

ALXN146W01
SEQUENCE LISTING

<110> ALEXION PHARMACEUTICALS, INC.

<120> Antibodies Containing Therapeutic Peptides

<130> ALXN-146-W01

<140>

<141>

<150> 61/208,487

<151> 2009-02-24

<160> 16

<170> PatentIn version 3.5

<210> 1

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide mimetic

<400> 1

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide mimetic

<400> 2

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Pro
1 5 10 15

<210> 3

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide mimetic

<400> 3

Asp Tyr His Cys Arg Met Gly Pro Leu Thr Trp Val Cys Lys Pro Leu
1 5 10 15

Gly Gly

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>
 <223> Peptide mimetic

<400> 4

Ala Phe Leu Ala Arg Ala Ala
 1 5

<210> 5
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Spacer sequence

<400> 5

Ala Arg Ser Leu
 1

<210> 6
 <211> 2
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Spacer sequence

<400> 6

Pro Ile
 1

<210> 7
 <211> 2
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Spacer sequence

<400> 7

Asn Pro
 1

<210> 8
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Spacer sequence

<400> 8

Leu Val Gly
 1

<210> 9
 <211> 705

ALXN146W01

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence encoding a recombinant light chain polypeptide

<220>
 <221> CDS
 <222> (1)..(705)

```

<400> 9
gac atc cag atg acc cag tct cca tcc tcc ctg tcc gca tct gta gga      48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

gac aga gtc acc ctc act tgc cgg gca agt cag ggc gtt aga aat gct      96
Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Gly Val Arg Asn Ala
20 25 30

tta gtc tgg tat cag cag aaa cca gga aaa gcc cct gag cgc ctg atc      144
Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Arg Leu Ile
35 40 45

tac gct gca tcc att ttg caa agt ggg gtc cca tca agg ttc agc ggc      192
Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt gga tct ggg aca gaa ttc act ctc aca atc ggc ggc ctg cag cct      240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Gly Gly Leu Gln Pro
65 70 75 80

gaa gat ttc gca act tat tac tgt cta cag cat aat agt tac ccg tgg      288
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Trp
85 90 95

acg ttc ggc caa ggg acc aag gtg gaa atc aag cga act gtg gct gca      336
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

cca tct gtc ttc atc ttc ccg cca tcc gat gag cag ttg aaa tct gga      384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc      432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag      480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc      528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac      576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc      624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

ttc aac agg gga gag tgt gcg aga tca ctg att gaa ggg ccg acg ctg      672
Phe Asn Arg Gly Glu Cys Ala Arg Ser Leu Ile Glu Gly Pro Thr Leu
210 215 220

```

cgg caa tgg ctg gcg gcg cgc gcg ccc atc taa
 Arg Gln Trp Leu Ala Ala Arg Ala Pro Ile
 225 230

<210> 10
 <211> 234
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Leu Thr Cys Arg Ala Ser Gln Gly Val Arg Asn Ala
 20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Arg Leu Ile
 35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Gly Gly Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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

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

ALXN146W01

Phe Asn Arg Gly Glu Cys Ala Arg Ser Leu Ile Glu Gly Pro Thr Leu
 210 215 220

Arg Gln Trp Leu Ala Ala Arg Ala Pro Ile
 225 230

<210> 11
 <211> 1389
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence encoding a recombinant heavy chain polypeptide

<220>
 <221> CDS
 <222> (1)..(1389)

<400> 11
 cag gtc cag ctt gtg cag tct ggg gct gag gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 tca gtg aag gtt tcc tgc aag gcc tct gga tac acc ttc act tac tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Tyr Tyr
 20 25 30
 gct atg cat tgg gtg cgc cag gcc ccc gga caa aga cct gag tgg atg 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Pro Glu Trp Met
 35 40 45
 gga tgg atc aac ggt ggc gat gga aaa aca aaa tat gca cag aag ttc 192
 Gly Trp Ile Asn Gly Gly Asp Gly Lys Thr Lys Tyr Ala Gln Lys Phe
 50 55 60
 cag ggc aga ctc gcc att acc agg gac aca tcc gcg agg acc gcc tac 240
 Gln Gly Arg Leu Ala Ile Thr Arg Asp Thr Ser Ala Arg Thr Ala Tyr
 65 70 75 80
 atg gag ctg atc agc ctg aca tct gaa gac acg gct gtg tat tac tgt 288
 Met Glu Leu Ile Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gca aaa ggg gcc gag atg acc gtg ggc tcc tgg ggc ccg gga acc ctg 336
 Ala Lys Gly Ala Glu Met Thr Val Gly Ser Trp Gly Pro Gly Thr Leu
 100 105 110
 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcc gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 gcg ccc tgc tcc agg agc acc tcc gag agc aca gcc gcc ctg ggc tgc 432
 Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
 130 135 140

ALXN146W01

ctg Leu 145	gtc Val	aag Lys	gac Asp	tac Tyr	ttc Phe 150	ccc Pro	gaa Glu	ccg Pro	gtg Val	acg Thr 155	gtg Val	tcg Ser	tgg Trp	aac Asn	tca Ser 160	480
ggc Gly	gcc Ala	ctg Leu	acc Thr	agc Ser 165	ggc Gly	gtg Val	cac His	acc Thr	ttc Phe 170	ccg Pro	gct Ala	gtc Val	cta Leu	cag Gln 175	tcc Ser	528
tca Ser	gga Gly	ctc Leu	tac Tyr 180	tcc Ser	ctc Leu	agc Ser	agc Ser	gtg Val 185	gtg Val	acc Thr	gtg Val	ccc Pro	tcc Ser 190	agc Ser	aac Asn	576
ttc Phe	ggc Gly	acc Thr 195	cag Gln	acc Thr	tac Tyr	acc Thr	tgc Cys 200	aac Asn	gta Val	gat Asp	cac His	aag Lys 205	ccc Pro	agc Ser	aac Asn	624
acc Thr	aag Lys 210	gtg Val	gac Asp	aag Lys	aca Thr	gtt Val 215	gag Glu	cgc Arg	aaa Lys	tgt Cys	tgt Cys 220	gtc Val	gag Glu	tgc Cys	cca Pro	672
ccg Pro 225	tgc Cys	cca Pro	gca Ala	cca Pro	cct Pro 230	gtg Val	gca Ala	aat Asn	ccg Pro	atc Ile 235	gaa Glu	ggc Gly	cca Pro	acc Thr	ctg Leu 240	720
cgc Arg	cag Gln	tgg Trp	ctg Leu	gct Ala 245	gct Ala	cgc Arg	gct Ala	cgt Arg	ggg Gly 250	gga Gly	ccg Pro	tca Ser	gtc Val	ttc Phe 255	ctc Leu	768
ttc Phe	ccc Pro	cca Pro	aaa Lys 260	ccc Pro	aag Lys	gac Asp	acc Thr	ctc Leu 265	atg Met	atc Ile	tcc Ser	cgg Arg	acc Thr 270	cct Pro	gag Glu	816
gtc Val	acg Thr	tgc Cys 275	gtg Val	gtg Val	gtg Val	gac Asp	gtg Val 280	agc Ser	cag Gln	gaa Glu	gac Asp	ccc Pro 285	gag Glu	gtc Val	cag Gln	864
ttc Phe 290	aac Asn	tgg Trp	tac Tyr	gtg Val	gat Asp	ggc Gly 295	gtg Val	gag Glu	gtg Val	cat His	aat Asn 300	gcc Ala	aag Lys	aca Thr	aag Lys	912
ccg Pro 305	cgg Arg	gag Glu	gag Glu	cag Gln	ttc Phe 310	aac Asn	agc Ser	acg Thr	tac Tyr	cgt Arg 315	gtg Val	gtc Val	agc Ser	gtc Val	ctc Leu 320	960
acc Thr	gtc Val	ctg Leu	cac His	cag Gln 325	gac Asp	tgg Trp	ctg Leu	aac Asn	ggc Gly 330	aag Lys	gag Glu	tac Tyr	aag Lys	tgc Cys 335	aag Lys	1008
gtc Val	tcc Ser	aac Asn	aaa Lys 340	ggc Gly	ctc Leu	ccg Pro	tcc Ser	tcc Ser 345	atc Ile	gag Glu	aaa Lys	acc Thr	atc Ile 350	tcc Ser	aaa Lys	1056
gcc Ala	aaa Lys	ggg Gly 355	cag Gln	ccc Pro	cga Arg	gag Glu	cca Pro 360	cag Gln	gtg Val	tac Tyr	acc Thr	ctg Leu 365	ccc Pro	cca Pro	tcc Ser	1104
cag Gln 370	gag Glu	gag Glu	atg Met	acc Thr	aag Lys	aac Asn 375	cag Gln	gtc Val	agc Ser	ctg Leu	acc Thr 380	tgc Cys	ctg Leu	gtc Val	aaa Lys	1152
ggc Gly 385	ttc Phe	tac Tyr	ccc Pro	agc Ser	gac Asp 390	atc Ile	gcc Ala	gtg Val	gag Glu	tgg Trp 395	gag Glu	agc Ser	aat Asn	ggg Gly	cag Gln 400	1200

ALXN146W01

ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc	1248
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly	
405 410 415	
tcc ttc ttc ctc tac agc agg cta acc gtg gac aag agc agg tgg cag	1296
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln	
420 425 430	
gag ggg aat gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac	1344
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn	
435 440 445	
cac tac aca cag aag agc ctc tcc ctg tct ctg ggt aaa tga tga	1389
His Tyr Thr Gln Lys Ser Leu Ser Leu Gly Lys	
450 455 460	

<210> 12
 <211> 461
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Tyr Tyr	
20 25 30	
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Pro Glu Trp Met	
35 40 45	
Gly Trp Ile Asn Gly Gly Asp Gly Lys Thr Lys Tyr Ala Gln Lys Phe	
50 55 60	
Gln Gly Arg Leu Ala Ile Thr Arg Asp Thr Ser Ala Arg Thr Ala Tyr	
65 70 75 80	
Met Glu Leu Ile Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Lys Gly Ala Glu Met Thr Val Gly Ser Trp Gly Pro Gly Thr Leu	
100 105 110	
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys	
130 135 140	
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
145 150 155 160	
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
 180 185 190
 Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Pro Val Ala Asn Pro Ile Glu Gly Pro Thr Leu
 225 230 235 240
 Arg Gln Trp Leu Ala Ala Arg Ala Arg Gly Gly Pro Ser Val Phe Leu
 245 250 255
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 260 265 270
 Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 275 280 285
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 290 295 300
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 305 310 315 320
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 325 330 335
 Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 340 345 350
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 355 360 365
 Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 370 375 380
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 385 390 395 400
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 405 410 415
 Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 420 425 430
 Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

435

440

445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 450 455 460

<210> 13
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 13

Glu Gln Trp Lys Ser His Lys
 1 5

<210> 14
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 14

Pro Ala Glu Cys Ser
 1 5

<210> 15
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 15

Ser Asp Glu Gln Leu Lys Ser
 1 5

<210> 16
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 16

Ala Asp Tyr Glu Lys His
 1 5