

SEQUENCE LISTING

<110> MATSUMORI, Akira

<120> A method for detecting a patient suffering from heart failure, a method for identifying a heart disease, a reagent for detecting heart failure

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<150> JP 2014-208914

<151> 2014-10-10

<160> 1

<170> PatentIn version 3.5

<210> 1

<211> 602

<212> PRT

<213> Homo sapiens

<400> 1

Met Pro Ser Ala Lys Gln Arg Gly Ser Lys Gly Gly His Gly Ala Ala
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Ser Pro Ser Glu Lys Gly Ala His Pro Ser Gly Gly Ala Asp Asp Val
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Ala Lys Lys Pro Pro Pro Ala Pro Gln Gln Pro Pro Pro Pro Pro Ala
35 40 45

Pro His Pro Gln Gln His Pro Gln Gln His Pro Gln Asn Gln Ala His
50 55 60

Gly Lys Gly Gly His Arg Gly Gly Gly Gly Gly Gly Gly Lys Ser Ser
65 70 75 80

Ser Ser Ser Ser Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Ser
85 90 95

Ser Ala Ser Cys Ser Arg Arg Leu Gly Arg Ala Leu Asn Phe Leu Phe
100 105 110

Tyr Leu Ala Leu Val Ala Ala Ala Ala Phe Ser Gly Trp Cys Val His
115 120 125

His Val Leu Glu Glu Val Gln Gln Val Arg Arg Ser His Gln Asp Phe
130 135 140

Ser Arg Gln Arg Glu Glu Leu Gly Gln Gly Leu Gln Gly Val Glu Gln
145 150 155 160

Lys Val Gln Ser Leu Gln Ala Thr Phe Gly Thr Phe Glu Ser Ile Leu
 165 170 175

Arg Ser Ser Gln His Lys Gln Asp Leu Thr Glu Lys Ala Val Lys Gln
 180 185 190

Gly Glu Ser Glu Val Ser Arg Ile Ser Glu Val Leu Gln Lys Leu Gln
 195 200 205

Asn Glu Ile Leu Lys Asp Leu Ser Asp Gly Ile His Val Val Lys Asp
 210 215 220

Ala Arg Glu Arg Asp Phe Thr Ser Leu Glu Asn Thr Val Glu Glu Arg
 225 230 235 240

Leu Thr Glu Leu Thr Lys Ser Ile Asn Asp Asn Ile Ala Ile Phe Thr
 245 250 255

Glu Val Gln Lys Arg Ser Gln Lys Glu Ile Asn Asp Met Lys Ala Lys
 260 265 270

Val Ala Ser Leu Glu Glu Ser Glu Gly Asn Lys Gln Asp Leu Lys Ala
 275 280 285

Leu Lys Glu Ala Val Lys Glu Ile Gln Thr Ser Ala Lys Ser Arg Glu
 290 295 300

Trp Asp Met Glu Ala Leu Arg Ser Thr Leu Gln Thr Met Glu Ser Asp
 305 310 315 320

Ile Tyr Thr Glu Val Arg Glu Leu Val Ser Leu Lys Gln Glu Gln Gln
 325 330 335

Ala Phe Lys Glu Ala Ala Asp Thr Glu Arg Leu Ala Leu Gln Ala Leu
 340 345 350

Thr Glu Lys Leu Leu Arg Ser Glu Glu Ser Val Ser Arg Leu Pro Glu
 355 360 365

Glu Ile Arg Arg Leu Glu Glu Glu Leu Arg Gln Leu Lys Ser Asp Ser
 370 375 380

His Gly Pro Lys Glu Asp Gly Gly Phe Arg His Ser Glu Ala Phe Glu
 385 390 395 400

3

Ala Leu Gln Gln Lys Ser Gln Gly Leu Asp Ser Arg Leu Gln His Val
405 410 415

Glu Asp Gly Val Leu Ser Met Gln Val Ala Ser Ala Arg Gln Thr Glu
420 425 430

Ser Leu Glu Ser Leu Leu Ser Lys Ser Gln Glu His Glu Gln Arg Leu
435 440 445

Ala Ala Leu Gln Gly Arg Leu Glu Gly Leu Gly Ser Ser Glu Ala Asp
450 455 460

Gln Asp Gly Leu Ala Ser Thr Val Arg Ser Leu Gly Glu Thr Gln Leu
465 470 475 480

Val Leu Tyr Gly Asp Val Glu Glu Leu Lys Arg Ser Val Gly Glu Leu
485 490 495

Pro Ser Thr Val Glu Ser Leu Gln Lys Val Gln Glu Gln Val His Thr
500 505 510

Leu Leu Ser Gln Asp Gln Ala Gln Ala Ala Arg Leu Pro Pro Gln Asp
515 520 525

Phe Leu Asp Arg Leu Ser Ser Leu Asp Asn Leu Lys Ala Ser Val Ser
530 535 540

Gln Val Glu Ala Asp Leu Lys Met Leu Arg Thr Ala Val Asp Ser Leu
545 550 555 560

Val Ala Tyr Ser Val Lys Ile Glu Thr Asn Glu Asn Asn Leu Glu Ser
565 570 575

Ala Lys Gly Leu Leu Asp Asp Leu Arg Asn Asp Leu Asp Arg Leu Phe
580 585 590

Val Lys Val Glu Lys Ile His Glu Lys Val
595 600