

SEQUENCE LISTING

<110> Seattle Children's Hospital (dba Seattle Children's Research Institute)
 ENDOCYTE, INC.
 PURDUE RESEARCH FOUNDATION

<120> METHODS OF USE FOR CAR T CELLS

<130> SCRI.200W0

<150> 62/620,414

<151> 2017-02-07

<150> 62/620,706

<151> 2018-01-23

<150> 62/656,233

<151> 2018-04-11

<150> 62/724,171

<151> 2018-08-29

<150> 62/735,627

<151> 2018-09-24

<150> 62/736,727

<151> 2018-09-26

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3198

<212> DNA

<213> Artificial Sequence

<220>

<223> E2 anti-fluorescein antibody fragment CAR nucleic
 acid sequence

<400> 1

```

atgcttctcc tgggtgacaag ctttctgctc tgtgagttac cacacccagc attcctcctg 60
atcccaagcg tgctgacaca gcctagctcc gtgtctgccg cccctggcca gaaagtgacc 120
atcagctgta gcggcagcac cagcaacatc ggcaacaact acgtgtcctg gtatcagcag 180
caccgccgga agggcccca gctgatgata tacgacgtgt ccaagcggcc cagcggcgtg 240
cccgatagat tttccggcag caagagcggc aacagcgcca gcctggatat cagcggcctg 300
cagtctgagg acgaggccga ctactattgc gccgcctggg acgatatgct gagcgagttc 360
ctgtttggca ccggcaccaa gctgacagtg ctgggcggag gcggaggatc tggcggcgga 420
  
```

ggaagtggcg	gagggggatc	tcaggtgcag	ctggtggaaa	gcggcggcaa	cctggtgcag	480
cctggcggat	ctctgagact	gagctgtgcc	gccagcggct	tcaccttcgg	cagcttcagc	540
atgagctggg	tgcgccaggc	tcctggggga	ggactggaat	gggtggcagg	actgagcgcc	600
agaagcagcc	tgaccacta	cgccgatagc	gtgaagggcc	ggttcaccat	cagccgggac	660
aacgccaaga	acagcgtgta	cctgcagatg	aacagcctgc	gggtggaaga	taccgcccgtg	720
tactactgcg	ccagacggtc	ctacgacagc	agcggctact	ggggccactt	ctacagctac	780
atggacgtgt	ggggccaggg	caccctcgtg	acagtgtctg	agagcaagta	cggaccgccc	840
tgccccctt	gccctgcccc	cgagttcgac	ggcggaccca	gcgtgttcct	gttccccccc	900
aagcccaagg	acaccctgat	gatcagccgg	acccccgagg	tgacctgcgt	ggtggtggac	960
gtgagccagg	aagatcccga	ggtccagttc	aattggtacg	tggacggcgt	ggaagtgcac	1020
aacgccaaga	ccaagcccag	agaggaacag	ttccagagca	cctaccgggt	ggtgtctgtg	1080
ctgaccgtgc	tgcaccagga	ctggctgaac	ggcaaagaat	acaagtgcaa	ggtgtccaac	1140
aagggcctgc	ccagcagcat	cgaaaagacc	atcagcaagg	ccaagggcca	gcctcgcgag	1200
ccccagggtg	acaccctgcc	tccctcccag	gaagagatga	ccaagaacca	ggtgtcccctg	1260
acctgcctgg	tgaagggtt	ctaccccagc	gacatcgccg	tggagtggga	gagcaacggc	1320
cagcctgaga	acaactacaa	gaccacccct	cccgtgctgg	acagcgacgg	cagcttcttc	1380
ctgtacagcc	ggctgaccgt	ggacaagagc	cggtggcagg	aaggcaacgt	ctttagctgc	1440
agcgtgatgc	acgaggccct	gcacaaccac	tacaccaga	agagcctgag	cctgtcccctg	1500
ggcaagatgt	tctgggtgct	ggtggtggtg	ggcgggggtg	tggcctgcta	cagcctgctg	1560
gtgacagtgg	ccttcatcat	cttttgggtg	aaacggggca	gaaagaaact	cctgtatata	1620
ttcaaacaac	catttatgag	accagtacaa	actactcaag	aggaagatgg	ctgtagctgc	1680
cgattttccag	aagaagaaga	aggaggatgt	gaactgcggg	tgaagttcag	cagaagcgcc	1740
gacggcccctg	cctaccagca	gggccagaat	cagctgtaca	acgagctgaa	cctgggcaga	1800
aggggaagagt	acgacgtcct	ggataagcgg	agaggccggg	accctgagat	gggcggcaag	1860
cctcggcgga	agaaccccc	ggaaggcctg	tataacgaac	tgcagaaaga	caagatggcc	1920
gaggcctaca	gcgagatcgg	catgaagggc	gagcggaggc	ggggcaaggg	ccacgacggc	1980
ctgtatcagg	gcctgtccac	cgccaccaag	gatacctacg	acgccctgca	catgcaggcc	2040
ctgcccccaa	ggctcgaggg	cggcggagag	ggcagaggaa	gtcttctaac	atgcggtgac	2100
gtggaggaga	atcccggccc	taggatgctt	ctcctgggtg	caagccttct	gctctgtgag	2160
ttaccacacc	cagcattcct	cctgatccca	cgcaaagtgt	gtaacggaat	aggtattggt	2220
gaattttaaag	actcactctc	cataaatgct	acgaatatta	aacacttcaa	aaactgcacc	2280
tccatcagtg	gcgatctcca	catcctgccg	gtggcattta	ggggtgactc	cttcacacat	2340
actcctcctc	tggatccaca	ggaactggat	attctgaaaa	ccgtaaagga	aatcacaggg	2400
tttttgctga	ttcaggcttg	gcctgaaaac	aggacggacc	tccatgcctt	tgagaaccta	2460
gaaatcatac	gcggcaggac	caagcaacat	ggtcagtttt	ctcttgagct	cgtcagcctg	2520
aacataacat	ccttgggatt	acgctccctc	aaggagataa	gtgatggaga	tgtgataatt	2580
tcaggaaaca	aaaatttgtg	ctatgcaaat	acaataaact	ggaaaaaact	gtttgggacc	2640
tccggtcaga	aaacaaaat	tataagcaac	agaggtgaaa	acagctgcaa	ggccacaggc	2700
caggtctgcc	atgccttgtg	ctcccccgag	ggctgctggg	gcccggagcc	cagggactgc	2760
gtctcttgcc	ggaatgtcag	ccgaggcagg	gaatgcgtgg	acaagtgcaa	ccttctggag	2820
ggtgagccaa	gggagtttgt	ggagaactct	gagtgcatat	agtgccaccc	agagtgcctg	2880
cctcaggcca	tgaacatcac	ctgcacagga	cggggaccag	acaactgtat	ccagtgtgcc	2940
cactacattg	acggcccca	ctgcgtcaag	acctgcccgg	caggagtcat	gggagaaaaac	3000
aacaccctgg	tctggaagta	cgcagacgcc	ggccatgtgt	gccacctgtg	ccatccaaac	3060
tgcacctacg	gatgcactgg	gccaggtctt	gaaggctgtc	caacgaatgg	gcctaagatc	3120
ccgtccatcg	ccactgggat	ggtgggggcc	ctcctcttgc	tgctggtggt	ggccctgggg	3180
atcggcctct	tcatgtga					3198

<210> 2

<211> 1065

<212> PRT

<213> Artificial Sequence

<220>

<223> E2 anti-fluorescein antibody fragment CAR amino
acid sequence

<400> 2

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

Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Gln	
			340					345					350			
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
		355					360					365				
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	
	370					375					380					
Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	
385					390					395					400	
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	
				405					410						415	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	
			420						425					430		
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	
		435					440					445				
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	
	450					455					460					
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	
465					470					475					480	
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	
				485					490						495	
Ser	Leu	Ser	Leu	Gly	Lys	Met	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	
		500						505								
Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	
		515					520					525				
Trp	Val	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	
	530					535					540					
Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	
545					550					555					560	
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	
				565					570						575	
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	
			580					585						590		
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	
		595					600					605				
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	
	610					615					620					
Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	
625					630					635					640	
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	
				645					650						655	
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	
		660						665						670		
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Leu	Glu	Gly	Gly	
		675					680							685		
Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	
	690					695					700					
Pro	Gly	Pro	Arg	Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	
705					710					715					720	
Leu	Pro	His	Pro	Ala	Phe	Leu	Leu	Ile	Pro	Arg	Lys	Val	Cys	Asn	Gly	
				725					730						735	

Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	Ala	Thr	Asn	
			740					745					750			
Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	Leu	His	Ile	
		755					760					765				
Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	Pro	Pro	Leu	
		770				775					780					
Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	Ile	Thr	Gly	
785					790					795					800	
Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp	Leu	His	Ala	
			805						810						815	
Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln	His	Gly	Gln	
			820					825					830			
Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile	Thr	Ser	Leu	Gly	Leu	Arg	
		835					840					845				
Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val	Ile	Ile	Ser	Gly	Asn	Lys	
	850					855					860					
Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys	Lys	Leu	Phe	Gly	Thr	
865					870					875						880
Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg	Gly	Glu	Asn	Ser	Cys	
			885						890						895	
Lys	Ala	Thr	Gly	Gln	Val	Cys	His	Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys	
		900						905					910			
Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn	Val	Ser	Arg	
		915					920						925			
Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	Asn	Leu	Leu	Glu	Gly	Glu	Pro	Arg	
	930					935					940					
Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys	Ile	Gln	Cys	His	Pro	Glu	Cys	Leu	
945					950					955					960	
Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly	Arg	Gly	Pro	Asp	Asn	Cys	
			965						970						975	
Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp	Gly	Pro	His	Cys	Val	Lys	Thr	Cys	
		980						985					990			
Pro	Ala	Gly	Val	Met	Gly	Glu	Asn	Asn	Thr	Leu	Val	Trp	Lys	Tyr	Ala	
		995					1000					1005				
Asp	Ala	Gly	His	Val	Cys	His	Leu	Cys	His	Pro	Asn	Cys	Thr	Tyr	Gly	
	1010					1015					1020					
Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly	Cys	Pro	Thr	Asn	Gly	Pro	Lys	Ile	
1025					1030					1035					1040	
Pro	Ser	Ile	Ala	Thr	Gly	Met	Val	Gly	Ala	Leu	Leu	Leu	Leu	Leu	Val	
			1045						1050						1055	
Val	Ala	Leu	Gly	Ile	Gly	Leu	Phe	Met								
		1060						1065								

<210> 3

<211> 1068

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M5.3-CAR AMINO ACID SEQUENCE

<400> 3

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	
Ala	Phe	Leu	Leu	Ile	Pro	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser
		20					25						30		
Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser
	35					40					45				
Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Arg	Trp	Tyr	Leu
	50					55					60				
Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Val	Leu	Ile	Tyr	Lys	Val	Ser	Asn
65					70					75					80
Arg	Val	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
			85					90						95	
Asp	Phe	Thr	Leu	Lys	Ile	Asn	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val
			100					105						110	
Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly
		115					120						125		
Thr	Lys	Leu	Glu	Ile	Lys	Ser	Ser	Ala	Asp	Asp	Ala	Lys	Lys	Asp	Ala
	130					135					140				
Ala	Lys	Lys	Asp	Asp	Ala	Lys	Lys	Asp	Asp	Ala	Lys	Lys	Asp	Gly	Gly
145					150					155					160
Val	Lys	Leu	Asp	Glu	Thr	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ala
				165					170					175	
Met	Lys	Leu	Ser	Cys	Val	Thr	Ser	Gly	Phe	Thr	Phe	Gly	His	Tyr	Trp
			180					185					190		
Met	Asn	Trp	Val	Arg	Gln	Ser	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Val	Ala
	195						200					205			
Gln	Phe	Arg	Asn	Lys	Pro	Tyr	Asn	Tyr	Glu	Thr	Tyr	Tyr	Ser	Asp	Ser
	210					215					220				
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ser	Val
225					230					235					240
Tyr	Leu	Gln	Met	Asn	Asn	Leu	Arg	Val	Glu	Asp	Thr	Gly	Ile	Tyr	Tyr
				245					250					255	
Cys	Thr	Gly	Ala	Ser	Tyr	Gly	Met	Glu	Tyr	Leu	Gly	Gln	Gly	Thr	Ser
		260					265						270		
Val	Thr	Val	Ser	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
		275					280					285			
Ala	Pro	Glu	Phe	Asp	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
	290				295						300				
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
305					310					315					320
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr
				325					330					335	
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
		340					345						350		
Gln	Phe	Gln	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
	355						360					365			
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys

370		375		380												
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
385					390					395					400	
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	
				405					410					415		
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
			420					425					430			
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
		435					440				445					
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
	450					455					460					
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	
465					470				475						480	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
				485					490					495		
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Met	Phe	Trp	Val	Leu	Val	Val	
			500					505					510			
Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	
		515					520					525				
Ile	Ile	Phe	Trp	Val	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	
	530					535					540					
Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	
545					550				555						560	
Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	
				565					570					575		
Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	
			580				585						590			
Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	
	595						600					605				
Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	
	610					615					620					
Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	
625					630					635					640	
Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	
				645					650					655		
Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	
			660				665						670			
Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Leu	
	675						680					685				
Glu	Gly	Gly	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	
	690					695					700					
Glu	Glu	Asn	Pro	Gly	Pro	Arg	Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	
705					710					715					720	
Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe	Leu	Leu	Ile	Pro	Arg	Lys	Val	
				725					730					735		
Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	
			740					745					750			
Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	
	755						760					765				
Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	

gcgagcatct	cttgtcggtc	ttcccagttc	ctgggtccatt	caaacggcaa	tacttacttg	180
cgggtgtact	tgcagaagcc	cgggtcaatcc	ccaaaagtgc	tgatatacaa	ggttagcaat	240
cgggtcagtg	gagtgcccga	ccgcttcagc	ggaagcggat	ccgggactga	cttcactctg	300
aagatcaacc	gggtagaagc	tgaagacctg	gggggtgtact	tctgtctctca	gtcaacacac	360
gtgccatgga	cctttggagg	tggcaccaag	ctggaaatca	aatcatcagc	ggacgatgcc	420
aaaaaagacg	cggccaagaa	ggacgatgcc	aagaaggatg	atgctaaaaa	ggatggcgga	480
gtcaaattgg	acgagacagg	cgggggactg	gtgcagcccg	gcgggtgcat	gaaactgtct	540
tgtgtgacca	gcggcctttac	cttcgggcat	tattggatga	actgggtgcg	acagtctcca	600
gagaaagggc	tcgagtgggt	ggcccagttt	cgaataaaac	cgtacaatta	tgagacctac	660
tattcagatt	ctgtgaaagg	gcgcttcact	atttcacgcg	acgacagcaa	aagtccgtc	720
taccttcaga	tgaacaacct	tagagtggag	gataccggaa	tatactactg	cacgggtgcc	780
agttatggca	tggagtactt	ggggcagggg	acatctgtga	ccgtttctga	gagcaagtac	840
ggaccgccct	gcccccttg	ccctgcccc	gagttcgacg	gcggaccag	cgtgttcctg	900
ttcccccca	agcccaagga	cacctgatg	atcagccgga	ccccgaggt	gacctgcgtg	960
gtggtggacg	tgagccagga	agatcccag	gtccagttca	attggtacgt	ggacggcgtg	1020
gaagtgcaca	acgccaagac	caagcccaga	gaggaacagt	tccagagcac	ctaccgggtg	1080
gtgtctgtgc	tgaccgtgct	gcaccaggac	tggctgaacg	gcaaagaata	caagtgcag	1140
gtgtccaaca	agggcctgcc	cagcagcatc	gaaaagacca	tcagcaaggc	caagggccag	1200
cctcgcgagc	cccaggtgta	cacctgcct	ccctcccagg	aagagatgac	caagaaccag	1260
gtgtccctga	cctgcctggg	gaagggttc	taccccagcg	acatcgccgt	ggagtgggag	1320
agcaacggcc	agcctgagaa	caactacaag	accacccctc	ccgtgctgga	cagcgacggc	1380
agcttcttcc	tgtacagccg	gctgaccgtg	gacaagagcc	ggtggcagga	aggcaacgtc	1440
tttagctgca	gcgtgatgca	cgaggccctg	cacaaccact	acaccagaa	gagcctgagc	1500
ctgtccctgg	gcaagatgtt	ctgggtgctg	gtggtgggtg	gcggggtgct	ggcctgctac	1560
agcctgctgg	tgacagtggc	cttcatcatc	ttttgggtga	aacggggcag	aaagaaactc	1620
ctgtatatat	tcaaacaacc	atztatgaga	ccagtacaaa	ctactcaaga	ggaagatggc	1680
tgtagctgcc	gattttccaga	agaagaagaa	ggaggatgtg	aactgcgggt	gaagttcagc	1740
agaagcgccg	acgcccctgc	ctaccagcag	ggccagaatc	agctgtacaa	cgagctgaac	1800
ctgggcagaa	gggaagagta	cgacgtcctg	gataagcgga	gaggccggga	ccctgagatg	1860
ggcggcaagc	ctcggcgga	gaacccccag	gaaggcctgt	ataacgaact	gcagaaagac	1920
aagatggccg	aggcctacag	cgagatcggc	atgaagggcg	agcggaggcg	gggcaagggc	1980
cacgacggcc	tgtatcaggg	cctgtccacc	gccaccaagg	atacctacga	cgccctgcac	2040
atgcaggccc	tgcccccaag	gctcgagggc	ggcggagagg	gcagagggaag	tcttctaaca	2100
tgcggtgacg	tggaggagaa	tcccggccct	aggatgcttc	tcctggtgac	aagccttctg	2160
ctctgtgagt	taccacacc	agcattcctc	ctgatccac	gcaaagtgtg	taacggaata	2220
ggtattgggtg	aattttaaga	ctcactctcc	ataaatgcta	cgaatattaa	acacttcaaa	2280
aactgcacct	ccatcagtgg	cgatctccac	atcctgccgg	tggcatttag	gggtgactcc	2340
ttcacacata	ctcctcctct	ggatccacag	gaactggata	ttctgaaaac	cgtaaaggaa	2400
atcacagggt	ttttgtgat	tcaggcttgg	cctgaaaaca	ggacggacct	ccatgccttt	2460
gagaacctag	aaatcatacg	cggcaggacc	aagcaacatg	gtcagttttc	tcttgagtc	2520
gtcagcctga	acataacatc	cttgggatta	cgctccctca	aggagataag	tgatggagat	2580
gtgataattt	caggaaacaa	aaatttgtgc	tatgcaaata	caataaactg	gaaaaaactg	2640
tttgggacct	ccggtcagaa	aaccaaatt	ataagcaaca	gaggtgaaaa	cagctgcaag	2700
gccacaggcc	aggctctgca	tgcttgtgc	tccccgagg	gctgctgggg	cccggagccc	2760
agggactgcg	tctcttgccg	gaatgtcagc	cgaggcaggg	aatgcgtgga	caagtgcac	2820
cttctggagg	gtgagccaag	ggagtttgtg	gagaactctg	agtgcataca	gtgccacca	2880
gagtgctgc	ctcaggccat	gaacatcacc	tgcacaggac	ggggaccaga	caactgtatc	2940
cagtgtgccc	actacattga	cggccccac	tgcgtcaaga	cctgcccggc	aggagtcatg	3000
ggagaaaaca	acaccctggg	ctggaagtac	gcagacgccg	gccatgtgtg	ccacctgtgc	3060
catccaaact	gcacctacgg	atgcactggg	ccaggctctg	aaggctgtcc	aacgaatggg	3120

```
cctaagatcc cgtccatcgc cactgggatg gtgggggccc tcctcttgct gctggtggtg 3180
gccctgggga tcggcctctt catgtga                                     3207
```