

SEQUENCE LISTING

<110> Molecular Partners AG

<120> RECOMBINANT BINDING PROTEINS AND THEIR USE

<130> MD41211

<150> EP 15 162 502

<151> 2015-04-02

<150> EP 15 162 511

<151> 2015-04-02

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<212> PRT

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<223> His-tag

<400> 1

Met Arg Gly Ser His His His His His His Gly Ser

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<213> Artificial Sequence

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<223> GS-linker

<400> 2

Gly Gly Gly Gly Ser

1

5

<210> 3

<211> 7

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<213> Artificial Sequence

<220>

eolf-seql

<223> GS-linker

<400> 3

Gly Gly Gly Gly Ser Gly Ser
1 5

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<211> 12

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<223> Polypeptide linker

<400> 4

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

<210> 5

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> GS-linker

<400> 5

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

<210> 6

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> GS-linker

<400> 6

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser Gly Ser
20

<210> 7

<211> 10

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> PT-linker

<400> 7

Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser
1				5				10	

<210> 8

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PT-linker

<400> 8

Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly
1				5					10						15

Ser

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> PT-linker

<400> 9

Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
1				5					10						15

Pro Thr Pro Thr Pro Thr Gly Ser

20

<210> 10

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 10

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp

eolf-seql

1				5					10					15			
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Thr	Asp		
			20					25					30				
Asn	Asp	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Asn	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Asn	Gly	Ala	Asp	Val	Asn	Ala	Ser		
	50					55					60						
Asp	Leu	Thr	Gly	Ile	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Thr	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala		
			85					90						95			
Tyr	Asp	Asn	Asp	Gly	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Tyr	Gly		
		100						105					110				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	His	Gly	Ala	Asp	Val	Asn			
	115						120				125						
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn		
130						135					140						
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala					
145					150					155							

<210> 11

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 11

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1				5				10					15				
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp		
		20						25					30				
Lys	Asp	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys		
	50					55					60						
Asp	Lys	Asp	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala		
			85					90						95			
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly		
		100						105					110				
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala						
	115						120										

<210> 12

<211> 157

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 12

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1          5          10          15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Phe Asp
20          25          30
Trp Met Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His Leu
35          40          45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Thr
50          55          60
Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Asp Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Thr
85          90          95
Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly
100         105         110
His Leu Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn
115         120         125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
130         135         140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145         150         155

```

<210> 13

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 13

```

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

```

eolf-seql

				85					90					95			
Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly		
			100					105					110				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn		
		115					120					125					
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn		
	130					135					140						
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala					
145					150					155							

<210> 14
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 14

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

<210> 15
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 15

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Thr	Ala	Asp

eolf-seql

		20						25					30				
Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Val	Pro	Trp	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala	Lys		
		50				55					60						
Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ile	Gly	His		
65					70					75					80		
Gln	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Asn	Gly	Ala	Asp	Val	Asn	Ala		
			85						90					95			
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly		
		100						105					110				
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala						
		115					120										

<210> 16
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 16

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1			5					10					15				
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp		
		20					25				30						
Ser	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Leu		
		35				40					45						
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys		
		50			55				60								
Asp	Tyr	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His		
65					70				75						80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala		
			85					90						95			
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly		
		100						105					110				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
		115					120										

<210> 17
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

eolf-seql

<400> 17

```

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Arg Asp
20     25     30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
35     40     45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Ala
50     55     60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65     70     75     80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85     90     95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100    105    110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115    120

```

<210> 18

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 18

```

Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20     25     30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
35     40     45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50     55     60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His
65     70     75     80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85     90     95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
100    105    110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
115    120

```

<210> 19

<211> 124

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Designed ankyrin repeat domain

<400> 19

```

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1           5           10           15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
          20           25           30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
          35           40           45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
          50           55           60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Gly His
65           70           75           80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
          85           90           95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
          100          105          110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
          115          120

```

<210> 20

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 20

```

Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1           5           10           15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
          20           25           30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
          35           40           45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
          50           55           60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65           70           75           80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
          85           90           95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
          100          105          110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
          115          120

```

eolf-seql

<210> 21
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 21
 Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
 20 25 30
 Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
 35 40 45
 Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
 50 55 60
 Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala Val Gly His
 65 70 75 80
 Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
 85 90 95
 Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
 100 105 110
 His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
 115 120

<210> 22
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 22
 Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
 20 25 30
 Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
 35 40 45
 Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
 50 55 60
 Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
 65 70 75 80
 Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
 85 90 95
 Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly

eolf-seql

	100	105	110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala			
115	120		

<210> 23
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 23

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp		
1	5	10
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp		
20	25	30
Arg Phe Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu		
35	40	45
Lys Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Glu		
50	55	60
Asp Trp Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Met Gly His		
65	70	75
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala		
85	90	95
Met Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly		
100	105	110
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn		
115	120	125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn		
130	135	140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala		
145	150	155

<210> 24
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 24

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp		
1	5	10
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp		
20	25	30
Arg Phe Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu		

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 26

```

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1           5           10           15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
          20           25           30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
          35           40           45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
          50           55           60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
          85          90          95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
          100         105         110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
          115         120         125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
          130         135         140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
145          150          155

```

<210> 27

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 27

```

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

```

eolf-seql

				85					90					95			
Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly		
			100					105					110				
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn		
		115					120					125					
Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala		
	130					135					140						
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
145					150					155							

<210> 28
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 28

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

<210> 29
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 29

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1			5					10					15				
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Tyr		

eolf-seql

			20					25					30				
Glu	Asp	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala	Ala	Phe	Tyr	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Thr		
	50					55					60						
Asp	Ala	Trp	Gly	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Tyr	Tyr	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Thr		
			85						90					95			
His	Asp	Lys	Glu	Gly	Met	Thr	Ala	Leu	His	Leu	Ala	Ala	Leu	Thr	Gly		
		100						105					110				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Asn	Gly	Ala	Asp	Val	Asn			
	115						120			125							
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn		
	130					135				140							
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala					
145					150					155							

<210> 30

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 30

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1				5				10					15				
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Thr	His	Asp		
		20					25					30					
Asn	Phe	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ile	Gly	His	Leu		
	35					40					45						
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Phe		
	50				55					60							
Asp	Ser	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ser	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala		
			85						90					95			
Leu	Asp	Tyr	Asn	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Ser	Gly		
		100						105					110				
Arg	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn		
	115						120				125						
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn		
	130					135				140							
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala					
145					150					155							

eolf-seql

<210> 31
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 31
 Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Val Asp
 20 25 30
 Ala Trp Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ile Gly His Leu
 35 40 45
 Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Ala
 50 55 60
 Asp Tyr Tyr Gly Asp Thr Pro Leu His Leu Ala Ser Ala Gly His
 65 70 75 80
 Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
 85 90 95
 Gln Asp Asp Asn Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
 100 105 110
 Arg Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
 115 120 125
 Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
 130 135 140
 Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
 145 150 155

<210> 32
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 32
 Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ile Asp
 20 25 30
 Thr Trp Gly Asn Thr Pro Leu His Leu Ala Ala Asp Tyr Gly His Leu
 35 40 45
 Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Leu
 50 55 60
 Asp Trp Phe Gly Asp Thr Pro Leu His Leu Ala Ala Ser Leu Gly His

eolf-seql

65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Asn	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Val	Asp	Thr	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly
			100					105					110		
Arg	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn
		115					120					125			
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn
	130					135					140				
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala			
145					150					155					

<210> 33
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 33

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp
		20					25					30			
Arg	Trp	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu
		35				40					45				
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala	Asp
	50				55				60						
Asp	Val	Phe	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Leu	Gly	His
65				70				75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala
			85					90					95		
Asp	Asp	Tyr	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly
		100					105					110			
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn
		115				120					125				
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn
	130					135					140				
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala			
145					150					155					

<210> 34
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>

eolf-seql

<223> Designed ankyrin repeat domain

<400> 34

```

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Gln Asp
      20      25      30
Arg Trp Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu
      35      40      45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Asp
      50      55      60
Asp Val Phe Gly Asp Thr Pro Leu His Leu Ala Ala Ser Leu Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
      85      90      95
Asp Asp Tyr Ala Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
      100      105      110
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
      115      120      125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
      130      135      140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145      150      155

```

<210> 35

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 35

```

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

```

eolf-seql

115	120	125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn		
130	135	140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala		
145	150	155

<210> 36
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 36

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp		
1	5	10
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Asn Asp		
20	25	30
Ser Ser Gly Leu Thr Pro Leu His Leu Ala Ala Phe Tyr Gly His Leu		
35	40	45
Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Asp		
50	55	60
Asp Asp Trp Gly His Thr Pro Leu His Leu Ala Ala His Tyr Gly His		
65	70	75
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala		
85	90	95
Ile Asp Thr Arg Gly Leu Thr Pro Leu His Leu Ala Ala Ile Ala Gly		
100	105	110
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn		
115	120	125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn		
130	135	140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala		
145	150	155

<210> 37
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 37

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp		
1	5	10
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ser Asp		

eolf-seql

			20					25					30				
Asp	Thr	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Arg	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Asn		
		50				55					60						
Asp	Phe	Ala	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Val	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala		
				85					90					95			
His	Asp	Asp	Tyr	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Trp	Arg		
			100					105					110				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Asn	Gly	Ala	Asp	Val	Asn			
		115					120					125					
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn		
		130				135					140						
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala					
145					150					155							

<210> 38

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 38

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1				5					10					15			
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp		
			20					25				30					
Lys	Ser	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Phe	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Phe	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys		
		50				55					60						
Asp	Glu	Thr	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Ile	Trp	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala		
				85					90					95			
Lys	Asp	Leu	Tyr	Gly	Arg	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Leu	Arg		
			100					105					110				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn		
		115					120					125					
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn		
		130				135					140						
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala					
145					150					155							

eolf-seql

<210> 39
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 39
 Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Leu Asp
 20 25 30
 Gln Ile Gly Trp Thr Pro Leu His Leu Ala Ala Asn Tyr Gly His Leu
 35 40 45
 Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
 50 55 60
 Asp Leu Trp Gly Gln Thr Pro Leu His Leu Ala Trp Lys Gly His
 65 70 75 80
 Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
 85 90 95
 Lys Asp Thr Asp Gly Leu Thr Pro Leu His Leu Ala Ala Ile Arg Gly
 100 105 110
 His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
 115 120 125
 Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
 130 135 140
 Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
 145 150 155

<210> 40
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 40
 Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Ile Leu Met Ala Ser Gly Ala Asp Val Asn Ala Ala Asp
 20 25 30
 Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asp Gly His Leu
 35 40 45
 Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asp Ala Ser
 50 55 60
 Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His

eolf-seql

65				70				75				80			
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Asp	Ala	Asp	Val	Asn	Ala
				85				90						95	
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly
			100					105					110		
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala				
		115					120								

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

<220>
 <223> Designed ankyrin repeat domain

<400> 41

Asp	Leu	Gly	Lys	Glu	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Ala	Asp
		20					25					30			
Tyr	Phe	Gly	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35				40					45				
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala	Ser
	50				55				60						
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65				70				75				80			
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
			85					90				95			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Ala	Phe	Glu	Ile	Ser	Ile	Asp	Asn	Gly
			100				105					110			
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala				
		115					120								

<210> 42
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 42

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Ala	Asp
		20					25					30			
Tyr	Phe	Gly	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asp	Gly	His	Leu

eolf-seql

	35				40				45								
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala	Ser		
	50					55					60						
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala		
				85					90					95			
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly		
			100					105						110			
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala						
	115						120										

<210> 43
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 43

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1				5					10					15			
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Ala	Asp		
			20					25					30				
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asp	Gly	His	Leu		
			35				40					45					
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala	Ser		
	50					55					60						
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala		
				85					90					95			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly		
			100					105						110			
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala						
	115						120										

<210> 44
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 44

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

eolf-seql

1				5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	
			20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	
		35					40					45				
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	
	50					55					60					
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	
65					70					75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	
			85					90					95			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	
		100					105						110			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		115					120									

<210> 45

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 45

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	
1				5				10					15			
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	
			20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	
		35					40					45				
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	
	50					55					60					
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	
65					70					75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	
			85					90					95			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	
		100					105						110			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		115					120									

<210> 46

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql

<223> Designed ankyrin repeat domain

<400> 46

```

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1          5          10          15
Glu Val Arg Ile Leu Leu Ala Ala Gly Ala Asp Val Asn Ala Lys Asp
          20          25          30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
          35          40          45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
          50          55          60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
          85          90          95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
          100          105          110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
          115          120

```

<210> 47

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 47

```

Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1          5          10          15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
          20          25          30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
          35          40          45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
          50          55          60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
          85          90          95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
          100          105          110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
          115          120

```

<210> 48

<211> 124

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 48

```

Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1           5           10           15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
          20           25           30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
          35           40           45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
          50           55           60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65           70           75           80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
          85           90           95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
          100          105          110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
          115          120

```

<210> 49

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 49

```

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

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eolf-seql

115

120

<210> 50
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

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

<210> 51
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 51
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala

eolf-seql

				85					90					95			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly		
			100					105					110				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
		115					120										

<210> 52
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 52

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1			5					10					15				
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp		
		20					25					30					
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu		
		35				40					45						
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys		
	50				55			60									
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His		
65					70			75						80			
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala		
			85					90					95				
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly		
		100					105						110				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
		115					120										

<210> 53
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 53

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1			5					10					15				
Glu	Val	Arg	Phe	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Ala	Asp		
		20					25					30					
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu		
		35				40					45						
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Asn	Gly	Ala	Asp	Val	Asn	Ala	Gln		

eolf-seql

50		55		60											
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly
			100					105					110		
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala				
		115					120								

<210> 54
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 54

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20						25				30			
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu
	35					40					45				
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50				55				60						
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His
65					70				75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85					90					95		
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly
		100						105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala				
		115					120								

<210> 55
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 55

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp

eolf-seql

		20						25					30				
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu		
		35					40					45					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys		
		50				55					60						
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His		
65					70					75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala		
			85						90					95			
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly		
		100						105					110				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
		115					120										

<210> 56
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain

<400> 56

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp		
1			5					10					15				
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp		
		20					25				30						
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu		
		35				40					45						
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys		
		50			55				60								
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His		
65					70				75						80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Ser	Ala	Asp	Val	Asn	Ala		
			85					90					95				
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly		
		100						105					110				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
		115					120										

<210> 57
 <211> 159
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed ankyrin repeat domain with a C-terminal polypeptide linker

eolf-seql

<400> 57

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
      20      25      30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
      35      40      45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
      50      55      60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
      85      90      95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
      100      105      110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
      115      120      125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
      130      135      140
Thr Gly Ser Arg Ser Asp Leu Asp Ile Thr Gly Leu Lys Leu Asn
145      150      155

```

<210> 58

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising two designed ankyrin repeat domains

<400> 58

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

```

eolf-seql

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg
	130					135				140					
Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
145					150					155					160
Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys
				165					170					175	
Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His
			180					185					190		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		195					200					205			
Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly
	210					215					220				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
225					230					235					240
Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr
				245					250					255	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			260					265					270		
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
		275					280					285			
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn		
	290					295					300				

<210> 59

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising two designed ankyrin repeat domains

<400> 59

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

eolf-seql

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg
	130					135				140					
Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
145					150					155					160
Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
				165					170					175	
Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His
			180					185					190		
Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		195					200					205			
Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly
	210					215					220				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
225					230					235					240
Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala
				245					250					255	
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn			
			260					265							

<210> 60

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising two designed ankyrin repeat domains

<400> 60

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5					10					15	
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70				75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160

eolf-seql

Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			165						170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180					185					190		
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
			245						250					255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
	275					280						285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				

Ala
305

<210> 61
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising two designed ankyrin repeat domains

<400> 61

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75				80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85						90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				

eolf-seql

Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	
145					150					155					160	
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	
				165					170					175		
Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	
			180					185					190			
Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	
	195						200					205				
Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	
	210					215					220					
Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	
225					230					235					240	
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	
			245					250						255		
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	
			260					265					270			

<210> 62

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising two designed ankyrin repeat domains

<400> 62

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	
1				5				10					15			
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	
			20					25				30				
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	
		35				40						45				
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	
	50				55						60					
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	
65					70				75					80		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	
				85				90						95		
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	
			100					105					110			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	
		115					120					125				
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	
	130					135					140					
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	
145					150					155					160	

eolf-seql

Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp
			165						170					175	
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
			180					185					190		
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		195					200					205			
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
	210					215					220				
Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly
225					230					235					240
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
			245						250					255	
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu
			260					265					270		

Asn

<210> 63
 <211> 269
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising two designed ankyrin repeat domains

<400> 63

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5				10						15	
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75				80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Gly	Gly	Gly	Ser
		115					120					125			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg
	130					135					140				
Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
145					150					155				160	
Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys
				165					170					175	

eolf-seql

Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His
			180					185					190		
Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		195					200					205			
Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly
	210					215					220				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn
225					230					235					240
Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala
			245						250					255	
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn			
		260						265							

<210> 64

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising two designed ankyrin repeat domains

<400> 64

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

eolf-seql

Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
210						215					220				
Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
225					230					235					240
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile
			245						250					255	
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu
			260					265					270		

Asn

<210> 65
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising two designed ankyrin repeat domains

<400> 65

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

eolf-seql

Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
225					230					235					240
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile
			245						250					255	
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu
			260					265					270		

Asn

<210> 66
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising two designed ankyrin repeat domains

<400> 66

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

eolf-seql

Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser
			245						250					255	
Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala
			260					265					270		

<210> 67
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising two designed ankyrin repeat domains

<400> 67

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

eolf-seql

Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260 265 270

<210> 68

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 68

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

eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	
		275					280					285				
Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	
	290					295					300					
Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys	
				325				330						335		
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	
			340					345					350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	
	355					360						365				
Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	
	370					375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	
385					390					395					400	
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	
			405					410						415		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	
			420					425					430			
Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	
		435				440						445				
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	
	450					455					460					
Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	
465					470				475						480	
Ala	Glu	Ile	Leu	Gln	Lys	Leu	Asn									
				485												

<210> 69

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 69

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

eolf-seql

Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
			85						90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro
		115					120					125			
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
	130					135					140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
145					150					155					160
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			165					170						175	
Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
		180					185					190			
His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	195					200						205			
Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala
	210				215					220					
Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
225					230				235						240
Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu
			245					250					255		
Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		260					265					270			
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp
	275					280						285			
Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys
	290				295						300				
Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys
			325					330						335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
		340					345					350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr
	355					360					365				
Pro	Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val
	370				375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
			405					410					415		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly
		420					425					430			
Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val
	435					440						445			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser
	450					455					460				

eolf-seql

Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile
 465 470 475 480
 Ala Glu Val Leu Gln Lys Leu Asn
 485

<210> 70

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 70

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

eolf-seql

Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
		275					280					285			
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Gly	Gly
	290					295				300					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
305					310					315					320
Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly
			325						330					335	
Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		340						345					350		
Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	His	Glu
	355					360					365				
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
	370				375					380					
Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala
385					390					395					400
Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			405					410						415	
Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser	Ala
		420					425						430		
Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	435					440						445			
Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser
	450				455					460					
Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Asn
465					470					475					480

<210> 71
 <211> 480
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 71

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

eolf-seql

Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
			85						90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Gly	Gly	Gly	Ser
		115					120					125			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg
	130					135					140				
Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
145				150					155						160
Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
			165						170					175	
Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His
		180						185					190		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		195				200						205			
Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly
	210				215						220				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
225				230					235						240
Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu
			245					250						255	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
		260						265					270		
Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp
		275					280					285			
Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Gly	Gly	Gly
	290					295					300				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
305				310					315						320
Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly
			325					330						335	
Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		340					345						350		
Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala
		355				360						365			
Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
	370				375						380				
Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser
385				390					395						400
Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			405					410						415	
Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		420						425					430		
Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	435					440						445			
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
	450					455						460			

eolf-seql

Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
465 470 475 480

<210> 72

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 72

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

eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp
		275					280					285			
Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys
		290				295					300				
Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys
				325				330						335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340				345						350		
Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Tyr	Thr
		355				360						365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		370				375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu
			405					410						415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420				425					430			
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435				440						445			
Glu	Val	Leu	Gln	Lys	Leu	Asn									
		450				455									

<210> 73

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 73

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

eolf-seql

His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	
		115					120					125				
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	
		130					135					140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	
145					150					155					160	
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	
				165					170					175		
Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	
			180					185					190			
Pro	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	
		195					200					205				
Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	
	210				215					220						
Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
225					230					235					240	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	
				245					250					255		
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	
			260					265					270			
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
		275					280					285				
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	
		290				295				300						
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	
305					310					315					320	
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	
				325					330					335		
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	
			340				345						350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	
		355					360				365					
Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	
		370				375					380					
Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	
385					390					395					400	
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	
				405					410					415		
Val	Leu	Gln	Lys	Leu	Asn											
			420													

<210> 74

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

eolf-seql

<400> 74

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20      25      30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35      40      45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50      55      60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85      90      95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100     105     110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
115     120     125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
130     135     140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145     150     155     160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
165     170     175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
180     185     190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
195     200     205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
210     215     220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225     230     235     240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
245     250     255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
260     265     270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275     280     285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys Leu
290     295     300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305     310     315     320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro
325     330     335
Leu His Leu Ala Ala Pro Trp Gly His Leu Glu Ile Val Glu Val Leu
340     345     350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr
355     360     365

```

eolf-seql

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Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val
  370                               375                               380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys
385                               390                               395                               400
Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu
                               405                               410                               415
Ile Leu Gln Lys Leu Asn
                               420

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<210> 75
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 75

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

```

eolf-seql

Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile
			245						250					255	
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu
	290					295					300				
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met
305					310					315					320
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
			325						330					335	
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr
	355						360					365			
Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys
385					390					395					400
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
			405						410					415	
Val	Leu	Gln	Lys	Leu	Asn										
			420												

<210> 76

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 76

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

eolf-seql

His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	
		115					120					125				
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	
		130					135					140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	
145					150					155					160	
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	
				165					170					175		
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	
			180					185					190			
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	
		195					200					205				
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	
	210					215					220					
Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	
225					230				235						240	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	
				245					250					255		
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	
			260					265					270			
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
		275					280					285				
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	
	290					295				300						
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	
305					310					315					320	
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	Pro	
				325					330					335		
Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	
			340				345						350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	
		355					360					365				
Pro	Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	
		370				375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	
385					390					395					400	
Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	
				405					410					415		
Ile	Leu	Gln	Lys	Leu	Asn											
			420													

<210> 77

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

eolf-seql

<400> 77

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5						10					15	
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu
		35					40					45			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala
			85						90					95	
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly
		100						105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val
			165						170					175	
Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val
		180						185					190		
Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp
	210					215					220				
Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
			245						250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
		260						265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His
			325						330					335	
Leu	Ala	Ala	Pro	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
		340						345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu
	355						360					365			

eolf-seql

His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala
385					390					395					400
Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu
				405					410					415	
Gln	Lys	Ala	Ala												
			420												

<210> 78
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 78

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

eolf-seql

Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser
				245					250					255	
Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His
			325						330					335	
Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu
	355						360					365			
His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro
385					390					395					400
Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu
			405						410					415	
Gln	Lys	Ala	Ala												
			420												

<210> 79

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 79

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

eolf-seql

<400> 80

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5						10					15	
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro
			180					185					190		
Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
	210						215				220				
Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser
				245					250					255	
Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu
		355					360					365			

eolf-seql

His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375				380					
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro
385					390					395					400
Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu
				405					410					415	
Gln	Lys	Ala	Ala												
			420												

<210> 81
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 81

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

eolf-seql

Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala
				245					250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His
			325						330					335	
Leu	Ala	Ala	Pro	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu
	355						360					365			
His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala
385					390					395					400
Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu
				405					410					415	
Gln	Lys	Ala	Ala												
			420												

<210> 82

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 82

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

eolf-seql

His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	
		115					120					125				
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	
		130					135					140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	
145					150					155					160	
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	
				165					170					175		
Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	
			180					185					190			
Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	
		195					200					205				
Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	
		210				215					220					
Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
225					230					235					240	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	
				245					250					255		
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	
			260					265					270			
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
		275					280					285				
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	
		290				295					300					
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	
305					310					315					320	
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	Pro	
				325					330					335		
Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	
			340					345					350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	
		355					360					365				
Pro	Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	
		370				375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	
385					390					395					400	
Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	
				405					410					415		
Ile	Leu	Gln	Lys	Leu	Asn											
			420													

<210> 83

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

eolf-seql

<400> 83

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5						10					15	
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Lys	Ser	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg
			180					185					190		
Phe	Gly	His	Leu	Glu	Ile	Val	Glu	Phe	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asp	Glu	Thr	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala
	210						215				220				
Ile	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Leu	Tyr	Gly	Arg	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Lys	Leu	Arg	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile
		275					280					285			
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305						310					315				320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly	Trp	Thr	Pro	Leu
		355					360					365			

eolf-seql

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His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
 370                      375                      380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp Gly Gln Thr Pro
385                      390                      395                      400
Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile Val Glu Val Leu
                      405                      410                      415
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr Asp Gly Leu Thr
                      420                      425                      430
Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu Ile Val Glu Val
                      435                      440                      445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys
                      450                      455                      460
Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465                      470                      475                      480
Val Leu Gln Lys Ala Ala
                      485

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<210> 84
 <211> 486
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 84

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1                      5                      10                      15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
                      20                      25                      30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
                      35                      40                      45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                      50                      55                      60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65                      70                      75                      80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                      85                      90                      95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
                      100                     105                     110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
                      115                     120                     125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
                      130                     135                     140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro
145                      150                      155                      160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Pro Thr Pro
                      165                      170                      175

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eolf-seql

Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			180					185					190		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
		210				215					220				
Asn	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp	Gly	Gln	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Trp	Lys	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr	Asp	Gly	Leu	Thr	Pro	Leu	His	Leu
		275					280					285			
Ala	Ala	Ile	Arg	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
	290					295				300					
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp
305					310					315					320
Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys
				325					330					335	
Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
			340					345				350			
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu
		355					360					365			
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu
	370					375				380					
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
				405					410				415		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr
			420					425				430			
Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		435					440					445			
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys
	450					455				460					
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
465					470					475					480
Val	Leu	Gln	Lys	Ala	Ala										
				485											

<210> 85

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

eolf-seql

<400> 85

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5						10					15	
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180					185					190		
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			

eolf-seql

His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
370						375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala											
450															

<210> 86

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 86

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
	35					40						45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50				55				60						
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65				70				75						80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85					90						95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
		100					105						110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly
	115					120						125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130				135					140					
Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
145				150					155						160
Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			165					170						175	
Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly
		180					185						190		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	195						200					205			

eolf-seql

Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr
210						215					220				
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
225					230					235					240
Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn
			245						250					255	
Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			260					265					270		
Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala
		275					280					285			
Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly
290					295						300				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
305					310					315					320
Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
				325					330					335	
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			340				345						350		
Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
		355					360					365			
Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		370				375					380				
Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
385					390					395					400
Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
				405					410					415	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
			420					425					430		
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		435					440						445		

Ala

<210> 87
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 87
 Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
 1 5 10 15
 Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
 20 25 30
 Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
 35 40 45

eolf-seql

Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu
50					55					60					
Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His
65				70					75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85						90					95	
Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly
			100					105					110		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		115					120					125			
Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala
	130					135					140				
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro
145					150					155					160
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
				165					170					175	
Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			180					185					190		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
			420					425					430		

eolf-seql

Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
 435 440 445
 Leu Gln Lys Ala Ala
 450

<210> 88

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 88

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

eolf-seql

Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp
		275					280					285			
Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Gly	Gly	Gly
	290					295					300				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
305					310					315					320
Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly
				325					330					335	
Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
			340					345					350		
Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala
		355				360						365			
Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
	370					375					380				
Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser
385					390					395					400
Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			405					410						415	
Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		420						425					430		
Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	435					440						445			
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
	450				455					460					
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn
465					470					475					480

<210> 89
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 89

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

eolf-seql

<210> 90

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 90

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1          5          10          15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20        25        30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35        40        45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50        55        60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65        70        75        80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85        90        95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100       105       110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115       120       125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130       135       140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145       150       155       160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165       170       175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180       185       190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195       200       205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210       215       220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225       230       235       240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
245       250       255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260       265       270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
275       280       285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290       295       300

```

eolf-seql

Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315				320	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	
			405					410						415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala											
	450														

<210> 91

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 91

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35				40						45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50				55					60					
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65				70					75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85					90						95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
		100						105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly
	115					120						125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				

eolf-seql

Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
145					150					155					160
Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				165					170					175	
Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly
			180					185					190		
His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		195					200					205			
Ala	Lys	Asp	Tyr	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val
	210					215					220				
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
225					230					235					240
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
				245					250					255	
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
			260					265				270			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		275					280					285			
Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
	290					295					300				
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
305					310					315					320
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
				325					330					335	
Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			340					345				350			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		355					360					365			
Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	370					375					380				
Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
385					390					395					400
Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
				405					410					415	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
			420					425					430		
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		435					440					445			

Ala

<210> 92

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

eolf-seql

<400> 92

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5						10					15	
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185						190		
Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260				265						270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			

eolf-seql

His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
370						375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala											
450															

<210> 93
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising three designed ankyrin repeat domains

<400> 93

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

eolf-seql

Val	Asn	Ala	Lys	Asp	Tyr	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
210						215					220				
Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
				245					250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala											
	450														

<210> 94

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising three designed ankyrin repeat domains

<400> 94

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5					10					15	
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Leu
		35					40					45			

eolf-seql

Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
50						55					60				
Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85						90					95
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly
			100					105						110	
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120						125		
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
		130				135						140			
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185						190		
Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195				200						205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		210				215					220				
Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265						270	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290				295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala
			340					345					350		
Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
		370				375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		

eolf-seql

Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
 435 440 445
 Leu Gln Lys Ala Ala
 450

<210> 95

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 95

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

eolf-seql

Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
	275						280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295				300					
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
		340						345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
	355						360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
			405					410						415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
	435						440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485					490					495		
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
	515						520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
			565					570					575		
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
	595						600								

<210> 96

<211> 601

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 96

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20      25      30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35      40      45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50      55      60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85      90      95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100     105     110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115     120     125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130     135     140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145     150     155     160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
165     170     175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180     185     190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195     200     205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210     215     220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225     230     235     240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
245     250     255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260     265     270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
275     280     285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290     295     300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305     310     315     320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
325     330     335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
340     345     350

```

eolf-seql

Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485						490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
				565					570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 97

<211> 637

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 97

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Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			

eolf-seql

Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
50					55					60					
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro
		115					120					125			
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
		130				135					140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
145					150					155					160
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			165					170						175	
Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala
		180					185					190			
Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		195				200						205			
Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
		210				215				220					
Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
225					230					235					240
Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu
			245						250					255	
Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		260						265					270		
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp
		275				280						285			
Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys
		290				295					300				
Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys
			325					330						335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340				345						350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr
		355				360						365			
Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		370				375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu
			405					410						415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly
			420					425						430	

eolf-seql

Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val
		435					440					445			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe
	450					455					460				
Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu
465					470					475					480
Ala	Glu	Ile	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
				485					490					495	
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg
			500					505					510		
Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
	515						520					525			
Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys
	530					535					540				
Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His
545					550					555					560
Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				565					570					575	
Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly
			580					585					590		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn
		595					600					605			
Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala
	610					615					620				
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn			
625					630					635					

<210> 98

<211> 637

<212> PRT

<213> Artificial Sequence

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<223> Protein comprising four designed ankyrin repeat domains

<400> 98

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

eolf-seql

Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro
		115					120					125			
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
	130					135					140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
145					150					155					160
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			165					170						175	
Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
		180					185					190			
His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	195					200						205			
Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala
	210				215						220				
Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
225					230					235					240
Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu
			245					250						255	
Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		260					265					270			
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp
	275					280						285			
Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys
	290				295						300				
Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys
			325					330						335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
		340					345						350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr
		355				360					365				
Pro	Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
			405					410						415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly
		420					425					430			
Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val
	435						440					445			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser
	450					455					460				
Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile
465					470				475						480

eolf-seql

Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
				485					490						495	
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	
			500					505					510			
Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	
		515					520					525				
Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	
	530					535					540					
Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	
545					550					555					560	
Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	
			565						570					575		
Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	
		580						585					590			
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	His	Gly	Ala	Asp	Val	Asn		
	595					600					605					
Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	
	610					615					620					
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn				
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<212> PRT

<213> Artificial Sequence

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<223> Protein comprising four designed ankyrin repeat domains

<400> 99

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	
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Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	
			20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	
		35					40					45				
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	
	50					55					60					
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	
65					70					75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	
			85						90					95		
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	
			100					105					110			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Gly	Gly	Gly	Ser	
		115					120					125				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg	
	130					135						140				

eolf-seql

Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
145					150					155					160
Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
				165					170					175	
Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His
			180					185					190		
Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		195					200					205			
Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly
	210					215					220				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
225					230					235					240
Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr
				245					250					255	
Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			260					265					270		
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
		275				280					285				
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Gly	Gly
	290					295				300					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
305					310				315						320
Ser	Arg	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly
				325					330					335	
Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
			340					345					350		
Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	His	Glu
		355					360					365			
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
	370					375					380				
Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala
385					390					395					400
Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
				405					410					415	
Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser	Ala
			420					425					430		
Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		435				440						445			
Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser
	450					455					460				
Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Gly
465					470					475					480
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
				485					490					495	
Gly	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			500					505					510		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp
		515					520						525		

eolf-seql

Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
530						535					540				
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
545					550					555					560
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
				565					570					575	
Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly
			580					585					590		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
		595				600						605			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu
	610					615					620				

Asn
625

<210> 100
 <211> 625
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 100

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5					10					15	
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75				80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Gly	Gly	Gly	Ser
		115				120						125			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg
	130					135					140				
Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp
145					150					155					160
Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
			165						170					175	
Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His
		180						185					190		

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Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		195					200					205			
Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly
	210					215					220				
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
225					230					235					240
Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu
				245					250					255	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
		260						265					270		
Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp
	275						280				285				
Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Gly	Gly	Gly
	290					295				300					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
305					310					315					320
Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly
				325					330					335	
Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
			340				345						350		
Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala
		355				360						365			
Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
	370					375					380				
Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser
385					390					395					400
Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
				405					410					415	
Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
			420					425					430		
Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		435				440						445			
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
	450					455					460				
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly
465					470					475					480
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
				485					490					495	
Gly	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			500					505					510		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp
		515					520						525		
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
	530					535						540			
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
545					550					555					560
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
				565					570						575

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Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly
			580					585					590		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
		595					600					605			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu
	610					615					620				

Asn
625

<210> 101
 <211> 595
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 101

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

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Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn
			245						250					255	
Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			260					265					270		
Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala
		275					280					285			
Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly
	290					295					300				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
305					310					315					320
Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
				325					330					335	
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		340						345					350		
Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
		355					360					365			
Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	370					375					380				
Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
385					390					395					400
Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
				405					410					415	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
			420					425					430		
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		435					440					445			
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	450					455					460				
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala
465					470					475					480
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly
				485					490					495	
Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu
			500					505					510		
Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		515					520					525			
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His
	530					535					540				
Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
545					550					555					560
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala
				565					570					575	
Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
			580					585					590		
Lys	Ala	Ala													
		595													

<210> 102

eolf-seql

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 102

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
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Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20        25        30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35        40        45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50        55        60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65        70        75        80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85        90        95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100       105       110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115       120       125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130       135       140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145       150       155       160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165       170       175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180       185       190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195       200       205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210       215       220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225       230       235       240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
245       250       255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260       265       270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
275       280       285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290       295       300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305       310       315       320

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eolf-seql

Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405					410					415		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485					490					495		
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
	515						520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
			565					570					575		
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
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Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
	595					600									

<210> 103

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 103

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
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eolf-seql

Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150				155						160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165				170						175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185					190			
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195				200						205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215				220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230				235						240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275				280						285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400

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Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410				415		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420				425						430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485						490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
			565						570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 104
 <211> 601
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 104

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

eolf-seql

Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
		130				135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180					185					190		
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		210				215					220				
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290					295				300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305						310					315				320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
		370				375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
		450					455					460			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470						475				480

eolf-seql

Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515						520					525		
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
			565						570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
		580						585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 105

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 105

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5					10					15	
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75				80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				
Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
145					150					155					160
Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				165					170					175	

eolf-seql

Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly
			180					185					190		
His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		195					200					205			
Ala	Lys	Asp	Tyr	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val
	210					215					220				
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
225					230					235					240
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
			245						250					255	
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		260						265					270		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		275					280					285			
Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
	290					295					300				
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
305					310					315					320
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			325					330						335	
Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		340						345					350		
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		355					360					365			
Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
	370					375					380				
Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
385					390					395					400
Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			405						410					415	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
			420				425						430		
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		435					440					445			
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	450					455					460				
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala
465					470					475					480
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly
			485						490					495	
Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu
			500					505					510		
Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		515					520					525			
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His
	530					535					540				
Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
545					550					555					560

eolf-seql

Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala
			565						570					575	
Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
			580					585					590		
Lys	Ala	Ala													
		595													

<210> 106

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 106

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

eolf-seql

Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290					295				300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
		370				375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
		450				455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
		530				535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
				565					570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 107

<211> 601

<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 107

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1          5          10          15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20          25          30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35          40          45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50          55          60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85          90          95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100         105         110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115         120         125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130         135         140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145         150         155         160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165         170         175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
180         185         190
Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195         200         205
Val Asn Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala
210         215         220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225         230         235         240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
245         250         255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260         265         270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275         280         285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
290         295         300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305         310         315         320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
325         330         335

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eolf-seql

```

Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
    340                      345                      350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
    355                      360                      365
His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                      375                      380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro
385                      390                      395                      400
Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu
    405                      410                      415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
    420                      425                      430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
    435                      440                      445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                      455                      460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                      470                      475                      480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
    485                      490                      495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
    500                      505                      510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
    515                      520                      525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                      535                      540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile
545                      550                      555                      560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
    565                      570                      575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
    580                      585                      590
Ile Ala Glu Val Leu Gln Lys Ala Ala
    595                      600

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<210> 108

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 108

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1          5          10          15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    20          25          30

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eolf-seql

Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105						110	
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			165					170						175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185						190		
Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195				200						205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215				220					
Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265						270	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	

eolf-seql

```

Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
      420                      425                      430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
      435                      440                      445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
      450                      455                      460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                      470                      475                      480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
      485                      490                      495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
      500                      505                      510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
      515                      520                      525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
      530                      535                      540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile
545                      550                      555                      560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
      565                      570                      575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
      580                      585                      590
Ile Ala Glu Val Leu Gln Lys Ala Ala
      595                      600

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<210> 109

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 109

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

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His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro
		115					120					125			
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
		130					135				140				
Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
145					150					155					160
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp
				165					170					175	
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
			180					185					190		
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		195					200					205			
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
		210				215					220				
Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly
225					230					235					240
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
				245					250					255	
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp	Leu	Gly	Lys	Lys	Leu
		290				295					300				
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met
305					310					315					320
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr	Pro
				325					330					335	
Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Asp	Gly	Tyr	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		370				375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys
385					390					395					400
Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu
			405						410					415	
Ile	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
			420					425					430		
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	Asp
		435					440					445			
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
						455					460				

eolf-seql

Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			500					505					510		
Lys	Asp	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Glu	Gly	His	Leu
		515					520					525			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
	530					535					540				
Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn
545					550					555					560
Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Asn					
				565					570						

<210> 110

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 110

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

eolf-seql

Ile	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	225	230	235	240
Asp	Val	Asn	Ala	Lys	Asp	Leu	Tyr	Gly	Arg	Thr	Pro	Leu	His	Leu	Ala	245	250	255	
Ala	Lys	Leu	Arg	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	260	265	270	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	275	280	285	
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	290	295	300	
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	305	310	315	320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	325	330	335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	340	345	350	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly	Trp	Thr	Pro	Leu	355	360	365	
His	Leu	Ala	Ala	Asn	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	370	375	380	
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp	Gly	Gln	Thr	Pro	385	390	395	400
Leu	His	Leu	Ala	Ala	Trp	Lys	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	405	410	415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr	Asp	Gly	Leu	Thr	420	425	430	
Pro	Leu	His	Leu	Ala	Ala	Ile	Arg	Gly	His	Leu	Glu	Ile	Val	Glu	Val	435	440	445	
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	450	455	460	
Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	465	470	475	480
Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	485	490	495	
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	500	505	510	
Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	515	520	525	
Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	530	535	540	
Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	545	550	555	560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	565	570	575	
Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	580	585	590	
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	595	600	605	

eolf-seql

Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu
610 615 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625 630

<210> 111

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 111

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

eolf-seql

Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile
		275					280					285			
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
			420					425				430			
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Tyr	Gly	His	Leu	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp
	530					535					540				
Gly	Gln	Thr	Pro	Leu	His	Leu	Ala	Ala	Trp	Lys	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr
				565					570					575	
Asp	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala	Ala	Ile	Arg	Gly	His	Leu	Glu
			580					585					590		
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp
		595					600					605			
Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu
	610					615					620				
Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
625					630										

<210> 112

eolf-seql

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 112

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1           5           10           15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20          25          30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35          40          45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50          55          60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85          90          95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100         105         110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115         120         125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130         135         140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145         150         155         160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
165         170         175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
180         185         190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195         200         205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
210         215         220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225         230         235         240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
245         250         255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260         265         270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275         280         285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
290         295         300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala
305         310         315         320

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eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Lys	Ser	Gly	Asn	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Arg	Phe	Gly	His	Leu	Glu	Ile	Val	Glu	Phe	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Thr	Gly	Lys	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Ile	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Leu	Tyr	Gly	Arg	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Lys	Leu	Arg	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr
			420					425					430		
Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Tyr	Gly	His	Leu	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp
	530					535					540				
Gly	Gln	Thr	Pro	Leu	His	Leu	Ala	Ala	Trp	Lys	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr
				565					570					575	
Asp	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala	Ala	Ile	Arg	Gly	His	Leu	Glu
			580					585					590		
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp
		595				600						605			
Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu
	610					615					620				
Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
625					630										

<210> 113

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

eolf-seql

<400> 113

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20      25      30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
35      40      45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50      55      60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85      90      95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
100     105     110
His Leu Glu Ile Val Glu Val Leu Lys Ala Gly Ala Asp Val Asn
115     120     125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
130     135     140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro
145     150     155     160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
165     170     175
Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
180     185     190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
195     200     205
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
210     215     220
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225     230     235     240
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
245     250     255
Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260     265     270
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
275     280     285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290     295     300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305     310     315     320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
325     330     335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
340     345     350
Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly Trp Thr Pro Leu
355     360     365

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eolf-seql

His	Leu	Ala	Ala	Asn	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
370						375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp	Gly	Gln	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Trp	Lys	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr	Asp	Gly	Leu	Thr
			420					425					430		
Pro	Leu	His	Leu	Ala	Ala	Ile	Arg	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		435					440					445			
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys
	450					455					460				
Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
465					470					475					480
Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro
				485					490						495
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu
			500					505					510		
Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val
		515					520					525			
Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe
	530					535					540				
Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe
				565					570					575	
Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu
			580					585					590		
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp
		595					600					605			
Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu
	610					615					620				
Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
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<210> 114

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 114

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
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Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		

eolf-seql

Lys	Ser	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Phe	Gly	His	Leu
		35					40					45			
Glu	Ile	Val	Glu	Phe	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Glu	Thr	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Ile	Trp	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Lys	Asp	Leu	Tyr	Gly	Arg	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Leu	Arg
			100					105						110	
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	
		115					120					125			
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn
	130					135					140				
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro
145					150					155					160
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
				165					170					175	
Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			180					185					190		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Asn	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp	Gly	Gln	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Trp	Lys	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr	Asp	Gly	Leu	Thr	Pro	Leu	His	Leu
		275					280					285			
Ala	Ala	Ile	Arg	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
	290					295					300				
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp
305					310					315					320
Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys
				325					330					335	
Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
			340					345					350		
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu
		355					360					365			
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
				405					410					415	

eolf-seql

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Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
      420      425      430
Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val
      435      440      445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
      450      455      460
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465      470      475      480
Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro
      485      490      495
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu
      500      505      510
Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
      515      520      525
Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe
      530      535      540
Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile
545      550      555      560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe
      565      570      575
Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu
      580      585      590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
      595      600      605
Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu
      610      615      620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625      630

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<210> 115

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 115

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
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Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
      20      25      30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
      35      40      45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
      50      55      60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65      70      75      80

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eolf-seql

Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	85	90	95
Lys	Asp	Leu	Tyr	Gly	Arg	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Leu	Arg	100	105	110
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	115	120	125
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	130	135	140
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	145	150	155
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	165	170	175
Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	180	185	190
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	195	200	205
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	210	215	220
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	225	230	235
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	245	250	255
Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	260	265	270
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	275	280	285
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	290	295	300
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	305	310	315
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	325	330	335
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	340	345	350
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	355	360	365
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	370	375	380
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	385	390	395
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	405	410	415
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	420	425	430
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	435	440	445
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	450	455	460

eolf-seql

Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470						475				480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Leu	Asp	Gln	Ile	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Tyr	Gly	His	Leu	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Leu	Trp
	530					535					540				
Gly	Gln	Thr	Pro	Leu	His	Leu	Ala	Ala	Trp	Lys	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Thr
			565						570					575	
Asp	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala	Ala	Ile	Arg	Gly	His	Leu	Glu
		580						585					590		
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp
		595					600					605			
Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu
	610					615					620				
Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
625					630										

<210> 116

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 116

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
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Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35				40					45				
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50				55				60						
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65				70					75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85					90					95		
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
		100					105					110			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly
		115				120						125			

eolf-seql

Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
130					135					140					
Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
145					150				155						160
Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				165					170					175	
Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly
			180					185					190		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		195					200					205			
Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr
		210				215					220				
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
225					230					235					240
Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn
			245						250					255	
Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			260					265					270		
Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala
		275					280					285			
Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly
		290				295					300				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
305					310					315					320
Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
				325					330					335	
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
			340					345					350		
Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
		355					360					365			
Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
		370				375						380			
Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
385					390					395					400
Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
				405					410					415	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
			420					425					430		
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		435					440					445			
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
		450				455					460				
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala
465					470					475					480
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly
				485					490					495	
Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu
			500					505					510		

eolf-seql

Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		515					520					525			
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His
	530					535					540				
Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
545					550					555					560
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala
			565					570						575	
Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
		580						585					590		
Lys	Ala	Ala													
		595													

<210> 117

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 117

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
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Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20					25					30			
Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His	Leu
	35					40						45			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu
	50				55					60					
Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His
65				70				75						80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85					90					95		
Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly
		100					105						110		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	115					120					125				
Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala
	130				135						140				
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro
145				150						155					160
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
			165					170					175		
Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
		180					185						190		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			

eolf-seql

Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
210						215				220					
Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
				245					250						255
Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290					295				300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
				325					330						335
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
		370				375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410						415
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490						495
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
		530				535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
				565					570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		

eolf-seql

Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 118

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 118

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20					25					30			
Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His	Leu
		35				40						45			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu
	50				55					60					
Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His
65				70				75						80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			85					90					95		
Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly
			100				105						110		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		115				120						125			
Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala
	130					135					140				
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro
145				150						155				160	
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
			165					170						175	
Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			180				185						190		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195				200						205			
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225				230						235				240	
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
			245					250						255	
Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		260					265						270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
	275					280						285			

eolf-seql

Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
290						295				300					
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
			405					410						415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
				565					570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 119

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

eolf-seql

<400> 119

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
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Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20      25      30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35      40      45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50      55      60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85      90      95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100     105     110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115     120     125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130     135     140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145     150     155     160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
165     170     175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
180     185     190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195     200     205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
210     215     220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225     230     235     240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
245     250     255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260     265     270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275     280     285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
290     295     300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305     310     315     320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
325     330     335
Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
340     345     350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
355     360     365

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eolf-seql

His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
370						375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val
		515				520						525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln
	530					535					540				
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
				565					570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580				585						590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 120

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 120

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
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Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His	Leu
		35					40					45			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu
		50				55					60				

eolf-seql

Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly
			100					105					110		
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		115					120					125			
Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala
	130						135				140				
Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro
145					150					155					160
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
				165					170					175	
Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
			180					185					190		
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290					295				300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			

eolf-seql

Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
450						455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln
	530					535					540				
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
				565					570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 121

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 121

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
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Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
		130					135					140			

eolf-seql

Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	
145					150					155					160	
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	
				165					170					175		
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	
			180					185					190			
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	
	195						200					205				
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	
	210					215					220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Ala	Gly	Ala		
225				230						235				240		
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	
			245						250					255		
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
			260					265					270			
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	
	275					280					285					
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	
	290					295				300						
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	
				325					330					335		
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	
			340					345					350			
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	
	355						360					365				
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	
	370					375					380					
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	
385				390						395				400		
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	
			405						410					415		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	
			420					425					430			
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	
		435					440					445				
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	
	450					455					460					
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	
465					470					475				480		
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	
				485					490					495		
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	
			500					505					510			
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	
		515					520					525				

eolf-seql

Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	
530				535				540								
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	
545				550				555				560				
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	
				565				570				575				
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	
				580				585				590				
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala								
595				600												

<210> 122

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 122

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

eolf-seql

Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	225	230	235	240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	245	250	255	
Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	260	265	270	
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	275	280	285	
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	290	295	300	
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	305	310	315	320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	325	330	335	
Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	340	345	350	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	355	360	365	
His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	370	375	380	
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	385	390	395	400
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	405	410	415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	420	425	430	
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	435	440	445	
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	450	455	460	
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	465	470	475	480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	485	490	495	
Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	500	505	510	
Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	515	520	525	
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	530	535	540	
Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	545	550	555	560
Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	565	570	575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	580	585	590	
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala								595	600		

eolf-seql

<210> 123
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 123
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Val Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180 185 190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210 215 220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
245 250 255
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
260 265 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
275 280 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290 295 300

eolf-seql

Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	305		310		315		320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu		325		330		335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala		340		345		350	
Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu		355		360		365	
His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu		370		375		380	
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	385		390		395		400
Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu		405		410		415	
Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr		420		425		430	
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val		435		440		445	
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr		450		455		460	
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	465		470		475		480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg		485		490		495	
Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly		500		505		510	
Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val		515		520		525	
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr		530		535		540	
Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	545		550		555		560
Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys		565		570		575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp		580		585		590	
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala								595		600				

<210> 124

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 124

eolf-seql

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5					10					15	
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu
		35					40					45			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly
		100						105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val
		180					185						190		
Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp
	210					215					220				
Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
				245					250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
		260					265						270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Pro	Trp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
		340						345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				

eolf-seql

Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala
385					390					395					400
Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu
				405					410					415	
Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
			420					425					430		
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys
		435					440					445			
Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile
	450					455					460				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp
465					470					475					480
Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu
			485						490					495	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly
			500					505					510		
Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val
		515					520						525		
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala
	530					535					540				
Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
			565						570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 125

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 125

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

eolf-seql

Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp
465				470					475					480	
Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu
			485						490					495	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly
			500					505					510		
Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala
	530					535					540				
Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
			565						570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 126

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 126

Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5				10					15		
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Leu
		35					40					45			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His
65					70				75					80	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly
			100					105					110		
Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160

eolf-seql

Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val
			180					185					190		
Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp
	210					215					220				
Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
				245					250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro
385					390					395					400
Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu
				405					410					415	
Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro
			420					425					430		
Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys
		435					440					445			
Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile
	450					455					460				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp
465					470					475					480
Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu
				485					490					495	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly
			500					505					510		
Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala
	530					535						540			

eolf-seql

Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
				565					570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 127

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 127

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

eolf-seql

Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	245	250	255
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	260	265	270
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	275	280	285
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	290	295	300
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	305	310	315
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	325	330	335
Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	340	345	350
Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	355	360	365
His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	370	375	380
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	385	390	395
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	405	410	415
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	420	425	430
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	435	440	445
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	450	455	460
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	465	470	475
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	485	490	495
Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	500	505	510
Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	515	520	525
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	530	535	540
Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	545	550	555
Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	565	570	575
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	580	585	590
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala								595	600	

<210> 128

eolf-seql

<211> 637

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 128

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1           5           10           15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20          25          30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35          40          45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50          55          60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65          70          75          80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85          90          95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100         105         110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
115         120         125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
130         135         140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145         150         155         160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
165         170         175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
180         185         190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
195         200         205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
210         215         220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225         230         235         240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
245         250         255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
260         265         270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275         280         285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
290         295         300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305         310         315         320

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eolf-seql

Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	325	330	335
Leu	His	Leu	Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	340	345	350
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	355	360	365
Pro	Leu	His	Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	370	375	380
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	385	390	395
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	405	410	415
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	420	425	430
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	435	440	445
Glu	Val	Leu	Gln	Lys	Leu	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	450	455	460
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Arg	Ser	465	470	475
Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	485	490	495
Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	500	505	510
Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	515	520	525
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	530	535	540
Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly	His	545	550	555
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	565	570	575
Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	580	585	590
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	595	600	605
Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	610	615	620
Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Leu	Asn				625	630	635

<210> 129

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

eolf-seql

<400> 129

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1      5      10      15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20      25      30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35      40      45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50      55      60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65      70      75      80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85      90      95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100     105     110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115     120     125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130     135     140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145     150     155     160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165     170     175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180     185     190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195     200     205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210     215     220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225     230     235     240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
245     250     255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260     265     270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
275     280     285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290     295     300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305     310     315     320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
325     330     335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
340     345     350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
355     360     365

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eolf-seql

His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
370						375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
450						455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485						490					495	
Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly
		500						505					510		
Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr
530						535					540				
Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
			565						570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 130

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 130

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1			5					10					15		
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		20					25					30			
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40				45				
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
		50				55					60				

eolf-seql

Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
		130				135					140				
Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185					190			
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195				200						205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		210				215				220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230				235						240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290					295				300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
		370				375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			

eolf-seql

Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
450						455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515					520						525		
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
				565					570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 131

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 131

Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
1				5					10					15	
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
			20					25					30		
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
		35					40					45			
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
	50					55					60				
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
65					70					75					80
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
				85					90					95	
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
			100					105					110		
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr
		115					120					125			
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
		130				135						140			

eolf-seql

Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	
145					150					155					160	
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	
				165					170					175		
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	
			180					185					190			
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	
	195						200					205				
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	
	210					215					220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Ala	Gly	Ala		
225				230						235				240		
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	
			245						250					255		
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
			260					265					270			
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	
	275					280					285					
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	
	290					295				300						
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	
			325						330					335		
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	
			340					345					350			
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	
	355						360					365				
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	
	370					375					380					
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	
385				390						395				400		
Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	
			405						410					415		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	
			420					425					430			
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	
		435					440					445				
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	
	450					455					460					
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	
465					470					475				480		
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	
				485					490					495		
Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg	Gly	
			500					505					510			
Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile	Val	
		515					520					525				

eolf-seql

Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu	Thr	
530				535				540								
Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu	Ile	
545				550				555				560				
Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	
				565				570				575				
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	
580				585				590								
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala								
595				600												

<210> 132

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 132

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

eolf-seql

Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala
				245					250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		275					280					285			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu
	290					295					300				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440						445		
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				485					490					495	
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln
	530					535					540				
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
				565					570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

eolf-seql

<210> 133

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 133

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
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Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20        25        30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35        40        45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50        55        60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65        70        75        80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85        90        95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100       105       110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115       120       125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130       135       140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145       150       155       160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
165       170       175
Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val
180       185       190
Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195       200       205
Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp
210       215       220
Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala
225       230       235       240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
245       250       255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260       265       270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275       280       285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
290       295       300

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eolf-seql

Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala
305					310					315					320
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His
				325					330					335	
Leu	Ala	Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485						490					495	
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly
			500					505					510		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val
		515					520					525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln
	530					535					540				
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
			565						570					575	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 134

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 134

eolf-seql

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40						45		
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50						55				60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
	115						120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
				165					170					175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
	195						200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
	210					215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
	275						280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310						315				320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr
	355						360					365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val
	370					375					380				

eolf-seql

Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Gly	Lys	Lys	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	
			485					490					495		
Val	Arg	Glu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	
		500					505					510			
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515				520						525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
			565						570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
		580						585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 135

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 135

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
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Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40					45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80

eolf-seql

Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	85	90	95
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	100	105	110
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	115	120	125
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	130	135	140
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	145	150	155
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	165	170	175
Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	180	185	190
Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	195	200	205
Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	210	215	220
Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	225	230	235
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	245	250	255
Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	260	265	270
Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	275	280	285
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	290	295	300
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	305	310	315
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	325	330	335
Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	340	345	350
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	355	360	365
Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	370	375	380
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	385	390	395
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	405	410	415
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	420	425	430
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	435	440	445
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	450	455	460

eolf-seql

Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
			565						570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
		580						585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 136

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 136

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
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Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40					45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120						125		
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160

eolf-seql

Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	165	170	175
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	180	185	190
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	195	200	205
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	210	215	220
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	225	230	235
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	245	250	255
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	260	265	270
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	275	280	285
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	290	295	300
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	305	310	315
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	325	330	335
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	340	345	350
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	355	360	365
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	370	375	380
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	385	390	395
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	405	410	415
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	420	425	430
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	435	440	445
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	450	455	460
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	465	470	475
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	485	490	495
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	500	505	510
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	515	520	525
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	530	535	540

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Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550				555						560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 137

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 137

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

eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	
				245					250					255		
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	
			260					265					270			
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	
		275					280					285				
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	
	290					295					300					
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	
			325						330					335		
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	
		340					345						350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	
	355					360					365					
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	
	370				375					380						
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	
385					390				395						400	
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	
			405					410						415		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	
		420						425					430			
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	
	435					440						445				
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
	450					455					460					
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	
465					470				475						480	
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	
			485					490						495		
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	
		500					505						510			
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	
	515					520						525				
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	
	530				535						540					
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	
545					550				555						560	
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	
			565					570						575		
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	
		580					585						590			
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
	595					600										

<210> 138

eolf-seql

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 138

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1          5          10          15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20        25        30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35        40        45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50        55        60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65        70        75        80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85        90        95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100       105       110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115       120       125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130       135       140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145       150       155       160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165       170       175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
180       185       190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
195       200       205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
210       215       220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225       230       235       240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
245       250       255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
260       265       270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
275       280       285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
290       295       300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305       310       315       320

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eolf-seql

Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys
			325						330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
			405						410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
		420						425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435				440						445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470				475						480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
			485						490					495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
		500						505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550				555						560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
			565						570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
		580						585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 139

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 139

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

eolf-seql

Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala		
			20					25					30				
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly		
		35					40					45					
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn		
	50					55					60						
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu		
65					70					75					80		
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val		
			85					90						95			
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp		
		100					105					110					
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser		
	115					120					125						
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr		
	130					135					140						
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala		
145					150					155					160		
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala		
			165					170						175			
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala		
		180						185					190				
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly		
	195					200					205						
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu		
	210					215				220							
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala		
225					230					235					240		
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His		
			245					250						255			
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys		
			260					265					270				
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala		
	275					280					285						
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln		
	290					295				300							
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr		
305					310					315					320		
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys		
			325					330						335			
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu		
			340				345						350				
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr		
	355					360						365					
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val		
	370					375					380						
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp		
385					390					395					400		

eolf-seql

Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Gly	Lys	Lys	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	
				485				490					495		
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
		500					505						510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
		580						585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 140

<211> 636

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 140

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

eolf-seql

Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	
			100					105					110			
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	
		115					120					125				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	
	130					135					140					
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	
145					150					155					160	
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	
			165						170					175		
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	
		180						185					190			
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
	195					200					205					
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	
	210					215					220					
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	
225					230					235					240	
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	
			245						250					255		
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	
			260					265					270			
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	
	275						280					285				
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	
	290					295					300					
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	
			325						330					335		
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	
			340				345						350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	
		355					360					365				
Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	
	370					375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	
385					390					395					400	
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	
			405						410					415		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	
			420					425					430			
Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	
		435					440					445				
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	
	450					455					460					
Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	
465					470					475					480	

eolf-seql

Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr
				485					490					495	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser
			500					505						510	
Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
		515					520					525			
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
545					550					555					560
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
			565						570					575	
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His
		580						585					590		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
	595					600						605			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
610					615					620					
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala				
625					630					635					

<210> 141

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 141

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		20						25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40					45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			85						90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
		100						105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
	115						120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135						140			

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Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	145	150	155	160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	165	170	175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	180	185	190	
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	195	200	205	
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	210	215	220	
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	225	230	235	240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	245	250	255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	260	265	270	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	275	280	285	
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	290	295	300	
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	305	310	315	320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	325	330	335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	340	345	350	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	355	360	365	
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	370	375	380	
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	385	390	395	400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	405	410	415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	420	425	430	
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	435	440	445	
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	450	455	460	
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	465	470	475	480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	485	490	495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	500	505	510	
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	515	520	525	

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Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
530				535				540							
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545		550				555				560					
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
565				570				575							
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
580				585				590							
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
595		600													

<210> 142

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 142

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

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Ala	Ala	Ser	Met	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Met	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe
		275					280					285			
Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310						315				320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

eolf-seql

<210> 143
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 143
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115 120 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130 135 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145 150 155 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165 170 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
180 185 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
195 200 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
210 215 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225 230 235 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
245 250 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
260 265 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
275 280 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
290 295 300

eolf-seql

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40						45		
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50						55				60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
	115						120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala
				165					170					175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
	195						200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
	210					215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
	275						280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310						315				320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr
	355						360					365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val
	370					375					380				

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Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 145

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 145

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

eolf-seql

Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	85	90	95
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	100	105	110
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	115	120	125
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	130	135	140
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	145	150	155
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	165	170	175
Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	180	185	190
Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	195	200	205
Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	210	215	220
Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	225	230	235
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	245	250	255
Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	260	265	270
Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	275	280	285
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	290	295	300
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	305	310	315
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	325	330	335
Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	340	345	350
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	355	360	365
Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	370	375	380
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	385	390	395
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	405	410	415
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	420	425	430
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	435	440	445
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	450	455	460

eolf-seql

Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser
			500					505					510		
Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Gly	His	Leu	
545					550				555					560	
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
			565						570					575	
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 146

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 146

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35				40						45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75				80	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			85					90						95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120						125		
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160

eolf-seql

Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	165	170	175
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	180	185	190
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	195	200	205
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	210	215	220
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	225	230	235
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	245	250	255
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	260	265	270
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	275	280	285
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	290	295	300
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	305	310	315
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	325	330	335
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	340	345	350
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	355	360	365
Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	370	375	380
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	385	390	395
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	405	410	415
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	420	425	430
Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	435	440	445
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	450	455	460
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	465	470	475
Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	485	490	495
Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	500	505	510
Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	515	520	525
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	530	535	540

eolf-seql

Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 147
 <211> 603
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 147

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

eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His			
				245					250					255				
Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys			
			260					265					270					
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala			
		275					280					285						
Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln			
	290					295					300							
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr			
305					310					315					320			
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys			
			325						330					335				
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu			
		340					345						350					
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr			
	355					360					365							
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val			
	370					375					380							
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp			
385					390					395					400			
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu			
			405						410					415				
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly			
		420						425					430					
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala			
	435						440						445					
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr			
	450					455					460							
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp			
465					470					475					480			
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu			
			485					490						495				
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr			
		500					505						510					
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys			
	515					520						525						
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp			
	530					535					540							
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu			
545					550					555					560			
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln			
			565					570						575				
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His			
	580						585						590					
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala								
	595						600											

<210> 148

eolf-seql

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 148

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1          5          10          15
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20        25        30
Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly
35        40        45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50        55        60
Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr
65        70        75        80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85        90        95
Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn
100       105       110
Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
115       120       125
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
130       135       140
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
145       150       155       160
Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Pro
165       170       175
Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala
180       185       190
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly
195       200       205
Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu
210       215       220
Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala
225       230       235       240
Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His
245       250       255
Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
260       265       270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
275       280       285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
290       295       300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305       310       315       320

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eolf-seql

Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys
			325						330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu
			405						410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470				475						480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
			485						490				495		
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550				555						560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
			565						570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 149

<211> 597

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 149

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

eolf-seql

Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	
			20					25					30			
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	
		35					40					45				
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	
	50					55					60					
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	
65					70					75					80	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	
				85				90						95		
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	
			100				105					110				
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	
	115					120					125					
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
	130					135					140					
Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	
145					150				155						160	
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	
				165				170						175		
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	
			180				185					190				
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	
	195					200						205				
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	
	210					215					220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	
225					230					235					240	
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	
				245				250						255		
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
			260				265						270			
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	
	275					280						285				
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	
	290					295					300					
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
305					310					315					320	
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	
				325				330						335		
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	
			340				345						350			
Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	
	355					360						365				
Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	
	370					375					380					
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	
385				390					395						400	

eolf-seql

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Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
      405                        410                        415
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
      420                        425                        430
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
      435                        440                        445
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
      450                        455                        460
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu
465                        470                        475                        480
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
      485                        490                        495
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
      500                        505                        510
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
      515                        520                        525
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
      530                        535                        540
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
545                        550                        555                        560
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
      565                        570                        575
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
      580                        585                        590
Leu Gln Lys Ala Ala
      595

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<210> 150
 <211> 603
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 150

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

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eolf-seql

Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	
			100					105					110			
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	
		115					120					125				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	
	130					135					140					
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	
145					150					155					160	
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	
			165						170					175		
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	
		180						185					190			
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
	195					200					205					
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	
	210					215					220					
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	
225					230					235					240	
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	
			245						250					255		
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	
			260					265					270			
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	
	275						280					285				
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	
	290					295					300					
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	
			325						330					335		
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	
			340					345					350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	
		355					360					365				
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	
	370					375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	
385					390					395					400	
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	
			405						410					415		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	
			420					425					430			
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	
		435					440					445				
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
	450					455					460					
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	
465					470					475					480	

eolf-seql

Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 151

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 151

Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly
		35					40					45			
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
			165						170					175	

eolf-seql

Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
		210					215					220			
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu
			500					505					510		
Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn
	530					535					540				
Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu
545					550					555					560

eolf-seql

Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln
			565						570					575	
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 152
 <211> 597
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 152

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

eolf-seql

Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
			275				280					285			
Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
			290			295					300				
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
305					310					315					320
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
				325					330					335	
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			340					345					350		
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
		355				360						365			
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
		370				375					380				
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
385					390					395					400
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
				405					410					415	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
			420					425					430		
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
		435				440						445			
Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		450				455					460				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
465					470					475					480
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
				485					490					495	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
			500					505					510		
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
		515				520						525			
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
		530				535					540				
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
545					550					555					560
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
				565					570					575	
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
			580					585					590		
Leu	Gln	Lys	Ala	Ala											
		595													

<210> 153

<211> 582

<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 153

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1          5          10          15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20        25        30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35        40        45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50        55        60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65        70        75        80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85        90        95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100       105       110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115       120       125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
130       135       140
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
145       150       155       160
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg
165       170       175
Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu Glu
180       185       190
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp
195       200       205
Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu
210       215       220
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
225       230       235       240
Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His
245       250       255
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
260       265       270
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
275       280       285
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
290       295       300
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
305       310       315       320
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
325       330       335

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eolf-seql

Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly			
			340					345					350					
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val			
		355					360					365						
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln			
	370					375					380							
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile			
385					390					395					400			
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys			
			405					410					415					
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp			
		420					425					430						
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro			
	435					440					445							
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu			
	450				455					460								
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu			
465				470				475							480			
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro			
			485				490						495					
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu			
		500				505					510							
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr			
	515					520				525								
Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val			
	530					535				540								
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys			
545				550				555							560			
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu			
			565				570						575					
Val	Leu	Gln	Lys	Ala	Ala													
		580																

<210> 154

<211> 561

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 154

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln			
1				5				10				15						
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala			
		20					25					30						
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly			
	35					40					45							

eolf-seql

His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
50					55					60					
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75				80	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
			85						90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu
	130					135					140				
Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala
145					150					155					160
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His
			165						170					175	
Leu	Ala	Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			180					185					190		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu
		195					200					205			
His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
	210					215					220				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro
225					230					235					240
Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				245						250				255	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			260					265					270		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		275					280					285			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
	290					295					300				
Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
305					310					315					320
Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser
				325					330					335	
Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu
			340					345					350		
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		355					360					365			
Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu
		370				375					380				
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
385					390					395					400
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
				405					410					415	
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro
			420					425					430		

eolf-seql

Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg
		435					440					445			
Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp
	450					455					460				
Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala
465					470					475					480
Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
				485					490					495	
Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala
		500						505					510		
Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
	515						520					525			
Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile
	530					535					540				
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
545					550					555					560
Ala															

<210> 155

<211> 582

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 155

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35				40						45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		115					120						125		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp
	130					135					140				
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
145					150					155					160

eolf-seql

Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg
			165						170					175	
Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Ile	Gly	His	Leu	Glu
			180					185					190		
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp
		195					200					205			
Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Tyr	Gly	His	Leu
	210					215					220				
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
225					230					235					240
Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His
				245					250					255	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			260					265					270		
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly
	275						280					285			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly
	290					295					300				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp
305					310					315					320
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				325					330					335	
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly
			340					345					350		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val
		355					360						365		
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln
	370					375					380				
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile
385					390					395					400
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
				405					410					415	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			420					425					430		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly
		435					440					445			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu
	450					455					460				
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu
465					470					475					480
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
				485					490					495	
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
			500					505					510		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr
		515					520					525			
Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
						535					540				

eolf-seql

Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys
545					550					555					560
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
				565					570						575
Val	Leu	Gln	Lys	Ala	Ala										
			580												

<210> 156
 <211> 567
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 156

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

eolf-seql

<400> 157

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40						45		
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85				90						95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
				165				170						175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
	210					215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
305					310					315					320
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			

eolf-seql

His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
370						375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405						410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
		420						425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			
Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
450						455					460				
Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly
465					470					475					480
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
			485						490					495	
Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser
			500					505					510		
His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val
		515				520						525			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala
	530					535					540				
Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile
545					550					555					560
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile
			565						570					575	
Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			580					585					590		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala							
		595					600								

<210> 158

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 158

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40					45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
		50				55					60				

eolf-seql

Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		115					120						125		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135						140			
Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185						190		
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
	195					200						205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215				220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230				235						240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265						270	
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
		290				295					300				
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
	370					375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
		435					440					445			

eolf-seql

Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
450					455					460					
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys
465				470					475						480
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu
			485						490					495	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr
		500						505					510		
Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val
	515						520					525			
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys
	530					535					540				
Thr	Pro	Leu	His	Leu	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	
545				550					555						560
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly
			565						570					575	
Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		580						585					590		
Glu	Val	Leu	Gln	Lys	Ala	Ala									
		595													

<210> 159

<211> 597

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 159

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40						45		
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		115					120						125		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130						135					140			

eolf-seql

Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	
145					150					155					160	
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	
				165					170					175		
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	
			180					185					190			
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	
	195						200					205				
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	
	210					215					220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Ala	Gly	Ala		
225				230						235				240		
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	
				245					250					255		
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
			260					265					270			
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	
	275					280					285					
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	
	290					295				300						
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
305					310					315					320	
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	
				325					330					335		
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	
			340					345					350			
Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	
	355					360						365				
Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	
	370					375				380						
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	
385				390					395					400		
Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	
				405					410					415		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	
			420					425					430			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	
	435					440						445				
Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
	450					455					460					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	
465					470					475				480		
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	
				485					490					495		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	
			500					505					510			
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	
	515					520						525				

eolf-seql

Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
530						535				540					
Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
545					550					555					560
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
				565					570					575	
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
			580					585					590		
Leu	Gln	Lys	Ala	Ala											
			595												

<210> 160

<211> 582

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 160

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

eolf-seql

Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
225					230					235					240
Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Thr	Gly	His
				245					250					255	
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			260					265					270		
Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly
		275					280					285			
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly
	290					295					300				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp
305					310					315					320
Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
				325					330					335	
Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly
			340					345					350		
Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val
		355				360						365			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln
	370					375				380					
Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile
385					390					395					400
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys
			405						410					415	
Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp
			420					425					430		
Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly
		435					440					445			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu
		450				455					460				
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu
465					470					475					480
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
				485					490					495	
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
			500				505						510		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr
		515					520					525			
Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		530				535					540				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys
545					550					555					560
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
				565					570					575	
Val	Leu	Gln	Lys	Ala	Ala										
			580												

<210> 161

eolf-seql

<211> 567

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 161

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1          5          10          15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20        25        30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35        40        45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50        55        60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65        70        75        80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85        90        95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100       105       110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
115       120       125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
130       135       140
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
145       150       155       160
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
165       170       175
Leu His Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu
180       185       190
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
195       200       205
Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val
210       215       220
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn
225       230       235       240
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu
245       250       255
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
260       265       270
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
275       280       285
Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
290       295       300
Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
305       310       315       320

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eolf-seql

Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
			325						330					335	
Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp
			340					345					350		
Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
		355					360					365			
Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala
	370					375					380				
Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
385					390					395					400
Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala
			405					410						415	
Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly
		420						425					430		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys
		435				440						445			
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu
	450				455						460				
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr
465					470					475					480
Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val
			485					490						495	
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys
		500						505					510		
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu	Glu	Ile	Val	Glu
		515					520						525		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly
	530					535					540				
Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
545					550					555					560
Glu	Val	Leu	Gln	Lys	Ala	Ala									
			565												

<210> 162

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 162

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
	35						40					45			

eolf-seql

His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
50						55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	
			165					170						175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
		210				215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
305					310					315					320
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325					330					335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340					345					350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
		355					360					365			
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
		370				375					380				
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385					390					395					400
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
				405					410					415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420					425					430		

eolf-seql

```

Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
    435                      440                      445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                      455                      460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                      470                      475                      480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
    485                      490                      495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
    500                      505                      510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
    515                      520                      525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                      535                      540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                      550                      555                      560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
    565                      570                      575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
    580                      585                      590
Ile Ala Glu Val Leu Gln Lys Ala Ala
    595                      600

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<210> 163

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 163

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1      5      10      15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
    20      25      30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
    35      40      45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50      55      60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65      70      75      80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
    85      90      95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
    100     105     110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
    115     120     125

```

eolf-seql

Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135				140					
Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145				150					155						160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165				170						175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180				185					190			
Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
	195					200					205				
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
210					215					220					
Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Lys	Ala	Gly	Ala	
225				230				235						240	
Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245				250						255	
Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260				265						270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
	275					280					285				
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
290					295					300					
Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr
305				310					315						320
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu
				325				330						335	
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys
			340				345						350		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu
	355					360					365				
His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu
370					375					380					
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr	Pro
385				390					395					400	
Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			405				410							415	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr
			420				425					430			
Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
	435					440					445				
Leu	Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
450					455					460					
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys
465				470					475					480	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu
			485					490						495	
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr
			500				505						510		

eolf-seql

```

Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
   515                               520                               525
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
   530                               535                               540
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
545                               550                               555                               560
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
   565                               570                               575
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
   580                               585                               590
Glu Val Leu Gln Lys Ala Ala
   595

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<210> 164
 <211> 603
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 164

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

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eolf-seql

Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
210						215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
	275						280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
290						295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr
	355						360					365			
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val
370						375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
450						455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Glu	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		

eolf-seql

Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 165

<211> 636

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 165

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1			5					10					15		
Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala
		20					25					30			
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
	35					40					45				
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50				55					60					
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70				75					80	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val
			85					90					95		
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
		100					105					110			
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
	115					120						125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150				155					160	
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
			165					170					175		
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
		180					185					190			
Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
	195					200					205				
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
	210					215					220				
Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230				235					240	
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His
			245					250						255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys
		260					265						270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
	275					280						285			

eolf-seql

Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
290						295				300					
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		370				375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu
			405						410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly
			420				425						430		
Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val
		435				440						445			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe
		450				455				460					
Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu
465					470					475					480
Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr
				485					490					495	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser
			500					505					510		
Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
		515					520					525			
Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		530				535					540				
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
545					550					555					560
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
				565					570					575	
Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
			580					585					590		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala
		595					600					605			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
	610					615					620				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Leu	Asn				
625					630					635					

<210> 166

<211> 636

<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 166

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1          5          10          15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
20        25        30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35        40        45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50        55        60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65        70        75        80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val
85        90        95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100       105       110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115       120       125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130       135       140
Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala
145       150       155       160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165       170       175
Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala
180       185       190
Ala His Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
195       200       205
Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu
210       215       220
Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225       230       235       240
Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His
245       250       255
Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
260       265       270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe
275       280       285
Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
290       295       300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305       310       315       320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
325       330       335

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eolf-seql

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35					40						45		
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50						55				60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		115					120					125			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp
			180					185					190		
Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Ala
		210					215				220				
Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala
				245					250					255	
Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu
		275					280					285			
Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
305					310					315					320
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala
				325					330					335	
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly
			340					345					350		
Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu
		355					360					365			
Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
	370					375					380				

eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His
385					390					395					400
Leu	Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
				405					410					415	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu
			420					425					430		
His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu
		435					440					445			
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala
	450					455					460				
Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu
465					470					475					480
Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
				485					490					495	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu
		500						505					510		
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met
		515					520					525			
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
	530					535				540					
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
545					550					555					560
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr
				565					570					575	
Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val
			580					585					590		
Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys
		595					600					605			
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
	610					615					620				
Val	Leu	Gln	Lys	Leu	Asn										
625					630										

<210> 168

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 168

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
	35						40					45			

eolf-seql

His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
50						55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		115					120					125			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170					175	
Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	His
			180				185						190		
Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195				200						205			
Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ser
				245					250					255	
Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			260					265					270		
Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe	Asp	Ile
		275					280					285			
Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys	Ala
	290					295					300				
Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
305					310					315					320
Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala
				325					330					335	
Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly
			340					345					350		
Ala	Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu
		355					360					365			
Ala	Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
	370					375					380				
Gly	Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His
385					390					395					400
Leu	Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
				405					410					415	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu
			420					425					430		

eolf-seql

His	Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
		435					440					445			
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro
	450					455					460				
Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu
465					470					475					480
Gln	Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
				485					490					495	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu
		500						505					510		
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met
	515						520					525			
Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro
	530					535					540				
Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu
545					550					555					560
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr
			565						570					575	
Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val
		580						585					590		
Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys
	595					600					605				
Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
	610					615					620				
Val	Leu	Gln	Lys	Leu	Asn										
625					630										

<210> 169

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 169

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

eolf-seql

Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	
			100					105					110			
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	
		115					120					125				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	
	130					135					140					
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	
145					150				155						160	
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	
			165					170						175		
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala	
		180						185					190			
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	
	195					200					205					
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu	
	210				215						220					
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	
225					230					235					240	
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His	
			245					250					255			
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	
			260					265					270			
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	
	275					280						285				
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	
	290					295					300					
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	
305					310					315					320	
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	
			325						330					335		
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	
			340				345						350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	
		355				360						365				
Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	
	370					375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	
385					390					395					400	
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	
			405					410						415		
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	
			420					425					430			
Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	
		435					440					445				
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	
	450					455					460					
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	
465					470					475					480	

eolf-seql

Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	
Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr
			500					505					510		
Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 170

<211> 597

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 170

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35				40						45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Gly
		115					120					125			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala
145					150					155					160
Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				165					170						175

eolf-seql

Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro
			180					185					190		
Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Lys	Asp	Tyr	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala
	210					215					220				
Ala	Val	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala
225					230					235					240
Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala
				245					250					255	
Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala
			260					265					270		
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
		275					280					285			
Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
	290					295					300				
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
305					310					315					320
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
				325					330					335	
Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
			340					345					350		
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
		355					360					365			
Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
						375					380				
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His
385					390					395					400
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys
					405				410					415	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
			420					425					430		
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
		435				440						445			
Lys	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	450					455					460				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu
465					470					475					480
Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys
				485					490					495	
Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu
			500					505					510		
His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu
		515					520					525			
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro
	530					535					540				
Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
545					550					555					560

eolf-seql

Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr
			565						570					575	
Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val
			580					585					590		
Leu	Gln	Lys	Ala	Ala											
			595												

<210> 171
 <211> 603
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein comprising four designed ankyrin repeat domains

<400> 171

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

eolf-seql

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Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
    260                265                270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
    275                280                285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                295                300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                310                315                320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
    325                330                335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
    340                345                350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
    355                360                365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                375                380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                390                395                400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
    405                410                415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
    420                425                430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
    435                440                445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                455                460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                470                475                480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
    485                490                495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
    500                505                510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
    515                520                525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                535                540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545                550                555                560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
    565                570                575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
    580                585                590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
    595                600

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<210> 172

<211> 603

<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 172

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1          5          10          15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20        25        30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35        40        45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50        55        60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65        70        75        80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85        90        95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100       105       110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115       120       125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130       135       140
Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala
145       150       155       160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165       170       175
Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala
180       185       190
Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly
195       200       205
Ala Asp Val Asn Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu
210       215       220
Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225       230       235       240
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
245       250       255
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
260       265       270
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
275       280       285
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
290       295       300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305       310       315       320
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
325       330       335

```

eolf-seql

```

Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu
      340      345      350
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
      355      360      365
Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val
      370      375      380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn
385      390      395      400
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu
      405      410      415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
      420      425      430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
      435      440      445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
      450      455      460
Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465      470      475      480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
      485      490      495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
      500      505      510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
      515      520      525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
      530      535      540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545      550      555      560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
      565      570      575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
      580      585      590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
      595      600

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<210> 173

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 173

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Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1      5      10      15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
      20      25      30

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eolf-seql

Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
	35						40					45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
				165					170						175
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185				190			
Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
	210					215					220				
Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	

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Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
			485						490					495	
Val	Arg	Ile	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	
		500					505					510			
Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu
	515					520						525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Gly	His	Leu	
545					550				555					560	
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
			565					570					575		
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
		580					585					590			
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 174

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 174

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

eolf-seql

Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
		130					135					140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala
				165					170					175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
		210				215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
		290				295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Glu	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Phe	Ser	His	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu	Lys	Ile	Val	Glu	Val
		370				375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Ala	Gly	Lys
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Ile	Phe	Gly
			420					425					430		
Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala
		435					440					445			
Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
		450					455				460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu
				485					490					495	

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Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser
			500					505					510		
Thr	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu
		515					520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
		530				535					540				
Phe	Gln	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Val	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
		595					600								

<210> 175

<211> 636

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 175

Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly
		35				40						45			
His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp
65					70					75				80	
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
		130				135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
				165					170					175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185						190	

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Ala	Asp	Ala	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
		210				215					220				
Ala	Ala	Ser	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Ala	Gly	Asn	Thr	Pro	Leu	His
				245					250					255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Lys	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr
		355					360					365			
Pro	Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val
	370					375					380				
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr
385					390					395					400
Thr	Pro	Leu	His	Leu	Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly
			420					425					430		
Trp	Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val
		435					440					445			
Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe
	450					455					460				
Gly	Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu
465					470					475					480
Ala	Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr
				485					490					495	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser
			500					505					510		
Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp
		515					520					525			
Glu	Val	Arg	Glu	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp
	530					535					540				
Tyr	Phe	Ser	His	Thr	Pro	Leu	His	Leu	Ala	Ala	Arg	Asn	Gly	His	Leu
545					550					555					560
Lys	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys
				565					570					575	

eolf-seql

Asp	Phe	Ala	Gly	Lys	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asp	Gly	His
			580					585					590		
Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala
		595					600					605			
Gln	Asp	Ile	Phe	Gly	Lys	Thr	Pro	Ala	Asp	Ile	Ala	Ala	Asp	Ala	Gly
	610					615					620				
His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala				
625					630					635					

<210> 176

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 176

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

eolf-seql

Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Gln	Phe	Gly	Lys	Thr	Ala	Phe	Asp
			245						250					255	
Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys
			260					265					270		
Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
		275					280					285			
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu
	290					295					300				
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu
305				310						315					320
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Ser	Thr	Gly	Trp	Thr	Pro
			325						330					335	
Leu	His	Leu	Ala	Ala	Pro	Trp	Gly	His	Pro	Glu	Ile	Val	Glu	Val	Leu
		340					345					350			
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Phe	Gln	Gly	Trp	Thr
	355					360					365				
Pro	Leu	His	Leu	Ala	Ala	Ala	Gly	His	Leu	Glu	Ile	Val	Glu	Val	
370					375					380					
Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys
385				390						395					400
Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu
			405						410					415	
Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro
		420						425				430			
Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu
	435					440						445			
Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val
	450					455					460				
Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu	Arg
465				470						475					480
Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu	Ile
			485						490					495	
Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn	Glu
		500					505						510		
Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu	Glu
	515						520					525			
Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln	Asp
	530					535					540				
Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu
545				550						555					560
Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala						
			565						570						

<210> 177

<211> 636

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 177

Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln
1				5					10					15	
Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly
		35					40					45			
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val
				85				90						95	
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
			100				105						110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
		130				135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
				165				170						175	
Asp	Val	Asn	Ala	Lys	Asp	Arg	Tyr	Gly	Asp	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Asp	Ile	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Glu	Asp	Tyr	Phe	Gly	Asn	Thr	Pro	Leu	His	Leu
	210					215					220				
Ala	Ala	Ser	Tyr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asp	Tyr	Gly	Asn	Thr	Pro	Leu	His
				245				250						255	
Leu	Ala	Ala	Asn	Thr	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
			260					265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala
		275					280					285			
Asp	Leu	Ala	Ala	Asp	Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln
	290					295					300				
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys
				325					330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
			340					345					350		

Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala
			20					25					30		
Lys	Asp	Glu	Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly
		35					40					45			
His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn
	50					55					60				
Ala	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser
65					70					75					80
Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val
				85					90					95	
Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
						135						140			
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Met	Lys	Leu	Leu	Glu	Ala	Ala
145					150					155					160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala
				165					170					175	
Asp	Val	Asn	Ala	His	Asp	Thr	Trp	Gly	Leu	Thr	Pro	Leu	His	Leu	Ala
			180					185					190		
Ala	Phe	His	Gly	His	Gln	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Gly
		195					200					205			
Ala	Asp	Val	Asn	Ala	Gln	Asp	Phe	Tyr	Gly	Lys	Thr	Pro	Leu	His	Leu
						215					220				
Ala	Ala	Leu	Arg	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Tyr
225					230					235					240
Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Gln	Phe	Gly	Lys	Thr	Ala	Phe	Asp
				245					250					255	
Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln	Lys
			260					265					270		
Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro
		275					280					285			
Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu
						295					300				
Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu
305					310					315					320
Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro
				325					330					335	
Leu	His	Leu	Ala	Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu
			340					345					350		
Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr
		355					360					365			
Pro	Leu														

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Thr	Pro	Leu	His	Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu
				405					410					415	
Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly
			420					425					430		
Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala
		435					440					445			
Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
	450					455					460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480
Leu	Asp	Lys	Lys	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	
				485				490					495		
Val	Arg	Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Glu
		500					505						510		
Arg	Gly	Thr	Thr	Pro	Leu	His	Leu	Ala	Ala	Val	Tyr	Gly	His	Leu	Glu
	515					520						525			
Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly	Ala	Asp	Val	Asn	Ala	Lys	Asn
	530					535					540				
Glu	Thr	Gly	Tyr	Thr	Pro	Leu	His	Leu	Ala	Asp	Ser	Ser	Gly	His	Leu
545					550					555					560
Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	His	Ser	Ala	Asp	Val	Asn	Ala	Gln
				565					570					575	
Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp	Ala	Gly	His
			580					585					590		
Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala					
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<210> 179

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein comprising four designed ankyrin repeat domains

<400> 179

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

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Asn	Ala	Gln	Asp	Lys	Ser	Gly	Lys	Thr	Pro	Ala	Asp	Leu	Ala	Ala	Asp
			100					105					110		
Ala	Gly	His	Glu	Asp	Ile	Ala	Glu	Val	Leu	Gln	Lys	Ala	Ala	Gly	Ser
		115					120					125			
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr
	130					135					140				
Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Asp	Lys	Lys	Leu	Leu	Glu	Ala	Ala
145					150				155						160
Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu	Leu	Lys	Ala	Gly	Ala
			165					170						175	
Asp	Val	Asn	Ala	Lys	Asp	Tyr	Leu	Gly	Trp	Thr	Pro	Leu	His	Leu	Ala
		180						185					190		
Ala	His	Glu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala	Gly
	195					200					205				
Ala	Asp	Val	Asn	Ala	Lys	Asp	Val	Ser	Gly	Tyr	Thr	Pro	Leu	His	Leu
210					215					220					
Ala	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys	Ala
225					230				235						240
Gly	Ala	Asp	Val	Asn	Ala	Lys	Asp	Asn	Thr	Gly	Trp	Thr	Pro	Leu	His
			245					250						255	
Leu	Ser	Ala	Asp	Leu	Gly	His	Leu	Glu	Ile	Val	Glu	Val	Leu	Leu	Lys
		260						265					270		
Ala	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Lys	Phe	Gly	Lys	Thr	Ala	Phe
	275					280						285			
Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gln
290					295					300					
Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr
305					310					315					320
Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp	Leu	Gly	Met	Lys
			325						330					335	
Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg	Ile	Leu
		340				345							350		
Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	His	Asp	Thr	Trp	Gly	Leu	Thr
	355					360						365			
Pro	Leu	His	Leu	Ala	Ala	Phe	His	Gly	His	Gln	Glu	Ile	Val	Glu	Val
370					375						380				
Leu	Leu	Lys	His	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Phe	Tyr	Gly	Lys
385					390				395						400
Thr	Pro	Leu	His	Leu	Ala	Ala	Leu	Arg	Gly	His	Leu	Glu	Ile	Val	Glu
			405					410						415	
Val	Leu	Leu	Lys	Tyr	Gly	Ala	Asp	Val	Asn	Ala	Gln	Asp	Gln	Phe	Gly
		420						425					430		
Lys	Thr	Ala	Phe	Asp	Ile	Ser	Ile	Asp	Asn	Gly	Asn	Glu	Asp	Leu	Ala
	435					440						445			
Glu	Ile	Leu	Gln	Lys	Ala	Ala	Gly	Ser	Pro	Thr	Pro	Thr	Pro	Thr	Thr
450					455						460				
Pro	Thr	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Ser	Asp
465					470					475					480

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<220>
 <221> VARIANT
 <222> 1..33
 <223> Optionally up to 5, 4, 3, 2, 1, 0 amino acids in other than the positions denoted with Xaa can be exchanged by any amino acid

<220>
 <221> VARIANT
 <222> 5
 <223> Xaa represents an amino acid residue selected from the group consisting of D, G and S

<220>
 <221> VARIANT
 <222> 15
 <223> Xaa represents an amino acid residue selected from the group consisting of E, N, D, H, S, A, Q, T and G

<220>
 <221> VARIANT
 <222> 16
 <223> Xaa represents an amino acid residue selected from the group consisting of G and D

<220>
 <221> VARIANT
 <222> 19
 <223> Xaa represents an amino acid residue selected from the group consisting of E, K and G

<220>
 <221> VARIANT
 <222> 27
 <223> Xaa represents an amino acid residue selected from the group consisting of H, Y, A and N

<400> 181
 Xaa Asp Tyr Phe Xaa His Thr Pro Leu His Leu Ala Ala Arg Xaa Xaa
 1 5 10 15
 His Leu Xaa Ile Val Glu Val Leu Leu Lys Xaa Gly Ala Asp Val Asn
 20 25 30
 Ala