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<110> EditForce Inc.
Kyushu University

<120> Low-cohesive PPR Proteins and Use thereof

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<150> JP2019-100553

<151> 2019-05-29

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<170> PatentIn version 3.5

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Pro	Ser	Val
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Glu Glu Ala Leu Lys Leu Phe Lys Glu Met Glu Glu Lys Gly Ile Thr
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Pro Ser Val
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Pro Ser Val
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Glu	Glu	Ala	Leu	Lys	Leu	Phe	Lys	Glu	Met	Glu	Glu	Lys	Gly	Ile	Thr
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Glu	Glu	Ala	Leu	Lys	Leu	Phe	Lys	Glu	Met	Glu	Glu	Lys	Gly	Ile	Thr
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Pro	Ser	Val
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 gactataagg accacgacgg agactacaag gatcatgata ttgattacaa agacgatgac 840
 gataagatgg ccggacgcta gmagvskgtg vvvdgdvngk ksvsgggdat ygktkcttgk 900

vwtvtttygv csrydhmkhd ksamgyvrtk ddgnyktrav kgdtvnrkgd kdgngkhyny	960
nshnvymadk kngkvnrhn dgsvadhynt gdgvdnhyst saskdnkrdh mvvtaagtgm	1020
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 cccacactgg tgaccacctt cggctacggc gtggcttggt tctctcgta ccccgaccat 240
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 aactggtga atcgtatcga actgaagggc atcgacttca aagaggacgg caacattctg 420
 ggccacaagc tggagtacaa cttcaacagc cactacgtgt acatcaccgc cgataagcag 480
 aagaactgca tcaaggccaa cttcaagatt cgtcacaacg tggaggatgg ctccgtgcag 540
 ctggccgatc actaccagca gaacacacc atcggcgatg gaccgtttt actgcccgac 600
 aaccactatt taagccacca gagcaagctg tccaaggacc ccaacgagaa gcgtgatcat 660
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 aagagccggc tccatatggg atccggcgga ctcagtagcc ccaagaagaa acgcaaagtc 780
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ravkgdtnr kgdkdngnhk ynnshyvyta dknckankr hnvdgsvadh yntgdgvdnh	1080
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<220>
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<220>
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 <223> n is a, c, g, t or u

<220>
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 agcggctccg gcggcagcgg gggaggcggg catcatcacc atcaccacgg acgctagmag 660
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gyvrtkddgn yktravkgdt vnrkgdkdgn ghkynynshn vymadkkngk vnkrhndgsv	780
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<220>
 <223> RNA probe

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<210> 39
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<220>
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<400> 39	
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<210> 40
 <211> 30
 <212> DNA
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<220>
 <223> RNA probe

<400> 40	
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<210> 41
 <211> 30
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<220>
 <223> RNA probe

<400> 41

gacaccgccg ccgccgccgc cgccggacug 30

<210> 42
<211> 30
<212> DNA
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<220>
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<400> 42
gacaugcugg uguaucuugu cuuuagacug 30

<210> 43
<211> 63
<212> DNA
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<220>
<223> Dest-a

<400> 43
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ttc 63

<210> 44
<211> 47
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<220>
<223> Dest-b

<400> 44
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<210> 45
<211> 47
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<213> Artificial sequence

<220>
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<400> 45
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<210> 46
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 <220>
 <223> Dest-d

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 <400> 47
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 <210> 50
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 <400> 52
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 <210> 53
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 <220>
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 <400> 53
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 <210> 54
 <211> 22
 <212> PRT
 <213> Artificial sequence

 <220>
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 <400> 54

Glu Leu Thr Tyr Asn Thr Leu Ile Ser Gly Leu Gly Lys Ala Gly Arg
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Ala Arg Asp Pro Pro Val
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<210> 55
 <211> 4
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 <213> Artificial sequence

<220>
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<400> 55
 Lys Asp Glu Leu
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<210> 56
 <211> 4
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<220>
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<400> 56
 Lys Glu Glu Leu
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<210> 57
 <211> 19
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<220>
 <223> signal sequence

<400> 57
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Ala His Ser

<210> 58
 <211> 35
 <212> PRT

<213> Artificial Sequence

<220>

<223> 1st_A (v3.2_A)

<400> 58

Val Thr Tyr Thr Thr Asn Ile Asp Gln Leu Cys Lys Ala Gly Lys Val
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Asp Glu Ala Leu Glu Leu Phe Lys Glu Met Arg Ser Lys Gly Val Lys
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Pro Asn Val
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<210> 59

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> 1st_G (v3.2_G)

<400> 59

Val Thr Tyr Thr Thr Asn Ile Asp Gln Leu Cys Lys Ala Gly Lys Val
1 5 10 15

Asp Glu Ala Leu Glu Leu Phe Asp Glu Met Lys Glu Arg Gly Ile Lys
20 25 30

Pro Asp Val
35

<210> 60

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> 1st_U (v3.2_U)

<400> 60

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Asp Glu Ala Glu Glu Leu Leu Glu Glu Met Glu Glu Lys Gly Ile Lys
20 25 30

Pro Asp Val
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<210> 61
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<212> DNA
<213> Artificial Sequence

<220>
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gcgttcgcta aaagacaggg taaggaaatg gactccttaa gattcttgta cgacgggtatt 240
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gccggcaagg tggatgaggc cctggagctg ttcgacgaga tgaaggagag gggcatcaag	2220
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 <211> 757
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<400> 62

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20 25 30

His Ile Asn Leu Lys Val Ser Asp Gly Ser Ser Glu Ile Phe Phe Lys
35 40 45

Ile Lys Lys Thr Thr Pro Leu Arg Arg Leu Met Glu Ala Phe Ala Lys
50 55 60

Arg Gln Gly Lys Glu Met Asp Ser Leu Arg Phe Leu Tyr Asp Gly Ile
65 70 75 80

Arg Ile Gln Ala Asp Gln Ala Pro Glu Asp Leu Asp Met Glu Asp Asn
85 90 95

Asp Ile Ile Glu Ala His Arg Glu Gln Ile Gly Gly Met Gly Asn Ser
100 105 110

Val Val Thr Tyr Asn Thr Leu Ile Asp Gly Leu Cys Lys Ser Gly Lys
115 120 125

Ile Glu Glu Ala Leu Lys Leu Phe Lys Glu Met Glu Glu Lys Gly Ile
130 135 140

Thr Pro Ser Val Val Thr Tyr Thr Thr Leu Ile Asp Gly Leu Cys Lys
145 150 155 160

Ala Gly Asp Val Asp Glu Ala Leu Glu Leu Phe Lys Glu Met Arg Ser
165 170 175

Lys Gly Val Lys Pro Asn Val Val Thr Tyr Thr Thr Leu Ile Asp Gly
180 185 190

Leu Cys Lys Ala Gly Lys Val Asp Glu Ala Leu Glu Leu Phe Asp Glu
195 200 205

Met Lys Glu Arg Gly Ile Lys Pro Asp Val Val Thr Tyr Asn Thr Leu
210 215 220

Ile Asp Gly Leu Cys Lys Ser Gly Lys Ile Glu Glu Ala Leu Lys Leu

225		230		235		240									
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Thr	Thr	Leu	Ile	Asp	Gly	Leu	Cys	Lys	Ala	Gly	Asp	Val	Asp	Glu	Ala
			260					265					270		
Leu	Glu	Leu	Phe	Lys	Glu	Met	Arg	Ser	Lys	Gly	Val	Lys	Pro	Asn	Val
		275					280					285			
Val	Thr	Tyr	Thr	Thr	Leu	Ile	Asp	Gly	Leu	Cys	Lys	Ala	Gly	Lys	Val
	290					295					300				
Asp	Glu	Ala	Leu	Glu	Leu	Phe	Asp	Glu	Met	Lys	Glu	Arg	Gly	Ile	Lys
305					310					315					320
Pro	Asp	Val	Val	Thr	Tyr	Asn	Thr	Leu	Ile	Asp	Gly	Leu	Cys	Lys	Ser
				325					330					335	
Gly	Lys	Ile	Glu	Glu	Ala	Leu	Lys	Leu	Phe	Lys	Glu	Met	Glu	Glu	Lys
			340					345					350		
Gly	Ile	Thr	Pro	Ser	Val	Val	Thr	Tyr	Thr	Thr	Leu	Ile	Asp	Gly	Leu
	355						360					365			
Cys	Lys	Ala	Gly	Asp	Val	Asp	Glu	Ala	Leu	Glu	Leu	Phe	Lys	Glu	Met
	370					375					380				
Arg	Ser	Lys	Gly	Val	Lys	Pro	Asn	Val	Val	Thr	Tyr	Thr	Thr	Leu	Ile
385					390					395					400
Asp	Gly	Leu	Cys	Lys	Ala	Gly	Lys	Val	Asp	Glu	Ala	Leu	Glu	Leu	Phe
				405					410					415	
Asp	Glu	Met	Lys	Glu	Arg	Gly	Ile	Lys	Pro	Asp	Val	Val	Thr	Tyr	Asn
			420					425					430		
Thr	Leu	Ile	Asp	Gly	Leu	Cys	Lys	Ser	Gly	Lys	Ile	Glu	Glu	Ala	Leu
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Lys Leu Phe Lys Glu Met Glu Glu Lys Gly Ile Thr Pro Ser Val Val
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Thr Tyr Thr Thr Leu Ile Asp Gly Leu Cys Lys Ala Gly Asp Val Asp
 465 470 475 480

Glu Ala Leu Glu Leu Phe Lys Glu Met Arg Ser Lys Gly Val Lys Pro
 485 490 495

Asn Val Val Thr Tyr Thr Thr Leu Ile Asp Gly Leu Cys Lys Ala Gly
 500 505 510

Lys Val Asp Glu Ala Leu Glu Leu Phe Asp Glu Met Lys Glu Arg Gly
 515 520 525

Ile Lys Pro Asp Val Val Thr Tyr Asn Thr Leu Ile Asp Gly Leu Cys
 530 535 540

Lys Ser Gly Lys Ile Glu Glu Ala Leu Lys Leu Phe Lys Glu Met Glu
 545 550 555 560

Glu Lys Gly Ile Thr Pro Ser Val Val Thr Tyr Thr Thr Leu Ile Asp
 565 570 575

Gly Leu Cys Lys Ala Gly Asp Val Asp Glu Ala Leu Glu Leu Phe Lys
 580 585 590

Glu Met Arg Ser Lys Gly Val Lys Pro Asn Val Val Thr Tyr Thr Thr
 595 600 605

Leu Ile Asp Gly Leu Cys Lys Ala Gly Lys Val Asp Glu Ala Leu Glu
 610 615 620

Leu Phe Asp Glu Met Lys Glu Arg Gly Ile Lys Pro Asp Val Val Thr
 625 630 635 640

Tyr Asn Thr Leu Ile Asp Gly Leu Cys Lys Ser Gly Lys Ile Glu Glu
 645 650 655

Ala Leu Lys Leu Phe Lys Glu Met Glu Glu Lys Gly Ile Thr Pro Ser
660 665 670

Val Val Thr Tyr Thr Thr Leu Ile Asp Gly Leu Cys Lys Ala Gly Asp
675 680 685

Val Asp Glu Ala Leu Glu Leu Phe Lys Glu Met Arg Ser Lys Gly Val
690 695 700

Lys Pro Asn Val Val Thr Tyr Thr Thr Leu Ile Asp Gly Leu Cys Lys
705 710 715 720

Ala Gly Lys Val Asp Glu Ala Leu Glu Leu Phe Asp Glu Met Lys Glu
725 730 735

Arg Gly Ile Lys Pro Asp Glu Leu Thr Tyr Asn Thr Leu Ile Ser Gly
740 745 750

Leu Gly Lys Ala Gly
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<212> DNA
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