

SEQUENCE LISTING

<110> The Regents of the University of California
 Dowdy, Steven F.
 Yoshioka, Naohisa

<120> GENERATION OF HUMAPN iPS CELLS BY A SYNTHETIC SELF-REPLICATIVE
 RNA

<130> 00015-219WO1

<140> Not yet assigned
 <141> 2013-05-21

<150> US 61/649,876
 <151> 2012-05-21

<150> US 61/798,229
 <151> 2013-03-15

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<170> PatentIn version 3.5

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Glu	Glu	Phe	Asn	Asp	Leu	Leu	Asp	Leu	Asp	Phe	Ile	Leu	Ser	Asn	Ser		

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165 170 175
 Ser Ala Pro Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp
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 Cys Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg
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 Tyr Gln Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu
 35 40 45

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ctcatatata	ctttagattg	atttaaaact	tcatTTTTaa	tttaaaagga	tctaggtgaa	16140
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tgagcattga	gaaagcgcca	cgcttcccga	aggagaaaag	gcggacaggt	atccggtaa	16680
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ttatagtcct gtcgggtttc gccacctctg acttgagcgt cgatttttgt gatgctcgtc      16800

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<211> 1863
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (1)..(1863)

<400> 33
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Met Ala Glu Ala Arg Thr Ser Leu Ser Ala His Cys Arg Gly Pro Leu
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gcc act ggc ctg cac cca gac ctg gac ctc ccg ggc cga agc ctc gcc      96
Ala Thr Gly Leu His Pro Asp Leu Asp Leu Pro Gly Arg Ser Leu Ala
20 25 30

acc cct gcg cct tcc tgc tac ctt ctg ggc agc gaa ccc agc tct ggc      144
Thr Pro Ala Pro Ser Cys Tyr Leu Leu Gly Ser Glu Pro Ser Ser Gly
35 40 45

ctg ggc ctc cag ccc gag acc cac ctc ccc gag ggc agc ctg aag cgg      192
Leu Gly Leu Gln Pro Glu Thr His Leu Pro Glu Gly Ser Leu Lys Arg
50 55 60

tgc tgc gtc ttg ggc cta ccc ccc acc tcc cca gcc tcc tcc tca ccc      240
Cys Cys Val Leu Gly Leu Pro Pro Thr Ser Pro Ala Ser Ser Ser Pro
65 70 75 80

tgt gcc tcc tcc gac gtc acc tcc atc atc cgc tcc tcc cag acg tct      288
Cys Ala Ser Ser Asp Val Thr Ser Ile Ile Arg Ser Ser Gln Thr Ser
85 90 95

ctg gtc acc tgt gta aat gga ctc cgg agc ccc cct ctg acg gga gat      336
Leu Val Thr Cys Val Asn Gly Leu Arg Ser Pro Pro Leu Thr Gly Asp
100 105 110

ctg ggg ggc cct tcc aag cgg gcc cgg cct ggc cct gca tcg acg gac      384
Leu Gly Gly Pro Ser Lys Arg Ala Arg Pro Gly Pro Ala Ser Thr Asp
115 120 125

agc cat gag ggc agc ttg caa ctt gaa gcc tgc cgg aag gcg agc ttc      432
Ser His Glu Gly Ser Leu Gln Leu Glu Ala Cys Arg Lys Ala Ser Phe
130 135 140

ctg aag cag gaa ccc gcg gat gag ttt tca gag ctc ttt ggg cct cac      480
Leu Lys Gln Glu Pro Ala Asp Glu Phe Ser Glu Leu Phe Gly Pro His
145 150 155 160

cag cag ggc ctg ccg ccc ccc tat ccc ctg tct cag ttg ccg cct ggc      528
Gln Gln Gly Leu Pro Pro Pro Tyr Pro Leu Ser Gln Leu Pro Pro Gly
165 170 175

cca agc ctt gga ggc ctg ggg ctg ggc ctg gca ggc agg gtg gtg gcc      576
Pro Ser Leu Gly Gly Leu Gly Leu Gly Leu Ala Gly Arg Val Val Ala
180 185 190

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ggg cgg cag gcg tgc cgc tgg gtg gac tgc tgt gca gcc tat gag cag Gly Arg Gln Ala Cys Arg Trp Val Asp Cys Cys Ala Ala Tyr Glu Gln 195 200 205	624
cag gag gag ctg gtg cgg cac atc gag aag agc cac atc gac cag cgc Gln Glu Glu Leu Val Arg His Ile Glu Lys Ser His Ile Asp Gln Arg 210 215 220	672
aag ggc gag gac ttc acc tgc ttc tgg gct ggc tgc gtg cgc cgc tac Lys Gly Glu Asp Phe Thr Cys Phe Trp Ala Gly Cys Val Arg Arg Tyr 225 230 235 240	720
aag ccc ttc aac gcc cgc tac aag ctg ctc atc cac atg cga gtg cac Lys Pro Phe Asn Ala Arg Tyr Lys Leu Leu Ile His Met Arg Val His 245 250 255	768
tcg ggc gag aag ccc aac aag tgc atg ttt gaa ggc tgc agc aag gcc Ser Gly Glu Lys Pro Asn Lys Cys Met Phe Glu Gly Cys Ser Lys Ala 260 265 270	816
ttc tca cgg ctg gag aac ctc aag atc cac ctg agg agc cac acg ggc Phe Ser Arg Leu Glu Asn Leu Lys Ile His Leu Arg Ser His Thr Gly 275 280 285	864
gag aag cgg tac ctg tgc cag cac ccg ggt tgc cag aag gcc ttc agc Glu Lys Pro Tyr Leu Cys Gln His Pro Gly Cys Gln Lys Ala Phe Ser 290 295 300	912
aac tcc agc gac cgc gcc aag cac cag cgc acc cac cta gac acg aag Asn Ser Ser Asp Arg Ala Lys His Gln Arg Thr His Leu Asp Thr Lys 305 310 315 320	960
ccg tac gcc tgt cag atc cct ggc tgc tcc aag cgc tac aca gac ccc Pro Tyr Ala Cys Gln Ile Pro Gly Cys Ser Lys Arg Tyr Thr Asp Pro 325 330 335	1008
agc tcc ctc cgc aag cac gtc aag gcc cat tca gcc aaa gag cag cag Ser Ser Leu Arg Lys His Val Lys Ala His Ser Ala Lys Glu Gln Gln 340 345 350	1056
gtg cgt aag aag ctg cat gcg ggc cct gac acc gag gcc gac gtc ctg Val Arg Lys Lys Leu His Ala Gly Pro Asp Thr Glu Ala Asp Val Leu 355 360 365	1104
acc gag tgt ctg gtc ctg cag cag ctc cac acg tcc aca cag ctg gct Thr Glu Cys Leu Val Leu Gln Gln Leu His Thr Ser Thr Gln Leu Ala 370 375 380	1152
gcc agc gac ggc aag ggt ggc tgt ggc ctg ggc cag gag ctg ctc cca Ala Ser Asp Gly Lys Gly Gly Cys Gly Leu Gly Gln Glu Leu Leu Pro 385 390 395 400	1200
ggt gtg tat cct ggc tcc atc acc ccc cat aac gga ctt gca tcg ggc Gly Val Tyr Pro Gly Ser Ile Thr Pro His Asn Gly Leu Ala Ser Gly 405 410 415	1248
ctc ctg ccc cca gcg cac gac gta cct tcc agg cac cac ccg ctg gat Leu Leu Pro Pro Ala His Asp Val Pro Ser Arg His His Pro Leu Asp 420 425 430	1296

gcc acc acc agt tcc cac cac cat ctg tcc cct ctg ccc atg gct gag 1344
Ala Thr Thr Ser Ser His His His Leu Ser Pro Leu Pro Met Ala Glu
435 440 445

agc acc cgg gat ggg ttg ggg ccc ggc ctc ctc tca cca ata gtc agc 1392
Ser Thr Arg Asp Gly Leu Gly Pro Gly Leu Leu Ser Pro Ile Val Ser
450 455 460

ccc ctg aag ggg ctg ggg cca ccg ccg ctg ccc cca tcc tct cag agc 1440
Pro Leu Lys Gly Leu Gly Pro Pro Pro Leu Pro Pro Ser Ser Gln Ser
465 470 475 480

cat tct ccg ggg ggc cag ccc ttc ccc aca ctc ccc agc aag ccg tcc 1488
His Ser Pro Gly Gly Gln Pro Phe Pro Thr Leu Pro Ser Lys Pro Ser
485 490 495

tac cca ccc ttc cag agc cct cca ccc ccg cct ctg ccc agc cca caa 1536
Tyr Pro Pro Phe Gln Ser Pro Pro Pro Pro Pro Leu Pro Ser Pro Gln
500 505 510

ggt tac cag ggc agt ttc cac tcc atc cag agt tgc ttc ccc tat ggc 1584
Gly Tyr Gln Gly Ser Phe His Ser Ile Gln Ser Cys Phe Pro Tyr Gly
515 520 525

gac tgc tac cgg atg gct gaa cca gca gcc ggt ggg gac gga ctg gtc 1632
Asp Cys Tyr Arg Met Ala Glu Pro Ala Ala Gly Gly Asp Gly Leu Val
530 535 540

ggg gag acc cac ggt ttc aac ccc ctg cgg ccc aat ggc tac cac agc 1680
Gly Glu Thr His Gly Phe Asn Pro Leu Arg Pro Asn Gly Tyr His Ser
545 550 555 560

ctc agc acg ccc ttg cct gcc aca ggc tat gag gcc ctg gct gag gcc 1728
Leu Ser Thr Pro Leu Pro Ala Thr Gly Tyr Glu Ala Leu Ala Glu Ala
565 570 575

tca tgc ccc aca gcg ctg cca cag cag cca tct gaa gat gtg gtg tcc 1776
Ser Cys Pro Thr Ala Leu Pro Gln Gln Pro Ser Glu Asp Val Val Ser
580 585 590

agc ggc ccc gag gac tgt ggc ttc ttc ccc aat gga gcc ttt gac cac 1824
Ser Gly Pro Glu Asp Cys Gly Phe Phe Pro Asn Gly Ala Phe Asp His
595 600 605

tgc ctg ggc cac atc ccc tcc atc tac aca gac acc tga 1863
Cys Leu Gly His Ile Pro Ser Ile Tyr Thr Asp Thr
610 615 620

<210> 34
<211> 620
<212> PRT
<213> Homo sapiens

<400> 34

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Thr Pro Ala Pro Ser Cys Tyr Leu Leu Gly Ser Glu Pro Ser Ser Gly
35 40 45

Leu Gly Leu Gln Pro Glu Thr His Leu Pro Glu Gly Ser Leu Lys Arg
 50 55 60
 Cys Cys Val Leu Gly Leu Pro Pro Thr Ser Pro Ala Ser Ser Ser Pro
 65 70 75 80
 Cys Ala Ser Ser Asp Val Thr Ser Ile Ile Arg Ser Ser Gln Thr Ser
 85 90 95
 Leu Val Thr Cys Val Asn Gly Leu Arg Ser Pro Pro Leu Thr Gly Asp
 100 105 110
 Leu Gly Gly Pro Ser Lys Arg Ala Arg Pro Gly Pro Ala Ser Thr Asp
 115 120 125
 Ser His Glu Gly Ser Leu Gln Leu Glu Ala Cys Arg Lys Ala Ser Phe
 130 135 140
 Leu Lys Gln Glu Pro Ala Asp Glu Phe Ser Glu Leu Phe Gly Pro His
 145 150 155 160
 Gln Gln Gly Leu Pro Pro Pro Tyr Pro Leu Ser Gln Leu Pro Pro Gly
 165 170 175
 Pro Ser Leu Gly Gly Leu Gly Leu Gly Leu Ala Gly Arg Val Val Ala
 180 185 190
 Gly Arg Gln Ala Cys Arg Trp Val Asp Cys Cys Ala Ala Tyr Glu Gln
 195 200 205
 Gln Glu Glu Leu Val Arg His Ile Glu Lys Ser His Ile Asp Gln Arg
 210 215 220
 Lys Gly Glu Asp Phe Thr Cys Phe Trp Ala Gly Cys Val Arg Arg Tyr
 225 230 235 240
 Lys Pro Phe Asn Ala Arg Tyr Lys Leu Leu Ile His Met Arg Val His
 245 250 255
 Ser Gly Glu Lys Pro Asn Lys Cys Met Phe Glu Gly Cys Ser Lys Ala
 260 265 270
 Phe Ser Arg Leu Glu Asn Leu Lys Ile His Leu Arg Ser His Thr Gly
 275 280 285
 Glu Lys Pro Tyr Leu Cys Gln His Pro Gly Cys Gln Lys Ala Phe Ser
 290 295 300
 Asn Ser Ser Asp Arg Ala Lys His Gln Arg Thr His Leu Asp Thr Lys
 305 310 315 320
 Pro Tyr Ala Cys Gln Ile Pro Gly Cys Ser Lys Arg Tyr Thr Asp Pro
 325 330 335
 Ser Ser Leu Arg Lys His Val Lys Ala His Ser Ala Lys Glu Gln Gln
 340 345 350
 Val Arg Lys Lys Leu His Ala Gly Pro Asp Thr Glu Ala Asp Val Leu
 355 360 365
 Thr Glu Cys Leu Val Leu Gln Gln Leu His Thr Ser Thr Gln Leu Ala
 370 375 380
 Ala Ser Asp Gly Lys Gly Gly Cys Gly Leu Gly Gln Glu Leu Leu Pro
 385 390 395 400
 Gly Val Tyr Pro Gly Ser Ile Thr Pro His Asn Gly Leu Ala Ser Gly
 405 410 415
 Leu Leu Pro Pro Ala His Asp Val Pro Ser Arg His His Pro Leu Asp
 420 425 430
 Ala Thr Thr Ser Ser His His His Leu Ser Pro Leu Pro Met Ala Glu
 435 440 445
 Ser Thr Arg Asp Gly Leu Gly Pro Gly Leu Leu Ser Pro Ile Val Ser
 450 455 460
 Pro Leu Lys Gly Leu Gly Pro Pro Pro Leu Pro Pro Ser Ser Gln Ser
 465 470 475 480
 His Ser Pro Gly Gly Gln Pro Phe Pro Thr Leu Pro Ser Lys Pro Ser
 485 490 495
 Tyr Pro Pro Phe Gln Ser Pro Pro Pro Pro Pro Leu Pro Ser Pro Gln
 500 505 510
 Gly Tyr Gln Gly Ser Phe His Ser Ile Gln Ser Cys Phe Pro Tyr Gly
 515 520 525
 Asp Cys Tyr Arg Met Ala Glu Pro Ala Ala Gly Gly Asp Gly Leu Val

530		535		540											
Gly	Glu	Thr	His	Gly	Phe	Asn	Pro	Leu	Arg	Pro	Asn	Gly	Tyr	His	Ser
545				550				555							560
Leu	Ser	Thr	Pro	Leu	Pro	Ala	Thr	Gly	Tyr	Glu	Ala	Leu	Ala	Glu	Ala
				565				570						575	
Ser	Cys	Pro	Thr	Ala	Leu	Pro	Gln	Gln	Pro	Ser	Glu	Asp	Val	Val	Ser
			580					585					590		
Ser	Gly	Pro	Glu	Asp	Cys	Gly	Phe	Phe	Pro	Asn	Gly	Ala	Phe	Asp	His
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 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer - hKlfGC2For

<400> 35
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<210> 36
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer - hKlf4GC2Rev

<400> 36
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<210> 37
 <211> 58
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer - EcoR1-Sac1-T7M1-VEE

<400> 37
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<210> 38
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer - Xba1-BstZ17I-VEE

<400> 38
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<210> 39
 <211> 1056
 <212> DNA
 <213> Vaccinia virus
 <220>

<221> CDS

<222> (1)..(1056)

<400> 39

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1 5 10 15	
ttg cta ttc cac agt tac gcc ata gac atc gaa aat gaa atc aca gaa	96
Leu Leu Phe His Ser Tyr Ala Ile Asp Ile Glu Asn Glu Ile Thr Glu	
20 25 30	
ttc ttc aat aaa atg aga gat act cta cca gct aaa gac tct aaa tgg	144
Phe Phe Asn Lys Met Arg Asp Thr Leu Pro Ala Lys Asp Ser Lys Trp	
35 40 45	
ttg aat cca gca tgt atg ttc gga ggc aca atg aat gat ata gcc gct	192
Leu Asn Pro Ala Cys Met Phe Gly Gly Thr Met Asn Asp Ile Ala Ala	
50 55 60	
cta gga gag cca ttc agc gca aag tgt cct cct att gaa gac agt ctt	240
Leu Gly Glu Pro Phe Ser Ala Lys Cys Pro Pro Ile Glu Asp Ser Leu	
65 70 75 80	
tta tcg cac aga tat aaa gac tat gtg gtt aaa tgg gaa agg cta gaa	288
Leu Ser His Arg Tyr Lys Asp Tyr Val Val Lys Trp Glu Arg Leu Glu	
85 90 95	
aaa aat aga cgg cga cag gtt tct aat aaa cgt gtt aaa cat ggt gat	336
Lys Asn Arg Arg Gln Val Ser Asn Lys Arg Val Lys His Gly Asp	
100 105 110	
tta tgg ata gcc aac tat aca tct aaa ttc agt aac cgt agg tat ttg	384
Leu Trp Ile Ala Asn Tyr Thr Ser Lys Phe Ser Asn Arg Arg Tyr Leu	
115 120 125	
tgc acc gta act aca aag aat ggt gac tgt gtt cag ggt ata gtt aga	432
Cys Thr Val Thr Thr Lys Asn Gly Asp Cys Val Gln Gly Ile Val Arg	
130 135 140	
tct cat att aga aaa cct cct tca tgc att cca aaa aca tat gaa cta	480
Ser His Ile Arg Lys Pro Pro Ser Cys Ile Pro Lys Thr Tyr Glu Leu	
145 150 155 160	
ggg act cat gat aag tat ggc ata gac tta tac tgt gga att ctt tac	528
Gly Thr His Asp Lys Tyr Gly Ile Asp Leu Tyr Cys Gly Ile Leu Tyr	
165 170 175	
gca aaa cat tat aat aat ata act tgg tat aaa gat aat aag gaa att	576
Ala Lys His Tyr Asn Asn Ile Thr Trp Tyr Lys Asp Asn Lys Glu Ile	
180 185 190	
aat atc gac gac att aag tat tca caa acg gga aag gaa tta att att	624
Asn Ile Asp Asp Ile Lys Tyr Ser Gln Thr Gly Lys Glu Leu Ile Ile	
195 200 205	
cat aat cca gag tta gaa gat agc gga aga tac gac tgt tac gtt cat	672
His Asn Pro Glu Leu Glu Asp Ser Gly Arg Tyr Asp Cys Tyr Val His	
210 215 220	
tac gac gac gtt aga atc aag aat gat atc gta gta tca aga tgt aaa	720

Tyr	Asp	Asp	Val	Arg	Ile	Lys	Asn	Asp	Ile	Val	Val	Ser	Arg	Cys	Lys	
225					230					235					240	
ata	ctt	acg	gtt	ata	ccg	tca	caa	gac	cac	agg	ttt	aaa	cta	ata	cta	768
Ile	Leu	Thr	Val	Ile	Pro	Ser	Gln	Asp	His	Arg	Phe	Lys	Leu	Ile	Leu	
				245					250					255		
gat	cca	aaa	atc	aac	gta	acg	ata	gga	gaa	cct	gcc	aat	ata	aca	tgc	816
Asp	Pro	Lys	Ile	Asn	Val	Thr	Ile	Gly	Glu	Pro	Ala	Asn	Ile	Thr	Cys	
			260					265					270			
act	gct	gtg	tca	acg	tca	tta	ttg	att	gac	gat	gta	ctg	att	gaa	tgg	864
Thr	Ala	Val	Ser	Thr	Ser	Leu	Leu	Ile	Asp	Asp	Val	Leu	Ile	Glu	Trp	
		275					280					285				
gaa	aat	cca	tcc	gga	tgg	ctt	ata	gga	ttc	gat	ttt	gat	gta	tac	tct	912
Glu	Asn	Pro	Ser	Gly	Trp	Leu	Ile	Gly	Phe	Asp	Phe	Asp	Val	Tyr	Ser	
	290					295					300					
gtt	tta	act	agt	aga	ggc	ggg	att	acc	gag	gcg	acc	ttg	tac	ttt	gaa	960
Val	Leu	Thr	Ser	Arg	Gly	Gly	Ile	Thr	Glu	Ala	Thr	Leu	Tyr	Phe	Glu	
305					310					315					320	
aat	gtt	act	gaa	gaa	tat	ata	ggg	aat	aca	tat	aaa	tgt	cgt	gga	cac	1008
Asn	Val	Thr	Glu	Glu	Tyr	Ile	Gly	Asn	Thr	Tyr	Lys	Cys	Arg	Gly	His	
				325					330					335		
aac	tat	tat	ttt	gaa	aaa	acc	ctt	aca	act	aca	gta	gta	ttg	gag	taa	1056
Asn	Tyr	Tyr	Phe	Glu	Lys	Thr	Leu	Thr	Thr	Thr	Val	Val	Leu	Glu		
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<210> 40
 <211> 351
 <212> PRT
 <213> Vaccinia virus

 <400> 40

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Leu	Leu	Phe	His	Ser	Tyr	Ala	Ile	Asp	Ile	Glu	Asn	Glu	Ile	Thr	Glu	
			20					25					30			
Phe	Phe	Asn	Lys	Met	Arg	Asp	Thr	Leu	Pro	Ala	Lys	Asp	Ser	Lys	Trp	
		35					40					45				
Leu	Asn	Pro	Ala	Cys	Met	Phe	Gly	Gly	Thr	Met	Asn	Asp	Ile	Ala	Ala	
	50					55					60					
Leu	Gly	Glu	Pro	Phe	Ser	Ala	Lys	Cys	Pro	Pro	Ile	Glu	Asp	Ser	Leu	
65					70					75					80	
Leu	Ser	His	Arg	Tyr	Lys	Asp	Tyr	Val	Val	Lys	Trp	Glu	Arg	Leu	Glu	
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Lys	Asn	Arg	Arg	Arg	Gln	Val	Ser	Asn	Lys	Arg	Val	Lys	His	Gly	Asp	
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Leu	Trp	Ile	Ala	Asn	Tyr	Thr	Ser	Lys	Phe	Ser	Asn	Arg	Arg	Tyr	Leu	
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Cys	Thr	Val	Thr	Thr	Lys	Asn	Gly	Asp	Cys	Val	Gln	Gly	Ile	Val	Arg	
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Ser	His	Ile	Arg	Lys	Pro	Pro	Ser	Cys	Ile	Pro	Lys	Thr	Tyr	Glu	Leu	
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Ala	Lys	His	Tyr	Asn	Asn	Ile	Thr	Trp	Tyr	Lys	Asp	Asn	Lys	Glu	Ile	

			180					185					190				
Asn	Ile	Asp	Asp	Ile	Lys	Tyr	Ser	Gln	Thr	Gly	Lys	Glu	Leu	Ile	Ile		
		195					200					205					
His	Asn	Pro	Glu	Leu	Glu	Asp	Ser	Gly	Arg	Tyr	Asp	Cys	Tyr	Val	His		
	210					215					220						
Tyr	Asp	Asp	Val	Arg	Ile	Lys	Asn	Asp	Ile	Val	Val	Ser	Arg	Cys	Lys		
225					230					235					240		
Ile	Leu	Thr	Val	Ile	Pro	Ser	Gln	Asp	His	Arg	Phe	Lys	Leu	Ile	Leu		
			245					250						255			
Asp	Pro	Lys	Ile	Asn	Val	Thr	Ile	Gly	Glu	Pro	Ala	Asn	Ile	Thr	Cys		
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Thr	Ala	Val	Ser	Thr	Ser	Leu	Leu	Ile	Asp	Asp	Val	Leu	Ile	Glu	Trp		
		275					280					285					
Glu	Asn	Pro	Ser	Gly	Trp	Leu	Ile	Gly	Phe	Asp	Phe	Asp	Val	Tyr	Ser		
	290				295						300						
Val	Leu	Thr	Ser	Arg	Gly	Gly	Ile	Thr	Glu	Ala	Thr	Leu	Tyr	Phe	Glu		
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Asn	Tyr	Tyr	Phe	Glu	Lys	Thr	Leu	Thr	Thr	Thr	Val	Val	Leu	Glu			
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