

Tube #5

Sequencing of clone pCMV-intron-myc-Rab2 S20N
Results received oct 8 2008

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1 50
453 (1) NNNNNNNNGANNCCGCCCGTTGNNNAATGGGCGGTAGGCGTGTACGGTG
hRab2 (1) -----
Consensus (1)

51 100
453 (51) GGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCACTAGAA
hRab2 (1) -----
Consensus (51)

101 150
453 (101) GCTTTATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGTGCT
hRab2 (1) -----
Consensus (101)

151 200
453 (151) TCTGACACAACAGTCTCGAACTTAAGCTGCAGTGACTCTCTTAAGGTAGC
hRab2 (1) -----
Consensus (151)

201 250
453 (201) CTTGCAGAAGTTGGTCGTGAGGCACTGGGCAGGTAAGTATCAAGGTTACA
hRab2 (1) -----
Consensus (201)

251 300
453 (251) AGACAGGTTTAAGGAGACCAATAGAACTGGGCTTGTCGAGACAGAGAAG
hRab2 (1) -----
Consensus (251)

301 350
453 (301) ACTCTTGCGTTTCTGATAGGCACCTATTGGTCTTACTGACATCCACTTTG
hRab2 (1) -----
Consensus (301)

351 400
453 (351) CCTTTCTCTCCACAGGTGTCCACTCCCAGTTCAATTACAGCTCTTAAGGC
hRab2 (1) -----
Consensus (351)

401 450
453 (401) TAGAGTACTTAATACGACTCACTATAGGCTAGCCTCGACATGGAACAGAA
hRab2 (1) -----
Consensus (401)

451 500
453 (451) ACTCATCTCTGAAGAGGATCTGTCTAGAGGATCCACCATGGGCGTACGCCT
hRab2 (1) -----ATGGCGTACGCCT
Consensus (451) ATGGCGTACGCCT

501 550
453 (501) ATCTCTTCAAGTACATCATAATCGGGCGACACAGGTGTTGGTAAAAACTGC
hRab2 (14) ATCTCTTCAAGTACATCATAATCGGGCGACACAGGTGTTGGTAAATCATGC
Consensus (501) ATCTCTTCAAGTACATCATAATCGGGCGACACAGGTGTTGGTAAA TGC

551 600
453 (551) TTATTGCTACAGTTTACAGACAAGAGGTTTCAGCCAGTGCATGACCTTAC
hRab2 (64) TTATTGCTACAGTTTACAGACAAGAGGTTTCAGCCAGTGCATGACCTTAC
Consensus (551) TTATTGCTACAGTTTACAGACAAGAGGTTTCAGCCAGTGCATGACCTTAC

601 650
453 (601) TATTGGTGTAGAGTTCGGTGCTCGAATGATAACTATTGATGGGAAACAGA
hRab2 (114) TATTGGTGTAGAGTTCGGTGCTCGAATGATAACTATTGATGGGAAACAGA
Consensus (601) TATTGGTGTAGAGTTCGGTGCTCGAATGATAACTATTGATGGGAAACAGA

651 700
453 (651) TAAAACCTCAGATATGGGATACGGCAGGGCAAGAATCCTTTCGTTCCATC
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AAC=N
TCA=S

hRab2 (164) TAAAACCTTCAGATATGGGATACGGCAGGGCAAGAATCCTTTTCGTTCCATC
Consensus (651) TAAAACCTTCAGATATGGGATACGGCAGGGCAAGAATCCTTTTCGTTCCATC
701 750

453 (701) ACAACGTCGTATTACNNNNNTGCAGCNNNNNCTTTACTAGTTTACGATAG
hRab2 (214) ACAACGTCGTATTACAGAGGTGCAGCAGGAGCTTTACTAGTTTACGATAG
Consensus (701) ACAAGGTCGTATTAC TGCAGC CTTTACTAGTTTACGATAT
751 800

453 (751) TACACGGAGAGATACATTCAACCACTTGACAACNNNNNAGANNNTGCC
hRab2 (264) TACACGGAGAGATACATTCAACCACTTGACAACCTGGTTAGAAGATGCC
Consensus (751) TACACGGAGAGATACATTCAACCACTTGACAACC AGA TGCCC
801 850

453 (801) GCCAGCATTCCAANNNNNANCATGGTTCATTATGCTNATTTGG-----
hRab2 (314) GCCAGCATTCCAATTCCAACATGCTCATTATGCTTATTGGAAATAAAAGT
Consensus (801) GCCAGCATTCCA A CATGGTTCATTATGCT ATTGG
851 900

453 (841) -----
hRab2 (364) GATTTAGAATCTAGAAGAGAAGTAAAAAAGAAGAAGGTGAAGCTTTTGC
Consensus (851) -----
901 950

453 (841) -----
hRab2 (414) ACGAGAACATGGACTCATCTTCATGGAAACGTCTGCTAAGACTGCTTCCA
Consensus (901) -----
951 1000

453 (841) -----
hRab2 (464) ATGTAGAAGAGGCATTTATTAATACAGCAAAAGAAATTTATGAAAAAATT
Consensus (951) -----
1001 1050

453 (841) -----
hRab2 (514) CAAGAAGGAGTCTTTGACATTAATAATGAGGCAAATGGCATTAAAATTGG
Consensus (1001) -----
1051 1100

453 (841) -----
hRab2 (564) CCCTCAGCATGCTGCTACCAATGCAACACATGCAGGCAATCAGGGAGGAC
Consensus (1051) -----
1101 1126

453 (841) -----
hRab2 (614) AGCAGGCTGGGGGCGGCTGCTGTTGA
Consensus (1101) -----

Theoretical Map
(If the end of Rab2a is ok)

== Enzymes that DO NOT MAP to this sequence:

AarI	AatII	AbsI	Acc65I	AclI	AfeI	AgeI	AhdI	AjuI	AjuI
AleI	AlfI	AloI	AloI	AlwNI	ApaLI	AscI	AsiSI	AvrII	BaeI
BaeI	BarI	BarI	BbeI	BcgI	BcgI	BclI	BglI	BglII	BlpI
BmgBI	BplI	BpmI	BpuEI	BsaBI	BsaXI	BsaXI	BseRI	BsmBI	BspEI
BspHI	BsrBI	BsrDI	BsrGI	BssHII	BstBI	BstEII	BstXI	BstZ17I	Bsu36I
BtgZI	ClaI	CspCI	CspCI	DraIII	EagI	EciI	EcoNI	EcoRI	EcoRV
FseI	FspI	FspAI	HpaI	KasI	KpnI	MauBI	MfeI	MluI	MreI
MscI	NaeI	NarI	NdeI	NgoMIV	NmeAIII	NotI	NruI	NsiI	PacI
PasI	PciI	PfiMI	PfoI	PmlI	PsiI	PsrI	PsrI	PvuI	PvuII

1 G S T M A Y A Y L F K Y I I I G D T G V G K S C L L L Q F T
AcuI~
541 gacaagaggtttcagccagtgcatgaccttactattggtgtagagttcgggtgctcgaatgataactattgatgggaaacagataaaactt 630
ctgttctccaaagtcgggtcactggaatgataaccacatctcaagccacgagcttactattgataactacccttcttattttgaa
D K R F Q P V H D L T I G V E F G A R M I T I D G K Q I K L
BciVI~ XmnI SpeI BsgI
631 cagatatgggatacggcagggcaagaatcctttcgttccatcacaaggtcgtattacagaggtgcagcaggagctttactagtttacgat 720
gtctataccctatgccgtcccgttcttaggaaagcaaggtagtggtccagcataatgtctccacgtcgtcctcgaatgatcaaatgcta
Q I W D T A G Q E S F R S I T R S Y Y R G A A G A L L V Y D
SexAI BsmI~ XcmI
721 attacacggagagatacattcaaccacttgacaacctggttagaagatgccgccagcattccaattccaacatggtcattatgcttatt 810
taatgtgcctctctatgtaagttgggtaactgttggaccaatcttctacggcggtcgttaaggttaaggtgtaccagtaatacgaataa
I T R R D T F N H L T T W L E D A R Q H S N S N M V I M L I
XbaI PpiI~
EarI~ HindIII BssSI
811 ggaataaaaagtgatttagaatctagaagagaagtaaaaaagaagaaggtgaagcttttgacagagaacatggactcatcttcatggaa 900
cctttattttcactaaatcttagatcttctctcattttttcttctccacttcgaaaacgtgctcttgtacctgagtagaagtaacctt
G N K S D L E S R R E V K K E E G E A F A R E H G L I F M E
PpiI EarI~ AseI XmnI BdaI
901 acgtctgctaagactgcttccaatgtagaagaggcatttattaatacagcaaaagaatttatgaaaaattcaagaaggagtctttgac 990
tgcagacgatctgacgaagttacatcttctccgtaataaattatgctgttttctttaaatacttttttaagttcttctcagaaactg
T S A K T A S N V E E A F I N T A K E I Y E K I Q E G V F D
Bpu10I
AseI BbvCI SphI BstAPI BseYI~
991 attaataatgaggcaaatggcattaaaattggccctcagcatgctgctaccaatgcaacacatgcaggcaatcagggaggacagcaggct 1080
taattattactccgtttaccgtaattttaaccgggagtcgtacgacgatggttacgttgtgtacgtccgttagtccctcctgctgctccga
I N N E A N G I K I G P Q H A A T N A T H A G N Q G G Q Q A
PshAI
GsaI~ PspXI ApaI DraI
XhoI XbaI PspOMI PmeI
1081 gggggcggctgctgttgactcgagtctagagggcccggtttaaac 1170
ccccgcgcgacgacaactgagctcagatctcccgggcaaatg
G G G C C * L E S R G P V *