

SEQUENCE LISTING

<110> Crescendo Biologics Limited

<120> Single domain antibodies that bind human serum albumin

<130> P35198W01

<160> 20

<170> PatentIn version 3.5

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<211> 122

<212> PRT

<213> homo sapiens

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1 5 10 15

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

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

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

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

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

Arg Asp Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Glu His Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

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His Tyr Ala Met His
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Gly Ile Ser Trp Asn Gly Asn Lys Ile Thr Tyr Ala Asp Ser Val Lys
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Gly

<210> 4
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<212> PRT
<213> homo sapiens

<400> 4

Asp Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Glu His
1 5 10

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<400> 5

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala

20

25

30

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

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
 50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
 65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
 85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
 100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
 115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
 130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
 145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
 165 170 175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
 180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
 195 200 205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Gly Leu Lys Cys
 210 215 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245 250 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Gly Ser
325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355 360 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
370 375 380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu

420

425

430

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
 435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
 450 455 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Cys Leu Ser Val Phe
 465 470 475 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
 485 490 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Gly Arg Pro Cys Phe
 500 505 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
 515 520 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
 530 535 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
 565 570 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
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Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
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Leu

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His His His His His His
1 5

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Gly Gly Gly Gly Ser
1 5

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<220>
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<400> 9

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10

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Gly Ser Gly Ser Gly Ser Gly Ser
1 5

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Gly Gly Ser Gly Ser Gly Ser Gly
1 5

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Gly Gly Ser Gly Ser Gly
1 5

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Gly Gly Ser Gly
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ggtttccctc tagaaataat tttgtttaac ttttaggagg taaaacatat gaagaaaacg 120

gcaatcgcaa	tcgcagtcgc	tctggcgggt	ttcgcaactg	tagcgcaagc	cgaggtgcaa	180
ctggtcgagt	ctggtggtgg	tttggtgcaa	cctggtagaa	gcttgcgttt	gagttgtgcc	240
gcttccggct	tcactttcca	tcattatgct	atgcactggg	ttcgtcaagc	tcccggaaaa	300
ggtttgagtg	gggtttccgg	aatttcctgg	aatggcaata	agattacgta	cgctgattca	360
gtgaaaggaa	ggttttacaat	cagtagagat	aatgctaaaa	actcattgta	tctacaaatg	420
aacagcctaa	gagcagaaga	taccgctctg	tactactgtg	ttagagatag	ctcgttattc	480
attgtaggtg	caccaacttt	tgaacattgg	ggtcggggta	ctcttgtgac	tgtctcatcc	540
gcggccgcac	accaccatca	tcaccactaa	ctcgagcgcc	taatgaaagc	ttccccaagg	600
gcgacacccc	ctaattagcc	cgggcgaaag	gcccagtcct	tcgactgagc	ctttcgtttt	660
atttgatgcc	tggcagttcc	ctactctcgc	atggggagtc	cccacactac	catcggcgct	720
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<211> 453
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<213> homo sapiens
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<400> 17

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr
20 25 30

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

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

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

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

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp Met Asn
180 185 190

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
195 200 205

Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys Gly Arg
210 215 220

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
245 250 255

Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser Gly Gln
260 265 270

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

275

280

285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 290 295 300

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 305 310 315 320

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 325 330 335

Phe Thr Phe His His Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly
 340 345 350

Lys Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Gly Asn Lys Ile
 355 360 365

Thr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 370 375 380

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 385 390 395 400

Thr Ala Leu Tyr Tyr Cys Val Arg Asp Ser Ser Leu Phe Ile Val Gly
 405 410 415

Ala Pro Thr Phe Glu His Trp Gly Arg Gly Thr Leu Val Thr Val Ser
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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 435 440 445

Gly Gly Gly Gly Ser
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<211> 1359

<212> DNA

<213> homo sapiens

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ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg	300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatatctg gggccaaggg	360
acaatggtca ccgtctctc aggtgggtggc gggtcaggcg gaggtggctc tggaggtgga	420
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gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa	600
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aactcacttc gtgctgagga caccgcagtg tactactgtg ctgcgggtgg tgaaggatac	780
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ggaggagggtg gttctggagg cgggtggctct gaagtacaac tggttgaatc ggggtgggtgga	960
ttggtccaac ctggaagatc attgaggctt tcttgtgcag cttccggatt cacctttcat	1020
cactatgcta tgcactgggt gagacaagcc cctggtaagg gcttggaatg ggtgtccgga	1080
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gaacattggg gtagaggtag cctagttacg gttagctcag gcggaggtag ctctggagga	1320
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<400> 19

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
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Ser Leu Lys Leu Ser Cys Ala Val Ser Gly Phe Thr Phe His His Tyr
20 25 30

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

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

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

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

Val Arg Asp Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Asp His
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
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Ser Leu Lys Leu Ser Cys Ala Val Ser Gly Phe Thr Phe His His Tyr
20 25 30

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

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

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

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

Val Arg Asp Ser Ser Leu Phe Ile Val Gly Ala Pro Thr Phe Asp His
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120