

# SEQUENCE LISTING

<110> Almirall S.A.

<120> Novel compounds activating the Nrf2 pathway

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<140> 17382558.9

<141> 2017-08-08

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<170> PatentIn version 3.5

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| Cys | Asp | Ala | Glu | Thr | Gly | Glu | Cys | Xaa | Arg | Lys | Lys | Arg | Arg | Gln | Arg |
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<400> 37

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
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<210> 38  
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<400> 38

Xaa Leu Gln Cys Asp Ala Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 39

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<220>

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<400> 39

Xaa Leu Gln Cys Asp Ala Glu Thr Gly Glu Cys Leu Pro  
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<400> 40

Xaa Leu Gln Phe Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

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<400> 41

Xaa Phe Asp Pro Glu Thr Gly Glu Cys  
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<220>

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<222> (22)..(22)

<223> AMIDATION

<400> 42

Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro Xaa Arg Lys Lys  
1 5 10 15

Arg Arg Gln Arg Arg Arg  
20

<210> 43

<211> 8

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<223> AMIDATION

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<400> 43

Cys Asp Ala Glu Thr Gly Glu Cys  
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<400> 44

Xaa Leu Leu Cys Asp Pro Glu Thr Gly Glu Cys Leu Leu  
1 5 10

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<400> 45

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 46  
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<400> 46

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

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<400> 47

Xaa Lys Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 48  
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<400> 48

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 49  
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<223> binding site for cyclization

<400> 49

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Lys | Gln | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

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<400> 51

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1 5 10

<210> 52  
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<400> 52

Xaa Val Val Cys Asp Pro Glu Thr Gly Glu Cys Val Val  
1 5 10

<210> 53  
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<400> 53

Xaa Lys Lys Cys Asp Pro Glu Thr Gly Glu Cys Lys Lys  
1 5 10

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<220>  
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<400> 54

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro Xaa Arg Lys  
1 5 10 15

Lys Arg Arg Gln Arg Arg Arg  
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<210> 55  
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<400> 55

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

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<222> (10)..(10)

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<223> bAla

<220>

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<222> (22)..(22)

<223> AMIDATION

<400> 56

Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro Xaa Arg Lys Lys  
1 5 10 15

Arg Arg Gln Arg Arg Arg  
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<222> (13)..(13)  
<223> AMIDATION

<400> 57

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Lys | Lys | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 58  
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Arg Arg Gln Arg Arg Arg  
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<210> 59

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<400> 59

Leu Leu Cys Asp Pro Glu Thr Gly Glu Cys Leu Leu Xaa Arg Lys Lys  
1 5 10 15

Arg Arg Gln Arg Arg Arg  
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<210> 60  
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<400> 60

Leu Leu Cys Asp Pro Glu Thr Gly Glu Cys Leu Leu Xaa Arg Lys Lys  
1 5 10 15

Arg Arg Gln Arg Arg Arg  
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<210> 61  
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<220>  
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<220>  
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<223> binding site for cyclization

<220>  
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<222> (13)..(13)  
<223> AMIDATION

<400> 61

Xaa Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 62  
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<220>  
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<220>  
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<223> binding site for cyclization

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<223> AMIDATION

<400> 62

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Leu | Gln | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 63

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<223> AMIDATION

<400> 63

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Leu | Xaa | Arg | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Gln | Arg | Arg | Arg |
|     |     | 20  |     |     |     |

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<220>  
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1 5 10

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<220>  
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<220>  
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<220>  
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<223> AMIDATION

<400> 65

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Leu | Gln | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 66  
<211> 22  
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<213> Artificial Sequence

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<222> (10)..(10)  
<223> binding site for cyclization

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<223> bAla

<220>

<221> MOD\_RES  
<222> (22)..(22)  
<223> AMIDATION

<400> 66

Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro Xaa Arg Lys Lys  
1 5 10 15

Arg Arg Gln Arg Arg Arg  
20

<210> 67  
<211> 22  
<212> PRT  
<213> Artificial Sequence

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<223> peptidic sequences of the compounds of formula (I)

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<223> binding site for cyclization

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<222> (10)..(10)  
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<222> (13)..(13)  
<223> bAla

<220>  
<221> MOD\_RES  
<222> (22)..(22)  
<223> AMIDATION

<400> 67

Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro Xaa Arg Lys Lys  
1 5 10 15

Arg Arg Gln Arg Arg Arg  
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<210> 68

<211> 21  
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<222> (10)..(10)  
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<223> bAla

<220>  
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<222> (21)..(21)  
<223> AMIDATION

<400> 68

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro | Xaa | Arg | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Arg | Arg | Arg | Arg | Arg |
|     |     |     |     | 20  |

<210> 69  
<211> 23  
<212> PRT  
<213> Artificial Sequence

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<222> (10)..(10)  
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<223> bAla

<220>  
<221> MOD\_RES  
<222> (23)..(23)  
<223> AMIDATION

<400> 69

Leu Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro Xaa Arg Arg Arg  
1 5 10 15

Arg Arg Arg Arg Arg Arg Arg  
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<210> 70  
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<220>  
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<223> Stearyl

<220>  
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<222> (1)..(1)  
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<223> D-Pro

<220>  
<221> BINDING  
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<223> binding site for cyclization

<400> 70

Pro Gln Cys Asp Arg Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 71  
<211> 22  
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<213> Artificial Sequence

<220>  
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<223> bAla

<220>  
<221> MOD\_RES  
<222> (22)..(22)  
<223> AMIDATION

<400> 71

Leu Gln Cys Asp Phe Glu Thr Gly Glu Cys Leu Pro Xaa Arg Lys Lys  
1                      5                      10                      15

Arg Arg Gln Arg Arg Arg  
20

<210> 72  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)

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<223> (4S)-aminoproline

<220>  
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<222> (1)..(1)  
<223> Stearyl

<220>  
<221> BINDING  
<222> (1)..(1)  
<223> binding site for cyclization

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<222> (3)..(3)  
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<220>  
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<220>  
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<220>

<221> BINDING  
<222> (12)..(12)  
<223> binding site for cyclization

<400> 72

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 73  
<211> 12  
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<220>  
<223> peptidic sequences of the compounds of formula (I)

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<222> (1)..(1)  
<223> Stearyl

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<222> (12)..(12)  
<223> D-Pro

<220>  
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<222> (12)..(12)  
<223> binding site for cyclization

<400> 73

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 74  
<211> 12  
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<213> Artificial Sequence

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<223> (4S)-aminoproline

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<220>  
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<400> 74

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 75

<211> 12

<212> PRT

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<220>

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<223> ACETYLTATION

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<220>

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<222> (10)..(10)

<223> binding site for cyclization

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<222> (12)..(12)

<223> D-Pro

<400> 75

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
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<210> 76

<211> 12  
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<222> (3)..(3)  
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<222> (10)..(10)  
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<223> D-Pro

<220>  
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<223> AMIDATION

<400> 76

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 77  
<211> 12  
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<213> Artificial Sequence

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<220>  
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<223> D-Pro

<220>  
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<400> 77

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
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<210> 78  
<211> 12  
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<220>  
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<222> (1)..(1)  
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<223> D-Pro

<220>  
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<222> (12)..(12)  
<223> binding site for cyclization

<400> 78

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 79  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)'

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<220>  
<221> BINDING  
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<223> D-Pro

<220>  
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<400> 79

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 80  
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<220>  
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<223> Miristoyl

<220>  
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<223> (4S)-aminoproline

<220>

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<222> (1)..(1)

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<220>

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<223> binding site for cyclization

<400> 80

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
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<210> 81

<211> 12

<212> PRT

<213> Artificial Sequence

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<223> (4S)-aminoproline

<220>

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<220>  
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<223> D-Pro

<400> 81

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 82  
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<223> Stearyl

<220>  
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<400> 82

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Lys Pro  
1 5 10

<210> 83  
<211> 12  
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<220>  
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<220>  
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<400> 83

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 84  
<211> 12  
<212> PRT  
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<220>  
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<220>  
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<220>  
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<220>  
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<400> 84

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 85  
<211> 12  
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<220>  
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<220>  
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<222> (1)..(1)  
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<220>  
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<222> (3)..(3)  
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<222> (10)..(10)  
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<223> binding site for cyclization

<220>

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<222> (12)..(12)

<223> D-Pro

<400> 85

|     |     |     |     |     |     |     |     |     |     |     |     |
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| Pro | Gln | Cys | Asp | Pro | Glu | Thr | Gly | Glu | Cys | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 86

<211> 12

<212> PRT

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<220>

<221> LIPID

<222> (1)..(1)

<223> alpha-linolenyl

<220>

<221> MOD\_RES

<222> (1)..(1)

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<220>

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<223> binding site for cyclization

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<222> (12)..(12)

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<223> D-Pro

<400> 86

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 87  
<211> 12  
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<220>  
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<220>  
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<220>  
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<223> D-Pro

<400> 87

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
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<210> 88  
<211> 12  
<212> PRT  
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<220>  
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<222> (1)..(1)  
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<400> 88

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 89  
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<220>  
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<400> 89

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 90  
<211> 12  
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<223> Arachidyl

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<221> MOD\_RES

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<220>

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<223> binding site for cyclization

<220>

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<222> (3)..(3)

<223> binding site for cyclization

<220>

<221> BINDING

<222> (10)..(10)

<223> binding site for cyclization

<220>

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<222> (12)..(12)

<223> binding site for cyclization

<220>

<221> MOD\_RES

<222> (12)..(12)

<223> D-Pro

<400> 90

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 91

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> peptidic sequences of the compounds of formula (I)'

<220>  
<221> LIPID  
<222> (1)..(1)  
<223> Stearyl (appended to lateral chain)

<220>  
<221> BINDING  
<222> (1)..(1)  
<223> binding site for cyclization

<220>  
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<222> (3)..(3)  
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<220>  
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<400> 91

Lys Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 92  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)'

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<222> (1)..(1)  
<223> Stearyl (appended to N-alpha atom)

<220>  
<221> BINDING

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<222> (10)..(10)  
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<400> 92

Lys Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 93  
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<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)'

<220>  
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<223> Arachidyl

<220>  
<221> MOD\_RES  
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<223> (4S)-aminoproline

<220>  
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<223> binding site for cyclization

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<221> BINDING  
<222> (3)..(3)  
<223> binding site for cyclization

<220>  
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<222> (5)..(5)  
<223> L-thioproline

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<222> (10)..(10)  
<223> binding site for cyclization

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<222> (12)..(12)  
<223> binding site for cyclization

<220>  
<221> MOD\_RES  
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<223> D-Pro

<400> 93

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 94  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)'

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<222> (1)..(1)  
<223> Arachidyl

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> (4S)-aminoproline

<220>  
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<220>  
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<223> binding site for cyclization

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<223> L-thioproline

<220>  
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<223> binding site for cyclization

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<222> (12)..(12)  
<223> D-Pro

<220>  
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<222> (12)..(12)  
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<400> 94

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 95  
<211> 12  
<212> PRT  
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<220>  
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<223> Arachidyl

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<223> binding site for cyclization

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<223> D-Pro

<220>  
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<400> 95

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 96  
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<222> (1)..(1)  
<223> Stearyl

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> (4S)-aminoproline

<220>  
<221> BINDING  
<222> (1)..(1)  
<223> binding site for cyclization

<220>  
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<223> binding site for cyclization

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<222> (5)..(5)

<223> L-thioprolin

<220>

<221> BINDING

<222> (10)..(10)

<223> binding site for cyclization

<220>

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<222> (12)..(12)

<223> D-Pro

<220>

<221> BINDING

<222> (12)..(12)

<223> binding site for cyclization

<400> 96

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 97

<211> 12

<212> PRT

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<223> peptidic sequences of the compounds of formula (I)'

<220>

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<222> (1)..(1)

<223> Stearyl

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> (4S)-aminoprolin

<220>

<221> BINDING

<222> (1)..(1)

<223> binding site for cyclization

<220>

<221> BINDING

<222> (3)..(3)  
<223> binding site for cyclization

<220>  
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<222> (5)..(5)  
<223> L-thioprolin

<220>  
<221> BINDING  
<222> (10)..(10)  
<223> binding site for cyclization

<220>  
<221> MOD\_RES  
<222> (12)..(12)  
<223> D-Pro

<220>  
<221> BINDING  
<222> (12)..(12)  
<223> binding site for cyclization

<400> 97

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 98  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)'

<220>  
<221> LIPID  
<222> (1)..(1)  
<223> Nonadecanoyl

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> (4S)-aminoprolin

<220>  
<221> BINDING  
<222> (1)..(1)  
<223> binding site for cyclization

<220>

<221> BINDING  
<222> (3)..(3)  
<223> binding site for cyclization

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<223> binding site for cyclization

<220>  
<221> MOD\_RES  
<222> (12)..(12)  
<223> D-Pro

<220>  
<221> BINDING  
<222> (12)..(12)  
<223> binding site for cyclization

<400> 98

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 99  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptidic sequences of the compounds of formula (I)'

<220>  
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<222> (1)..(1)  
<223> Stearyl

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> bAla

<220>  
<221> BINDING  
<222> (4)..(4)  
<223> binding site for cyclization

<220>  
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<222> (11)..(11)  
<223> binding site for cyclization

<220>  
<221> MOD\_RES  
<222> (13)..(13)  
<223> Amidation

<400> 99

Xaa Leu Leu Cys Asp Pro Glu Thr Gly Glu Cys Leu Leu  
1 5 10

<210> 100  
<211> 12  
<212> PRT  
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<220>  
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<220>  
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<222> (1)..(1)  
<223> Stearyl

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> (4S)-aminoproline

<220>  
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<222> (1)..(1)  
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<223> binding site for cyclization

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<223> binding site for cyclization

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<222> (12)..(12)  
<223> D-Pro

<220>  
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<222> (12)..(12)  
<223> binding site for cyclization

<400> 100

Pro Gln Cys Asp Pro Glu Thr Gly Glu Cys Leu Pro  
1 5 10

<210> 101

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> sequence motif of Nrf2

<400> 101

Glu Thr Gly Glu  
1

<210> 102

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> high affinity sequence domain between Nrf2 and the kelch domain  
of Keap1

<400> 102

Asp Glu Glu Thr Gly Glu  
1 5

<210> 103

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> motif containing a beta turn region stablilized by aspartate and  
threonine residues

<220>

<221> MOD\_RES

<222> (2)..(2)

<223> Xaa can be any naturally occurring amino acid

<400> 103

Asp Xaa Glu Thr Gly Glu

1 5

<210> 104  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 104

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

<210> 105  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 105

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Gln  
1 5 10

<210> 106  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 106

Arg Arg Arg Arg Arg Arg Arg Arg  
1 5

<210> 107  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 107

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys  
1 5 10 15

<210> 108  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 108

Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro  
1 5 10 15

<210> 109  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 109

Lys Leu Ala Leu Lys Leu Ala Leu Lys Ala Leu Lys Ala Ala Leu Lys  
1 5 10 15

Leu Ala

<210> 110  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 110

Arg Gln Ile Lys Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys  
1 5 10 15

<210> 111  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 111

Arg Gly Gly Arg Leu Ser Tyr Ser Arg Arg Arg Phe Ser Thr Ser Thr  
1 5 10 15

Gly Arg

<210> 112  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 112

Arg Arg Leu Ser Tyr Ser Arg Arg Arg Phe  
1 5 10

<210> 113  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 113

Pro Ile Arg Arg Arg Lys Lys Leu Arg Arg Leu Lys  
1 5 10

<210> 114  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>

<223> cell penetrating peptide

<400> 114

Arg Arg Gln Arg Arg Thr Ser Lys Leu Met Lys Arg  
1 5 10

<210> 115

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> cell penetrating peptide

<400> 115

Arg Arg Arg Arg Asn Arg Thr Arg Arg Asn Arg Arg Arg Val Arg  
1 5 10 15

<210> 116

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> cell penetrating peptide

<400> 116

Lys Met Thr Arg Ala Gln Arg Arg Ala Ala Ala Arg Arg Asn Arg Trp  
1 5 10 15

Thr Ala Arg

<210> 117

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> cell penetrating peptide

<400> 117

Thr Arg Arg Gln Arg Thr Arg Arg Ala Arg Arg Asn Arg  
1 5 10

<210> 118  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 118

Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Pro Pro Gln  
1 5 10

<210> 119  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell penetrating peptide

<400> 119

Lys Leu Ala Leu Lys Leu Ala Leu Lys Leu Ala Leu Ala Leu Lys Leu  
1 5 10 15

Ala

<210> 120  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tag2 sequence

<220>  
<221> MOD\_RES  
<222> (10)..(10)  
<223> AMIDATION

<400> 120

Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg  
1 5 10

<210> 121  
<211> 8  
<212> PRT

<213> Artificial Sequence

<220>

<223> Tag2 sequence

<220>

<221> MOD\_RES

<222> (8)..(8)

<223> AMIDATION

<400> 121

Arg Arg Arg Arg Arg Arg Arg Arg  
1 5

<210> 122

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag2 sequence

<220>

<221> MOD\_RES

<222> (9)..(9)

<223> AMIDATION

<400> 122

Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5

<210> 123

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag2 sequence

<220>

<221> MOD\_RES

<222> (11)..(11)

<223> AMIDATION

<400> 123

Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala  
1 5 10