

pctgb2014052994-seq1
SEQUENCE LISTING

<110> F-star Biotechnology Limited
F-star Biotechnologische Forschungs- Und Entwicklungsges
m.b.H

<120> Cancer Biomarkers and Uses Thereof

<130> TEK/CP7067424

<150> GB 1317622.7

<151> 2013-10-04

<160> 19

<170> PatentIn version 3.3

<210> 1

<211> 681

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence: Nucleotide sequence of antigen-binding Fc
fragment H561-4

<400> 1

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acctgcccc cttgtcctgc ccccgagctg ctgggaggcc cttccgtgtt tctgttcccc      60
ccaaagccca aggacaccct gatgatctcc cggacccccg aagtgacctg cgtggtggtg      120
gacgtgtccc acgaggacct tgaagtgaag ttcaattggt acgtggacgg cgtggaagtg      180
cacaacgcca agaccaagcc cagagaggaa cagtacaact ccacctaccg ggtggtgtcc      240
gtgctgaccg tgctgcacca ggactggctg aacggcaaag agtacaagtg caaggtgtcc      300
aacaaggccc tgctgcccc catcgaaaag accatctcca aggccaaggg ccagccccgc      360
gagccccagg tgtacaccct gccccctagc cgggacgagt tcttcaccta ctgggtgtcc      420
ctgacctgcc tgggtcaaggg cttctacccc tccgatatcg ccgtggaatg ggagtccaac      480
ggccagcccc agaacaacta caagaccacc ccccctgtgc tggactccga cggctcattc      540
ttcctgtact ccaagctgac cgtggaccgg cggagatgga ccgccggcaa cgtgttctcc      600
tgcagcgtga tgcacgaggc cctgcacaac cactacaccc agaagtcctt gtccctgagc      660
cccggcaagt gatgagaatt c                                          681
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<210> 2

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence: Nucleotide sequence of the antigen-binding Fc
fragment H561-4 hinge region

<400> 2

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acctgcccc cttgtcct                                          18
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<210> 3

<211> 330

<212> DNA

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<213> Artificial sequence

<220>

<223> Synthetic sequence: Nucleotide sequence of the antigen-binding Fc fragment H561-4 CH2 domain

<400> 3

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gcccccgagc tgctgggagg cccttcctgtg tttctgttcc ccccaaagcc caaggacacc      60
ctgatgatct cccggacccc cgaagtgacc tgcgtggtgg tggacgtgtc ccacgaggac      120
cctgaagtga agttcaattg gtacgtggac ggcgtggaag tgcacaacgc caagaccaag      180
cccagagagg aacagtacaa ctccacctac cgggtggtgt ccgtgctgac cgtgctgcac      240
caggactggc tgaacggcaa agagtacaag tgcaaggtgt ccaacaaggc cctgcctgcc      300
cccatcgaaa agaccatctc caaggccaag                                     330
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<210> 4

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence: Nucleotide sequence of the antigen-binding Fc fragment H561-4 CH3 domain

<400> 4

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gaaaagacca tctccaaggc caagggccag cccgcgagc cccaggtgta caccctgccc      60
cctagccggg acgagttctt cacctactgg gtgtccctga cctgcctggt caagggcttc      120
taccctccg atatcgccgt ggaatgggag tccaacggcc agcccgagaa caactacaag      180
accaccccc ctgtgctgga ctccgacggc tcattcttcc tgtactcaa gctgaccgtg      240
gaccggcgga gatggaccgc cggcaacgtg ttctcctgca gcgtgatgca cgaggccctg      300
cacaaccact acaccagaa gtccctgtcc ctgagccccg gcaag                                     345
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<210> 5

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence: Nucleotide sequence encoding the part of the H561-4 AB structural loop region believed to be involved in antigen binding

<400> 5

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ttcttcacct actgg                                     15
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<210> 6

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence: Nucleotide sequence encoding part of the H561-4 CD structural loop region

<400> 6

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aacggccagc ccgag                                     15
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<210> 7
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic sequence: Nucleotide sequence encoding the part of the
 H561-4 EF structural loop region believed to be involved in
 antigen binding

<400> 7
 gaccggcgga gatggaccgc c 21

<210> 8
 <211> 223
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic sequence: Amino acid sequence of antigen-binding Fc
 fragment H561-4

<400> 8
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 1 5 10 15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 20 25 30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 50 55 60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 65 70 75 80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 85 90 95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 100 105 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 115 120 125

Pro Ser Arg Asp Glu Phe Phe Thr Tyr Trp Val Ser Leu Thr Cys Leu
 130 135 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 145 150 155 160

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
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165

170

175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Arg Arg Arg
180 185 190

Trp Thr Ala Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
195 200 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 9

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Amino acid sequence of the H561-4 hinge region

<400> 9

Thr Cys Pro Pro Cys Pro
1 5

<210> 10

<211> 110

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Amino acid sequence of the H561-4 CH2 domain

<400> 10

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

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

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

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<210> 11
 <211> 107
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> Synthetic sequence: Amino acid sequence of the H561-4 CH3 domain
 <400> 11

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 1 5 10 15

Glu Phe Phe Thr Tyr Trp Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Arg Arg Arg Trp Thr Ala Gly
 65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

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

<220>
 <223> Synthetic sequence: Amino acid sequence of the part of the H561-4
 AB structural loop region believed to be involved in antigen
 binding

<400> 12

Phe Phe Thr Tyr Trp
 1 5

<210> 13
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic sequence: Amino acid sequence of part of the H561-4 CD
 structural loop region

<400> 13

Asn Gly Gln Pro Glu
 1 5

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<210> 14
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
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<400> 14

Asp Arg Arg Arg Trp Thr Ala
 1 5

<210> 15
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 15

Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu
 1 5 10 15

<210> 16
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 16

Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr
 1 5 10 15

<210> 17
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 17

Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser
 1 5 10 15

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

Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro
 35 40 45

His Gln Ala Leu
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<210> 18
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 <212> PRT
 <213> Homo sapiens

<400> 18

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

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

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Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545 550 555 560

Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
565 570 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
580 585 590

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
595 600 605

Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln
610 615 620

Arg Ala Ser Pro Leu Thr
625 630

<210> 19
<211> 223
<212> PRT
<213> Homo sapiens

<400> 19

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1 5 10 15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
20 25 30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50 55 60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65 70 75 80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
85 90 95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
100 105 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
115 120 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
130 135 140

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Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145 150 155 160

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
165 170 175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
180 185 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
195 200 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220