

16. März 2011

558-29 PCT\_Sequence Listing\_ST25.txt  
SEQUENCE LISTING

<110> AMSilk GmbH, et al.  
<120> Method for production of polymer containing fibres  
<130> 558-29 PCT  
<150> PCT/EP2010/001694  
>151> 2010-03-17  
<160> 44  
<170> PatentIn version 3.5  
<210> 1  
<211> 636  
<212> PRT  
<213> Araneus diadematus

<220>  
<221> PEPTIDE  
<222> (1)..(636)  
<223> ADF-3

<400> 1

Ala Arg Ala Gly Ser Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly  
1 5 10 15

Gln Gln Gly Pro Gly Gln Gln Gly Pro Tyr Gly Pro Gly Ala Ser Ala  
20 25 30

Ala Ala Ala Ala Ala Gly Gly Tyr Gly Pro Gly Ser Gly Gln Gln Gly  
35 40 45

Pro Ser Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gly Gln Gly Pro  
50 55 60

Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala Ala Ala Gly Gly Tyr Gly  
65 70 75 80

Pro Gly Ser Gly Gln Gln Gly Pro Gly Gly Gln Gly Pro Tyr Gly Pro  
85 90 95

Gly Ser Ser Ala Ala Ala Ala Ala Ala Gly Gly Asn Gly Pro Gly Ser  
100 105 110

Gly Gln Gln Gly Ala Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly  
115 120 125

Ala Ser Ala Ala Ala Ala Ala Ala Gly Gly Tyr Gly Pro Gly Ser Gly  
130 135 140

Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gly Gln Gly Pro Tyr Gly  
145 150 155 160

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Pro Gly Ala Ser Ala Ala Ala Ala Ala Gly Gly Tyr Gly Pro Gly  
165 170 175

Ser Gly Gln Gly Pro Gly Gln Gln Gly Pro Gly Gly Gln Gly Pro Tyr  
180 185 190

Gly Pro Gly Ala Ser Ala Ala Ala Ala Ala Gly Gly Tyr Gly Pro  
195 200 205

Gly Ser Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly  
210 215 220

Pro Gly Gly Gln Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala  
225 230 235 240

Ala Ala Gly Gly Tyr Gly Pro Gly Tyr Gly Gln Gln Gly Pro Gly Gln  
245 250 255

Gln Gly Pro Gly Gly Gln Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala  
260 265 270

Ser Ala Ala Ser Gly Gly Tyr Gly Pro Gly Ser Gly Gln Gln Gly Pro  
275 280 285

Gly Gln Gln Gly Pro Gly Gly Gln Gly Pro Tyr Gly Pro Gly Ala Ser  
290 295 300

Ala Ala Ala Ala Ala Ala Gly Gly Tyr Gly Pro Gly Ser Gly Gln Gln  
305 310 315 320

Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly  
325 330 335

Pro Gly Gly Gln Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala  
340 345 350

Ala Ala Gly Gly Tyr Gly Pro Gly Ser Gly Gln Gln Gly Pro Gly Gln  
355 360 365

Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln  
370 375 380

Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly  
385 390 395 400

Pro Gly Gln Gln Gly Pro Gly Gly Gln Gly Ala Tyr Gly Pro Gly Ala  
405 410 415

Ser Ala Ala Ala Gly Ala Ala Gly Gly Tyr Gly Pro Gly Ser Gly Gln  
420 425 430

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Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln  
435 440 445

Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly  
450 455 460

Pro Gly Gln Gln Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala  
465 470 475 480

Ala Ala Gly Gly Tyr Gly Pro Gly Ser Gly Gln Gln Gly Pro Gly Gln  
485 490 495

Gln Gly Pro Gly Gln Gln Gly Pro Gly Gly Gln Gly Pro Tyr Gly Pro  
500 505 510

Gly Ala Ala Ser Ala Ala Val Ser Val Gly Gly Tyr Gly Pro Gln Ser  
515 520 525

Ser Ser Val Pro Val Ala Ser Ala Val Ala Ser Arg Leu Ser Ser Pro  
530 535 540

Ala Ala Ser Ser Arg Val Ser Ser Ala Val Ser Ser Leu Val Ser Ser  
545 550 555 560

Gly Pro Thr Lys His Ala Ala Leu Ser Asn Thr Ile Ser Ser Val Val  
565 570 575

Ser Gln Val Ser Ala Ser Asn Pro Gly Leu Ser Gly Cys Asp Val Leu  
580 585 590

Val Gln Ala Leu Leu Glu Val Val Ser Ala Leu Val Ser Ile Leu Gly  
595 600 605

Ser Ser Ser Ile Gly Gln Ile Asn Tyr Gly Ala Ser Ala Gln Tyr Thr  
610 615 620

Gln Met Val Gly Gln Ser Val Ala Gln Ala Leu Ala  
625 630 635

<210> 2  
<211> 410  
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<213> Araneus diadematus

<220>  
<221> PEPTIDE  
<222> (1)..(410)  
<223> ADF-4

<400> 2

Ala Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Ser Gly Gly  
1 5 10 15

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

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Gly Pro Ser Gly Pro Gly Tyr Gln Gly Pro Ser Gly Pro Gly Ala Tyr  
290 295 300

Gly Pro Ser Pro Ser Ala Ser Ala Ser Val Ala Ala Ser Val Tyr Leu  
305 310 315 320

Arg Leu Gln Pro Arg Leu Glu Val Ser Ser Ala Val Ser Ser Leu Val  
325 330 335

Ser Ser Gly Pro Thr Asn Gly Ala Ala Val Ser Gly Ala Leu Asn Ser  
340 345 350

Leu Val Ser Gln Ile Ser Ala Ser Asn Pro Gly Leu Ser Gly Cys Asp  
355 360 365

Ala Leu Val Gln Ala Leu Leu Glu Leu Val Ser Ala Leu Val Ala Ile  
370 375 380

Leu Ser Ser Ala Ser Ile Gly Gln Val Asn Val Ser Ser Val Ser Gln  
385 390 395 400

Ser Thr Gln Met Ile Ser Gln Ala Leu Ser  
405 410

<210> 3  
<211> 5  
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<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> REPEAT  
<222> (1)..(5)  
<223> consensus peptide motif

<400> 3

Gly Pro Gly Xaa Xaa  
1 5

<210> 4  
<211> 5  
<212> PRT  
<213> Araneus diadematus

<220>  
<221> VARIANT  
<222> (4)..(4)  
<223> Q at position 4 may also be alanine, serine, glycine, tyrosine,  
proline, or glutamine

<220>  
<221> VARIANT  
<222> (5)..(5)

<223> Q at position 5 may also be alanine, serine, glycine, tyrosine, proline, or glutamine

<400> 4

Gly Pro Gly Gln Gln  
1 5

<210> 5

<211> 5

<212> PRT

<213> Araneus diadematus

<220>

<221> REPEAT

<222> (1)..(5)

<223> peptide motif (ADF-3)

<400> 5

Gly Pro Gly Ala Ser  
1 5

<210> 6

<211> 5

<212> PRT

<213> Araneus diadematus

<220>

<221> REPEAT

<222> (1)..(5)

<223> peptide motif (ADF-3)

<400> 6

Gly Pro Gly Ser Gly  
1 5

<210> 7

<211> 5

<212> PRT

<213> Araneus diadematus

<220>

<221> REPEAT

<222> (1)..(5)

<223> peptide motif (ADF-4)

<400> 7

Gly Pro Gly Gly Tyr  
1 5

<210> 8

<211> 5

<212> PRT

<213> Araneus diadematus

<220>

<221> REPEAT

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<222> (1)..(5)  
<223> peptide motif (ADF-4)

<400> 8

Gly Pro Gly Gly Pro  
1 5

<210> 9  
<211> 5  
<212> PRT  
<213> *Nephila clavipes*

<220>  
<221> REPEAT  
<222> (1)..(5)  
<223> peptide motif (flagelliform protein)

<400> 9

Gly Pro Gly Gly Ala  
1 5

<210> 10  
<211> 5  
<212> PRT  
<213> *Arthropoda*

<220>  
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<222> (1)..(5)  
<223> peptide motif (resilin)

<400> 10

Gly Pro Gly Gly Gly  
1 5

<210> 11  
<211> 5  
<212> PRT  
<213> *Nephila clavipes*

<220>  
<221> REPEAT  
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<223> peptide motif (flagelliform protein)

<400> 11

Gly Pro Gly Gly Ser  
1 5

<210> 12  
<211> 5  
<212> PRT  
<213> Artificial sequence

<220>  
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<220>  
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 <222> (1)..(5)  
 <223> Ax peptide motif

<400> 12

Ala Ala Ala Ala Ala  
 1 5

<210> 13  
 <211> 6  
 <212> PRT  
 <213> Araneus diadematus

<220>  
 <221> REPEAT  
 <222> (1)..(6)  
 <223> Ax peptide motif (ADF 3)

<400> 13

Ala Ala Ala Ala Ala Ala  
 1 5

<210> 14  
 <211> 7  
 <212> PRT  
 <213> Araneus diadematus

<220>  
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 <222> (1)..(7)  
 <223> Ax peptide motif (ADF-4)

<400> 14

Ala Ala Ala Ala Ala Ala Ala  
 1 5

<210> 15  
 <211> 8  
 <212> PRT  
 <213> Araneus diadematus

<220>  
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 <222> (1)..(8)  
 <223> Ax peptide motif (ADF-4)

<400> 15

Ala Ala Ala Ala Ala Ala Ala Ala  
 1 5

<210> 16  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence



<220>

<223> synthetic

<220>

<221> REPEAT

<222> (1)..(9)

<223> Ax peptide motif

<400> 16

Ala Ala Ala Ala Ala Ala Ala Ala Ala  
1 5

<210> 17

<211> 10

<212> PRT

<213> Araneus diadematus

<220>

<221> REPEAT

<222> (1)..(10)

<223> Ax peptide motif (ADF-4)

<400> 17

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
1 5 10

<210> 18

<211> 9

<212> PRT

<213> Arthropoda

<220>

<221> REPEAT

<222> (1)..(9)

<223> peptide motif (based on resilin)

<400> 18

Gly Gly Arg Pro Ser Asp Thr Tyr Gly  
1 5

<210> 19

<211> 9

<212> PRT

<213> Arthropoda

<220>

<221> REPEAT

<222> (1)..(9)

<223> peptide motif (based on resilin)

<400> 19

Gly Gly Arg Pro Ser Ser Ser Tyr Gly  
1 5

<210> 20

<211> 24

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<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<222> (1)..(24)  
<223> Module A (ADF-3)

<400> 20

Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala Ala Gly Gly  
1 5 10 15

Tyr Gly Pro Gly Ser Gly Gln Gln  
20

<210> 21  
<211> 35  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(35)  
<223> Module C (ADF-4)

<400> 21

Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly Gly  
1 5 10 15

Tyr Gly Pro Glu Asn Gln Gly Pro Ser Gly Pro Gly Gly Tyr Gly Pro  
20 25 30

Gly Gly Pro  
35

<210> 22  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(20)  
<223> Module Q (ADF-3)

<400> 22

Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly Pro Gly Gln Gln Gly  
1 5 10 15

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Pro Gly Gln Gln  
20

<210> 23  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(27)  
<223> Module K (flagelliform protein)

<400> 23

Gly Pro Gly Gly Ala Gly Gly Pro Tyr Gly Pro Gly Gly Ala Gly Gly  
1 5 10 15

Pro Tyr Gly Pro Gly Gly Ala Gly Gly Pro Tyr  
20 25

<210> 24  
<211> 28  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(28)  
<223> Module sp (flagelliform protein)

<400> 24

Gly Gly Thr Thr Ile Ile Glu Asp Leu Asp Ile Thr Ile Asp Gly Ala  
1 5 10 15

Asp Gly Pro Ile Thr Ile Ser Glu Glu Leu Thr Ile  
20 25

<210> 25  
<211> 34  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(34)  
<223> Module S (Resilin)

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<400> 25

Pro Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly  
1 5 10 15

Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Gly Arg Pro Ser Asp Thr  
20 25 30

Tyr Gly

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

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(39)  
<223> Module R (Resilin)

<400> 26

Ser Ala Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly Gly Gly Asn Gly  
1 5 10 15

Gly Arg Pro Ser Asp Thr Tyr Gly Ala Pro Gly Gly Gly Asn Gly Gly  
20 25 30

Arg Pro Ser Ser Ser Tyr Gly  
35

<210> 27  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(18)  
<223> Module X (flagelliform protein)

<400> 27

Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ser Gly Gly Ala Gly  
1 5 10 15

Gly Ser

<210> 28  
<211> 30

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(30)  
<223> Module Y (flagelliform protein)

<400> 28

Gly Pro Gly Gly Ala Gly Pro Gly Gly Tyr Gly Pro Gly Gly Ser Gly  
1 5 10 15

Pro Gly Gly Tyr Gly Pro Gly Gly Ser Gly Pro Gly Gly Tyr  
20 25 30

<210> 29  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(24)  
<223> Module Ac

<400> 29

Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala Ala Ala Gly Gly  
1 5 10 15

Tyr Gly Pro Gly Cys Gly Gln Gln  
20

<210> 30  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(24)  
<223> Module Ak

<400> 30

Gly Pro Tyr Gly Pro Gly Ala Ser Ala Ala Ala Ala Ala Ala Gly Gly  
1 5 10 15

Tyr Gly Pro Gly Lys Gly Gln Gln  
20

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<210> 31  
 <211> 35  
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<220>  
 <223> synthetic

<220>  
 <221> DOMAIN  
 <222> (1)..(35)  
 <223> Module Cc

<400> 31

Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly Gly  
 1 5 10 15

Tyr Gly Pro Glu Asn Gln Gly Pro Cys Gly Pro Gly Gly Tyr Gly Pro  
 20 25 30

Gly Gly Pro  
 35

<210> 32  
 <211> 35  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<220>  
 <221> DOMAIN  
 <222> (1)..(35)  
 <223> Module Ck1

<400> 32

Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly Gly  
 1 5 10 15

Tyr Gly Pro Glu Asn Gln Gly Pro Lys Gly Pro Gly Gly Tyr Gly Pro  
 20 25 30

Gly Gly Pro  
 35

<210> 33  
 <211> 35  
 <212> PRT  
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<220>  
 <223> synthetic

<220>

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<221> DOMAIN  
<222> (1)..(35)  
<223> Module Ck2

<400> 33

Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly Gly  
1 5 10 15

Tyr Gly Pro Lys Asn Gln Gly Pro Ser Gly Pro Gly Gly Tyr Gly Pro  
20 25 30

Gly Gly Pro  
35

<210> 34  
<211> 35  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(35)  
<223> Module Ckc

<400> 34

Gly Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly Gly  
1 5 10 15

Tyr Gly Pro Lys Asn Gln Gly Pro Cys Gly Pro Gly Gly Tyr Gly Pro  
20 25 30

Gly Gly Pro  
35

<210> 35  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(13)  
<223> TAG cys1

<400> 35

Gly cys Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly  
1 5 10

<210> 36  
<211> 8

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(8)  
<223> TAG cys2

<400> 36

Gly cys Gly Gly Gly Gly Gly Gly  
1 5

<210> 37  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(14)  
<223> TAG cys3

<400> 37

Gly cys Gly Gly ser Gly Gly Gly Gly ser Gly Gly Gly Gly  
1 5 10

<210> 38  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>  
<221> DOMAIN  
<222> (1)..(13)  
<223> TAG lys1

<400> 38

Gly Lys Gly Gly Gly Gly Gly Gly ser Gly Gly Gly Gly  
1 5 10

<210> 39  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<220>



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<221> DOMAIN  
<222> (1)..(8)  
<223> TAG lys2

<400> 39

Gly Lys Gly Gly Gly Gly Gly Gly  
1 5

<210> 40  
<211> 5  
<212> PRT  
<213> Arthropoda

<220>  
<221> REPEAT  
<222> (1)..(5)  
<223> peptide motif (resilin)

<400> 40

Gly Pro Gly Gln Gly  
1 5

<210> 41  
<211> 124  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> based on ADF-3

<220>  
<221> DOMAIN  
<222> (1)..(124)  
<223> NR3 (ADF-3)

<400> 41

Gly Ala Ala Ser Ala Ala Val Ser Val Gly Gly Tyr Gly Pro Gln Ser  
1 5 10 15

Ser Ser Ala Pro Val Ala Ser Ala Ala Ala Ser Arg Leu Ser Ser Pro  
20 25 30

Ala Ala Ser Ser Arg Val Ser Ser Ala Val Ser Ser Leu Val Ser Ser  
35 40 45

Gly Pro Thr Asn Gln Ala Ala Leu Ser Asn Thr Ile Ser Ser Val Val  
50 55 60

Ser Gln Val Ser Ala Ser Asn Pro Gly Leu Ser Gly Cys Asp Val Leu  
65 70 75 80

Val Gln Ala Leu Leu Glu Val Val Ser Ala Leu Val Ser Ile Leu Gly  
85 90 95

Ser Ser Ser Ile Gly Gln Ile Asn Tyr Gly Ala Ser Ala Gln Tyr Thr  
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100

105

110

Gln Met Val Gly Gln Ser Val Ala Gln Ala Leu Ala  
 115 120

<210> 42  
 <211> 109  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> based on ADF-4

<220>  
 <221> DOMAIN  
 <222> (1)..(109)  
 <223> NR4 (ADF-4)

<400> 42

Gly Ala Tyr Gly Pro Ser Pro Ser Ala Ser Ala Ser Val Ala Ala Ser  
 1 5 10 15

Arg Leu Ser Ser Pro Ala Ala Ser Ser Arg Val Ser Ser Ala Val Ser  
 20 25 30

Ser Leu Val Ser Ser Gly Pro Thr Asn Gly Ala Ala Val Ser Gly Ala  
 35 40 45

Leu Asn Ser Leu Val Ser Gln Ile Ser Ala Ser Asn Pro Gly Leu Ser  
 50 55 60

Gly Cys Asp Ala Leu Val Gln Ala Leu Leu Glu Leu Val Ser Ala Leu  
 65 70 75 80

Val Ala Ile Leu Ser Ser Ala Ser Ile Gly Gln Val Asn Val Ser Ser  
 85 90 95

Val Ser Gln Ser Thr Gln Met Ile Ser Gln Ala Leu Ser  
 100 105

<210> 43  
 <211> 747  
 <212> PRT  
 <213> Araneus diadematus

<220>  
 <221> PEPTIDE  
 <222> (1)..(747)  
 <223> MaSp I

<400> 43

Gln Gly Ala Gly Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly  
 1 5 10 15

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Gly Tyr Gly Gly Leu Gly Gly Gln Gly Ala Gly Gln Gly Gly Tyr Gly  
20 25 30

Gly Leu Gly Gly Gln Gly Ala Gly Gln Gly Ala Gly Ala Ala Ala Ala  
35 40 45

Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Ser  
50 55 60

Gln Gly Ala Gly Arg Gly Gly Gln Gly Ala Gly Ala Ala Ala Ala Ala  
65 70 75 80

Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly  
85 90 95

Ala Gly Arg Gly Gly Leu Gly Gly Gln Gly Ala Gly Ala Ala Ala Ala  
100 105 110

Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Asn  
115 120 125

Gln Gly Ala Gly Arg Gly Gly Gln Gly Ala Ala Ala Ala Ala Ala Gly  
130 135 140

Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly Ala Gly  
145 150 155 160

Arg Gly Gly Leu Gly Gly Gln Gly Ala Gly Ala Ala Ala Ala Ala Ala  
165 170 175

Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Gly Gln Gly Ala  
180 185 190

Gly Gln Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly  
195 200 205

Gly Leu Gly Gly Gln Gly Ala Gly Ala Ala Ala Ala Ala Ala Ala Gly  
210 215 220

Gly Ala Gly Gln Gly Gly Leu Gly Gly Gln Gly Ala Gly Gln Gly Ala  
225 230 235 240

Gly Ala Ser Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly  
245 250 255

Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Glu Gly Ala Gly Ala  
260 265 270

Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu  
275 280 285

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Gly Gly Gln Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Ser Gln  
290 295 300

Gly Ala Gly Arg Gly Gly Leu Gly Gly Gln Gly Ala Gly Ala Ala Ala  
305 310 315 320

Ala Gly Gly Ala Gly Gln Gly Gly Leu Gly Gly Gln Gly Ala Gly Gln  
325 330 335

Gly Ala Gly Ala Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly  
340 345 350

Tyr Gly Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Leu Gly Gly  
355 360 365

Gln Gly Ala Gly Ala Val Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln  
370 375 380

Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Gln  
385 390 395 400

Gly Ala Gly Ala Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Arg Gly  
405 410 415

Tyr Gly Gly Leu Gly Asn Gln Gly Ala Gly Arg Gly Gly Leu Gly Gly  
420 425 430

Gln Gly Ala Gly Ala Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln  
435 440 445

Gly Gly Tyr Gly Gly Leu Gly Asn Gln Gly Ala Gly Arg Gly Gly Gln  
450 455 460

Gly Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly  
465 470 475 480

Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Gln Gly Ala Gly Ala Ala  
485 490 495

Ala Ala Ala Ala Val Gly Ala Gly Gln Glu Gly Ile Arg Gly Gln Gly  
500 505 510

Ala Gly Gln Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly Ser Gly Arg  
515 520 525

Gly Gly Leu Gly Gly Gln Gly Ala Gly Ala Ala Ala Ala Ala Gly  
530 535 540

Gly Ala Gly Gln Gly Gly Leu Gly Gly Gln Gly Ala Gly Gln Gly Ala  
545 550 555 560

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Gly Ala Ala Ala Ala Ala Ala Gly Gly Val Arg Gln Gly Gly Tyr Gly  
565 570 575

Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Gln Gly Ala Gly Ala  
580 585 590

Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Leu  
595 600 605

Gly Gly Gln Gly Val Gly Arg Gly Gly Leu Gly Gly Gln Gly Ala Gly  
610 615 620

Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Tyr Gly Gly Val Gly  
625 630 635 640

Ser Gly Ala Ser Ala Ala Ser Ala Ala Ala Ser Arg Leu Ser Ser Pro  
645 650 655

Gln Ala Ser Ser Arg Val Ser Ser Ala Val Ser Asn Leu Val Ala Ser  
660 665 670

Gly Pro Thr Asn Ser Ala Ala Leu Ser Ser Thr Ile Ser Asn Val Val  
675 680 685

Ser Gln Ile Gly Ala Ser Asn Pro Gly Leu Ser Gly Cys Asp Val Leu  
690 695 700

Ile Gln Ala Leu Leu Glu Val Val Ser Ala Leu Ile Gln Ile Leu Gly  
705 710 715 720

Ser Ser Ser Ile Gly Gln Val Asn Tyr Gly Ser Ala Gly Gln Ala Thr  
725 730 735

Gln Ile Val Gly Gln Ser Val Tyr Gln Ala Leu  
740 745

<210> 44  
<211> 627  
<212> PRT  
<213> Araneus diadematus

<220>  
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<222> (1)..(627)  
<223> MaSp II

<400> 44

Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro  
1 5 10 15

Gly Gln Gln Gly Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala  
20 25 30

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Ala Ala Ala Ala Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro  
35 40 45

Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Arg Tyr Gly Pro Gly  
50 55 60

Gln Gln Gly Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Gly  
65 70 75 80

Ser Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Arg Gln Gln Gly Pro  
85 90 95

Gly Gly Tyr Gly Gln Gly Gln Gln Gly Pro Ser Gly Pro Gly Ser Ala  
100 105 110

Ala Ala Ala Ser Ala Ala Ala Ser Ala Glu Ser Gly Gln Gln Gly Pro  
115 120 125

Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly  
130 135 140

Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Ser Gly  
145 150 155 160

Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro Gly Gln  
165 170 175

Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr  
180 185 190

Gly Pro Gly Gln Gln Gly Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala  
195 200 205

Ala Ala Ala Ala Ser Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly  
210 215 220

Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Leu  
225 230 235 240

Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly Gln  
245 250 255

Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Ser Gly Pro  
260 265 270

Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly Gly Tyr  
275 280 285

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly  
290 295 300

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Pro Ser Gly Ala Gly Ser Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly  
305 310 315 320

Gln Gln Gly Leu Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly  
325 330 335

Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Ser Ala  
340 345 350

Ser Ala Ala Ala Ala Ala Ala Gly Pro Gly Gln Gln Gly Pro Gly Gly  
355 360 365

Tyr Gly Pro Gly Gln Gln Gly Pro Ser Gly Pro Gly Ser Ala Ser Ala  
370 375 380

Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly Gly Tyr Gly Pro Gly Gln  
385 390 395 400

Gln Gly Pro Gly Gly Tyr Ala Pro Gly Gln Gln Gly Pro Ser Gly Pro  
405 410 415

Gly Ser Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly Gly  
420 425 430

Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Ala Pro Gly Gln Gln  
435 440 445

Gly Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala  
450 455 460

Gly Pro Gly Gly Tyr Gly Pro Ala Gln Gln Gly Pro Ser Gly Pro Gly  
465 470 475 480

Ile Ala Ala Ser Ala Ala Ser Ala Gly Pro Gly Gly Tyr Gly Pro Ala  
485 490 495

Gln Gln Gly Pro Ala Gly Tyr Gly Pro Gly Ser Ala Val Ala Ala Ser  
500 505 510

Ala Gly Ala Gly Ser Ala Gly Tyr Gly Pro Gly Ser Gln Ala Ser Ala  
515 520 525

Ala Ala Ser Arg Leu Ala Ser Pro Asp Ser Gly Ala Arg Val Ala Ser  
530 535 540

Ala Val Ser Asn Leu Val Ser Ser Gly Pro Thr Ser Ser Ala Ala Leu  
545 550 555 560

Ser Ser Val Ile Ser Asn Ala Val Ser Gln Ile Gly Ala Ser Asn Pro  
565 570 575

558-29 PCT\_Sequence Listing\_ST25.txt

Gly Leu Ser Gly Cys Asp Val Leu Ile Gln Ala Leu Leu Glu Ile Val  
580 585 590

Ser Ala Cys Val Thr Ile Leu Ser Ser Ser Ile Gly Gln Val Asn  
595 600 605

Tyr Gly Ala Ala Ser Gln Phe Ala Gln Val Val Gly Gln Ser Val Leu  
610 615 620

Ser Ala Phe  
625