

SEQUENCE LISTING

<110> Denali Therapeutics Inc.
Dennis, Mark S.
Silverman, Adam P.
Zuchero, Joy Yu

<120> TRANSFERRIN RECEPTOR TRANSGENIC MODELS

<130> 1076191

<150> US 62/460,692

<151> 2017-02-17

<150> US 62/543,559

<151> 2017-08-10

<150> US 62/543,658

<151> 2017-08-10

<150> US 62/583,314

<151> 2017-11-08

<160> 11

<170> PatentIn version 3.5

<210> 1

<211> 184

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<213> Homo sapiens

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Val	Thr	Gly	Lys	Leu	Val	His	Ala	Asn	Phe	Gly	Thr	Lys	Lys	Asp	Phe
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Glu	Asp	Leu	Tyr	Thr	Pro	Val	Asn	Gly	Ser	Ile	Val	Ile	Val	Arg	Ala
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Gly	Lys	Ile	Thr	Phe	Ala	Glu	Lys	Val	Ala	Asn	Ala	Glu	Ser	Leu	Asn
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Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val
85 90 95

Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly Thr Gly Asp
100 105 110

Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln Phe Pro Pro
115 120 125

Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg
130 135 140

Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser
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Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys
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Asn Val Lys Leu Thr Val Ser Asn
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aacttcggaa ccaagaagga ctttgaggat ctgtacacac cagtgaacgg ctctatcgtg 180
atcgtgcgcg ctggaaagat caccttcgcc gagaaggtgg ctaacgccga gaggcctgaac 240
gccatcggcg tgctgatcta catggatcag acaaagtttc ccatcgtgaa cgctgagctg 300
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tttaaccaca ccagttccc cccttcagg tctagcggac tgccaaacat ccccgatcag 420
acaatcagca gagccgctgc cgagaagctg tttggcaaca tggagggaga ctgccctcc 480
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 <213> Artificial Sequence

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 <223> Transmembrane Domain

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 <223> Apical Domain

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Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
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Asn Ser His Val Glu Met Lys Leu Ala Ala Asp Glu Glu Glu Asn Ala
 35 40 45

Asp Asn Asn Met Lys Ala Ser Val Arg Lys Pro Lys Arg Phe Asn Gly
 50 55 60

Arg Leu Cys Phe Ala Ala Ile Ala Leu Val Ile Phe Phe Leu Ile Gly
 65 70 75 80

Phe Met Ser Gly Tyr Leu Gly Tyr Cys Lys Arg Val Glu Gln Lys Glu

85

90

95

Glu Cys Val Lys Leu Ala Glu Thr Glu Glu Thr Asp Lys Ser Glu Thr
 100 105 110

Met Glu Thr Glu Asp Val Pro Thr Ser Ser Arg Leu Tyr Trp Ala Asp
 115 120 125

Leu Lys Thr Leu Leu Ser Glu Lys Leu Asn Ser Ile Glu Phe Ala Asp
 130 135 140

Thr Ile Lys Gln Leu Ser Gln Asn Thr Tyr Thr Pro Arg Glu Ala Gly
 145 150 155 160

Ser Gln Lys Asp Glu Ser Leu Ala Tyr Tyr Ile Glu Asn Gln Phe His
 165 170 175

Glu Phe Lys Phe Ser Lys Val Trp Arg Asp Glu His Tyr Val Lys Ile
 180 185 190

Gln Val Lys Ser Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn
 195 200 205

Gly Arg Leu Val Tyr Leu Val Glu Asn Pro Gly Gly Tyr Val Ala Tyr
 210 215 220

Ser Lys Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly
 225 230 235 240

Thr Lys Lys Asp Phe Glu Asp Leu Tyr Thr Pro Val Asn Gly Ser Ile
 245 250 255

Val Ile Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn
 260 265 270

Ala Glu Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr
 275 280 285

Lys Phe Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His
 290 295 300

Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His
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Thr Gln Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val
325 330 335

Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu
340 345 350

Gly Asp Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val
355 360 365

Thr Ser Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys
370 375 380

Glu Arg Arg Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Tyr Glu Glu
385 390 395 400

Pro Asp Arg Tyr Val Val Val Gly Ala Gln Arg Asp Ala Leu Gly Ala
405 410 415

Gly Val Ala Ala Lys Ser Ser Val Gly Thr Gly Leu Leu Leu Lys Leu
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Ala Gln Val Phe Ser Asp Met Ile Ser Lys Asp Gly Phe Arg Pro Ser
435 440 445

Arg Ser Ile Ile Phe Ala Ser Trp Thr Ala Gly Asp Phe Gly Ala Val
450 455 460

Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys
465 470 475 480

Ala Phe Thr Tyr Ile Asn Leu Asp Lys Val Val Leu Gly Thr Ser Asn
485 490 495

Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr Leu Met Gly Lys Ile
500 505 510

Met Gln Asp Val Lys His Pro Val Asp Gly Lys Ser Leu Tyr Arg Asp

515

520

525

Ser Asn Trp Ile Ser Lys Val Glu Lys Leu Ser Phe Asp Asn Ala Ala
 530 535 540

Tyr Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe
 545 550 555 560

Cys Glu Asp Ala Asp Tyr Pro Tyr Leu Gly Thr Arg Leu Asp Thr Tyr
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Glu Ala Leu Thr Gln Lys Val Pro Gln Leu Asn Gln Met Val Arg Thr
 580 585 590

Ala Ala Glu Val Ala Gly Gln Leu Ile Ile Lys Leu Thr His Asp Val
 595 600 605

Glu Leu Asn Leu Asp Tyr Glu Met Tyr Asn Ser Lys Leu Leu Ser Phe
 610 615 620

Met Lys Asp Leu Asn Gln Phe Lys Thr Asp Ile Arg Asp Met Gly Leu
 625 630 635 640

Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp Tyr Phe Arg Ala Thr
 645 650 655

Ser Arg Leu Thr Thr Asp Phe His Asn Ala Glu Lys Thr Asn Arg Phe
 660 665 670

Val Met Arg Glu Ile Asn Asp Arg Ile Met Lys Val Glu Tyr His Phe
 675 680 685

Leu Ser Pro Tyr Val Ser Pro Arg Glu Ser Pro Phe Arg His Ile Phe
 690 695 700

Trp Gly Ser Gly Ser His Thr Leu Ser Ala Leu Val Glu Asn Leu Lys
 705 710 715 720

Leu Arg Gln Lys Asn Ile Thr Ala Phe Asn Glu Thr Leu Phe Arg Asn
 725 730 735

Gln Leu Ala Leu Ala Thr Trp Thr Ile Gln Gly Val Ala Asn Ala Leu
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Ser Gly Asp Ile Trp Asn Ile Asp Asn Glu Phe
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35 40 45

Asp Asn Asn Met Lys Ala Ser Val Arg Lys Pro Lys Arg Phe Asn Gly
50 55 60

Arg Leu Cys Phe Ala Ala Ile Ala Leu Val Ile Phe Phe Leu Ile Gly
65 70 75 80

Phe Met Ser Gly Tyr Leu Gly Tyr Cys Lys Arg Val Glu Gln Lys Glu
85 90 95

Glu Cys Val Lys Leu Ala Glu Thr Glu Glu Thr Asp Lys Ser Glu Thr
100 105 110

Met Glu Thr Glu Asp Val Pro Thr Ser Ser Arg Leu Tyr Trp Ala Asp
115 120 125

Leu Lys Thr Leu Leu Ser Glu Lys Leu Asn Ser Ile Glu Phe Ala Asp
130 135 140

Thr Ile Lys Gln Leu Ser Gln Asn Thr Tyr Thr Pro Arg Glu Ala Gly
145 150 155 160

Ser Gln Lys Asp Glu Ser Leu Ala Tyr Tyr Ile Glu Asn Gln Phe His
165 170 175

Glu Phe Lys Phe Ser Lys Val Trp Arg Asp Glu His Tyr Val Lys Ile
180 185 190

Gln Val Lys Ser Ser Ile Gly Gln Asn Met Val Thr Ile Val Gln Ser
195 200 205

Asn Gly Asn Leu Asp Pro Val Glu Ser Pro Glu Gly Tyr Val Ala Phe
210 215 220

Ser Lys Pro Thr Glu Val Ser Gly Lys Leu Val His Ala Asn Phe Gly
225 230 235 240

Thr Lys Lys Asp Phe Glu Glu Leu Ser Tyr Ser Val Asn Gly Ser Leu
245 250 255

Val Ile Val Arg Ala Gly Glu Ile Thr Phe Ala Glu Lys Val Ala Asn
260 265 270

Ala Gln Ser Phe Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Lys Asn
275 280 285

Lys Phe Pro Val Val Glu Ala Asp Leu Ala Leu Phe Gly His Ala His
290 295 300

Leu Gly Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His
305 310 315 320

Thr Gln Phe Pro Pro Ser Gln Ser Ser Gly Leu Pro Asn Ile Pro Val
325 330 335

Gln Thr Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Lys Met Glu
340 345 350

Gly Ser Cys Pro Ala Arg Trp Asn Ile Asp Ser Ser Cys Lys Leu Glu
355 360 365

Leu Ser Gln Asn Gln Asn Val Lys Leu Ile Val Lys Asn Val Leu Lys
370 375 380

Glu Arg Arg Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Tyr Glu Glu
385 390 395 400

Pro Asp Arg Tyr Val Val Val Gly Ala Gln Arg Asp Ala Leu Gly Ala
405 410 415

Gly Val Ala Ala Lys Ser Ser Val Gly Thr Gly Leu Leu Leu Lys Leu
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Ala Gln Val Phe Ser Asp Met Ile Ser Lys Asp Gly Phe Arg Pro Ser
435 440 445

Arg Ser Ile Ile Phe Ala Ser Trp Thr Ala Gly Asp Phe Gly Ala Val
450 455 460

Gly Ala Thr Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys
465 470 475 480

Ala Phe Thr Tyr Ile Asn Leu Asp Lys Val Val Leu Gly Thr Ser Asn
485 490 495

Phe Lys Val Ser Ala Ser Pro Leu Leu Tyr Thr Leu Met Gly Lys Ile
500 505 510

Met Gln Asp Val Lys His Pro Val Asp Gly Lys Ser Leu Tyr Arg Asp
515 520 525

Ser Asn Trp Ile Ser Lys Val Glu Lys Leu Ser Phe Asp Asn Ala Ala
530 535 540

Tyr Pro Phe Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe
545 550 555 560

Cys Glu Asp Ala Asp Tyr Pro Tyr Leu Gly Thr Arg Leu Asp Thr Tyr
565 570 575

Glu Ala Leu Thr Gln Lys Val Pro Gln Leu Asn Gln Met Val Arg Thr
580 585 590

Ala Ala Glu Val Ala Gly Gln Leu Ile Ile Lys Leu Thr His Asp Val
595 600 605

Glu Leu Asn Leu Asp Tyr Glu Met Tyr Asn Ser Lys Leu Leu Ser Phe
610 615 620

Met Lys Asp Leu Asn Gln Phe Lys Thr Asp Ile Arg Asp Met Gly Leu
625 630 635 640

Ser Leu Gln Trp Leu Tyr Ser Ala Arg Gly Asp Tyr Phe Arg Ala Thr
645 650 655

Ser Arg Leu Thr Thr Asp Phe His Asn Ala Glu Lys Thr Asn Arg Phe
660 665 670

Val Met Arg Glu Ile Asn Asp Arg Ile Met Lys Val Glu Tyr His Phe
675 680 685

Leu Ser Pro Tyr Val Ser Pro Arg Glu Ser Pro Phe Arg His Ile Phe
690 695 700

Trp Gly Ser Gly Ser His Thr Leu Ser Ala Leu Val Glu Asn Leu Lys
705 710 715 720

Leu Arg Gln Lys Asn Ile Thr Ala Phe Asn Glu Thr Leu Phe Arg Asn
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Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
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Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro
100 105 110

Gly Glu Asp Phe Pro Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys
115 120 125

Arg Lys Leu Ser Glu Lys Leu Asp Ser Thr Asp Phe Thr Gly Thr Ile
130 135 140

Lys Leu Leu Asn Glu Asn Ser Tyr Val Pro Arg Glu Ala Gly Ser Gln
145 150 155 160

Lys Asp Glu Asn Leu Ala Leu Tyr Val Glu Asn Gln Phe Arg Glu Phe
165 170 175

Lys Leu Ser Lys Val Trp Arg Asp Gln His Phe Val Lys Ile Gln Val
180 185 190

Lys Asp Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn Gly Arg
195 200 205

Leu Val Tyr Leu Val Glu Asn Pro Gly Gly Tyr Val Ala Tyr Ser Lys
210 215 220

Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys
225 230 235 240

Lys Asp Phe Glu Asp Leu Tyr Thr Pro Val Asn Gly Ser Ile Val Ile
245 250 255

Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu
260 265 270

Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
275 280 285

Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly
290 295 300

Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
305 310 315 320

Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
325 330 335

Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
340 345 350

Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser
355 360 365

Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
370 375 380

Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
385 390 395 400

His Tyr Val Val Val Gly Ala Gln Arg Asp Ala Trp Gly Pro Gly Ala
405 410 415

Ala Lys Ser Gly Val Gly Thr Ala Leu Leu Lys Leu Ala Gln Met
420 425 430

Phe Ser Asp Met Val Leu Lys Asp Gly Phe Gln Pro Ser Arg Ser Ile
435 440 445

Ile Phe Ala Ser Trp Ser Ala Gly Asp Phe Gly Ser Val Gly Ala Thr
450 455 460

Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr
465 470 475 480

Tyr Ile Asn Leu Asp Lys Ala Val Leu Gly Thr Ser Asn Phe Lys Val
485 490 495

Ser Ala Ser Pro Leu Leu Tyr Thr Leu Ile Glu Lys Thr Met Gln Asn
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Val Lys His Pro Val Thr Gly Gln Phe Leu Tyr Gln Asp Ser Asn Trp
515 520 525

Ala Ser Lys Val Glu Lys Leu Thr Leu Asp Asn Ala Ala Phe Pro Phe
530 535 540

Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe Cys Glu Asp
545 550 555 560

Thr Asp Tyr Pro Tyr Leu Gly Thr Thr Met Asp Thr Tyr Lys Glu Leu
565 570 575

Ile Glu Arg Ile Pro Glu Leu Asn Lys Val Ala Arg Ala Ala Glu
580 585 590

Val Ala Gly Gln Phe Val Ile Lys Leu Thr His Asp Val Glu Leu Asn
595 600 605

Leu Asp Tyr Glu Arg Tyr Asn Ser Gln Leu Leu Ser Phe Val Arg Asp
610 615 620

Leu Asn Gln Tyr Arg Ala Asp Ile Lys Glu Met Gly Leu Ser Leu Gln
625 630 635 640

Trp Leu Tyr Ser Ala Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu
645 650 655

Thr Thr Asp Phe Gly Asn Ala Glu Lys Thr Asp Arg Phe Val Met Lys
660 665 670

Lys Leu Asn Asp Arg Val Met Arg Val Glu Tyr His Phe Leu Ser Pro
675 680 685

Tyr Val Ser Pro Lys Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser
690 695 700

Gly Ser His Thr Leu Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
705 710 715 720

Gln Asn Asn Gly Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
725 730 735

Leu Ala Thr Trp Thr Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp
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Val Trp Asp Ile Asp Asn Glu Phe
755 760

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<213> Macaca mulatta

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Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys Lys Asp Phe
35 40 45

Glu Asp Leu Asp Ser Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala
50 55 60

Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu Ser Leu Asn
65 70 75 80

Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val
85 90 95

Lys Ala Asp Leu Ser Phe Phe Gly His Ala His Leu Gly Thr Gly Asp
100 105 110

Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln Phe Pro Pro

115

120

125

Ser Gln Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg
 130 135 140

Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser
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Asp Trp Lys Thr Asp Ser Thr Cys Lys Met Val Thr Ser Glu Asn Lys
 165 170 175

Ser Val Lys Leu Thr Val Ser Asn
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<213> Pan troglodytes

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Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys Lys Asp Phe
 35 40 45

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

Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu Ser Leu Asn
 65 70 75 80

Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val
 85 90 95

Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly Thr Gly Asp
 100 105 110

Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln Phe Pro Pro
115 120 125

Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr Val Ser Arg
130 135 140

Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser
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Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser Glu Ser Lys
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Asn Val Lys Leu Thr Val Ser Asn
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Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys Lys Asp Phe
35 40 45

Glu Asp Leu Asp Ser Pro Val Asn Gly Ser Ile Val Ile Val Arg Ala
50 55 60

Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu Ser Leu Asn
65 70 75 80

Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe Pro Ile Val
85 90 95

Lys Ala Asp Leu Ser Phe Phe Gly His Ala His Leu Gly Thr Gly Asp
100 105 110

Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln Phe Pro Pro
115 120 125

Ser Gln Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr Ile Ser Arg
130 135 140

Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp Cys Pro Ser
145 150 155 160

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