

Key	From	To	Length	Description
DOMAIN	46	53	8	PRO-RICH.
MOD_RES	118	118	1	PHOSPHORYLATION (BY PAK1) (BY SIMILARITY).
DOMAIN	324	374	51	LIM 1.
DOMAIN	381	432	51	LIM 2.
DOMAIN	442	492	51	LIM 3.
DOMAIN	501	551	51	LIM 4. PAXI-HUMAN

Sequence information  
 Length: 557 Molecular weight: 60936 CRC64: B379BED63E8E63A5 [This is a d  
 AA Da sequence]

MMH - [

10	20	30	40	50	60
MDLDALLAG	LESTTSHISK	RPVFLSEKTP	YSYPTGHTY	QEIAPPPVP	PFPSGALNO
70	80	90	100	110	120
TILDPLQWQ	PGSRFHIHQ	QSSSPVYGS	SARTSSVSNP	QDSVGSPCR	VGRKHVYEF
130	140	150	160	170	180
PNKQSAEFS	PTVMSTLGS	NLSELDRLLL	ELNAVQHPP	GFPADENSS	FFLPHALSFL
190	200	210	220	230	240
YGVFETNSPL	GGKAGPLTKE	KPKRNGRGL	EDVRSVESL	LDELESSVPS	EVFAITVNOG
250	260	270	280	290	300
EMSSPQVTS	TOQOTRISAS	SATRELDLIM	ASLSDPKFMA	QKGTGSSSPP	GGFKKPSQL
310	320	330	340	350	360
DSMLGSLQSD	LMLGLOVATVA	KGVCGACKKP	IAGQVVTAMG	KTWHPHFVC	THCQREIGSR
370	380	390	400	410	420
HFFERDQOPY	CEKDYHNLFS	PRCYCHGPI	LQKVVTALDR	TWHPHFPCA	QDAPFQPEG
430	440	450	460	470	480
FHEKDGKAYC	RKDYFDMFAP	KCGGCARAIL	ENYISALNTL	WHPECFVCRE	CTFFVYNSF
490	500	510	520	530	540
FEHQGFYCE	WHYHRSGL	CSGQKPTIC	RCITAMAGY	HPHFVCAFC	LQRLGRTK
550					
EQDRFVCG	CFALPFC				

Magnitude:

0.2 g of Gly-loaded TGT resin  
 (↑ loading 0.2 mmol / gram)

5 x excess of reagents

HOBt (mw: 153.1) 0.0306 g / vial

HBTU (mw: 379.3) 0.076 g / vial

(amino acids and HBTU should be measured accurately, but an HOBt excess is just fine)

run started at 2:45 pm 11/16/03

Some general tips:

- if machine is on, turn the power off. Click the power button to on and wait for beeping. Then press on the other button on the synthesizer, one on the left side of the computer and one on top of the ~~printer~~ monitor.
- Return on notebook → add and give name. Enter seq. N → C (≡) for DC between each and (?) for space at end, (\*) at N-terminus (takes off Fmoc at end) and spaces (?) after each DC to add a capping step.) Esc. back to main menu.
- Chemistry: Chemistry: comes up as calibration. hit return and change to A sys. prep. (first SPC) others are N-Acetylimidazole
- Magnitude: ie. .2 g resin .2 mmol/g loading 5 fold XS
- Protocol: Check that the amino acids are for B-couple w/ no monitor, spacer at the end is N, change spaces for capping to J (I think) ↑ COOH end
- Resources: Weigh out amino acids (2 for each if DC used), and an equimolar amount (ie. .2 mmol HBTU and HOBt if .2 mmol of amino acid is used) of HBTU and HOBt (← can be less precise with HOBt) into the brown 9050 vials.