

SEQUENCE LISTING

<110> iOmx Therapeutics AG

<120> INTRACELLULAR KINASE ASSOCIATED WITH RESISTANCE AGAINST T-CELL
MEDIATED CYTOTOXICITY, AND USES THEREOF

<130> I33723W0

<150> EP20175030.4

<151> 2020-05-15

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 385

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala
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Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly
20 25 30

Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu
35 40 45

Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser
50 55 60

Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn
65 70 75 80

Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu
85 90 95

Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu
100 105 110

Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val
115 120 125

Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp
130 135 140

Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys
145 150 155 160

Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp
165 170 175

Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
180 185 190

Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
195 200 205

Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu
210 215 220

Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe
225 230 235 240

Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile
245 250 255

Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln
260 265 270

Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn
275 280 285

Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser
290 295 300

Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
305 310 315 320

Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser
325 330 335

Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Leu Ala Pro Ser Thr

340

345

350

Leu Cys Ser Phe Ile Ser Ser Ser Ser Gly Val Ser Gly Val Gly Ala
 355 360 365

Glu Arg Arg Pro Arg Pro Thr Thr Val Thr Ala Val His Ser Gly Ser
 370 375 380

Lys
 385

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 <213> Homo sapiens

<400> 2

Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala
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Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly
 20 25 30

Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu
 35 40 45

Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser
 50 55 60

Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn
 65 70 75 80

Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu
 85 90 95

Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu
 100 105 110

Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val
 115 120 125

Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp
130 135 140

Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys
145 150 155 160

Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp
165 170 175

Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
180 185 190

Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
195 200 205

Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu
210 215 220

Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe
225 230 235 240

Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile
245 250 255

Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln
260 265 270

Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn
275 280 285

Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser
290 295 300

Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
305 310 315 320

Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser
325 330 335

Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys
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Pro Glu Ser Leu Ser
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<213> artificial

<220>
<223> siRNA sequence targeting CAMK1D

<400> 3
ugaaguguau cccuaagaa 19

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<212> RNA
<213> artificial

<220>
<223> siRNA sequence targeting CAMK1D

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caaaucaccu guacuuggu 19

<210> 5
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<212> RNA
<213> artificial

<220>
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<400> 5
ccgaaaaucu cuuguacua 19

<210> 6
<211> 19
<212> RNA
<213> artificial

<220>
<223> siRNA sequence targeting CAMK1D

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gagaaggacc cgaauaaaa 19

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 <212> DNA
 <213> artificial

 <220>
 <223> gRNA sequence for targeting mouse CAMK1D by gene editing

 <400> 7
 tcgatcggat agtggagaag 20

<210> 8
 <211> 20
 <212> DNA
 <213> artificial

 <220>
 <223> gRNA sequence for targeting mouse CAMK1D by gene editing

 <400> 8
 ggagatagta tacggcatcc 20

<210> 9
 <211> 20
 <212> DNA
 <213> artificial

 <220>
 <223> gRNA sequence for targeting CAMK1D by gene editing

 <400> 9
 tagccgagga gaaagctact 20

<210> 10
 <211> 20
 <212> DNA
 <213> Mus musculus

 <400> 10
 ggagatagta tacggcatcc 20

<210> 11
 <211> 149
 <212> PRT
 <213> Homo sapiens

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Met Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala
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Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu
20 25 30

Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu
35 40 45

Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile
50 55 60

Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr
65 70 75 80

Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp
85 90 95

Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn
100 105 110

Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu
115 120 125

Ala Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln
130 135 140

Met Met Thr Ala Lys
145

<210> 12
<211> 505
<212> PRT
<213> Homo sapiens

<400> 12

Met Glu Gly Gly Pro Ala Val Cys Cys Gln Asp Pro Arg Ala Glu Leu
1 5 10 15

Val Glu Arg Val Ala Ala Ile Asp Val Thr His Leu Glu Glu Ala Asp
20 25 30

Gly Gly Pro Glu Pro Thr Arg Asn Gly Val Asp Pro Pro Pro Arg Ala

35

40

45

Arg Ala Ala Ser Val Ile Pro Gly Ser Thr Ser Arg Leu Leu Pro Ala
 50 55 60

Arg Pro Ser Leu Ser Ala Arg Lys Leu Ser Leu Gln Glu Arg Pro Ala
 65 70 75 80

Gly Ser Tyr Leu Glu Ala Gln Ala Gly Pro Tyr Ala Thr Gly Pro Ala
 85 90 95

Ser His Ile Ser Pro Arg Ala Trp Arg Arg Pro Thr Ile Glu Ser His
 100 105 110

His Val Ala Ile Ser Asp Ala Glu Asp Cys Val Gln Leu Asn Gln Tyr
 115 120 125

Lys Leu Gln Ser Glu Ile Gly Lys Gly Ala Tyr Gly Val Val Arg Leu
 130 135 140

Ala Tyr Asn Glu Ser Glu Asp Arg His Tyr Ala Met Lys Val Leu Ser
 145 150 155 160

Lys Lys Lys Leu Leu Lys Gln Tyr Gly Phe Pro Arg Arg Pro Pro Pro
 165 170 175

Arg Gly Ser Gln Ala Ala Gln Gly Gly Pro Ala Lys Gln Leu Leu Pro
 180 185 190

Leu Glu Arg Val Tyr Gln Glu Ile Ala Ile Leu Lys Lys Leu Asp His
 195 200 205

Val Asn Val Val Lys Leu Ile Glu Val Leu Asp Asp Pro Ala Glu Asp
 210 215 220

Asn Leu Tyr Leu Val Phe Asp Leu Leu Arg Lys Gly Pro Val Met Glu
 225 230 235 240

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

Arg Asp Val Ile Leu Gly Leu Glu Tyr Leu His Cys Gln Lys Ile Val
260 265 270

His Arg Asp Ile Lys Pro Ser Asn Leu Leu Leu Gly Asp Asp Gly His
275 280 285

Val Lys Ile Ala Asp Phe Gly Val Ser Asn Gln Phe Glu Gly Asn Asp
290 295 300

Ala Gln Leu Ser Ser Thr Ala Gly Thr Pro Ala Phe Met Ala Pro Glu
305 310 315 320

Ala Ile Ser Asp Ser Gly Gln Ser Phe Ser Gly Lys Ala Leu Asp Val
325 330 335

Trp Ala Thr Gly Val Thr Leu Tyr Cys Phe Val Tyr Gly Lys Cys Pro
340 345 350

Phe Ile Asp Asp Phe Ile Leu Ala Leu His Arg Lys Ile Lys Asn Glu
355 360 365

Pro Val Val Phe Pro Glu Glu Pro Glu Ile Ser Glu Glu Leu Lys Asp
370 375 380

Leu Ile Leu Lys Met Leu Asp Lys Asn Pro Glu Thr Arg Ile Gly Val
385 390 395 400

Pro Asp Ile Lys Leu His Pro Trp Val Thr Lys Asn Gly Glu Glu Pro
405 410 415

Leu Pro Ser Glu Glu Glu His Cys Ser Val Val Glu Val Thr Glu Glu
420 425 430

Glu Val Lys Asn Ser Val Arg Leu Ile Pro Ser Trp Thr Thr Val Ile
435 440 445

Leu Val Lys Ser Met Leu Arg Lys Arg Ser Phe Gly Asn Pro Phe Glu
450 455 460

Pro Gln Ala Arg Arg Glu Glu Arg Ser Met Ser Ala Pro Gly Asn Leu

465					470					475					480
Leu	Val	Lys	Glu	Gly 485	Phe	Gly	Glu	Gly	Gly 490	Lys	Ser	Pro	Glu	Leu 495	Pro
Gly	Val	Gln	Glu 500	Asp	Glu	Ala	Ala	Ser 505							
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Gly	Gly	Pro 35	Glu	Pro	Thr	Arg	Asn 40	Gly	Val	Asp	Pro	Pro 45	Pro	Arg	Ala
Arg	Ala 50	Ala	Ser	Val	Ile	Pro 55	Gly	Ser	Thr	Ser	Arg 60	Leu	Leu	Pro	Ala
Arg 65	Pro	Ser	Leu	Ser	Ala 70	Arg	Lys	Leu	Ser	Leu 75	Gln	Glu	Arg	Pro	Ala 80
Gly	Ser	Tyr	Leu 85	Glu	Ala	Gln	Ala	Gly 90	Pro	Tyr	Ala	Thr	Gly	Pro 95	Ala
Ser	His	Ile	Ser 100	Pro	Arg	Ala	Trp	Arg 105	Arg	Pro	Thr	Ile	Glu 110	Ser	His
His	Val	Ala 115	Ile	Ser	Asp	Ala	Glu 120	Asp	Cys	Val	Gln	Leu 125	Asn	Gln	Tyr
Lys	Leu 130	Gln	Ser	Glu	Ile	Gly 135	Lys	Gly	Ala	Tyr	Gly 140	Val	Val	Arg	Leu

Ala Tyr Asn Glu Ser Glu Asp Arg His Tyr Ala Met Lys Val Leu Ser
145 150 155 160

Lys Lys Lys Leu Leu Lys Gln Tyr Gly Phe Pro Arg Arg Pro Pro Pro
165 170 175

Arg Gly Ser Gln Ala Ala Gln Gly Gly Pro Ala Lys Gln Leu Leu Pro
180 185 190

Leu Glu Arg Val Tyr Gln Glu Ile Ala Ile Leu Lys Lys Leu Asp His
195 200 205

Val Asn Val Val Lys Leu Ile Glu Val Leu Asp Asp Pro Ala Glu Asp
210 215 220

Asn Leu Tyr Leu Ala Leu Gln Asn Gln Ala Gln Asn Ile Gln Leu Asp
225 230 235 240

Ser Thr Asn Ile Ala Lys Pro His Ser Leu Leu Pro Ser Glu Gln Gln
245 250 255

Asp Ser Gly Ser Thr Trp Ala Ala Arg Ser Val Phe Asp Leu Leu Arg
260 265 270

Lys Gly Pro Val Met Glu Val Pro Cys Asp Lys Pro Phe Ser Glu Glu
275 280 285

Gln Ala Arg Leu Tyr Leu Arg Asp Val Ile Leu Gly Leu Glu Tyr Leu
290 295 300

His Cys Gln Lys Ile Val His Arg Asp Ile Lys Pro Ser Asn Leu Leu
305 310 315 320

Leu Gly Asp Asp Gly His Val Lys Ile Ala Asp Phe Gly Val Ser Asn
325 330 335

Gln Phe Glu Gly Asn Asp Ala Gln Leu Ser Ser Thr Ala Gly Thr Pro
340 345 350

Ala Phe Met Ala Pro Glu Ala Ile Ser Asp Ser Gly Gln Ser Phe Ser
355 360 365

Gly Lys Ala Leu Asp Val Trp Ala Thr Gly Val Thr Leu Tyr Cys Phe
370 375 380

Val Tyr Gly Lys Cys Pro Phe Ile Asp Asp Phe Ile Leu Ala Leu His
385 390 395 400

Arg Lys Ile Lys Asn Glu Pro Val Val Phe Pro Glu Glu Pro Glu Ile
405 410 415

Ser Glu Glu Leu Lys Asp Leu Ile Leu Lys Met Leu Asp Lys Asn Pro
420 425 430

Glu Thr Arg Ile Gly Val Pro Asp Ile Lys Leu His Pro Trp Val Thr
435 440 445

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

Val Glu Val Thr Glu Glu Glu Val Lys Asn Ser Val Arg Leu Ile Pro
465 470 475 480

Ser Trp Thr Thr Val Ile Leu Val Lys Ser Met Leu Arg Lys Arg Ser
485 490 495

Phe Gly Asn Pro Phe Glu Pro Gln Ala Arg Arg Glu Glu Arg Ser Met
500 505 510

Ser Ala Pro Gly Asn Leu Leu Val
515 520