

SEQUENCE LISTING

<110> ETH Zurich

<120> New compounds for use as a therapeutically active substance and in particular for use in the treatment of tumors

<130> AB2120 PCT BS

<140> XX

<150> EP17205416.5

<151> 2017-12-05

<160> 4

<170> BiSSAP 1.3.6

<210> 1

<211> 629

<212> PRT

<213> Homo sapiens

<220>

<223> DYRK1B_HUMAN Dual specificity tyrosine-phosphorylation-regulated kinase 1B

<400> 1

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Met Ala Val Pro Pro Gly His Gly Pro Phe Ser Gly Phe Pro Gly Pro
1      5      10      15
Gln Glu His Thr Gln Val Leu Pro Asp Val Arg Leu Leu Pro Arg Arg
      20      25      30
Leu Pro Leu Ala Phe Arg Asp Ala Thr Ser Ala Pro Leu Arg Lys Leu
      35      40      45
Ser Val Asp Leu Ile Lys Thr Tyr Lys His Ile Asn Glu Val Tyr Tyr
      50      55      60
Ala Lys Lys Lys Arg Arg Ala Gln Gln Ala Pro Pro Gln Asp Ser Ser
65      70      75      80
Asn Lys Lys Glu Lys Lys Val Leu Asn His Gly Tyr Asp Asp Asp Asn
      85      90      95
His Asp Tyr Ile Val Arg Ser Gly Glu Arg Trp Leu Glu Arg Tyr Glu
      100      105      110
Ile Asp Ser Leu Ile Gly Lys Gly Ser Phe Gly Gln Val Val Lys Ala
      115      120      125
Tyr Asp His Gln Thr Gln Glu Leu Val Ala Ile Lys Ile Ile Lys Asn
      130      135      140
Lys Lys Ala Phe Leu Asn Gln Ala Gln Ile Glu Leu Arg Leu Leu Glu
145      150      155      160
Leu Met Asn Gln His Asp Thr Glu Met Lys Tyr Tyr Ile Val His Leu
      165      170      175
Lys Arg His Phe Met Phe Arg Asn His Leu Cys Leu Val Phe Glu Leu
      180      185      190
Leu Ser Tyr Asn Leu Tyr Asp Leu Leu Arg Asn Thr His Phe Arg Gly
      195      200      205
Val Ser Leu Asn Leu Thr Arg Lys Leu Ala Gln Gln Leu Cys Thr Ala
      210      215      220
Leu Leu Phe Leu Ala Thr Pro Glu Leu Ser Ile Ile His Cys Asp Leu
225      230      235      240
Lys Pro Glu Asn Ile Leu Leu Cys Asn Pro Lys Arg Ser Ala Ile Lys
      245      250      255
Ile Val Asp Phe Gly Ser Ser Cys Gln Leu Gly Gln Arg Ile Tyr Gln
      260      265      270
Tyr Ile Gln Ser Arg Phe Tyr Arg Ser Pro Glu Val Leu Leu Gly Thr
      275      280      285
Pro Tyr Asp Leu Ala Ile Asp Met Trp Ser Leu Gly Cys Ile Leu Val
      290      295      300
Glu Met His Thr Gly Glu Pro Leu Phe Ser Gly Ser Asn Glu Val Asp
305      310      315      320
Gln Met Asn Arg Ile Val Glu Val Leu Gly Ile Pro Pro Ala Ala Met
      325      330      335
Leu Asp Gln Ala Pro Lys Ala Arg Lys Tyr Phe Glu Arg Leu Pro Gly
      340      345      350
Gly Gly Trp Thr Leu Arg Arg Thr Lys Glu Leu Arg Lys Asp Tyr Gln
      355      360      365
Gly Pro Gly Thr Arg Arg Leu Gln Glu Val Leu Gly Val Gln Thr Gly
      370      375      380
Gly Pro Gly Gly Arg Arg Ala Gly Glu Pro Gly His Ser Pro Ala Asp
385      390      395      400
Tyr Leu Arg Phe Gln Asp Leu Val Leu Arg Met Leu Glu Tyr Glu Pro
      405      410      415
Ala Ala Arg Ile Ser Pro Leu Gly Ala Leu Gln His Gly Phe Phe Arg
      420      425      430
Arg Thr Ala Asp Glu Ala Thr Asn Thr Gly Pro Ala Gly Ser Ser Ala
      435      440      445
Ser Thr Ser Pro Ala Pro Leu Asp Thr Cys Pro Ser Ser Ser Thr Ala
      450      455      460
Ser Ser Ile Ser Ser Ser Gly Gly Ser Ser Gly Ser Ser Ser Asp Asn
465      470      475      480
Arg Thr Tyr Arg Tyr Ser Asn Arg Tyr Cys Gly Gly Pro Gly Pro Pro
      485      490      495
Ile Thr Asp Cys Glu Met Asn Ser Pro Gln Val Pro Pro Ser Gln Pro
      500      505      510
Leu Arg Pro Trp Ala Gly Gly Asp Val Pro His Lys Thr His Gln Ala
      515      520      525
Pro Ala Ser Ala Ser Ser Leu Pro Gly Thr Gly Ala Gln Leu Pro Pro

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      530      535      540
Gln Pro Arg Tyr Leu Gly Arg Pro Pro Ser Pro Thr Ser Pro Pro Pro
545      550      555      560
Pro Glu Leu Met Asp Val Ser Leu Val Gly Gly Pro Ala Asp Cys Ser
      565      570      575
Pro Pro His Pro Ala Pro Ala Pro Gln His Pro Ala Ala Ser Ala Leu
      580      585      590
Arg Thr Arg Met Thr Gly Gly Arg Pro Pro Leu Pro Pro Asp Asp
      595      600      605
Pro Ala Thr Leu Gly Pro His Leu Gly Leu Arg Gly Val Pro Gln Ser
      610      615      620
Thr Ala Ala Ser Ser
625

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<210> 2
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>
<223> primer (forward)

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<400> 2
ggacctcatc aaaacttaca agcacatc
28

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<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> primer (reverse)

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<400> 3
acagagagct tacgcagcgg ggc
23

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<210> 4
<211> 763
<212> PRT
<213> Homo sapiens

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<220>
<223> DYRK1A_human dual specificity tyrosine-phosphorylation-regulated
kinase 1A

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<400> 4
Met His Thr Gly Gly Glu Thr Ser Ala Cys Lys Pro Ser Ser Val Arg
1      5      10      15
Leu Ala Pro Ser Phe Ser Phe His Ala Ala Gly Leu Gln Met Ala Gly
20     25     30
Gln Met Pro His Ser His Gln Tyr Ser Asp Arg Arg Gln Pro Asn Ile
35     40     45
Ser Asp Gln Gln Val Ser Ala Leu Ser Tyr Ser Asp Gln Ile Gln Gln
50     55     60
Pro Leu Thr Asn Gln Val Met Pro Asp Ile Val Met Leu Gln Arg Arg
65     70     75     80
Met Pro Gln Thr Phe Arg Asp Pro Ala Thr Ala Pro Leu Arg Lys Leu
85     90     95
Ser Val Asp Leu Ile Lys Thr Tyr Lys His Ile Asn Glu Val Tyr Tyr
100    105    110
Ala Lys Lys Lys Arg Arg His Gln Gln Gly Gln Gly Asp Ser Ser
115    120    125
His Lys Lys Glu Arg Lys Val Tyr Asn Asp Gly Tyr Asp Asp Asp Asn
130    135    140
Tyr Asp Tyr Ile Val Lys Asn Gly Glu Lys Trp Met Asp Arg Tyr Glu
145    150    155    160
Ile Asp Ser Leu Ile Gly Lys Gly Ser Phe Gly Gln Val Val Lys Ala
165    170    175
Tyr Asp Arg Val Glu Gln Glu Trp Val Ala Ile Lys Ile Ile Lys Asn
180    185    190
Lys Lys Ala Phe Leu Asn Gln Ala Gln Ile Glu Val Arg Leu Leu Glu
195    200    205
Leu Met Asn Lys His Asp Thr Glu Met Lys Tyr Tyr Ile Val His Leu
210    215    220
Lys Arg His Phe Met Phe Arg Asn His Leu Cys Leu Val Phe Glu Met
225    230    235    240
Leu Ser Tyr Asn Leu Tyr Asp Leu Leu Arg Asn Thr Asn Phe Arg Gly
245    250    255
Val Ser Leu Asn Leu Thr Arg Lys Phe Ala Gln Gln Met Cys Thr Ala
260    265    270
Leu Leu Phe Leu Ala Thr Pro Glu Leu Ser Ile Ile His Cys Asp Leu
275    280    285
Lys Pro Glu Asn Ile Leu Leu Cys Asn Pro Lys Arg Ser Ala Ile Lys
290    295    300
Ile Val Asp Phe Gly Ser Ser Cys Gln Leu Gly Gln Arg Ile Tyr Gln
305    310    315    320
Tyr Ile Gln Ser Arg Phe Tyr Arg Ser Pro Glu Val Leu Leu Gly Met
325    330    335
Pro Tyr Asp Leu Ala Ile Asp Met Trp Ser Leu Gly Cys Ile Leu Val
340    345    350

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Glu Met His Thr Gly Glu Pro Leu Phe Ser Gly Ala Asn Glu Val Asp
355 360 365
Gln Met Asn Lys Ile Val Glu Val Leu Gly Ile Pro Pro Ala His Ile
370 375 380
Leu Asp Gln Ala Pro Lys Ala Arg Lys Phe Phe Glu Lys Leu Pro Asp
385 390 395 400
Gly Thr Trp Asn Leu Lys Lys Thr Lys Asp Gly Lys Arg Glu Tyr Lys
405 410 415
Pro Pro Gly Thr Arg Lys Leu His Asn Ile Leu Gly Val Glu Thr Gly
420 425 430
Gly Pro Gly Gly Arg Arg Ala Gly Glu Ser Gly His Thr Val Ala Asp
435 440 445
Tyr Leu Lys Phe Lys Asp Leu Ile Leu Arg Met Leu Asp Tyr Asp Pro
450 455 460
Lys Thr Arg Ile Gln Pro Tyr Tyr Ala Leu Gln His Ser Phe Phe Lys
465 470 475 480
Lys Thr Ala Asp Glu Gly Thr Asn Thr Ser Asn Ser Val Ser Thr Ser
485 490 495
Pro Ala Met Glu Gln Ser Gln Ser Ser Gly Thr Thr Ser Ser Thr Ser
500 505 510
Ser Ser Ser Gly Gly Ser Ser Gly Thr Ser Asn Ser Gly Arg Ala Arg
515 520 525
Ser Asp Pro Thr His Gln His Arg His Ser Gly Gly His Phe Thr Ala
530 535 540
Ala Val Gln Ala Met Asp Cys Glu Thr His Ser Pro Gln Val Arg Gln
545 550 555 560
Gln Phe Pro Ala Pro Leu Gly Trp Ser Gly Thr Glu Ala Pro Thr Gln
565 570 575
Val Thr Val Glu Thr His Pro Val Gln Glu Thr Thr Phe His Val Ala
580 585 590
Pro Gln Gln Asn Ala Leu His His His His Gly Asn Ser Ser His His
595 600 605
His His His His His His His His His Gly Gln Gln Ala Leu
610 615 620
Gly Asn Arg Thr Arg Pro Arg Val Tyr Asn Ser Pro Thr Asn Ser Ser
625 630 635 640
Ser Thr Gln Asp Ser Met Glu Val Gly His Ser His His Ser Met Thr
645 650 655
Ser Leu Ser Ser Ser Thr Thr Ser Ser Ser Thr Ser Ser Ser Ser Thr
660 665 670
Gly Asn Gln Gly Asn Gln Ala Tyr Gln Asn Arg Pro Val Ala Ala Asn
675 680 685
Thr Leu Asp Phe Gly Gln Asn Gly Ala Met Asp Val Asn Leu Thr Val
690 695 700
Tyr Ser Asn Pro Arg Gln Glu Thr Gly Ile Ala Gly His Pro Thr Tyr
705 710 715 720
Gln Phe Ser Ala Asn Thr Gly Pro Ala His Tyr Met Thr Glu Gly His
725 730 735
Leu Thr Met Arg Gln Gly Ala Asp Arg Glu Glu Ser Pro Met Thr Gly
740 745 750
Val Cys Val Gln Gln Ser Pro Val Ala Ser Ser
755 760

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