

Foreignfiling_text P18-218 Seq List
SEQUENCE LISTING

<110> Merck Patent GmbH

<120> ABITUZUMAB FOR THE TREATMENT OF COLORECTAL CANCER

<130> P18-218 PCT

<150> US62/748,114

<151> 2018-10-19

<160> 7

<170> BiSSAP 1.3.6

 $\langle 210 \rangle$ 1

$\langle 211 \rangle$ 214

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> DI17E6 light chain

$\langle 400 \rangle$ 1

[illegible]

Foreignfiling_text P18-218 Seq List

<210> 2

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> DI17E6 heavy chain

<400> 2

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Gly	Glu	Leu	Ala	Lys	Pro	Gly	Ala	1	5	10	15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Ser	Phe	20	25	30	
Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Tyr	Ile	Asn	Pro	Arg	Ser	Gly	Tyr	Thr	Glu	Tyr	Asn	Glu	Ile	Phe	50	55	60	
Arg	Asp	Lys	Ala	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	65	70	75	80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Ser	Phe	Leu	Gly	Arg	Gly	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	100	105	110	
Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	115	120	125	
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	130	135	140	
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	145	150	155	160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	165	170	175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	180	185	190	
Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	195	200	205	
Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	210	215	220	
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	225	230	235	240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	245	250	255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	260	265	270	
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	275	280	285	
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Ala	Gln	Ser	Thr	Phe	Arg	Val	Val	Ser	290	295	300	
Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	305	310	315	320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	325	330	335	
Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	340	345	350	

Foreignfiling_text P18-218 Seq List

```

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
      355                      360                      365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
      370                      375                      380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385                      390                      395                      400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
      405                      410                      415
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
      420                      425                      430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
      435                      440                      445

```

<210> 3

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> modified IgG1 hinge region

<400> 3

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1          5          10          15

```

<210> 4

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain framework region

<400> 4

```

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Glu Pro Gly Ala
1          5          10          15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser
      20          25          30

```

<210> 5

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain framework region

<400> 5

```

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1          5          10

```

Foreignfiling_text P18-218 Seq List

<210> 6

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain framework region

<400> 6

Lys Ala Thr Met Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln

1 5 10 15

Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ser

20 25 30

<210> 7

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain framework region

<400> 7

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser

1 5 10