

AB\_Enzymes.ST25.txt  
SEQUENCE LISTING

<110> AB Enzymes Oy

<120> Method and DNA Constructs for Increasing the Production Level of Carbohydrate Degrading Enzymes in Filamentous Fungi

<130> A3834PFI

<150> FI 20040551

<151> 2004-04-16

<160> 25

<170> PatentIn version 3.2

<210> 1

<211> 1375

<212> DNA

<213> Nonomuraea flexuosa

<220>

<221> Nf xyn11A nucleotide sequence (AJ508952), the coding region is from nt 303 to nt 1337

<222> (1)..(1375)

<400> 1

cccgggtatt catgtgaatg attagcaaca gttatgttac ggagatattt ctgagagtgt	60
tgacaggtcg tgaagtcggt ccgatacttt cgagctagct ccgatagttt tcgatacgcc	120
ggcacatcga gcacgtcggg cgagtcacgc gccacgtcgg ttttccgccg caccgccgcg	180
agagcggccg gagaaccccc gcgtgtccgc ggcatcgggt ccggtccgtc gttcggccgc	240
gaccgcgcgc cgggtcgcga caccgccagcc cccatcggcc cttcttcacg aggaagccgt	300
acatgaacga acccctcacc atcacgcagg ccaggcgccg cagacgcctc ggccctccggc	360
gcatcgtcac cagtgccttc gccctggcac tcgccatcgc cggtcgcgtg ctgcccggca	420
cggcccacgc cgacaccacc atcaccaga accagaccgg gtacgacaac ggctacttct	480
actcgttctg gaccgacgcg cccgggaccg tctccatgac cctccactcg ggcggcagct	540
acagcacctc gtggcggaac accgggaact tcgtcgccgg caagggtctg tccaccggcg	600
gacggcggac cgtgacctac aacgcctcct tcaaccgctc gggtaacgcc tacctcacgc	660
tctacggctg gaccaggaac ccgctcgtcg agtactacat cgtcgagagc tggggcacct	720
accggcccac cggcacctac aagggcaccg tcaccaccga cggcggcacg tacgacatct	780
acgagacctg gcggtacaac gcgccgtcca tcgagggcac ccggaccttc cagcagttct	840
ggagcgtccg gcagcagaag cggaccagcg gcaccatcac catcggaac cacttcgacg	900
cctggggccc cgccggcatg aacctgggca gccacgacta ccagatcatg gcgaccgagg	960
gctaccagag cagcggtagc tccaccgtct ccatcagcga gggtaggaac cccggcaacc	1020
cgggtaacc cggcaacccc ggcaacccc gtaacccggg taaccccggc ggtggctgcg	1080
tcgcgaccct ctccgccggc cagcagtggg gcgaccgcta caacctcaac gtctcggtca	1140
gcggctcgaa caactggacg gtccggatgg acgtgcccta cccggcccg atcatcgcca	1200
cctggaacat ccacgcccag tggcccaggt cccaggtgct catcgccaga cccaacggca	1260

AB\_Enzymes.ST25.txt

acggcaacaa ctggggcgctg acgatccagc acaacggcaa ctggacctgg ccgacgggtca 1320  
cctgtaccgc gaactgagtt cccgccccca aagggtggcgc ggcggctccc ggccc 1375

<210> 2  
<211> 906  
<212> DNA  
<213> *Nonomuraea flexuosa*

<220>  
<221> am35, Nf xyn11A coding region for the mature Nf Xyn11A (AM35)  
protein  
<222> (1)..(906)

<400> 2  
gacaccacca tcacccagaa ccagaccggg tacgacaacg gctacttcta ctcgttcttg 60  
accgacgcg cggggaccgt ctccatgacc ctccactcgg gcggcagcta cagcacctcg 120  
tggcggaaca ccgggaactt cgtcgccggc aagggtctgg ccaccggcgg acggcggacc 180  
gtgacctaca acgcctcctt caaccgctcg ggtaacgcct acctcacgct ctacggctgg 240  
accaggaacc cgctcgtcga gtactacatc gtcgagagct ggggcaccta ccggccccacc 300  
ggcacctaca agggcaccgt caccaccgac ggcggcacgt acgacatcta cgagacctgg 360  
cgggtacaacg cgccgtccat cgagggcacc cggaccttcc agcagttctg gagcgtccgg 420  
cagcagaagc ggaccagcgg caccatcacc atcggcaacc acttcgacgc ctgggccccgc 480  
gccggcatga acctgggcag ccacgactac cagatcatgg cgaccgaggg ctaccagagc 540  
agcggtagct ccaccgtctc catcagcgag ggtggcaacc ccggcaaccc gggtaacccc 600  
ggcaaccccc gcaacccccg taacccgggt aaccccggcg gtggctgcgt cgcgaccctc 660  
tccgccggcc agcagtggag cgaccgctac aacctcaacg tctcggtcag cggctcgaac 720  
aactggacgg tccggtatga cgtgccctac ccggcccgca tcatcgccac ctggaacatc 780  
cacgcccagt ggcccagatc ccaggtgctc atcgccagac ccaacggcaa cggcaacaac 840  
tggggcgctga cgatccagca caacggcaac tggacctggc cgacgggtcac ctgtaccgcg 900  
aactga 906

<210> 3  
<211> 663  
<212> DNA  
<213> *Nonomuraea flexuosa*

<220>  
<221> am24, shortened form of am35, includes a STOP codon  
<222> (1)..(663)

<400> 3  
gacaccacca tcacccagaa ccagaccggg tacgacaacg gctacttcta ctcgttcttg 60  
accgacgcg cggggaccgt ctccatgacc ctccactcgg gcggcagcta cagcacctcg 120  
tggcggaaca ccgggaactt cgtcgccggc aagggtctgg ccaccggcgg acggcggacc 180  
gtgacctaca acgcctcctt caaccgctcg ggtaacgcct acctcacgct ctacggctgg 240

AB\_Enzymes.ST25.txt

```
accaggaacc cgctcgtcga gtactacatc gtcgagagct ggggcaccta ccggcccacc 300
ggcacctaca agggcaccgt caccaccgac ggcggcacgt acgacatcta cgagacctgg 360
cgggtacaacg cgccgtccat cgagggcacc cggaccttcc agcagttctg gagcgtccgg 420
cagcagaagc ggaccagcgg caccatcacc atcggcaacc acttcgacgc ctggggcccgc 480
gccggcatga acctgggcag ccacgactac cagatcatgg cgaccgaggg ctaccagagc 540
agcggtagct ccaccgtctc catcagcgag ggtggcaacc ccggcaaccc gggtaacccc 600
ggcaaccccg gcaaccccg taacccgggt aaccccggcg gtggctgcgt cgcgaccctc 660
taa 663
```

```
<210> 4
<211> 906
<212> DNA
<213> Nonomuraea flexuosa
```

```
<220>
<221> am35*, like am35 but 9 codons are changed in the sequence
      (Example 10) (the changes do not alter the encoded amino acid
      sequence)
<222> (1)..(906)
```

```
<400> 4
gacaccacca tcaccagaa ccagaccggc tacgacaacg gctacttcta ctcgttctgg 60
accgacgccc ccggcaccgt ctccatgacc ctccactcgg gcggcagcta cagcacctcg 120
tggcgcaaca ccggcaactt cgtcgccggc aagggtgtgt ccaccggcgg ccgccgcacc 180
gtcacctaca acgcctcctt caaccgctcg ggtaacgcct acctcacgct ctacggctgg 240
accaggaacc cgctcgtcga gtactacatc gtcgagagct ggggcaccta ccggcccacc 300
ggcacctaca agggcaccgt caccaccgac ggcggcacgt acgacatcta cgagacctgg 360
cgggtacaacg cgccgtccat cgagggcacc cggaccttcc agcagttctg gagcgtccgg 420
cagcagaagc ggaccagcgg caccatcacc atcggcaacc acttcgacgc ctggggcccgc 480
gccggcatga acctgggcag ccacgactac cagatcatgg cgaccgaggg ctaccagagc 540
agcggtagct ccaccgtctc catcagcgag ggtggcaacc ccggcaaccc gggtaacccc 600
ggcaaccccg gcaaccccg taacccgggt aaccccggcg gtggctgcgt cgcgaccctc 660
tccgccggcc agcagtggag cgaccgtac aacctcaacg tctcggtcag cggtcgaac 720
aactggacgg tccggatgga cgtgccctac ccggcccgcg tcatcgccac ctggaacatc 780
cacgcccagt ggcccagtc ccaggtgctc atcgccagac ccaacggcaa cggcaacaac 840
tggggcgtga cgatccagca caacggcaac tggacctggc cgacgggtcac ctgtaccgcg 900
aactga 906
```

```
<210> 5
<211> 663
<212> DNA
<213> Nonomuraea flexuosa
```

<220>  
 <221> am24\*, like am24 but 9 codons are changed in the sequence like in  
 am35\* (Example 10)  
 <222> (1)..(663)

<400> 5  
 gacaccacca tcacccagaa ccagaccggc tacgacaacg gctacttcta ctcgttcttg 60  
 accgacgccc ccggcaccgt ctccatgacc ctccactcgg gcggcagcta cagcacctcg 120  
 tggcgcaaca ccggcaactt cgtcgccggc aagggctggt ccaccggcgg ccgccgcacc 180  
 gtcacctaca acgcctcctt caacccgtcg ggtaacgcct acctcacgct ctacggcttg 240  
 accaggaacc cgctcgtcga gtactacatc gtcgagagct ggggcaccta ccggccccacc 300  
 ggacactaca agggcaccgt caccaccgac ggcggcacgt acgacatcta cgagacctgg 360  
 cgggtacaacg cgccgtccat cgagggcacc cggaccttcc agcagttctg gagcgtccgg 420  
 cagcagaagc ggaccagcgg caccatcacc atcggcaacc acttcgacgc ctgggccccgc 480  
 gccggcatga acctgggcag ccacgactac cagatcatgg cgaccgaggg ctaccagagc 540  
 agcggtagct ccaccgtctc catcagcgag ggtggcaacc ccggcaaccc gggtaacccc 600  
 ggcaaccccc gcaacccccg taacccgggt aaccccggcg gtggctgcgt cgcgaccctc 660  
 taa 663

<210> 6  
 <211> 1864  
 <212> DNA  
 <213> *Nonomuraea flexuosa*

<220>  
 <221> Nf xyn10A nucleotide sequence (AJ508953), the coding region is  
 from nt 194 to nt 1672  
 <222> (1)..(1864)

<400> 6  
 ttcggcagcc tattgacaaa tttcgtgaat gtttcccaca cttgctctgc agacggcccc 60  
 gccgatcatg ggtgcaccgg tcggcgggac cgtgctccga cgccattcgg ggggtgtgcgc 120  
 ctgcggggcgc ggctcgcac ccgcggggac tcccgcgggt ccctttccgt gtccctctaa 180  
 tggaggctca ggcatgggag tgaacgcctt cccagacccc ggagctcggc ggttcaccgg 240  
 cgggctgtac cgggccctgg ccgcggccac ggtgagcgtg gtcggcgtgg tcacggccct 300  
 gacggtgacc cagcccgcga gcgccgcggc gagcacgctc gccgaggggt ccgcgcagca 360  
 caaccggtac ttcggcgtgg ccatcgccgc gaacaggctc accgactcgg tctacaccaa 420  
 catcgcaaac cgcgagttca actcgggtgac ggccgagaac gagatgaaga tcgacgccac 480  
 cgagccgcag caggggcggt tcgacttcac ccaggccgac cggatctaca actgggcgcg 540  
 ccagaacggc aagcagggtc gcggccacac cctggcctgg cactcgcagc agccgcagtg 600  
 gatgcagaac ctacgaggcc aggcgctgcg ccaggcgatg atcaaccaca tccagggggg 660  
 catgtcctac taccggggca agatcccgat ctgggacgtg gtgaacgagg cgttcgagga 720  
 cggaaactcc ggccgcccgt gcgactccaa cctccagcgc accggtaacg attggatcga 780

AB\_Enzymes.ST25.txt

```

ggtcgcgttc cgcaccgccc gccaggggga cccctcggcc aagctctgct acaacgacta 840
caacatcgag aactggaacg cgccaagac ccaggcggtc tacaacatgg tgcgggactt 900
caagtcccg cgcgtgcca tcgactgctt gggcttccag tcgcacttca acagcggtaa 960
cccggtacaac ccgaacttcc gcaccaccct gcagcagttc gcggccctcg gcgtggacgt 1020
cgaggtcacc gagctggaca tcgagaacgc cccggcccag acctacgcca gcgtgatccg 1080
ggactgcctg gccgtggacc gctgcaccgg catcaccgtc tgggggtgtcc gcgacagcga 1140
ctcctggcgc tcgtaccaga acccgctgct gttcgacaac aacggcaaca agaagcaggc 1200
ctactacgcy gtgctcgacy ccctgaacga gggctccgac gacggtggcg gcccgtccaa 1260
cccgccggtc tcgccggcgc cgggtggcgg ttccgggcag atccggggcg tggcctccaa 1320
ccggtgcatc gacgtgccga acggcaaacac cgccgacggc acccaggtcc agctgtacga 1380
ctgccacagc ggttccaacc agcagtggac ctacacctcg tccggtgagt tccgcatctt 1440
cggcaacaag tgcctggacg cgggcggctc cagcaacggt gcggtgggtcc agatctacag 1500
ctgctggggc ggcgccaacc agaagtggga gctccgggcc gacggcacca tcgtgggcgt 1560
gcagtccggg ctgtgcctcg acgcggtggg tggcggcacc ggcaacggca cgcggtgca 1620
gctctactcc tgctggggcg gcaacaacca gaagtgggtcc tacaacgcct gatccccggc 1680
tgatcgaccc tagttgaggc cgtctccggt acggcaccgt cggaccggag gcggtccctt 1740
gttcgtccag gacggaagga ccggtctgag caggcgcggc gatcggaacac catggtggga 1800
ggcacgaaaag cgggaggggg tcgtattccg agactccggg aagtggaggt gttcctccac 1860
ctga

```

```

<210> 7
<211> 1347
<212> DNA
<213> Nonomuraea flexuosa

```

```

<220>
<221> am50, Nf xyn10A coding region for the mature Nf xyn10A (AM50)
      protein
<222> (1)..(1347)

```

```

<400> 7
gcggcgagca cgctcgccga gggtgccgcy cagcacaacc ggtacttcgg cgtggccatc 60
gccgcaaca ggctcaccga ctcggtctac accaaccatcg cgaaccgcga gttcaactcg 120
gtgacggccg agaacgagat gaagatcgac gccaccgagc cgcagcaggg gcggttcgac 180
ttcaccagg cgcaccggat ctacaactgg gcgcgccaga acggcaagca ggtccgcggc 240
cacaccctgg cctggcactc gcagcagccg cagtggatgc agaacctcag cggccaggcg 300
ctgcgccagg cgatgatcaa ccacatccag ggggtcatgt cctactaccg gggcaagatc 360
ccgatctggg acgtggtgaa cgaggcggtc gaggacggaa actccggccg ccggtgcgac 420
tccaacctcc agcgaccggg taacgattgg atcgagggtc cgttccgcac cgcccggcag 480
ggggacccct cggccaagct ctgctacaac gactacaaca tcgagaactg gaacgcggcc 540

```

AB\_Enzymes.ST25.txt

aagacccagg	cggtctacaa	catggtgcgg	gacttcaagt	cccgcggcgt	gccccatcgac	600
tgctgtgggct	tccagtcgca	cttcaacagc	ggtaacccgt	acaacccgaa	cttccgcacc	660
accctgcagc	agttcgcggc	cctcggcgtg	gacgtcgagg	tcaccgagct	ggacatcgag	720
aacgccccgg	cccagaccta	cgccagcgtg	atccgggact	gcctggccgt	ggaccgctgc	780
accggcatca	ccgtctgggg	tgtccgcgac	agcgactcct	ggcgctcgta	ccagaacccg	840
ctgctgttcg	acaacaacgg	caacaagaag	caggcctact	acgcggtgct	cgacgccctg	900
aacgaggggt	ccgacgacgg	tggcgggccc	tccaacccgc	cggtctcgcc	gccgcccgggt	960
ggcggttccg	ggcagatccg	gggcgtggcc	tccaacccgt	gcatcgacgt	gccgaacggc	1020
aacaccgccg	acggcaccca	ggtccagctg	tacgactgcc	acagcggttc	caaccagcag	1080
tggacctaca	cctcgtccgg	tgagttccgc	atcttcggca	acaagtgcct	ggacgcgggc	1140
ggctccagca	acggtgcggt	ggtccagatc	tacagctgct	ggggcggcgc	caaccagaag	1200
tgggagctcc	gggccgacgg	caccatcgct	ggcgtgcagt	ccgggctgtg	cctcgacgcg	1260
gtgggtggcg	gcaccggcaa	cggcacgcgg	ctgcagctct	actcctgctg	gggcggcaac	1320
aaccagaagt	ggtcctacaa	cgccctaa				1347

<210> 8  
 <211> 972  
 <212> DNA  
 <213> *Nonomuraea flexuosa*

<220>  
 <221> The sequence encoding the AM50 core and linker regions, includes  
 a STOP codon  
 <222> (1)..(972)

<400> 8						
gcggcgagca	cgctcgccga	gggtgccg	cagcacaacc	ggtacttcgg	cgtagccatc	60
gccgcgaaca	ggctcaccga	ctcgggtctac	accaacatcg	cgaaccgcga	gttcaactcg	120
gtgacggccg	agaacgagat	gaagatcgac	gccaccgagc	cgacgcaggg	gcggttcgac	180
ttcaccagg	ccgaccgat	ctacaactgg	gcgcgccaga	acggcaagca	ggtccgcggc	240
cacaccctgg	cctggcactc	gcagcagccg	cagtggatgc	agaacctcag	cggccaggcg	300
ctgcgccagg	cgatgatcaa	ccacatccag	ggggatcatgt	cctactaccg	gggcaagatc	360
ccgatctggg	acgtggtgaa	cgaggcggtc	gaggacggaa	actccggccg	ccggtgcgac	420
tccaacctcc	agcgcaccgg	taacgattgg	atcgaggctg	cgttccgcac	cggccgccag	480
ggggaccct	cggccaagct	ctgctacaac	gactacaaca	tcgagaactg	gaacgcggcc	540
aagacccagg	cggtctacaa	catggtgcgg	gacttcaagt	cccgcggcgt	gccccatcgac	600
tgctgtgggct	tccagtcgca	cttcaacagc	ggtaacccgt	acaacccgaa	cttccgcacc	660
accctgcagc	agttcgcggc	cctcggcgtg	gacgtcgagg	tcaccgagct	ggacatcgag	720
aacgccccgg	cccagaccta	cgccagcgtg	atccgggact	gcctggccgt	ggaccgctgc	780
accggcatca	ccgtctgggg	tgtccgcgac	agcgactcct	ggcgctcgta	ccagaacccg	840

AB\_Enzymes.ST25.txt

```
ctgctgttcg acaacaacgg caacaagaag caggcctact acgcggtgct cgacgccctg 900
aacgaggggct ccgacgacgg tggcgggccc tccaaccgcg cggtctcgcc gccgccgggt 960
ggcggttcct aa 972
```

```
<210> 9
<211> 906
<212> DNA
<213> Nonomuraea flexuosa
```

```
<220>
<221> The sequence encoding the AM50 core region, includes a STOP codon
<222> (1)..(906)
```

```
<400> 9
gcggcgagca cgctcgccga gggtgccgcg cagcacaacc ggtacttcgg cgtggccatc 60
gccgcgaaca ggctcaccga ctcggtctac accaaccatcg cgaaccgcga gttcaactcg 120
gtgacggccg agaacgagat gaagatcgac gccaccgagc cgcagcaggg gcggttcgac 180
ttcaccagg cgcaccgat ctacaactgg gcgcgccaga acggcaagca ggtccgcggc 240
cacaccctgg cctggcactc gcagcagccg cagtggatgc agaacctcag cggccaggcg 300
ctgcgccagg cgatgatcaa ccacatccag ggggtcatgt cctactaccg gggcaagatc 360
ccgatctggg acgtggtgaa cgaggcggtc gaggacggaa actccggccg ccggtgcgac 420
tccaacctcc agcgcaccgg taacgattgg atcgaggctc cgttccgcac cgcccgccag 480
ggggacccct cggccaagct ctgctacaac gactacaaca tcgagaactg gaacgcggcc 540
aagaccagg cgggtctaca catggtgcgg gacttcaagt cccgcggcgt gcccatcgac 600
tgcgtgggct tccagtcgca cttcaacagc ggtaaccctg acaaccgaa cttccgcacc 660
accctgcagc agttcgcgcc cctcggcgtg gacgtcgagg tcaccgagct ggacatcgag 720
aacgccccgg cccagacccta cgccagcgtg atccgggact gcctggccgt ggaccgctgc 780
accggcatca ccgtctgggg tgtccgcgac agcgactcct ggcgctcgta ccagaaccgg 840
ctgctgttcg acaacaacgg caacaagaag caggcctact acgcggtgct cgacgccctg 900
aactaa 906
```

```
<210> 10
<211> 344
<212> PRT
<213> Nonomuraea flexuosa
```

```
<220>
<221> Nf Xyn11A amino acid sequence (AJ508952) encoded by the Nf xyn11A
gene
<222> (1)..(344)
```

```
<400> 10
```

```
Met Asn Glu Pro Leu Thr Ile Thr Gln Ala Arg Arg Arg Arg Arg Leu
1 5 10 15
```

Gly Leu Arg Arg Ile Val Thr Ser Ala Phe Ala Leu Ala Leu Ala Ile  
 20 25 30  
 Ala Gly Ala Leu Leu Pro Gly Thr Ala His Ala Asp Thr Thr Ile Thr  
 35 40 45  
 Gln Asn Gln Thr Gly Tyr Asp Asn Gly Tyr Phe Tyr Ser Phe Trp Thr  
 50 55 60  
 Asp Ala Pro Gly Thr Val Ser Met Thr Leu His Ser Gly Gly Ser Tyr  
 65 70 75 80  
 Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val Ala Gly Lys Gly Trp  
 85 90 95  
 Ser Thr Gly Gly Arg Arg Thr Val Thr Tyr Asn Ala Ser Phe Asn Pro  
 100 105 110  
 Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp Thr Arg Asn Pro Leu  
 115 120 125  
 Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr Tyr Arg Pro Thr Gly  
 130 135 140  
 Thr Tyr Lys Gly Thr Val Thr Thr Asp Gly Gly Thr Tyr Asp Ile Tyr  
 145 150 155 160  
 Glu Thr Trp Arg Tyr Asn Ala Pro Ser Ile Glu Gly Thr Arg Thr Phe  
 165 170 175  
 Gln Gln Phe Trp Ser Val Arg Gln Gln Lys Arg Thr Ser Gly Thr Ile  
 180 185 190  
 Thr Ile Gly Asn His Phe Asp Ala Trp Ala Arg Ala Gly Met Asn Leu  
 195 200 205  
 Gly Ser His Asp Tyr Gln Ile Met Ala Thr Glu Gly Tyr Gln Ser Ser  
 210 215 220  
 Gly Ser Ser Thr Val Ser Ile Ser Glu Gly Gly Asn Pro Gly Asn Pro  
 225 230 235 240  
 Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly  
 245 250 255  
 Gly Gly Cys Val Ala Thr Leu Ser Ala Gly Gln Gln Trp Ser Asp Arg  
 260 265 270  
 Tyr Asn Leu Asn Val Ser Val Ser Gly Ser Asn Asn Trp Thr Val Arg  
 275 280 285  
 Met Asp Val Pro Tyr Pro Ala Arg Ile Ile Ala Thr Trp Asn Ile His



290

295

300

Ala Gln Trp Pro Glu Ser Gln Val Leu Ile Ala Arg Pro Asn Gly Asn  
 305 310 315 320

Gly Asn Asn Trp Gly Val Thr Ile Gln His Asn Gly Asn Trp Thr Trp  
 325 330 335

Pro Thr Val Thr Cys Thr Ala Asn  
 340

<210> 11  
 <211> 301  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> r33.4 kDa = AM35 = full length mature Nf xyn11A protein, encoded  
 by am35 and am35\* genes  
 <222> (1)..(301)

<400> 11

Asp Thr Thr Ile Thr Gln Asn Gln Thr Gly Tyr Asp Asn Gly Tyr Phe  
 1 5 10 15

Tyr Ser Phe Trp Thr Asp Ala Pro Gly Thr Val Ser Met Thr Leu His  
 20 25 30

Ser Gly Gly Ser Tyr Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val  
 35 40 45

Ala Gly Lys Gly Trp Ser Thr Gly Gly Arg Arg Thr Val Thr Tyr Asn  
 50 55 60

Ala Ser Phe Asn Pro Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp  
 65 70 75 80

Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr  
 85 90 95

Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Thr Thr Asp Gly Gly  
 100 105 110

Thr Tyr Asp Ile Tyr Glu Thr Trp Arg Tyr Asn Ala Pro Ser Ile Glu  
 115 120 125

Gly Thr Arg Thr Phe Gln Gln Phe Trp Ser Val Arg Gln Gln Lys Arg  
 130 135 140

Thr Ser Gly Thr Ile Thr Ile Gly Asn His Phe Asp Ala Trp Ala Arg  
 145 150 155 160

Ala Gly Met Asn Leu Gly Ser His Asp Tyr Gln Ile Met Ala Thr Glu

165

170

175

Gly Tyr Gln Ser Ser Gly Ser Ser Thr Val Ser Ile Ser Glu Gly Gly  
 180 185 190

Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn  
 195 200 205

Pro Gly Asn Pro Gly Gly Gly Cys Val Ala Thr Leu Ser Ala Gly Gln  
 210 215 220

Gln Trp Ser Asp Arg Tyr Asn Leu Asn Val Ser Val Ser Gly Ser Asn  
 225 230 235 240

Asn Trp Thr Val Arg Met Asp Val Pro Tyr Pro Ala Arg Ile Ile Ala  
 245 250 255

Thr Trp Asn Ile His Ala Gln Trp Pro Glu Ser Gln Val Leu Ile Ala  
 260 265 270

Arg Pro Asn Gly Asn Gly Asn Asn Trp Gly Val Thr Ile Gln His Asn  
 275 280 285

Gly Asn Trp Thr Trp Pro Thr Val Thr Cys Thr Ala Asn  
 290 295 300

<210> 12  
 <211> 220  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> AM24, truncated form from AM35, encoded by am24 and am24\* genes  
 <222> (1)..(220)

<400> 12

Asp Thr Thr Ile Thr Gln Asn Gln Thr Gly Tyr Asp Asn Gly Tyr Phe  
 1 5 10 15

Tyr Ser Phe Trp Thr Asp Ala Pro Gly Thr Val Ser Met Thr Leu His  
 20 25 30

Ser Gly Gly Ser Tyr Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val  
 35 40 45

Ala Gly Lys Gly Trp Ser Thr Gly Gly Arg Arg Thr Val Thr Tyr Asn  
 50 55 60

Ala Ser Phe Asn Pro Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp  
 65 70 75 80

Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr  
 85 90 95

AB\_Enzymes.ST25.txt

Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Thr Thr Asp Gly Gly  
100 105 110

Thr Tyr Asp Ile Tyr Glu Thr Trp Arg Tyr Asn Ala Pro Ser Ile Glu  
115 120 125

Gly Thr Arg Thr Phe Gln Gln Phe Trp Ser Val Arg Gln Gln Lys Arg  
130 135 140

Thr Ser Gly Thr Ile Thr Ile Gly Asn His Phe Asp Ala Trp Ala Arg  
145 150 155 160

Ala Gly Met Asn Leu Gly Ser His Asp Tyr Gln Ile Met Ala Thr Glu  
165 170 175

Gly Tyr Gln Ser Ser Gly Ser Ser Thr Val Ser Ile Ser Glu Gly Gly  
180 185 190

Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn  
195 200 205

Pro Gly Asn Pro Gly Gly Gly Cys Val Ala Thr Leu  
210 215 220

<210> 13  
<211> 217  
<212> PRT  
<213> Nonomuraea flexuosa

<220>  
<221> r23.8 kDa, truncated form from AM35  
<222> (1)..(217)  
<400> 13

Asp Thr Thr Ile Thr Gln Asn Gln Thr Gly Tyr Asp Asn Gly Tyr Phe  
1 5 10 15

Tyr Ser Phe Trp Thr Asp Ala Pro Gly Thr Val Ser Met Thr Leu His  
20 25 30

Ser Gly Gly Ser Tyr Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val  
35 40 45

Ala Gly Lys Gly Trp Ser Thr Gly Gly Arg Arg Thr Val Thr Tyr Asn  
50 55 60

Ala Ser Phe Asn Pro Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp  
65 70 75 80

Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr  
85 90 95

AB\_Enzymes.ST25.txt

Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Thr Thr Asp Gly Gly  
 100 105 110  
 Thr Tyr Asp Ile Tyr Glu Thr Trp Arg Tyr Asn Ala Pro Ser Ile Glu  
 115 120 125  
 Gly Thr Arg Thr Phe Gln Gln Phe Trp Ser Val Arg Gln Gln Lys Arg  
 130 135 140  
 Thr Ser Gly Thr Ile Thr Ile Gly Asn His Phe Asp Ala Trp Ala Arg  
 145 150 155 160  
 Ala Gly Met Asn Leu Gly Ser His Asp Tyr Gln Ile Met Ala Thr Glu  
 165 170 175  
 Gly Tyr Gln Ser Ser Gly Ser Ser Thr Val Ser Ile Ser Glu Gly Gly  
 180 185 190  
 Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn Pro Gly Asn  
 195 200 205  
 Pro Gly Asn Pro Gly Gly Gly Cys Val  
 210 215

<210> 14  
 <211> 193  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> r22.0 kDa, truncated form from AM35  
 <222> (1)..(193)

<400> 14

Asp Thr Thr Ile Thr Gln Asn Gln Thr Gly Tyr Asp Asn Gly Tyr Phe  
 1 5 10 15  
 Tyr Ser Phe Trp Thr Asp Ala Pro Gly Thr Val Ser Met Thr Leu His  
 20 25 30  
 Ser Gly Gly Ser Tyr Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val  
 35 40 45  
 Ala Gly Lys Gly Trp Ser Thr Gly Gly Arg Arg Thr Val Thr Tyr Asn  
 50 55 60  
 Ala Ser Phe Asn Pro Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp  
 65 70 75 80  
 Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr  
 85 90 95

Tyr Arg Pro Thr Gly Thr Tyr Lys Gly Thr Val Thr Thr Asp Gly Gly  
 100 105 110  
 Thr Tyr Asp Ile Tyr Glu Thr Trp Arg Tyr Asn Ala Pro Ser Ile Glu  
 115 120 125  
 Gly Thr Arg Thr Phe Gln Gln Phe Trp Ser Val Arg Gln Gln Lys Arg  
 130 135 140  
 Thr Ser Gly Thr Ile Thr Ile Gly Asn His Phe Asp Ala Trp Ala Arg  
 145 150 155 160  
 Ala Gly Met Asn Leu Gly Ser His Asp Tyr Gln Ile Met Ala Thr Glu  
 165 170 175  
 Gly Tyr Gln Ser Ser Gly Ser Ser Thr Val Ser Ile Ser Glu Gly Gly  
 180 185 190

Asn

<210> 15  
 <211> 492  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> Nf xyn10A, the amino acid sequence (AJ508953) encoded by the Nf  
 xyn10A gene  
 <222> (1)..(492)  
 <400> 15

Met Gly Val Asn Ala Phe Pro Arg Pro Gly Ala Arg Arg Phe Thr Gly  
 1 5 10 15  
 Gly Leu Tyr Arg Ala Leu Ala Ala Ala Thr Val Ser Val Val Gly Val  
 20 25 30  
 Val Thr Ala Leu Thr Val Thr Gln Pro Ala Ser Ala Ala Ala Ser Thr  
 35 40 45  
 Leu Ala Glu Gly Ala Ala Gln His Asn Arg Tyr Phe Gly Val Ala Ile  
 50 55 60  
 Ala Ala Asn Arg Leu Thr Asp Ser Val Tyr Thr Asn Ile Ala Asn Arg  
 65 70 75 80  
 Glu Phe Asn Ser Val Thr Ala Glu Asn Glu Met Lys Ile Asp Ala Thr  
 85 90 95  
 Glu Pro Gln Gln Gly Arg Phe Asp Phe Thr Gln Ala Asp Arg Ile Tyr  
 100 105 110

Asn Trp Ala Arg Gln Asn Gly Lys Gln Val Arg Gly His Thr Leu Ala  
 115 120 125  
 Trp His Ser Gln Gln Pro Gln Trp Met Gln Asn Leu Ser Gly Gln Ala  
 130 135 140  
 Leu Arg Gln Ala Met Ile Asn His Ile Gln Gly Val Met Ser Tyr Tyr  
 145 150 155 160  
 Arg Gly Lys Ile Pro Ile Trp Asp Val Val Asn Glu Ala Phe Glu Asp  
 165 170 175  
 Gly Asn Ser Gly Arg Arg Cys Asp Ser Asn Leu Gln Arg Thr Gly Asn  
 180 185 190  
 Asp Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Gln Gly Asp Pro Ser  
 195 200 205  
 Ala Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Asn Trp Asn Ala Ala  
 210 215 220  
 Lys Thr Gln Ala Val Tyr Asn Met Val Arg Asp Phe Lys Ser Arg Gly  
 225 230 235 240  
 Val Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe Asn Ser Gly Asn  
 245 250 255  
 Pro Tyr Asn Pro Asn Phe Arg Thr Thr Leu Gln Gln Phe Ala Ala Leu  
 260 265 270  
 Gly Val Asp Val Glu Val Thr Glu Leu Asp Ile Glu Asn Ala Pro Ala  
 275 280 285  
 Gln Thr Tyr Ala Ser Val Ile Arg Asp Cys Leu Ala Val Asp Arg Cys  
 290 295 300  
 Thr Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp Ser Trp Arg Ser  
 305 310 315 320  
 Tyr Gln Asn Pro Leu Leu Phe Asp Asn Asn Gly Asn Lys Lys Gln Ala  
 325 330 335  
 Tyr Tyr Ala Val Leu Asp Ala Leu Asn Glu Gly Ser Asp Asp Gly Gly  
 340 345 350  
 Gly Pro Ser Asn Pro Pro Val Ser Pro Pro Pro Gly Gly Gly Ser Gly  
 355 360 365  
 Gln Ile Arg Gly Val Ala Ser Asn Arg Cys Ile Asp Val Pro Asn Gly  
 370 375 380  
 Asn Thr Ala Asp Gly Thr Gln Val Gln Leu Tyr Asp Cys His Ser Gly  
 Page 14



AB\_Enzymes.ST25.txt

Ala Phe Glu Asp Gly Asn Ser Gly Arg Arg Cys Asp Ser Asn Leu Gln  
130 135 140

Arg Thr Gly Asn Asp Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Gln  
145 150 155 160

Gly Asp Pro Ser Ala Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Asn  
165 170 175

Trp Asn Ala Ala Lys Thr Gln Ala Val Tyr Asn Met Val Arg Asp Phe  
180 185 190

Lys Ser Arg Gly Val Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe  
195 200 205

Asn Ser Gly Asn Pro Tyr Asn Pro Asn Phe Arg Thr Thr Leu Gln Gln  
210 215 220

Phe Ala Ala Leu Gly Val Asp Val Glu Val Thr Glu Leu Asp Ile Glu  
225 230 235 240

Asn Ala Pro Ala Gln Thr Tyr Ala Ser Val Ile Arg Asp Cys Leu Ala  
245 250 255

Val Asp Arg Cys Thr Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp  
260 265 270

Ser Trp Arg Ser Tyr Gln Asn Pro Leu Leu Phe Asp Asn Asn Gly Asn  
275 280 285

Lys Lys Gln Ala Tyr Tyr Ala Val Leu Asp Ala Leu Asn Glu Gly Ser  
290 295 300

Asp Asp Gly Gly Gly Pro Ser Asn Pro Pro Val Ser Pro Pro Pro Gly  
305 310 315 320

Gly Gly Ser Gly Gln Ile Arg Gly Val Ala Ser Asn Arg Cys Ile Asp  
325 330 335

Val Pro Asn Gly Asn Thr Ala Asp Gly Thr Gln Val Gln Leu Tyr Asp  
340 345 350

Cys His Ser Gly Ser Asn Gln Gln Trp Thr Tyr Thr Ser Ser Gly Glu  
355 360 365

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

Gly Ala Val Val Gln Ile Tyr Ser Cys Trp Gly Gly Ala Asn Gln Lys  
385 390 395 400



AB\_Enzymes.ST25.txt

Trp Glu Leu Arg Ala Asp Gly Thr Ile Val Gly Val Gln Ser Gly Leu  
405 410 415

Cys Leu Asp Ala Val Gly Gly Gly Thr Gly Asn Gly Thr Arg Leu Gln  
420 425 430

Leu Tyr Ser Cys Trp Gly Gly Asn Asn Gln Lys Trp Ser Tyr Asn Ala  
435 440 445

<210> 17  
<211> 323  
<212> PRT  
<213> Nonomuraea flexuosa

<220>  
<221> AM50 core + linker, truncated form from AM50  
<222> (1)..(323)

<400> 17

Ala Ala Ser Thr Leu Ala Glu Gly Ala Ala Gln His Asn Arg Tyr Phe  
1 5 10 15

Gly Val Ala Ile Ala Ala Asn Arg Leu Thr Asp Ser Val Tyr Thr Asn  
20 25 30

Ile Ala Asn Arg Glu Phe Asn Ser Val Thr Ala Glu Asn Glu Met Lys  
35 40 45

Ile Asp Ala Thr Glu Pro Gln Gln Gly Arg Phe Asp Phe Thr Gln Ala  
50 55 60

Asp Arg Ile Tyr Asn Trp Ala Arg Gln Asn Gly Lys Gln Val Arg Gly  
65 70 75 80

His Thr Leu Ala Trp His Ser Gln Gln Pro Gln Trp Met Gln Asn Leu  
85 90 95

Ser Gly Gln Ala Leu Arg Gln Ala Met Ile Asn His Ile Gln Gly Val  
100 105 110

Met Ser Tyr Tyr Arg Gly Lys Ile Pro Ile Trp Asp Val Val Asn Glu  
115 120 125

Ala Phe Glu Asp Gly Asn Ser Gly Arg Arg Cys Asp Ser Asn Leu Gln  
130 135 140

Arg Thr Gly Asn Asp Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Gln  
145 150 155 160

Gly Asp Pro Ser Ala Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Asn  
165 170 175

Trp Asn Ala Ala Lys Thr Gln Ala Val Tyr Asn Met Val Arg Asp Phe  
180 185 190

Lys Ser Arg Gly Val Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe  
195 200 205

Asn Ser Gly Asn Pro Tyr Asn Pro Asn Phe Arg Thr Thr Leu Gln Gln  
210 215 220

Phe Ala Ala Leu Gly Val Asp Val Glu Val Thr Glu Leu Asp Ile Glu  
225 230 235 240

Asn Ala Pro Ala Gln Thr Tyr Ala Ser Val Ile Arg Asp Cys Leu Ala  
245 250 255

Val Asp Arg Cys Thr Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp  
260 265 270

Ser Trp Arg Ser Tyr Gln Asn Pro Leu Leu Phe Asp Asn Asn Gly Asn  
275 280 285

Lys Lys Gln Ala Tyr Tyr Ala Val Leu Asp Ala Leu Asn Glu Gly Ser  
290 295 300

Asp Asp Gly Gly Gly Pro Ser Asn Pro Pro Val Ser Pro Pro Pro Gly  
305 310 315 320

Gly Gly Ser

<210> 18  
<211> 301  
<212> PRT  
<213> Nonomuraea flexuosa

<220>  
<221> AM50 core, truncated form from AM50  
<222> (1)..(301)

<400> 18

Ala Ala Ser Thr Leu Ala Glu Gly Ala Ala Gln His Asn Arg Tyr Phe  
1 5 10 15

Gly Val Ala Ile Ala Ala Asn Arg Leu Thr Asp Ser Val Tyr Thr Asn  
20 25 30

Ile Ala Asn Arg Glu Phe Asn Ser Val Thr Ala Glu Asn Glu Met Lys  
35 40 45

Ile Asp Ala Thr Glu Pro Gln Gln Gly Arg Phe Asp Phe Thr Gln Ala  
50 55 60

Asp Arg Ile Tyr Asn Trp Ala Arg Gln Asn Gly Lys Gln Val Arg Gly  
Page 18

```

65                               70                75                80
His Thr Leu Ala Trp His Ser Gln Gln Pro Gln Trp Met Gln Asn Leu
      85                      90
Ser Gly Gln Ala Leu Arg Gln Ala Met Ile Asn His Ile Gln Gly Val
      100                   105                   110
Met Ser Tyr Tyr Arg Gly Lys Ile Pro Ile Trp Asp Val Val Asn Glu
      115                   120                   125
Ala Phe Glu Asp Gly Asn Ser Gly Arg Arg Cys Asp Ser Asn Leu Gln
      130                   135                   140
Arg Thr Gly Asn Asp Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Gln
      145                   150                   155                   160
Gly Asp Pro Ser Ala Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Asn
      165                   170                   175
Trp Asn Ala Ala Lys Thr Gln Ala Val Tyr Asn Met Val Arg Asp Phe
      180                   185                   190
Lys Ser Arg Gly Val Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe
      195                   200                   205
Asn Ser Gly Asn Pro Tyr Asn Pro Asn Phe Arg Thr Thr Leu Gln Gln
      210                   215                   220
Phe Ala Ala Leu Gly Val Asp Val Glu Val Thr Glu Leu Asp Ile Glu
      225                   230                   235                   240
Asn Ala Pro Ala Gln Thr Tyr Ala Ser Val Ile Arg Asp Cys Leu Ala
      245                   250                   255
Val Asp Arg Cys Thr Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp
      260                   265                   270
Ser Trp Arg Ser Tyr Gln Asn Pro Leu Leu Phe Asp Asn Asn Gly Asn
      275                   280                   285
Lys Lys Gln Ala Tyr Tyr Ala Val Leu Asp Ala Leu Asn
      290                   295                   300

```

```

<210> 19
<211> 406
<212> PRT
<213> Nonomuraea flexuosa

```

```

<220>
<221> AM50 core + linker + alpha/beta domains of the tail
<222> (1)..(406)

```

&lt;400&gt; 19

Ala Ala Ser Thr Leu Ala Glu Gly Ala Ala Gln His Asn Arg Tyr Phe  
 1 5 10 15  
 Gly Val Ala Ile Ala Ala Asn Arg Leu Thr Asp Ser Val Tyr Thr Asn  
 20 25 30  
 Ile Ala Asn Arg Glu Phe Asn Ser Val Thr Ala Glu Asn Glu Met Lys  
 35 40 45  
 Ile Asp Ala Thr Glu Pro Gln Gln Gly Arg Phe Asp Phe Thr Gln Ala  
 50 55 60  
 Asp Arg Ile Tyr Asn Trp Ala Arg Gln Asn Gly Lys Gln Val Arg Gly  
 65 70 75 80  
 His Thr Leu Ala Trp His Ser Gln Gln Pro Gln Trp Met Gln Asn Leu  
 85 90 95  
 Ser Gly Gln Ala Leu Arg Gln Ala Met Ile Asn His Ile Gln Gly Val  
 100 105 110  
 Met Ser Tyr Tyr Arg Gly Lys Ile Pro Ile Trp Asp Val Val Asn Glu  
 115 120 125  
 Ala Phe Glu Asp Gly Asn Ser Gly Arg Arg Cys Asp Ser Asn Leu Gln  
 130 135 140  
 Arg Thr Gly Asn Asp Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Gln  
 145 150 155 160  
 Gly Asp Pro Ser Ala Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Asn  
 165 170 175  
 Trp Asn Ala Ala Lys Thr Gln Ala Val Tyr Asn Met Val Arg Asp Phe  
 180 185 190  
 Lys Ser Arg Gly Val Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe  
 195 200 205  
 Asn Ser Gly Asn Pro Tyr Asn Pro Asn Phe Arg Thr Thr Leu Gln Gln  
 210 215 220  
 Phe Ala Ala Leu Gly Val Asp Val Glu Val Thr Glu Leu Asp Ile Glu  
 225 230 235 240  
 Asn Ala Pro Ala Gln Thr Tyr Ala Ser Val Ile Arg Asp Cys Leu Ala  
 245 250 255  
 Val Asp Arg Cys Thr Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp  
 260 265 270

AB\_Enzymes.ST25.txt

Ser Trp Arg Ser Tyr Gln Asn Pro Leu Leu Phe Asp Asn Asn Gly Asn  
275 280 285

Lys Lys Gln Ala Tyr Tyr Ala Val Leu Asp Ala Leu Asn Glu Gly Ser  
290 295 300

Asp Asp Gly Gly Gly Pro Ser Asn Pro Pro Val Ser Pro Pro Pro Gly  
305 310 315 320

Gly Gly Ser Gly Gln Ile Arg Gly Val Ala Ser Asn Arg Cys Ile Asp  
325 330 335

Val Pro Asn Gly Asn Thr Ala Asp Gly Thr Gln Val Gln Leu Tyr Asp  
340 345 350

Cys His Ser Gly Ser Asn Gln Gln Trp Thr Tyr Thr Ser Ser Gly Glu  
355 360 365

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

Gly Ala Val Val Gln Ile Tyr Ser Cys Trp Gly Gly Ala Asn Gln Lys  
385 390 395 400

Trp Glu Leu Arg Ala Asp  
405

<210> 20  
<211> 366  
<212> PRT  
<213> Nonomuraea flexuosa

<220>  
<221> AM50 core + linker + alpha domain of the tail  
<222> (1)..(366)  
<400> 20

Ala Ala Ser Thr Leu Ala Glu Gly Ala Ala Gln His Asn Arg Tyr Phe  
1 5 10 15

Gly Val Ala Ile Ala Ala Asn Arg Leu Thr Asp Ser Val Tyr Thr Asn  
20 25 30

Ile Ala Asn Arg Glu Phe Asn Ser Val Thr Ala Glu Asn Glu Met Lys  
35 40 45

Ile Asp Ala Thr Glu Pro Gln Gln Gly Arg Phe Asp Phe Thr Gln Ala  
50 55 60

Asp Arg Ile Tyr Asn Trp Ala Arg Gln Asn Gly Lys Gln Val Arg Gly  
65 70 75 80

His Thr Leu Ala Trp His Ser Gln Gln Pro Gln Trp Met Gln Asn Leu  
85 90 95

Ser Gly Gln Ala Leu Arg Gln Ala Met Ile Asn His Ile Gln Gly Val  
100 105 110

Met Ser Tyr Tyr Arg Gly Lys Ile Pro Ile Trp Asp Val Val Asn Glu  
115 120 125

Ala Phe Glu Asp Gly Asn Ser Gly Arg Arg Cys Asp Ser Asn Leu Gln  
130 135 140

Arg Thr Gly Asn Asp Trp Ile Glu Val Ala Phe Arg Thr Ala Arg Gln  
145 150 155 160

Gly Asp Pro Ser Ala Lys Leu Cys Tyr Asn Asp Tyr Asn Ile Glu Asn  
165 170 175

Trp Asn Ala Ala Lys Thr Gln Ala Val Tyr Asn Met Val Arg Asp Phe  
180 185 190

Lys Ser Arg Gly Val Pro Ile Asp Cys Val Gly Phe Gln Ser His Phe  
195 200 205

Asn Ser Gly Asn Pro Tyr Asn Pro Asn Phe Arg Thr Thr Leu Gln Gln  
210 215 220

Phe Ala Ala Leu Gly Val Asp Val Glu Val Thr Glu Leu Asp Ile Glu  
225 230 235 240

Asn Ala Pro Ala Gln Thr Tyr Ala Ser Val Ile Arg Asp Cys Leu Ala  
245 250 255

Val Asp Arg Cys Thr Gly Ile Thr Val Trp Gly Val Arg Asp Ser Asp  
260 265 270

Ser Trp Arg Ser Tyr Gln Asn Pro Leu Leu Phe Asp Asn Asn Gly Asn  
275 280 285

Lys Lys Gln Ala Tyr Tyr Ala Val Leu Asp Ala Leu Asn Glu Gly Ser  
290 295 300

Asp Asp Gly Gly Gly Pro Ser Asn Pro Pro Val Ser Pro Pro Pro Gly  
305 310 315 320

Gly Gly Ser Gly Gln Ile Arg Gly Val Ala Ser Asn Arg Cys Ile Asp  
325 330 335

Val Pro Asn Gly Asn Thr Ala Asp Gly Thr Gln Val Gln Leu Tyr Asp  
340 345 350

Cys His Ser Gly Ser Asn Gln Gln Trp Thr Tyr Thr Ser Ser

<210> 21  
 <211> 4  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> A synthetic linker sequence coding for a Kex2-like protease  
 cleavage signal Lys-Arg included in all the constructs to ensure  
 cleavage of the fusion protein.  
 <222> (1)..(4)

<400> 21

Arg Asp Lys Arg  
 1

<210> 22  
 <211> 5  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> An additional sequence preceding the Kex2 site in the expression  
 cassette pALK1264, pALK1131 and pALK1134  
 <222> (1)..(5)

<400> 22

Gly Gln Cys Gly Gly  
 1 5

<210> 23  
 <211> 6  
 <212> PRT  
 <213> Nonomuraea flexuosa

<220>  
 <221> The N-terminal sequence of mature Nf Xyn11A and recombinant  
 Xyn11A polypeptides, named as r33.4 kDa, r23.8 kDa and r22.0 kDa  
 <222> (1)..(6)

<400> 23

Asp Thr Thr Ile Thr Gln  
 1 5

<210> 24  
 <211> 6  
 <212> DNA  
 <213> Nonomuraea flexuosa

<220>  
 <221> An NruI recognition site introduced into a Kex2 linker  
 <222> (1)..(6)

<400> 24  
 tcgcga

<210> 25  
<211> 12  
<212> DNA  
<213> *Nonomuraea flexuosa*

<220>  
<221> Kex2 linker which facilitates the construction of fusions  
<222> (1)..(12)

<400> 25  
cgcgacaagc gc

12