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S E Q U E N C E L I S T I N G

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<110>  Friedrich-Alexander-Universität Erlangen-Nürnberg
<120>  Microarray for the detection of an angiostatic tumor stage of
        colorectal carcinoma
<130>  P23867
<150>  US 60/861,624
<151>  2006-11-29
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<170>  Patent In version 3.3
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eol f - seq l . t x t

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eol f - seq l . t x t

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Page 3

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20

25

30

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eol f - seq l . t x t

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Ala Ile Thr Gl n Pro Met Val Val Val Ala Ile Val Gly Leu Tyr Arg
 35 40 45

Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys Lys Gly
 50 55 60

Phe Ser Leu Gly Ser Thr Val Gl n Ser His Thr Lys Gly Ile Trp Met
 65 70 75 80

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Trp Oys Val Pro His Pro Lys Lys Pro Gly His Ile Leu Val Leu Leu
85 90 95

Asp Thr Glu Gly Leu Gly Asp Val Glu Lys Gly Asp Asn Gln Asn Asp
100 105 110

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115 120 125

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355

360

365

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G l u G l n G l u A r g T h r L e u A l a L e u L y s L e u G l n G l u G l n G l u G l n L e u
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gagct t t cgc t aaagct aag aaaaggt act gat aagaaaa gt aaaagct t t aat gat cct 660
cgg t t gt gca t ccgaaagt t ct t ccccaag aggaagt gct t cgt ct t cga t t ggcccgt 720
cct aagaagt acct t gct ca cct agagcag ct aaaggagg aagagct gaa ccct gat t t c 780
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 <212> PRT
 <213> Homo sapiens

<400> 10

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 Page 9

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20

25

30

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Thr 50 Gly Lys Ser Tyr Leu 55 Met Asn Lys Leu Ala 60 Gly Lys Lys Asn Gly

Phe 65 Ser Leu Gly Ser 70 Thr Val Lys Ser His 75 Thr Lys Gly Ile Trp 80 Met

Trp 90 Cys Val Pro 85 His Pro Lys Lys Pro 90 Glu His Thr Leu Val 95 Leu Leu

Asp 100 Thr Glu 100 Gly Leu Gly Asp 105 Ile Glu 105 Lys Gly Asp Asn 110 Glu Asn Asp

Ser 115 Trp Ile 115 Phe Ala Leu Ala 120 Ile Leu Leu Ser Ser 125 Thr Phe Val Tyr

Asn 130 Ser 130 Met Gly Thr 135 Ile Asn 135 Gln Gln Ala Met 140 Asp Gln Leu His Tyr

Val 145 Thr Glu Leu Thr 150 Asp Arg 150 Ile Lys Ala 155 Asn Ser Ser Pro Gly Asn 160

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Arg 225 Lys Phe Phe Pro 230 Lys Arg Lys Cys Phe 235 Val Phe Asp Trp Pro Ala 240

Pro 245 Lys Lys Tyr 245 Leu Ala His Leu Glu 250 Gln Leu Lys Glu Glu Glu 255 Leu

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eof - seq1 . t x t

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 355 360 365
 Asn Ser Phe Lys Asp Val Asp G n Met Phe G n Arg Lys Leu G y Al a
 370 375 380
 G n Leu G u Al a Arg Arg Asp Asp Phe Cys Lys G n Asn Ser Lys Al a
 385 390 395 400
 Ser Ser Asp Cys Cys Met Al a Leu Leu G n Asp I l e Phe G y Pro Leu
 405 410 415
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 420 425 430
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 Pro Arg Lys G y I l e G n Al a Lys G u Val Leu Lys Lys Tyr Leu G u
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 Ser Lys G u Asp Val Al a Asp Al a Leu Leu G n Thr Asp G n Ser Leu
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 485 490 495
 Al a G u Al a Al a Lys Lys Met Leu G u G u I l e G n Lys Lys Asn G u
 500 505 510
 G u Met Met G u G n Lys G u Lys Ser Tyr G n G u H i s Val Lys G n
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 Leu Thr G u Lys Met G u Arg Asp Arg Al a G n Leu Met Al a G u G n
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 G u Lys Thr Leu Al a Leu Lys Leu G n G u G n G u Arg Leu Leu Lys
 545 550 555 560
 G u G y Phe G u Asn G u Ser Lys Arg Leu G n Lys Asp I l e Tr p Asp
 565 570 575

Ile Gl n Met Arg Ser Lys Ser Leu Gl u Pro Ile Cys Asn Ile Leu
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eol f - seq1 . t x t

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<212> DNA
<213> Homo sapi ens

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eol f - seq1 . t xt

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 <212> PRT
 <213> Homo sapiens

<400> 13

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 35 40 45

Ile Ser Gln Pro Val Val Val Val Ala Ile Val Gly Leu Tyr Arg Thr
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eof - seq1 . t x t

Gly Lys Ser Tyr Leu Met Asn Arg Leu Ala Gly Lys Arg Asn Gly Phe
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 100 105 110
 Thr Glu Gly Leu Gly Asp Val Glu Lys Ser Asn Pro Lys Asn Asp Ser
 115 120 125
 Trp Ile Phe Ala Leu Ala Val Leu Leu Ser Ser Ser Phe Val Tyr Asn
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 Ser Val Ser Thr Ile Asn His Gln Ala Leu Glu Gln Leu His Tyr Val
 145 150 155 160
 Thr Glu Leu Ala Glu Leu Ile Arg Ala Lys Ser Cys Pro Arg Pro Asp
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 Glu Ala Glu Asp Ser Ser Glu Phe Ala Ser Phe Phe Pro Asp Phe Ile
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 Ile Thr Glu Asp Glu Tyr Leu Glu Asn Ala Leu Lys Leu Ile Pro Gly
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eol f - seq1 . t x t

G u A s n P r o A l a A l a V a l G n A r g A l a A l a A s p H i s T y r S e r G n G n
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M e t A l a G n G n L e u A r g L e u P r o T h r A s p T h r L e u G n G u L e u L e u
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A s p V a l H i s A l a A l a C y s G u A r g G u A l a I l e A l a V a l P h e M e t G u
 370 375 380

H i s S e r P h e L y s A s p G u A s n H i s G u P h e G n L y s L y s L e u V a l A s p
 385 390 400

T h r I l e G u L y s L y s L y s G y A s p P h e V a l L e u G n A s n G u G u A l a
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S e r A l a L y s T y r C y s G n A l a G u L e u L y s A r g L e u S e r G u H i s L e u
 420 425 430

T h r G u S e r I l e L e u A r g G y I l e P h e S e r V a l P r o G y G y H i s A s n
 435 440 445

L e u T y r L e u G u G u L y s L y s G n V a l G u T r p A s p T y r L y s L e u V a l
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P r o A r g L y s G y V a l L y s A l a A s n G u V a l L e u G n A s n P h e L e u G n
 465 470 475 480

S e r G n V a l V a l V a l G u G u S e r I l e L e u G n S e r A s p L y s A l a L e u
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T h r A l a G y G u L y s A l a I l e A l a A l a G u A r g A l a M e t L y s G u A l a
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A l a G u L y s G u G n G u L e u L e u A r g G u L y s G n L y s G u G n G n
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G n M e t M e t G u A l a G n G u A r g S e r P h e G n G u A s n I l e A l a G n
 530 535 540

L e u L y s L y s L y s M e t G u A r g G u A r g G u A s n L e u L e u A r g G u H i s
 545 550 555 560

G u A r g L e u L e u L y s H i s L y s L e u L y s V a l G n G u G u M e t L e u L y s
 565 570 575

G u G u P h e G n L y s L y s S e r G u G n L e u A s n L y s G u I l e A s n G n
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L e u L y s G u L y s I l e G u S e r T h r L y s A s n G u G n L e u A r g L e u L e u
 595 600 605

L y s I l e L e u A s p M e t A l a S e r A s n I l e M e t I l e V a l T h r L e u P r o G y
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610

615

eol f - seq1 . t xt
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<213> Homo sapi ens

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agt cagt gag accaagaacc caccaat t cc ggacacgct a at t gt t gt ag at cat cact t 420
caaggt gccc at at ct t t ct agt ggaaaaa t t at t ct ggc ct ccgct gca t aaaaat cag 480
gcaaccagaa t t ct acat at at aaggcaaa gt aacat cct agacat ggct t t agagat cc 540
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t ct at cgcac t ggcaaat cc t acct gat ga acaagct ggc t gggaagaac aagggt t ct 720
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eol f - seq1 . t x t

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 <213> Homo sapi ens

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 50 55 60

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Trp Cys Val Pro His Pro Asn Trp Pro Asn His Thr Leu Val Leu Leu
 85 90 95

Asp Thr Glu Gly Leu Gly Asp Val Glu Lys Ala Asp Asn Lys Asn Asp
 100 105 110

Ile Gln Ile Phe Ala Leu Ala Leu Leu Ser Ser Thr Phe Val Tyr
 115 120 125

Asn Thr Val Asn Lys Ile Asp Gln Gly Ala Ile Asp Leu Leu His Asn
 130 135 140

eof - seq1 . t x t

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Asp Arg Val Glu Asp Pro Ala Asp Ser Ala Ser Phe Phe Pro Asp Leu
165 170 175

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180 185 190

Leu Val Thr Pro Asp Glu Tyr Leu Glu Asn Ser Leu Arg Pro Lys Gln
195 200 205

Gly Ser Asp Gln Arg Val Gln Asn Phe Asn Leu Pro Arg Leu Cys Ile
210 215 220

Gln Lys Phe Phe Pro Lys Lys Lys Cys Phe Ile Phe Asp Leu Pro Ala
225 230 235 240

His Gln Lys Lys Leu Ala Gln Leu Glu Thr Leu Pro Asp Asp Glu Leu
245 250 255

Glu Pro Glu Phe Val Gln Gln Val Thr Glu Phe Cys Ser Tyr Ile Phe
260 265 270

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275 280 285

Ser Arg Leu Lys Asn Leu Val Leu Thr Tyr Val Asn Ala Ile Ser Ser
290 295 300

Gly Asp Leu Pro Cys Ile Glu Asn Ala Val Leu Ala Leu Ala Gln Arg
305 310 315 320

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325 330 335

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340 345 350

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370 375 380

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385 390 395 400

Ser Ser Asp Tyr Cys Ser Ala Leu Leu Lys Asp Ile Phe Gly Pro Leu
405 410 415

eol f - seq1 . txt
 G u G u A l a V a l L y s G n G y I l e T y r S e r L y s P r o G y G y H i s A s n
 420 425 430
 L e u P h e I l e G n L y s T h r G u G u L e u L y s A l a L y s T y r T y r A r g G u
 435 440 445
 P r o A r g L y s G y I l e G n A l a G u G u V a l L e u G n L y s T y r L e u L y s
 450 455 460
 S e r L y s G u S e r V a l S e r H i s A l a I l e L e u G n T h r A s p G n A l a L e u
 465 470 475 480
 T h r G u T h r G u L y s L y s L y s L y s G u A l a G n V a l L y s A l a G u A l a
 485 490 495
 G u L y s A l a G u A l a G n A r g L e u A l a A l a I l e G n A r g G n A s n G u
 500 505 510
 G n M e t M e t G n G u A r g G u A r g L e u H i s G n G u G n V a l A r g G n
 515 520 525
 M e t G u I l e A l a L y s G n A s n T r p L e u A l a G u G n G n L y s M e t G n
 530 535 540
 G u G n G n M e t G n G u G n A l a A l a G n L e u S e r T h r T h r P h e G n
 545 550 555
 A l a G n A s n A r g S e r L e u L e u S e r G u L e u G n H i s A l a G n A r g T h r
 560 565 570 575
 V a l A s n A s n A s p A s p P r o C y s V a l L e u L e u
 580 585