

Sequence Listing Information:

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General Information:

Current application / IP Office: KR

Current application / Application number: PCT/KR2021/012872

Current application / Filing date: 2021-09-17

Current application / Applicant file reference: PF-B2898

Earliest priority application / IP Office: KR

Earliest priority application / Application number: 10-2020-0120399

Earliest priority application / Filing date: 2020-09-18

Applicant name: INSTITUTE FOR BASIC SCIENCE

Applicant name / Language: ko

Invention title: TARGETED DEAMINASE AND BASE EDITING USING SAME (ko)

Sequence Total Quantity: 571

Sequences:

Sequence Number (ID): 1

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138

> note, Deaminase

- source, 1..138

> mol_type, protein

> organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60

SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKRGATGET 120

KVFTGNSNSP KSPTKGGC

138

Sequence Number (ID): 2

Length: 123

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..123
 - > note, Zinc Finger Protein
- source, 1..123
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSRSDNLS RHIRTHTGEK PFACDICGRK FAISSNLNSH 60
TKIHTGSQKP FQCRICMRNF SRSDNLARHI RHTHTGEKPFA CDICGRKFAT SGNLTRHTKI 120
HLR 123

Sequence Number (ID): 3

Length: 122

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..122
 - > note, Zinc Finger Protein
- source, 1..122
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSRSDNLS VHIRTHTGEK PFACDICGRK FAQKINLQVH 60
TKIHTGEKPF QCRICMRNFS RSDVLSEHIR THTGEKPFAC DICGRKFAQR NHRTTHTKI 120
LR 122

Sequence Number (ID): 4

Length: 408

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..408
 - > note, TALE
- source, 1..408
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
gatatagctg attgaggac cctcgggtac tcacagcagc aacaagaaaa aatcaaacca 60
aaggtacgta gcacggttgc ccaacatcat gaagccctag ttggtcacgg attactcat 120
gcccatattg ttgcactgag tcaacaccct gctgcattag gcacagtggc tgtgaaatat 180
caagatatga ttctgtctct tcctgaggcc acacacgagg caattgtggg tgttgaaaaa 240
caatggtctg gtgcgcgagc gcttgaagct ctctaaccg tagctggaga gttgagaggc 300
ccaccgcttc agcttgacac agggcagctg ttgaagatag caaagagggg ggggtgtaact 360
gctgttgaag cagtccatgc atggagaaat gcattaactg gagctcca      408
```

Sequence Number (ID): 5

Length: 411

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..411
 - > note, TALE
- source, 1..411
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
gatattgctg atcttcgaac attgggttat tctcagcagc aacaagagaa aatcaaaccg 60
aaagtccgtt caaccgtagc tcaacatcat gaagcccttg ttggtcatgg attactcat 120
gctcacattg ttgctctaag tcagcaccct gccgcgctag gcacagtgc cgtaagtat 180
caagatatga tagctgcttt acctgaagca acccagagg caatagtggg ggttggaag 240
```

aggggtgcag gcgccagggc actggaggca ctctaacag tagctggaga acttcgggga 300
ccaccattgc agcttgatac tggacaactc ttgaagatcg caaaaagagg ggggtgtgact 360
gctgtggaag ctgttcatgc atggagaaat gctttgacgg gagcaccct g 411

Sequence Number (ID): 6

Length: 123

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..123
 - > note, TALE
- source, 1..123
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

agcatagttg ctacgctaag tagacctgat ccagcacttg ctgcattgac gaacgatcat 60
ctcgtagcgc tggcttgttt gggcggcagg ccagccttgg acgccgtgaa gaaaggatta 120
ggt 123

Sequence Number (ID): 7

Length: 123

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..123
 - > note, TALE
- source, 1..123
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tcgatagtag cacaattaag caggcctgac cctgcacttg ctgctcttac aaatgatcat 60
cttgttgctc tggcctgttt ggggtggcgt cccgcgttgg atgctgttaa gaaaggactt 120
ggt 123

Sequence Number (ID): 8

Length: 5

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..5
 - > note, Synthetic Sequence
- source, 1..5
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

TGEKQ 5

Sequence Number (ID): 9

Length: 10

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..10
 - > note, Synthetic Sequence
- source, 1..10
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGAQGSTLDF 10

Sequence Number (ID): 10

Length: 16

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..16
 - > note, Synthetic Sequence

- source, 1..16
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGSETPGTSE SATPES 16

Sequence Number (ID): 11

Length: 33

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..33
 - > note, Synthetic Sequence
- source, 1..33
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGGSSGGSS GSETPGTSES ATPSSGGSS GGS 33

Sequence Number (ID): 12

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, A1341D KRKKA
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YDNAGHVEGQ 60
 SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKRGATGET 120
 KVFTGNSNSP KSPTAGGC 138

Sequence Number (ID): 13

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, AAAAA
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTPYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVAAGATGET 120
AVFTGNSNSP ASPTAGGC 138

Sequence Number (ID): 14

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, AAAAK
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTPYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVAAGATGET 120
AVFTGNSNSP ASPTKGGC 138

Sequence Number (ID): 15

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, AAKAA
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVAAGATGET 120
KVFTGNSNSP ASPTAGGC 138

Sequence Number (ID): 16

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, AAKAK
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVAAGATGET 120
KVFTGNSNSP ASPTKGGC 138

Sequence Number (ID): 17

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138

- > note, KAAAA
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKAGATGET 120
AVFTGNSNSP ASPTAGGC 138

Sequence Number (ID): 18

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, E1347A
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVAGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKRGATGET 120
KVFTGNSNSP KSPTKGGC 138

Sequence Number (ID): 19

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, GSVG
- source, 1..138
 - > mol_type, protein

> organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLEKGVF SSGGPTPYPN YANAGHVESQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGVI PVKRGATGET 120
KVFTGNSNGP KSPTKGGC 138

Sequence Number (ID): 20

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, SSVG
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTPYPN YANAGHVESQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGVI PVKRGATGET 120
KVFTGNSNGP KSPTKGGC 138

Sequence Number (ID): 21

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, GSAG
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLEKGVF SSGGPTPYPN YANAGHVESQ 60

SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKRGATGET 120
KVFTGNSNGP KSPTKGGC 138

Sequence Number (ID): 22

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, GSVS
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLEKVF SSGGPTPYPN YANAGHVESQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGVI PVKRGATGET 120
KVFTGNSNSP KSPTKGGC 138

Sequence Number (ID): 23

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Wild-type DddAtox G1333-N
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 24

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Wild-type G1333-C
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 25

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Wild-type DddAtox G1397-N
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEG 108

Sequence Number (ID): 26

Length: 30

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..30
 - > note, Wild-type DddAtox G1397-C
- source, 1..30

- > mol_type, protein
- > organism, synthetic construct

Residues:

AIPVKRGATG ETKVFTGNSN SPKSPTKGGC 30

Sequence Number (ID): 27

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Wild-type DddAtox G1333-N
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacgccct gggccatat cagattagtg ctccccaact cccgcctac 60
 aacggtcaga cagtggggac cttttactat gtcaacgacg ccggggggatt ggaatccaag 120
 gttttctcta gcggtggg 138

Sequence Number (ID): 28

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Wild-type G1333-C
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
 atgagagata acggcattag cgaagggtt gtgtccata ataatcctga gggcacctgt 120

ggcttctgtg taaatatgac cgaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaaccg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 29

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Wild-type DddAtox G1397-N
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttgggcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
caaaccgtcg ggacctttta ctacgtaaac gatgctgggt ggctggaatc caaagtattc 120
tcctcagggg gccctacacc ctacccaac tacgccaatg ctggctcatgt agaagggcag 180
tcagcactgt ttatgcgcga taatggtata agcgaggggg tggtcttcca taacaacca 240
gagggtactt gtggcttctg tgtgaatatg actgaaaccc ttctgccga aaatgccaag 300
atgactgtcg tcccactga aggc 324

Sequence Number (ID): 30

Length: 90

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..90
 - > note, Wild-type DddAtox G1397-C
- source, 1..90
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gccatacctg tgaagcgggg agcaacaggg gagacaaagg tggtcacagg caactctaac 60
agtccaaaga gccccaccaa aggcgggtgt 90

Sequence Number (ID): 31

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSAALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 32

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt ccgcagccct ggtccatat cagattagtg ctcccaact cccgcctac 60
aacggtcaga cagtggggac ctttactat gtcaacgacg ccgggggatt ggaatccaag 120
gtttctcta gcggtggg 138

Sequence Number (ID): 33

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYAAGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 34

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacccgc aggtccatat cagattagtg ctccccaact cccgcctac 60
aacggtcaga cagtggggac ctttactat gtcaacgacg ccgggggatt ggaatccaag 120
gttttctcta gcggtggg 138

Sequence Number (ID): 35

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44

> mol_type, protein
> organism, synthetic construct

Residues:

GSYALGPYQA SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 36

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 > note, Deaminase Variant
- source, 1..138
 > mol_type, other DNA
 > organism, synthetic construct

Residues:

ggctctggtt cctacgccct gggtccatat caggcaagtg ctccccaact ccccgctac 60
aacggtcaga cagtggggac cttttactat gtcaacgacg ccggggggatt ggaatccaag 120
gttttctcta gcggtggg 138

Sequence Number (ID): 37

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 > note, Deaminase Variant
- source, 1..44
 > mol_type, protein
 > organism, synthetic construct

Residues:

GSYALGPYQI AAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 38

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggctctggtt cctacgcct ggtccatat cagattgcag ctccccaact cccgcctac 60
aacggtcaga cagtggggac ctttactat gtcaacgacg ccggggggatt ggaatccaag 120
gttttctcta gcggtggg                                     138
```

Sequence Number (ID): 39

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
GSYALGPYQI SAPQLPAYNG QTAGTFYYVN DAGGLESKVF SSGG 44
```

Sequence Number (ID): 40

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138

- > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggctctggtt cctacgccct ggtccatat cagattagtg ctcccaact cccgcctac 60
aacggtcaga cagcaggac ctttactat gtcaacgacg ccgggggatt ggaatccaag 120
gttttctcta gcggtggg                                     138
```

Sequence Number (ID): 41

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
GSYALGPYQI SAPQLPAYNG QTVATFYVN DAGGLESKVF SSGG          44
```

Sequence Number (ID): 42

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacgccct ggtccatat cagattagtg ctcccaact cccgcctac 60
aacggtcaga cagtggcaac ctttactat gtcaacgacg ccgggggatt ggaatccaag 120
gttttctcta gcggtggg 138

Sequence Number (ID): 43

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGAFYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 44

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacgccct ggtccatat cagattagtg ctcccaact cccgcctac 60
aacggtcaga cagtgggggc atttactat gtcaacgacg ccgggggatt ggaatccaag 120
gttttctcta gcggtggg 138

Sequence Number (ID): 45

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTAYYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 46

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacgccct ggttccatat cagattagtg ctccccaact ccccgcttac 60
aacggtcaga cagtggggac cgcatactat gtcaacgacg ccggggggatt ggaatccaag 120
gttttctcta gcggtggg 138

Sequence Number (ID): 47

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant

- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFAYVN DAGGLESKVF SSGG 44

Sequence Number (ID): 48

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacgcct ggtccatat cagattagtg ctcccaact cccgcctac 60
 aacggtcaga cagtggggac cttgcatat gtcaacgacg ccgggggatt ggaatccaag 120
 gttttctcta gcggtggg 138

Sequence Number (ID): 49

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYAVN DAGGLESKVF SSGG 44

Sequence Number (ID): 50

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggctctggtt cctacgccct gggccatat cagattagtg ctccccaact cccgcctac 60
aacggtcaga cagtggggac cttttacgca gtcaacgacg ccggggggatt ggaatccaag 120
gttttctcta gcggtggg                                     138
```

Sequence Number (ID): 51

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
GSYALGPYQI SAPQLPAYNG QTVGTFYYAN DAGGLESKVF SSGG 44
```

Sequence Number (ID): 52

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggctctggtt cctacgccct ggttccatat cagattagtg ctccccaact cccgcctac 60
aacggtcaga cagtggggac cttttactat gcaaacgacg ccggggggatt ggaatccaag 120
gttttctcta gcggtggg                                     138
```

Sequence Number (ID): 53

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESASF SSGG 44
```

Sequence Number (ID): 54

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggctctggtt cctacgccct ggtccatat cagattagtg ctcccaact cccgcctac 60
aacggtcaga cagtggggac ctttactat gtcaacgacg ccgggggatt ggaatccgca 120
gttttctcta gcggtggg                                     138
```

Sequence Number (ID): 55

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVA SSGG          44
```

Sequence Number (ID): 56

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggctctggtt cctacgccct ggtccatat cagattagtg ctcccaact cccgcctac 60
aacggtcaga cagtggggac ctttactat gtcaacgacg ccgggggatt ggaatccaag 120
gttgcatcta gcggtggg                                     138
```

Sequence Number (ID): 57

Length: 44

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..44
 - > note, Deaminase Variant
- source, 1..44
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF ASGG 44

Sequence Number (ID): 58

Length: 138

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..138
 - > note, Deaminase Variant
- source, 1..138
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggctctggtt cctacgcctt ggtccatat cagattagt ctcccaact cccgcctac 60
aacggtcaga cagtggggac ctttactat gtcaacgacg ccgggggatt ggaatccaag 120
gttttcgcaa gcggtggg 138

Sequence Number (ID): 59

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94

- > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHAEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 60

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgcag aggggcagtc agctctttt 60
atgagagata acggcattag cgaagggtt gtgtccata ataactctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaagg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 61

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94

> mol_type, protein
> organism, synthetic construct

Residues:

PTPYPNYANA GHVEGASALF MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 62

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 > note, Deaminase Variant
- source, 1..282
 > mol_type, other DNA
 > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgtcg agggggcatc agctcttttt 60
atgagagata acggcattag cgaagggtt gtgttcata ataactctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaaccg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 63

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 > note, Deaminase Variant
- source, 1..94
 > mol_type, protein
 > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQAALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 64

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgtaacgcc gggcacgtcg aggggcaggc agctctttt 60
atgagagata acggcattag cgaagggtt gtgttcata ataactctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaagg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 65

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALA MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60

PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC

94

Sequence Number (ID): 66

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctcttgca 60
atgagagata acggcattag cgaagggtt gtgtccata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaaccg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc                282
```

Sequence Number (ID): 67

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF ARDNGISEGL VFHNNPEGTC GFCVNMTE TL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                94
```

Sequence Number (ID): 68

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgtaacgcc gggcacgtcg aggggcagtc agctctttt 60
gcaagagata acggcattag cgaagggtt gtgtccata ataactctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaagg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc                282
```

Sequence Number (ID): 69

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF MRDNGISAGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                94
```

Sequence Number (ID): 70

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgcagggctt gtgtccata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc                282
```

Sequence Number (ID): 71

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF MRDNGISEAL VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                94
```

Sequence Number (ID): 72

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgaagcactt gtgttcata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtcaaaa gtccccacc aaggagggtt gc                282
```

Sequence Number (ID): 73

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF MRDNGISEGA VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                94
```

Sequence Number (ID): 74

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant

- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgaaggggca gtgtccata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc                282
```

Sequence Number (ID): 75

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF MRDNGISEGL AFHNNPEGTC GFCVNMTE TL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                94
```

Sequence Number (ID): 76

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgtaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgaagggtt gcattccata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
ccacccgaag gcgcaatccc agttaaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc                282
```

Sequence Number (ID): 77

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF MRDNGISEGL VAHNNPEGTC GFCVNMTE TL LPENAKMTVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                94
```

Sequence Number (ID): 78

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
 atgagagata acggcattag cgaagggtt gtggcacata ataactctga gggcacctgt 120
 ggcttctgtg taaatatgac cgaacactt ctgcctgaga acgctaaaat gactgtcgta 180
 ccacccgaag gcgcaatccc agttaaagg ggcgcaaccg gcgaaaccaa agtattcacc 240
 ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 79

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALF MRDNGISEGL VFANNPEGTC GFCVNMETEL LPENAKMTVV 60
 PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 80

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
 atgagagata acggcattag cgaagggtt gtgttcgcaa ataactctga gggcacctgt 120

ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgta 180
 ccacccgaag gcgcaatccc agttaaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240
 ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 81

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAAMTVV 60
 PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 82

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgtaacgcc gggcacgtcg aggggcagtc agctctttt 60
 atgagagata acggcattag cgaagggtt gtgttcata ataatcctga gggcacctgt 120
 ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctgcaat gactgtcgta 180
 ccacccgaag gcgcaatccc agttaaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240

ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 83

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKATVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 84

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgaagggtt gtgtccata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaacactt ctgcctgaga acgctaaagc aactgtcgta 180
ccacccgaag gcgcaatccc agttaacgg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 85

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
PTPYPNYANA GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMAVV 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC                                     94
```

Sequence Number (ID): 86

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ccaacacctt atcctaacta cgtaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgaagggtt gtgtccata ataactctga gggcacctgt 120
ggcttctgtg taaatatgac cgaacacgtt ctgcctgaga acgctaaaat ggcagtcgta 180
ccacccgaag gcgcaatccc agttaaagg ggcgaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc                                     282
```

Sequence Number (ID): 87

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Deaminase Variant
- source, 1..94
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVA 60
PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 88

Length: 282

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..282
 - > note, Deaminase Variant
- source, 1..282
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaacacctt atcctaacta cgctaacgcc gggcacgtcg aggggcagtc agctctttt 60
atgagagata acggcattag cgaagggtt gtgtccata ataatcctga gggcacctgt 120
ggcttctgtg taaatatgac cgaaacactt ctgcctgaga acgctaaaat gactgtcgca 180
ccacccgaag gcgcaatccc agttaaagg ggcgcaaccg gcgaaaccaa agtattcacc 240
ggaaacagca atagtccaaa gtccccacc aaggagggtt gc 282

Sequence Number (ID): 89

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPYN YANAGHVEGQ 60
 SALFMRDNGI SEGLVFHNNP EGTCGFAVNM TETLLPENAK MTVVPPEG 108

Sequence Number (ID): 90

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
 caaaccgtcg ggaccttta ctacgtaaac gatgctggtg ggctggaatc caaagtattc 120
 tcctcagggg gccctacacc ctacccaac tacgccaatg ctggcatgt agaaggcag 180
 tcagcactgt ttatgcgcga taatggtata agcgagggtg tggctttcca taacaacca 240
 gagggctactt gtggcttcgc agtgaatatg actgaaacct ttctgccga aaatgccaaag 300
 atgactgtcg tccacactga aggc 324

Sequence Number (ID): 91

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108

- > note, Deaminase Variant
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
 SALFMRDNGI SEGLVFHNNP EGTCGFCANM TETLLPENAK MTVVPPEG 108

Sequence Number (ID): 92

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttgggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
 caaaccgtcg ggacctttta ctacgtaaac gatgctggtg ggctggaatc caaagtattc 120
 tcctcagggg gccctacacc ctacccaac tacgccaatg ctggtcatgt agaagggcag 180
 tcagcactgt ttatgcgcga taatggtata agcgagggtg tggcttcca taacaacca 240
 gagggactct gtggcttctg tgcaaatatg actgaaaccc ttctgccga aaatgccaag 300
 atgactgtcg tcccactga aggc 324

Sequence Number (ID): 93

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant

- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
 SALFMRDNGI SEGLVFHNNP EGTCGFCVNM AETLLPENAK MTVVPPEG 108

Sequence Number (ID): 94

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
 caaaccgtcg ggacctttta ctacgtaaac gatgctggtg ggctggaatc caaagtattc 120
 tcctcagggg gccctacacc ctacccaac tacgccaatg ctggtcatgt agaagggcag 180
 tcagcactgt ttatgcgcga taatggtata agcgagggtg tggctttcca taacaacca 240
 gaggggtactt gtggcttctg tgtgaatatg gcagaaaccc ttctgcccga aaatgccaag 300
 atgactgtcg tcccactga aggc 324

Sequence Number (ID): 95

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant
- source, 1..108

> mol_type, protein
> organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPYN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TATLLPENAK MTVPVPEG 108

Sequence Number (ID): 96

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 > note, Deaminase Variant
- source, 1..324
 > mol_type, other DNA
 > organism, synthetic construct

Residues:

ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
caaaccgtcg ggaccttta ctacgtaaac gatgctggtg ggctggaatc caaagtattc 120
tcctcagggg gccctacacc ctacccaac tacgccaatg ctggatcatgt agaagggcag 180
tcagcactgt ttatgcgcga taatggtata agcgaggggt tggctttcca taacaaccca 240
gagggtactt gtggcttctg tgtgaatatg actgcaacc ttctgccga aaatgccaag 300
atgactgtcg tcccactga aggc 324

Sequence Number (ID): 97

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 > note, Deaminase Variant
- source, 1..108
 > mol_type, protein

> organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPYN YANAGHVEGQ 60

SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLAPENAK MTVVPPEG 108

Sequence Number (ID): 98

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
caaaccgtcg ggaccttta ctacgtaac gatgctggtg ggctggaatc caaagtattc 120
tcctcagggg gccctacacc ctacccaac tacgccaatg ctggtcatgt agaaggcag 180
tcagcactgt ttatgcgcga taatggtata agcgagggtg tggctttcca taacaacca 240
gagggtactt gtggcttctg tgtgaatatg actgaaacc ttgcaccga aaatgccaag 300
atgactgtcg tccacactga aggc 324

Sequence Number (ID): 99

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAA MTVVPPEG 108

Sequence Number (ID): 100

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
caaaccgtcg ggaccttta ctacgtaaac gatgctgggt ggctggaatc caaagtattc 120
tcctcagggg gccctacacc ctacccaac tacgccaatg ctggctcatgt agaagggcag 180
tcagcactgt ttatgcgcga taatggtata agcgaggggt tggctttcca taacaacca 240
gagggtactt gtggcttctg tgtgaatatg actgaaaccc ttctgcccga aaatgccgca 300
atgactgtcg tcccactga aggc 324

Sequence Number (ID): 101

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK ATVVPPEG 108

Sequence Number (ID): 102

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
caaaccgtcg ggaccttta ctacgtaaac gatgctggtg ggctggaatc caaagtattc 120
tcctcagggg gccctacacc ctacccaac tacgccaatg ctggtcatgt agaagggcag 180
tcagcactgt ttatgcgcga taatggtata agcgaggggt tggctttcca taacaacca 240
gagggtactt gtggcttctg tgtgaatatg actgaaaccc ttctgcccgga aaatgccaag 300
gcaactgtcg tcccacctga aggc 324

Sequence Number (ID): 103

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60

Sequence Number (ID): 104

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtagctacg cacttgggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
 caaacctcg ggaccttta ctacgtaac gatgctgggt ggctggaatc caaagtattc 120
 tcctcagggg gccctacacc ctacccaac tacgccaatg ctggatcatgt agaagggcag 180
 tcagcactgt ttatgcgcga taatggtata agcgagggtg tggctttcca taacaacca 240
 gagggctact gtggcttctg tgtgaatatg actgaaacc ttctgccga aaatccaag 300
 atggcagtcg tccacactga aggc 324

Sequence Number (ID): 105

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Deaminase Variant
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60
 SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTAVPPEG 108

Sequence Number (ID): 106

Length: 324

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..324
 - > note, Deaminase Variant
- source, 1..324
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
ggtagctacg cacttggtcc ttaccagatt agcgaccccc aactccccgc ctataatggt 60
caaaccgtcg ggaccttta ctacgtaaac gatgctgggt ggctggaatc caaagtattc 120
tcctcagggg gccctacacc ctacccaac tacgccaatg ctggtcatgt agaagggcag 180
tcagcactgt ttatgcgcga taatggtata agcgaggggt tggctttcca taacaacca 240
gagggtactt gtggcttctg tgtgaatatg actgaaacc ttctgccga aaatgccaag 300
atgactgcag tccacactga aggc                                     324
```

Sequence Number (ID): 107

Length: 30

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..30
 - > note, Deaminase Variant
- source, 1..30
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
AIPVKRGATG ETAVFTGNSN SPKSPTKGGC                                     30
```

Sequence Number (ID): 108

Length: 90

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..90
 - > note, Deaminase Variant
- source, 1..90
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```
gccatacctg tgaagcgggg agcaacaggg gagacagcag tggtcacagg caactctaac 60
agtccaaaga gcccaccaa aggcgggtgt                               90
```

Sequence Number (ID): 109

Length: 30

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..30
 - > note, Deaminase Variant
- source, 1..30
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

```
AIPVKRGATG ETKAFTGNSN SPKSPTKGGC                               30
```

Sequence Number (ID): 110

Length: 90

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..90
 - > note, Deaminase Variant
- source, 1..90

- > mol_type, other DNA
- > organism, synthetic construct

Residues:

gccatacctg tgaagcgggg agcaacaggg gagacaaagg cattcacagg caactctaac 60
 agtccaaaga gccccaccaa aggcgggtgt 90

Sequence Number (ID): 111

Length: 30

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..30
 - > note, Deaminase Variant
- source, 1..30
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

AIPVKRGATG ETKVATGNSN SPKSPTKGGC 30

Sequence Number (ID): 112

Length: 90

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..90
 - > note, Deaminase Variant
- source, 1..90
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gccatacctg tgaagcgggg agcaacaggg gagacaaagg tggcaacagg caactctaac 60
 agtccaaaga gccccaccaa aggcgggtgt 90

Sequence Number (ID): 113

Length: 30

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..30
 - > note, Deaminase Variant
- source, 1..30
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

AIPVKRGATG ETKVFAGNSN SPKSPTKGGC 30

Sequence Number (ID): 114

Length: 90

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..90
 - > note, Deaminase Variant
- source, 1..90
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gccatacctg tgaagcgggg agcaacaggg gagacaaagg tggtcgcagg caactctaac 60
agtccaaaga gcccaccaa aggcgggtgt 90

Sequence Number (ID): 115

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Linker

- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGTPHEVG VY TL 24

Sequence Number (ID): 116

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Primer
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

catcaatggg cgtggatag 19

Sequence Number (ID): 117

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Primer
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

catcaatggg cgtggatag 19

Sequence Number (ID): 118

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Primer
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gacacctact cagacaatgc 20

Sequence Number (ID): 119

Length: 12

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..12
 - > note, Left-ZFD DNA binding region
- source, 1..12
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtcatcctca tc 12

Sequence Number (ID): 120

Length: 12

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..12
 - > note, Synthetic Sequence
- source, 1..12
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

aaactgcaaa ag 12

Sequence Number (ID): 121

Residues:

000

Sequence Number (ID): 122

Residues:

000

Sequence Number (ID): 123

Residues:

000

Sequence Number (ID): 124

Residues:

000

Sequence Number (ID): 125

Residues:

000

Sequence Number (ID): 126

Residues:

000

Sequence Number (ID): 127

Residues:

000

Sequence Number (ID): 128

Length: 10

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..10
 - > note, Synthetic Sequence
- source, 1..10
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc 10

Sequence Number (ID): 129

Length: 11

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..11
 - > note, Synthetic Sequence
- source, 1..11
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc g 11

Sequence Number (ID): 130

Length: 12

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..12
 - > note, Synthetic Sequence
- source, 1..12
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc ga 12

Sequence Number (ID): 131

Length: 13

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gat 13

Sequence Number (ID): 132

Length: 14

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..14
 - > note, Synthetic Sequence

- source, 1..14
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatc 14

Sequence Number (ID): 133

Length: 15

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..15
 - > note, Synthetic Sequence
- source, 1..15
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcg 15

Sequence Number (ID): 134

Length: 16

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..16
 - > note, Synthetic Sequence
- source, 1..16
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcga 16

Sequence Number (ID): 135

Length: 17

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..17
 - > note, Synthetic Sequence
- source, 1..17
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgat 17

Sequence Number (ID): 136

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgatc 18

Sequence Number (ID): 137

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

ctgatcgatc gatcgatcg 19

Sequence Number (ID): 138

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgatcga 20

Sequence Number (ID): 139

Length: 21

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..21
 - > note, Synthetic Sequence
- source, 1..21
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgatcga t 21

Sequence Number (ID): 140

Length: 22

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..22
 - > note, Synthetic Sequence
- source, 1..22
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgatcga tc 22

Sequence Number (ID): 141

Length: 23

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgatcga tcg 23

Sequence Number (ID): 142

Length: 24

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgatcgatc gatcgatcga tcga 24

Sequence Number (ID): 143

Length: 33

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..33
 - > note, Synthetic Sequence
- source, 1..33
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtttactcaa tcctctgatc agggtagagca tca 33

Sequence Number (ID): 144

Length: 11

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..11
 - > note, Synthetic Sequence
- source, 1..11
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

VYSILWSGWA S 11

Sequence Number (ID): 145

Length: 33

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..33

> note, Synthetic Sequence

- source, 1..33

> mol_type, other DNA

> organism, synthetic construct

Residues:

gtttactcaa tcctctgatt agggtagca tca 33

Sequence Number (ID): 146

Length: 11

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..11

> note, Synthetic Sequence

- source, 1..11

> mol_type, protein

> organism, synthetic construct

Residues:

VYSILWLGWA S 11

Sequence Number (ID): 147

Length: 33

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..33

> note, Synthetic Sequence

- source, 1..33

> mol_type, other DNA

> organism, synthetic construct

Residues:

gtttactcaa tcctctaac agggtagca tca 33

Sequence Number (ID): 148

Length: 10

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..10
 - > note, Synthetic Sequence
- source, 1..10
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

VYSILSGWAS 10

Sequence Number (ID): 149

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctacgcctaa tctactccac ctcaatcaca ctactcccc 39

Sequence Number (ID): 150

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39

- > mol_type, other DNA
- > organism, synthetic construct

Residues:

ctacgcctaa tctactttac ctcaatcaca ctactcccc 39

Sequence Number (ID): 151

Length: 13

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LRLIYFTSIT LLP 13

Sequence Number (ID): 152

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctacgcctaa tctactccac ctcaatcaca ctactcccc 39

Sequence Number (ID): 153

Length: 13

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LRLIYSTSIT LLP 13

Sequence Number (ID): 154

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctacgcctaa tctactttat ttcaatcaca ctactcccc 39

Sequence Number (ID): 155

Length: 13

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LRLIYFISIT LLP

13

Sequence Number (ID): 156

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctacgcctaa tctacttcac ctcaatcaca ctactcccc

39

Sequence Number (ID): 157

Length: 13

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LRLIYFISIT LLP

13

Sequence Number (ID): 158

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctacgcctaa tctactttat ctcaatcaca ctactcccc 39

Sequence Number (ID): 159

Length: 13

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LRLIYFISIT LLP 13

Sequence Number (ID): 160

Length: 39

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..39
 - > note, Synthetic Sequence
- source, 1..39
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctacgcctaa tctactttac cttaatcaca ctactcccc 39

Sequence Number (ID): 161

Length: 13

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..13
 - > note, Synthetic Sequence
- source, 1..13
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LRLIYFTLIT LLP 13

Sequence Number (ID): 162

Length: 917

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..917
 - > note, Synthetic Sequence
- source, 1..917
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctagcaacga ttgtacaatt gcttctttaa aaaaggaaga aagaaagaaa gaaaagaatc 60
aacatcagcg ttaacaaacg gccccgttac ggcccaaacg gtcatataga gtaacggcgt 120
taagcgttga aagactccta tcgaaatacg taaccgcaaa cgtgtcatag tcagatcccc 180
tcttccttca ccgcctcaaa cacaaaaata atcttctaca gcctatatat acaaccccc 240
cttctatctc tcctttctca caattcatca tcttcttctc tctaccccca attttaagaa 300
atctctctt ctctcttca ttttaaggt aaatctctct ctctctctct ctctctgtta 360
ttccttgttt taattaggta tgtattattg ctagttgtt aatctgctta tcttatgtat 420
gccttatgtg aatatcttta tcttggtcat ctcatccgtt tagaagctat aaatttgttg 480

atttgactgt gtatctacac gtggttatgt ttatatctaa tcagatatga atttcttcat 540
 attgttgcgt ttgtgtgtac caatccgaaa tcgttgattt ttttcattta atcgtgtagc 600
 taattgtacg tatacatatg gatctacgta tcaattgttc atctgtttgt gttgtatgt 660
 atacagatct gaaaacatca ctctctcat ctgattgtgt tgttacatac atagatatag 720
 atctgttata tcattttttt tattaattgt gtatatatat atgtgcatag atctggatta 780
 catgattgtg attatttaca tgattttgtt attacgtat gtatatatgt agatctggac 840
 ttttggagt tgttgacttg attgtatttg tgtgtgtata tgtgtgttct gatcttgata 900
 tgttatgtat gtgcagc 917

Sequence Number (ID): 163

Length: 469

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..469
 - > note, Synthetic Sequence
- source, 1..469
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

caggcctccc agctttcgtc cgtatcatcg gtttcgacaa cgttcgtaa gttcaatgca 60
 tcagtttcat tgccacaca ccagaatcct actaagtttg agtattatgg cattggaaaa 120
 gctgttttct tctatcattt gttctgcttg taattactg tgttcttca gttttgttt 180
 tcggacatca aaatgcaaat ggatggataa gagttaataa atgatatggt cttttgttc 240
 atttcaaat tattattatc tgttgttttt actttaatgg gttgaattta agtaagaaag 300
 gaactaacag tgtgatatta aggtgcaatg ttagacatat aaaacagtct ttacctctc 360
 tttggttatg tcttgaattg gttgttttct tcacttatct gtgtaatcaa gtttactatg 420
 agtctatgat caagtaatta tgcaatcaag ttaagtacag tataggctt 469

Sequence Number (ID): 164

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

taatacgact cactatagg 19

Sequence Number (ID): 165

Length: 308

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..308
 - > note, Synthetic Sequence
- source, 1..308
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MLQLCSTFRP QLLPCQFRF TNGVLIPQIN YVASNSVVNI RPMIRCQRAS GGRGGANRSK 60
PAKPQVKEGS NKTVIEGLVT ESLPNGMFRV DLENGDNILG YICGKIRKNF IRILPGDKVK 120
VEMSVYDSTK GRIIFRMSSR DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA MDIADLRTL 180
YSQQQQEKIK PKVRSTVAQH HEALVGHGFT HAHIVALSQH PAALGTVAVK YQDMIAALPE 240
ATHEAIVGVG KQWSGARALE ALLTVAGELR GPPLQLDTGQ LLKIAKGGV TAVEAVHAWR 300
NALTGAPL 308

Sequence Number (ID): 166

Length: 240

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..240

> note, Synthetic Sequence

- source, 1..240

> mol_type, protein

> organism, synthetic construct

Residues:

MASSMLSSAT MVASPAQATM VAPFNGLKSS AAFPATRKAN NDITSITSNG GRVNCMQVWP 60
PIGKKKFETL SYLPDLTDSE DYKDHDGDYK DHDIDYKDDD DKMDIADLRT LGYSQQQKEK 120
IKPKVRSTVA QHHEALVGHG FTHAHIVALS QHPAALGTVA VKYQDMIAAL PEATHEAIVG 180
VGKRGAGARA LEALLTVAGE LRGPPLQLDT GQLLKIARKG GVTAVEAVHA WRNALTGAPL 240

Sequence Number (ID): 167

Length: 244

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..244

> note, Synthetic Sequence

- source, 1..244

> mol_type, protein

> organism, synthetic construct

Residues:

MAMAVFRREG RRLPSIAAR PIAAIRSPLS SDQEEGLLGV RSISTQVVRN RMKSVKNIQK 60
ITKAMKMVAA SKLRAVQYPY DVPDYAGYPY DVPDYAGYPY DVPDYAMDIA DLRTLGYSSQ 120
QQEKIKPKVR STVAQHHEAL VGHGFTHAHI VALSQHPAAL GTVAVKYQDM IAALPEATHE 180
AIVGVGKQWS GARALEALLT VAGELRGPPL QLDTGQLLKI AKRGGVTAVE AVHAWRNALT 240
GAPL 244

Sequence Number (ID): 168

Length: 196

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..196

> note, Synthetic Sequence

- source, 1..196

> mol_type, protein

> organism, synthetic construct

Residues:

MFKQASRLLS RSVAAASSKS VTTRAFSTEL PSTLDSYKD HDGDYKDHI DYKDDDDKMD 60
IADLRTLGY S QQQQEKIKPK VRSTVAQHHE ALVGHGFTHA HIVALSQHPA ALGTVAVKYQ 120
DMIAALPEAT HEAIVGVGKR GAGARALEAL LTVAGELRGP PLQLDTGQLL KIAKRGGVTA 180
VEAVHAWRNA LTGAPL 196

Sequence Number (ID): 169

Length: 195

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..195

> note, Synthetic Sequence

- source, 1..195

> mol_type, protein

> organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLG R PALDAVKKG 60
LGGSGSYALG PYQISAPQLP AYNGQTVGTF YYVNDAGGLE SKVFSSGGSG GSTNLSDIIE 120
KETGKQLVIQ ESILMLPEEV EEVIGNKPES DILVHTAYDE STDENVMLLT SDAPEYKPWA 180
LVIQDSNGEN KIKML 195

Sequence Number (ID): 170

Length: 245

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..245

> note, Synthetic Sequence

- source, 1..245
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLGG RPALDAVKKG 60
LGGSPTPYPN YANAGHVEGQ SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK 120
MTVVPPEGAI PVKRGATGET KVFTGNSNSP KSPTKGGCSG GSTNLSDIIE KETGKQLVIQ 180
ESILMLPEEV EEVIGNKPES DILVHTAYDE STDENVMLLT SDAPEYKPWA LVIQDSNGEN 240
KIKML 245

Sequence Number (ID): 171

Length: 259

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..259
 > note, Synthetic Sequence
- source, 1..259
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLGG RPALDAVKKG 60
LGGSGSYALG PYQISAPQLP AYNGQTVGTF YYVNDAGGLE SKVFSSGGPT PYPNYANAGH 120
VEGQSALFMR DNGISEGLVF HNNPEGTCGF CVNMTETLLP ENAKMTVVPP EGSGGSTNLS 180
DIIEKETGKQ LVIQESILML PEEVEEVIGN KPESDILVHT AYDESTDENV MLLTSDAPEY 240
KPWALVIQDS NGENKIKML 259

Sequence Number (ID): 172

Length: 181

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..181

> note, Synthetic Sequence

- source, 1..181

> mol_type, protein

> organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLG G RPALDAVKKG 60
LGGSAIPVKR GATGETKVFT GNSNSPKSPT KGGCSGGSTN LSDIEKETG KQLVIQESIL 120
MLPEEVEEVI GNKPESDILV HTAYDESTDE NVMLLTSDAP EYKPWALVIQ DSNGENKIKM 180
L 181

Sequence Number (ID): 173

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68

> note, Synthetic Sequence

- source, 1..68

> mol_type, protein

> organism, synthetic construct

Residues:

NLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 174

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68

> note, Synthetic Sequence

- source, 1..68

> mol_type, protein

> organism, synthetic construct

Residues:

GLTPEQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETVQRL 60

LPVLCQDH 68

Sequence Number (ID): 175

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQRL 60

LPVLCQAH 68

Sequence Number (ID): 176

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETVQRL 60

LPVLCQAH 68

Sequence Number (ID): 177

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNNGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 178

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNNGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 179

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68

- > note, Synthetic Sequence
- source, 1..68
- > mol_type, protein
- > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 180

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
- > note, Synthetic Sequence
- source, 1..68
- > mol_type, protein
- > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 181

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
- > note, Synthetic Sequence
- source, 1..68
- > mol_type, protein
- > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 182

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 183

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 184

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNNGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 185

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNNGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 186

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68

> mol_type, protein
> organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 187

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASHDGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 188

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 189

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 190

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 191

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASHDGG KQALETVQRL 60
 LPVLCQDH 68

Sequence Number (ID): 192

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
 LPVLCQDH 68

Sequence Number (ID): 193

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 194

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 195

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 196

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 197

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 198

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence

- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNGGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 199

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNGGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 200

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETQRL 60

LPVLCQAH 68

Sequence Number (ID): 201

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNGGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 202

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASHDGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 203

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 204

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 205

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein

> organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETVQRL 60

LPVLCQDH 68

Sequence Number (ID): 206

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNNGG KQALETVQRL 60

LPVLCQDH 68

Sequence Number (ID): 207

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNIGG KQALETVQRL 60

LPVLCQAH 68

Sequence Number (ID): 208

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNNGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 209

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 210

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68

- > note, Synthetic Sequence
- source, 1..68
- > mol_type, protein
- > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 211

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
- > note, Synthetic Sequence
- source, 1..68
- > mol_type, protein
- > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 212

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
- > note, Synthetic Sequence
- source, 1..68
- > mol_type, protein
- > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 213

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 214

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 215

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 216

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 217

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68

> mol_type, protein
> organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 218

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

NLTPEQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 219

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASHDGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 220

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 221

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASHDGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 222

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNNGG KQALETVQRL 60
 LPVLCQAH 68

Sequence Number (ID): 223

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETVQRL 60
 LPVLCQAH 68

Sequence Number (ID): 224

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 225

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 226

Length: 34

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..34
 - > note, Synthetic Sequence
- source, 1..34
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQAH 34

Sequence Number (ID): 227

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 228

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 229

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68

> mol_type, protein
> organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 230

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 231

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 232

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 233

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 234

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNNGG KQALETVQRL 60
 LPVLCQDH 68

Sequence Number (ID): 235

Length: 34

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..34
 - > note, Synthetic Sequence
- source, 1..34
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNNGGKQAL ETVQRLLPVL CQDH 34

Sequence Number (ID): 236

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPEQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 237

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 238

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 239

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 240

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 241

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68

> mol_type, protein
> organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 242

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASHDGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 243

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 > note, Synthetic Sequence
- source, 1..68
 > mol_type, protein
 > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNIGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 244

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPEQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 245

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 246

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETVQRL 60
 LPVLCQAH 68

Sequence Number (ID): 247

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNGGG KQALETVQRL 60
 LPVLCQAH 68

Sequence Number (ID): 248

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 249

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 250

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 251

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNIGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 252

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNNGG KQALETQRL 60
LPVLCQDH 68

Sequence Number (ID): 253

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence

- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 254

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNGGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 255

Length: 69

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..69
 - > note, Synthetic Sequence
- source, 1..69
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNGGG KQALETVQRL 60

LPVLCQDHG

69

Sequence Number (ID): 256

Length: 67

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..67
 - > note, Synthetic Sequence
- source, 1..67
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNGGGK QALETQVQRL 60
PVLCQAH 67

Sequence Number (ID): 257

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVLC QDHGLTPDQ VVAIASNGGG KQALETQVQRL 60
LPVLCQAH 68

Sequence Number (ID): 258

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 259

Length: 34

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..34
 - > note, Synthetic Sequence
- source, 1..34
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNNGGKQAL ETVQRLLPVL CQAH 34

Sequence Number (ID): 260

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 261

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQDH 68

Sequence Number (ID): 262

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL 60
LPVLCQAH 68

Sequence Number (ID): 263

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNNGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 264

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETQRL 60
LPVLCQAH 68

Sequence Number (ID): 265

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence

- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETQRL 60
 LPVLCQAH 68

Sequence Number (ID): 266

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPDQVVAI ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASHDGG KQALETQRL 60
 LPVLCQAH 68

Sequence Number (ID): 267

Length: 68

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..68
 - > note, Synthetic Sequence
- source, 1..68
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNIGG KQALETQRL 60

LPVLCQAH

68

Sequence Number (ID): 268

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

catcaatggg cgtggatag 19

Sequence Number (ID): 269

Length: 136

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..136
 - > note, Synthetic Sequence
- source, 1..136
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

DIADLRTLGY SQQQKEIKP KVRSTVAQHH EALVGHGFTH AHIVALSQHP AALGTVAVKY 60
QDMIAALPEA THEAIVGVGK QWSGARALEA LLTVAGELRG PPLQLDTGQL LKIAKGGVT 120
AVEAVHAWRN ALTGAP 136

Sequence Number (ID): 270

Length: 137

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..137
 - > note, Synthetic Sequence
- source, 1..137
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

DIADLRTLGY SQQQQEKIKP KVRSTVAQHH EALVGHGFTH AHIVALSQHP AALGTVAVKY 60
QDMIAALPEA THEAIVGVGK RGAGARALEA LLTVAGELRG PPLQLDTGQL LKIAKRGGVT 120
AVEAVHAWRN ALTGAPL 137

Sequence Number (ID): 271

Length: 41

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..41
 - > note, Synthetic Sequence
- source, 1..41
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SIVAQLSRPD PALAALTNDH LVALACLGGR PALDAVKKGL G 41

Sequence Number (ID): 272

Length: 94

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..94
 - > note, Synthetic Sequence
- source, 1..94
 - > mol_type, protein

> organism, synthetic construct

Residues:

PTPYPNYANA GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV 60

PPEGAIPVKR GATGETKVFT GNSNSPKSPT KGGC 94

Sequence Number (ID): 273

Length: 108

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..108
 - > note, Synthetic Sequence
- source, 1..108
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPN YANAGHVEGQ 60

SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEG 108

Sequence Number (ID): 274

Length: 49

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..49
 - > note, Synthetic Sequence
- source, 1..49
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MLGFVGRVAA APASGALRRL TPSASLPPAQ LLLRAAPTAV HPVRDYAAQ 49

Sequence Number (ID): 275

Length: 8

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..8
 - > note, Synthetic Sequence
- source, 1..8
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

DYKDDDDK 8

Sequence Number (ID): 276

Length: 9

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..9
 - > note, Synthetic Sequence
- source, 1..9
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YPYDVPDYA 9

Sequence Number (ID): 277

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

tttcctact ggtccgatt 19

Sequence Number (ID): 278

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttgcaggtat taattgctt 19

Sequence Number (ID): 279

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttccctaaac ataaactcat 20

Sequence Number (ID): 280

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttaaaataaa gttattatt 19

Sequence Number (ID): 281

Length: 19

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..19
 - > note, Synthetic Sequence
- source, 1..19
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttcctaacag ggttctact 19

Sequence Number (ID): 282

Length: 17

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..17
 - > note, Synthetic Sequence
- source, 1..17
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttgttggg agaatat

17

Sequence Number (ID): 283

Length: 199

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..199
 - > note, Synthetic Sequence
- source, 1..199
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRG 180
VTAVEAVHAW RNALTGAPL 199

Sequence Number (ID): 284

Length: 191

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..191
 - > note, Synthetic Sequence
- source, 1..191
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHS L DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAGR GGVTAVEAVH 180
AWRNALTGAP L 191

Sequence Number (ID): 285

Length: 197

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..197
 - > note, Synthetic Sequence
- source, 1..197
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLGG RPALDAVKKG 60
LGGSGSGSYA LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LESKVFSSGG SGGSTNLSDI 120
IEKETGKQLV IQESILMLPE EVEEVIGNKP ESDILVHTAY DESTDENVML LTSDAPEYKP 180
WALVIQDSNG ENKIKML 197

Sequence Number (ID): 286

Length: 247

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..247
 - > note, Synthetic Sequence
- source, 1..247
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLGG RPALDAVKKG 60
LGGSGSPTPY PNYANAGHVE GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN 120
AKMTVPPEG AIPVKRGATG ETKVFTGNSN SPKSPTKGGC SGGSTNLSDI IEKETGKQLV 180
IQESILMLPE EVEEVIGNKP ESDILVHTAY DESTDENVML LTSDAPEYKP WALVIQDSNG 240
ENKIKML 247

Sequence Number (ID): 287

Length: 261

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..261
 - > note, Synthetic Sequence
- source, 1..261
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLG G RPALDAVKKG 60
LGGSGSGSYA LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LESKVFSSGG PTPYPNYANA 120
GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV PPEGSGGSTN 180
LSDIIEKETG KQLVIQESIL MLPEEVEEVI GNKPESDILV HTAYDESTDE NVMLLTSDAP 240
EYKPWALVIQ DSNGENKIKM L 261

Sequence Number (ID): 288

Length: 183

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..183
 - > note, Synthetic Sequence
- source, 1..183
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GLTPEQVVAI ASNGGGKQAL ESIVAQLSRP DPALAALTND HLVALACLG G RPALDAVKKG 60
LGGSGSAIPV KRGATGETKV FTGNSNSPKS PTKGGCSGGS TNLSDIIEKE TGKQLVIQES 120
ILMLPEEVEE VIGNKPESDI LVHTAYDEST DENVMMLTSD APEYKPWALV IQDSNGENKI 180
KML 183

Sequence Number (ID): 289

Length: 577

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..577
 - > note, Synthetic Sequence
- source, 1..577
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPDQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNGGG KQALETVQRL 60
LPVLCQAHGL TPEQVVAIAS NGGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASHDGGKQ 120
ALETVQRLLP VLCQAHGLTP AQVVAIASHD GGKQALETVQ RLLPVLCQDH GLTPAQVVAI 180
ASNGGGKQAL ETVQRLLPVL CQDHGLTPEQ VVAIASNIGG KQALETVQRL LPVLCQAHGL 240
TPDQVVAIAS HDGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASNGGGKQ ALETVQRLLP 300
VLCQAHGLTP AQVVAIASNN GGKQALETVQ RLLPVLCQDH GLTPAQVVAI ASNNGGKQAL 360
ETVQRLLPVL CQDHGLTPDQ VVAIASNGGG KQALETVQRL LPVLCQAHGL TPAQVVAIAS 420
HDGGKQALET VQRLLPVLCQ DHGLTPDQVV AIASHDGGKQ ALETVQRLLP VLCQAHGLTP 480
EQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPEQVVAI ASNIGGKQAL ETVQRLLPVL 540
CQAHGLTPDQ VVAIASNGGG KQALETVQRL LPVLCQD 577

Sequence Number (ID): 290

Length: 577

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..577
 - > note, Synthetic Sequence
- source, 1..577
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPEQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL 60
LPVLCQDHGL TPAQVVAIAS NIGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASNIGGKQ 120
ALETVQRLLP VLCQAHGLTP DQVVAIASNI GGKQALETVQ RLLPVLCQDH GLTPDQVVAI 180
ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL LPVLCQAHGL 240
TPAQVVAIAS NIGGKQALET VQRLLPVLCQ DHGLTPAQVV AIASNIGGKQ ALETVQRLLP 300
VLCQAHGLTP AQVVAIASNN GGKQALETVQ RLLPVLCQDH GLTPEQVVAI ASNGGGKQAL 360
ETVQRLLPVL CQAHGLTPAQ VVAIASNIGG KQALETVQRL LPVLCQDHGL TPAQVVAIAS 420
NIGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASNIGGKQ ALETVQRLLP VLCQAHGLTP 480
DQVVAIASNG GGKQALETVQ RLLPVLCQAH GLTPEQVVAI ASNIGGKQAL ETVQRLLPVL 540
CQAHGLTPDQ VVAIASNIGG KQALETVQRL LPVLCQD 577

Sequence Number (ID): 291

Length: 577

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..577
 - > note, Synthetic Sequence
- source, 1..577
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETVQRL 60
LPVLCQAHGL TPAQVVAIAS HDGGKQALET VQRLLPVLCQ AHGLTPAQVV AIASNIGGKQ 120
ALETVQRLLP VLCQAHGLTP AQVVAIASNN GGKQALETVQ RLLPVLCQDH GLTPAQVVAI 180
ASNNGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNIGG KQALETVQRL LPVLCQAHGL 240
TPDQVVAIAS NIGGKQALET VQRLLPVLCQ DHGLTPDQVV AIASNIGGKQ ALETVQRLLP 300
VLCQAHGLTP EQVVAIASNG GGKQALETVQ RLLPVLCQAH GLTPAQVVAI ASNIGGKQAL 360
ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETVQRL LPVLCQAHGL TPEQVVAIAS 420
NIGGKQALET VQRLLPVLCQ AHGLTPAQVV AIASNIGGKQ ALETVQRLLP VLCQAHGLTP 480
DQVVAIASNN GGKQALETVQ RLLPVLCQDH GLTPDQVVAI ASHDGGKQAL ETVQRLLPVL 540

CQAHGLTPAQ VVAIASNGGG KQALETVQRL LPVLCQD

577

Sequence Number (ID): 292

Length: 577

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..577
 - > note, Synthetic Sequence
- source, 1..577
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQAHGL TPEQVVAIAS HDGGKQALET VQRLLPVLCQ AHGLTPEQVV AIASNGGGKQ 120
ALETVQRLLP VLCQAHGLTP AQVVAIASNI GGKQALETVQ RLLPVLCQDH GLTPAQVVAI 180
ASNIGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASHDGG KQALETVQRL LPVLCQAHGL 240
TPAQVVAIAS NIGGKQALET VQRLLPVLCQ AHGLTPAQVV AIASNNGGKQ ALETVQRLLP 300
VLCQAHGLTP AQVVAIASNN GGKQALETVQ RLLPVLCQDH GLTPAQVVAI ASNNGGKQAL 360
ETVQRLLPVL CQDHGLTPDQ VVAIASNGGG KQALETVQRL LPVLCQAHGL TPEQVVAIAS 420
NNGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASHDGGKQ ALETVQRLLP VLCQDHGLTP 480
DQVVAIASNG GGKQALETVQ RLLPVLCQAH GLTPEQVVAI ASNIGGKQAL ETVQRLLPVL 540
CQAHGLTPAQ VVAIASHDGG KQALETVQRL LPVLCQD 577

Sequence Number (ID): 293

Length: 611

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..611
 - > note, Synthetic Sequence
- source, 1..611
 - > mol_type, protein

> organism, synthetic construct

Residues:

NLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQDHGLTPAQ VVAIASHDGG KQALETVQRL 60
LPVLCQAHGL TPEQVVAIAS HDGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASHDGGKQ 120
ALETVQRLLP VLCQAHGLTP DQVVAIASNG GGKQALETVQ RLLPVLCQDH GLTPAQVVAI 180
ASNIGGKQAL ETVQRLLPVL CQDHGLTPDQ VVAIASNIGG KQALETVQRL LPVLCQAHGL 240
TPDQVVAIAS NIGGKQALET VQRLLPVLCQ AHGLTPAQVV AIASHDGGKQ ALETVQRLLP 300
VLCQAHGLTP AQVVAIASNI GGKQALETVQ RLLPVLCQDH GLTPAQVVAI ASNGGGKQAL 360
ETVQRLLPVL CQDHGLTPDQ VVAIASNIGG KQALETVQRL LPVLCQDHGL TPDQVVAIAS 420
NIGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASNIGGKQ ALETVQRLLP VLCQAHGLTP 480
AQVVAIASHD GGKQALETVQ RLLPVLCQAH GLTPAQVVAI ASNGGGKQAL ETVQRLLPVL 540
CQDHGLTPEQ VVAIASHDGG KQALETVQRL LPVLCQAHGL TPAQVVAIAS NIGGKQALET 600
VQRLLPVLCQ D 611

Sequence Number (ID): 294

Length: 509

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..509
 - > note, Synthetic Sequence
- source, 1..509
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

NLTPAQVVAI ASNGGGKQAL ETVQRLLPVL CQAHGLTPDQ VVAIASNNGG KQALETVQRL 60
LPVLCQAHGL TPAQVVAIAS NNGGKQALET VQRLLPVLCQ DHGLTPAQVV AIASNNGGKQ 120
ALETVQRLLP VLCQAHGLTP DQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPAQVVAI 180
ASNGGGKQAL ETVQRLLPVL CQDHGLTPEQ VVAIASNNGG KQALETVQRL LPVLCQAHGL 240
TPAQVVAIAS NNGGKQALET VQRLLPVLCQ DHGLTPDQVV AIASNNGGKQ ALETVQRLLP 300
VLCQAHGLTP DQVVAIASNI GGKQALETVQ RLLPVLCQDH GLTPAQVVAI ASNNGGKQAL 360
ETVQRLLPVL CQDHGLTPAQ VVAIASNIGG KQALETVQRL LPVLCQAHGL TPEQVVAIAS 420

NIGGKQALET VQRLLPVLCQ AHGLTPDQVV AIASNGGGKQ ALETVQRLLP VLCQDHGLTP 480
DQVVAIASNI GGKQALETVQ RLLPVLCQA 509

Sequence Number (ID): 295

Length: 28

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..28
 - > note, Synthetic Sequence
- source, 1..28
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

agtggggacc gcatactatg tcaacgac 28

Sequence Number (ID): 296

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtctgaccgt tgtaggcg 18

Sequence Number (ID): 297

Length: 30

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..30
 - > note, Synthetic Sequence
- source, 1..30
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

atccaagggtt gcatctagcg gtgggtccgg 30

Sequence Number (ID): 298

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tccaatcccc cgcgctcg 18

Sequence Number (ID): 299

Length: 33

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..33
 - > note, Synthetic Sequence
- source, 1..33
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cagacagtgg caaccttta ctatgtcaac gac 33

Sequence Number (ID): 300

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

accgtttag gcggggag 18

Sequence Number (ID): 301

Length: 30

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..30
 - > note, Synthetic Sequence
- source, 1..30
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tccatatcag gcaagtgctc cccaactccc 30

Sequence Number (ID): 302

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence

- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccagggcgt aggaacca 18

Sequence Number (ID): 303

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

attggaatcc gcagtttct ctagcgtgg gtccgg 36

Sequence Number (ID): 304

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccccggcgt cgttgaca 18

Sequence Number (ID): 305

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctctggtcc tacgccgag gtccatatca gattag 36

Sequence Number (ID): 306

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctaactgat atggacctgc ggcgtaggaa ccagag 36

Sequence Number (ID): 307

Length: 30

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..30
 - > note, Synthetic Sequence
- source, 1..30
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

atatcagatt gcagctcccc aactccccgc 30

Sequence Number (ID): 308

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggacccaggg cgtaggaa 18

Sequence Number (ID): 309

Length: 24

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

caaggtttc gcaagcgtg ggtc 24

Sequence Number (ID): 310

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gattccaatc ccccggcg 18

Sequence Number (ID): 311

Length: 30

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..30
 - > note, Synthetic Sequence
- source, 1..30
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtcagacag tgggggcatt ttactatgtc 30

Sequence Number (ID): 312

Length: 30

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..30
 - > note, Synthetic Sequence
- source, 1..30
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gacatagtaa aatgccccca ctgtctgacc

30

Sequence Number (ID): 313

Length: 28

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..28
 - > note, Synthetic Sequence
- source, 1..28
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtcagacag cagggacctt ttactatg

28

Sequence Number (ID): 314

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gttgtaggcg gggagttg

18

Sequence Number (ID): 315

Length: 25

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..25

- > note, Synthetic Sequence
- source, 1..25
- > mol_type, other DNA
- > organism, synthetic construct

Residues:

ttttactatg caaacgacgc cgggg 25

Sequence Number (ID): 316

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtccccact gtctgacc 18

Sequence Number (ID): 317

Length: 42

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..42
 - > note, Synthetic Sequence
- source, 1..42
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctctgggtcc gcagccctgg gtccatatca gattagtgc cc 42

Sequence Number (ID): 318

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccagagcccc ccaacccc 18

Sequence Number (ID): 319

Length: 31

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..31
 - > note, Synthetic Sequence
- source, 1..31
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cagtggggac cttgcatat gtcaacgacg c 31

Sequence Number (ID): 320

Length: 31

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..31
 - > note, Synthetic Sequence
- source, 1..31

- > mol_type, other DNA
- > organism, synthetic construct

Residues:

gcgtcgttga catatgcaaa ggtccccact g 31

Sequence Number (ID): 321

Length: 28

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..28
 - > note, Synthetic Sequence
- source, 1..28
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gaccttttac gcagtcaacg acgccggg 28

Sequence Number (ID): 322

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccactgtct gaccgttg 18

Sequence Number (ID): 323

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgtggcttcg cagtgaatat gactgaaacc cttctg 36

Sequence Number (ID): 324

Length: 32

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..32
 - > note, Synthetic Sequence
- source, 1..32
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

catattcact gcgaagccac aagtaccctc tg 32

Sequence Number (ID): 325

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtgtgaatat gactgcaacc cttctgcccg aaaatg 36

Sequence Number (ID): 326

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

catttcggg cagaagggtt gcagtcatat tcacac 36

Sequence Number (ID): 327

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gaaaatgccg caatgactgt cgtcccacct gaagg 35

Sequence Number (ID): 328

Length: 31

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..31
 - > note, Synthetic Sequence
- source, 1..31
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gacagtcatt gcggcattt cgggcagaag g 31

Sequence Number (ID): 329

Length: 32

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..32
 - > note, Synthetic Sequence
- source, 1..32
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gaaacccttg cacccgaaaa tgccaagatg ac 32

Sequence Number (ID): 330

Length: 40

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..40
 - > note, Synthetic Sequence
- source, 1..40
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

atttcgggt gcaagggtt cagtcattt cacacagaag 40

Sequence Number (ID): 331

Length: 32

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..32
 - > note, Synthetic Sequence
- source, 1..32
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

aatgccaagg caactgtcgt ccacactgaa gg 32

Sequence Number (ID): 332

Length: 34

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..34
 - > note, Synthetic Sequence
- source, 1..34
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gacgacagtt gccttgcat ttctggcag aagg 34

Sequence Number (ID): 333

Length: 34

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..34
 - > note, Synthetic Sequence

- source, 1..34
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtgaatatgg cagaaaccct tctgcccgaa aatg 34

Sequence Number (ID): 334

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

aagggtttct gccatattca cacagaagcc acaag 35

Sequence Number (ID): 335

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cgaaaatgcc aagatggcag tcgtcccacc tgaag 35

Sequence Number (ID): 336

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cttcaggtgg gacgactgcc atcttggcat tttcg 35

Sequence Number (ID): 337

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggtacttgtg gcttctgtgc aaatatgact gaaacc 36

Sequence Number (ID): 338

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

ggtttcagtc atattgcac agaagccaca agtacc 36

Sequence Number (ID): 339

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gaaaatgcca agatgactgc agtcccacct gaagg 35

Sequence Number (ID): 340

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccttcaggtg ggactgcagt catcttgca ttttc 35

Sequence Number (ID): 341

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggcattagcg caggccttgt gttccataat aatcc 35

Sequence Number (ID): 342

Length: 42

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..42
 - > note, Synthetic Sequence
- source, 1..42
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cacaagccct gcgctaagtc cggtatctct cataaaaaga gc 42

Sequence Number (ID): 343

Length: 40

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..40
 - > note, Synthetic Sequence
- source, 1..40
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtcagctctt gcaatgagag ataacggcat tagcgaaggg 40

Sequence Number (ID): 344

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgcccctcga cgtgcccg 18

Sequence Number (ID): 345

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gggcttgtag cacataataa tcctgagggc acctg 35

Sequence Number (ID): 346

Length: 32

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..32

- > note, Synthetic Sequence
- source, 1..32
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gattattatg tgccacaagc ccttcgctaa tg 32

Sequence Number (ID): 347

Length: 23

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cattagcgaa gcacttgtgt tcc 23

Sequence Number (ID): 348

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccgttatctc tcataaaaag 20

Sequence Number (ID): 349

Length: 30

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..30
 - > note, Synthetic Sequence
- source, 1..30
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gcttggttc gcaaataatc ctgagggcac 30

Sequence Number (ID): 350

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccttcgctaa tgccgtta 18

Sequence Number (ID): 351

Length: 23

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..23
 - > note, Synthetic Sequence
- source, 1..23

- > mol_type, other DNA
- > organism, synthetic construct

Residues:

tgagaacgct gcaatgactg tcg 23

Sequence Number (ID): 352

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggcagaagtg ttcggtc 18

Sequence Number (ID): 353

Length: 37

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..37
 - > note, Synthetic Sequence
- source, 1..37
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tagcgaaggg gcagtgtcc ataataatcc tgagggc 37

Sequence Number (ID): 354

Length: 35

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..35
 - > note, Synthetic Sequence
- source, 1..35
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

atggaacact gcccttcgc taatgccgtt atctc 35

Sequence Number (ID): 355

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

agctctttt gcaagagata acggcattag cgaagg 36

Sequence Number (ID): 356

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gactgcccct cgacgtgc 18

Sequence Number (ID): 357

Length: 26

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..26
 - > note, Synthetic Sequence
- source, 1..26
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gaacgctaaa gcaactgtcg taccac 26

Sequence Number (ID): 358

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tcaggcagaa gtgtttcg 18

Sequence Number (ID): 359

Length: 40

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..40
 - > note, Synthetic Sequence
- source, 1..40
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cgtcgagggg gcatcagctc ttttatgag agataacggc 40

Sequence Number (ID): 360

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgcccggcgt tagcgtag 18

Sequence Number (ID): 361

Length: 25

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..25
 - > note, Synthetic Sequence
- source, 1..25
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cgaggggcag gcagctcttt ttatg 25

Sequence Number (ID): 362

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

acgtgcccg cgtagcg 18

Sequence Number (ID): 363

Length: 23

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cgctaaaatg gcagtcgtac cac 23

Sequence Number (ID): 364

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence

- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttctcaggca gaagtgttc 20

Sequence Number (ID): 365

Length: 22

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..22
 - > note, Synthetic Sequence
- source, 1..22
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gccgggcacg cagaggggca gt 22

Sequence Number (ID): 366

Length: 26

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..26
 - > note, Synthetic Sequence
- source, 1..26
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gttagcgtag ttaggataag gtgttg 26

Sequence Number (ID): 367

Length: 27

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..27
 - > note, Synthetic Sequence
- source, 1..27
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cgaaggcctt gcattccata ataatcc 27

Sequence Number (ID): 368

Length: 18

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..18
 - > note, Synthetic Sequence
- source, 1..18
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctaatgccgt tatctctc 18

Sequence Number (ID): 369

Length: 23

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

aatgactgtc gcaccacccg aag 23

Sequence Number (ID): 370

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttagcgttct caggcagaag 20

Sequence Number (ID): 371

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

acaaaggtgg caacaggcaa ctctaacagt ccaaag 36

Sequence Number (ID): 372

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gttgctgtt gccaccttg tctccctgt tgctcc 36

Sequence Number (ID): 373

Length: 31

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..31
 - > note, Synthetic Sequence
- source, 1..31
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

caacagggga gacagcagtg ttacaggca a 31

Sequence Number (ID): 374

Length: 31

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..31
 - > note, Synthetic Sequence
- source, 1..31
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ttgcctgtga acactgctgt ctcccctgtt g

31

Sequence Number (ID): 375

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggagacaaag gtgttcgcag gcaactctaa cagtcc 36

Sequence Number (ID): 376

Length: 36

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..36
 - > note, Synthetic Sequence
- source, 1..36
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggactgttag agttgcctgc gaacaccttt gtctcc 36

Sequence Number (ID): 377

Length: 34

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..34

- > note, Synthetic Sequence
- source, 1..34
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gagacaaagg cattcacagg caactctaac agtc 34

Sequence Number (ID): 378

Length: 33

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..33
 - > note, Synthetic Sequence
- source, 1..33
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gcctgtgaat gcctttgtct cccctgttgc tcc 33

Sequence Number (ID): 379

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, Synthetic Sequence
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTPYPN YANAGHVAGQ 60

SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKRGATGET 120

Sequence Number (ID): 380

Length: 51

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..51
 - > note, Synthetic Sequence
- source, 1..51
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccaagcttg ccaccatggg atccggcagc tacgccctgg gtccgtatca g 51

Sequence Number (ID): 381

Length: 49

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..49
 - > note, Synthetic Sequence
- source, 1..49
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccgaggatc tcgctgccgc tgcaaccgcc ttggtcggg ctcttcggg 49

Sequence Number (ID): 382

Length: 110

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..110

- > note, Synthetic Sequence
- source, 1..110
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```

ccgggagtc tcgctgccg tgcaaccgcc ttggtcggg ctctcgggc tggctgtt 60
accggtaac acttggttt caccggtagc gccgcgcgcc actggaatg          110

```

Sequence Number (ID): 383

Length: 108

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..108
 - > note, Synthetic Sequence
- source, 1..108
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

```

ccgggagtc tcgctgccg tgcaaccgcc ttggtcggg ctctcgggc tggctgtt 60
accggtaac acttggttt caccggtagc gccgccttc ttactgg          108

```

Sequence Number (ID): 384

Length: 110

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..110
 - > note, Synthetic Sequence
- source, 1..110
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccgggagtc tcgctgccgc tgcaaccgcc ttggtcggg ctctcgggc tgttgctgtt 60
accggtaaac actttggtt caccgtagc gccggccgcc actggaatgg 110

Sequence Number (ID): 385

Length: 84

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..84
 - > note, Synthetic Sequence
- source, 1..84
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccgggagtc tcgctgccgc tgcaaccgcc ttggtcggg ctctcgggc tgttgctgtt 60
accggtaaac acggcggtt cacc 84

Sequence Number (ID): 386

Length: 58

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..58
 - > note, Synthetic Sequence
- source, 1..58
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccgggagtc tcgctgccgc tgcaaccgcc ttggtcggg ctggccgggc tgttgctg 58

Sequence Number (ID): 387

Length: 49

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..49
 - > note, Synthetic Sequence
- source, 1..49
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cccgaggagtc tcgctgccgc tgcaaccgcc ggcggtcggg ctcttcggg 49

Sequence Number (ID): 388

Length: 46

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..46
 - > note, Synthetic Sequence
- source, 1..46
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctatgccaat gccgggtcatg tggccgggtca gagcgccctg ttcattg 46

Sequence Number (ID): 389

Length: 46

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..46
 - > note, Synthetic Sequence
- source, 1..46
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

catgaacagg gcgctctgac cggccacatg accggcattg gcatag 46

Sequence Number (ID): 390

Length: 88

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..88
 - > note, Synthetic Sequence
- source, 1..88
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgagccagct gggcggcgac agcggcagcg agactcccgg gacctcagag tccgccacac 60
ccgaaagtgg cagctacgcc ctgggtcc 88

Sequence Number (ID): 391

Length: 50

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..50
 - > note, Synthetic Sequence
- source, 1..50
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

aatagggccc tctagatgca tgctcgagtt agcaaccgcc ttggtcggg 50

Sequence Number (ID): 392

Length: 50

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..50
 - > note, Synthetic Sequence
- source, 1..50
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgaagaaagg tctgggcgga tccggcagct acgccctggg tccgtatcag 50

Sequence Number (ID): 393

Length: 50

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..50
 - > note, Synthetic Sequence
- source, 1..50
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgaagaaagg cctgggtgga tccggcagct acgccctggg tccgtatcag 50

Sequence Number (ID): 394

Length: 50

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..50
 - > note, Synthetic Sequence
- source, 1..50
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tcagattagt tgagccgcca gagcaaccgc ctttggtcgg gctcttcggg 50

Sequence Number (ID): 395

Length: 34

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..34
 - > note, Synthetic Sequence
- source, 1..34
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tctggcggct caactaatct gagcgacatc attg 34

Sequence Number (ID): 396

Length: 29

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..29
 - > note, Synthetic Sequence
- source, 1..29
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

cagatccgaa aatggatata caagctccc 29

Sequence Number (ID): 397

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence

- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggcccagact gagcacgtga 20

Sequence Number (ID): 398

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ggccacacta gcgttgctgc 20

Sequence Number (ID): 399

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gccatagatg gtggaccgaa 20

Sequence Number (ID): 400

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccatctatgg ctctcggtg 20

Sequence Number (ID): 401

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccgcagccga gagccataga 20

Sequence Number (ID): 402

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA

> organism, synthetic construct

Residues:

ggaatccctt ctgcagcacc 20

Sequence Number (ID): 403

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ctgccccac agggcagtaa 20

Sequence Number (ID): 404

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

tgcccctccc tccctggccc 20

Sequence Number (ID): 405

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

ccctggccca ggtgaagtg 20

Sequence Number (ID): 406

Length: 21

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..21
 - > note, Synthetic Sequence
- source, 1..21
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtgaaggtgt ggttcagaa c 21

Sequence Number (ID): 407

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

aaagtacaaa cggcagaagc 20

Sequence Number (ID): 408

Length: 21

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..21
 - > note, Synthetic Sequence
- source, 1..21
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

gtggtagcgg aactcactaa g 21

Sequence Number (ID): 409

Length: 20

Molecule Type: DNA

Features Location/Qualifiers:

- misc_feature, 1..20
 - > note, Synthetic Sequence
- source, 1..20
 - > mol_type, other DNA
 - > organism, synthetic construct

Residues:

caccagcct gctctgcctt 20

Sequence Number (ID): 410

Length: 434

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..434

> note, Synthetic Sequence

- source, 1..434

> mol_type, protein

> organism, synthetic construct

Residues:

MLGFVGRVAA APASGALRRL TPSASLPPAQ LLLRAAPTAV HPVRDYAAQD YKDDDDKVDE 60
MTKKFGTLTI HDTEKAAEFG IRIPGEKPFQ CRICMRNFSD SGNLRVHIRT HTGEKPYKCP 120
DCGKSFSQSS SLIRHQRTHT GEKPYECDHC GKSFSQSSHL NVHKRTHTGE KPYRCKYCDR 180
SFSISSNLQR HVRNIHLRSG TPHEVGVTYTL SGTPHEVGVIY TLAIPVKRGA TGETKVFTGN 240
SNSPKSPTKG GCSGSETPGT SESATPESE VEFSEYWMR HALTLAKRAR DEREVPVGAV 300
LVLNNRVIGE GWNRAIGLHD PTAHAEIMAL RQGGLVMQNY RLIDATLYVT FEPCVMCAGA 360
MIHSRIGRVV FGVRNSKRGAGAGSLMNVNLN PGMNHRVEIT EGILADECAA LLCDFYRMMPR 420
QVFNAQKKAQ SSIN 434

Sequence Number (ID): 411

Length: 339

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..339

> note, Synthetic Sequence

- source, 1..339

> mol_type, protein

> organism, synthetic construct

Residues:

MLGFVGRVAA APASGALRRL TPSASLPPAQ LLLRAAPTAV HPVRDYAAQD YKDDDDKVDE 60
MTKKFGTLTI HDTEKAAEFG IRIPGEKPFQ CRICMRNFSD SGNLRVHIRT HTGEKPYKCP 120
DCGKSFSQSS SLIRHQRTHT GEKPYECDHC GKSFSQSSHL NVHKRTHTGE KPYRCKYCDR 180
SFSISSNLQR HVRNIHLRSG TPHEVGVTYTL SGTPHEVGVIY TLAIPVKRGA TGETKVFTGN 240
SNSPKSPTKG GCSGGSTNLS DIIEKETGKQ LVIQESILML PEEVEEVIGN KPESDILVHT 300
AYDESTDENV MLLTSDAPEY KPWALVIQDS NGENKIKML 339

Sequence Number (ID): 412

Length: 419

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..419
 - > note, Synthetic Sequence
- source, 1..419
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MLGFVGRVAA APASGALRRL TPSASLPPAQ LLLRAAPTAV HPVRDYAAQY PYDVPDYAVD 60
EMTKKFGLTL IHDTEKAAEF GIHGVPAAMG GSYALGPYQI SAPQLPAYNG QTVGTFYYVN 120
DAGGLESKVF SSGGPTYPYN YANAGHVEGQ SALFMRDNGI SEGLVFHNNP EGTCGFCVNM 180
TETLLPENAK MTVPVPEGSG TPHEVGVTLS SGTPEHVGVT TLYKCPECVK SFSTKNSLTE 240
HQRTHTEGKP YKCPECVKSF SSKKALTEHQ RTHTEGKPYE CNYCGKTFVS SSSLIRHQRI 300
HTGEKPYRCK YCDRSFSISS NLQRHVRNIH LRSGGSTNLS DIIEKETGKQ LVIQESILML 360
PEEVEEVIGN KPESDILVHT AYDESTDENV MLLTSDAPEY KPWALVIQDS NGENKIKML 419

Sequence Number (ID): 413

Length: 380

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..380
 - > note, Synthetic Sequence
- source, 1..380
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MAPKKKRKVG IHGVPAAMGG SYALGPYQIS APQLPAYNGQ TVGTFYYVND AGGLESKVFS 60
SSGGPTYPNY ANAGHVEGQS ALFMRDNGIS EGLVFHNNPE GTCGFCVNMT ETLLPENAKM 120
TVVPPEGSGT PHEVGVTLS GTPHEVGVT LFQCRICMRK FATSGSLTRH TKIHTGEKPF 180

QCRICMRNFS RSDHLSTHIR THTGEKPFAC DICGRKFATS SNRTKHTKIH THPRAPIPKP 240
FQCRICMRNF SRSDNLSEHI RHTHTGEKPFA CDICGRKFAW HSSLRVHTKI HLRSGGSTNL 300
SDIIEKETGK QLVIQESILM LP EEVEEVIG NK PESDILVH TAYDESTDEN VMLLTSDAPE 360
YKPWALVIQD SNGENKIKML 380

Sequence Number (ID): 414

Length: 396

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..396
 - > note, Synthetic Sequence
- source, 1..396
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MAPKKKRKVG IHGVPAAMAE RPFQCRICMR NFSRSDHLST HIRHTHTGEKP FACDICGRKF 60
ADRSHLARHT KIHTGSQKPF QCRICMRKFA LKQHLNEHTK IHTGEKPFQC RICMRNFSQS 120
GNLARHIRTH TGEKPFACDI CGRKFAHNSS LKDHTKIHLR SGTPHEVG VY TLSGTPHEVG 180
VYT LAIPVKR GATGETKVFT GNSNSPKSPT KGGCSGSETP GTS ESATPES SEVEFSHEYW 240
MRHALTLAKR ARDEREVPVG AVLVLNNRVI GEGWNRAIGL HDPTAHAEIM ALRQGGLVMQ 300
NYRLIDATLY VTFEPCVMCA GAMIH SRIGR VVFGVRNSKR GAAGSLMNVL NYPGMNHRVE 360
ITEGILADEC AALLCDFYRM PRQVFNAQKK AQSSIN 396

Sequence Number (ID): 415

Length: 911

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..911
 - > note, Synthetic Sequence
- source, 1..911
 - > mol_type, protein

> organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETQVRLP PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETQVR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETQVRLP PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETQVR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETQVRLP 600
PVLCQAHGLT PAQVVAIASN GGGKQALETQ QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALA ALLVSGSGSYA 720
LGPYQISAPQ LPAYNGQTVG TFYVNDAGG LESKVFSSGG PTPYPNYANA GHVEGQSALF 780
MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV PEGSGGSTN LSDIEKETG 840
KQLVIQESIL MLPEEVEEVI GNKPESDILV HTAYDESTDE NVMLLTSDAP EYKPWALVIQ 900
DSNGENKIKM L 911

Sequence Number (ID): 416

Length: 833

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..833
 - > note, Synthetic Sequence
- source, 1..833
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120

KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
 VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
 VAIASNNGGK QALETQVRL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
 HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
 LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
 QALETQVRL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
 IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETQVRL 600
 PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
 LETVQRLLPV LCQAHGLTPE QVVAIASNNG GKQALESIVA QLSRPDPA LA ALLVGS AIPV 720
 KRGATGETKV FTGNSNSPKS PTKGGCSGGS TNLSDIIEKE TGKQLVIQES ILMLPEEVEE 780
 VIGNKPESDI LVHTAYDEST DENVMMLTSD APEYKPWALV IQDSNGENKI KML 833

Sequence Number (ID): 417

Length: 1005

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1005
 - > note, Synthetic Sequence
- source, 1..1005
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHS L DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
 TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
 LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAR GGVTAVEAVH 180
 AWRNALTGAP LNLTDPQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
 GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
 VAIASNNGGK QALETQVRL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
 HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
 LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480

QALETQVRL PVLCQAHGLT PDQVVAIASN NGGKQALETQ QRLLPVLCQA HGLTPAQVVA 540
 IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNGG GKQALETQVR LLPVLCQAHG 600
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETQVRL 660
 PVLCQAHGLT PAQVVAIASH DGGKQALETQ QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
 LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETQVR LLPVLCQAHG LTPEQVVAIA 780
 SNGGGKQALE SIVAQLSRPD PALAALLVGS GSYALGPYQI SAPQLPAYNG QTVGTFYYVN 840
 DAGGLESKVF SSGGPTYPN YANAGHVEGQ SALFMRDNGI SEGLVFHNNP EGTGFCVNM 900
 TETLLPENAK MTVVPPEGSG GSTNLSDIIE KETGKQLVIQ ESILMLPEEV EEVIGNKPES 960
 DILVHTAYDE STDENVMLLT SDAPEYKPWA LVIQDSNGEN KIKML 1005

Sequence Number (ID): 418

Length: 927

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..927
 - > note, Synthetic Sequence
- source, 1..927
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSI DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
 TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
 LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAGR GGVTAVEAVH 180
 AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
 GKQALETQVR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
 VAIASNNGGK QALETQVRL PVLCQAHGLT PAQVVAIASN GGGKQALETQ QRLLPVLCQA 360
 HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETQVR 420
 LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
 QALETQVRL PVLCQAHGLT PDQVVAIASN NGGKQALETQ QRLLPVLCQA HGLTPAQVVA 540
 IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNGG GKQALETQVR LLPVLCQAHG 600
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETQVRL 660

PVLCQAHGLT PAQVVAIASH DGGKQALETQ QRLPVLCQA HGLTPAQVVA IASHDGGKQA 720
 LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETQQR LLPVLCQAHG LTPEQVVAIA 780
 SNGGGKQALE SIVAQLSRPD PALAALLVGS AIPVKRGATG ETKVFTGNSN SPKSPTKGGC 840
 SGGSTNLSDI IEKETGKQLV IQESILMLPE EVEEVIGNKP ESDILVHTAY DESTDENVML 900
 LTSDAPEYKP WALVIQDSNG ENKIKML 927

Sequence Number (ID): 419

Length: 988

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..988
 - > note, Synthetic Sequence
- source, 1..988
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
 MDIADLRTLQ YSQQQQEKIK PKVRSTVAQH HEALVGHGFT HAHIVALSQH PAALGTVAVK 120
 YQDMIAALPE ATHEAIVGVG KQWSGARALE ALLTVAGELR GPPLQLDTGQ LLKIAKRGV 180
 TAVEAVHAWR NALTGAPLNL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPQQVV 240
 AIASHDGGKQ ALETQQRLLP VLCQAHGLTP QQVVAIASNG GGKQALETQV RLLPVLCQAH 300
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETQVQAL 360
 LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNIGGKQ 420
 ALETQQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETQV ALLPVLCQAH GLTPEQVVAI 480
 ASHDGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASHDGG KQALETQVQAL LPVLCQAHGL 540
 TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASHDGGKQ ALETQVALLP 600
 VLCQAHGLTP EQVVAIASNN GGKQALETQV RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 660
 ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETQVQAL LPVLCQAHGL TPEQVVAIAS 720
 HDGGKQALET VQALLPVLCQ AHGLTPQQVV AIASNNGGRP ALESIVAQLS RPDPALAALT 780
 NDHLVALACL GGRPALDAVK KGLGGSSGSE TPGTSESATP ESSEVEFSHE YWMRHALTLA 840
 KRARDEREVP VGAVLVLNNR VIGEGWNRAI GLHDPTAHAE IMALRQGGLV MQNYRLIDAT 900

LYVTFEPCVM CAGAMIHSRI GRVVFGRNS KRGAAAGSLMN VLNYPGMNHR VEITEGILAD 960
ECAALLCDFY RMPRQVFNAQ KKAQSSIN 988

Sequence Number (ID): 420

Length: 980

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..980
 - > note, Synthetic Sequence
- source, 1..980
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSI DYKDHDGDYK DHDIDYKDDD DKMDIADLRT 60
LGYSQQQKEK IKPKVRSTVA QHHEALVGHG FTHAHIVALS QHPAALGTVA VKYQDMIAAL 120
PEATHEAIVG VGKQWSGARA LEALLTVAGE LRGPPLQLDT GQLLKIARKG GVTAVEAVHA 180
WRNALTGAPL NLTPEQVVAI ASHDGGKQAL ETVQALLPVL CQAHGLTPQQ VVAIASHDGG 240
KQALETVQRL LPVLCQAHGL TPQQVVAIAS NGGGKQALET VQRLLPVLCQ AHGLTPEQVV 300
AIASNNGGKQ ALETQALLP VLCQAHGLTP EQVVAIASNG GGKQALETVQ ALLPVLCQAH 360
GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNIGG KQALETVQRL 420
LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ 480
ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPEQVVAI 540
ASNNGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL 600
TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ ALETVQRLLP 660
VLCQAHGLTP QQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 720
ETVQRLLPVL CQAHGLTPQQ VVAIASNNGG RPALESIVAQ LSRPDPALAA LTNDHLVALA 780
CLGGRPALDA VKKGLGGSSG SETPGTSESA TPESSEVEFS HEYWMRHALT LAKRARDERE 840
VPVGAVLVLN NRVIGEGWNR AIGLHDPTAH AEIMALRQGG LVMQNYRLID ATLYVTFEPC 900
VMCAGAMIHS RIGRVVFGVR NSKRGAAAGSL MNVLNYPGMN HRVEITEGIL ADECAALLCD 960
FYRMPRQVFN AQKKAQSSIN 980

Sequence Number (ID): 421

Length: 942

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..942
 - > note, Synthetic Sequence
- source, 1..942
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALE ALLVSGSGSYA 720
LGPYQISAPQ LPAYNGQTVG TFYVNDAGG LESKVFSSGG SGSETPGTSE SATPESSEVE 780
FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW NRAIGLHDPT AHAEIMALRQ 840
GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG VRNSKRGAAQ SLMNVLNYPG 900
MNHREITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS IN 942

Sequence Number (ID): 422

Length: 992

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..992
 - > note, Synthetic Sequence
- source, 1..992
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
 GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
 KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
 VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
 VAIASNNGGK QALETQVRLP PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQD 300
 HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETQVR 360
 LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
 QALETQVRLP PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQA HGLTPDQVVA 480
 IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETQVR LLPVLCQDHG 540
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETQVRLP 600
 PVLCQAHGLT PAQVVAIASN GGGKQALETQ QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
 LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALE ALLVGSPTPY 720
 PNYANAGHVE GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG 780
 AIPVKRGATG ETKVFTGNSN SPKSPTKGGC SGSETPGTSE SATPESSEVE FSHEYWMRHA 840
 LTLAKRARDE REVPVGAVLV LNNRVIGEGW NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL 900
 IDATLYVTFE PCVMCAGAMI HSRIGRVVFG VRNSKRGAA SLMNVLNYPG MNHRVEITEG 960
 ILADECAALL CDFYRMPRQV FNAQKKAQSS IN 992

Sequence Number (ID): 423

Length: 1036

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1036
 - > note, Synthetic Sequence
- source, 1..1036

> mol_type, protein
> organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSI DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAGR GGVTAVEAVH 180
AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
VAIASNNGGK QALETVQRLL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
QALETVQRLL PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNNGGK QALETVQRLL 660
PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
SNGGGKQALE SIVAQLSRPD PALAALLVGS GSYALGPYQI SAPQLPAYNG QTVGTFYVYN 840
DAGGLESKVF SSGGSGSETP GTSESATPES SEVEFSHEYW MRHALTLAKR ARDEREVPVG 900
AVLVLNRRVI GEGWNRAIGL HDPTAHAEIM ALRQGGLVMQ NYRLIDATLY VTFEPCVMCA 960
GAMIHSRIGR VVFGVRNSKR GAAGSLMNVL NYPGMNHRVE ITEGILADEC AALLCDFYRM 1020
PRQVFNAQKK AQSSIN 1036

Sequence Number (ID): 424

Length: 1086

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1086
 - > note, Synthetic Sequence
- source, 1..1086
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSI DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAGR GGVTAVEAVH 180
AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
VAIASNNGGK QALETVQRLL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
QALETVQRLL PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETVQRLL 660
PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
SNNGGKQALE SIVAQLSRPD PALAALLVGS PTPYPNYANA GHVEGQSALF MRDNGISEGL 840
VFHNNPEGTC GFCVNMETEL LPENAKMTVV PEGAIPVKR GATGETKVFT GNSNSPKSPT 900
KGGCSGSETP GTSESATPES SEVEFSHEYW MRHALTLAKR ARDEREVPVG AVLVLNNRVI 960
GEGWNRAIGL HDPTAHAEIM ALRQGGLVMQ NYRLIDATLY VTFEPCVMCA GAMIHSRIGR 1020
VVFGVRNSKR GAAGSLMNVL NYPGMNHRVE ITEGILADEC AALLCDFYRM PRQVFNAQKK
1080
AQSSIN 1086

Sequence Number (ID): 425

Length: 952

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..952
 - > note, Synthetic Sequence
- source, 1..952
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETQVRL PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETQVQR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETQVRL PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETQVQR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETQVRL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETQ QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPAAL ALTNDHLVAL 720
ACLGGRPALD AVKKGLLVGS AIPVKRGATG ETKVFTGNSN SPKSPTKGGC SGSETPGTSE 780
SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW NRAIGLHDPT 840
AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG VRNSKRGAA 900
SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS IN 952

Sequence Number (ID): 426

Length: 1047

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1047
 - > note, Synthetic Sequence
- source, 1..1047
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHL DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAR GGVTAVEAVH 180

AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
 GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
 VAIASNNGGK QALETVQRLL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
 HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
 LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
 QALETVQRLL PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
 IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETVQRLL 660
 PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
 LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
 SNGGGKQALE SIVAQLSRPD PALAALTNDH LVALACLGGR PALDAVKKGL GSGSAIPVK 840
 RGATGETKVF TGNSNSPKSP TKGGCSGSET PGTSESATPE SSEVEFSHEY WMRHALTLAK 900
 RARDEREVPV GAVLVNNRV IGEGWNRAIG LHDPTAHAEI MALRQGGLVM QNYRLIDATL 960
 YVTFEPCVMC AGAMIHSRIG RVVFGVRNSK RGAAGSLMNV LNYPGMNHRV EITEGILADE 1020
 CAALLCDFYR MPRQVFNAQK KAQSSIN 1047

Sequence Number (ID): 427

Length: 785

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..785
 - > note, Synthetic Sequence
- source, 1..785
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSPL DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
 GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
 KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
 VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
 VAIASNNGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300

HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
 LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNGGGK 420
 QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
 IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
 PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNGGGKQA 660
 LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPAAL ALTNDHLVAL 720
 ACLGGRPALD AVKKGLGGSG SGSYALGPYQ ISAPQLPAYN GQTVGTFYYV NDAGGLESKV 780
 FSSGG 785

Sequence Number (ID): 428

Length: 835

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..835
 - > note, Synthetic Sequence
- source, 1..835
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSPL DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
 GIRIQDLRTL GYSQQQKEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
 KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
 VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
 VAIASNGGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
 HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
 LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNGGGK 420
 QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
 IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
 PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNGGGKQA 660

LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALA ALTNDHLVAL 720
ACLGGRPALD AVKKGLGGSG SPTYPNYAN AGHVEGQSAL FMRDNGISEG LVFHNNPEGT 780
CGFCVNMTET LLPENAKMTV VPPEGAIPVK RGATGETKVF TGNSNSPKSP TKGGC 835

Sequence Number (ID): 429

Length: 849

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..849
 - > note, Synthetic Sequence
- source, 1..849
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQKEI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTAVV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALA ALTNDHLVAL 720
ACLGGRPALD AVKKGLGGSG SGSYALGPYQ ISAPQLPAYN GQTVGTFYYV NDAGGLESKV 780
FSSGGPTYP NYANAGHVEG QSALFMRDNG ISEGLVFHNN PEGTCGFCVN MTETLLPENA 840
KMTVVPPEG 849

Sequence Number (ID): 430

Length: 854

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..854
 - > note, Synthetic Sequence
- source, 1..854
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSL DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAR GGVTAVEAVH 180
AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
VAIASNNGGK QALETQVRLP PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
QALETQVRLP PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETQVRLP 660
PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
SNNGGKQALE SIVAQLSRPD PALAALLVGS GSYALGPYQI SAPQLPAYNG QTVGTFYYVN 840
DAGGLESKVF SSGG 854

Sequence Number (ID): 431

Length: 904

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..904
 - > note, Synthetic Sequence

- source, 1..904
 > mol_type, protein
 > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSL DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAGR GGVTAVEAVH 180
AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
VAIASNNGGK QALETVQRLL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
QALETVQRLL PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETVQRLL 660
PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
SNGGGKQALE SIVAQLSRPD PALAALLVGS PTPYPNYANA GHVEGQSALF MRDNGISEGL 840
VFHNNPEGTC GFCVNMETEL LPENAKMTVV PEGAIPVKR GATGETKVFT GNSNSPKSPT 900
KGGC 904

Sequence Number (ID): 432

Length: 918

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..918
 > note, Synthetic Sequence
- source, 1..918
 > mol_type, protein
 > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSI DYKDHGDYK DHDIDYKDDD DKGIRIQDLR 60
 TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
 LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAR GGVTAVEAVH 180
 AWRNALTGAP LNLTDPQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
 GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
 VAIASNNGGK QALETVQRLL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
 HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
 LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
 QALETVQRLL PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
 IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETVQRLL 660
 PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
 LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
 SNNGGKQALE SIVAQLSRPD PALAALLVGS GSYALGPYQI SAPQLPAYNG QTVGTFYYVN 840
 DAGGLESKVF SSGGPTYPN YANAGHVEGQ SALFMRDNGI SEGLVFHNNP EGTGFCVNM 900
 TETLLPENAK MTVVPPEG 918

Sequence Number (ID): 433

Length: 1032

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1032
 - > note, Synthetic Sequence
- source, 1..1032
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
 MDIADLRTLG YSQQQQEKIK PKVRSTVAQH HEALVGHGFT HAHIVALSQH PAALGTVAVK 120
 YQDMIAALPE ATHEAIVGVG KQWSGARALE ALLTVAGELR GPPLQLDTGQ LLKIARGGV 180
 TAVEAVHAWR NALTGAPLNL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPQQVV 240

AIASHDGGKQ ALETVQRLLP VLCQAHGLTP QQVVAIASNG GGKQALETVQ RLLPVLCQAH 300
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL 360
 LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNIGGKQ 420
 ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ ALLPVLCQAH GLTPEQVVAI 480
 ASHDGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASHDGG KQALETVQAL LPVLCQAHGL 540
 TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASHDGGKQ ALETVQALLP 600
 VLCQAHGLTP EQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 660
 ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL TPEQVVAIAS 720
 HDGGKQALET VQALLPVLCQ AHGLTPQQVV AIASNNGGRP ALESIVAQLS RPDPALAALT 780
 NDHLVALACL GGRPALDAVK KGLGGSGSYA LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG 840
 LESKVFSSGG SGSETPGTSE SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV 900
 LNNRVIGEGW NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI 960
 HSRIGRVVFG VRNSKRGAA G SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV 1020
 FNAQKKAQSS IN 1032

Sequence Number (ID): 434

Length: 1082

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1082
 - > note, Synthetic Sequence
- source, 1..1082
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
 MDIADLRTL GYSQQQKEIK PKVRSTVAQH HEALVGHGFT HAHIVALSQH PAALGTVAVK 120
 YQDMIAALPE ATHEAIVGVG KQWSGARALE ALLTVAGELR GPPLQLDTGQ LLKIAKRGGV 180
 TAVEAVHAWR NALTGAPLNL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPQQVV 240
 AIASHDGGKQ ALETVQRLLP VLCQAHGLTP QQVVAIASNG GGKQALETVQ RLLPVLCQAH 300
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL 360

LPVLCQAHGL TPEQVVAIAS NGGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNIGGKQ 420
 ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ ALLPVLCQAH GLTPEQVVAI 480
 ASHDGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASHDGG KQALETVQAL LPVLCQAHGL 540
 TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASHDGGKQ ALETVQALLP 600
 VLCQAHGLTP EQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 660
 ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL TPEQVVAIAS 720
 HDGGKQALET VQALLPVLCQ AHGLTPQQVV AIASNNGGRP ALESIVAQLS RPDPALAALT 780
 NDHLVALACL GGRPALDAVK KGLGGSPTPY PNYANAGHVE GQSALFMRDN GISEGLVFHN 840
 NPEGTCGFCV NMTETLLPEN AKMTVVPPEG AIPVKGATG ETKVFTGNSN SPKSPTKGGC 900
 SGSETPGTSE SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW 960
 NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG 1020
 VRNSKRGAAG SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS
 1080

IN 1082

Sequence Number (ID): 435

Length: 1020

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1020
 - > note, Synthetic Sequence
- source, 1..1020
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
 MDIADLRTLQ YSQQQQEKIK PKVRSTVAQH HEALVGHGFT HAHIVALSQH PAALGTVAVK 120
 YQDMIAALPE ATHEAIVGVG KQWSGARALE ALLTVAGELR GPPLQLDTGQ LLKIAKRGV 180
 TAVEAVHAWR NALTGAPLNL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPQQVV 240
 AIASHDGGKQ ALETVQRLLP VLCQAHGLTP QQVVAIASNG GGKQALETVQ RLLPVLCQAH 300
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL 360

LPVLCQAHGL TPEQVVAIAS NGGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNIGGKQ 420
 ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ ALLPVLCQAH GLTPEQVVAI 480
 ASHDGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASHDGG KQALETVQAL LPVLCQAHGL 540
 TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASHDGGKQ ALETVQALLP 600
 VLCQAHGLTP EQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 660
 ETVQRLLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL TPEQVVAIAS 720
 HDGGKQALET VQALLPVLCQ AHGLTPQQVV AIASNNGGRP ALESIVAQLS RPDPALAALT 780
 NDHLVALACL GGRPALDAVK KGLGGSGSAI PVKRGATGET KVFTGNSNSP KSPTKGGCSG 840
 SETPGTSESA TPESSEVEFS HEYWMRHALT LAKRARDERE VPVGAVLVN NRVIGEGWNR 900
 AIGLHDPTAH AEIMALRQGG LVMQNYRLID ATLYVTFEPC VMCAGAMIHS RIGRVVFGVR 960
 NSKRGAGSL MNVLNYPGMN HRVEITEGIL ADECAALLCD FYRMPRQVFN AQKKAQSSIN 1020

Sequence Number (ID): 436

Length: 1024

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1024
 - > note, Synthetic Sequence
- source, 1..1024
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSL DYKDHDGDYK DHDIDYKDDD DKMDIADLRT 60
 LGYSQQQQEK IKPKVRSTVA QHHEALVGHG FTHAHIVALS QHPAALGTVA VKYQDMIAAL 120
 PEATHEAIVG VGKQWSGARA LEALLTVAGE LRGPPLQLDT GQLLKIAKRG GVTAVEAVHA 180
 WRNALTGAPL NLTPEQVVAI ASHDGGKQAL ETVQALLPVL CQAHGLTPQQ VVAIASHDGG 240
 KQALETVQRL LPVLCQAHGL TPQQVVAIAS NGGGKQALET VQRLLPVLCQ AHGLTPEQVV 300
 AIASNNGGKQ ALETVQALLP VLCQAHGLTP EQVVAIASNG GGKQALETVQ ALLPVLCQAH 360
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNIGG KQALETVQRL 420
 LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ 480
 ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPEQVVAI 540

ASNNGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL 600
 TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ ALETVQRLLP 660
 VLCQAHGLTP QQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 720
 ETVQRLLPVL CQAHGLTPQQ VVAIASNGGG RPALESIVAQ LSRPDPALAA LTNDHLVALA 780
 CLGGRPALDA VKKGLGGSGS YALGPYQISA PQLPAYNGQT VGTFYYVNDG GGLESKFSS 840
 GSGSETPGT SESATPESE VEFSEYWMR HALTLAKRAR DEREVPVGAV LVLNNRVIGE 900
 GWNRAIGLHD PTAHAEIMAL RQGGLVMQNY RLIDATLYVT FEPCVMCAGA MIHSRIGRVV 960
 FGVRNSKRGV AGSLMNVLNY PGMNHRVEIT EGILADECAA LLCDFYRMPR QVFNAQKKAQ
 1020
 SSIN 1024

Sequence Number (ID): 437

Length: 1074

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1074
 - > note, Synthetic Sequence
- source, 1..1074
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSI DYKDHDGDYK DHDIDYKDDD DKMDIADLRT 60
 LGYSQQQQEK IKPKVRSTVA QHHEALVGHG FTHAHIVALS QHPAALGTVA VKYQDMIAAL 120
 PEATHEAIVG VGKQWSGARA LEALLTVAGE LRGPPLQLDT GQLLKIAKRG GVTAVEAVHA 180
 WRNALTGAPL NLTPEQVVAI ASHDGGKQAL ETVQALLPVL CQAHGLTPQQ VVAIASHDGG 240
 KQALETVQRL LPVLCQAHGL TPQQVVAIAS NIGGKQALET VQRLLPVLCQ AHGLTPEQVV 300
 AIASNNGGKQ ALETVQALLP VLCQAHGLTP EQVVAIASNG GGKQALETVQ ALLPVLCQAH 360
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNIGG KQALETVQRL 420
 LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ 480
 ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPEQVVAI 540
 ASNNGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL 600

TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ ALETVQRLLP 660
 VLCQAHGLTP QQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 720
 ETVQRLLPVL CQAHGLTPQQ VVAIASNNGG RPALESIVAQ LSRPDPALAA LTNDHLVALA 780
 CLGGRPALDA VKKGLGGSPT PYPNYANAGH VEGQSALFMR DNGISEGLVF HNNPEGTCGF 840
 CVNMTETLLP ENAKMTVVPP EGAIPVKRGA TGETKVFTGN SNSPKSPTKG GCSGSETPGT 900
 SESATPESSE VEFSEHYWMR HALTLAKRAR DEREVPVGAV LVLNNRVIGE GWNRAIGLHD 960
 PTAHAEIMAL RQGGLVMQNY RLIDATLYVT FEPCVMCAGA MIHSRIGRVV FGVRNSKRG 1020
 AGSLMNVLNY PGMNHRVEIT EGILADECAA LLCDFYRMPR QVFNAQKKAQ SSIN 1074

Sequence Number (ID): 438

Length: 1012

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1012
 - > note, Synthetic Sequence
- source, 1..1012
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHS L DYKDHDGDYK DHDIDYKDDD DKMDIADLRT 60
 LGYSQQQQEK IKPKVRSTVA QHHEALVGHG FTHAHIVALS QHPAALGTVA VKYQDMIAAL 120
 PEATHEAIVG VGKQWSGARA LEALLTVAGE LRGPPLQLDT GQLLKIARG GVTAVEAVHA 180
 WRNALTGAPL NLTPEQVVAI ASHDGGKQAL ETVQALLPVL CQAHGLTPQQ VVAIASHDGG 240
 KQALETVQRL LPVLCQAHGL TPQQVVAIAS NNGGKQALET VQRLLPVLCQ AHGLTPEQVV 300
 AIASNNGGKQ ALETVQALLP VLCQAHGLTP EQVVAIASNG GGKQALETVQ ALLPVLCQAH 360
 GLTPEQVVAI ASNIGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNIGG KQALETVQRL 420
 LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ 480
 ALETVQRLLP VLCQAHGLTP EQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPEQVVAI 540
 ASNNGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNNGG KQALETVQAL LPVLCQAHGL 600
 TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ ALETVQRLLP 660
 VLCQAHGLTP QQVVAIASNI GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNNGGKQAL 720

ETVQRLLPVL CQAHGLTPQQ VVAIASNGGG RPALESIVAQ LSRPDPALAA LTNDHLVALA 780
CLGGRPALDA VKKGLGGSGS AIPVKRGATG ETKVFTGNSN SPKSPTKGGC SGSETPGTSE 840
SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW NRAIGLHDPT 900
AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG VRNSKRGAAAG 960
SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS IN 1012

Sequence Number (ID): 439

Length: 1038

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1038
 - > note, Synthetic Sequence
- source, 1..1038
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
GIRIQDLRTL GYSQQQKEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVL CQAHGLTPDQV 240
VAIASNGGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVL CQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
LLPVL CQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVL CQAHGLTPAQV VAIASNGGGK 420
QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVL CQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVL CQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVL CQAHGLTPEQV VAIASNNGGK QALETVQRLL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVL CQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALA ALLVSGSETP 720
GTSESATPES SEVEFSHEYW MRHALTLAKR ARDEREVPVG AVLVLNNRVI GEGWNRAIGL 780
HDPTAHAEIM ALRQGGLVMQ NYRLIDATLY VTFEPCVMCA GAMIHRSRIGR VVFGVRNSKR 840
GAAGSLMNVL NYPGMNHRVE ITEGILADEC AALLCDFYRM PRQVFNAQKK AQSSINLVGS 900

GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLEGKVF SSGGPTPYPN YANAGHVESQ 960
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGVI PVKRGATGET 1020
KVFTGNSNGP KSPTKGGC 1038

Sequence Number (ID): 440

Length: 1038

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1038
 - > note, Synthetic Sequence
- source, 1..1038
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQKEI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPAI ALLVSGSETP 720
GTSESATPES SEVEFSHEYW MRHALTLAKR ARDEREVPVG AVLVLNNRVI GEGWNRAIGL 780
HDPTAHAEIM ALRQGGLVMQ NYRLIDATLY VTFEPCVMCA GAMIHSRIGR VVFGVRNSKR 840
GAAGSLMNVL NYPGMNHRVE ITEGILADEC AALLCDFYRM PRQVFNAQKK AQSSINLVGS 900
GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTPYPN YANAGHVAGQ 960
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVVPPEGAI PVKRGATGET 1020

KVFTGNSNSP KSPTKGGC

1038

Sequence Number (ID): 441

Length: 1038

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..1038
 - > note, Synthetic Sequence
- source, 1..1038
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPAI ALLVSGSETP 720
GTSESATPES SEVEFSHEYW MRHALTLAKR ARDEREVPVG AVLVLNNRVI GEGWNRAIGL 780
HDPTAHAEIM ALRQGGLVMQ NYRLIDATLY VTFEPCVMCA GAMHSRIGR VVFGVRNSKR 840
GAAGSLMNVL NYPGMNHRVE ITEGILADEC AALLCDFYRM PRQVFNAQKK AQSSINLVGS 900
GSYALGPYQI SAPQLPAYNG QTVGTFYYVN DAGGLESKVF SSGGPTYPYN YANAGHVEGQ 960
SALFMRDNGI SEGLVFHNNP EGTCGFCVNM TETLLPENAK MTVPVPEGAI PVAAGATGET 1020
AVFTGNSNSP ASPTAGGC

1038

Sequence Number (ID): 442

Length: 990

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..990
 - > note, Synthetic Sequence
- source, 1..990
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHS L DYKDHDGDYK DHDIDYKDDD DKGIRIQDLR 60
TLGYSQQQQE KIKPKVRSTV AQHHEALVGH GFTHAHIVAL SQHPAALGTV AVKYQDMIAA 120
LPEATHEAIV GVGKQWSGAR ALEALLTVAG ELRGPPLQLD TGQLLKIAGR GGVTAVEAVH 180
AWRNALTGAP LNLTPDQVVA IASNNGGKQA LETVQRLLPV LCQDHGLTPA QVVAIASNIG 240
GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPDQV 300
VAIASNNGGK QALETVQRLL PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA 360
HGLTPEQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASNNG GKQALETVQR 420
LLPVLCQDHG LTPAQVVAIA SNIGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK 480
QALETVQRLL PVLCQAHGLT PDQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPAQVVA 540
IASHDGGKQA LETVQRLLPV LCQDHGLTPD QVVAIASNNG GKQALETVQR LLPVLCQAHG 600
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV VAIASNIGGK QALETVQRLL 660
PVLCQAHGLT PAQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPAQVVA IASHDGGKQA 720
LETVQRLLPV LCQDHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 780
SNGGGKQALE SIVAQLSRPD PALAALLVSG SETPGTSESA TPESSEVEFS HEYWMRHALT 840
LAKRARDERE VPVGAVLVLN NRVIGEGWNR AIGLHDPTAH AEIMALRQGG LVMQNYRLID 900
ATLYVTFEPC VMCAGAMIHS RIGRVVFGVR NSKRGAAAGSL MNVLNYPGMN HRVEITEGIL 960
ADECAALLCD FYRMPRQVFN AQKKAQSSIN 990

Sequence Number (ID): 443

Length: 854

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..854
 - > note, Synthetic Sequence
- source, 1..854
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNGGGK QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETVQR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNGGGK 420
QALETVQRLL PVLCQDHGLT PAQVVAIASN IGGKQALETV QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETVQR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETVQRLL 600
PVLCQAHGLT PAQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALA ALLVGSGSYA 720
LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LEGKVFSSGG PTPYPNYANA GHVESQSALF 780
MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV PPEGVIPVKR GATGETKVFT 840
GNSNGPKSPT KGGC 854

Sequence Number (ID): 444

Length: 854

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..854
 - > note, Synthetic Sequence
- source, 1..854
 - > mol_type, protein

> organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180
VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
VAIASNNGGK QALETQVRLP PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQD 300
HGLTPDQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPD QVVAIASHDG GKQALETQVR 360
LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
QALETQVRLP PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLLPVLCQA HGLTPDQVVA 480
IASNNGGKQA LETVQRLLPV LCQAHGLTPA QVVAIASHDG GKQALETQVR LLPVLCQDHG 540
LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETQVRLP 600
PVLCQAHGLT PAQVVAIASN GGGKQALETQ QRLLPVLCQA HGLTPAQVVA IASNNGGKQA 660
LETVQRLLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPALA ALLVGSGSYA 720
LGPYQISAPQ LPAYNGQTVG TFYVNDAGG LESKVFSSGG PTPYPNYANA GHVAGQSALF 780
MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV PPGAIPVKR GATGETKVFT 840
GNSNSPKSPT KGGC 854

Sequence Number (ID): 445

Length: 854

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..854
 - > note, Synthetic Sequence
- source, 1..854
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MALSRAVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVDPYA GYPYDVDPYA GYPYDVDPYA 60
GIRIQDLRTL GYSQQQQEKI KPKVRSTVAQ HHEALVGHGF THAHIVALSQ HPAALGTVAV 120
KYQDMIAALP EATHEAIVGV GKQWSGARAL EALLTVAGEL RGPPLQLDTG QLLKIAKRGG 180

VTAVEAVHAW RNALTGAPLN LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPDQV 240
 VAIASNNGGK QALETQVQRL PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLPVLCQD 300
 HGLTPDQVVA IASNNGGKQA LETVQRLPV LCQAHGLTPD QVVAIASHDG GKQALETQVQR 360
 LLPVLCQDHG LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPAQV VAIASNNGGK 420
 QALETQVQRL PVLCQDHGLT PAQVVAIASN IGGKQALETQ QRLPVLCQA HGLTPDQVVA 480
 IASNNGGKQA LETVQRLPV LCQAHGLTPA QVVAIASHDG GKQALETQVQR LLPVLCQDHG 540
 LTPDQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNNGGK QALETQVQRL 600
 PVLCQAHGLT PAQVVAIASN GGGKQALETQ QRLPVLCQA HGLTPAQVVA IASNNGGKQA 660
 LETVQRLPV LCQAHGLTPE QVVAIASNGG GKQALESIVA QLSRPDPA LA ALLVSGSYA 720
 LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LESKVFSSGG PTPYPNYANA GHVEGQSALF 780
 MRDNGISEGL VFHNNPEGTC GFCVNMETEL LPENAKMTVV PPEGAIPVAA GATGETAVFT 840
 GNSNSPASPT AGGC 854

Sequence Number (ID): 446

Length: 647

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..647
 - > note, Synthetic Sequence
- source, 1..647
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

DLRTLGYSSQ QQEKIKPKVR STVAQHHEAL VGHGFTHAHI VALSQHPAAL GTVAVKYQDM 60
 IAALPEATHE AIVGVGKQWS GARALEALLT VAGELRGPP LQLDTGQLLKI AKRGGVTAVE 120
 AVHAWRNALT GAPLNLTDPQ VVAIASHDGG KQALETQVQL PVLCQAHGL TPDQVVAIAS 180
 NNGGKQALET VQRLPVLCQ DHGLTPAQVV AIASNIGGKQ ALETQVQRLPVLCQDHGLTP 240
 DQVVAIASNN GGGKQALETQV RLLPVLCQAH GLTPDQVVAI ASHDGGKQAL ETVQRLPV 300
 CQDHGLTPDQ VVAIASHDGG KQALETQVQL PVLCQAHGL TPAQVVAIAS NNGGKQALET 360
 VQRLPVLCQ DHGLTPAQVV AIASNIGGKQ ALETQVQRLPVLCQAHGLTP DQVVAIASNN 420
 GGGKQALETQV RLLPVLCQAH GLTPAQVVAI ASHDGGKQAL ETVQRLPVLCQDHGLTPDQ 480

VVAIASHDGG KQALETQRL LPVLCQAHGL TPEQVVAIAS NNGGKQALET VQRLLPVLCQ 540
AHGLTPAQVV AIASNNGGKQ ALETQVRLLP VLCQAHGLTP AQVVAIASNG GGKQALETQV 600
RLLPVLCQAH GLTPEQVVAI ASNNGGKQAL ESIVAQLSRP DPALAAL 647

Sequence Number (ID): 447

Length: 749

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..749
 - > note, Synthetic Sequence
- source, 1..749
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

DLRTLGYSSQ QQEKIKPKVR STVAQHHEAL VGHGFTHAHI VALSQHPAAL GTVAVKYQDM 60
IAALPEATHE AIVGVGKQWS GARALEALLT VAGELRGPPL QLDTGQLLKI AKRGGVTAVE 120
AVHAWRNALT GAPLNLTDPQ VVAIASNNGG KQALETQRL LPVLCQDHGL TPAQVVAIAS 180
NIGGKQALET VQRLLPVLCQ AHGLTPEQVV AIASNNGGKQ ALETQVRLLP VLCQAHGLTP 240
DQVVAIASNG GGKQALETQV RLLPVLCQAH GLTPAQVVAI ASNNGGKQAL ETVQRLLPVL 300
CQAHGLTPEQ VVAIASNNGG KQALETQRL LPVLCQAHGL TPAQVVAIAS NNGGKQALET 360
VQRLLPVLCQ DHGLTPAQVV AIASNIGGKQ ALETQVRLLP VLCQAHGLTP EQVVAIASNG 420
GGKQALETQV RLLPVLCQAH GLTPDQVVAI ASNNGGKQAL ETVQRLLPVL CQAHGLTPAQ 480
VVAIASHDGG KQALETQRL LPVLCQDHGL TPDQVVAIAS NNGGKQALET VQRLLPVLCQ 540
AHGLTPDQVV AIASHDGGKQ ALETQVRLLP VLCQAHGLTP DQVVAIASNI GGKQALETQV 600
RLLPVLCQAH GLTPAQVVAI ASHDGGKQAL ETVQRLLPVL CQAHGLTPAQ VVAIASHDGG 660
KQALETQRL LPVLCQDHGL TPAQVVAIAS HDGGKQALET VQRLLPVLCQ AHGLTPEQVV 720
AIASNNGGKQ ALESIVAQLS RPDALAAL 749

Sequence Number (ID): 448

Length: 744

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..744
 - > note, Synthetic Sequence
- source, 1..744
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MDIADLRTLGSYSQQQKEIKPKVRSTVAQHHEALVGHGFTHAHIVALSQLPAALGTVAVK 60
YQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIARGGV 120
TAVEAVHAWRNALTGAPLNLTPSEQVVAIASNNGGKQALETVQALLPVLCQAHGLTPQQVV 180
AIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGKQALETVQRLLPVLCQAH 240
GLTPEQVVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASNNGGKQALETVQAL 300
LPVLCQAHGLTPEQVVAIASNNGGKQALETVQALLPVLCQAHGLTPEQVVVAIASNIGGKQ 360
ALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVVA 420
ASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHGGKQALETVQALLPVLCQAHGL 480
TPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVVAIASHGGKQALETVQALLP 540
VLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVVAIASNIGGKQAL 600
ETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVVAIAS 660
HDGGKQALETVQALLPVLCQAHGLTPEQVVVAIASNIGGGRPALESIVAQLSRPDPALAA 720
NDHLVALACLGGRPALDAVKKGLG 744

Sequence Number (ID): 449

Length: 744

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..744
 - > note, Synthetic Sequence
- source, 1..744
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

MDIADLRTLQ YSQQQQEKIK PKVRSTVAQH HEALVGHGFT HAHIVALSQH PAALGTVAVK 60
 YQDMIAALPE ATHEAIVGVG KQWSGARALE ALLTVAGELR GPPLQLDTGQ LLKIAKRGGV 120
 TAVEAVHAWR NALTGAPLNL TPEQVVAIAS HDGGKQALET VQALLPVLCQ AHGLTPQQVV 180
 AIASHDGGKQ ALETVQRLLP VLCQAHGLTP QQVVAIASNG GGKQALETVQ RLLPVLCQAH 240
 GLTPEQVVAI ASNNGGKQAL ETVQALLPVL CQAHGLTPEQ VVAIASNGGG KQALETVQAL 300
 LPVLCQAHGL TPEQVVAIAS NIGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNIGGKQ 360
 ALETVQRLLP VLCQAHGLTP EQVVAIASNN GGKQALETVQ ALLPVLCQAH GLTPEQVVAI 420
 ASNNGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASNIGG KQALETVQRL LPVLCQAHGL 480
 TPEQVVAIAS NNGGKQALET VQALLPVLCQ AHGLTPEQVV AIASNNGGKQ ALETVQALLP 540
 VLCQAHGLTP EQVVAIASNI GGKQALETVQ ALLPVLCQAH GLTPEQVVAI ASNNGGKQAL 600
 ETVQRLLPVL CQAHGLTPQQ VVAIASNIGG KQALETVQRL LPVLCQAHGL TPQQVVAIAS 660
 NNGGKQALET VQRLLPVLCQ AHGLTPQQVV AIASNGGGRP ALESIVAQLS RPDPALAALT 720
 NDHLVALACL GGRPALDAVK KGLG 744

Sequence Number (ID): 450

Length: 142

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..142
 - > note, Synthetic Sequence
- source, 1..142
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRKF ATSGSLTRHT KIHTGEKPFQ CRICMRNFSS SDHLSTHIRT HTGEKPFACD 60
 ICGRKFATSS NRTKHTKIHT HPRAPIPKPF QCRICMRNFS RSDNLSEHIR THTGEKPFAC 120
 DICGRKFAWH SSLRVHTKIH LR 142

Sequence Number (ID): 451

Length: 138

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..138
 - > note, Synthetic Sequence
- source, 1..138
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRNF SRSDHLSTHI RTHTGEKPFA CDICGRKFAD RSHLARHTKI HTGSQKPFQC 60
RICMRKFALK QHLNEHTKIH TGEKPFQCRI CMRNFSQSGN LARHIRTHTG EKPACDICG 120
RKFAHNSSLK DHTKIHLR 138

Sequence Number (ID): 452

Length: 110

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..110
 - > note, Synthetic Sequence
- source, 1..110
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRNF SDSGNLRVHI RTHTGEKPYK CPDCGKSFSQ SSSLIRHQRT HTGEKPYECD 60
HCGKSFSQSS HLNVHKRTHT GEKPYRCKYC DRSFSSSNL QRHVRNIHLR 110

Sequence Number (ID): 453

Length: 110

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..110
 - > note, Synthetic Sequence
- source, 1..110

> mol_type, protein
> organism, synthetic construct

Residues:

YKCECGKSF STKNSLTEHQ RTHTEGKPYK CPECGKSFSS KKALTEHQRT HTGEKPYECN 60
YCGKTFVSSTLIRHQRIHT GEKPYRCKYC DRSFSSSNL QRHVRNIHLR 110

Sequence Number (ID): 454

Length: 46

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..46
 > note, Synthetic Sequence
- source, 1..46
 > mol_type, protein
 > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGG 46

Sequence Number (ID): 455

Length: 96

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..96
 > note, Synthetic Sequence
- source, 1..96
 > mol_type, protein
 > organism, synthetic construct

Residues:

GSPTYPNYA NAGHVEGQSA LFMRDNGISE GLVFHNNPEG TCGFCVNMTE TLLPENAKMT 60
VVPPEGAIPV KRGATGETKV FTGNSNSPKS PTKGGC 96

Sequence Number (ID): 456

Length: 110

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..110
 - > note, Synthetic Sequence
- source, 1..110
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSQSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGGPTPY PNYANAGHVE 60
GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG 110

Sequence Number (ID): 457

Length: 32

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..32
 - > note, Synthetic Sequence
- source, 1..32
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSAIPVKRGA TGETKVFTGN SNSPKSPTKG GC 32

Sequence Number (ID): 458

Length: 166

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..166
 - > note, Synthetic Sequence

- source, 1..166
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SEVEFSHEYW MRHALTLAKR ARDEREVPVG AVLVLNNRVI GEGWNRAIGL HDPTAHAEIM 60
ALRQGGLVMQ NYRLIDATLY VTFEPCVMCA GAMIHSRIGR VVFGVRNSKR GAAGSLMNVL 120
NYPGMNHRVE ITEGILADEC AALLCDFYRM PRQVFNAQKK AQSSIN 166

Sequence Number (ID): 459

Length: 140

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..140
 - > note, Synthetic Sequence
- source, 1..140
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLEGK VFSSGGPTPY PNYANAGHVE 60
SQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG VIPVKRGATG 120
ETKVFTGNSN GPKSPTKGGC 140

Sequence Number (ID): 460

Length: 140

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..140
 - > note, Synthetic Sequence
- source, 1..140
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGGPTPY PNYANAGHVA 60
GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG AIPVKRGATG 120
ETKVFTGNSN SPKSPTKGGC 140

Sequence Number (ID): 461

Length: 140

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..140
 - > note, Synthetic Sequence
- source, 1..140
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGGPTPY PNYANAGHVE 60
GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG AIPVAAGATG 120
ETAVFTGNSN SPASPTAGGC 140

Sequence Number (ID): 462

Length: 83

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..83
 - > note, Synthetic Sequence
- source, 1..83
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

TNLSDIIEKE TGKQLVIQES ILMLPEEVVEE VIGNKPESDI LVHTAYDEST DENVMMLTSD 60
APEYKPWALV IQDSNGENKI KML 83

Sequence Number (ID): 463

Length: 324

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..324
 - > note, Synthetic Sequence
- source, 1..324
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGSETPGTSE SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW 60
NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG 120
VRNSKRGAA G SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS 180
INLVGSGSYA LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LEGKVFSSGG PTPYPNYANA 240
GHVESQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV PPEGVIPVKR 300
GATGETKVFT GNSNGPKSPT KGGC 324

Sequence Number (ID): 464

Length: 324

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..324
 - > note, Synthetic Sequence
- source, 1..324
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGSETPGTSE SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW 60
NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG 120
VRNSKRGAA G SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS 180

INLVGSGSYA LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LESKVFSSGG PTPYPNYANA 240
GHVAGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV PPEGAI PVKR 300
GATGETKVFT GNSNSPKSPT KGGC 324

Sequence Number (ID): 465

Length: 324

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..324
 - > note, Synthetic Sequence
- source, 1..324
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGSETPGTSE SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPGAVLV LNNRVIGEGW 60
NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG 120
VRNSKRGAA G SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS 180
INLVGSGSYA LGPYQISAPQ LPAYNGQTVG TFYYVNDAGG LESKVFSSGG PTPYPNYANA 240
GHVEGQSALF MRDNGISEGL VFHNNPEGTC GFCVNMETL LPENAKMTVV PPEGAI PVAA 300
GATGETAVFT GNSNSPASPT AGGC 324

Sequence Number (ID): 466

Length: 182

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..182
 - > note, Synthetic Sequence
- source, 1..182
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGSETPGTSE SATPESSEVE FSHEYWMRHA LTLAKRARDE REVPVGAVLV LNNRVIGEGW 60
NRAIGLHDPT AHAEIMALRQ GGLVMQNYRL IDATLYVTFE PCVMCAGAMI HSRIGRVVFG 120
VRNSKRGAAAG SLMNVLNYPG MNHRVEITEG ILADECAALL CDFYRMPRQV FNAQKKAQSS 180
IN 182

Sequence Number (ID): 467

Length: 140

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..140
 - > note, Synthetic Sequence
- source, 1..140
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLEGK VFSSGGPTPY PNYANAGHVE 60
SQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG VIPVKGATG 120
ETKVFTGNSN GPKSPTKGGC 140

Sequence Number (ID): 468

Length: 140

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..140
 - > note, Synthetic Sequence
- source, 1..140
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGGPTPY PNYANAGHVA 60
GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG AIPVKGATG 120

ETKVFTGNSN SPKSPTKGGC

140

Sequence Number (ID): 469

Length: 140

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..140
 - > note, Synthetic Sequence
- source, 1..140
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSGSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGGPTPY PNYANAGHVE 60
GQSALFMRDN GISEGLVFHN NPEGTCGFCV NMTETLLPEN AKMTVVPPEG AIPVAAGATG 120
ETAVFTGNSN SPASPTAGGC 140

Sequence Number (ID): 470

Length: 214

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..214
 - > note, Synthetic Sequence
- source, 1..214
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSAIPVKRGA TGETKVFTGN SNSPKSPTKG GCSGSETPGT SESATPESSSE VEFSEYWMR 60
HALTLAKRAR DEREVPVGAV LVLNNRVIGE GWNRAIGLHD PTAHAEIMAL RQGGLVMQNY 120
RLIDATLYVT FEPCVMCAGA MIHSRIGRVV FGVRNSKRGA AGSLMNVNLNY PGMNHRVEIT 180
EGILADECAA LLCDFYRMMPR QVFNAQKKAQ SSIN 214

Sequence Number (ID): 471

Length: 228

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..228
 - > note, Synthetic Sequence
- source, 1..228
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSQSYALGPY QISAPQLPAY NGQTVGTFYY VNDAGGLESK VFSSGGSGSE TPGTSESATP 60
ESSEVEFSHE YWMRHALTLA KRARDEREVP VGAVLVNNR VIGEGWNRAI GLHDPTAHAE 120
IMALRQGGLV MQNYRLIDAT LYVTFEPCVM CAGAMIHSRI GRVVFGRNS KRGAAGSLMN 180
VLNYPGMNHR VEITEGILAD ECAALLCDFY RMPRQVFNAQ KKAQSSIN 228

Sequence Number (ID): 472

Length: 278

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..278
 - > note, Synthetic Sequence
- source, 1..278
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GSPTYPNYA NAGHVEGQSA LFMRDNGISE GLVFHNNPEG TCGFCVNMTE TLLPENAKMT 60
VVPPEGAIPV KRGATGETKV FTGNSNSPKS PTKGGCSGSE TPGTSESATP ESSEVEFSHE 120
YWMRHALTLA KRARDEREVP VGAVLVNNR VIGEGWNRAI GLHDPTAHAE IMALRQGGLV 180
MQNYRLIDAT LYVTFEPCVM CAGAMIHSRI GRVVFGRNS KRGAAGSLMN VLNYPGMNHR 240
VEITEGILAD ECAALLCDFY RMPRQVFNAQ KKAQSSIN 278

Sequence Number (ID): 473

Length: 8

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..8
 - > note, Synthetic Sequence
- source, 1..8
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGGGLGST 8

Sequence Number (ID): 474

Length: 16

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..16
 - > note, Synthetic Sequence
- source, 1..16
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGSETPGTSE SATPES 16

Sequence Number (ID): 475

Length: 32

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..32
 - > note, Synthetic Sequence
- source, 1..32

> mol_type, protein
> organism, synthetic construct

Residues:

SGGSSGGSSG SETPGTSESA TPESGGSSG GS 32

Sequence Number (ID): 476

Length: 60

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..60
 > note, Synthetic Sequence
- source, 1..60
 > mol_type, protein
 > organism, synthetic construct

Residues:

MALSRVCGT SRQLAPVLGY LGSRQKHSLP DYPYDVPDYA GYPYDVPDYA GYPYDVPDYA 60

Sequence Number (ID): 477

Length: 52

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..52
 > note, Synthetic Sequence
- source, 1..52
 > mol_type, protein
 > organism, synthetic construct

Residues:

MASVLTPLLL RGLTGSARRL PVPRAKIHSL DYKDHDGDYK DHDIDYKDDD DK 52

Sequence Number (ID): 478

Length: 7

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..7
 - > note, Synthetic Sequence
- source, 1..7
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

PKKKRKV 7

Sequence Number (ID): 479

Length: 5

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..5
 - > note, Synthetic Sequence
- source, 1..5
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

TGEKP 5

Sequence Number (ID): 480

Length: 4

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..4
 - > note, Synthetic Sequence
- source, 1..4
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

SGGS 4

Sequence Number (ID): 481

Length: 83

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..83
 - > note, Synthetic Sequence
- source, 1..83
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

TNLSDIIEKE TKGQLVIQES ILMPLPEEVVEE VIGNKPESDI LVHTAYDEST DENVMLLTSD 60
APEYKPWALV IQDSNGENKI KML 83

Sequence Number (ID): 482

Length: 123

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..123
 - > note, Synthetic Sequence
- source, 1..123
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSQSGDLR RHIRTHTGEK PFACDICGRK FARSDNLSVH 60
TKIHGTSQKP FQCRICMRNF SQKINLQVHI RTHHTGEKPFA CDICGRKFAR SDVLSEHTKI 120
HLR 123

Sequence Number (ID): 483

Length: 123

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..123
 - > note, Synthetic Sequence
- source, 1..123
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSQSNLR AHIRHTGEEK PFACDICGRK FATSSNRKTH 60
TKIHGTSQKP FQCRICMRNF SLQQTLDHI RHTGEEKPFA CDICGRKFAQ SGNLARHTKI 120
HLR 123

Sequence Number (ID): 484

Length: 142

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..142
 - > note, Synthetic Sequence
- source, 1..142
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRKF ATSGSLTRHT KIHTGEEKPFQ CRICMRNFSR SDHLSTHIRT HTGEEKPFACD 60
ICGRKFATSS NRTKHTKIHT HPRAPIPKPF QCRICMRNFS RSDNLSEHIR THTGEEKPFAC 120
DICGRKFAWH SSLRVHTKIH LR 142

Sequence Number (ID): 485

Length: 151

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..151
 - > note, Synthetic Sequence
- source, 1..151
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSRSDHLS THIRHTGEK PFACDICGRK FADRSHLARH 60
 TKIHTGSQKP FQCRICMRKF ALKQHLNEHT KIHTGEKPFQ CRICMRNFSQ SGNLARHIRT 120
 HTGEKPFACD ICGRKFAHNS SLKDHTKIHL R 151

Sequence Number (ID): 486

Length: 118

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..118
 - > note, Synthetic Sequence
- source, 1..118
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRIPGEKPY SCGICGKSFS DSSAKRRHCI LHTGEKPYTC SDCGKAFRDK SCLNRHRRTH 60
 TGEKPYKCME CGKAFNRRSH LTRHQRIHTG EKPYESNYCG KTFVSSTLI RHQRIHLR 118

Sequence Number (ID): 487

Length: 117

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..117
 - > note, Synthetic Sequence
- source, 1..117
 - > mol_type, protein

> organism, synthetic construct

Residues:

GIRERPYPACP VESCDRRFST SGSLVRHIRI HTGQKPFQCR ICMRNFSRSD ELTRHIRTHT 60

GEKPFACDIC GRKFARSDHL THTKIHTGE KPFQCRICMR KFAQSSNLVR HTKIHLR 117

Sequence Number (ID): 488

Length: 117

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..117

> note, Synthetic Sequence

- source, 1..117

> mol_type, protein

> organism, synthetic construct

Residues:

GIRERPYPACP VESCDRRFSD PGHLVRHIRI HTGQKPFQCR ICMRNFSRSD ELTRHIRTHT 60

GEKPFACDIC GRKFARSDHL THTKIHTGE KPFQCRICMR KFARSDKLVR HTKIHLR 117

Sequence Number (ID): 489

Length: 122

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..122

> note, Synthetic Sequence

- source, 1..122

> mol_type, protein

> organism, synthetic construct

Residues:

GIRIPGEKPY ECNYCGKTFS VSSTLIRHQR IHTGEKPYHC DWDGCGWKFA RSEDLTRHYR 60

KHTGEKPFEC KDCGKAFIQK SNLIRHQRTHT TGEKPYHCDW DGCGWKFARS DELTRHYRKH 120

LR

122

Sequence Number (ID): 490

Length: 117

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..117
 - > note, Synthetic Sequence
- source, 1..117
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRERPACPV VESCDRRFSD CRDLARHIRI HTGQKPFQCR ICMRNFSRSD ELTRHIRTHT 60
GEKPFACDIC GRKFARSDHL TTHTKIHTGE KPFQCRICMR KFARSDKLVR HTKIHLR 117

Sequence Number (ID): 491

Length: 118

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..118
 - > note, Synthetic Sequence
- source, 1..118
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRIPGEKPF ECKDCGKAFI QKSNLIRHQR THTGEKPYRC EECGKAFRWP SNLTRHKRIH 60
TGEKPYRCEE CGKAFRWPSN LTRHKRIHTG EKPYSCGICG KSFSDDSAKR RHCILHLR 118

Sequence Number (ID): 492

Length: 117

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..117
 - > note, Synthetic Sequence
- source, 1..117
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRERPYPACP VESCDRRFSD CRDLARHIRI HTGQKPFQCR ICMRNFSRSD ELTRHIRTHT 60
 GEKPFACDIC GRKFARSDHL TTHTKIHTGE KPFQCRICMR KFARSDKLVR HTKIHLR 117

Sequence Number (ID): 493

Length: 120

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..120
 - > note, Synthetic Sequence
- source, 1..120
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRIPGEKPY TCSDCGKAFR DKSLNRHRR THTGEKPYKC GQCGKFYSQV SHLTRHQKIH 60
 TGEKPFECKD CGKAFIQKSN LIRHQRTHTG EKPYPHCDWDG CGWKFARSDE LTRHYRKHLR 120

Sequence Number (ID): 494

Length: 117

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..117
 - > note, Synthetic Sequence
- source, 1..117
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRERPYACP VESCDRRFSR SDKLVRHIRI HTGQKPFQCR ICMRNFSRSD ELTRHIRTHT 60
GEKPFACDIC GRKFARSDHL TTHTKIHTGE KPFQCRICMR KFARSDKLVR HTKIHLR 117

Sequence Number (ID): 495

Length: 118

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..118
 - > note, Synthetic Sequence
- source, 1..118
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRIPGEKPY TCSDCGKA FR DKSCLNRHRR THTGEKPYEC NYCGKTFSVS STLIRHQRIH 60
TGEKPYTCSD CGKA FRDKSC LNRHRRTHTG EKPYTCSDCG KA FRDKSCLN RHRRTHLR 118

Sequence Number (ID): 496

Length: 117

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..117
 - > note, Synthetic Sequence
- source, 1..117
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRERPYACP VESCDRRFSR SDKLVRHIRI HTGQKPFQCR ICMRNFSRSD ELTRHIRTHT 60
GEKPFACDIC GRKFARSDHL TTHTKIHTGE KPFQCRICMR KFARSDKLVR HTKIHLR 117

Sequence Number (ID): 497

Length: 118

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..118
 - > note, Synthetic Sequence
- source, 1..118
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIRIPGEKPY ECNYCGKTFS VSSTLIRHQR IHTGEKPYTC SDCGKAFRDK SCLNRHRRTH 60
TGEKPYTCSD CGKAFRDKSC LNRHRRHTGT EKPYHCDWDG CGWKFARSDE LTRHYRKH 118

Sequence Number (ID): 498

Length: 122

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..122
 - > note, Synthetic Sequence
- source, 1..122
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSTSGHLV RHIRTHTGEK PFACDICGRK FATSGHLVRH 60
TKIHTGEKPF QCRICMRNFS TSGELVRHIR THTGEKPFAC DICGRKFAQS SNLVRHTKIH 120
LR 122

Sequence Number (ID): 499

Length: 123

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..123

> note, Synthetic Sequence

- source, 1..123

> mol_type, protein

> organism, synthetic construct

Residues:

GIHGVPAAMA ERPFQCRICM RNFSDRSNLS RHIRTHTGEK PFACDICGRK FAISSNLNSH 60
TKIHTGSQKP FQCRICMRNF SRSDNLARHI RHTHTGEKPFA CDICGRKFAT SGNLTRHTKI 120
HLR 123

Sequence Number (ID): 500

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

> note, Synthetic Sequence

- source, 1..23

> mol_type, protein

> organism, synthetic construct

Residues:

FQCRICMRNF SDSGNLRVHI RTH 23

Sequence Number (ID): 501

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

> note, Synthetic Sequence

- source, 1..23

> mol_type, protein

> organism, synthetic construct

Residues:

YKCPECGKSF STKNSLTEHQ RTH 23

Sequence Number (ID): 502

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 503

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECDHCGKSF SQSSHLNVHK RTH 23

Sequence Number (ID): 504

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

- > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECHDCGKSF RQSTHLTQHR RIH 23

Sequence Number (ID): 505

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPDCGKSF SQSSSLIRHQ RTH 23

Sequence Number (ID): 506

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SDPGHLVRHQ RTH 23

Sequence Number (ID): 507

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YGCHLCGKAF SKSSNLRRHE MIH 23

Sequence Number (ID): 508

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SDPGHLVRHQ RTH 23

Sequence Number (ID): 509

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23

- > mol_type, protein
- > organism, synthetic construct

Residues:

YKCPECGKSF SDPGHLVRHQ RTH 23

Sequence Number (ID): 510

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FHCGYCEKSF SVKDYLTKHI RTH 23

Sequence Number (ID): 511

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FHCGYCEKSF SVKDYLTKHI RTH 23

Sequence Number (ID): 512

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FHCGYCEKSF SVKDYLTKHI RTH 23

Sequence Number (ID): 513

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FACPECPKRF MRSDNLTQHI KTH 23

Sequence Number (ID): 514

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECHDCGKSF RQSTHLTQHR RIH 23

Sequence Number (ID): 515

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCEECGKAF RWPSNLTRHK RIH 23

Sequence Number (ID): 516

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FECKDCGKAF IQKSNLIRHQ RTH 23

Sequence Number (ID): 517

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YTCSYCGKSF TQSNLTKQHT RIH 23

Sequence Number (ID): 518

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPDCGKSF SQSSSLIRHQ RTH 23

Sequence Number (ID): 519

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SSKKALTEHQ RTH 23

Sequence Number (ID): 520

Length: 25

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..25
 - > note, Synthetic Sequence
- source, 1..25
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YHCDWDGCGW KFARSDLTR HYRKH 25

Sequence Number (ID): 521

Length: 25

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..25
 - > note, Synthetic Sequence
- source, 1..25
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YHCDWDGCGW KFARSDLTR HYRKH 25

Sequence Number (ID): 522

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence

- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YSCGICGKSF SDSSAKRRHC ILH 23

Sequence Number (ID): 523

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCGQCGKFY SQVSHLTRHQ KIH 23

Sequence Number (ID): 524

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SISSNLQRHV RNIH 24

Sequence Number (ID): 525

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCKTCQRKF SRSDHLKTHT RTH 23

Sequence Number (ID): 526

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 527

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein

> organism, synthetic construct

Residues:

FHCGYCEKSF SVKDYLTKEI RTH 23

Sequence Number (ID): 528

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

> note, Synthetic Sequence

- source, 1..23

> mol_type, protein

> organism, synthetic construct

Residues:

YECVQCGKGF TQSSNLITHQ RVH 23

Sequence Number (ID): 529

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

> note, Synthetic Sequence

- source, 1..23

> mol_type, protein

> organism, synthetic construct

Residues:

YKCECGKSF STHLDLIRHQ RTH 23

Sequence Number (ID): 530

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECDHCGKSF SQSSHLNVHK RTH 23

Sequence Number (ID): 531

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECNYCGKTF SVSSTLIRHQ RIH 23

Sequence Number (ID): 532

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECHDCGKSF RQSTHLTQHR RIH 23

Sequence Number (ID): 533

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 534

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FHCGYCEKSF SVKDYLTKHI RTH 23

Sequence Number (ID): 535

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

- > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCDECGKNF TQSSNLIVHK RIH 23

Sequence Number (ID): 536

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECDHCGKSF SQSSHLNVHK RTH 23

Sequence Number (ID): 537

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECNYCGKTF SVSSTLIRHQ RIH 23

Sequence Number (ID): 538

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 539

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPDCGKSF SQSSSLIRHQ RTH 23

Sequence Number (ID): 540

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23

- > mol_type, protein
- > organism, synthetic construct

Residues:

YECHDCGKSF RQSTHLTQHR RIH 23

Sequence Number (ID): 541

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPDCGKSF SQSSSLIRHQ RTH 23

Sequence Number (ID): 542

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SISSNLQRHV RNIH 24

Sequence Number (ID): 543

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCGQCGKFY SQVSHLTRHQ KIH 23

Sequence Number (ID): 544

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 545

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SSPADLTRHQ RTH 23

Sequence Number (ID): 546

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YTCSYCGKSF TQSNTLKQHT RIH 23

Sequence Number (ID): 547

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SSKKALTEHQ RTH 23

Sequence Number (ID): 548

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRNF SDSGNLRVHI RTH 23

Sequence Number (ID): 549

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECDHCGKAF SVSSNLNVHR RIH 23

Sequence Number (ID): 550

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCGQCGKFY SQVSHLTRHQ KIH 23

Sequence Number (ID): 551

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YGCHLCGKAF SKSSNLRRHE MIH 23

Sequence Number (ID): 552

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YTCSDCGKAF RDKSCLNRHR RTH 23

Sequence Number (ID): 553

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence

- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SDPGHLVRHQ RTH 23

Sequence Number (ID): 554

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SISSNLQRHV RNIH 24

Sequence Number (ID): 555

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SISSNLQRHV RNIH 24

Sequence Number (ID): 556

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SISSNLQRHV RNIH 24

Sequence Number (ID): 557

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCGQCGKFY SQVSHLTRHQ KIH 23

Sequence Number (ID): 558

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein

> organism, synthetic construct

Residues:

YKCPDCGKSF SQSSSLIRHQ RTH 23

Sequence Number (ID): 559

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

> note, Synthetic Sequence

- source, 1..23

> mol_type, protein

> organism, synthetic construct

Residues:

YECDHCGKSF SQSSHLNVHK RTH 23

Sequence Number (ID): 560

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

> note, Synthetic Sequence

- source, 1..23

> mol_type, protein

> organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 561

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 562

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SDSSNLQRHV RNIH 24

Sequence Number (ID): 563

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRNF SDGSLRVHI RTH 23

Sequence Number (ID): 564

Length: 24

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..24
 - > note, Synthetic Sequence
- source, 1..24
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YRCKYCDRSF SISSNLQRHV RNIH 24

Sequence Number (ID): 565

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

FQCRICMRNF SDGSLRVHI RTH 23

Sequence Number (ID): 566

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23

- > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECDHCGKSF SQSSHLNVHK RTH 23

Sequence Number (ID): 567

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YECDHCGKAF SVSSNLNVHR RIH 23

Sequence Number (ID): 568

Length: 25

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..25
 - > note, Synthetic Sequence
- source, 1..25
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YHCDWDGCGW KFARSDELTR HYRKH 25

Sequence Number (ID): 569

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YKCPECGKSF SREDNLHTHQ RTH 23

Sequence Number (ID): 570

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23
 - > mol_type, protein
 - > organism, synthetic construct

Residues:

YTCSYCGKSF TQSNLTKQHT RIH 23

Sequence Number (ID): 571

Length: 23

Molecule Type: AA

Features Location/Qualifiers:

- REGION, 1..23
 - > note, Synthetic Sequence
- source, 1..23

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> mol_type, protein
> organism, synthetic construct
```

Residues:

YECDHCGKSF SQSSHLNVHK RTH

23

END