5' GTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAA 110

5' TATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGT 220

AmpR

5' AAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGA 330

AmpR

BcgI' BcgI

5' GCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCA 440

AmpR

PvuI

5' CCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGG 550

AmpR

5' AGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACA 660

AmpR

5' CCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTT 770

AmpR

5' GCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGTTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGG 880

AmpR

5' TAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAAC 990

AmpR

5' TGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCT 1100

AmpR

5' TAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACC 1210

AmpR Col E1 origin

5' ACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGC 1320

Col E1 origin

5' CGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGG 1430

Col E1 origin

5' TTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCT 1540

Col E1 origin

5' ACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGG 1650

Col E1 origin

5' GAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAAC 1760

Col E1 origin

5' GCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCATTAGGCACCCCAGGCTTTACCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAGAGC 1870

Col E1 origin

5' GCCCAATACGCAAGGAAACAGCTATGACCATGTTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGGAAGGCCCATGAGGCCAGTTAATTAAG 1980

Acc65I
KpnI

5' AGGTACCTTAATTAAGGCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGC 2090

5'ITR

AflII

5' AGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTGTAGTTAATGATTAACCCGCCATGCTACTTATCTACGTAGCCATGCTCTAGGAAGATCGCAATTCGCCCTTA 2200

5'ITR

NheI
BmtI

5' AGCTAGCTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCC 2310

CMV Promoter

5' AACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTT 2420

CMV Promoter

NdeI

5' GGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTA 2530

CMV Promoter

5' CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 2640

CMV Promoter

5' CACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACG 2750

CMV Promoter

5' GTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCTGCAGAAGTTGGTCGTGAGGCACTGGGCAGGTAAGTATCAAGGTTACAAGACAGGTTTAAGGA 2860

CMV Promoter | Artificial Intron

NotI
EagI

5' GACCAATAGAAACTGGGCTTGTCGAGACAGAGAAGACTCTTGCGTTTCTGATAGGCACCTATTGGTCTTACTGACATCCACTTTGCCTTTCTCTCCACAGGTGTCCAgcg 2970

Artificial Intron

5' gccgcGCCACcATGAGACTGCTGACCGCCCTGTTCGCCTACTTCATCGTGGCCCTGATCCTGGCCTTCAGCGTGTCCGCCAAGAGCATGCACCACCACCATCACCATCAT 3080

Koz...seq | TCM signal sequence | His tag

M	R	L	L	T	A	L	F	A	Y	F	I	V	A	L	I	L	A	F	S	V	S	A	K	S	M	H	H	H	H	H	H	H
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

SgrAI

5' CACATGAGCGGCCTGAACGACATCTTCGAGGCCCAGAAAATCGAGTGGCACGAGATGAGCAAGGGCGAGGAACTGTTCACCGGCGTGGTGCCCATCCTGGTGGAACTGGA 3190

H... | AviTag | Superfolder GFP

H	M	S	G	L	N	D	I	F	E	A	Q	K	I	E	W	H	E	M	S	K	G	E	E	L	F	T	G	V	V	P	I	L	V	E	L	D
34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70

5' CGGCGACGTGAACGGCCACAAGTTCTCTGTGCGGGGCGAGGGCGAGGGGGACGCCACAAATGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGAAAGCTGCCCGTGC 3300

Superfolder GFP

G D V N G H K F S V R G E G E G D A T N G K L T L K F I C T T G K L P V
71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106

5' CCTGGCCTACCCTGGTCACAACCCTGACCTACGGCGTGCAGTGCTTCAGCAGATACCCCGACCACATGAAGCGGCACGATTTCTTCAAGAGCGCCATGCCCGAGGGCTAC 3410

Superfolder GFP

P W P T L V T T L T Y G V Q C F S R Y P D H M K R H D F F K S A M P E G Y
107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143

5' GTGCAAGAACGGACCATCAGCTTCAAGGACGACGGCACCTACAAGACCAGAGCCGAAGTGAAGTTCGAGGGCGACACCCTGGTCAACCGGATCGAGCTGAAGGGCATCGA 3520

Superfolder GFP

V Q E R T I S F K D D G T Y K T R A E V K F E G D T L V N R I E L K G I D
144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180

AflIII

5' CTTCAAAGAGGACGGCAACATCCTGGGCCACAAGCTCGAGTACAACTTCAACAGCCACAACGTGTACATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCA 3630

Superfolder GFP

F K E D G N I L G H K L E Y N F N S H N V Y I T A D K Q K N G I K A N F
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216

5' AGATCCGGCACAACGTGGAAGATGGCAGCGTGCAGCTGGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAATCACTACCTGAGC 3740

Superfolder GFP

K I R H N V E D G S V Q L A D H Y Q Q N T P I G D G P V L L P D N H Y L S
217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253

BlpI EcoO109I PpuMI EcoRI

5' ACCCAGAGCGTGCTGAGCAAGGACCCCAACGAGAAGCGGGACCACATGGTGCTGCTGGAATTTGTGACCGCCGCTGGCATCACCCACGGCGAATTCgagcccaaatcttg 3850

Superfolder GFP Fc domain

T Q S V L S K D P N E K R D H M V L L E F V T A A G I T H G E F E P K S C
254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290

5' tgacaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggaccc 3960

Fc domain

D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I S R T
291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326

5' ctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggag 4070

Fc domain

P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K P R E
327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363

EcoNI

5' gagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagc 4180

Fc domain

E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K A L P A
364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400

SexAI

5' ccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcctgacct 4290

Fc domain

P I E K T I S K A K G Q P R E P Q V Y T L P P S R D E L T K N Q V S L T
401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436

5' gcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctcc 4400

Fc domain

C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S
437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473

AarI NsiI SapI

5' ttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagag 4510

Fc domain

F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S
474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510

EcoRI

5' cctctccctgtctccgggtaaagaattcgcATCAACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATATTAAATTAGATTTTGCATA 4620

Fc domain attR1

L S L S P G K E F A
511 512 513 514 515 516 517 518 519 520

5' AAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGGCGGCaGCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATAATGTGTGGA 4730

attR1

5' TTTTGAGTTAGGATCCGTCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACAT 4840

Chloramphenicol resistance (CmR) gene

5' TTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGC 4950

Chloramphenicol resistance (CmR) gene

BspEI

5' CTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTtCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTT 5060

Chloramphenicol resistance (CmR) gene

5' TCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTG 5170

Chloramphenicol resistance (CmR) gene

BsmBI PasI

5' GCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGC 5280

Chloramphenicol resistance (CmR) gene

5' CCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTTTGTGATGGCTTCCATGTCGGCAGAATGC 5390

Chloramphenicol resistance (CmR) gene

5' TTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAAGATCTGGATCCGGCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGC 5500

Chloramphenicol resistance (CmR) gene

BstZ17I

5' GGTATAAGAATATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTATGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAG 5610

BbvCI

5' GCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCATGCAGAATGAAGCCCGTCGTCTGCGTGCCGAACGCTGGAAAGCGGAAAATCAGGAAGGGATGGCTGAG 5720

5' GTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACAGGGGCTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTG 5830

ccdB gene

5' TGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTG 5940

ccdB gene

5' CATATCGGGGATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAA 6050

ccdB gene

SalI

5' AAACGCCATTAACCTGATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGACCATAGTGACTGGATATGTTGTGTTTTACAGTATTAT 6160

ccdB gene attR2

5' GTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTGGTTGATAGCTTGGATCCAATCAA 6270

attR2 WPRE

XcmI

5' CCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTC 6380

WPRE

5' CCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTG 6490

WPRE

5' ACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCC 6600

WPRE

5' CGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCG 6710

WPRE

NgoMIV
NaeI

5' CGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGAGATCTGCCTCGAC 6820

WPRE BGH pA

5' TGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCAT 6930

BGH pA

5' CGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGACTCGAGTTAAGGG 7040

BGH pA

5' CGAATTGCCGATTAGGATCTTCCTAGAGCATGGCTACGTAGATAAGTAGCATGGCGGGTTAATCATTAACTACAAGGAACCCCTAGTGATGGAGTTGGCCACTCCCTCTC 7150

3'-ITR

EcoICRI
SacI

5' TGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGCCTTAATTAAGAGCTC 7260

3'-ITR

AscI AvrII StuI

5' ATGGCGCGCCTAGGCCTTGACGGCCTTCCGCCAATTCGCCCTATAGTGAGTCGTATTACGTCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGG 7370

5' CGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGAAACGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC 7480

PsiI

5' GAATGGGAGCGCCCTGTAGCGGCCACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAAC 7590

5' AAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTAG 7637