

SEQUENCE LISTING

<110> INSERM

<120> Methods for treating and diagnosing a cancer secreting cath-D or Alzheimer's disease

<130> BEP 070419

<160> 10

<170> PatentIn version 3.3

<210> 1

<211> 601

<212> PRT

<213> Homo sapiens

<400> 1

Gln Ile Asp Arg Gly Val Thr His Leu Asn Ile Ser Gly Leu Lys Met
1 5 10 15

Pro Arg Gly Ile Ala Ile Asp Trp Val Ala Gly Asn Val Tyr Trp Thr
20 25 30

Asp Ser Gly Arg Asp Val Ile Glu Val Ala Gln Met Lys Gly Glu Asn
35 40 45

Arg Lys Thr Leu Ile Ser Gly Met Ile Asp Glu Pro His Ala Ile Val
50 55 60

Val Asp Pro Leu Arg Gly Thr Met Tyr Trp Ser Asp Trp Gly Asn His
65 70 75 80

Pro Lys Ile Glu Thr Ala Ala Met Asp Gly Thr Leu Arg Glu Thr Leu
85 90 95

Val Gln Asp Asn Ile Gln Trp Pro Thr Gly Leu Ala Val Asp Tyr His
100 105 110

Asn Glu Arg Leu Tyr Trp Ala Asp Ala Lys Leu Ser Val Ile Gly Ser
115 120 125

Ile Arg Leu Asn Gly Thr Asp Pro Ile Val Ala Ala Asp Ser Lys Arg
130 135 140

Gly Leu Ser His Pro Phe Ser Ile Asp Val Phe Glu Asp Tyr Ile Tyr
145 150 155 160

Gly Val Thr Tyr Ile Asn Asn Arg Val Phe Lys Ile His Lys Phe Gly

165

170

175

His Ser Pro Leu Val Asn Leu Thr Gly Gly Leu Ser His Ala Ser Asp
180 185 190

Val Val Leu Tyr His Gln His Lys Gln Pro Glu Val Thr Asn Pro Cys
195 200 205

Asp Arg Lys Lys Cys Glu Trp Leu Cys Leu Leu Ser Pro Ser Gly Pro
210 215 220

Val Cys Thr Cys Pro Asn Gly Lys Arg Leu Asp Asn Gly Thr Cys Val
225 230 235 240

Pro Val Pro Ser Pro Thr Pro Pro Pro Asp Ala Pro Arg Pro Gly Thr
245 250 255

Cys Asn Leu Gln Cys Phe Asn Gly Gly Ser Cys Phe Leu Asn Ala Arg
260 265 270

Arg Gln Pro Lys Cys Arg Cys Gln Pro Arg Tyr Thr Gly Asp Lys Cys
275 280 285

Glu Leu Asp Gln Cys Trp Glu His Cys Arg Asn Gly Gly Thr Cys Ala
290 295 300

Ala Ser Pro Ser Gly Met Pro Thr Cys Arg Cys Pro Thr Gly Phe Thr
305 310 315 320

Gly Pro Lys Cys Thr Gln Gln Val Cys Ala Gly Tyr Cys Ala Asn Asn
325 330 335

Ser Thr Cys Thr Val Asn Gln Gly Asn Gln Pro Gln Cys Arg Cys Leu
340 345 350

Pro Gly Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln Cys Ser Gly Tyr
355 360 365

Cys Glu Asn Phe Gly Thr Cys Gln Met Ala Ala Asp Gly Ser Arg Gln
370 375 380

Cys Arg Cys Thr Ala Tyr Phe Glu Gly Ser Arg Cys Glu Val Asn Lys
385 390 395 400

Cys Ser Arg Cys Leu Glu Gly Ala Cys Val Val Asn Lys Gln Ser Gly
405 410 415

Asp Val Thr Cys Asn Cys Thr Asp Gly Arg Val Ala Pro Ser Cys Leu
420 425 430

Thr Cys Val Gly His Cys Ser Asn Gly Gly Ser Cys Thr Met Asn Ser
435 440 445

Lys Met Met Pro Glu Cys Gln Cys Pro Pro His Met Thr Gly Pro Arg
450 455 460

Cys Glu Glu His Val Phe Ser Gln Gln Gln Pro Gly His Ile Ala Ser
465 470 475 480

Ile Leu Ile Pro Leu Leu Leu Leu Leu Leu Val Leu Val Ala Gly
485 490 495

Val Val Phe Trp Tyr Lys Arg Arg Val Gln Gly Ala Lys Gly Phe Gln
500 505 510

His Gln Arg Met Thr Asn Gly Ala Met Asn Val Glu Ile Gly Asn Pro
515 520 525

Thr Tyr Lys Met Tyr Glu Gly Gly Glu Pro Asp Asp Val Gly Gly Leu
530 535 540

Leu Asp Ala Asp Phe Ala Leu Asp Pro Asp Lys Pro Thr Asn Phe Thr
545 550 555 560

Asn Pro Val Tyr Ala Thr Leu Tyr Met Gly Gly His Gly Ser Arg His
565 570 575

Ser Leu Ala Ser Thr Asp Glu Lys Arg Glu Leu Leu Gly Arg Gly Pro
580 585 590

Glu Asp Glu Ile Gly Asp Pro Leu Ala
595 600

<210> 2
<211> 476
<212> PRT
<213> Homo sapiens

<400> 2

Gln Ile Asp Arg Gly Val Thr His Leu Asn Ile Ser Gly Leu Lys Met
1 5 10 15

Pro Arg Gly Ile Ala Ile Asp Trp Val Ala Gly Asn Val Tyr Trp Thr
20 25 30

Asp Ser Gly Arg Asp Val Ile Glu Val Ala Gln Met Lys Gly Glu Asn
35 40 45

Arg Lys Thr Leu Ile Ser Gly Met Ile Asp Glu Pro His Ala Ile Val
50 55 60

Val Asp Pro Leu Arg Gly Thr Met Tyr Trp Ser Asp Trp Gly Asn His
65 70 75 80

Pro Lys Ile Glu Thr Ala Ala Met Asp Gly Thr Leu Arg Glu Thr Leu
85 90 95

Val Gln Asp Asn Ile Gln Trp Pro Thr Gly Leu Ala Val Asp Tyr His
100 105 110

Asn Glu Arg Leu Tyr Trp Ala Asp Ala Lys Leu Ser Val Ile Gly Ser
115 120 125

Ile Arg Leu Asn Gly Thr Asp Pro Ile Val Ala Ala Asp Ser Lys Arg
130 135 140

Gly Leu Ser His Pro Phe Ser Ile Asp Val Phe Glu Asp Tyr Ile Tyr
145 150 155 160

Gly Val Thr Tyr Ile Asn Asn Arg Val Phe Lys Ile His Lys Phe Gly
165 170 175

His Ser Pro Leu Val Asn Leu Thr Gly Gly Leu Ser His Ala Ser Asp
180 185 190

Val Val Leu Tyr His Gln His Lys Gln Pro Glu Val Thr Asn Pro Cys
195 200 205

Asp Arg Lys Lys Cys Glu Trp Leu Cys Leu Leu Ser Pro Ser Gly Pro
210 215 220

Val Cys Thr Cys Pro Asn Gly Lys Arg Leu Asp Asn Gly Thr Cys Val
225 230 235 240

Pro Val Pro Ser Pro Thr Pro Pro Pro Asp Ala Pro Arg Pro Gly Thr
245 250 255

Cys Asn Leu Gln Cys Phe Asn Gly Gly Ser Cys Phe Leu Asn Ala Arg

260

265

270

Arg Gln Pro Lys Cys Arg Cys Gln Pro Arg Tyr Thr Gly Asp Lys Cys
 275 280 285

Glu Leu Asp Gln Cys Trp Glu His Cys Arg Asn Gly Gly Thr Cys Ala
 290 295 300

Ala Ser Pro Ser Gly Met Pro Thr Cys Arg Cys Pro Thr Gly Phe Thr
 305 310 315 320

Gly Pro Lys Cys Thr Gln Gln Val Cys Ala Gly Tyr Cys Ala Asn Asn
 325 330 335

Ser Thr Cys Thr Val Asn Gln Gly Asn Gln Pro Gln Cys Arg Cys Leu
 340 345 350

Pro Gly Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln Cys Ser Gly Tyr
 355 360 365

Cys Glu Asn Phe Gly Thr Cys Gln Met Ala Ala Asp Gly Ser Arg Gln
 370 375 380

Cys Arg Cys Thr Ala Tyr Phe Glu Gly Ser Arg Cys Glu Val Asn Lys
 385 390 395 400

Cys Ser Arg Cys Leu Glu Gly Ala Cys Val Val Asn Lys Gln Ser Gly
 405 410 415

Asp Val Thr Cys Asn Cys Thr Asp Gly Arg Val Ala Pro Ser Cys Leu
 420 425 430

Thr Cys Val Gly His Cys Ser Asn Gly Gly Ser Cys Thr Met Asn Ser
 435 440 445

Lys Met Met Pro Glu Cys Gln Cys Pro Pro His Met Thr Gly Pro Arg
 450 455 460

Cys Glu Glu His Val Phe Ser Gln Gln Gln Pro Gly
 465 470 475

<210> 3

<211> 173

<212> PRT

<213> Artificial

<220>

<223> fragment of the beta chain of LRP1

<400> 3

Pro Ser Gly Met Pro Thr Cys Arg Cys Pro Thr Gly Phe Thr Gly Pro
1 5 10 15

Lys Cys Thr Gln Gln Val Cys Ala Gly Tyr Cys Ala Asn Asn Ser Thr
20 25 30

Cys Thr Val Asn Gln Gly Asn Gln Pro Gln Cys Arg Cys Leu Pro Gly
35 40 45

Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln Cys Ser Gly Tyr Cys Glu
50 55 60

Asn Phe Gly Thr Cys Gln Met Ala Ala Asp Gly Ser Arg Gln Cys Arg
65 70 75 80

Cys Thr Ala Tyr Phe Glu Gly Ser Arg Cys Glu Val Asn Lys Cys Ser
85 90 95

Arg Cys Leu Glu Gly Ala Cys Val Val Asn Lys Gln Ser Gly Asp Val
100 105 110

Thr Cys Asn Cys Thr Asp Gly Arg Val Ala Pro Ser Cys Leu Thr Cys
115 120 125

Val Gly His Cys Ser Asn Gly Gly Ser Cys Thr Met Asn Ser Lys Met
130 135 140

Met Pro Glu Cys Gln Cys Pro Pro His Met Thr Gly Pro Arg Cys Glu
145 150 155 160

Glu His Val Phe Ser Gln Gln Gln Pro Gly His Ile Ala
165 170

<210> 4

<211> 46

<212> PRT

<213> Artificial

<220>

<223> fragment of the beta chain of LRP1

<400> 4

Cys Arg Cys Leu Pro Gly Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln
1 5 10 15

Cys Ser Gly Tyr Cys Glu Asn Phe Gly Thr Cys Gln Met Ala Ala Asp
20 25 30

Gly Ser Arg Gln Cys Arg Cys Thr Ala Tyr Phe Glu Gly Ser
35 40 45

<210> 5
<211> 49
<212> PRT
<213> Artificial

<220>
<223> fragment of the beta chain of LRP1

<400> 5

Cys Arg Cys Leu Pro Gly Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln
1 5 10 15

Cys Ser Gly Tyr Cys Glu Asn Phe Gly Thr Cys Gln Met Ala Ala Asp
20 25 30

Gly Ser Arg Gln Cys Arg Cys Thr Ala Tyr Phe Glu Gly Ser Arg Cys
35 40 45

Glu

<210> 6
<211> 21
<212> DNA
<213> Artificial

<220>
<223> target sequence

<400> 6
aagcagtttg cctgcagaga t 21

<210> 7
<211> 21
<212> DNA
<213> Artificial

<220>
<223> target sequence

<400> 7
aagctatgag tttaagaagt t 21

<210> 8
<211> 21

<212> RNA	
<213> Artificial	
<220>	
<223> target sequence	
<400> 8	
aagcauca guagacuauc a	21
<210> 9	
<211> 21	
<212> DNA	
<213> Artificial	
<220>	
<223> target sequence	
<400> 9	
aagcagtttg cctgcagaga c	21
<210> 10	
<211> 21	
<212> DNA	
<213> Artificial	
<220>	
<223> target sequence	
<400> 10	
aacgtacgcg gaatacttcg a	21