

9869SG4396-seq1-000001
SEQUENCE LISTING

<110> AGENCY FOR SCIENCE, TECHNOLOGY AND RESEARCH
<120> ANTI-AXL TYROSINE KINASE RECEPTOR ANTIBODIES AND USES THEREOF
<130> 9869SG4396
<160> 15
<170> PatentIn version 3.5
<210> 1
<211> 119
<212> PRT
<213> Artificial Sequence
<220>
<223> Isolated peptide sequence
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Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Ser Tyr
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Tyr Met Tyr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Val Ser Pro Ser Asn Gly Gly Ala Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Leu Tyr Gly Pro Arg Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 2
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<213> Artificial Sequence

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<223> Isolated peptide sequence

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Asp Ile Glu Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr
20 25 30

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Gly Ala Ser Asn Gln Gly Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Met Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys Gln Gln Ser Lys
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Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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Gly	Val	Ser	Pro	Ser	Asn	Gly	Gly	Ala	Asn	Phe	Asn	Glu	Lys	Phe	Lys
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Thr

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Phe	Leu	Tyr	Gly	Pro	Arg	Tyr	Phe	Asp	Val
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<210> 6

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<212> PRT

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<223> Isolated peptide sequence

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Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn
1 5 10 15

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<223> Isolated peptide sequence

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Gly Ala Ser Asn Gln Gly Ser
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<210> 8

<211> 9

<212> PRT

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<223> Isolated peptide sequence

<400> 8

Gln Gln Ser Lys Glu Val Pro Tyr Thr
1 5

<210> 9

<211> 20

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<223> Primer sequence

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ggtggctgtg aagacgatga

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<210> 10
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 <213> Artificial Sequence

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 <223> Primer sequence

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 ctcagatact ccatgccact 20

<210> 11
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 cagcgagauu uaugacuaut t 21

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<400> 12
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 cctggacaag gccttgagtg gattgggggg gttagtccta gcaatgggtg tgctaacttc 180
 aatgagaagt tcaagaccaa ggccacactg actgtagaca aatcctccag cacagcctac 240
 atgcaactca gcagcctgac atctgaggac tctgcggtct attactgtac aagattcctt 300
 tatgggccga ggtacttcga tgtctggggc caagggacca cggtcaccgt ctcctca 357

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caacagaaac caggacagcc acccaaactc ctcatTTatg gtgcatccaa ccagggatcc      180
ggggTccctg ccaggTttag tggcagTggg tctgggacag acttcagcct caacatccat      240
cctatggagg aggatgatac tgcaatgtat ttctgtcagc aaagtaagga ggTtccgtac      300
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<210> 14

<211> 894

<212> PRT

<213> Homo sapiens

<400> 14

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Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp Cys
1           5           10           15
  
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Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr Gln Ala
20           25           30
  
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Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35           40           45
  
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Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50           55           60
  
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Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65           70           75           80
  
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Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
  
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85

90

95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr
 100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser
 115 120 125

Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
 130 135 140

Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys
 145 150 155 160

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
 165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
 180 185 190

His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His
 195 200 205

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
 210 215 220

Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu
 225 230 235 240

Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr
 245 250 255

His Cys Thr Leu Gln Ala Val Leu Ser Asn Asp Gly Met Gly Ile Gln
 260 265 270

Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser

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275

280

285

Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Thr Pro
 290 295 300

Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp
 305 310 315 320

Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro
 325 330 335

Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His
 340 345 350

Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg
 355 360 365

Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly
 370 375 380

Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser
 385 390 395 400

Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro
 405 410 415

Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Gln Ala Gln
 420 425 430

Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp
 435 440 445

Pro Trp Trp Tyr Val Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val
 450 455 460

Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg

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465		470		475		480									
Tyr	Gly	Glu	Val	Phe	Glu	Pro	Thr	Val	Glu	Arg	Gly	Glu	Leu	Val	Val
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Arg	Tyr	Arg	Val	Arg	Lys	Ser	Tyr	Ser	Arg	Arg	Thr	Thr	Glu	Ala	Thr
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Leu	Asn	Ser	Leu	Gly	Ile	Ser	Glu	Glu	Leu	Lys	Glu	Lys	Leu	Arg	Asp
		515					520					525			
Val	Met	Val	Asp	Arg	His	Lys	Val	Ala	Leu	Gly	Lys	Thr	Leu	Gly	Glu
	530					535					540				
Gly	Glu	Phe	Gly	Ala	Val	Met	Glu	Gly	Gln	Leu	Asn	Gln	Asp	Asp	Ser
545					550					555					560
Ile	Leu	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	Ile	Ala	Ile	Cys	Thr	Arg
			565						570					575	
Ser	Glu	Leu	Glu	Asp	Phe	Leu	Ser	Glu	Ala	Val	Cys	Met	Lys	Glu	Phe
			580					585					590		
Asp	His	Pro	Asn	Val	Met	Arg	Leu	Ile	Gly	Val	Cys	Phe	Gln	Gly	Ser
		595					600					605			
Glu	Arg	Glu	Ser	Phe	Pro	Ala	Pro	Val	Val	Ile	Leu	Pro	Phe	Met	Lys
	610					615					620				
His	Gly	Asp	Leu	His	Ser	Phe	Leu	Leu	Tyr	Ser	Arg	Leu	Gly	Asp	Gln
625					630					635					640
Pro	Val	Tyr	Leu	Pro	Thr	Gln	Met	Leu	Val	Lys	Phe	Met	Ala	Asp	Ile
			645						650					655	
Ala	Ser	Gly	Met	Glu	Tyr	Leu	Ser	Thr	Lys	Arg	Phe	Ile	His	Arg	Asp

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660

665

670

Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
 675 680 685

Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg
 690 695 700

Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
 705 710 715 720

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
 725 730 735

Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly
 740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu
 755 760 765

Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
 770 775 780

Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
 785 790 795 800

Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
 805 810 815

Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
 820 825 830

Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro
 835 840 845

Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly

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850

855

860

Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala
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Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp Gly Ala
885 890

<210> 15
<211> 894
<212> PRT
<213> Homo sapiens

<400> 15

Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp Cys
1 5 10 15

Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr Gln Ala
20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
85 90 95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr
100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser
115 120 125

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Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
130 135 140

Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys
145 150 155 160

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
180 185 190

His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His
195 200 205

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
210 215 220

Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu
225 230 235 240

Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr
245 250 255

His Cys Thr Leu Gln Ala Val Leu Ser Asn Asp Gly Met Gly Ile Gln
260 265 270

Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser
275 280 285

Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Thr Pro
290 295 300

Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp
305 310 315 320

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Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro
325 330 335

Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His
340 345 350

Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg
355 360 365

Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly
370 375 380

Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser
385 390 395 400

Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro
405 410 415

Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Gln Ala Gln
420 425 430

Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp
435 440 445

Pro Trp Trp Tyr Val Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val
450 455 460

Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg
465 470 475 480

Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly Glu Leu Val Val
485 490 495

Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr
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Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp
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Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu
530 535 540

Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn Gln Asp Asp Ser
545 550 555 560

Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg
565 570 575

Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe
580 585 590

Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys Phe Gln Gly Ser
595 600 605

Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys
610 615 620

His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Asp Gln
625 630 635 640

Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile
645 650 655

Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp
660 665 670

Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
675 680 685

Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg
690 695 700

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Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
705 710 715 720

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
725 730 735

Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly
740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu
755 760 765

Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
770 775 780

Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
785 790 795 800

Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
805 810 815

Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
820 825 830

Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro
835 840 845

Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly
850 855 860

Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala
865 870 875 880

Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp Gly Ala
885 890

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