

P6023132EP seq ST25 (2)
SEQUENCE LISTING

<110> MosaMedix B.V.

<120> Radiolabeled Annexins

<130> P6023132EP

<160> 8

<170> PatentIn version 3.3

<210> 1

<211> 13

<212> PRT

<213> Artificial

<220>

<223> N-terminus is a sequence of at least 15 amino acids and includes between 2 and 20 histidine residues separated by no more than one other amino acid residue

<400> 1

Glu Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys
1 5 10

<210> 2

<211> 16

<212> PRT

<213> Artificial

<220>

<223> N-terminus is a sequence of at least 12 amino acids and includes between 2 and 20 histidine residues separated by no more than one other amino acid residue

<400> 2

Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys
1 5 10 15

<210> 3

<211> 19

<212> PRT

<213> Artificial

<220>

<223> N-terminus is a sequence of at least 9 amino acids and includes between 2 and 20 histidine residues separated by no more than one other amino acid residue

<400> 3

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

Ala Met Lys

<210> 4

<211> 22

<212> PRT

<213> Artificial

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<220>

<223> N-terminus is a sequence of at least 6 amino acids and includes between 2 and 20 histidine residues separated by no more than one other amino acid residue

<400> 4

Thr Val Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr
1 5 10 15

Leu Arg Lys Ala Met Lys
20

<210> 5

<211> 25

<212> PRT

<213> Artificial

<220>

<223> N-terminus is a sequence of at least 3 amino acids and includes between 2 and 20 histidine residues separated by no more than one other amino acid residue

<400> 5

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

Ala Glu Thr Leu Arg Lys Ala Met Lys
20 25

<210> 6

<211> 28

<212> PRT

<213> Artificial

<220>

<223> N-terminus is a sequence of at least 2 amino acids and includes between 2 and 20 histidine residues separated by no more than one other amino acid residue

<400> 6

Ala Gln Val Leu Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Glu
1 5 10 15

Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys
20 25

<210> 7

<211> 319

<212> PRT

<213> Homo sapiens

<400> 7

Ala Gln Val Leu Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Glu
1 5 10 15

Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr
20 25 30

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

P6023132EP seq ST25 (2)
 Gly Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Glu Asp Asp
 305 310 315

<210> 8
 <211> 325
 <212> PRT
 <213> Artificial

<220>
 <223> annexin variant

<400> 8

His His His His His His Ala Gln Val Leu Arg Gly Thr Val Thr Asp
 1 5 10 15

Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala
 20 25 30

Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu Leu Thr
 35 40 45

Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr
 50 55 60

Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly
 65 70 75 80

Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg Leu Tyr
 85 90 95

Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr Asn Glu
 100 105 110

Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg
 115 120 125

Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp
 130 135 140

Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu Val Val
 145 150 155 160

Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln
 165 170 175

Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp
 180 185 190

Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg Ser Val
 195 200 205

Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe
 210 215 220

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|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gln 225 | Ile | Glu | Glu | Thr | Ile 230 | Asp | Arg | Glu | Thr | Ser 235 | Gly | Asn | Leu | Glu | Gln 240 |
| Leu | Leu | Leu | Ala | Val 245 | Val | Lys | Ser | Ile | Arg 250 | Ser | Ile | Pro | Ala | Tyr 255 | Leu |
| Ala | Glu | Thr | Leu 260 | Tyr | Tyr | Ala | Met | Lys 265 | Gly | Ala | Gly | Thr | Asp 270 | Asp | His |
| Thr | Leu | Ile 275 | Arg | Val | Met | Val | Ser 280 | Arg | Ser | Glu | Ile | Asp 285 | Leu | Phe | Asn |
| Ile | Arg 290 | Lys | Glu | Phe | Arg | Lys 295 | Asn | Phe | Ala | Thr | Ser 300 | Leu | Tyr | Ser | Met |
| Ile 305 | Lys | Gly | Asp | Thr | Ser 310 | Gly | Asp | Tyr | Lys | Lys 315 | Ala | Leu | Leu | Leu | Leu 320 |
| Cys | Gly | Glu | Asp | Asp 325 | | | | | | | | | | | |