

Seq list TQD (GB)  
SEQUENCE LISTING

<110> ANGANY GENETICS

<120> Viral-like particles and uses thereof

<130> BFF160322

<160> 35

<170> PatentIn version 3.5

<210> 1

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA encoding Der p2 natural form

<400> 1

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tctagaggt  | ccatgaagac | caacctgttc | ttgttcctga | tcttcagcct | gctgctgagc  | 60  |
| ctgtcatctg | ctgatcaagt | ggatgtgaag | gattgcgcta | accacgagat | caagaagggtg | 120 |
| ttggttcctg | gttgccatgg | ttctgagcct | tgcattattc | acaggggtaa | gcctttccag  | 180 |
| cttgaggctg | ttttcgaggc | taaccagaat | accaagaccg | ctaagattga | gatcaaggct  | 240 |
| agcatcgatg | gtctggaagt | tgatgtgcct | ggatcgcgac | ctaacgcttg | ccactatatg  | 300 |
| aagtgccctc | ttgtgaaggg | tcagcagtac | gatatcaagt | acacctggaa | cgtgccaaag  | 360 |
| atcgctccta | agtctgagaa | tgtggtggtg | accgttaagg | tgatgggtga | tgatgggtgtt | 420 |
| ctggcttgcg | ctattgctac | ccatgctaag | attagggatc | atcaccacca | ccatcacgat  | 480 |
| tacaaggacg | atgatgataa | agtcgctagg | taagtcgac  |            |             | 519 |

<210> 2

<211> 166

<212> PRT

<213> Dermatophagoides pteronyssinus

<400> 2

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Asn | Leu | Phe | Leu | Phe | Leu | Ile | Phe | Ser | Leu | Leu | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Ala | Asp | Gln | Val | Asp | Val | Lys | Asp | Cys | Ala | Asn | His | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Lys | Val | Leu | Val | Pro | Gly | Cys | His | Gly | Ser | Glu | Pro | Cys | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | His | Arg | Gly | Lys | Pro | Phe | Gln | Leu | Glu | Ala | Val | Phe | Glu | Ala | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asn | Thr | Lys | Thr | Ala | Lys | Ile | Glu | Ile | Lys | Ala | Ser | Ile | Asp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Glu | Val | Asp | Val | Pro | Gly | Ile | Asp | Pro | Asn | Ala | Cys | His | Tyr | Met |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

## Seq list TQD (GB)

85

90

95

Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp  
 100 105 110

Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val  
 115 120 125

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
 130 135 140

Ala Lys Ile Arg Asp His His His His His His Asp Tyr Lys Asp Asp  
 145 150 155 160

Asp Asp Lys Val Pro Arg  
 165

<210> 3  
 <211> 695  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> cDNA according to invention B

<400> 3  
 tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
 ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaagggtg 120  
 ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 180  
 cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct 240  
 agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg 300  
 aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag 360  
 atcgctccta agtctgagaa tgtggtggtg accgttaagg tgatgggtga tgatggtggt 420  
 ctggcttgcg ctattgctac ccatgctaag attagggatg gtggtggttc tgggtggtgga 480  
 tctcttaagc agattgagga taagatcgaa gagatcctga gcaagatcta ccacatcgag 540  
 aacgagatcg ctaggatcaa gaagctgac ggagaatctg ctgctggtgg tggtagttac 600  
 cagatcctgt ctatctacag caccgtggct tcatctcttg ctctggctat tatgatggct 660  
 ggtctgtctc tgtggatgtg ctctaacggt tctct 695

<210> 4  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> protein according to invention B

<400> 4

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
 Page 2

| 1   | 5   | Seq list TQD (GB) | 10         | 15                                                                 |
|-----|-----|-------------------|------------|--------------------------------------------------------------------|
| Leu | Ser | Ser               | Ala<br>20  | Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu<br>25 30           |
| Ile | Lys | Lys               | Val<br>35  | Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile<br>40 45           |
| Ile | His | Arg               | Gly<br>50  | Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn<br>55 60           |
| Gln | Asn | Thr               | Lys        | Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly<br>65 70 75 80     |
| Leu | Glu | Val               | Asp        | Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met<br>85 90 95        |
| Lys | Cys | Pro               | Leu<br>100 | Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp<br>105 110         |
| Asn | Val | Pro               | Lys        | Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val<br>115 120 125     |
| Lys | Val | Met               | Gly        | Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His<br>130 135 140     |
| Ala | Lys | Ile               | Arg        | Asp Gly Gly Gly Ser Gly Gly Gly Ser Leu Lys Gln<br>145 150 155 160 |
| Ile | Glu | Asp               | Lys        | Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu<br>165 170 175     |
| Asn | Glu | Ile               | Ala        | Arg Ile Lys Lys Leu Ile Gly Glu Ser Ala Ala Gly<br>180 185 190     |
| Gly | Gly | Ser               | Tyr        | Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser<br>195 200 205     |
| Leu | Ala | Leu               | Ala        | Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser<br>210 215 220     |
| Asn | Gly | Ser               | Leu        | Gln Cys Arg Ile Cys Ile<br>225 230                                 |

<210> 5  
 <211> 726  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> cDNA according to invention C

<400> 5

## Seq list TQD (GB)

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc  | 60  |
| ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaagggtg | 120 |
| ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag  | 180 |
| cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct  | 240 |
| agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg  | 300 |
| aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag  | 360 |
| atcgctccta agtctgagaa tgtggtggtg accgttaagg tgatgggtga tgatggtgtt  | 420 |
| ctggcttgcg ctattgctac ccatgctaag attagggatg gtggtggttc tgggtggtga  | 480 |
| tctaggatga agcagatcga ggataagctg gaagagatcc tgagcaagct gtaccacatt  | 540 |
| gagaacgagc tggctaggat caagaagctg cttggagaaa ggggtggtgg tagttaccag  | 600 |
| atcctgtcca tctactctac cgtggcttct tctcttgctc tggctatcat gatggctggt  | 660 |
| ctgtctcttt ggatgtgcag caacggttct cttcagtgca ggatctgcat ctaaactagt  | 720 |
| gtcgac                                                             | 726 |

&lt;210&gt; 6

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Protein according to invention C

&lt;400&gt; 6

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Asn | Leu | Phe | Leu | Phe | Leu | Ile | Phe | Ser | Leu | Leu | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Ala | Asp | Gln | Val | Asp | Val | Lys | Asp | Cys | Ala | Asn | His | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Lys | Val | Leu | Val | Pro | Gly | Cys | His | Gly | Ser | Glu | Pro | Cys | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | His | Arg | Gly | Lys | Pro | Phe | Gln | Leu | Glu | Ala | Val | Phe | Glu | Ala | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asn | Thr | Lys | Thr | Ala | Lys | Ile | Glu | Ile | Lys | Ala | Ser | Ile | Asp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Glu | Val | Asp | Val | Pro | Gly | Ile | Asp | Pro | Asn | Ala | Cys | His | Tyr | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Cys | Pro | Leu | Val | Lys | Gly | Gln | Gln | Tyr | Asp | Ile | Lys | Tyr | Thr | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Pro | Lys | Ile | Ala | Pro | Lys | Ser | Glu | Asn | Val | Val | Val | Thr | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

# Seq list TQD (GB)

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
130 135 140

Ala Lys Ile Arg Asp Gly Gly Gly Ser Gly Gly Gly Ser Arg Met Lys  
145 150 155 160

Gln Ile Glu Asp Lys Leu Glu Glu Ile Leu Ser Lys Leu Tyr His Ile  
165 170 175

Glu Asn Glu Leu Ala Arg Ile Lys Lys Leu Leu Gly Glu Arg Gly Gly  
180 185 190

Gly Ser Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu  
195 200 205

Ala Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn  
210 215 220

Gly Ser Leu Gln Cys Arg Ile Cys Ile  
225 230

<210> 7  
<211> 723  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> cDNA according to invention D

<400> 7  
tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaaggct 120  
ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 180  
cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct 240  
agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg 300  
aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag 360  
atcgctccta agtctgagaa tgtggtggtg accgttaagg tgatgggtga tgatggtggt 420  
ctggcttgcg ctattgctac ccatgctaag attagggatg gtggtggttc tgggtggtga 480  
tctgtgaagc agcttgctga tgctgttgag gaactggctt ctgctaacta ccaccttgct 540  
aacgctgttg ctaggttggc taaggctggt ggtgaaaggg gtggtggttag ttaccagatc 600  
ctgtccatct actctaccgt ggcttcttct cttgctctgg ctatcatgat ggctggtctg 660  
tctctttgga tgtgcagcaa cggttctctt cagtgcagga tctgcatcta aactagtgtc 720  
gac 723

<210> 8  
<211> 232  
<212> PRT

## Seq list TQD (GB)

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Protein according to invention D

&lt;400&gt; 8

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu  
20 25 30

Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile  
35 40 45

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

Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly  
65 70 75 80

Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met  
85 90 95

Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp  
100 105 110

Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val  
115 120 125

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
130 135 140

Ala Lys Ile Arg Asp Gly Gly Gly Ser Gly Gly Gly Ser Val Lys Gln  
145 150 155 160

Leu Ala Asp Ala Val Glu Glu Leu Ala Ser Ala Asn Tyr His Leu Ala  
165 170 175

Asn Ala Val Ala Arg Leu Ala Lys Ala Val Gly Glu Arg Gly Gly Gly  
180 185 190

Ser Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala  
195 200 205

Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly  
210 215 220

Ser Leu Gln Cys Arg Ile Cys Ile  
225 230

&lt;210&gt; 9

## Seq list TQD (GB)

<211> 723  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> cDNA according to invention E

<400> 9  
 tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
 ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaagggtg 120  
 ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 180  
 cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct 240  
 agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg 300  
 aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag 360  
 atcgtcctta agtctgagaa tgtgggtgtg accgttaagg tgatgggtga tgatgggtgtt 420  
 ctggccttgcg ctattgctac ccatgctaag attagggatg gtgggtgggtc tgggtgggtga 480  
 tctaagcaga tcgaggataa gatcgagaac atcaccagca agatctacaa cattaccaac 540  
 gagatcgcta ggatcaagaa gctgatcggt aacaggaccg gtgggtggtag ttaccagatc 600  
 ctgtccatct actctaccgt ggcttcttct cttgctctgg ctatcatgat ggctgggtctg 660  
 tctctttgga tgtgcagcaa cggttctctt cagtgcagga tctgcatcta aactagtgtc 720  
 gac 723

<210> 10  
 <211> 232  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein according to invention E

<400> 10

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
 1 5 10 15

Leu Ser Ser Ala Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu  
 20 25 30

Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile  
 35 40 45

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

Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly  
 65 70 75 80

Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met  
 85 90 95

# Seq list TQD (GB)

Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp  
100 105 110

Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val  
115 120 125

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
130 135 140

Ala Lys Ile Arg Asp Gly Gly Gly Ser Gly Gly Gly Ser Lys Gln Ile  
145 150 155 160

Glu Asp Lys Ile Glu Asn Ile Thr Ser Lys Ile Tyr Asn Ile Thr Asn  
165 170 175

Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Asn Arg Thr Gly Gly Gly  
180 185 190

Ser Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala  
195 200 205

Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly  
210 215 220

Ser Leu Gln Cys Arg Ile Cys Ile  
225 230

<210> 11  
<211> 705  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> cDNA according to invention F

<400> 11  
tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaaggctg 120  
ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 180  
cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct 240  
agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg 300  
aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag 360  
atcgctccta agtctgagaa tgtggtggtg accgttaagg tgatgggtga tgatggtggt 420  
ctggcttgcg ctattgctac ccatgctaag attagggatg gtggtggttc tgggtggtga 480  
tctctgaagt ccaggcttga taccctgtct caagaggctg cacttctgaa agaacagcag 540  
gctctgcaga ctgtgtgtct ggggtggtggt agttaccaga tcctgtccat ctactctacc 600  
gtggcttctt ctcttgctct ggctatcatg atggctggtc tgtctctttg gatgtgcagc 660

aacggttctc ttcagtcgag gatctgcac taaactagtg tcgac

<210> 12  
 <211> 226  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein according to invention F

<400> 12

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
 1 5 10 15

Leu Ser Ser Ala Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu  
 20 25 30

Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile  
 35 40 45

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

Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly  
 65 70 75 80

Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met  
 85 90 95

Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp  
 100 105 110

Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val  
 115 120 125

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
 130 135 140

Ala Lys Ile Arg Asp Gly Gly Gly Ser Gly Gly Gly Ser Leu Lys Ser  
 145 150 155 160

Arg Leu Asp Thr Leu Ser Gln Glu Val Ala Leu Leu Lys Glu Gln Gln  
 165 170 175

Ala Leu Gln Thr Val Cys Leu Gly Gly Gly Ser Tyr Gln Ile Leu Ser  
 180 185 190

Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met Met Ala  
 195 200 205

Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile  
 210 215 220

# Seq list TQD (GB)

Cys Ile  
225

<210> 13  
<211> 705  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> cDNA according to invention G

<400> 13  
tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaagggtg 120  
ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 180  
cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct 240  
agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg 300  
aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag 360  
atcgctccta agtctgagaa tgtgggtggtg accgttaagg tgatgggtga tgatgggtgtt 420  
ctggcttgcg ctattgctac ccatgctaag attagggatg gtgggtggttc tgggtggtgga 480  
tctatcaacg agactgctga tgatatcgtg tacaggctga ccgtgattat cgatgatagg 540  
tacgagagcc tgaagaacct tgggtggtggt agttaccaga tcctgtccat ctactctacc 600  
gtggcttctt ctcttgctct ggctatcatg atggctggtc tgtctctttg gatgtgcagc 660  
aacggttctc ttcagtgcag gatctgcatc taaactagtg tcgac 705

<210> 14  
<211> 226  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Protein according to invention G

<400> 14

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu  
20 25 30

Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile  
35 40 45

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

Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly  
65 70 75 80

# Seq list TQD (GB)

Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met  
85 90 95

Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp  
100 105 110

Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val  
115 120 125

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
130 135 140

Ala Lys Ile Arg Asp Gly Gly Gly Ser Gly Gly Gly Ser Ile Asn Glu  
145 150 155 160

Thr Ala Asp Asp Ile Val Tyr Arg Leu Thr Val Ile Ile Asp Asp Arg  
165 170 175

Tyr Glu Ser Leu Lys Asn Leu Gly Gly Gly Ser Tyr Gln Ile Leu Ser  
180 185 190

Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met Met Ala  
195 200 205

Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile  
210 215 220

Cys Ile  
225

<210> 15  
<211> 573  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> cDNA according to invention H

<400> 15  
tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
ctgtcatctg cttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 120  
cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagggtgg tggtagtgaa 180  
gttgatgtgc ctggtatcga tcctaacgct tgccactata tgaagtgcc tcttgatgaag 240  
ggtcagcagt acgatatcaa gtacacctgg aacgtgccaa agatcgctcc taagtctgag 300  
aatggtggtg gatctggtgg tggatccctt aagcagattg aggataagat cgaagagatc 360  
ctgagcaaga tctaccacat cgagaacgag atcgctagga tcaagaagct gatcggagaa 420  
tctgctgctg gtggtggtag ttaccagatc ctgtccatct actctaccgt ggcttcttct 480  
cttgctctgg ctatcatgat ggctggtctg tctctttgga tgtgcagcaa cggttctctt 540

cagtgcagga tctgcatcta aactagtgtc gac

<210> 16  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein according to invention H

<400> 16

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
 1 5 10 15

Leu Ser Ser Ala Cys His Gly Ser Glu Pro Cys Ile Ile His Arg Gly  
 20 25 30

Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln Asn Thr Lys  
 35 40 45

Thr Ala Lys Gly Gly Gly Ser Glu Val Asp Val Pro Gly Ile Asp Pro  
 50 55 60

Asn Ala Cys His Tyr Met Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr  
 65 70 75 80

Asp Ile Lys Tyr Thr Trp Asn Val Pro Lys Ile Ala Pro Lys Ser Glu  
 85 90 95

Asn Gly Gly Gly Ser Gly Gly Gly Ser Leu Lys Gln Ile Glu Asp Lys  
 100 105 110

Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala  
 115 120 125

Arg Ile Lys Lys Leu Ile Gly Glu Ser Ala Ala Gly Gly Gly Ser Tyr  
 130 135 140

Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala  
 145 150 155 160

Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu  
 165 170 175

Gln Cys Arg Ile Cys Ile  
 180

<210> 17  
 <211> 579  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> cDNA according to invention I

## Seq list TQD (GB)

<400> 17  
 tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
 ctgtcatctg ctgagatctg cccagctgtt aagagggacg tcgatctatt tcttacggga 120  
 actcctgatg agtacgtcga acaagttgca cagtacaaag cactaccagt agtactcgag 180  
 aacgctagga tacttaagaa ttgtgtggac gcaaaaatga ccgaggaaga caaggaaaac 240  
 gcattgagct tgcttgataa aatatacacc tctccacttt gccatcacca ccaccatcac 300  
 actagtgggtg gtggttcttg tggtggatcc cttaaagcaga ttgaggataa gatcgaagag 360  
 atcctgagca agatctacca catcgagaac gagatcgcta ggatcaagaa gctgatcgga 420  
 gaatctgctg ctgggtgggtg tagttaccag atcctgtcta tctacagcac cgtggcttca 480  
 tctcttgctc tggctattat gatggctggg ctgtctctgt ggatgtgctc taacggttct 540  
 cttcagtgcg ggatctgcat ttaaactagt taagtcgac 579

<210> 18  
 <211> 183  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein according to invention I

<400> 18

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala Glu Ile Cys Pro Ala Val Lys Arg Asp Val Asp Leu  
20 25 30

Phe Leu Thr Gly Thr Pro Asp Glu Tyr Val Glu Gln Val Ala Gln Tyr  
35 40 45

Lys Ala Leu Pro Val Val Leu Glu Asn Ala Arg Ile Leu Lys Asn Cys  
50 55 60

Val Asp Ala Lys Met Thr Glu Glu Asp Lys Glu Asn Ala Leu Ser Leu  
65 70 75 80

Leu Asp Lys Ile Tyr Thr Ser Pro Leu Cys His His His His His His  
85 90 95

Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Leu Lys Gln Ile Glu Asp  
100 105 110

Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile  
115 120 125

Ala Arg Ile Lys Lys Leu Ile Gly Glu Ser Ala Ala Gly Gly Gly Ser  
130 135 140

# Seq list TQD (GB)

Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu  
145 150 155 160

Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser  
165 170 175

Leu Gln Cys Arg Ile Cys Ile  
180

<210> 19  
<211> 709  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> cDNA according to invention J

<400> 19  
tctagaggta ccatgaagac caacctgttc ttgttcctga tcttcagcct gctgctgagc 60  
ctgtcatctg ctgatcaagt ggatgtgaag gattgcgcta accacgagat caagaagggtg 120  
ttggttcctg gttgccatgg ttctgagcct tgcattattc acaggggtaa gcctttccag 180  
cttgaggctg ttttcgaggc taaccagaat accaagaccg ctaagattga gatcaaggct 240  
agcatcgatg gtctggaagt tgatgtgcct ggtatcgatc ctaacgcttg ccactatatg 300  
aagtgccctc ttgtgaaggg tcagcagtac gatatcaagt acacctggaa cgtgccaaag 360  
atcgctccta agtctgagaa tgtggtggtg accgttaagg tgatgggtga tgatggtgtt 420  
ctggcttgcg ctattgctac ccatgctaag attagggatg gtggtggttc tgggtggtgga 480  
tctcttaagc agattgagga taagatcgaa gagatcctga gcaagatcta ccacatcgag 540  
aacgagatcg ctaggatcaa gaagctgatc ggagaatctg ctgctggtgg tggtagtatt 600  
gctcttgctg ttggtggtgt tgctgtgctg ggtttcgtta ttgtgtgcct tctggtgctg 660  
aagtccgcta tgaagaagaa gtccaagtac gatagctact agtgtcgac 709

<210> 20  
<211> 229  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Protein according to invention J

<400> 20

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu  
20 25 30

Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile  
35 40 45

# Seq list TQD (GB)

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

Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly  
65 70 75 80

Leu Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met  
85 90 95

Lys Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp  
100 105 110

Asn Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val  
115 120 125

Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His  
130 135 140

Ala Lys Ile Arg Asp Gly Gly Gly Ser Gly Gly Gly Ser Leu Lys Gln  
145 150 155 160

Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu  
165 170 175

Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Ser Ala Ala Gly  
180 185 190

Gly Gly Ser Ile Ala Leu Ala Val Gly Gly Val Ala Val Leu Gly Phe  
195 200 205

Val Ile Val Cys Leu Leu Val Leu Lys Ser Ala Met Lys Lys Lys Ser  
210 215 220

Lys Tyr Asp Ser Tyr  
225

<210> 21  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> signal peptide of the tobacco chitinase  
<400> 21

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala  
20

<210> 22  
<211> 129

Seq list TQD (GB)

<212> PRT  
 <213> Dermatophagoides pteronyssinus  
 <400> 22  
 Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu Ile Lys Lys Val  
 1 5 10 15  
 Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile Ile His Arg Gly  
 20 25 30  
 Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln Asn Thr Lys  
 35 40 45  
 Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly Leu Glu Val Asp  
 50 55 60  
 Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met Lys Cys Pro Leu  
 65 70 75 80  
 Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn Val Pro Lys  
 85 90 95  
 Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Val Met Gly  
 100 105 110  
 Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile Arg  
 115 120 125  
 Asp

<210> 23  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker

<400> 23  
 Gly Gly Gly Ser Gly Gly Gly Ser  
 1 5

<210> 24  
 <211> 34  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCN4-pII coiled-coil domain

<400> 24  
 Leu Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr  
 1 5 10 15

Seq list TQD (GB)

His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Ser  
 20 25 30

Ala Ala

<210> 25  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker

<400> 25

Gly Gly Gly Ser  
 1

<210> 26  
 <211> 39  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Anchoring sequence of the H5N1 influenza virus H5 hemagglutinin

<400> 26

Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu  
 1 5 10 15

Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser  
 20 25 30

Leu Gln Cys Arg Ile Cys Ile  
 35

<210> 27  
 <211> 33  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCN4-pLI Coiled-coil domain

<400> 27

Arg Met Lys Gln Ile Glu Asp Lys Leu Glu Glu Ile Leu Ser Lys Leu  
 1 5 10 15

Tyr His Ile Glu Asn Glu Leu Ala Arg Ile Lys Lys Leu Leu Gly Glu  
 20 25 30

Arg

<210> 28

Seq list TQD (GB)

<211> 32  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCN4-pAA coiled-coil domain

<400> 28

Val Lys Gln Leu Ala Asp Ala Val Glu Glu Leu Ala Ser Ala Asn Tyr  
 1 5 10 15

His Leu Ala Asn Ala Val Ala Arg Leu Ala Lys Ala Val Gly Glu Arg  
 20 25 30

<210> 29  
 <211> 32  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IZN4 coiled-coil domain

<400> 29

Lys Gln Ile Glu Asp Lys Ile Glu Asn Ile Thr Ser Lys Ile Tyr Asn  
 1 5 10 15

Ile Thr Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Asn Arg Thr  
 20 25 30

<210> 30  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SNARE coiled-coil domain

<400> 30

Ile Asn Glu Thr Ala Asp Asp Ile Val Tyr Arg Leu Thr Val Ile Ile  
 1 5 10 15

Asp Asp Arg Tyr Glu Ser Leu Lys Asn Leu  
 20 25

<210> 31  
 <211> 34  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Anchoring sequence of the PDLP1 protein

<400> 31

Ile Ala Leu Ala Val Gly Gly Val Ala Val Leu Gly Phe Val Ile Val  
 1 5 10 15

Cys Leu Leu Val Leu Lys Ser Ala Met Lys Lys Lys Ser Lys Tyr Asp

Ser Tyr

<210> 32  
<211> 78  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Sequence of the CH1 chain of the feline allergen Fel d 1  
<400> 32

Glu Ile Cys Pro Ala Val Lys Arg Asp Val Asp Leu Phe Leu Thr Gly  
1 5 10 15

Thr Pro Asp Glu Tyr Val Glu Gln Val Ala Gln Tyr Lys Ala Leu Pro  
20 25 30

Val Val Leu Glu Asn Ala Arg Ile Leu Lys Asn Cys Val Asp Ala Lys  
35 40 45

Met Thr Glu Glu Asp Lys Glu Asn Ala Leu Ser Leu Leu Asp Lys Ile  
50 55 60

Tyr Thr Ser Pro Leu Cys His His His His His His Thr Ser  
65 70 75

<210> 33  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Coiled-coil synthetic domain  
<400> 33

Leu Lys Ser Arg Leu Asp Thr Leu Ser Gln Glu Val Ala Leu Leu Lys  
1 5 10 15

Glu Gln Gln Ala Leu Gln Thr Val Cys Leu  
20 25

<210> 34  
<211> 328  
<212> PRT  
<213> Influenza A virus

<400> 34

Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly  
1 5 10 15

His His Ala Val Pro Asn Gly Thr Leu Val Lys Thr Ile Thr Asp Asp  
20 25 30

# Seq list TQD (GB)

Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser Thr  
 35 40 45  
 Gly Lys Ile Cys Asn Asn Pro His Arg Ile Leu Asp Gly Ile Asp Cys  
 50 55 60  
 Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His Cys Asp Val Phe Gln  
 65 70 75 80  
 Asn Glu Thr Trp Asp Leu Phe Val Glu Arg Ser Lys Ala Phe Ser Asn  
 85 90 95  
 Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Arg Ser Leu Val  
 100 105 110  
 Ala Ser Ser Gly Thr Leu Glu Phe Ile Thr Glu Gly Phe Thr Trp Thr  
 115 120 125  
 Gly Val Thr Gln Asn Gly Gly Ser Asn Ala Cys Lys Arg Gly Pro Gly  
 130 135 140  
 Ser Gly Phe Phe Ser Arg Leu Asn Trp Leu Thr Lys Ser Gly Ser Thr  
 145 150 155 160  
 Tyr Pro Val Leu Asn Val Thr Met Pro Asn Asn Asp Asn Phe Asp Lys  
 165 170 175  
 Leu Tyr Ile Trp Gly Ile His His Pro Ser Thr Asn Gln Glu Gln Thr  
 180 185 190  
 Ser Leu Tyr Val Gln Ala Ser Gly Arg Val Thr Val Ser Thr Arg Arg  
 195 200 205  
 Ser Gln Gln Thr Ile Ile Pro Asn Ile Gly Ser Arg Pro Trp Val Arg  
 210 215 220  
 Gly Leu Ser Ser Arg Ile Ser Ile Tyr Trp Thr Ile Val Lys Pro Gly  
 225 230 235 240  
 Asp Val Leu Val Ile Asn Ser Asn Gly Asn Leu Ile Ala Pro Arg Gly  
 245 250 255  
 Tyr Phe Lys Met Arg Thr Gly Lys Ser Ser Ile Met Arg Ser Asp Ala  
 260 265 270  
 Pro Ile Asp Thr Cys Ile Ser Glu Cys Ile Thr Pro Asn Gly Ser Ile  
 275 280 285  
 Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Lys Ile Thr Tyr Gly Ala  
 290 295 300

# Seq list TQD (GB)

Cys Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Gly Met  
305 310 315 320

Arg Asn Val Pro Glu Lys Gln Thr  
325

<210> 35  
<211> 500  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> zika virus envelope protein

<400> 35

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser  
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr  
20 25 30

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

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser  
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala  
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu  
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser  
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys  
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His  
130 135 140

Gly Ser Gln His Ser Gly Met Ile Gly Tyr Glu Thr Asp Glu Asp Arg  
145 150 155 160

Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu  
165 170 175

Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu  
180 185 190

Seq list TQD (GB)

Asp Phe Ser<sub>195</sub> Asp Leu Tyr Tyr Leu<sub>200</sub> Thr Met Asn Asn Lys<sub>205</sub> His Trp Leu  
 Val His<sub>210</sub> Lys Glu Trp Phe His<sub>215</sub> Asp Ile Pro Leu Pro<sub>220</sub> Trp His Ala Gly  
 Ala Asp Thr Gly Thr Pro<sub>230</sub> His Trp Asn Asn Lys<sub>235</sub> Glu Ala Leu Val Glu<sub>240</sub>  
 Phe Lys Asp Ala His<sub>245</sub> Ala Lys Arg Gln Thr<sub>250</sub> Val Val Val Leu Gly<sub>255</sub> Ser  
 Gln Glu Gly Ala Val His Thr Ala Leu<sub>265</sub> Ala Gly Ala Leu Glu<sub>270</sub> Ala Glu  
 Met Asp Gly<sub>275</sub> Ala Lys Gly Arg Leu<sub>280</sub> Phe Ser Gly His Leu<sub>285</sub> Lys Cys Arg  
 Leu Lys<sub>290</sub> Met Asp Lys Leu Arg<sub>295</sub> Leu Lys Gly Val Ser<sub>300</sub> Tyr Ser Leu Cys  
 Thr Ala Ala Phe Thr Phe<sub>310</sub> Thr Lys Val Pro Ala<sub>315</sub> Glu Thr Leu His Gly<sub>320</sub>  
 Thr Val Thr Val Glu<sub>325</sub> Val Gln Tyr Ala Gly<sub>330</sub> Thr Asp Gly Pro Cys<sub>335</sub> Lys  
 Ile Pro Val Gln<sub>340</sub> Met Ala Val Asp Met<sub>345</sub> Gln Thr Leu Thr Pro<sub>350</sub> Val Gly  
 Arg Leu Ile<sub>355</sub> Thr Ala Asn Pro Val<sub>360</sub> Ile Thr Glu Ser Thr<sub>365</sub> Glu Asn Ser  
 Lys Met<sub>370</sub> Met Leu Glu Leu Asp<sub>375</sub> Pro Pro Phe Gly Asp<sub>380</sub> Ser Tyr Ile Val  
 Ile Gly Val Gly Asp Lys<sub>390</sub> Lys Ile Thr His His<sub>395</sub> Trp His Arg Ser Gly<sub>400</sub>  
 Ser Thr Ile Gly Lys<sub>405</sub> Ala Phe Glu Ala Thr<sub>410</sub> Val Arg Gly Ala Lys<sub>415</sub> Arg  
 Met Ala Val Leu<sub>420</sub> Gly Asp Thr Ala Trp<sub>425</sub> Asp Phe Gly Ser Val<sub>430</sub> Gly Gly  
 Val Phe Asn<sub>435</sub> Ser Leu Gly Lys Gly<sub>440</sub> Ile His Gln Ile Phe<sub>445</sub> Gly Ala Ala  
 Phe Lys<sub>450</sub> Ser Leu Phe Gly Gly<sub>455</sub> Met Ser Trp Phe Ser<sub>460</sub> Gln Ile Leu Ile

# Seq list TQD (GB)

Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile  
 465 470 475 480

Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr  
 485 490 495

Ala Val Ser Ala  
 500