

SEQUENCE LISTING

<110> NovaGo Therapeutics AG

<120> Novel anti-Nogo-A antibodies

<130> NO48A05/P-WO

<160> 24

<170> PatentIn version 3.5

<210> 1

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

<223> NG004 variable heavy chain (VH) sequence

<400> 1

gag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	agg	48
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agg	agc	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Ser	His	
			20					25					30			

gct	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35				40						45				

gca	gtt	aca	tca	tat	gat	gga	acc	aat	aaa	tac	tac	gca	gac	tcc	gtg	192
Ala	Val	Thr	Ser	Tyr	Asp	Gly	Thr	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					

aag	ggc	cga	ttc	acc	atc	tcc	aaa	gac	aat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		

ctg	caa	atg	gac	agc	ctc	aga	gtt	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asp	Ser	Leu	Arg	Val	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcg	aga	ggc	cga	gca	gtg	gct	ggt	acg	agg	gaa	gat	tat	tgg	ggc	cag	336
Ala	Arg	Gly	Arg	Ala	Val	Ala	Gly	Thr	Arg	Glu	Asp	Tyr	Trp	Gly	Gln	
		100					105						110			

gga	acc	ctg	gtc	acc	gtc	tcc	tcg									360
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Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 2
<211> 120
<212> PRT
<213> Homo sapiens

<400> 2

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser His
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Thr Ser Tyr Asp Gly Thr Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Arg Ala Val Ala Gly Thr Arg Glu Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
<211> 5
<212> PRT
<213> Homo sapiens

<400> 3

Ser His Ala Met His
1 5

<210> 4
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 4

Val	Thr	Ser	Tyr	Asp	Gly	Thr	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 5
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 5

Gly	Arg	Ala	Val	Ala	Gly	Thr	Arg	Glu	Asp	Tyr
1				5				10		

<210> 6
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(339)
 <223> NG004 variable kappa chain (VK) sequence

<400> 6

gac	atc	cag	atg	acc	cag	tct	cca	gac	tcc	ctg	gct	gtg	tct	ctg	ggc	48
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	
1				5				10						15		

gag	agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	ttc	agc	96
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Phe	Ser	
			20					25					30			

tcc	aac	agt	aag	aac	tac	tta	gct	tgg	tac	cag	cag	aaa	cca	gga	cag	144
Ser	Asn	Ser	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
			35				40					45				

cct	cct	aag	gtg	ctc	att	tac	tgg	gca	tct	acc	cgg	gaa	tcc	ggg	gtc	192
Pro	Pro	Lys	Val	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	

50	55	60	
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc			240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr			
65	70	75	80
atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa			288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln			
	85	90	95
tat tat act act cgc cct acg ttc ggc cta ggg acc aaa gtg gat atc			336
Tyr Tyr Thr Thr Arg Pro Thr Phe Gly Leu Gly Thr Lys Val Asp Ile			
	100	105	110
aaa			339
Lys			

<210> 7
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 7

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Phe Ser
20 25 30

Ser Asn Ser Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Tyr Tyr Thr Thr Arg Pro Thr Phe Gly Leu Gly Thr Lys Val Asp Ile
100 105 110

Lys

<210> 8
<211> 17
<212> PRT
<213> Homo sapiens

<400> 8

Lys Ser Ser Gln Ser Val Leu Phe Ser Ser Asn Ser Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 9
<211> 7
<212> PRT
<213> Homo sapiens

<400> 9

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 10
<211> 9
<212> PRT
<213> Homo sapiens

<400> 10

Gln Gln Tyr Tyr Thr Thr Arg Pro Thr
1 5

<210> 11
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(342)
<223> NG034 variable heavy chain (VH) sequence

<400> 11

gag	gtg	cag	ctg	gtg	gag	act	ggg	gga	ggc	ttg	gtc	cca	ccg	ggg	ggg		48
Glu	Val	Gln	Leu	Val	Glu	Thr	Gly	Gly	Gly	Leu	Val	Pro	Pro	Gly	Gly		
1				5					10					15			

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	acc	aac	tat		96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asn	Tyr		
			20					25					30				

tct	atg	cac	tgg	gtc	cgc	ctg	gct	cca	ggg	aag	aga	ctg	gaa	tat	att		144
Ser	Met	His	Trp	Val	Arg	Leu	Ala	Pro	Gly	Lys	Arg	Leu	Glu	Tyr	Ile		
		35					40					45					

tca	gct	att	agt	agt	gat	ggc	ggt	gac	cca	ttt	tat	gca	agc	tct	gtg		192
Ser	Ala	Ile	Ser	Ser	Asp	Gly	Gly	Asp	Pro	Phe	Tyr	Ala	Ser	Ser	Val		
	50					55					60						

aag	ggc	aga	gtc	gcc	atc	tcc	aga	gac	aat	tcc	aag	aag	acg	ttg	tat		240
Lys	Gly	Arg	Val	Ala	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Lys	Thr	Leu	Tyr		
65					70					75				80			

ctt	caa	atg	ggc	aga	ctg	aga	cct	gag	gac	acg	gct	gta	tat	tat	tgt		288
Leu	Gln	Met	Gly	Arg	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			

gtg	agt	gat	gct	ttt	gat	gtc	tgg	ggc	cag	ggg	aca	atg	gtc	acc	gtc		336
Val	Ser	Asp	Ala	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val		
			100					105					110				

tct	tcg																342
Ser	Ser																

<210> 12
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 12

Glu	Val	Gln	Leu	Val	Glu	Thr	Gly	Gly	Gly	Leu	Val	Pro	Pro	Gly	Gly		
1				5					10					15			

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asn	Tyr		
			20					25					30				

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

Ser Ala Ile Ser Ser Asp Gly Gly Asp Pro Phe Tyr Ala Ser Ser Val
50 55 60

Lys Gly Arg Val Ala Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
65 70 75 80

Leu Gln Met Gly Arg Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Ser Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val
100 105 110

Ser Ser

<210> 13
<211> 5
<212> PRT
<213> Homo sapiens

<400> 13

Asn Tyr Ser Met His
1 5

<210> 14
<211> 17
<212> PRT
<213> Homo sapiens

<400> 14

Ala Ile Ser Ser Asp Gly Gly Asp Pro Phe Tyr Ala Ser Ser Val Lys
1 5 10 15

Gly

<210> 15
<211> 5
<212> PRT
<213> Homo sapiens

<400> 15

Asp Ala Phe Asp Val
1 5

<210> 16
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(336)
<223> NG034 variable kappa chain (VK) sequence

<400> 16
gaa att gtg ctg acc cag tct cca ctc tcc ctg tcc gtc acc ctt gga 48
Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Leu Gly
1 5 10 15

cag ccg gcc tcc atc tcc tgc agg tct agt caa agc ctc cta tac agt 96
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

aat ggc aac acc tac ttg aat tgg ttt cag cag agg cca ggc caa tct 144
Asn Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

cca agg cgc cta ctt tat agg gtt tct aac cgg gac tct ggg gtc cca 192
Pro Arg Arg Leu Leu Tyr Arg Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60

gac aga ttc agc ggc agt ggg tca ggc act cat ttc aca ctg aaa att 240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr His Phe Thr Leu Lys Ile
65 70 75 80

agt agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa ggt 288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

aca cac tgg cct cgc acg ttc ggc caa ggg acc aag gtg gag atc aaa 336
Thr His Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 17
<211> 112
<212> PRT
<213> Homo sapiens

<400> 17

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Leu Gly

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

<210> 18
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 18

Arg	Ser	Ser	Gln	Ser	Leu	Leu	Tyr	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Asn
1				5					10					15	

<210> 19
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 19

Arg	Val	Ser	Asn	Arg	Asp	Ser
1				5		

<210> 20
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Gln Gly Thr His Trp Pro Arg Thr
1 5

<210> 21

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> minimal epitope recognized by NG004

<220>

<221> PEPTIDE

<222> (1)..(7)

<223> minimal epitope recognized by antibody NG004

<400> 21

Ile Asn Ala Ala Leu Gln Glu
1 5

<210> 22

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 34

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Peptide 34: amino acids 133-147 of the Nogo-A d20plus region

<400> 22

Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu
1 5 10 15

<210> 23

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 35

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Peptide 35: amino acids 137-151 of the Nogo-A d20plus region

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Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln	Glu	Thr	Glu	Ala	Pro
1			5					10					15	

<210> 24

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 36

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Peptide 36: amino acids 141-155 of the Nogo-A d20plus region

<400> 24

Ile	Asn	Ala	Ala	Leu	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile
1				5				10					15	