arg Gly Asp Gly Tyr Arg Tyr Ser Leu Ala Leu Pro Arg
420 425 430

Thr Glu His Ala Ile Arg Pro Ser Ser Val Ala
435 440

<210> 321

<211> 35

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-273 effector

<400> 321

Met	Ala	Val	Phe	Val	Leu	Asp	Thr	Gln	Gly	Gln	Ala	Leu	Met	Pro	Cys
1				5					10					15	

Thr	Glu	Lys	Arg	Ala	Arg	Leu	Leu	Leu	Ala	Arg	Gly	Arg	Ala	Arg	Val
			20					25					30		

His	Arg	Leu
		35

<210> 322

<211> 53

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-274 effector

<400> 322

Met	Ala	Val	Phe	Val	Leu	Ser	Lys	Asn	Lys	Lys	Pro	Leu	Met	Pro	Cys
1				5					10					15	

Ser	Glu	Lys	Arg	Ala	Arg	Ile	Leu	Leu	Ser	Lys	Lys	Gln	Ala	Val	Val
			20					25					30		

His	Gln	His	His	Pro	Phe	Thr	Ile	Arg	Leu	Lys	Lys	Gln	Thr	Gly	Asn
		35					40					45			

Glu	Thr	Gln	Pro	Ile
				50

<210> 323

<211> 430

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-275 effector

<400> 323

Met Ala Val Phe Val Leu Ser Lys Asn Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Ile Leu Leu Ser Lys Lys Gln Ala Val Val
20 25 30

His Gln His Tyr Pro Phe Thr Ile Arg Leu Lys Lys Gln Thr Gly Asn
35 40 45

Glu Thr Gln Pro Ile Gln Leu Lys Ile Asp Pro Gly Ser Arg Tyr Thr
50 55 60

Gly Val Ala Leu Val Met Asp Leu Pro Thr Leu Met Arg Ala Leu Cys
65 70 75 80

Leu Phe Glu Ile Gln His Arg Gly His Gln Ile Ser Glu Ala Leu Thr
85 90 95

Gln Arg Arg Ala Phe Arg Arg Arg Arg Arg Asn Gln Leu Arg Tyr Arg
100 105 110

Pro Ala Arg Phe Asn Asn Arg Thr Arg Lys Ala Gly Trp Leu Pro Pro
115 120 125

Ser Val Gln His Leu Leu Asp Thr Thr Phe Ala Leu Val Gln Lys Leu
130 135 140

Lys Arg Arg Cys Pro Ile Ser Ala Ile Val Phe Glu Gln Val Lys Phe
145 150 155 160

Asp Met Gln Lys Met Gln Asn Pro Asn Ile Gln Gly Val Glu Tyr Gln

165

170

175

His Gly Thr Leu Phe Gln Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys
 180 185 190

His Arg His Thr Cys Ala Tyr Cys Gly Gly Glu Ser Gln Asp Ala Ile
 195 200 205

Leu Glu Val Glu His Lys His Pro Arg Ala Gln Gly Gly Ser Asn Ser
 210 215 220

Ile Arg Asn Leu Val Ile Ala Cys His Thr Cys Asn Gln Thr Lys Gly
 225 230 235 240

Asn Arg Thr Leu Ser Glu Phe Leu Thr Val Leu Lys Asn Thr Lys Leu
 245 250 255

Asp Lys Val Arg Lys Val Asn Ile Ala Gln Ile Leu Ala Gly Lys Val
 260 265 270

Phe Leu Leu Arg Asp Ala Ser Ala Val Asn Ala Cys Arg His Gln Leu
 275 280 285

Gly Lys Thr Leu Leu Thr Leu Ser Leu Pro Val Ser Thr Gly Thr Gly
 290 295 300

Ala Gln Thr Lys Tyr Asn Arg Met His Tyr Gln Leu Pro Lys Ser His
 305 310 315 320

Ala Leu Asp Ala Leu Met Thr Gly Asn Met Glu Lys Pro Ile Glu Ala
 325 330 335

Trp His Lys Pro Thr Leu Ile Val Lys Ala Met Gly Arg Gly Cys Tyr
 340 345 350

Lys Arg Thr Arg Leu Asn Gln Tyr Gly Phe Pro Arg Gly Tyr Leu Gln
 355 360 365

Arg Lys Lys Ile Tyr Phe Gly Phe Gln Thr Gly Asp Leu Val Val Ser
 370 375 380

Thr Val Leu Lys Gly Lys Lys Ile Gly Thr Tyr Ile Gly Arg Leu Ala
385 390 395 400

Val Arg Asp Ser Gly Tyr Phe Asn Ile Gln Thr Pro Thr Gly Val Ile
405 410 415

Gln Gly Ile Ser His Lys Thr Cys Arg Leu Ile Gln Arg Asn
420 425 430

<210> 324
<211> 31
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-276 effector

<400> 324
Met Ala Val Phe Val Val Asp Lys Arg Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Lys Ala Val
20 25 30

<210> 325
<211> 281
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-277 effector

<400> 325
Met Ala Val Phe Val Val Asp Arg His Lys Lys Pro Leu Met Pro Cys

1	5	10	15												
Ser	Glu	Lys	Arg	Ala	Arg	Lys	Leu	Leu	Ala	Arg	Gly	Arg	Ala	Arg	Val
			20				25						30		
His	Arg	Leu	Met	Pro	Phe	Ala	Ile	Arg	Leu	Val	Asp	Arg	Thr	Val	Asn
		35					40					45			
Glu	Ser	Val	Leu	Gln	Pro	Ala	Lys	Ile	Lys	Leu	Asp	Pro	Gly	Ser	Lys
	50					55					60				
Thr	Thr	Gly	Ile	Ala	Val	Val	Arg	Glu	Ser	Ala	Thr	Ala	Asp	Glu	Glu
65					70					75					80
Thr	Gly	Glu	Ile	His	Thr	Thr	Val	His	Val	Leu	Asn	Leu	Leu	Glu	Leu
				85					90					95	
His	His	Arg	Gly	Lys	Gln	Ile	Ser	Glu	Ser	Leu	Thr	Ala	Arg	Arg	Gln
			100					105					110		
Leu	Arg	Arg	Arg	Arg	Arg	Gly	Asn	Leu	Arg	Tyr	Arg	Lys	Pro	Arg	Phe
		115					120					125			
Leu	Asn	Arg	Ala	Lys	Pro	Lys	Gly	Trp	Leu	Ala	Pro	Ser	Leu	Gln	His
	130					135					140				
Arg	Val	Asp	Thr	Ile	Gly	Ala	Trp	Val	Asn	Arg	Phe	Gln	Gln	Leu	Ala
145					150					155					160
Pro	Ile	Thr	Gly	Ile	Asp	Gln	Glu	Leu	Val	Arg	Phe	Asp	Leu	Gln	His
				165					170					175	
Leu	Glu	Asn	Pro	Glu	Ile	Ser	Gly	Ile	Glu	Tyr	Gln	Gln	Gly	Thr	Leu
			180					185					190		
Ala	Gly	Tyr	Glu	Thr	Arg	Glu	Tyr	Leu	Leu	Asn	Lys	Trp	Asn	Arg	Ala
		195					200					205			
Cys	Ala	Tyr	Cys	Gly	Ala	Lys	Asn	Val	Pro	Phe	Gln	Ile	Asp	His	Ile
	210					215					220				

His Pro Arg Ala Gly Gly Gly Ser His Arg Val Ser Asn Leu Thr Leu
225 230 235 240

Ala Cys Gln Pro Cys Asn Gln Lys Lys Gly Ala Gln Glu Ile Asn Ile
245 250 255

Phe Leu Ala Lys Asp Pro Lys Arg Leu Ala Arg Ile Gln Ala Gln Ala
260 265 270

Lys Ala Pro Leu Lys Asp Ala Ala Ala
275 280

<210> 326
<211> 455
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-278 effector

<400> 326
Met Ala Val Phe Val Val Asp Arg His Lys Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Lys Leu Leu Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Met Pro Phe Ala Ile Arg Leu Val Asp Arg Thr Val Asn
35 40 45

Glu Ser Val Leu Gln Pro Ala Lys Ile Lys Leu Asp Pro Gly Ser Lys
50 55 60

Thr Thr Gly Ile Ala Val Val Arg Glu Ser Ala Thr Ala Asp Glu Glu
65 70 75 80

Thr Gly Glu Ile His Thr Thr Val His Val Leu Asn Leu Leu Glu Leu

85

90

95

His His Arg Gly Lys Gln Ile Ser Glu Ser Leu Thr Ala Arg Arg Gln
 100 105 110

Leu Arg Arg Arg Arg Arg Gly Asn Leu Arg Tyr Arg Lys Pro Arg Phe
 115 120 125

Leu Asn Arg Ala Lys Pro Lys Gly Trp Leu Ala Pro Ser Leu Gln His
 130 135 140

Arg Val Asp Thr Ile Gly Ala Trp Val Asn Arg Phe Gln Gln Leu Ala
 145 150 155 160

Pro Ile Thr Gly Ile Asp Gln Glu Leu Val Arg Phe Asp Leu Gln His
 165 170 175

Leu Glu Asn Pro Glu Ile Ser Gly Ile Glu Tyr Gln Gln Gly Thr Leu
 180 185 190

Ala Gly Tyr Glu Thr Arg Glu Tyr Leu Leu Asn Lys Trp Asn Arg Ala
 195 200 205

Cys Ala Tyr Cys Gly Ala Lys Gln Ile Pro Leu Gln Ile Asp His Ile
 210 215 220

His Pro Arg Ala Arg Gly Gly Ser Asp Arg Val Ser Asn Leu Thr Leu
 225 230 235 240

Ala Cys Gly Pro Cys Asn Gln Glu Lys Gly Ser Leu Leu Ile Ala Glu
 245 250 255

Tyr Leu Lys Asp His Thr Asp Arg Leu Lys Arg Ile Gln Ala Gln Ala
 260 265 270

Gln Ala Pro Leu Lys Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala
 275 280 285

Leu Phe Asn Thr Leu Lys Thr Met Gly Leu Pro Val Thr Thr Gly Ser
 290 295 300

Gly Gly Gln Thr Lys Phe Asn Arg Ala Arg Leu Glu Ile Pro Lys Thr
305 310 315 320

His Ala Leu Asp Ala Ala Cys Val Gly Thr Met Glu Ala Ile Arg Asp
325 330 335

Trp Asn Arg Pro Thr Leu Leu Ile Lys Ala Thr Gly Arg Gly Ser Tyr
340 345 350

Gln Arg Thr Arg Leu Asn Ala Tyr Gly Phe Pro Arg Gly Tyr Leu Thr
355 360 365

Arg Gln Lys Arg Ile Lys Gly Phe Gln Thr Gly Asp Met Val Lys Ala
370 375 380

Glu Val Thr Lys Gly Lys Lys Thr Gly Ser Tyr Leu Gly Arg Val Ala
385 390 395 400

Val Arg Ala Ser Gly Ser Phe Asn Leu Gln Thr Ala Gln Gly Val Ile
405 410 415

Gln Gly Val Gly Tyr Arg Tyr Cys Lys Val Ile Gln Arg Ala Asp Gly
420 425 430

Tyr Gly Tyr Ser Gln Gln Leu Asn Pro Lys Glu Ala Glu Leu Arg Ser
435 440 445

Ala Arg Tyr Pro Ser Pro Ala
450 455

<210> 327

<211> 227

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-279 effector

<400> 327

Met Ala Val Phe Val Val Asp Arg Arg Gln Ala Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Ala Gln Gly Arg Ala Arg Val
20 25 30

His Arg Leu Ile Pro Phe Thr Ile Arg Leu Ile Asp Arg Glu Val Val
35 40 45

Gln Ser Thr Leu Gln Pro Leu Glu Leu Lys Ile Asp Pro Gly Ser Lys
50 55 60

Thr Ser Gly Leu Ala Leu Val Arg Asn Asn Asn Thr Val Asn Ala Glu
65 70 75 80

Thr Gly Lys Ile Thr Ala Thr Ala His Val Leu Asn Leu Phe Glu Leu
85 90 95

Thr His Arg Gly Phe Gln Ile Ser His Thr Leu Thr Ala Arg Arg Gln
100 105 110

Met Arg Arg Arg Arg Arg Ser Ala Asn Leu Arg Tyr Arg Ala Pro Arg
115 120 125

Phe Leu Asn Arg Lys Asn Lys Gly Lys Gly Trp Leu Ala Pro Ser Leu
130 135 140

Gln His Arg Ile Asp Thr Thr Leu Ser Trp Val Val Arg Leu Arg Asn
145 150 155 160

Val Ala Pro Ser Thr His Leu Ala Gln Glu Leu Val Arg Phe Asp Met
165 170 175

Gln Gln Leu Glu Asn Pro Glu Ile Ala Gly Val Gln Tyr Gln Gln Gly
180 185 190

Glu Leu Arg Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp Gly
195 200 205

Arg Gln Cys Ala Tyr Cys Asp Val Ser Asn Val Pro Leu Gln Ile Glu
210 215 220

His Ile His
225

<210> 328
<211> 191
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-280 effector

<400> 328
Met Ala Val Leu Val Leu Asp Arg Glu Asp Arg Leu Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Phe Ala Arg Gly Arg Ala Arg Val
20 25 30

His Arg Val Leu Pro Phe Val Ile Arg Leu Val Asp Arg Arg Ala Asp
35 40 45

Asp Cys Asp Phe Gln Pro Leu Arg Leu Lys Leu Asp Pro Gly Ser Lys
50 55 60

Ile Thr Gly Met Val Leu Val Arg Gln Thr Gly Asn Asp Gly Ile Ala
65 70 75 80

Val Leu Asn Leu Phe Glu Leu Ile His Arg Gly Arg Gln Ile Ser Glu
85 90 95

Ala Leu Thr Ala Arg Arg Asn Met Arg Arg Arg Arg Arg Ala Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Arg Met Pro Ala Gly Trp

115

120

125

Leu Pro Pro Ser Leu Gln His Leu Val Asp Thr Thr Met Ala Trp Ile
 130 135 140

Arg Arg Leu Tyr Arg Trp Ala Pro Ile Ser Ala Leu Ser Thr Glu Leu
 145 150 155 160

Val Gln Phe Asp Met Gln Ala Met Glu Asp Pro Asp Ile Glu Gly Val
 165 170 175

Glu Tyr Gln Gln Gly Ala Leu Ala Ala Tyr Glu Leu Arg Glu Tyr
 180 185 190

<210> 329

<211> 436

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-281 effector

<400> 329

Met Ala Val Tyr Val Leu Asp Lys Ser Gly Lys Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Val Arg Gly Arg Ala Arg Val
 20 25 30

His Arg Leu Met Pro Phe Ala Ile Arg Leu Thr Asp Arg Lys Gln Ala
 35 40 45

Glu Ser Leu Leu Gln Pro Leu Ala Ile Lys Val Asp Pro Gly Ser Arg
 50 55 60

Tyr Thr Gly Met Ala Leu Val Arg Gln Gln Ala Lys Cys Val Ser Val
 65 70 75 80

Leu Ser Leu Met Glu Leu Ala His Arg Gly Ala Ala Ile Arg Lys Ala
85 90 95

Leu Glu Gln Arg Ala Gly Tyr Arg Arg Arg Arg Arg Ser Gln Asn Leu
100 105 110

Arg His Arg Glu Ala Arg Phe Asp Asn Arg Ser Arg Pro Asp Gly Trp
115 120 125

Leu Pro Pro Ser Leu Gln His Arg Val Asp Thr Thr Leu Ser Trp Val
130 135 140

Gln Arg Leu Arg Arg Leu Ala Pro Val Cys Glu Met Ala Ile Glu Arg
145 150 155 160

Val Lys Phe Asp Met Gln Ala Met His Asn Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Gly Arg Cys Cys Ala Tyr Cys Phe Ala Glu Asn Thr
195 200 205

Pro Leu Glu Val Glu His Ile Gln Ala Arg Ser Asn Gly Gly Ser Asp
210 215 220

Arg Val Ser Asn Leu Thr Leu Ala Cys His Pro Cys Asn Gln Arg Lys
225 230 235 240

Gly Asn Gln Pro Val Glu Leu Phe Leu Lys Gly Lys Pro Glu Leu Leu
245 250 255

Ala Arg Ile Lys Ala Asn Ala Lys Val Pro Leu Arg Asp Ala Ala Ala
260 265 270

Val Asn Ala Thr Arg Asn Thr Leu Phe Gln Ala Leu Leu Ala Thr Gly
275 280 285

Leu Pro Val Ala Thr Gly Thr Gly Ala Gln Thr Lys Tyr Asn Arg Arg

290

295

300

Arg Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Val Cys Val Gly
 305 310 315 320

Glu Val Asp Thr Val Thr Gly Trp Gln Arg Pro Thr Leu Ser Ile Lys
 325 330 335

Ala Thr Gly Arg Gly Glu Tyr Gln Arg Thr Arg Leu Thr Ala His Gly
 340 345 350

Phe Pro Arg Gly Tyr Leu Thr Arg Gln Lys Arg His Phe Gly Phe Gln
 355 360 365

Thr Gly Asp Gln Ile Ile Ala Thr Val Pro Ser Gly Lys Lys Ala Gly
 370 375 380

Val His Lys Val Arg Ala Ala Val Arg Lys Ser Gly Ser Phe Asn Val
 385 390 395 400

Gln Met Leu Ser Thr Val Ile Gln Gly Ile His His Arg His Cys Arg
 405 410 415

Ile Ile Gln Arg Ala Asp Gly Tyr Ser Tyr Ala Gln Ile Ser Thr Gln
 420 425 430

Asp Ser Gln Pro
 435

<210> 330

<211> 305

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-282 effector

<400> 330

Met Ala Val Tyr Val Leu Asp Lys Ser Gly Met Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Cys Gly Arg Ala Arg Ile
20 25 30

His Arg Gln Leu Pro Phe Val Ile Arg Leu Val Asp Arg Arg Val Asn
35 40 45

Asp Ser Ala Leu Gln Leu Leu Thr Leu Lys Leu Asp Pro Gly Ser Arg
50 55 60

Ile Thr Gly Leu Ala Leu Ile Arg Glu Gln Gly Gln Arg Val Ser Val
65 70 75 80

Leu Ser Leu Leu Glu Met Ile His Arg Gly Ala Ala Ile Arg Gln Ala
85 90 95

Met Gln Gln Arg Ala Ala Phe Arg Arg Arg Arg Arg Ser Ala Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Asp Asn Arg Thr Leu Pro Gln Gly Trp
115 120 125

Leu Pro Pro Ser Leu Arg His Arg Pro Ala Ile Thr Leu Gly Trp Val
130 135 140

Glu Arg Met Arg Asn Trp Thr Pro Ile Ser Cys Leu Ala Val Glu Arg
145 150 155 160

Val Lys Phe Asp Met Gln Ala Met Gln Asn Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Ile Glu
180 185 190

His Ile Val Ala Arg Ser Asn Gly Gly Ser Asp Arg Val Phe Asn Leu
195 200 205

Thr Leu Ala Cys Arg Pro Cys Asn Gln Arg Lys Gly Asn Gln Pro Val

210

215

220

Glu Val Phe Leu Lys Arg Asp Pro Asp Arg Leu Ser Arg Ile Lys Ala
 225 230 235 240

Arg Ala Lys Ala Pro Leu Arg Asp Ala Ala Glu Ile Asn Ala Thr Arg
 245 250 255

Asn Ala Leu Phe Val Asp Met Leu Asn Thr Gly Leu Pro Val Ser Thr
 260 265 270

Gly Thr Gly Ala Gln Thr Lys Tyr Asn Arg Gln Arg Leu Gly Val Pro
 275 280 285

Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Lys Ala Ile
 290 295 300

Glu
 305

<210> 331
 <211> 425
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 uncultivated organism

<220>
 <223> Category: MG35 effectors

<220>
 <223> Description: MG35-283 effector

<400> 331
 Met Ala Val Tyr Val Leu Asp Lys Ser Gly Met Pro Leu Met Pro Cys
 1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Cys Gly Arg Ala Arg Ile
 20 25 30

His Arg Gln Leu Pro Phe Val Ile Arg Leu Val Asp Arg Arg Val Asn
 35 40 45

Asp Ser Ala Leu Gln Leu Leu Thr Leu Lys Leu Asp Pro Gly Ser Arg
50 55 60

Ile Thr Gly Leu Ala Leu Ile Arg Glu Gln Gly Gln Arg Val Ser Val
65 70 75 80

Leu Ser Leu Leu Glu Met Ile His Arg Gly Ala Ala Ile Arg Gln Ala
85 90 95

Met Gln Gln Arg Ala Ala Phe Arg Arg Arg Arg Arg Ser Ala Asn Leu
100 105 110

Arg Tyr Arg Ala Pro Arg Phe Asp Asn Arg Thr Leu Pro Gln Gly Trp
115 120 125

Leu Pro Pro Ser Leu Arg His Arg Pro Ala Ile Thr Leu Gly Trp Val
130 135 140

Glu Arg Met Arg Asn Trp Thr Pro Ile Ser Cys Leu Ala Val Glu Arg
145 150 155 160

Val Lys Phe Asp Met Gln Ala Met Gln Asn Pro Glu Ile Ser Gly Val
165 170 175

Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Ile Glu
180 185 190

His Ile Val Ala Arg Ser Asn Gly Gly Ser Asp Arg Val Phe Asn Leu
195 200 205

Thr Leu Ala Cys Arg Pro Cys Asn Gln Arg Lys Gly Asn Gln Pro Val
210 215 220

Glu Val Phe Leu Lys Arg Asp Pro Asp Arg Leu Ser Arg Ile Lys Ala
225 230 235 240

Arg Ala Lys Ala Pro Leu Arg Asp Ala Ala Glu Ile Asn Ala Thr Arg
245 250 255

Asn Ala Leu Phe Val Asp Met Leu Asn Thr Gly Leu Pro Val Ser Thr

260

265

270

Gly Thr Gly Ala Gln Thr Lys Tyr Asn Arg Gln Arg Leu Gly Val Pro
 275 280 285

Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Glu Val Lys Ala Ile
 290 295 300

Glu His Trp Gln Arg Pro Thr Leu Ala Ile Lys Ala Thr Gly Arg Gly
 305 310 315 320

Gly Tyr Gln Arg Thr Arg Leu Thr Ala His Gly Phe Pro Leu Gly Cys
 325 330 335

Leu Thr Arg Gln Lys Arg His Leu Gly Phe Gln Thr Gly Asp Gln Val
 340 345 350

Arg Ala Phe Val Pro Thr Gly Lys Lys Ser Gly Ile His Gln Gly Arg
 355 360 365

Phe Ala Val Arg Gln Thr Gly Ser Phe Asn Ile Gln Thr Pro Asp Gly
 370 375 380

Leu Val Leu Gly Ile His Tyr Arg His Cys Ala Leu Asn Gln Arg Ala
 385 390 395 400

Asp Gly Tyr Ala Tyr Ser Gln Leu Pro Phe Asp Ser Ala Gln Pro Gln
 405 410 415

Lys Glu Ala Ala Arg Ala Gly Ala Arg
 420 425

<210> 332

<211> 447

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-284 effector

<400> 332

Met Ala Val Tyr Val Leu Asp Asn Thr Gly Lys Pro Leu Met Pro Cys
1 5 10 15

Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg Ala Arg Val
20 25 30

His Arg Leu Ala Pro Leu Val Ile Arg Leu Val Asp Arg Arg Leu Ala
35 40 45

Asp Ser Ala Val Gln Pro Leu Thr Leu Lys Leu Asp Pro Gly Ser Arg
50 55 60

Phe Thr Gly Met Ala Leu Val Arg Glu Arg Gln Lys Arg Val Ser Val
65 70 75 80

Leu Ser Leu Leu Glu Leu Val His Arg Gly Ala Ala Ile Arg Lys Ala
85 90 95

Leu Glu Gln Arg Ala Gly Phe Arg Arg Arg Arg Arg Ser Gln Asn Leu
100 105 110

Arg His Arg Ala Pro Arg Phe Asn Asn Arg Thr Arg Pro Ala Gly Trp
115 120 125

Leu Ala Pro Ser Leu Arg His Arg Leu Asp Thr Thr Leu Ser Trp Val
130 135 140

Ala Arg Ile Arg Arg Trp Ala Pro Ile Thr Ala Leu Ala Val Glu Arg
145 150 155 160

Val Lys Phe Asp Pro Gln Ala Met Gln Ser Pro Glu Ile Ser Gly Leu
165 170 175

Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Thr Val Arg Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Ser Arg Arg Cys Ala Tyr Cys Ala Ala Glu Asn Val

195

200

205

Pro Leu Glu Ile Glu His Ile Ile Pro Arg Ser Asn Gly Gly Ser Asp
 210 215 220

Arg Val Ser Asn Leu Thr Leu Ala Cys Arg Pro Cys Asn Gln Arg Lys
 225 230 235 240

Gly Asn Arg Pro Ile Asp Ala Phe Leu Lys Asp Gln Pro Glu Leu Leu
 245 250 255

Ala Arg Ile Thr Ala Arg Ala Lys Thr Pro Leu His Asp Ala Ala Ala
 260 265 270

Val Asn Ala Thr Arg Asn Ala Leu Phe Ser Ala Leu Leu Asn Thr Gly
 275 280 285

Leu Pro Val Ala Thr Gly Ser Gly Ala Gln Thr Lys Tyr Asn Arg Arg
 290 295 300

Arg Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala Val Cys Val Gly
 305 310 315 320

Glu Val Glu Ala Val Ser Gly Trp Gln Arg Pro Thr Leu Ser Ile Lys
 325 330 335

Ala Thr Gly Arg Gly Glu Tyr Gln Arg Thr Arg Leu Thr Ala His Gly
 340 345 350

Phe Pro Arg Gly Tyr Leu Thr Arg Gln Lys Arg His Phe Gly Phe Gln
 355 360 365

Thr Gly Asp Gln Val Lys Ala Ser Val Pro Gly Gly Lys Lys Ala Gly
 370 375 380

Ile His Arg Gly Arg Val Ala Val Arg Gln Ser Gly Ser Phe Asn Ile
 385 390 395 400

Gln Thr Pro Ala Gly Val Val Gln Gly Ile Ser His Arg His Cys Ile
 405 410 415

Leu Ile Gln Arg Ala Asp Gly Tyr Ala Tyr Ala Gln Asn Pro Thr Leu
420 425 430

Asp Ser Ala Gln Pro Gln Gln Glu Ala Ala Arg Thr Gly Ala Arg
435 440 445

<210> 333
<211> 322
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-285 effector

<400> 333
Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile
1 5 10 15

Ser Thr Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu
20 25 30

Ile Glu Gly Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val
35 40 45

Arg Glu Tyr Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly
50 55 60

Ala Lys Asp Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys
65 70 75 80

Asn Gly Ser Asp Arg Ile Asn Asn Leu Ala Leu Ala Cys Gln Cys Cys
85 90 95

Asn Gln Lys Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys
100 105 110

Pro Lys Leu Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys

115

120

125

Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Thr Leu
 130 135 140

Lys Thr Thr Gly Leu Val Val Glu Thr Ala Ser Gly Gly Gln Thr Lys
 145 150 155 160

Phe Asn Arg Asn Gln Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala
 165 170 175

Val Cys Val Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr
 180 185 190

Leu Ala Ile Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu
 195 200 205

Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ser
 210 215 220

Thr Gly Phe Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Thr Gly
 225 230 235 240

Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val Ala Ile Arg Ala Thr Gly
 245 250 255

Ser Phe Asn Ile Gln Thr Ser Thr Gly Leu Val Gln Gly Val Ser His
 260 265 270

Arg Tyr Cys Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu
 275 280 285

Val Ala Lys Thr Asp Val Arg Gly Thr Pro Pro Gln His Arg Asp Ala
 290 295 300

Ser His Pro Ala Leu Tyr Leu Pro Gly Leu Lys Ala Glu Val Ser Arg
 305 310 315 320

Ala Asn

<210> 334
<211> 489
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-286 effector

<400> 334
Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala
20 25 30

Arg Val Val Cys Thr Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
50 55 60

Asn Ile Gly Val Ala Ala Val Lys Glu Asp Gly Gln Cys Val Phe Ser
65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Asp Val Pro Leu Leu Met Glu Lys
85 90 95

Arg Ala Ala Phe Arg Arg Asn His Arg Asn Leu Asp Arg Arg Arg Lys
100 105 110

Arg Gln Arg Arg Ala Lys Ala Ala Gly Thr Ile Val Glu Asn Glu Thr
115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Val Val Cys His Tyr
130 135 140

Val Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Cys Arg Pro Gln Gly

145		150		155		160									
Trp	Leu	Thr	Pro	Thr	Ala	Asn	His	Leu	Leu	Gln	Thr	His	Ile	Asn	Leu
				165					170					175	
Ile	Ala	Lys	Ile	Ala	Lys	Leu	Leu	Pro	Val	Thr	Lys	Val	Val	Val	Glu
			180					185					190		
Leu	Asn	Arg	Phe	Ala	Phe	Met	Ala	Met	Asp	Asn	Pro	Asn	Ile	Arg	Arg
		195					200					205			
Trp	Glu	Tyr	Gln	Gln	Gly	Pro	Leu	Tyr	Gly	Leu	Gly	Ser	Val	Glu	Asp
	210					215					220				
Ala	Val	Tyr	Ala	Gln	Gln	Asp	Gly	His	Cys	Leu	Phe	Cys	Lys	Lys	Pro
225					230					235					240
Ile	Asp	His	Tyr	His	His	Val	Val	Pro	Arg	Asn	Lys	Asn	Gly	Ser	Glu
				245					250					255	
Thr	Leu	Ala	Asn	Arg	Cys	Gly	Leu	Cys	Ala	Lys	His	His	Asp	Leu	Val
			260					265					270		
His	Lys	Asp	Lys	Ala	Trp	Thr	Asp	Lys	Leu	Val	Thr	Arg	Lys	Glu	Gly
		275					280					285			
Met	Asn	Lys	Lys	Tyr	His	Ala	Leu	Ser	Val	Leu	Asn	Gln	Ile	Ile	Pro
	290					295					300				
His	Leu	Met	Glu	Tyr	Leu	Gly	Ser	Lys	Thr	Leu	Tyr	Asp	Val	Tyr	Ala
305					310					315					320
Thr	Asp	Gly	Lys	Ser	Thr	Lys	Gly	Phe	Arg	Ile	Ala	Lys	Asn	Val	Pro
				325					330					335	
Lys	Glu	His	Tyr	Thr	Asp	Ala	Tyr	Cys	Ile	Ala	Cys	Ser	Ile	Leu	Asp
			340					345					350		
Thr	Ala	Ile	Glu	Val	Ser	Ala	Pro	Thr	Ser	Pro	Phe	Lys	Leu	Lys	Gln
		355					360					365			

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Ala Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Arg Pro His Leu Pro Gln His
420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Asp Phe Asn Gly
435 440 445

Thr Ile Gly Val Met Gln Ser Ser Thr Val Gly Ser Phe Tyr Lys Ser
450 455 460

Thr Glu Gly His Lys Ser Thr Pro Arg Lys Cys Val Leu Leu Met Arg
465 470 475 480

Asn Ala Gly Met Val Phe Ile Pro Ala
485

<210> 335

<211> 489

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-287 effector

<400> 335

Met Asp Met Val Tyr Val Leu Asn Lys Asp Gly Lys Pro Leu Met Ala
1 5 10 15

Thr Thr Arg Gly Gly Arg Val Arg Tyr Leu Leu Lys Glu Lys Lys Ala

20

25

30

Arg Val Val Ser Ser Thr Pro Phe Thr Ile Gln Leu Asn Tyr Asp Thr
 35 40 45

Pro Asp Ile Thr Gln Asp Leu Ile Leu Gly Ile Asp Pro Gly Arg Thr
 50 55 60

Asn Ile Gly Val Ala Val Val Lys Glu Asp Gly Gln Cys Val Phe Ser
 65 70 75 80

Ala His Leu Glu Thr Arg Asn Lys Glu Val Pro Leu Leu Met Lys Lys
 85 90 95

Arg Ala Ala Phe Arg Arg Gln His Arg Thr Gln Asp Arg Arg Arg Lys
 100 105 110

Arg Gln Arg Arg Ala Ile Ala Ala Gly Thr Thr Val Glu Ser Asn Thr
 115 120 125

Ile Glu Arg Leu Leu Pro Gly Tyr Glu Lys Pro Ile Val Cys His His
 130 135 140

Ile Arg Asn Lys Glu Ala Arg Phe Asn Asn Arg Ser Arg Pro Ala Gly
 145 150 155 160

Trp Leu Thr Pro Thr Ala Asn His Leu Leu Gln Thr His Ile Asn Leu
 165 170 175

Ile Ala Lys Ile Ala Lys Val Leu Pro Ile Thr Lys Val Val Val Glu
 180 185 190

Leu Asn Arg Phe Ala Phe Met Ala Met Asp Asn Pro Asn Ile Arg Arg
 195 200 205

Trp Glu Tyr Gln Gln Gly Ser Leu Tyr Gly Leu Gly Ser Val Glu Asp
 210 215 220

Ala Val Tyr Ala Gln Gln Asp Gly His Cys Leu Phe Cys Lys Lys Pro
 225 230 235 240

Ile Asp His Tyr His His Val Val Pro Arg His Lys Gly Gly Ser Glu
245 250 255

Thr Leu Ala Asn Arg Cys Gly Leu Cys Glu Lys His His Ala Leu Val
260 265 270

His Lys Asp Lys Ala Trp Ala Glu Lys Leu Val Thr Arg Lys Gly Gly
275 280 285

Met Asn Lys Lys Tyr His Ala Leu Ser Val Leu Asn Gln Ile Ile Pro
290 295 300

Phe Leu Met Glu Tyr Leu Gly Glu Glu Thr Pro Tyr Asp Val Tyr Ala
305 310 315 320

Thr Asp Gly Lys Ser Thr Lys Gly Phe Arg Ile Ala Lys Asn Val Pro
325 330 335

Lys Glu His Tyr Thr Asp Ala Tyr Cys Ile Ala Cys Ser Ile Leu Asp
340 345 350

Ala Asp Thr Lys Val Ser Ala Pro Ala Glu Pro Phe Lys Leu Lys Gln
355 360 365

Phe Arg Arg His Asp Arg Gln Ser Cys Ile Arg Gln Met Val Asp Arg
370 375 380

Lys Tyr Leu Leu Asp Gly Lys Val Val Ala Thr Asn Arg His Lys Ala
385 390 395 400

Ile Glu Gln Lys Ser Asp Ser Leu Glu Glu Phe Arg Glu Ala Tyr Gly
405 410 415

Asp Ala Ala Val Ser Gln Leu Thr Val Arg Pro His Leu Pro Gln Tyr
420 425 430

Lys Asp Met Thr Arg Ile Met Pro Gly Ala Val Met Ala Phe Asn Gly
435 440 445

Ser Val Gly Val Met Gln Ser Ser Ile Val Gly Ser Phe Tyr Lys Ser

450

455

460

Thr Lys Gly His Lys Ala Thr Pro Arg Arg Cys Val Leu Leu Ala Gln
 465 470 475 480

Asn Ala Gly Met Val Phe Asn Pro Ala
 485

<210> 336

<211> 289

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-288 effector

<400> 336

Met Glu Asp Ser Thr Leu Gln Pro Val Arg Leu Lys Leu Asp Pro Gly
 1 5 10 15

Ser Lys Thr Thr Gly Met Ala Leu Val Arg Glu Ser Glu Glu Val Tyr
 20 25 30

Pro Asp Thr Gly Glu Val Gln Arg Thr Ala His Val Leu Lys Leu Ala
 35 40 45

Asp Leu Gln His Arg Gly His Val Ile Arg Glu Ala Leu Thr Gln Arg
 50 55 60

Ala Ser Phe Arg Arg Arg Arg Gly Ala Asn Leu Arg His Arg Ala
 65 70 75 80

Pro Arg Phe Cys Asn Arg Thr Arg Pro Ala Gly Trp Leu Ala Pro Ser
 85 90 95

Leu Gln His Arg Ala Asp Thr Thr Leu Ala Trp Val Arg Arg Leu Gln
 100 105 110

Arg Trp Ser Pro Ile Thr Ala Leu Ser Gln Glu Leu Val Arg Phe Asp
115 120 125

Met Gln Leu Ile Gln Asn Pro Glu Ile Ser Gly Val Glu Tyr Gln His
130 135 140

Gly Thr Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys Trp
145 150 155 160

His Arg Thr Cys Ala Tyr Cys Pro Ala Thr Asn Val Pro Leu Gln Val
165 170 175

Glu His Ile Val Pro Arg Ala Lys Gly Gly Ser His Arg Val Ser Asn
180 185 190

Leu Thr Leu Ala Cys Gly Pro Cys Asn Thr Ala Lys Gly Thr Gln Asp
195 200 205

Val Arg Ala Phe Leu Ala Gln Asp Pro Lys Arg Leu Ala Arg Val Leu
210 215 220

Ala Gln Ala Lys Ala Pro Leu Arg Asp Ala Ala Ala Met Lys Leu Phe
225 230 235 240

Thr Gln Ala Glu Phe Asp Asn Leu Pro Val Ile Asp Gly Val Lys Gln
245 250 255

Cys Pro Thr Gly Asp Tyr Ser Ser Val Arg Asn Phe Gly Glu Arg Cys
260 265 270

Val Phe Gly Ala Glu Ser Ile Phe Cys Arg Asp Ser Arg Phe Ala Asp
275 280 285

Ser

<210> 337

<211> 257

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-289 effector

<400> 337

Met Glu Asn Ala Asp Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu
1 5 10 15

Gln Gly Tyr Glu Val Arg Gln Tyr Val Leu Glu Arg Gly Gly His Thr
20 25 30

Cys Ser Tyr Cys Asp Ala Lys Asp Val Ala Leu His Leu Asp His Val
35 40 45

Leu Pro Arg Ser Arg Gly Gly Ser Asn Arg Val Ser Asn Leu Val Pro
50 55 60

Ala Cys Lys Pro Cys Asn Asp Ala Lys Ser Asn Arg Ala Val Glu Asp
65 70 75 80

Tyr Leu Val Asp Arg Pro Glu Val Leu Arg Gln Val Lys Ala Gln Leu
85 90 95

Arg Ser Pro Leu Lys Asp Ala Ala Val Met Asn Ala Thr Arg Phe Ala
100 105 110

Ile Val Asp Ala Leu Arg Asp Phe Gly Leu Glu Val Gln Met Trp Ser
115 120 125

Gly Gly Arg Thr Lys Trp Asn Arg Thr Asn Leu Gly Leu Pro Lys Asp
130 135 140

His Trp Ile Asp Ala Ala Cys Val Gly Glu Thr Gly Ala Ala Val Arg
145 150 155 160

Val Pro Ala Leu Arg Pro Leu Thr Ile Thr Ala Met Gly Arg Gly His
165 170 175

Arg Arg Val His Gly Asn Asp Arg Tyr Gly Phe Pro Arg Gly Thr Ala
180 185 190

Arg Arg Ala Lys Arg Val Ala Gly Phe Gln Thr Gly Asp Leu Val Arg
195 200 205

Leu Val Cys Leu Gly Gly Lys Ser Ala Gly Ile His Thr Gly Arg Leu
210 215 220

Ser Ser Ile Arg Thr Arg Gly Gln Phe Val Leu Gly Lys His Asp Arg
225 230 235 240

Pro Ala Arg Glu Phe Thr Leu Leu Gln Arg Ser Asp Gly Tyr Ala Tyr
245 250 255

Gly

<210> 338

<211> 54

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-290 effector

<400> 338

Met Gly Arg Val Ala Val Arg Ala Ser Gly Ser Phe Asn Ile Gln Thr
1 5 10 15

Gly Asn Gly Leu Val Gln Gly Val Ser His Arg Tyr Cys Thr Val Val
20 25 30

Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu Val Ala Lys Thr Asp Val
35 40 45

Arg Gly Thr Pro Pro Gln

<210> 339

<211> 187

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-291 effector

<400> 339

Met	Gly	Tyr	His	Asp	Tyr	Pro	Ile	Leu	Thr	Gly	Ile	Leu	Phe	Ile	Arg
1				5					10					15	

Glu	Ser	Leu	Thr	Leu	Ala	Cys	His	Asp	Cys	Asn	Gln	Lys	Lys	Gly	Asn
			20					25					30		

Gln	Asp	Val	Arg	Glu	Phe	Leu	Ala	Thr	Lys	Pro	Asp	Leu	Leu	Asn	Arg
		35					40					45			

Ile	Leu	Gln	Gln	Ala	Lys	Leu	Pro	Leu	Lys	Asp	Ala	Ala	Ala	Val	Asn
	50					55					60				

Ser	Thr	Arg	Trp	Ala	Leu	Phe	Arg	Ala	Leu	Lys	Glu	Thr	Gly	Leu	Pro
65					70					75					80

Val	Thr	Asp	Gly	Thr	Gly	Gly	Gln	Thr	Lys	Phe	Asn	Arg	Asn	Arg	Leu
				85					90					95	

Gly	Leu	Pro	Lys	Ser	His	Trp	Leu	Asp	Ala	Ala	Cys	Val	Gly	Asn	Val
			100					105						110	

Glu	Thr	Leu	Lys	Val	Leu	Thr	Ser	Lys	Pro	Leu	Leu	Ile	Ala	Ala	Lys
		115					120					125			

Gly	His	Gly	Thr	Arg	Gln	Met	Cys	Gly	Thr	Asn	Lys	Tyr	Gly	Phe	Pro
	130					135					140				

Thr Arg His Lys Ser Arg Val Gln Ile His Lys Gly Phe Arg Thr Gly
145 150 155 160

Asp Ile Val Ser Ala Thr Val Thr Ala Gly Lys Lys Val Gly Ser Tyr
165 170 175

Val Gly Arg Val Leu Cys Arg Ala Ser Gly Ser
180 185

<210> 340

<211> 173

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-292 effector

<400> 340

Met Ile Pro Val Glu Pro Lys Asn Thr Pro Thr Asp Ala Ser Pro Val
1 5 10 15

Cys Ser Ser Val Thr Asp Ala Leu Asn Ser Thr Ser Arg Asp Leu Arg
20 25 30

Gln Cys Ala Pro Glu Val Leu Ala Gly Ile Phe Val Glu Glu Thr Val
35 40 45

Arg Arg Lys Ala Ser Gly Glu Ser Gln Ile Phe Val Leu Asp Asn Arg
50 55 60

Arg Ile Pro Leu Met Pro Cys Arg Pro Ala Arg Ala Trp Arg Leu Leu
65 70 75 80

Lys Ala Gly Lys Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
85 90 95

Leu Lys Arg Asp Val Asp Pro Asp Pro Gln Pro Val Glu Phe Lys Val

100

105

110

Asp Pro Gly Ser Arg Thr Thr Gly Ile Ala Leu Val Ala Leu Phe Pro
 115 120 125

Asn Arg Gly Arg Val Val Leu Trp Ala Ala Asn Leu His His Arg Gly
 130 135 140

Leu Lys Ile Lys Ser Ala Ile Asp Arg Arg Arg Ala Leu Arg Arg Gly
 145 150 155 160

Arg Arg Ala Arg Asn Thr Arg Tyr Arg Ala Ala Arg Ala
 165 170

<210> 341

<211> 482

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-293 effector

<400> 341

Met Ile Pro Val Glu Pro Lys Asn Thr Pro Thr Asp Ala Ser Pro Val
 1 5 10 15

Cys Ser Ser Val Thr Asp Ala Leu Asn Ser Thr Ser Arg Asp Leu Arg
 20 25 30

Gln Cys Ala Pro Glu Val Leu Ala Gly Ile Phe Val Glu Glu Thr Val
 35 40 45

Arg Arg Lys Ala Ser Gly Glu Ser Gln Ile Phe Val Leu Asp Asn Arg
 50 55 60

Arg Ile Pro Leu Met Pro Cys Arg Pro Ala Arg Ala Trp Arg Leu Leu
 65 70 75 80

Lys Ala Gly Lys Ala Ser Val Phe Arg Arg Phe Pro Phe Thr Ile Ile
85 90 95

Leu Lys Arg Asp Val Asp Pro Asp Pro Gln Pro Val Glu Phe Lys Val
100 105 110

Asp Pro Gly Ser Arg Thr Thr Gly Ile Ala Leu Val Ala Leu Phe Pro
115 120 125

Asn Arg Gly Arg Val Val Leu Trp Ala Ala Asn Leu His His Arg Gly
130 135 140

Leu Lys Ile Lys Ser Ala Ile Asp Arg Arg Arg Ala Leu Arg Arg Gly
145 150 155 160

Arg Arg Ala Arg Asn Thr Arg Tyr Arg Ala Ala Arg Phe Asp Asn Arg
165 170 175

Val Arg Ala Lys Gly Trp Leu Pro Pro Ser Ile Gln Ser Arg Val Asp
180 185 190

Asn Val His Ser Trp Tyr Leu Lys Leu Leu Ala Arg Val Pro Ile Ser
195 200 205

Glu Ala His Ile Glu Thr Val Arg Phe Asp Met Gln Lys Ile Gln Asn
210 215 220

Pro Glu Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu Leu Gly Tyr
225 230 235 240

Glu Ile Arg Glu Tyr Leu Leu Glu Lys Phe Ser Arg Arg Cys Ala Tyr
245 250 255

Cys Gly Ala Lys Asp Val Gln Leu Gln Ile Glu His Ile Lys Pro Lys
260 265 270

Ala Leu Gly Gly Thr Asn Arg Val Ser Asn Leu Thr Leu Ala Cys Glu
275 280 285

Pro Cys Asn Leu Arg Lys Gly Lys Met Pro Ile Glu Asp Phe Leu Arg

290

295

300

Lys Lys Pro Asp Leu Leu Ser Lys Ile Lys Ser Arg Ala Gln Ser Pro
 305 310 315 320

Leu Thr Asp Ala Ala Ser Val Asn Ala Ser Arg Tyr Ala Ile Gly Asp
 325 330 335

Lys Ile Arg Ser Ile Gly Leu Pro Thr Cys Phe Trp Ser Gly Gly Arg
 340 345 350

Thr Lys Lys Asn Arg Val Phe Gln Gly Tyr Ala Lys Asp His Trp Ile
 355 360 365

Asp Ala Ala Cys Val Gly Glu Ser Gly Val Ser Val Asn Ile Gly Ser
 370 375 380

Val Lys Pro Ile Ser Ile Ser Ala Ile Gly Arg Gly Ser Arg Gln Val
 385 390 395 400

Ser Cys Val Asp Lys Tyr Gly Phe Pro Arg Gly Lys Ala Gly Thr Val
 405 410 415

Lys Arg Val Phe Gly Phe Ser Thr Gly Asp Phe Val Arg Leu Thr Arg
 420 425 430

Leu Ser Gly Lys Tyr Ala Gly Val Trp Val Gly Ile Ile Ala Gly Thr
 435 440 445

Arg Lys Ser Gly Tyr Leu Asp Ile Lys Cys Gly Lys Lys Lys Ile Thr
 450 455 460

Ala Lys His Ser Glu Phe Arg Leu Leu Asn His Gly Asp Gly Tyr Val
 465 470 475 480

Tyr Ala

<210> 342

<211> 110

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-294 effector

<400> 342

Met Leu Gly Leu His Lys Glu His Trp Leu Asp Ala Ala Cys Val Gly
1 5 10 15

Glu Ser Gly Ala Asn Ile Val Ile Pro Leu Gly Leu Gln Pro Leu Gly
20 25 30

Ile Lys Ala Ala Gly His Gly Asn Arg Gln Met Cys Ala Thr Asp Ala
35 40 45

Phe Gly Phe Pro Lys Arg His Arg Thr Asn Gln Lys Ser Phe Phe Gly
50 55 60

Phe Gln Thr Gly Asp Met Ala Arg Ala Ser Ile Pro Ser Gly Lys Lys
65 70 75 80

Gln Gly Val His Thr Gly Arg Val Leu Val Arg Ala Thr Gly Ser Phe
85 90 95

Asp Ile His Val Leu Val Lys Asp Phe His Pro Gly Asn Leu
100 105 110

<210> 343

<211> 125

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-295 effector

<400> 343

Met Leu Gly Leu His Lys Glu His Trp Leu Asp Ala Ala Cys Val Gly
1 5 10 15

Glu Ser Gly Ala Asn Ile Val Ile Pro Leu Gly Leu Gln Pro Leu Gly
20 25 30

Ile Lys Ala Ala Gly His Gly Asn Arg Gln Met Cys Ala Thr Asp Ala
35 40 45

Phe Gly Phe Pro Lys Thr His Arg Thr Asn Gln Lys Ser Tyr Tyr Gly
50 55 60

Phe Gln Thr Gly Asp Met Ala Arg Ala Ser Ile Pro Ser Gly Lys Lys
65 70 75 80

Gln Gly Val His Thr Gly Arg Val Leu Val Arg Ala Thr Gly Ser Phe
85 90 95

Asp Ile Gln Thr Lys Ala Gly Arg Val Ala Gly Ile Ser His Lys His
100 105 110

Cys Val Ala Val His Arg Lys Asp Gly Tyr Thr Tyr Gln
115 120 125

<210> 344

<211> 476

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-296 effector

<400> 344

Met Leu His Gln Pro Gln Ala Leu Ser Pro Thr Thr Lys Lys Arg Ala
1 5 10 15

Ala Thr Arg Leu Pro Thr Ser Arg Leu Asn Asp Leu Arg Ala Pro Gly
20 25 30

Glu Val Thr Ile Thr Cys Ala Ser Arg Arg Gly Arg Leu Arg Ala His
35 40 45

Leu Arg Pro Lys Thr Pro Arg Val Phe Val Phe Ser Asn Thr Leu Lys
50 55 60

Pro Leu Met Pro Cys Arg Pro Ala Arg Ala Gln Asp Leu Leu Ala Tyr
65 70 75 80

Gly Arg Ala Ala Val Tyr Arg Leu Gln Pro Phe Thr Ile Val Leu Lys
85 90 95

Asp Arg Ala Ala Gly Asp Val Gln Pro Val Glu Phe Lys Val Asp Pro
100 105 110

Gly Ser Lys Val Thr Gly Leu Ala Leu Val Ala Glu Phe Glu Met Arg
115 120 125

Gly Arg Thr Val Val Trp Ala Ala Asn Leu Ala His Arg Gly His Arg
130 135 140

Val Lys Ala Ser Met Thr Asp Arg Ala Met Phe Arg Arg Gly Arg Arg
145 150 155 160

Gly Arg Lys Thr Arg Tyr Arg Ala Ala Arg Phe Glu Asn Arg Thr Arg
165 170 175

Pro Thr Asn Trp Leu Ala Pro Ser Leu Gln Ser Arg Val Leu Asn Val
180 185 190

Lys Asn Trp Tyr Ser Arg Leu Leu Ser Arg Ala Ser Ile Ser Val Ala
195 200 205

Gln Val Glu Thr Ser Ser Phe Asp Thr Gln Leu Met Glu Asn Ala Asp
210 215 220

Ile Ser Gly Val Glu Tyr Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val

225					230						235					240
Arg	Gln	Tyr	Val	Leu	Glu	Arg	Gly	Gly	His	Thr	Cys	Ser	Tyr	Cys	Asp	
				245					250					255		
Ala	Lys	Asp	Val	Ala	Leu	His	Leu	Asp	His	Val	Leu	Pro	Arg	Ser	Arg	
			260					265					270			
Gly	Gly	Ser	Asn	Arg	Val	Ser	Asn	Leu	Val	Pro	Ala	Cys	Lys	Pro	Cys	
		275					280					285				
Asn	Asp	Ala	Lys	Ser	Asn	Arg	Ala	Val	Glu	Asp	Tyr	Leu	Val	Asp	Arg	
	290					295					300					
Pro	Glu	Val	Leu	Arg	Gln	Val	Lys	Ala	Gln	Leu	Arg	Ser	Pro	Leu	Lys	
305					310					315					320	
Asp	Ala	Ala	Val	Met	Asn	Ala	Thr	Arg	Phe	Ala	Ile	Val	Asp	Ala	Leu	
				325					330					335		
Arg	Asp	Phe	Gly	Leu	Glu	Val	Gln	Met	Trp	Ser	Gly	Gly	Arg	Thr	Lys	
			340					345					350			
Trp	Asn	Arg	Thr	Asn	Leu	Gly	Leu	Pro	Lys	Asp	His	Trp	Ile	Asp	Ala	
		355					360					365				
Ala	Cys	Val	Gly	Glu	Thr	Gly	Ala	Ala	Val	Arg	Val	Pro	Ala	Leu	Arg	
	370					375					380					
Pro	Leu	Thr	Ile	Thr	Ala	Met	Gly	Arg	Gly	His	Arg	Arg	Val	His	Gly	
385					390					395					400	
Asn	Asp	Arg	Tyr	Gly	Phe	Pro	Arg	Gly	Thr	Ala	Arg	Arg	Ala	Lys	Arg	
				405					410					415		
Val	Ala	Gly	Phe	Gln	Thr	Gly	Asp	Leu	Val	Arg	Leu	Val	Cys	Leu	Gly	
			420					425					430			
Gly	Lys	Ser	Ala	Gly	Ile	His	Thr	Gly	Arg	Leu	Ser	Ser	Ile	Arg	Thr	
		435					440					445				

Arg Gly Gln Phe Val Leu Gly Lys His Asp Arg Pro Ala Arg Glu Phe
450 455 460

Thr Leu Leu Gln Arg Ser Asp Gly Tyr Ala Tyr Gly
465 470 475

<210> 345
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-297 effector

<400> 345
Met Leu Lys Leu Leu Arg Leu Ala Pro Leu Thr Gln Ile Ala Val Glu
1 5 10 15

Thr Val Arg Phe Asp Thr Gln Lys Met Gln Lys Pro Glu Ile Ser Gly
20 25 30

Val Glu Tyr Gln Gln Gly Glu Leu Ala Gly Tyr Glu Leu Arg Ala Tyr
35 40 45

Leu Leu Glu Lys Val Asn Ala Leu Ile Val Val Pro Lys Met Tyr Arg
50 55 60

Leu Lys Leu Ser Thr
65

<210> 346
<211> 275
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-298 effector

<400> 346

Met Leu Lys Pro Asn Phe Val Phe Val Leu Asp Ala Ser Lys Lys Pro
1 5 10 15

Leu Thr Pro Cys Lys Pro Ser Met Ala Arg Arg Leu Leu Gly Leu Gly
20 25 30

Lys Ala Ala Ile Phe His Arg Tyr Pro Phe Thr Ile Ile Leu Lys Lys
35 40 45

Glu Val Glu Ser Thr Pro Glu Pro Ile Thr Leu Lys Ile Asp Pro Gly
50 55 60

Ser Lys Thr Thr Gly Phe Ala Leu Leu Asn Ser Asn Lys Val Val Tyr
65 70 75 80

Gly Ala Glu Leu Thr His Arg Gly Thr Val Ile Lys Leu Ser Leu Glu
85 90 95

Leu Arg Arg Asn Leu Arg Arg Gly Arg Arg Asn Arg His Thr Arg Tyr
100 105 110

Arg Gln Ala Arg Phe Leu Asn Arg Lys Arg Pro Glu Gly Trp Leu Ala
115 120 125

Pro Ser Leu Gln His Arg Val Glu Thr Thr Leu Thr Trp Val Glu Lys
130 135 140

Phe Arg Lys Tyr Ala Pro Ile Gly Asn Ile Val Gln Glu Leu Val Arg
145 150 155 160

Phe Asp Leu Gln Gln Met Glu Asn Pro Glu Ile Ser Trp Ile Glu Tyr
165 170 175

Gln Gln Gly His Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Asn
180 185 190

Lys Trp Glu Arg Lys Cys Ala Tyr Cys Ser Val Glu Asn Val Pro Leu
195 200 205

Gln Val Glu His Ile His Pro Lys Ala Glu Gly Gly Ser Asn Arg Ser
210 215 220

Ser Asn Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu Lys Lys Gly Thr
225 230 235 240

Gln Asp Ile Glu Val Phe Leu Lys Lys Lys Pro Glu Val Leu Lys Thr
245 250 255

Ile Lys Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn
260 265 270

Ser Thr Arg
275

<210> 347
<211> 425
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-299 effector

<400> 347
Met Leu Lys Pro Asn Phe Val Phe Val Leu Asp Ala Ser Lys Lys Pro
1 5 10 15

Leu Thr Pro Cys Lys Pro Ser Met Ala Arg Arg Leu Leu Gly Leu Gly
20 25 30

Lys Ala Ala Ile Phe His Arg Tyr Pro Phe Thr Ile Ile Leu Lys Lys
35 40 45

Glu Val Glu Ser Thr Pro Glu Pro Ile Thr Leu Lys Ile Asp Pro Gly

50

55

60

Ser Lys Thr Thr Gly Phe Ala Leu Leu Asn Ser Asn Lys Val Val Tyr
 65 70 75 80

Gly Ala Glu Leu Thr His Arg Gly Thr Val Ile Lys Leu Ser Leu Glu
 85 90 95

Leu Arg Arg Asn Leu Arg Arg Gly Arg Arg Asn Arg His Thr Arg Tyr
 100 105 110

Arg Gln Ala Arg Phe Leu Asn Arg Lys Arg Pro Glu Gly Trp Leu Ala
 115 120 125

Pro Ser Leu Gln His Arg Val Glu Thr Thr Leu Thr Trp Val Glu Lys
 130 135 140

Phe Arg Lys Tyr Ala Pro Ile Gly Asn Ile Val Gln Glu Leu Val Arg
 145 150 155 160

Phe Asp Leu Gln Gln Met Glu Asn Pro Glu Ile Ser Trp Ile Glu Tyr
 165 170 175

Gln Gln Gly His Leu Gln Gly Tyr Glu Val Arg Glu Tyr Leu Leu Asn
 180 185 190

Lys Trp Glu Arg Lys Cys Ala Tyr Cys Ser Val Glu Asn Val Pro Leu
 195 200 205

Gln Val Glu His Ile His Pro Lys Ala Glu Gly Gly Ser Asn Arg Ser
 210 215 220

Ser Asn Leu Cys Leu Ala Cys Glu Lys Cys Asn Leu Lys Lys Gly Thr
 225 230 235 240

Gln Asp Ile Glu Val Phe Leu Lys Lys Lys Pro Glu Val Leu Lys Thr
 245 250 255

Ile Lys Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala Ala Ala Val Asn
 260 265 270

Ser Thr Arg Trp Glu Leu Phe Arg Arg Leu Glu Lys Thr Gly Leu Pro
275 280 285

Val Ser Val Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg Thr Arg Leu
290 295 300

Glu Leu Pro Lys Thr His Trp Leu Asp Ala Ala Cys Val Gly Glu Ile
305 310 315 320

Glu Ser Leu Lys Val Leu Thr Asp Lys Pro Leu Leu Ile Lys Cys Asn
325 330 335

Gly His Gly Thr Arg Gln Met Tyr Arg Thr Asp Lys Tyr Gly Phe Pro
340 345 350

Ser Arg Tyr Val Pro Arg Ile Lys Phe Val His Gly Phe Gln Thr Gly
355 360 365

Asp Ile Ala Lys Ala Val Ile Thr Thr Gly Lys Lys Leu Gly Thr Tyr
370 375 380

Thr Gly Arg Ile Ala Val Arg Ser Thr Gly Ser Phe Asn Ile Ser Asp
385 390 395 400

Lys Ser Gly Leu Ile Gln Gly Met Asn His Lys Asn Phe Arg Thr Ile
405 410 415

Tyr Lys Lys Asp Gly Tyr Ser Tyr Ala
420 425

<210> 348

<211> 252

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-300 effector

<400> 348

Met Leu Leu Ser Gln Arg Lys Ala Ala Val Phe Arg Pro Tyr Pro Tyr
1 5 10 15

Arg Leu Ile Leu Lys Glu Glu Val Leu Asn Pro Asp Ile Glu Pro Leu
20 25 30

Leu Ile Lys Ile Asp Pro Gly Ala Lys Thr Thr Gly Leu Ala Leu Val
35 40 45

Asn Asp Arg Thr Gly Glu Val Val Trp Val Ala Glu Leu Gln His Arg
50 55 60

Gly Phe Gln Leu Arg Asp Ala Leu Thr Ser Arg Arg Gln Leu Arg Arg
65 70 75 80

Ser Arg Arg Asn Arg Lys Thr Arg Tyr Arg Lys Pro Arg Gly Leu Asn
85 90 95

Arg Thr Arg Asn Thr Gly Trp Leu Pro Pro Ser Leu Asn Ser Arg Val
100 105 110

Ala Asn Ile Leu Thr Trp Val Lys Arg Leu Ser Leu Leu Cys Gln Ile
115 120 125

Asn Ala Ile Ser Gln Glu Leu Val Arg Phe Asp Thr Gln Gln Met Ala
130 135 140

Asn Pro Glu Ile Ser Gly Ile Ala Tyr Gln Gln Gly Thr Leu Ala Gly
145 150 155 160

Tyr Glu Val Arg Glu Phe Leu Leu Phe Lys Trp Asp Arg Thr Cys Ala
165 170 175

Tyr Cys Gly Ala Lys Asp Thr Lys Leu Glu Val Glu His Ile Gln Ser
180 185 190

Arg Ser Lys Gly Gly Ser Asn Arg Val Ser Asn Leu Cys Leu Ala Cys
195 200 205

Val Pro Cys Asn Arg Glu Lys Gly Asn Gln Asp Ile Lys Asp Phe Leu
210 215 220

Lys Gly Lys Pro Asp Leu Leu Lys Gln Ile Leu Ala Gln Ala Lys Arg
225 230 235 240

Pro Leu Ala Asn Ala Ala Ala Val Asn Thr Thr Arg
245 250

<210> 349
<211> 197
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-301 effector

<400> 349
Met Leu Asn Gln Ile Ile Pro His Leu Met Glu Tyr Leu Gly Asn Glu
1 5 10 15

Thr Leu Tyr Asp Val Tyr Ala Thr Asp Gly Cys Ser Thr Lys Gly Phe
20 25 30

Arg Ile Ala Lys Asn Val Pro Lys Glu His Tyr Thr Asp Ala Tyr Cys
35 40 45

Ile Ala Cys Ser Ile Leu Asp Thr Asp Ile Glu Val Ser Ala Pro Thr
50 55 60

Arg Pro Phe Glu Leu Lys Gln Phe Arg Arg His Asp Arg Gln Ala Cys
65 70 75 80

Ile Arg Gln Met Val Asp Arg Lys Tyr Leu Leu Asp Gly Lys Val Val
85 90 95

Ala Thr Asn Arg His Lys Ala Ile Glu Gln Lys Ser Asp Ser Leu Glu

100

105

110

Glu Phe Arg Glu Ala His Gly Asn Ala Ala Val Ser Gln Leu Thr Val
 115 120 125

Lys Pro His His Pro Gln Cys Lys Asp Met Ala Arg Ile Met Pro Gly
 130 135 140

Ala Val Met Val Phe Asp Gly Ala Val Gly Val Phe Gln Gly Ser Ser
 145 150 155 160

Gly Gln Asn Asn Gly Thr Pro Asn Tyr Tyr Asn Ser Thr Lys Gly Glu
 165 170 175

Arg Phe Leu Met Arg Ser Cys Val Leu Leu Ala Gln Asn Ala Gly Met
 180 185 190

Val Phe Ile Pro Ala
 195

<210> 350

<211> 164

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-302 effector

<400> 350

Met Leu Pro Val Glu Ile Gly Ser Gly Gly Leu Thr Lys Phe Asn Arg
 1 5 10 15

Thr Arg Leu Gln Ile Pro Lys Ser His Ala Leu Asp Ala Ala Cys Val
 20 25 30

Gly Gln Val Asp Ala Ile His Ala Trp Ser Arg Pro Thr Leu Gln Ile
 35 40 45

Lys Cys Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Thr Gln Tyr
50 55 60

Gly Phe Ala Arg Gly Tyr Leu Met Arg Thr Lys Ser Val Lys Gly Phe
65 70 75 80

Arg Thr Gly Asp Leu Val Arg Ala Ser Val Thr Ser Gly Lys Lys Ile
85 90 95

Gly Glu Tyr Leu Gly Arg Val Ala Gly Arg Ala Thr Gly Ser Phe Asn
100 105 110

Ile Gln Thr Val Asp Ala Val Val Gln Gly Ile Ser His Lys Tyr Cys
115 120 125

Arg Ile Val His Arg Gly Asp Gly Tyr Gly Tyr Ala Trp Ser Ile Thr
130 135 140

Pro Ser Ser Thr Gly Lys Asn Asn Phe Pro Val Ser Ser Arg Leu Leu
145 150 155 160

Thr Gly Arg Leu

<210> 351

<211> 517

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-303 effector

<400> 351

Met Leu Thr Arg Asp Ser Glu Ser Arg His Gly Lys Pro Gly Lys Ala
1 5 10 15

Arg Tyr Val Asp Pro Lys Ala Glu Ala Gly Arg Arg Gly Ala Ser Ser

20

25

30

Ala Ser Pro Ser Pro Thr Ala Arg Ser Arg Gln Pro Gly Ser Gly Thr
 35 40 45

Lys Arg Ala Arg Gly Asp Gly Leu Gly Pro Thr Phe Pro Arg Gly Ala
 50 55 60

Ala Gly Ala Ala Asn Pro Asp Val Ser Arg Pro Gln Gly Gln Val Gly
 65 70 75 80

Gly Asn Ala His Val Phe Val Leu Asp Arg Lys His His Pro Leu Met
 85 90 95

Pro Thr Thr Ala Ala Arg Ala Arg Glu Leu Leu Lys Lys Arg Arg Ala
 100 105 110

Val Val Ala Arg Leu His Pro Phe Thr Ile Arg Ile Lys Asp Arg Thr
 115 120 125

Gly Gly Ala Val Gln Thr Val Ile Val Lys Ile Asp Pro Gly Ser Lys
 130 135 140

Thr Thr Gly Leu Ala Val Ala Arg Val Ala Gly Asp Gly Glu His Ala
 145 150 155 160

Leu Trp Leu Ala Glu Val Gly His Arg Gly Leu Ala Ile Arg Arg Ser
 165 170 175

Leu Glu Gln Arg Arg Gly Tyr Arg His Gly Arg Arg Ser Arg Asn Leu
 180 185 190

Arg Tyr Arg Ala Pro Arg Ile Asp Asn Arg Thr Lys Pro Ala Asp Trp
 195 200 205

Leu Pro Pro Ser Leu Gln His Arg Val Asp Ala Val Val His Trp Ala
 210 215 220

Asp Arg Leu Arg Arg Leu Cys Pro Val Ala Gly Ile Val Met Glu Ala
 225 230 235 240

Val Arg Phe Asp Thr Gln Leu Leu Ala Asp Pro Asp Ile Ser Gly Val
245 250 255

Glu Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Ile Arg Glu Trp Val
260 265 270

Leu Glu Lys Trp Gly Arg Ala Cys Val Tyr Cys Gly Ala Glu Gly Val
275 280 285

Pro Leu Gln Leu Asp His Val Val Ala Arg Gly Arg Leu Gly Gln Gly
290 295 300

Arg Pro Lys Asp Phe Val Pro Ser Cys Gly Pro Cys Asn Gln Lys Lys
305 310 315 320

Gly Met Arg Leu Val Glu Glu Phe Leu Ala Lys Lys Pro Ala Leu Leu
325 330 335

Ala Gln Ile Leu Ala Gly Leu Glu Lys Pro Val Arg Asp Ala Ala Ala
340 345 350

Val Asn Ser Thr Arg Val Ala Leu His Arg Ala Leu Ala Ala Thr Gly
355 360 365

Leu Pro Val Arg Thr Gly Ser Gly Gly Arg Thr Lys Trp Asn Arg Ser
370 375 380

Arg Phe Gly Val Pro Lys Thr His Ala Leu Asp Ala Leu Cys Ala Gly
385 390 395 400

Glu Thr Gln Ala Val His Gly Trp Gln Arg Leu Pro Thr Leu Val Ile
405 410 415

Gly Cys Ser Gly Arg Gly Ser His Gln Arg Thr Arg Val Thr Ala Asp
420 425 430

Gly Phe Pro Arg Gly Tyr Leu Met Arg Arg Lys Arg Val Phe Gly Phe
435 440 445

Ala Thr Gly Asp Leu Val Arg Ala Val Val Pro Ala Gly Lys Lys Ala

450

455

460

Gly Thr His Val Gly Arg Val Ala Val Arg Ser Arg Gly Ser Phe Asn
 465 470 475 480

Ile Arg Thr Thr Ala Gly Val Ile Asp Ser Val Ser His Lys His Cys
 485 490 495

Arg Leu Leu Gln Arg Ala Asp Gly Tyr Asn Tyr Asn Thr Arg Ser Gly
 500 505 510

Ala Ser Ser Pro Pro
 515

<210> 352

<211> 183

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-304 effector

<400> 352

Met Leu Thr Arg Thr Gly Leu Ala Val Glu Ala Thr Thr Gly Gly Arg
 1 5 10 15

Thr Lys Trp Asn Arg Ala Arg Met Gly Ile Pro Lys Arg Asp Ala Trp
 20 25 30

Asp Ala Ala Cys Ala Gly Thr Val Asp Gln Ile Leu Gly Trp Asp Arg
 35 40 45

Pro Ile Gln Arg Ile Asp Cys Leu Gly Arg Gly Ser His Gln Arg Thr
 50 55 60

Arg Val Thr Lys Asp Gly Phe Pro Arg Gly Tyr Leu Pro Arg Thr Lys
 65 70 75 80

Thr Val Gln Gly Phe Arg Thr Gly Asp His Val Arg Ala Ile Val Pro
85 90 95

Thr Gly Lys Lys Thr Gly Thr Trp Ala Gly Arg Val Ala Val Arg Thr
100 105 110

Thr Gly Ser Phe Asn Ile Gln Thr Val Ala Glu Thr Val Gln Gly Val
115 120 125

Ser Ala Arg Trp Cys Val Leu Leu Gln Arg Gly Asp Gly Tyr Arg Tyr
130 135 140

Ser Gln Val Gly Ser Glu Pro Leu Leu Ala Val Arg Pro Ser Ser Arg
145 150 155 160

Arg Leu Lys Ala Thr Val Ser Gly Pro Leu Ala Pro Asp Val Thr Thr
165 170 175

His Thr Leu Glu Gly Phe Glu
180

<210> 353
<211> 290
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-305 effector

<400> 353
Met Asn Asn Asn Ser Val Phe Val Leu Asp Thr Asn Lys Lys Pro Cys
1 5 10 15

Asn Pro Val His Pro Ala Val Ala Arg Lys Leu Leu Thr Gln Gly Lys
20 25 30

Ala Ala Val Phe Arg Arg Tyr Pro Phe Thr Ile Val Leu Lys Glu Glu

35

40

45

Ser Lys Asp Glu Val Lys Glu Leu Arg Val Lys Ile Asp Pro Gly Ala
 50 55 60

Lys Thr Thr Gly Leu Ala Ile Val Ser Asp Thr Asn Val Val Trp Cys
 65 70 75 80

Ala Glu Leu Glu His Arg Gly Phe Gln Val Arg Glu Lys Phe Asn Asp
 85 90 95

Arg Arg Thr Leu Arg Arg Ser Arg Gly Asn Arg Lys Thr Arg Tyr Arg
 100 105 110

Lys Pro Arg Phe Leu Asn Arg Lys Arg Pro Lys Gly Trp Leu Pro Ser
 115 120 125

Ser Leu Met Ser Arg Val Phe Asn Ile Glu Ser Trp Val Lys Lys Leu
 130 135 140

Cys Arg Leu Ala Pro Ile Thr Ala Ile Ile Gln Glu Leu Val Arg Leu
 145 150 155 160

Asp Thr His Lys Ile Ile Asn Pro Glu Ile Asn Gly Thr Glu Tyr Gln
 165 170 175

Lys Gly Glu Leu Phe Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys
 180 185 190

Phe Asn Arg Thr Cys Val Tyr Cys Asn Thr Lys Glu Gly Pro Phe Asn
 195 200 205

Leu Asp Leu Phe His Pro Lys Ser Lys Gly Gly Ser Asp Arg Val Ser
 210 215 220

Asn Leu Val Leu Ile Cys Val Lys Cys Asn Gln Lys Lys Asp Asn Gln
 225 230 235 240

Leu Pro Ala Asp Phe Leu Ser Asp Lys Pro Lys Leu Leu Ala Ile Ile
 245 250 255

Glu Lys Gln Arg Lys Gln Pro Leu Ala Asp Ala Ala Ala Val Asn Ala
260 265 270

Thr Arg Trp Lys Leu Lys Glu Val Leu Glu Asn Thr Gly Leu Pro Val
275 280 285

Glu Thr
290

<210> 354
<211> 433
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-307 effector

<400> 354
Met Pro Cys His Pro Ala Arg Ala Arg Glu Met Leu Arg Lys Gly Arg
1 5 10 15

Ala Val Val Val Arg Met Tyr Pro Phe Thr Ile Arg Ile Lys Asp Arg
20 25 30

Val Gly Gly Thr Met Gln Pro Val Ser Leu Lys Leu Asp Pro Gly Ser
35 40 45

Lys Thr Thr Gly Val Ala Val Ala Arg Glu Asp Glu Asp Lys Thr Glu
50 55 60

Ala Leu Trp Leu Gly Glu Ile Thr His Arg Gly Ala Gln Ile Arg Lys
65 70 75 80

Ser Leu Glu Gln Arg Gly Gly Tyr Arg Arg Arg Arg Arg Asn Ala Asn
85 90 95

Leu Arg His Arg Ala Pro Arg Phe Asn Asn Arg Arg Thr Pro Glu Gly

	100		105		110														
Arg	Leu	Met	Pro	Ser	Leu	Arg	His	Arg	Val	Asp	Asn	Val	Val	Ser	Trp				
	115						120				125								
Thr	Arg	Arg	Leu	Met	Arg	Trp	Cys	Pro	Ile	Thr	Arg	Ile	Ala	Met	Glu				
	130					135					140								
Leu	Val	Arg	Phe	Asp	Met	Gln	Ala	Met	Gln	Asn	Pro	Glu	Ile	Arg	Gly				
145					150					155					160				
Val	Glu	Tyr	Gln	Arg	Gly	Ala	Leu	Phe	Gly	Tyr	Glu	Val	Arg	Glu	Tyr				
				165					170					175					
Leu	Leu	Glu	Lys	Trp	Gly	Arg	Lys	Cys	Ala	Tyr	Cys	Gly	Ala	Glu	Gly				
			180					185					190						
Val	Pro	Leu	Gln	Val	Glu	His	Ile	Gln	Pro	Lys	Ala	Arg	Gly	Gly	Ser				
		195					200					205							
Asn	Arg	Val	Ser	Asn	Leu	Ala	Leu	Ala	Cys	Arg	Pro	Cys	Asn	Glu	Gln				
	210					215					220								
Lys	Gly	Ala	Arg	Pro	Val	Glu	Glu	Phe	Leu	Arg	Gly	Lys	Pro	Glu	Val				
225					230					235					240				
Leu	Arg	Arg	Val	Leu	Ala	Gln	Ala	Lys	Val	Ser	Leu	Lys	Asp	Ala	Ala				
				245					250					255					
Ala	Val	Asn	Ala	Thr	Arg	Trp	Thr	Leu	Trp	Arg	Ala	Leu	Lys	Ala	Thr				
			260					265					270						
Gly	Leu	Pro	Leu	Glu	Thr	Gly	Ser	Gly	Gly	Arg	Thr	Lys	Tyr	Asn	Arg				
		275					280					285							
Cys	Arg	Leu	Gly	Val	Pro	Lys	Thr	His	Ala	Leu	Asp	Ala	Leu	Cys	Val				
	290					295					300								
Gly	Arg	Val	Glu	Ala	Val	Ser	Gly	Trp	Gln	Ile	Pro	Thr	Leu	Ala	Ile				
305					310					315					320				

Arg Ala Thr Gly Arg Gly Ala Tyr Arg Arg Thr Gln Val Thr Ala Ser
325 330 335

Gly Phe Pro Arg Gly Tyr Leu Met Arg Lys Lys Thr Val Phe Gly Phe
340 345 350

Arg Thr Gly Asp Met Val Val Ala Ser Val Pro Thr Gly Lys Lys Ala
355 360 365

Gly Ile His Arg Gly Arg Val Ala Val Arg Glu Thr Gly Ser Phe Asn
370 375 380

Ile Gln Thr Ser Ala Gly Val Val Gln Gly Ile Gly His Lys Arg Cys
385 390 395 400

Arg Leu Arg Met Arg Ala Asp Gly Tyr Gly Tyr Gln Thr Asn Leu Glu
405 410 415

Thr Ala Leu Leu Pro Ser Leu Lys Gly Gly Val Ser Ala Pro Glu Ile
420 425 430

Arg

<210> 355
<211> 418
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-308 effector

<400> 355
Met Pro Cys His Pro Ala Arg Ala Arg Gln Met Leu Arg Glu Gly Arg
1 5 10 15

Ala Val Ile His Arg Thr Thr Pro Met Val Ile Arg Leu Lys Asp Arg

20

25

30

Thr Asp Gly Asp Thr Gln Ala Val Arg Leu Lys Phe Asp Pro Gly Ser
 35 40 45

Lys Thr Thr Gly Ile Ala Leu Val Arg Gln Thr Pro Ser Ala Asp Leu
 50 55 60

Ala Val Leu Asn Leu Met Glu Leu Ala His Arg Gly His Gln Ile Ser
 65 70 75 80

Glu Ala Leu Thr Ala Arg Arg Gln Met Arg Arg Arg Arg Arg Gly Ser
 85 90 95

Leu Arg Tyr Arg Ala Pro Arg Phe Leu Asn Arg Gly Asn Lys Ala Arg
 100 105 110

Gly Trp Val Ala Pro Ser Leu Gln His Arg Val Asp Thr Ala Val Ala
 115 120 125

Trp Val His Arg Leu Gln Arg Trp Thr Pro Ile Ala Ala Ile Ser Ser
 130 135 140

Glu Leu Val Arg Phe Asp Met Gln Ala Leu Asp Asn Pro Asp Ile Glu
 145 150 155 160

Gly Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val Arg Glu
 165 170 175

Tyr Leu Leu Glu Lys Trp Gly Arg Ala Cys Ala Tyr Cys Gly Ala Lys
 180 185 190

Asp Thr Pro Leu Gln Ile Glu His Ile Gln Pro Lys Ala Arg Gly Gly
 195 200 205

Ser Asn Arg Ile Ser Asn Leu Thr Leu Ala Cys Gln Cys Cys Asn Glu
 210 215 220

Ala Lys Ala Ala Gln Pro Ile Glu Ala Phe Leu Ala Lys Lys Pro Asp
 225 230 235 240

Val Leu Arg Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys Asp Ala
245 250 255

Ala Ala Val Asn Ala Thr Arg Trp Ala Leu Val Asn Arg Leu Gln Ala
260 265 270

Thr Gly Leu Pro Val Glu Met Ala Ser Gly Gly Arg Thr Lys Phe Asn
275 280 285

Arg Ser Arg Leu Gln Val Pro Lys Thr His Ala Leu Asp Ala Ala Cys
290 295 300

Val Gly Ala Phe Gly Ser Leu Leu Arg Trp Arg Gln Pro Thr Leu His
305 310 315 320

Ile Lys Cys Thr Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu Thr Lys
325 330 335

His Gly Phe Pro Arg Gly Tyr Leu Met Arg Ser Lys Gln Val His Gly
340 345 350

Phe Gln Thr Gly Asp Leu Val Lys Ala Gln Val Pro Gln Gly Lys Lys
355 360 365

Ala Gly Ala Tyr Arg Gly Arg Val Ala Val Arg Ala Thr Gly Ser Phe
370 375 380

Asn Ile Gln Thr Gly Asn Gly Val Val Gln Gly Ile Ser Tyr Arg His
385 390 395 400

Cys Ser Leu Ile Gln Arg Gly Asp Gly Tyr Gly Tyr Leu Met Gln Pro
405 410 415

Ile Ala

<210> 356

<211> 254

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-309 effector

<400> 356

Met Pro Cys Arg Pro Ala Arg Ala Gln Asp Leu Leu Ala Cys Gly Arg
1 5 10 15

Ala Ala Val Tyr Arg Leu Gln Pro Phe Thr Ile Val Leu Lys Asp Arg
20 25 30

Ala Ala Gly Asp Val Gln Pro Val Glu Phe Lys Val Asp Pro Gly Ser
35 40 45

Lys Val Thr Gly Leu Ala Leu Val Ala Glu Phe Glu Lys Arg Gly Arg
50 55 60

Thr Val Val Trp Ala Ala Asn Leu Ala His Arg Gly His Arg Val Lys
65 70 75 80

Ala Ser Met Thr Asp Arg Ala Met Phe Arg Arg Gly Arg Arg Gly Arg
85 90 95

Lys Thr Arg Tyr Arg Ala Ala Arg Phe Glu Asn Arg Thr Arg Pro Thr
100 105 110

Asn Trp Leu Ala Pro Ser Leu Gln Ser Arg Val Leu Asn Val Lys Ser
115 120 125

Trp Tyr Ser Arg Leu Leu Ser Arg Ala Ser Ile Ser Val Ala Gln Val
130 135 140

Glu Thr Ser Ser Phe Asp Thr Gln Leu Met Glu Asn Ala Asp Ile Ser
145 150 155 160

Gly Val Glu Tyr Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Leu
165 170 175

Tyr Val Leu Glu Arg Gly Gly His Thr Cys Ser Tyr Cys Asp Ala Lys
180 185 190

Asp Val Ala Leu His Leu Asp His Val Leu Pro Arg Ser Arg Gly Gly
195 200 205

Ser Asn Arg Val Ser Asn Leu Val Pro Ala Cys Lys Pro Cys Asn Asp
210 215 220

Ala Lys Ser Asn Arg Ala Val Glu Asp Tyr Leu Val Asp Arg Pro Glu
225 230 235 240

Val Leu Arg Gln Val Lys Ala Gln Leu Arg Ser Pro Leu Lys
245 250

<210> 357

<211> 186

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-310 effector

<400> 357

Met Pro Cys Ser Glu Lys Arg Ala Gln Leu Leu Leu Arg Arg Arg Lys
1 5 10 15

Ala Val Val His Lys Ile Ala Pro Phe Thr Ile Arg Leu Lys Glu Arg
20 25 30

Ile Gly Gly Val Val Gln Pro Val Arg Ile Lys Leu Asp Pro Gly Ser
35 40 45

Lys Thr Thr Gly Ile Ala Leu Val Arg Glu Glu Glu Thr Val Ser Pro
50 55 60

Asp Ser Gly Lys Ile Glu Thr Thr Ala His Val Leu Phe Leu Ala Asp

65

70

75

80

Leu Glu His Arg Gly Gly Arg Ile Arg Asp Arg Leu Thr Ala Arg Arg
85 90 95

Ala Phe Arg Arg Arg Arg Arg Gly Asn Leu Arg Tyr Arg Lys Pro Arg
100 105 110

Phe Asp Asn Arg Thr Arg Pro Asp Gly Trp Leu Ala Pro Ser Leu Gln
115 120 125

His Arg Val Asp Thr Thr Met Ala Trp Val Asn Arg Phe Arg Lys Leu
130 135 140

Ser Pro Val Thr Gly Ile Ser Gln Glu Leu Val Arg Phe Asp Leu Gln
145 150 155 160

Lys Ile Glu Asn Pro Glu Ile Ala Gly Val Glu Tyr Gln His Gly Thr
165 170 175

Leu Ala Gly Tyr Glu Ile Arg Glu Tyr Leu
180 185

<210> 358

<211> 45

<212> PRT

<213> Unknown

 $\langle 220 \rangle$

<223> Description of Unknown:
uncultivated organism

 $\langle 220 \rangle$

<223> Category: MG35 effectors

 $\langle 220 \rangle$

<223> Description: MG35-311 effector

<400> 358

Met Pro Cys Ser Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg
1 5 10 15

Ala Arg Val His Arg Leu Val Pro Phe Thr Ile Arg Leu Ile Asp Arg
20 25 30

Glu Gln Glu Asp Cys Ala Leu Gln Pro Val Arg Leu Lys
35 40 45

<210> 359

<211> 440

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-312 effector

<400> 359

Met Pro Cys Ser Glu Lys Arg Ala Arg Leu Met Leu Gln Arg Gly Arg
1 5 10 15

Ala Arg Val Ala Arg Arg Phe Pro Phe Thr Ile Arg Leu Val Asp Arg
20 25 30

Leu Val Ala Asp Ser Ala Val Gln Pro Val Arg Ile Lys Ile Asp Pro
35 40 45

Gly Ser Lys Thr Thr Gly Leu Ala Val Val Arg Asp Glu Gly Gly Asn
50 55 60

Gln Gly Ser Ala Val Leu Tyr Leu Thr Glu Leu Gln His Arg Gly Lys
65 70 75 80

Gln Ile Ser Glu Ala Leu Thr Ala Arg Arg Ala Met Arg Arg Arg Arg
85 90 95

Arg Gly Asn Leu Arg Tyr Arg Pro Ala Arg Phe Asp Asn Arg Thr Arg
100 105 110

Pro Ala Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Thr
115 120 125

Ala Ser Trp Val Ser Arg Leu Arg Arg Leu Ala Pro Val Ser Gly Ile

130

135

140

Ala Met Glu Leu Val Arg Phe Asp Met Gln Leu Leu Glu Asn Pro Asp
 145 150 155 160

Ile Ser Gly Val Gly Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Leu
 165 170 175

Arg Glu Phe Leu Leu Asn Lys Trp Asp Arg Ala Cys Ala Tyr Cys Gly
 180 185 190

Val Val Asn Val Pro Leu Gln Ile Glu His Ile His Ser Lys Ala Arg
 195 200 205

Gly Gly Ser Asn Arg Glu Ser Asn Leu Thr Leu Ala Cys Glu Pro Cys
 210 215 220

Asn Gln Glu Lys Gly Ala Gln Pro Val Glu Val Tyr Leu Ala Lys Arg
 225 230 235 240

Pro Ala Val Leu Ala Arg Ile Lys Ala Thr Ala Lys Arg Pro Leu Lys
 245 250 255

Asp Ala Ala Ala Val Asn Ala Thr Arg Trp Ala Leu Phe Asn Arg Leu
 260 265 270

Lys Gln Thr Asp Leu Pro Val Thr Thr Gly Ser Gly Gly Arg Thr Lys
 275 280 285

Trp Asn Arg Ser Arg Leu Gly Ile Pro Lys Thr His Gly Leu Asp Ala
 290 295 300

Ala Cys Val Gly Glu Val Asp Ala Leu Ser Gly Trp Asp Val Ser Ser
 305 310 315 320

Leu Ser Ile Lys Ala Thr Gly Arg Gly Ser Tyr Cys Arg Thr Arg Leu
 325 330 335

Asp Lys Phe Gly Phe Pro Arg Gly Tyr Leu Thr Arg Gln Lys Arg Ile
 340 345 350

Lys Gly Phe Gln Thr Gly Asp Ile Val Gln Ala Val Leu Ser Ala Gly
355 360 365

Val His Val Gly Thr Trp Ile Gly Arg Val Ala Val Arg Ala Thr Gly
370 375 380

Ser Phe Asn Ile Gln Thr Ala Ser Gly Val Arg Gln Gly Ile Gly Trp
385 390 395 400

Lys Phe Cys Arg Val Leu Gln Arg Ala Asp Gly Tyr Gly Tyr Ser Ala
405 410 415

Thr Pro Thr Glu Arg Lys Val Ala Thr Ser Ser Pro Cys Leu Lys Ala
420 425 430

Gly Val Ser Val Ala Lys Ser Arg
435 440

<210> 360
<211> 124
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-313 effector

<400> 360
Met Pro Cys Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg
1 5 10 15

Ala Cys Val His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu
20 25 30

Lys Ala Glu Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro
35 40 45

Gly Ser Lys Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys

50

55

60

Gly Val Ala Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln
65 70 75 80

Ile Ser Glu Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg
85 90 95

Ser Lys Leu Arg Tyr Arg Ala Pro Arg Phe Asp Asn Arg Gly Asn Gln
100 105 110

Lys Lys Ala Gly Tyr Arg Gln Val Cys Asn Thr Gly
115 120

<210> 361

<211> 422

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-314 effector

<400> 361

Met Pro Cys Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg
1 5 10 15

Ala Cys Val His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu
20 25 30

Lys Ala Glu Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro
35 40 45

Gly Ser Lys Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys
50 55 60

Gly Val Ala Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln
65 70 75 80

Ile Ser Glu Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg
85 90 95

Ser Lys Leu Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Lys
100 105 110

Gln Arg Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser
115 120 125

Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile
130 135 140

Ser Thr Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu
145 150 155 160

Ile Glu Gly Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val
165 170 175

Arg Glu Tyr Leu Leu Glu Lys Trp Gly Arg Thr Cys Ala Tyr Cys Gly
180 185 190

Ala Lys Asp Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys
195 200 205

Asn Gly Ser Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys
210 215 220

Asn Gln Lys Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys
225 230 235 240

Pro Glu Leu Leu Lys Arg Ile Leu Ala Gln Ala Lys Arg Pro Leu Lys
245 250 255

Asp Ala Ala Ala Val Asn Ser Thr Arg Trp Ala Leu Val Asn Pro Leu
260 265 270

Lys Ala Thr Gly Leu Pro Val Glu Thr Ala Ser Gly Gly Lys Thr Lys
275 280 285

Phe Asn Arg Asn Gln Leu Gly Ile Pro Lys Thr His Ala Leu Asp Ala

290

295

300

Ala Cys Val Gly Glu Val Gly Ser Ile Thr Asp Trp Gln Lys Pro Thr
 305 310 315 320

Leu Ser Ile Lys Ala Met Gly Arg Gly Ser Tyr Gln Arg Thr Arg Leu
 325 330 335

Asp Lys Phe Gly Cys Val Arg Gly Tyr Leu Thr Arg Ser Lys Ser Ile
 340 345 350

Lys Gly Phe Gln Thr Gly Asp Met Val Lys Ala Glu Val Thr Lys Gly
 355 360 365

Lys Lys Ile Gly Ser Tyr Thr Gly Arg Val Ala Val Arg Ala Ser Gly
 370 375 380

Ser Phe Asn Ile Gln Thr Ser Ala Gly Leu Val Gln Gly Val Ser Asp
 385 390 395 400

Arg Tyr Cys Thr Val Val Gln Arg Gly Asn Gly Tyr Gly Tyr Ser Leu
 405 410 415

Val Ala Lys Asn Gly Arg
 420

<210> 362

<211> 450

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-315 effector

<400> 362

Met Pro Cys Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg
 1 5 10 15

Ala Cys Val His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu
20 25 30

Lys Ala Glu Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro
35 40 45

Gly Ser Lys Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Lys
50 55 60

Gly Val Ala Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln
65 70 75 80

Ile Ser Glu Ala Leu Thr Ala Arg Arg Gly Asn Arg Arg Leu Arg Arg
85 90 95

Ser Lys Leu Arg Tyr Arg Pro Pro Arg Phe Asn Asn Arg Gly Asn Lys
100 105 110

Gln Arg Gly Trp Leu Ala Pro Ser Leu Gln His Arg Val Asp Thr Ser
115 120 125

Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile
130 135 140

Ser Thr Glu Leu Val Arg Phe Asp Ala Gln Ala Leu Glu Asn Pro Glu
145 150 155 160

Ile Glu Gly Ala Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val
165 170 175

Arg Glu Tyr Leu Leu Glu Lys Trp Asp Arg Thr Cys Ala Tyr Cys Gly
180 185 190

Ala Lys Asp Val Pro Leu Gln Ile Glu His Ile His Pro Lys Ser Lys
195 200 205

Asn Gly Ser Asp Arg Ile Asn Asn Leu Thr Leu Ala Cys Gln Cys Cys
210 215 220

Asn Gln Lys Lys Ala Ala Leu Pro Val Glu Met Phe Leu Ala Lys Lys

225		230		235		240									
Pro	Glu	Leu	Leu	Glu	Arg	Ile	Leu	Ala	Gln	Ala	Lys	Arg	Pro	Leu	Lys
				245					250					255	
Asp	Ala	Ala	Ala	Val	Asn	Ser	Thr	Arg	Trp	Ala	Leu	Val	Asn	Thr	Leu
			260					265					270		
Lys	Thr	Thr	Gly	Leu	Val	Val	Glu	Thr	Gly	Thr	Gly	Gly	Gln	Thr	Lys
		275					280					285			
Phe	Asn	Arg	Ser	Gln	Phe	Asp	Ile	Pro	Lys	Thr	His	Ala	Leu	Asp	Ala
	290					295					300				
Ala	Cys	Val	Gly	Glu	Val	Gly	Ser	Ile	Thr	Asp	Trp	Gln	Lys	Pro	Thr
305					310					315					320
Leu	Ala	Ile	Lys	Ala	Met	Gly	Arg	Gly	Ser	Tyr	Gln	Arg	Thr	Arg	Leu
				325					330					335	
Asp	Lys	Phe	Gly	Cys	Val	Arg	Gly	Tyr	Leu	Thr	Arg	Ser	Lys	Ser	Ile
			340					345					350		
Lys	Gly	Phe	Gln	Thr	Gly	Asp	Met	Val	Lys	Ala	Glu	Val	Thr	Thr	Gly
		355					360					365			
Lys	Lys	Ile	Gly	Ser	Tyr	Thr	Gly	Arg	Val	Ala	Val	Arg	Ala	Thr	Gly
	370					375					380				
Ser	Phe	Asn	Ile	Gln	Thr	Ser	Thr	Gly	Leu	Val	Gln	Gly	Val	Ser	His
385					390					395					400
Arg	Tyr	Cys	Thr	Val	Val	Gln	Arg	Gly	Asn	Gly	Tyr	Gly	Tyr	Ser	Leu
				405					410					415	
Gly	Ala	Lys	Thr	Asp	Val	Arg	Gly	Thr	Pro	Pro	Gln	His	Arg	Asp	Ala
			420					425					430		
Ser	His	Pro	Ala	Leu	Tyr	Leu	Pro	Gly	Leu	Lys	Ala	Glu	Val	Ser	Arg
		435					440					445			

Ala Asn
450

<210> 363
<211> 226
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
uncultivated organism

<220>
<223> Category: MG35 effectors

<220>
<223> Description: MG35-316 effector

<400> 363
Met Pro Cys Thr Glu Lys Arg Ala Arg Leu Leu Leu Glu Arg Gly Arg
1 5 10 15

Ala Cys Val His Leu Val Met Pro Phe Thr Ile Arg Ile Val Asp Leu
20 25 30

Lys Ala Glu Asn Cys Ala Phe Gln Ala Leu Arg Val Lys Leu Asp Pro
35 40 45

Gly Ser Lys Ala Thr Gly Ile Ala Leu Val Arg Glu Thr Glu Gly Asn
50 55 60

Gly Val Ala Val Val Asn Leu Phe Glu Leu Val His Arg Gly Arg Gln
65 70 75 80

Ile Ser Glu Ala Leu Thr Ala Arg Arg Gly His Arg Arg Leu Arg Arg
85 90 95

Ser Lys Leu Arg Tyr Arg Pro Pro Arg Phe Asp Asn Arg Gly Asn Gln
100 105 110

Lys Lys Gly Trp Leu Pro Pro Ser Leu Gln His Arg Val Asp Thr Ser
115 120 125

Met Ala Trp Val Ser Arg Ile Gln Arg Leu Ala Pro Val Ser Ala Ile

130

135

140

Ser Thr Glu Leu Val Arg Phe Asp Met Gln Ala Met Glu Asn Pro Glu
145 150 155 160

Ile Glu Gly Met Gln Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Val
165 170 175

Arg Glu Tyr Leu Leu Glu Lys Trp Lys Arg Thr Cys Ala Tyr Cys Asp
180 185 190

Ala Lys Asp Val Pro Leu Gln Val Glu His Ile Gln Pro Lys Ala Lys
195 200 205

Gly Gly Ser Asn Arg Ile Ser Asn Leu Ala Leu Ala Cys Pro Ser Cys
210 215 220

Asn Ser
225

<210> 364

<211> 377

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-317 effector

<400> 364

Met Pro Cys Thr Pro Lys Arg Ala Arg Lys Leu Leu Glu Ala Gly Arg
1 5 10 15

Ala Arg Val His Gln Leu Ile Pro Phe Ala Ile Arg Leu Thr Asp Arg
20 25 30

Val Ala Gln Thr Ser Asn Phe Gln Pro Leu Lys Ile Lys Leu Asp Pro
35 40 45

Gly Ser Lys Ala Ser Gly Leu Ala Val Cys Arg Val Ser Glu Lys Thr
50 55 60

Asp Gly Asp Gly Val Val Gln Pro Thr Met His Ile Leu Phe Leu Met
65 70 75 80

Glu Leu Val His Arg Gly Ala Ala Ile Lys Lys Ser Leu Gln Ala Arg
85 90 95

Ala Ala Met Arg Gly Arg Arg Arg Gly Asn Leu Arg Tyr Arg Ala Pro
100 105 110

Arg Phe Asn Asn Arg Thr Lys Ser Lys Gly Trp Leu Pro Pro Ser Leu
115 120 125

Gln His Arg Val Asp Thr Leu Ser Ser Trp Val Asn Arg Ile Gly Arg
130 135 140

Leu Ala Pro Ile Thr His Leu Ala Gln Glu Leu Val Arg Phe Asp Met
145 150 155 160

Gln Leu Met Gln Asn Ala Glu Ile Ser Gly Val Ala Tyr Gln Gln Gly
165 170 175

Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Ala Lys Phe Asn
180 185 190

Arg Thr Cys Ala Tyr Cys Asp Ala Thr Glu Val Pro Leu Gln Ile Glu
195 200 205

His Ile Gln Ala Lys Ala Asn Ala Gly Ser Asn Arg Val Ser Asn Leu
210 215 220

Thr Leu Ala Cys Lys Lys Cys Asn Gln Ala Lys Gly Ser Leu Asp Ile
225 230 235 240

Arg Thr Phe Leu Ala Lys Asp Pro Ala Arg Leu Ala Arg Ile Leu Lys
245 250 255

Gln Val Lys Ala Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr Arg

260

265

270

Trp Ala Val Phe Asn Met Leu Lys Gln Thr Gly Leu Pro Val Glu Thr
 275 280 285

Gly Ser Gly Gly Gln Thr Lys Tyr Asn Arg Thr Arg Leu Gly Val Ile
 290 295 300

Lys Thr His Ala Leu Asp Ala Ala Cys Val Gly Gln Val Gly Glu Val
 305 310 315 320

Gln Gly Thr His Phe Asn Thr Leu Arg Val Thr Cys Thr Gly Arg Gly
 325 330 335

Ser Arg Cys Lys Thr Arg Leu Asp Lys Tyr Gly Phe Pro Arg Thr Tyr
 340 345 350

Leu Thr Arg Thr Lys Thr Ala Phe Gly Phe Arg Thr Gly Asp Thr Val
 355 360 365

Ser Ala Val Val Pro Lys Gly Lys Lys
 370 375

<210> 365

<211> 380

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-318 effector

<400> 365

Met Pro Glu Ala Val Val Lys Ala Leu Ile Thr Lys Ile Asp Pro Gly
 1 5 10 15

Ser Lys Tyr Thr Gly Ile Val Leu Val Asp Asn Asn Asp Arg Val Leu
 20 25 30

Phe Ala Ala Glu Ile Glu His Arg Gly Leu Phe Ile Lys Asn Lys Leu
35 40 45

Asp Ser Arg Arg Val Leu Arg Arg Gly Arg Arg Gly Arg Asn Thr Arg
50 55 60

Tyr Arg Gln Pro Arg Phe Leu Asn Arg Thr Arg Pro Asp Gly Trp Leu
65 70 75 80

Pro Pro Ser Leu Gln His Arg Leu Leu Thr Thr Met Thr Trp Ile Asp
85 90 95

Lys Phe Arg Arg Tyr Ala Glu Ile Ser Lys Leu Ala Val Glu Arg Val
100 105 110

Lys Phe Asp Met Gln Lys Met Gln Asn Pro Gly Ile Ser Gly Val Glu
115 120 125

Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Met Arg Glu Tyr Leu Leu
130 135 140

Glu Lys Trp Asn Arg Thr Cys Ala Tyr Cys Gly Lys Gln Asp Ile Pro
145 150 155 160

Leu Glu Ile Glu His Ile His Pro Lys Ser Lys Gly Gly Ser Asn Arg
165 170 175

Ile Ser Asn Leu Thr Leu Ala Cys Arg Ser Cys Asn Glu Lys Lys Gly
180 185 190

Asn Met Leu Ile Glu Glu Phe Leu Lys Asn Lys Pro Asp Val Leu Lys
195 200 205

Ile Ile Leu Ala Gln Ala Lys Ala Pro Leu Lys Asp Ala Ala Ala Val
210 215 220

Asn Ala Thr Arg Asn Met Leu Phe Lys Lys Leu Leu Asn Thr Gly Leu
225 230 235 240

Leu Val Glu Thr Gly Thr Gly Ala Gln Thr Lys Phe Asn Arg Ile Gly

245

250

255

Leu Lys Leu Pro Lys Glu His Trp Ile Asp Ala Ala Cys Val Gly Asp
 260 265 270

Ser Gly Cys Asn Val Lys Val Asp Ser Asn Leu Lys Pro Leu Lys Ile
 275 280 285

Lys Ala Thr Gly His Gly Asn Arg Arg Met Cys Ser Thr Asn Lys Tyr
 290 295 300

Gly Phe Pro Ile Gln His Arg Thr Asn Lys Lys Phe His Phe Gly Phe
 305 310 315 320

Gln Thr Gly Asp Ile Val Lys Ala Val Val Thr Lys Gly Lys Asn Ile
 325 330 335

Gly Ile His Ile Gly Lys Val Met Cys Arg Ala Lys Gly Asn Phe Asp
 340 345 350

Val Gln Thr Leu Lys Gly Lys Ile Gly Ala Ser Tyr Lys Asn Cys Ser
 355 360 365

Ile Leu Ser Arg Lys Asp Gly Tyr Ile Tyr Asn Thr
 370 375 380

<210> 366

<211> 412

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-319 effector

<400> 366

Met Pro Thr Ser Ala Val Arg Ala Arg Lys Leu Leu Gly Ser Gly Lys
 1 5 10 15

Ala Ala Val Ile Arg Arg Phe Pro Phe Thr Ile Ile Leu Lys Glu Arg
20 25 30

Ser Ser Gly Glu Val Gln Ser Leu Arg Leu Lys Leu Asp Pro Gly Ser
35 40 45

Lys Glu Thr Gly Met Ala Ile Val Asn Glu Thr Met Lys Val Val Val
50 55 60

Phe Ala Ala Val Leu Ala His Arg Gly Ala Ala Ile Lys Ala Lys Leu
65 70 75 80

Asp Ser Arg Arg Ala Thr Arg Arg Gly Arg Arg Asn Arg Ser Thr Arg
85 90 95

Tyr Arg Gly Pro Arg Phe Asn Asn Arg Arg Arg Pro Ala Gly Trp Leu
100 105 110

Pro Pro Ser Leu Gln His Arg Val Glu Thr Ile Met Thr Trp Val Arg
115 120 125

Arg Phe Ser Trp Leu Ala Pro Ile Thr Ala Ile Ser Gln Glu Leu Val
130 135 140

Arg Phe Asp Leu Gln Lys Ile Glu Asn Pro Glu Ile Ser Gly Ile Glu
145 150 155 160

Tyr Gln Gln Gly Thr Leu Ala Gly Tyr Glu Ala Arg Gln Tyr Leu Leu
165 170 175

Gln Lys Trp Gly His Ala Cys Ala Tyr Cys Gly Val Gln Asn Val Pro
180 185 190

Leu Glu Val Glu His Ile His Pro Lys Ala Lys Gly Gly Thr Asn Arg
195 200 205

Val Ser Asn Leu Ala Ile Ala Cys Lys Pro Cys Asn Thr Arg Lys Gly
210 215 220

Cys Leu Asp Val Ala Ile Phe Leu Lys Gly Lys Pro Asp Leu Leu Lys

225		230		235		240									
Lys	Ile	Glu	Ala	Gln	Ala	Lys	Arg	Pro	Leu	Lys	Asp	Ala	Thr	Ala	Val
				245					250					255	
Asn	Ala	Thr	Arg	Trp	Ala	Leu	Tyr	Glu	Arg	Leu	Gln	Ala	Thr	Ser	Leu
			260					265					270		
Pro	Val	Glu	Thr	Gly	Ser	Gly	Gly	Arg	Thr	Lys	Tyr	Asn	Arg	Thr	Leu
		275					280					285			
Leu	Gly	Leu	Pro	Lys	Glu	His	Trp	Ile	Asp	Ala	Ala	Cys	Val	Gly	Glu
	290					295					300				
Ser	Gly	Ala	Ser	Thr	Asn	Val	Pro	Lys	Gly	Met	Met	Pro	Leu	Val	Ala
305					310					315					320
Arg	Ala	Ala	Gly	His	Gly	Asn	Arg	Gln	Ile	Cys	Ala	Thr	Asp	Ala	Phe
				325					330					335	
Gly	Phe	Pro	Lys	Arg	His	Arg	Thr	Ser	Gln	Lys	Ser	Phe	Phe	Gly	Phe
			340					345					350		
Gln	Thr	Gly	Asp	Met	Val	Cys	Ala	Ile	Val	Pro	Ser	Gly	Lys	Lys	Gln
		355					360					365			
Gly	Ile	His	Thr	Gly	Arg	Leu	Leu	Val	Arg	Ala	Thr	Gly	Ser	Phe	Asp
	370					375					380				
Ile	Gln	Thr	Ala	Ala	Gly	Arg	Val	Ser	Gly	Ile	Asn	His	Arg	His	Cys
385					390					395					400
Gly	Ala	Ile	His	Arg	Lys	Asp	Gly	Tyr	Ala	Tyr	Gln				
				405					410						

<210> 367

<211> 190

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-320 effector

<400> 367

Met Gln His Arg Val Ala Thr Ile Met Thr Trp Val Gly Arg Leu Ser
1 5 10 15

Arg Ile Ala Thr Ile Thr Ala Leu Ser Gln Glu Leu Val Arg Phe Asp
20 25 30

Leu Gln Lys Ile Glu Lys Pro Glu Ile Ser Gly Val Asp Leu Ala Gly
35 40 45

Tyr Glu Ala Arg Gln Tyr Leu Leu Gln Lys Trp Gly His Ala Cys Ala
50 55 60

Tyr Cys Gly Val Gln Asn Val Pro Leu Glu Val Glu His Ile His Pro
65 70 75 80

Lys Ala Lys Gly Gly Thr Asn Arg Val Ser Asn Leu Cys Ile Ala Cys
85 90 95

Asn Pro Cys Asn Thr Lys Lys Gly Cys Ser Asp Ile Ala Val Phe Trp
100 105 110

Lys Asp Lys Pro Asp Leu Leu Arg Lys Ile Glu Thr Gln Ala Lys His
115 120 125

Pro Leu Lys Asp Ala Thr Ala Val Asn Ala Thr Arg Trp Ala Leu Phe
130 135 140

Glu Lys Leu Lys Ala Ile Gly Leu Pro Phe Glu Val Gly Ser Gly Gly
145 150 155 160

Arg Tyr Ser Asn Leu Ile Val Gln Cys Trp Ser Ser Thr Lys Ser Thr
165 170 175

Gly Ser Met Pro Leu Val Ser Gly Ser Leu Val Pro Ile Ser

180

185

190

<210> 368

<211> 428

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-321 effector

<400> 368

Met	Gln	Lys	Val	Phe	Val	Val	Asp	Lys	Asn	Gly	Arg	Pro	Leu	Met	Pro
1				5					10					15	

Cys	Ser	Pro	Thr	Arg	Cys	Lys	Gln	Phe	Lys	Lys	Glu	Gly	Arg	Ser	Arg
			20					25					30		

Val	Tyr	Arg	Leu	Lys	Pro	Phe	Thr	Ile	Gln	Leu	Ile	Asp	Val	Glu	Gly
		35					40					45			

Gly	Glu	Thr	Lys	Asp	Val	Glu	Tyr	Lys	Val	Asp	Ala	Gly	Ser	Lys	Phe
	50					55					60				

Thr	Gly	Leu	Ala	Leu	Val	Gly	Asn	Phe	Glu	Lys	Gln	Gly	Asn	Val	Leu
65					70					75					80

Leu	Trp	Ala	Ala	Asn	Leu	Gln	His	Arg	Gly	Gln	Glu	Ile	Lys	Asn	Ala
				85					90					95	

Leu	Glu	Ser	Arg	Arg	Ser	Leu	Arg	Arg	Gly	Arg	Arg	Asn	Arg	Lys	Lys
			100					105					110		

Arg	Tyr	Arg	Ala	Ala	Arg	Trp	Arg	Phe	Arg	Asn	Gly	Ile	Lys	Gly	Gly
		115					120					125			

Leu	Ala	Pro	Ser	Leu	Met	Ser	Arg	Val	Asn	Asn	Ile	Thr	Asn	Trp	Leu
	130						135				140				

Lys Lys Leu Met Lys Tyr Val Pro Val Thr Lys Ile Val Ser Glu Leu
145 150 155 160

Val Arg Phe Asp Leu Gln Lys Leu Val Asn Pro Glu Ile Ser Ser Ile
165 170 175

Glu Tyr Gln Gln Gly Thr Leu Gln Gly Tyr Glu Val Lys Glu Tyr Leu
180 185 190

Leu Glu Lys Trp Gly Arg Gln Cys Val Tyr Cys Asn Lys Lys Asp Val
195 200 205

Pro Leu Gln Val Glu His Ile His Pro Arg Ala Lys Gly Gly Thr Asn
210 215 220

Arg Ile Gly Asn Leu Thr Ile Ser Cys Ala Lys Cys Asn Glu Lys Lys
225 230 235 240

Ser Ala Arg Ser Ile Gly Asp Phe Leu Ser Gly Lys Pro Thr Leu Leu
245 250 255

Lys Lys Ile Lys Ala Gln Met Gly Lys Pro Leu Lys Asp Ala Thr Ala
260 265 270

Val Asn Thr Thr Arg Trp Arg Leu Lys Glu Glu Leu Glu Ser Phe Gly
275 280 285

Leu Pro Leu Glu Leu Ser Ser Gly Gly Arg Thr Lys Phe Asn Arg Leu
290 295 300

Gln Gln Gly Tyr Lys Lys Asp His Trp Leu Asp Ala Ala Cys Thr Gly
305 310 315 320

Ser Ser Gly Glu Ser Val Ser Leu Asn Arg Ile Lys Pro Leu Gln Ile
325 330 335

Lys Ala Met Gly Arg Gly Ser Arg Gln Val Met Lys Thr Asp Lys Tyr
340 345 350

Gly Phe Pro Arg Gly Ser Ala Gly Thr Val Lys Arg Val Asn Gly Phe

355

360

365

Gln Thr Gly Asp Leu Val Lys Leu Asp Gln Pro Lys Gly Lys Tyr Ala
 370 375 380

Gly Thr Trp Ile Gly Arg Leu Val Gly Val Arg Ser Arg Gly Ile Leu
 385 390 395 400

Asp Ile Met Thr Pro Leu Gly Lys Ala Gly Ala Thr Trp Lys Asn Phe
 405 410 415

Thr Leu Leu Gln His Ser Asp Gly Tyr Glu Tyr Ala
 420 425

<210> 369

<211> 424

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-322 effector

<400> 369

Met Gln Asn Tyr Val Phe Val Leu Asp Thr Asn Lys Gln Pro Leu Asn
 1 5 10 15

Pro Val Thr Pro Lys Arg Ala Arg Glu Leu Leu Thr Lys Gln Lys Ala
 20 25 30

Ser Val Phe Arg Met Tyr Pro Phe Thr Ile Ile Leu Lys His Ala Val
 35 40 45

Pro Asn Pro Ala Ser Lys Ile Leu Thr Ile Lys Leu Asp Pro Gly Ser
 50 55 60

Lys Val Thr Gly Ile Ala Val Leu Asp Gly Glu Asn Val Ile Trp Val
 65 70 75 80

Ala Glu Leu Glu His Arg Gly Trp Gln Ile Lys Asp Ser Leu Leu Thr
85 90 95

Arg Arg Ser Leu Arg Arg Asn Arg Arg Asn Arg Lys Thr Arg Tyr Arg
100 105 110

Gln Ala Lys Phe Asn Asn Arg Lys Arg Lys Glu Gly Trp Leu Ala Pro
115 120 125

Ser Leu Met His Arg Val Leu Thr Ile Glu Thr Trp Val Lys Arg Leu
130 135 140

Cys Arg Tyr Ala Pro Ile Thr Ser Ile Ala Met Glu Leu Val Lys Phe
145 150 155 160

Asp Thr Gln Lys Leu Gln Asn Pro Glu Ile Asp Gly Val Glu Tyr Gln
165 170 175

Gln Gly Glu Leu Ala Gly Tyr Glu Val Arg Glu Tyr Leu Leu Glu Lys
180 185 190

Trp Gly Arg Lys Cys Val Tyr Cys Asp Lys Gln Asp Val Pro Leu Gln
195 200 205

Ile Glu His Ile His Pro Arg Ser Lys Gly Gly Ser Asn Arg Val Ser
210 215 220

Asn Leu Thr Leu Ser Cys Glu Gln Cys Asn Ile Lys Lys Gly Thr Lys
225 230 235 240

Phe Ile Asp Glu Phe Leu Lys Lys Asp Gly Ala Arg Leu Glu Lys Ile
245 250 255

Lys His Gln Ala Lys Gln Pro Leu Lys Asp Ala Ala Thr Val Asn Ala
260 265 270

Thr Arg Trp Thr Leu Phe Arg Ile Leu Lys Asn Ile Leu Pro Thr Thr
275 280 285

Thr Gly Thr Gly Gly Gln Thr Lys Tyr Asn Arg Thr Arg Leu Glu Leu

290

295

300

Pro Lys His His Trp Val Asp Ala Ala Cys Val Gly Lys Val Glu Lys
 305 310 315 320

Leu Asn Ile Leu Thr Thr His Pro Leu Arg Ile Lys Cys Thr Gly Trp
 325 330 335

Gly Thr Arg Gln Met Cys Gly Thr Asn Lys Tyr Gly Phe Pro Ile Arg
 340 345 350

His Arg Glu Arg Lys Gln Val His Phe Gly Phe Arg Thr Gly Asp Ile
 355 360 365

Ala Lys Ala Val Val Thr Ser Gly Lys Lys Val Gly Gln Tyr Val Gly
 370 375 380

Arg Val Leu Cys Arg Lys Thr Gly Asn Phe Asp Ile Ala Thr Lys Ala
 385 390 395 400

Gly Arg Val Ala Gly Ile Ser His Lys Phe Cys Ser Pro Ile His Lys
 405 410 415

Asn Asp Gly Tyr Ser Tyr Ala Phe
 420

<210> 370

<211> 339

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-323 effector

<400> 370

Met Gln Pro Val Glu Phe Lys Val Asp Pro Gly Ser Lys Val Thr Gly
 1 5 10 15

Leu Ala Leu Val Ala Glu Phe Glu Lys Arg Gly Arg Thr Val Val Trp
20 25 30

Ala Ala Asn Leu Ala His Arg Gly Tyr Arg Val Lys Ala Ser Ile Thr
35 40 45

Asp Arg Ala Met Phe Arg Arg Gly Arg Arg Gly Arg Lys Thr Arg Tyr
50 55 60

Arg Ala Ala Arg Phe Glu Asn Arg Thr Arg Pro Thr His Trp Leu Ala
65 70 75 80

Pro Ser Leu Gln Ser Arg Val Leu Asn Val Lys Ser Trp Tyr Ser Arg
85 90 95

Leu Leu Ser Arg Ala Pro Ile Ser Val Ala Gln Val Glu Thr Ser Ser
100 105 110

Phe Asp Thr Gln Leu Met Glu Asn Ala Asp Ile Ser Gly Val Glu Tyr
115 120 125

Gln Gln Gly Glu Leu Gln Gly Tyr Glu Val Arg Gln Tyr Val Leu Glu
130 135 140

Arg Gly Gly His Thr Cys Ser Tyr Cys Asp Ala Lys Asp Val Ala Leu
145 150 155 160

His Leu Asp His Val Leu Pro Arg Ser Arg Gly Gly Ser Asn Arg Val
165 170 175

Ser Asn Leu Val Pro Ala Cys Lys Pro Cys Asn Asp Ala Lys Ser Asn
180 185 190

Arg Ala Val Glu Asp Tyr Leu Val Asp Arg Pro Glu Val Leu Arg Gln
195 200 205

Val Lys Ala Gln Leu Arg Ser Pro Leu Lys Asp Ala Ala Val Met Asn
210 215 220

Ala Thr Arg Phe Ala Ile Val Asp Ala Leu Arg Glu Phe Gly Leu Glu

Gly Arg Thr Cys Val Tyr Cys Asp His Thr Asp Arg Pro Leu Gln Val
35 40 45

Glu His Leu Thr Pro Thr Gly Ser Gly Gly Ser Asp Gln Val Ser Asn
50 55 60

Leu Ala Leu Ala Cys Glu Ser Cys Asn Ala Ala Lys Gly Asn Gln Thr
65 70 75 80

Val Glu Val Tyr Leu Ala Asp Asp Pro Val Arg Arg Asp Arg Ile Leu
85 90 95

Arg Gln Ala Gln Gln Pro Leu Arg Asp Ala Ala Ala Val Asn Ala Thr
100 105 110

Arg Trp Ala Ile Trp Glu Met Leu Thr Arg Thr Gly Val Pro Val Glu
115 120 125

Ala Thr Thr Gly Gly Arg Thr Lys Trp Asn Arg Thr Arg Met Gly Ile
130 135 140

Pro Lys Arg Asp Ala Trp Asp Ala Ala Cys Ala Gly Thr Val Asp Gln
145 150 155 160

Val Leu Gly Trp Asp Arg Pro Ile Gln Arg Val Asp Cys Leu Gly Arg
165 170 175

Gly Ser His Gln Arg Thr Arg Val Thr Lys Asp Gly Phe Pro Arg Gly
180 185 190

Tyr Leu Pro Arg Thr Lys Met Val Gln Gly Phe Arg Thr Gly Asp His
195 200 205

Val Arg Ala Ile Val Glu Thr Gly Ala His Arg Gly Thr Trp Thr Gly
210 215 220

Arg Val Ala Val Arg Ser Thr Gly Ser Phe Asn Ile Gln Thr Gly Ala
225 230 235 240

Ala Thr Ile Gln Gly Ile Ala Ala Arg Trp Cys Val Leu Leu Gln Arg

245

250

255

Gly Asp Gly Tyr Arg Tyr Ser Leu Ala Leu Pro Arg Thr Glu His Ala
 260 265 270

Ile Arg Pro Ser Ser Val Ala
 275

<210> 372

<211> 77

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-325 effector

<400> 372

Met Gln Arg Ala Phe Val Leu Ser Lys Thr Lys Lys Pro Leu Met Pro
 1 5 10 15

Cys His Pro Ala Arg Ala Arg Glu Leu Leu Lys Lys Lys Lys Ala Lys
 20 25 30

Val Tyr Arg Leu Lys Ala Phe Thr Ile Ile Leu Thr Glu Arg Glu Asp
 35 40 45

Gly Glu Thr Gln Glu Val Glu Leu Lys Val Asp Pro Gly Ser Lys Thr
 50 55 60

Ser Gly Met Ala Leu Val Ala Thr Cys Lys Arg Gly Lys
 65 70 75

<210> 373

<211> 151

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

uncultivated organism

<220>

<223> Category: MG35 effectors

<220>

<223> Description: MG35-326 effector

<400> 373

Met	Gln	Arg	Val	Phe	Val	Leu	Asp	Ala	Lys	Gly	Glu	Pro	Leu	Met	Pro
1				5					10					15	

Cys	Arg	Pro	Thr	Arg	Ala	Arg	Arg	Leu	Leu	Lys	Ala	Gly	Arg	Ala	Ala
			20					25					30		

Val	Phe	Lys	Arg	Tyr	Pro	Phe	Thr	Ile	Val	Leu	Lys	Ala	Arg	Glu	Gly
		35					40					45			

Gly Glu Thr Gln Gly Thr Gln Leu Lys Ile Asp Pro Gly Ala Arg T