

P107883_ST25.txt
SEQUENCE LISTING

<110> Nanyang Technological University

<120> PEPTIDES BINDING TO PARALLEL-STRANDED G-QUADRUPLEXES

<130> 107883

<160> 31

<170> PatentIn version 3.5

<210> 1

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> peptide of human Rhau protein

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His Pro Gly His Leu Lys Gly Arg Glu Ile Gly Met Trp Tyr Ala Lys
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Met Ser Tyr Asp Tyr His Gln Asn Trp Gly Arg Asp Gly Gly Pro Arg
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Ser Ser Gly Gly Gly Tyr Gly Gly Gly Pro Ala Gly Gly His Gly Gly
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Asn Arg Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Arg Gly
35 40 45

Gly Arg Gly Arg
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Lys Gln Gly Gln Lys Asn Lys Glu Ala Glu Arg Gln Glu Arg Ala Val
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Val His Met Asp Glu Arg Arg Glu Glu Gln Ile Val Gln Leu Leu Asn
20 25 30

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

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Lys Phe Ser Glu Tyr Phe Gly Asn Cys Pro Met Ile His Ile Pro Gly
305 310 315 320

Phe Thr Phe Pro Val Val Glu Tyr Leu Leu Glu Asp Val Ile Glu Lys
325 330 335

Ile Arg Tyr Val Pro Glu Gln Lys Glu His Arg Ser Gln Phe Lys Arg
340 345 350

Gly Phe Met Gln Gly His Val Asn Arg Gln Glu Lys Glu Glu Lys Glu
355 360 365

Ala Ile Tyr Lys Glu Arg Trp Pro Asp Tyr Val Arg Glu Leu Arg Arg
370 375 380

Arg Tyr Ser Ala Ser Thr Val Asp Val Ile Glu Met Met Glu Asp Asp
385 390 395 400

Lys Val Asp Leu Asn Leu Ile Val Ala Leu Ile Arg Tyr Ile Val Leu
405 410 415

Glu Glu Glu Asp Gly Ala Ile Leu Val Phe Leu Pro Gly Trp Asp Asn
420 425 430

Ile Ser Thr Leu His Asp Leu Leu Met Ser Gln Val Met Phe Lys Ser
435 440 445

Asp Lys Phe Leu Ile Ile Pro Leu His Ser Leu Met Pro Thr Val Asn
450 455 460

Gln Thr Gln Val Phe Lys Arg Thr Pro Pro Gly Val Arg Lys Ile Val
465 470 475 480

Ile Ala Thr Asn Ile Ala Glu Thr Ser Ile Thr Ile Asp Asp Val Val
485 490 495

Tyr Val Ile Asp Gly Gly Lys Ile Lys Glu Thr His Phe Asp Thr Gln
500 505 510

Asn Asn Ile Ser Thr Met Ser Ala Glu Trp Val Ser Lys Ala Asn Ala
515 520 525

Lys Gln Arg Lys Gly Arg Ala Gly Arg Val Gln Pro Gly His Cys Tyr
530 535 540

His Leu Tyr Asn Gly Leu Arg Ala Ser Leu Leu Asp Asp Tyr Gln Leu
545 550 555 560

Pro Glu Ile Leu Arg Thr Pro Leu Glu Glu Leu Cys Leu Gln Ile Lys
565 570 575

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Ile Leu Arg Leu Gly Gly Ile Ala Tyr Phe Leu Ser Arg Leu Met Asp
 580 585 590

Pro Pro Ser Asn Glu Ala Val Leu Leu Ser Ile Arg His Leu Met Glu
 595 600 605

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

Leu Ala Arg Leu Pro Val Glu Pro His Ile Gly Lys Met Ile Leu Phe
 625 630 635 640

Gly Ala Leu Phe Cys Cys Leu Asp Pro Val Leu Thr Ile Ala Ala Ser
 645 650 655

Leu Ser Phe Lys Asp Pro Phe Val Ile Pro Leu Gly Lys Glu Lys Ile
 660 665 670

Ala Asp Ala Arg Arg Lys Glu Leu Ala Lys Asp Thr Arg Ser Asp His
 675 680 685

Leu Thr Val Val Asn Ala Phe Glu Gly Trp Glu Glu Ala Arg Arg Arg
 690 695 700

Gly Phe Arg Tyr Glu Lys Asp Tyr Cys Trp Glu Tyr Phe Leu Ser Ser
 705 710 715 720

Asn Thr Leu Gln Met Leu His Asn Met Lys Gly Gln Phe Ala Glu His
 725 730 735

Leu Leu Gly Ala Gly Phe Val Ser Ser Arg Asn Pro Lys Asp Pro Glu
 740 745 750

Ser Asn Ile Asn Ser Asp Asn Glu Lys Ile Ile Lys Ala Val Ile Cys
 755 760 765

Ala Gly Leu Tyr Pro Lys Val Ala Lys Ile Arg Leu Asn Leu Gly Lys
 770 775 780

Lys Arg Lys Met Val Lys Val Tyr Thr Lys Thr Asp Gly Leu Val Ala
 785 790 795 800

Val His Pro Lys Ser Val Asn Val Glu Gln Thr Asp Phe His Tyr Asn
 805 810 815

Trp Leu Ile Tyr His Leu Lys Met Arg Thr Ser Ser Ile Tyr Leu Tyr
 820 825 830

Asp Cys Thr Glu Val Ser Pro Tyr Cys Leu Leu Phe Phe Gly Gly Asp
 835 840 845

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Ile Ser Ile Gln Lys Asp Asn Asp Gln Glu Thr Ile Ala Val Asp Glu
850 855 860

Trp Ile Val Phe Gln Ser Pro Ala Arg Ile Ala His Leu Val Lys Glu
865 870 875 880

Leu Arg Lys Glu Leu Asp Ile Leu Leu Gln Glu Lys Ile Glu Ser Pro
885 890 895

His Pro Val Asp Trp Asn Asp Thr Lys Ser Arg Asp Cys Ala Val Leu
900 905 910

Ser Ala Ile Ile Asp Leu Ile Lys Thr Gln Glu Lys Ala Thr Pro Arg
915 920 925

Asn Phe Pro Pro Arg Phe Gln Asp Gly Tyr Tyr Ser
930 935 940

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ggguuaggggu

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<223> G-quadruplex forming DNA

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Ala Lys Lys Gln Gly Gln Lys Asn Lys Glu Ala Glu Arg Gln Glu Arg
 20 25 30

Ala Val Val His Met Asp Glu Arg Arg Glu Glu Gln Ile Val Gln Leu
 35 40 45

Leu Asn Ser Val Gln Ala Lys
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Lys Gln Gly Gln Lys Asn Lys Glu Ala Glu Arg Gln Glu
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Ala Lys Lys Gln
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Lys Gln Gly Gln
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P107883_ST25.txt

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<400> 31

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Lys Gln Gly Gln
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