

MATS Sequence 371.txt
SEQUENCE LISTING

<110> Eisai R&D Management Co., Ltd.
Kim, Dae-Shik
Fang, Frank
Endo, Atsushi
Choi, Hyeong-Wook
Hao, Ming-Hong
Bao, Xingfeng
Huang, Kuan-Chun

<120> Compounds for the Treatment of Cancer

<130> 0080171-000371

<150> 62/460562

<151> 2017-02-17

<150> 62/479169

<151> 2017-03-30

<150> 62/551645

<151> 2017-08-29

<150> 62/551647

<151> 2017-08-29

<150> 62/551668

<151> 2017-08-29

<160> 7

<170> PatentIn version 3.5

<210> 1

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 1

atgccccact ccagcctgca tccatccatc ccgtgtccca ggggtcacgg ggcccagaag 60

gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca 120

gagcacactc tccggtacct ggtgctccac cttagcctccc tgcagctggg actgctgtta 180

aacgggggtct gcagcctggc tgaggagctg cgccacatcc actccaggta ccgggggcagc 240

MATS Sequence 371.txt

tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg	300
ctgtccatct atttctacta ctccctccca aatgcggtcg gcccgcctt cacttggatg	360
cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc	420
ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca	480
tggatcatatt acatcgata tctgcggctg atcctgccag agctccaggc ccggattcga	540
acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt	600
ctcctcccat tggactgtgg ggtgcctgat aacctgagta tggctgacct caacattcgc	660
ttcctggata aactgcccc gcagaccggt gaccgggctg gcatcaagga tcgggtttac	720
agcaacagca tctatgagct tctggagaac gggcagcggg cgggcacctg tgtcctggag	780
tacgccacc ccttgagac tttgtttgcc atgtcacaat acagtcaagc tggcttttagc	840
cgggaggata ggcttgagca ggccaaactc ttctgccgga cacttgagga catcctggca	900
gatgcccctg agtctcagaa caactgccgc ctcatcgcct accaggaacc tgcagatgac	960
agcagcttct cgctgtccca ggaggttctc cggcacctgc ggcaggagga aaaggaagag	1020
gttactgtgg gcagcttgaa gacctcagcg gtgcccagta cctccacgat gtcccaagag	1080
cctgagctcc tcatcagtgg aatggaaaag cccctccctc tccgcacgga tttctcttga	1140

<210> 2

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 2

atgccccact ccagcctgca tccatccatc ccgtgtccca ggggtcacgg ggcccagaag	60
gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca	120
gagcacactc tccggtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta	180
aacgggggtct gcagcctggc tgaggagctg cgccacatcc actccaggta ccggggcagc	240
tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg	300
ctgtccatct atttctacta ctccctccca aatgcggtcg gcccgcctt cacttggatg	360

MATS Sequence 371.txt

cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc	420
ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca	480
tggatcatatt acatcgata tctgcggctg atcctgccag agctccaggc ccggattcga	540
acttacaatc agcattacaa caacctgcta cgggggtgcag tgagccagcg gctgtatatt	600
ctcctcccat tggactgtgg ggtgcctgat aacctgagta tggctgaccc caacattcgc	660
ttcctggata aactgcccc a gcagaccggt gaccatgctg gcatcaagga tcgggtttac	720
agcaacagca tctatgagct tctggagaac gggcagcggg cgggcacctg tgtcctggag	780
tacgccaccc ctttgagac tttgtttgcc atgtcacaat acagtcaagc tggctttagc	840
cgggaggata ggcttgagca ggccaaactc ttctgccgga cacttgagga catcctggca	900
gatgcccctg agtctcagaa caactgccgc ctcatcgcct accaggaacc tgcagatgac	960
agcagcttct cgctgtccca ggaggttctc cggcacctgc ggcaggagga aaaggaagag	1020
gttactgtgg gcagcttgaa gacctcagcg gtgcccagta cctccacgat gtccaagag	1080
cctgagctcc tcatcagtgg aatggaaaag cccctccctc tccgcacgga tttctcttga	1140

<210> 3
 <211> 1140
 <212> DNA
 <213> Homo sapiens

<400> 3 atgccccact ccagcctgca tccatccatc ccgtgtccca ggggtcacgg ggcccagaag	60
gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca	120
gagcacactc tccggtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta	180
aacgggggtct gcagcctggc tgaggagctg cgccacatcc actccaggta ccgggggcagc	240
tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg	300
ctgtccatct atttctacta ctccctccca aatgcggtcg gcccgccctt cacttggatg	360
cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc	420

MATS Sequence 371.txt

```

ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca      480
tgggtcatatt acatcggata tctgcggctg atcctgccag agctccaggc ccggattcga      540
acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt      600
ctcctcccat tggactgtgg ggtgcctgat aacctgagta tggctgaccc caacattcgc      660
ttcctggata aactgcccca gcagaccgct gaccgagctg gcatcaagga tcgggtttac      720
agcaacagca tctatgagct tctggagaac gggcagcggg cgggcacctg tgtcctggag      780
tacgccaccc ctttgagac tttgtttgcc atgtcacaat acagtcaagc tggcttttagc      840
cgggaggata ggcttgagca ggccaaactc ttctgccaga cacttgagga catcctggca      900
gatgcccttg agtctcagaa caactgccgc ctcatcgcct accaggaacc tgcagatgac      960
agcagcttct cgctgtccca ggaggttctc cggcacctgc ggcaggagga aaaggaagag     1020
gttactgtgg gcagcttgaa gacctcagcg gtgcccagta cctccacgat gtcccaagag     1080
cctgagctcc tcatcagtgg aatggaaaag cccctccctc tccgcacgga tttctcttga     1140

```

<210> 4
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 4

```

Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu
1           5           10          15

```

```

Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr
          20           25           30

```

```

Asn Asn Leu Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu
          35           40           45

```

```

Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn
          50           55           60

```

MATS Sequence 371.txt

Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly
65 70 75 80

Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn
85 90 95

Gly Gln Arg Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln
100 105 110

Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu
115 120 125

Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile
130 135 140

Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr
145 150 155 160

Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu
165 170 175

Arg His Leu Arg Gln Glu Glu Lys Glu Glu Val
180 185

<210> 5

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> His-TEV-Sumo-WT STING construct

<400> 5

Met His His His His His His Ser Ser Gly Val Asp Leu Gly Thr Glu
1 5 10 15

Asn Leu Tyr Phe Gln Ser Asn Ala Met Ser Asp Ser Glu Val Asn Gln
20 25 30

MATS Sequence 371.txt

Glu Ala Lys Pro Glu Val Lys Pro Glu Val Lys Pro Glu Thr His Ile
35 40 45

Asn Leu Lys Val Ser Asp Gly Ser Ser Glu Ile Phe Phe Lys Ile Lys
50 55 60

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

Gly Lys Glu Met Asp Ser Leu Arg Phe Leu Tyr Asp Gly Ile Arg Ile
85 90 95

Gln Ala Asp Gln Thr Pro Glu Asp Leu Asp Met Glu Asp Asn Asp Ile
100 105 110

Ile Glu Ala His Arg Glu Gln Ile Gly Gly Gly Ser Val Ala His Gly
115 120 125

Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu
130 135 140

Leu Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu
145 150 155 160

Arg Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys
165 170 175

Gly Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu
180 185 190

Asp Lys Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg
195 200 205

Val Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala
210 215 220

MATS Sequence 371.txt

Gly Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala
225 230 235 240

Met Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu
245 250 255

Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala
260 265 270

Pro Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala
275 280 285

Asp Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg
290 295 300

Gln Glu Glu Lys Glu Glu Val
305 310

<210> 6
<211> 187
<212> PRT
<213> Homo sapiens

<400> 6

Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu
1 5 10 15

Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr
20 25 30

Asn Asn Leu Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu
35 40 45

Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn
50 55 60

MATS Sequence 371.txt

Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp His Ala Gly
65 70 75 80

Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn
85 90 95

Gly Gln Arg Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln
100 105 110

Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu
115 120 125

Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile
130 135 140

Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr
145 150 155 160

Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu
165 170 175

Arg His Leu Arg Gln Glu Glu Lys Glu Glu Val
180 185

<210> 7

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> His-TEV-Sumo-REF STING 155-341 construct

<400> 7

Met His His His His His His Ser Ser Gly Val Asp Leu Gly Thr Glu
1 5 10 15

Asn Leu Tyr Phe Gln Ser Asn Ala Met Ser Asp Ser Glu Val Asn Gln

MATS Sequence 371.txt

20

25

30

Glu Ala Lys Pro Glu Val Lys Pro Glu Val Lys Pro Glu Thr His Ile
35 40 45

Asn Leu Lys Val Ser Asp Gly Ser Ser Glu Ile Phe Phe Lys Ile Lys
50 55 60

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

Gly Lys Glu Met Asp Ser Leu Arg Phe Leu Tyr Asp Gly Ile Arg Ile
85 90 95

Gln Ala Asp Gln Thr Pro Glu Asp Leu Asp Met Glu Asp Asn Asp Ile
100 105 110

Ile Glu Ala His Arg Glu Gln Ile Gly Gly Gly Ser Val Ala His Gly
115 120 125

Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu
130 135 140

Leu Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu
145 150 155 160

Arg Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys
165 170 175

Gly Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu
180 185 190

Asp Lys Leu Pro Gln Gln Thr Gly Asp His Ala Gly Ile Lys Asp Arg
195 200 205

Val Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala

MATS Sequence 371.txt

210

215

220

Gly Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala
225 230 235 240

Met Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu
245 250 255

Gln Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala
260 265 270

Pro Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala
275 280 285

Asp Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg
290 295 300

Gln Glu Glu Lys Glu Glu Val
305 310