

GRIN1 ATD

== Enzymes that DO NOT MAP to this sequence:

AarI	AclI	AflII	AgeI	AscI	AseI	AvrII
BbvCI	BclI	BsaI	BsiWI	BspEI	BsrGI	BstBI
BstEII	Bsu36I	ClaI	EagI	HindIII	KflI	MauBI
MfeI	MluI	MreI	NcoI	NdeI	NheI	NotI
PciI	RsrII	SalI	SgrAI	SgrDI	SpeI	XbaI

== Total Number of Hits per Enzyme:

AbsI	1	BseYI	1	EcoNI	1	PspOMI	1
Acc65I	1	BsmBI	1	EcoRI	1	PspXI	1
ApaLI	2	BspHI	1	KasI	1	SapI	1
BamHI	1	BspMI	2	KroI	1	SexAI	1
BbsI	2	BssHII	2	NarI	1	Tth111I	1
BglII	1	BssSI	3	NgoMIV	1	XhoI	2
BlpI	2	BtgZI	1	PasI	1	XmaI	1
Bpu10I	1	EarI	2	PfoI	1		

== Linear Map of Sequence:

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      BamHI          start GRIN1
      \
1  ggatccgccaccatgagcaccatgcgccctgctgacgctcgccctgctgttctcctgctcc 60
   cctaggcgggtggtactctgggtacgcggacgactgcgagcgggacgacaagaggacgagg
      ^      *      ^      *      ^      *      ^      *      ^      *
1  G  S  A  T  M S T M R L L T L A L L F S C S

                                     BlpI
                                     \
61  gtcgcccgtgccgctgcgaccccaagatcgtcaacattggcgcggtgctgagcacgcgg 120
   cagcgggcacggcgcacgctggggttctagcagttgtaaccgcgccacgactcgtgcgcc
      ^      *      ^      *      ^      *      ^      *      ^      *
1  V A  R  A  A  C  D  P  K  I  V  N  I  G  A  V  L  S  T  R

      BssSI                                     PfoI
      \                                     \
121  aagcacgagcagatgttccgcgaggccgtgaaccaggccaacaagcgggcacggctcctgg 180
   ttcgtgctcgtctacaaggcgctccggcacttggtccggttggttcgccgtgccgaggacc
      ^      *      ^      *      ^      *      ^      *      ^      *
1  K  H  E  Q  M  F  R  E  A  V  N  Q  A  N  K  R  H  G  S  W

                                     PfoI
                                     \
181  aagattcagctcaatgccacctccgtcacgcacaagcccaacgccatccagatggctctg 240
   ttctaagtcgagttacgggtggaggcagtgcggtgttcgggttgcggtaggtctaccgagac
      ^      *      ^      *      ^      *      ^      *      ^      *
1  K  I  Q  L  N  A  T  S  V  T  H  K  P  N  A  I  Q  M  A  L
```

241	tcggtgtg	cgaggac	ctcatct	ccagcc	agggtct	acgccat	cctagtt	agccatc	ccacct	300										
	agccacac	gctcctg	gagtaga	gggtcgg	tccagatg	cggtagg	atcaatc	ggtaggt	gga											
	^	*	^	*	^	*	^	*	^	*										
1	S	V	C	E	D	L	I	S	S	Q	V	Y	A	I	L	V	S	H	P	P

NgoMIV
 KroI
 \

301	accccc	aacgacc	acttcact	cccaccc	ctgtctc	ctacacag	ccggctt	ctaccgc	ata	360										
	tgggggt	tgtggtg	aagtga	gggtggg	gacagagg	atgtgtc	ggccga	agatggc	gtat											
	^	*	^	*	^	*	^	*	^	*										
1	T	P	N	D	H	F	T	P	T	P	V	S	Y	T	A	G	F	Y	R	I

BseYI
 \

Bpu10I
 \

361	cccgtg	ctgggg	ctgacc	acccgc	atgtcc	atctact	cggaca	aagagca	tccac	ctgagc	420									
	gggcac	gacccc	gactgg	tggggc	gtacagg	tagatga	gcctgtt	ctcgtag	gtggac	tgcg										
	^	*	^	*	^	*	^	*	^	*										
1	P	V	L	G	L	T	T	R	M	S	I	Y	S	D	K	S	I	H	L	S

421	ttcctg	cgccacc	gtgccgc	ccctact	cccacc	agtc	cagcgt	gtgg	tttgag	atgatgc	gt	480								
	aaggac	gcgtgg	cacggc	gggatg	aggggt	gggtcag	gtcgca	caccaa	actctac	tacgca										
	^	*	^	*	^	*	^	*	^	*	^	*								
1	F	L	R	T	V	P	P	Y	S	H	Q	S	S	V	W	F	E	M	M	R

BssSI
 \

481	gtctacagctggaaccacatcatcctgctgggtcagcgacgaccacgagggccgggcggt	540
	cagatgtcgcaccttggtgtagtaggacgaccagtcgctgctggtgctcccggcccgcga	
	^ * ^ * ^ * ^ * ^ *	
1	V Y S W N H I I L L V S D D H E G R A A	
	BsmBI \ 541	
	cagaaacgcctggagacgctgctggaggagcgtgagtccaaggcagagaaggtgctgcag	600
	gtcttttgcggacctctgcgcacgacctcctcgccactcagggttccgtctcttccacgacgtc	
	^ * ^ * ^ * ^ * ^ *	
1	Q K R L E T L L E E R E S K A E K V L Q	
	PasI \ 601	
	tttgacccagggaccaagaacgtgacggccctgctgatggaggcgaaagagctggaggcc	660
	aaactgggtccctgggttcttgccactgcccgggacgactacctccgctttctcgacctccgg	
	^ * ^ * ^ * ^ * ^ *	
1	F D P G T K N V T A L L M E A K E L E A	
	XmaI \ 661	
	cgggtcatcatccttttctgccagcgaggacgatgctgccactgtataccgcgcagccgcg	720
	gcccagtagtaggaaagacgggtcgctcctgctacgacggtgacatatggcgcgtcggcgc	
	^ * ^ * ^ * ^ * ^ *	
1	R V I I L S A S E D D A A T V Y R A A A	
	BtgZI \ 721	
	atgctgaacatgacgggctccgggtacgtgtggctgggtcggcgagcgcgagatctcgggg	780
	tacgacttgtagtgcgggagggccatgcacaccgaccagccgctcgcgctctagagcccc	
	^ * ^ * ^ * ^ * ^ *	

1	M L N M T G S G Y V W L V G E R E I S G	
781	aacgccttgcgctacgccccagacggcatcctcgggctgcagctcatcaacggcaagaac	840
	ttgcgggacgcgatgcggggctctgccgtaggagcccgacgtcgagtagttgccgttcttg	
	^ * ^ * ^ * ^ * ^ *	
1	N A L R Y A P D G I L G L Q L I N G K N	
		BssSI
		ApaLI XhoI
		\ \ \
841	gagtcggcccacatcagcgacgccgtgggctgggtggcccaggccgtgcacgagctcctc	900
	ctcagccgggtgtagtcgctgcggcacccgcaccaccgggtccggcacgtgctcgaggag	
	^ * ^ * ^ * ^ * ^ *	
1	E S A H I S D A V G V V A Q A V H E L L	
	EcoNI	
	\	
901	gagaaggagaacatcacccgacccgcccggggctgcgtgggcaacaccaacatctggaag	960
	ctcttcctcttgtagtggctgggcgggcgccccgacgcacccggttggtggtgtagaccttc	
	^ * ^ * ^ * ^ * ^ *	
1	E K E N I T D P P R G C V G N T N I W K	
		EarI
	BbsI SapI BbsI	
	\ \ \	
961	accgggcccgtcttcaagagagtgcgtgatgtcttccaagtatgcggatgggggtgactggt	1020
	tggcccgcgagaagttctctcacgactacagaaggttcatacgccctacccactgacca	
	^ * ^ * ^ * ^ * ^ *	
1	T G P L F K R V L M S S K Y A D G V T G	

[illegible]

[illegible]

1501	gagtggaatgggatgatgggcgagctgctcagcgggcaggcagacatgatcgtggcgccg	1560
	ctcaccttaccctactacccgctcgcagagtcgcccgtccgtctgtactagcaccgcggc	
	^ * ^ * ^ * ^ * ^ * ^ *	
1	E W N G M M G E L L S G Q A D M I V A P	
	BssHII	
	BssHII	
	\ \	
1561	ctaaccataaacaacgagcgcgcgcagtacatcgagttttccaagcccttcaagtaccag	1620
	gattgggtatttgttgctcgcgcgcgcatgtagctcaaaagggttcgggaagttcatggtc	
	^ * ^ * ^ * ^ * ^ * ^ *	
1	L T I N N E R A Q Y I E F S K P F K Y Q	
1621	ggcctgactatttctgggtcaagaaggagattccccggagcacgctggactcgttcatgcag	1680
	ccggactgataagaccagtttcttccctctaaggggcctcgtgcgacctgagcaagtacgtc	
	^ * ^ * ^ * ^ * ^ * ^ *	
1	G L T I L V K K E I P R S T L D S F M Q	
	<i>myc tag</i> EarI HIS TAG	
	\	
1681	ccgttccagagcacagaacaaaaactcatctcagaagaggatctgcatcatcaccatcac	1740
	ggcaagggtctcgtgtcttgtttttgagtagagtcttctcctagacgtagtagtggtagtg	*T modified
	^ * ^ * ^ * ^ * ^ * ^ *	by Furukawa
1	P F Q S T* <u>E Q K L I S E E D L</u> H H H H H	
	<u>AcTEV protease site</u> <u>Asp</u> PDGF TM domain>>>	
1741	cacgaaaacctgtatttttcagggcggcaacgctgtgggccaggacacgcaggaggtcatc	1800
	gtgcttttggacataaaaagtccccgccgttgcgacacccggtcctgtgcgtcctccagtag	

1		[^] <u>H E N L Y F Q G G</u> [*] [^] <u>N</u> [*] [^] A V G Q D T Q E V I [*]	
1801	gtggtgccacactccttgccctttaagggtggtggtgatctcagccatcctggccctggtg caccacggtgtgaggaacgggaaattccaccaccactagagtcggtaggaccgggaccac	1860	
1	[^] V V P H S L P F K V V V I S A I L A L V [*]		
1861	gtgctcaccatcatctcccttatcatcctcatcatgctttggcagaagaagccacgttag cacgagtggtagtagagggaaatagtaggagtagtacgaaaccgtcttcttcggtgcaatc	1920	
1	[^] V L T I I S L I I L I M L W Q K K P R * [*]		
1921	EcoRI \ gaattc cttaag	1980	
1	[^] E F [*] [^] [*] [^] [*] [^] [*] [^] [*] [^] [*]		

===== End of Analysis =====

>GRIN1 ATD fusion protein

GGATCCGCCACCATGAGCACCATGCGCCTGCTGACGCTCGCCCTGCTGTTCTCCTGCTCCGTCGCCCCGTG
CCGCGTGCGACCCCAAGATCGTCAACATTGGCGCGGTGCTGAGCACGCGGAAGCACGAGCAGATGTTCCG
CGAGGCCGTGAACGAGCCAACAAGCGGCACGGCTCCTGGAAGATTGAGCTCAATGCCACCTCCGTCACG
CACAAGCCCAACGCCATCCAGATGGCTCTGTGCGGTGTGCGAGGACCTCATCTCCAGCCAGGTCTACGCCA
TCCTAGTTAGCCATCCACCTACCCCCAACGACCACTTCACTCCCACCCCTGTCTCCTACACAGCCGGCTT
CTACCGCATACCCGTGCTGGGGCTGACCACCCGCATGTCCATCTACTCGGACAAGAGCATCCACCTGAGC
TTCTTGCGCACCGTGCCGCCCTACTCCCACCAGTCCAGCGTGTGGTTTGAGATGATGCGTGTCTACAGCT
GGAACCACATCATCTGCTGGTCAGCGACGACCACGAGGGCCGGGCGGCTCAGAAACGCCTGGAGACGCT
GCTGGAGGAGCGTGAGTCCAAGGCAGAGAAGGTGCTGCAGTTTGACCCAGGGACCAAGAACGTGACGGCC
CTGCTGATGGAGGCGAAAGAGCTGGAGGCCCGGGTCATCATCCTTTCTGCCAGCGAGGACGATGCTGCCA
CTGTATACCGCGCAGCCGCGATGCTGAACATGACGGGCTCCGGGTACGTGTGGCTGGTCGGCGAGCGCGA
GATCTCGGGGAACGCCCTGCGCTACGCCCCAGACGGCATCCTCGGGCTGCAGCTCATCAACGGCAAGAAC
GAGTCGGCCACATCAGCGACGCCGTGGGCGTGGTGGCCAGGCCGTGCACGAGCTCCTCGAGAAGGAGA
ACATCACCGACCCGCCGCGGGGCTGCGTGGGCAACACCAACATCTGGAAGACCGGGCCGCTCTTCAAGAG
AGTGCTGATGTCTTCCAAGTATGCGGATGGGGTGACTGGTCGCGTGGAGTTCAATGAGGATGGGGACCGG
AAGTTCGCCAACTACAGCATCATGAACCTGCAGAACCGCAAGCTGGTGCAAGTGGGCATCTACAATGGCA
CCCACGTCATCCCTAATGACAGGAAGATCATCTGGCCAGGCGGAGAGACAGAGAAGCCTCGAGGGTACCA
GATGTCCACCAGACTGAAGATTGTGACGATCCACCAGGAGCCCTTCGTGTACGTCAAGCCCACGCTGAGT
GATGGGACATGCAAGGAGGAGTTCACAGTCAACGGCGACCCAGTCAAGAAGGTGATCTGCACCGGGCCCA
ACGACACGTCGCGGGCAGCCCCCGCCACACGGTGCCTCAGTGTGCTACGGCTTTTGCATCGACCTGCT
CATCAAGCTGGCACGGACCATGAACTTCACCTACGAGGTGCACCTGGTGGCAGATGGCAAGTTCGGCACA
CAGGAGCGGGTGAACAACAGCAACAAGAAGGAGTGGAATGGGATGATGGGCGAGCTGCTCAGCGGGCAGG
CAGACATGATCGTGGCGCCGCTAACCATAAACAACGAGCGCGCGCAGTACATCGAGTTTTTCCAAGCCCTT
CAAGTACCAGGGCCTGACTATTCTGGTCAAGAAGGAGATTCCCCGGAGCACGCTGGACTCGTTCATGCAG
CCGTTCCAGAGCACAGAACAAAACTCATCTCAGAAGAGGATCTGCATCATCACCATCACCACGAAAACC
TGTATTTTCAGGGCGGCAACGCTGTGGGCCAGGACACGCAGGAGGTATCGTGGTGGCACACTCCTTGCC
CTTTAAGGTGGTGGTGTCTCAGCCATCCTGGCCCTGGTGGTGTCTACCATCATCTCCCTTATCATCCTC
ATCATGCTTTGGCAGAAGAAGCCACGTTAGGAATTC

>GRIN1 ATD FUSION PROTEIN amino acid sequence

MSTMRLTLALLFSCSVARAACDPKIVNIGAVLSTRKHEQMFAVNQANKRHGSWKIQLNATSVTHKPNAIQMALSVCEDLISSQVYA
ILVSHPPTPNDHFTPTPVSYTAGFYRIPVLGLTTRMSIYSDKSIHLSFLRTVPPYSHQSSVWFEMMRVYSWNHIILLVSDDEGAAQK
RLETLLEERESKAQKVLQFDPGTKNVTALLMEAKELEARVILSASEDDAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIL
GLQLINGKNESAHISDAVGVAQAVHELLEKENITDPPRGCVGNTNIWKTGPLFKRVLMSKYADGVTGRVEFNEDGDRKFANYSIMNL
QNRKLVQVGIYNGTHVIPNDRKIIWPGGETEKPRGYQMSTRLKIVTIHQEPFVYVKPTLSDGTCKEEFTVNGDPVKKVICTGPNDTSPG
SPRHTVPQCCYGFCIDLLIKLARTMNFTYEVHLVADGKFGTQERVNNSNKKEWNGMMGELLSGQADMIVAPLTINNERAQYIEFSKPFK
YQGLTILVKKEIPRSTLDSFMQPFQSTEQKLISEEDLHHHHHHENLYFQGGNAVQDTQEVIVPHSLPFKVVVISAILALVVLTIISL
IILIMLWQKKPR