

SEQUENCE LISTING

<110> Algomedix

<120> Pyridyl Pyrazole TRPA1 Modulators

<130> 97682-925619

<140> WO Not yet assigned

<141> Not yet assigned

<150> US 61/924,119

<151> 2014-01-06

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1119

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(1119)

<223> wild-type transient receptor potential cation channel subfamily
A member 1 (TRPA1), ankyrin-like with transmembrane domains
protein 1 (ANKTM1), transformation sensitive protein p120

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Lys	Glu	Ser	Leu	Lys	Val	Val	Phe	Glu	Gly	Ser	Ala	Tyr	Gly	Leu	Gln
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Asn	Phe	Asn	Lys	Gln	Lys	Lys	Leu	Lys	Arg	Cys	Asp	Asp	Met	Asp	Thr
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Phe	Phe	Leu	His	Tyr	Ala	Ala	Ala	Glu	Gly	Gln	Ile	Glu	Leu	Met	Glu
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Lys	Ile	Thr	Arg	Asp	Ser	Ser	Leu	Glu	Val	Leu	His	Glu	Met	Asp	Asp
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Tyr	Gly	Asn	Thr	Pro	Leu	His	Cys	Ala	Val	Glu	Lys	Asn	Gln	Ile	Glu
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Ser	Val	Lys	Phe	Leu	Leu	Ser	Arg	Gly	Ala	Asn	Pro	Asn	Leu	Arg	Asn
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Phe	Asn	Met	Met	Ala	Pro	Leu	His	Ile	Ala	Val	Gln	Gly	Met	Asn	Asn
			130				135				140				
Glu	Val	Met	Lys	Val	Leu	Leu	Glu	His	Arg	Thr	Ile	Asp	Val	Asn	Leu
145					150				155					160	
Glu	Gly	Glu	Asn	Gly	Asn	Thr	Ala	Val	Ile	Ile	Ala	Cys	Thr	Thr	Asn
			165					170					175		
Asn	Ser	Glu	Ala	Leu	Gln	Ile	Leu	Leu	Lys	Lys	Gly	Ala	Lys	Pro	Cys
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Lys	Ser	Asn	Lys	Trp	Gly	Cys	Phe	Pro	Ile	His	Gln	Ala	Ala	Phe	Ser
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Gly	Ser	Lys	Glu	Cys	Met	Glu	Ile	Ile	Leu	Arg	Phe	Gly	Glu	Glu	His
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Gly	Tyr	Ser	Arg	Gln	Leu	His	Ile	Asn	Phe	Met	Asn	Asn	Gly	Lys	Ala
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Thr	Pro	Leu	His	Leu	Ala	Val	Gln	Asn	Gly	Asp	Leu	Glu	Met	Ile	Lys
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Met	Cys	Leu	Asp	Asn	Gly	Ala	Gln	Ile	Asp	Pro	Val	Glu	Lys	Gly	Arg
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Cys	Thr	Ala	Ile	His	Phe	Ala	Ala	Thr	Gln	Gly	Ala	Thr	Glu	Ile	Val
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Lys	Leu	Met	Ile	Ser	Ser	Tyr	Ser	Gly	Ser	Val	Asp	Ile	Val	Asn	Thr
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Thr	Asp	Gly	Cys	His	Glu	Thr	Met	Leu	His	Arg	Ala	Ser	Leu	Phe	Asp
305					310					315					320
His	His	Glu	Leu	Ala	Asp	Tyr	Leu	Ile	Ser	Val	Gly	Ala	Asp	Ile	Asn
				325					330					335	
Lys	Ile	Asp	Ser	Glu	Gly	Arg	Ser	Pro	Leu	Ile	Leu	Ala	Thr	Ala	Ser
			340					345					350		
Ala	Ser	Trp	Asn	Ile	Val	Asn	Leu	Leu	Leu	Ser	Lys	Gly	Ala	Gln	Val
		355					360					365			
Asp	Ile	Lys	Asp	Asn	Phe	Gly	Arg	Asn	Phe	Leu	His	Leu	Thr	Val	Gln
	370					375					380				
Gln	Pro	Tyr	Gly	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Phe	Met	Gln	Met	Gln
385					390					395					400
Gln	Ile	Lys	Glu	Leu	Val	Met	Asp	Glu	Asp	Asn	Asp	Gly	Cys	Thr	Pro
				405					410					415	
Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu
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Leu	Gly	Phe	Asn	Val	Ser	Ile	His	Ser	Lys	Ser	Lys	Asp	Lys	Lys	Ser
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Pro	Leu	His	Phe	Ala	Ala	Ser	Tyr	Gly	Arg	Ile	Asn	Thr	Cys	Gln	Arg
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Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu
465					470					475					480
His	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Asn	Gly	His	Asp	Lys
				485					490					495	
Val	Val	Gln	Leu	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His
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Asn	Gly	Trp	Thr	Ala	Leu	His	His	Ala	Ser	Met	Gly	Gly	Tyr	Thr	Gln
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Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu
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Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His
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Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu
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Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg
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Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys
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Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr
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Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile
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Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys
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Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala
		675					680					685			
Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys
	690					695					700				

Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met	705		710		715		720
Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu		725		730		735	
Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile		740		745		750	
Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr		755		760		765	
Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly		770		775		780	
Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe		785		790		800	
Met	Asp	Ile	Ser	Asn	Val	Leu	Glu	Trp	Ile	Ile	Tyr	Thr	Thr	Gly	Ile		805		810		815	
Ile	Phe	Val	Leu	Pro	Leu	Phe	Val	Glu	Ile	Pro	Ala	His	Leu	Gln	Trp		820		825		830	
Gln	Cys	Gly	Ala	Ile	Ala	Val	Tyr	Phe	Tyr	Trp	Met	Asn	Phe	Leu	Leu		835		840		845	
Tyr	Leu	Gln	Arg	Phe	Glu	Asn	Cys	Gly	Ile	Phe	Ile	Val	Met	Leu	Glu		850		855		860	
Val	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Ser	Thr	Val	Val	Phe	Ile	Phe	Leu		865		870		875	
Leu	Leu	Ala	Phe	Gly	Leu	Ser	Phe	Tyr	Ile	Leu	Leu	Asn	Leu	Gln	Asp		885		890		895	
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Asn	Glu	Leu	Ala	His	Pro	Val	Leu	Ser	Phe	Ala	Gln	Leu	Val	Ser	Phe		930		935		940	
Thr	Ile	Phe	Val	Pro	Ile	Val	Leu	Met	Asn	Leu	Leu	Ile	Gly	Leu	Ala		945		950		955	
Val	Gly	Asp	Ile	Ala	Glu	Val	Gln	Lys	His	Ala	Ser	Leu	Lys	Arg	Ile		965		970		975	
Ala	Met	Gln	Val	Glu	Leu	His	Thr	Ser	Leu	Glu	Lys	Lys	Leu	Pro	Leu		980		985		990	
Trp	Phe	Leu	Arg	Lys	Val	Asp	Gln	Lys	Ser	Thr	Ile	Val	Tyr	Pro	Asn		995		1000		1005	
Lys	Pro	Arg	Ser	Gly	Gly	Met	Leu	Phe	His	Ile	Phe	Cys	Phe	Leu	Phe		1010		1015		1020	
Cys	Thr	Gly	Glu	Ile	Arg	Gln	Glu	Ile	Pro	Asn	Ala	Asp	Lys	Ser	Leu		1025		1030		1035	
Glu	Met	Glu	Ile	Leu	Lys	Gln	Lys	Tyr	Arg	Leu	Lys	Asp	Leu	Thr	Phe		1045		1050		1055	
Leu	Leu	Glu	Lys	Gln	His	Glu	Leu	Ile	Lys	Leu	Ile	Ile	Gln	Lys	Met		1060		1065		1070	
Glu	Ile	Ile	Ser	Glu	Thr	Glu	Asp	Asp	Asp	Ser	His	Cys	Ser	Phe	Gln		1075		1080		1085	
Asp	Arg	Phe	Lys	Lys	Glu	Gln	Met	Glu	Gln	Arg	Asn	Ser	Arg	Trp	Asn		1090		1095		1100	
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<211> 1119

<212> PRT

<213> Homo sapiens

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 <221> VARIANT
 <222> (1)...(1119)
 <223> transient receptor potential cation channel subfamily A member 1
 (TRPA1), variant rs13268757, VAR_020660, ankyrin-like with
 transmembrane domains protein 1 (ANKTM1), transformation
 sensitive protein p120

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 Met Lys Cys Ser Leu Arg Lys Met Trp Arg Pro Gly Glu Lys Lys Glu
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 Pro Gln Gly Val Tyr Glu Asp Val Pro Asp Asp Thr Glu Asp Phe
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 Lys Glu Ser Leu Lys Val Val Phe Glu Gly Ser Ala Tyr Gly Leu Gln
 35 40 45
 Asn Phe Asn Lys Gln Lys Lys Leu Lys Arg Cys Asp Asp Met Asp Thr
 50 55 60
 Phe Phe Leu His Tyr Ala Ala Ala Glu Gly Gln Ile Glu Leu Met Glu
 65 70 75 80
 Lys Ile Thr Arg Asp Ser Ser Leu Glu Val Leu His Glu Met Asp Asp
 85 90 95
 Tyr Gly Asn Thr Pro Leu His Cys Ala Val Glu Lys Asn Gln Ile Glu
 100 105 110
 Ser Val Lys Phe Leu Leu Ser Arg Gly Ala Asn Pro Asn Leu Arg Asn
 115 120 125
 Phe Asn Met Met Ala Pro Leu His Ile Ala Val Gln Gly Met Asn Asn
 130 135 140
 Glu Val Met Lys Val Leu Leu Glu His Arg Thr Ile Asp Val Asn Leu
 145 150 155 160
 Glu Gly Glu Asn Gly Asn Thr Ala Val Ile Ile Ala Cys Thr Thr Asn
 165 170 175
 Asn Ser Glu Ala Leu Gln Ile Leu Leu Lys Lys Gly Ala Lys Pro Cys
 180 185 190
 Lys Ser Asn Lys Trp Gly Cys Phe Pro Ile His Gln Ala Ala Phe Ser
 195 200 205
 Gly Ser Lys Glu Cys Met Glu Ile Ile Leu Arg Phe Gly Glu Glu His
 210 215 220
 Gly Tyr Ser Arg Gln Leu His Ile Asn Phe Met Asn Asn Gly Lys Ala
 225 230 235 240
 Thr Pro Leu His Leu Ala Val Gln Asn Gly Asp Leu Glu Met Ile Lys
 245 250 255
 Met Cys Leu Asp Asn Gly Ala Gln Ile Asp Pro Val Glu Lys Gly Arg
 260 265 270
 Cys Thr Ala Ile His Phe Ala Ala Thr Gln Gly Ala Thr Glu Ile Val
 275 280 285
 Lys Leu Met Ile Ser Ser Tyr Ser Gly Ser Val Asp Ile Val Asn Thr
 290 295 300
 Thr Asp Gly Cys His Glu Thr Met Leu His Arg Ala Ser Leu Phe Asp
 305 310 315 320
 His His Glu Leu Ala Asp Tyr Leu Ile Ser Val Gly Ala Asp Ile Asn
 325 330 335
 Lys Ile Asp Ser Glu Gly Arg Ser Pro Leu Ile Leu Ala Thr Ala Ser
 340 345 350
 Ala Ser Trp Asn Ile Val Asn Leu Leu Leu Ser Lys Gly Ala Gln Val
 355 360 365
 Asp Ile Lys Asp Asn Phe Gly Arg Asn Phe Leu His Leu Thr Val Gln
 370 375 380
 Gln Pro Tyr Gly Leu Lys Asn Leu Arg Pro Glu Phe Met Gln Met Gln
 385 390 395 400
 Gln Ile Lys Glu Leu Val Met Asp Glu Asp Asn Asp Gly Cys Thr Pro
 405 410 415

Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu			
			420					425					430					
Leu	Gly	Phe	Asn	Val	Ser	Ile	His	Ser	Lys	Ser	Lys	Asp	Lys	Lys	Ser			
			435					440					445					
Pro	Leu	His	Phe	Ala	Ala	Ser	Tyr	Gly	Arg	Ile	Asn	Thr	Cys	Gln	Arg			
			450					455					460					
Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu			
465						470					475				480			
His	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Asn	Gly	His	Asp	Lys			
						485				490					495			
Val	Val	Gln	Leu	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His			
			500					505						510				
Asn	Gly	Trp	Thr	Ala	Leu	His	His	Ala	Ser	Met	Gly	Gly	Tyr	Thr	Gln			
			515					520					525					
Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu			
			530				535					540						
Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His			
545						550				555					560			
Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu			
						565				570				575				
Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg			
						580				585				590				
Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys			
			595				600						605					
Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr			
			610				615					620						
Glu	Met	Ile	Glu	Tyr	Leu	Pro	Glu	Cys	Met	Lys	Val	Leu	Leu	Asp	Phe			
625						630				635				640				
Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile			
						645				650				655				
Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys			
			660					665					670					
Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala			
			675					680					685					
Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys			
			690				695				700							
Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met			
705						710				715				720				
Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu			
						725				730				735				
Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile			
			740					745					750					
Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr			
			755					760					765					
Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly			
			770				775				780							
Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe			
785						790				795				800				
Met	Asp	Ile	Ser	Asn	Val	Leu	Glu	Trp	Ile	Ile	Tyr	Thr	Thr	Gly	Ile			
						805				810				815				
Ile	Phe	Val	Leu	Pro	Leu	Phe	Val	Glu	Ile	Pro	Ala	His	Leu	Gln	Trp			
			820					825					830					
Gln	Cys	Gly	Ala	Ile	Ala	Val	Tyr	Phe	Tyr	Trp	Met	Asn	Phe	Leu	Leu			
			835					840					845					
Tyr	Leu	Gln	Arg	Phe	Glu	Asn	Cys	Gly	Ile	Phe	Ile	Val	Met	Leu	Glu			
			850				855				860							
Val	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Ser	Thr	Val	Val	Phe	Ile	Phe	Leu			
865						870				875				880				
Leu	Leu	Ala	Phe	Gly	Leu	Ser	Phe	Tyr	Ile	Leu	Leu	Asn	Leu	Gln	Asp			
						885				890				895				

Pro Phe Ser Ser Pro Leu Leu Ser Ile Ile Gln Thr Phe Ser Met Met
 900 905 910
 Leu Gly Asp Ile Asn Tyr Arg Glu Ser Phe Leu Glu Pro Tyr Leu Arg
 915 920 925
 Asn Glu Leu Ala His Pro Val Leu Ser Phe Ala Gln Leu Val Ser Phe
 930 935 940
 Thr Ile Phe Val Pro Ile Val Leu Met Asn Leu Leu Ile Gly Leu Ala
 945 950 955 960
 Val Gly Asp Ile Ala Glu Val Gln Lys His Ala Ser Leu Lys Arg Ile
 965 970 975
 Ala Met Gln Val Glu Leu His Thr Ser Leu Glu Lys Lys Leu Pro Leu
 980 985 990
 Trp Phe Leu Arg Lys Val Asp Gln Lys Ser Thr Ile Val Tyr Pro Asn
 995 1000 1005
 Lys Pro Arg Ser Gly Gly Met Leu Phe His Ile Phe Cys Phe Leu Phe
 1010 1015 1020
 Cys Thr Gly Glu Ile Arg Gln Glu Ile Pro Asn Ala Asp Lys Ser Leu
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 Glu Met Glu Ile Leu Lys Gln Lys Tyr Arg Leu Lys Asp Leu Thr Phe
 1045 1050 1055
 Leu Leu Glu Lys Gln His Glu Leu Ile Lys Leu Ile Ile Gln Lys Met
 1060 1065 1070
 Glu Ile Ile Ser Glu Thr Glu Asp Asp Asp Ser His Cys Ser Phe Gln
 1075 1080 1085
 Asp Arg Phe Lys Lys Glu Gln Met Glu Gln Arg Asn Ser Arg Trp Asn
 1090 1095 1100
 Thr Val Leu Arg Ala Val Lys Ala Lys Thr His His Leu Glu Pro
 1105 1110 1115

<210> 3

<211> 1119

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(1119)

<223> transient receptor potential cation channel subfamily A member 1
 (TRPA1), variant rs16937976, VAR_047471, ankyrin-like with
 transmembrane domains protein 1 (ANKTM1), transformation
 sensitive protein p120

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Met Lys Arg Ser Leu Arg Lys Met Trp Arg Pro Gly Glu Lys Lys Glu
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 Pro Gln Gly Val Val Tyr Glu Asp Val Pro Asp Asp Thr Glu Asp Phe
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 35 40 45
 Asn Phe Asn Lys Gln Lys Lys Leu Lys Thr Cys Asp Asp Met Asp Thr
 50 55 60
 Phe Phe Leu His Tyr Ala Ala Ala Glu Gly Gln Ile Glu Leu Met Glu
 65 70 75 80
 Lys Ile Thr Arg Asp Ser Ser Leu Glu Val Leu His Glu Met Asp Asp
 85 90 95
 Tyr Gly Asn Thr Pro Leu His Cys Ala Val Glu Lys Asn Gln Ile Glu
 100 105 110
 Ser Val Lys Phe Leu Leu Ser Arg Gly Ala Asn Pro Asn Leu Arg Asn
 115 120 125

Phe	Asn	Met	Met	Ala	Pro	Leu	His	Ile	Ala	Val	Gln	Gly	Met	Asn	Asn	
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Glu	Val	Met	Lys	Val	Leu	Leu	Glu	His	Arg	Thr	Ile	Asp	Val	Asn	Leu	
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Glu	Gly	Glu	Asn	Gly	Asn	Thr	Ala	Val	Ile	Ile	Ala	Cys	Thr	Thr	Asn	
				165					170						175	
Asn	Ser	Glu	Ala	Leu	Gln	Ile	Leu	Leu	Lys	Lys	Gly	Ala	Lys	Pro	Cys	
			180					185						190		
Lys	Ser	Asn	Lys	Trp	Gly	Cys	Phe	Pro	Ile	His	Gln	Ala	Ala	Phe	Ser	
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Gly	Ser	Lys	Glu	Cys	Met	Glu	Ile	Ile	Leu	Arg	Phe	Gly	Glu	Glu	His	
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Gly	Tyr	Ser	Arg	Gln	Leu	His	Ile	Asn	Phe	Met	Asn	Asn	Gly	Lys	Ala	
225					230					235					240	
Thr	Pro	Leu	His	Leu	Ala	Val	Gln	Asn	Gly	Asp	Leu	Glu	Met	Ile	Lys	
				245					250						255	
Met	Cys	Leu	Asp	Asn	Gly	Ala	Gln	Ile	Asp	Pro	Val	Glu	Lys	Gly	Arg	
			260					265					270			
Cys	Thr	Ala	Ile	His	Phe	Ala	Ala	Thr	Gln	Gly	Ala	Thr	Glu	Ile	Val	
		275				280					285					
Lys	Leu	Met	Ile	Ser	Ser	Tyr	Ser	Gly	Ser	Val	Asp	Ile	Val	Asn	Thr	
		290				295					300					
Thr	Asp	Gly	Cys	His	Glu	Thr	Met	Leu	His	Arg	Ala	Ser	Leu	Phe	Asp	
305					310					315					320	
His	His	Glu	Leu	Ala	Asp	Tyr	Leu	Ile	Ser	Val	Gly	Ala	Asp	Ile	Asn	
				325					330					335		
Lys	Ile	Asp	Ser	Glu	Gly	Arg	Ser	Pro	Leu	Ile	Leu	Ala	Thr	Ala	Ser	
			340					345						350		
Ala	Ser	Trp	Asn	Ile	Val	Asn	Leu	Leu	Ser	Lys	Gly	Ala	Gln	Val		
		355					360				365					
Asp	Ile	Lys	Asp	Asn	Phe	Gly	Arg	Asn	Phe	Leu	His	Leu	Thr	Val	Gln	
		370				375					380					
Gln	Pro	Tyr	Gly	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Phe	Met	Gln	Met	Gln	
385					390					395					400	
Gln	Ile	Lys	Glu	Leu	Val	Met	Asp	Glu	Asp	Asn	Asp	Gly	Cys	Thr	Pro	
				405					410					415		
Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu	
			420					425						430		
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		435					440						445			
Pro	Leu	His	Phe	Ala	Ala	Ser	Tyr	Gly	Arg	Ile	Asn	Thr	Cys	Gln	Arg	
		450				455					460					
Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu	
465					470					475					480	
His	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Asn	Gly	His	Asp	Lys	
				485					490					495		
Val	Val	Gln	Leu	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His	
			500					505						510		
Asn	Gly	Trp	Thr	Ala	Leu	His	His	Ala	Ser	Met	Gly	Gly	Tyr	Thr	Gln	
		515					520							525		
Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu	
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Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His	
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Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu	
				565					570					575		
Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg	
			580					585					590			
Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys	
		595					600						605			

Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr	
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Glu	Met	Ile	Glu	Tyr	Leu	Pro	Glu	Cys	Met	Lys	Val	Leu	Leu	Asp	Phe	
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Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile	
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Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys	
			660					665						670		
Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala	
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Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys	
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Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met	
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Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu	
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Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile	
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Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr	
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Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly	
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Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe	
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Met	Asp	Ile	Ser	Asn	Val	Leu	Glu	Trp	Ile	Ile	Tyr	Thr	Thr	Gly	Ile	
				805					810					815		
Ile	Phe	Val	Leu	Pro	Leu	Phe	Val	Glu	Ile	Pro	Ala	His	Leu	Gln	Trp	
		820						825					830			
Gln	Cys	Gly	Ala	Ile	Ala	Val	Tyr	Phe	Tyr	Trp	Met	Asn	Phe	Leu	Leu	
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Tyr	Leu	Gln	Arg	Phe	Glu	Asn	Cys	Gly	Ile	Phe	Ile	Val	Met	Leu	Glu	
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Val	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Ser	Thr	Val	Val	Phe	Ile	Phe	Leu	
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Leu	Leu	Ala	Phe	Gly	Leu	Ser	Phe	Tyr	Ile	Leu	Leu	Asn	Leu	Gln	Asp	
				885					890					895		
Pro	Phe	Ser	Ser	Pro	Leu	Leu	Ser	Ile	Ile	Gln	Thr	Phe	Ser	Met	Met	
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	915					920						925				
Asn	Glu	Leu	Ala	His	Pro	Val	Leu	Ser	Phe	Ala	Gln	Leu	Val	Ser	Phe	
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Thr	Ile	Phe	Val	Pro	Ile	Val	Leu	Met	Asn	Leu	Leu	Ile	Gly	Leu	Ala	
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Ala	Met	Gln	Val	Glu	Leu	His	Thr	Ser	Leu	Glu	Lys	Lys	Leu	Pro	Leu	
		980						985					990			
Trp	Phe	Leu	Arg	Lys	Val	Asp	Gln	Lys	Ser	Thr	Ile	Val	Tyr	Pro	Asn	
	995						1000					1005				
Lys	Pro	Arg	Ser	Gly	Gly	Met	Leu	Phe	His	Ile	Phe	Cys	Phe	Leu	Phe	
	1010					1015					1020					
Cys	Thr	Gly	Glu	Ile	Arg	Gln	Glu	Ile	Pro	Asn	Ala	Asp	Lys	Ser	Leu	
1025					1030					1035					1040	
Glu	Met	Glu	Ile	Leu	Lys	Gln	Lys	Tyr	Arg	Leu	Lys	Asp	Leu	Thr	Phe	
				1045					1050					1055		
Leu	Leu	Glu	Lys	Gln	His	Glu	Leu	Ile	Lys	Leu	Ile	Ile	Gln	Lys	Met	
		1060						1065					1070			
Glu	Ile	Ile	Ser	Glu	Thr	Glu	Asp	Asp	Asp	Ser	His	Cys	Ser	Phe	Gln	
	1075						1080					1085				

Asp Arg Phe Lys Lys Glu Gln Met Glu Gln Arg Asn Ser Arg Trp Asn
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Thr Val Leu Arg Ala Val Lys Ala Lys Thr His His Leu Glu Pro
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<223> transient receptor potential cation channel subfamily A member 1
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transmembrane domains protein 1 (ANKTM1), transformation
sensitive protein p120

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

His	His	Glu	Leu	Ala	Asp	Tyr	Leu	Ile	Ser	Val	Gly	Ala	Asp	Ile	Asn	
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Lys	Ile	Asp	Ser	Glu	Gly	Arg	Ser	Pro	Leu	Ile	Leu	Ala	Thr	Ala	Ser	
			340					345					350			
Ala	Ser	Trp	Asn	Ile	Val	Asn	Leu	Leu	Leu	Ser	Lys	Gly	Ala	Gln	Val	
		355					360					365				
Asp	Ile	Lys	Asp	Asn	Phe	Gly	Arg	Asn	Phe	Leu	His	Leu	Thr	Val	Gln	
	370					375					380					
Gln	Pro	Tyr	Gly	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Phe	Met	Gln	Met	Gln	
385					390					395					400	
Gln	Ile	Lys	Glu	Leu	Val	Met	Asp	Glu	Asp	Asn	Asp	Gly	Cys	Thr	Pro	
			405					410					415			
Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu	
			420					425					430			
Leu	Gly	Phe	Asn	Val	Ser	Ile	His	Ser	Lys	Ser	Lys	Asp	Lys	Lys	Ser	
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Pro	Leu	His	Phe	Ala	Ala	Ser	Tyr	Gly	Arg	Ile	Asn	Thr	Cys	Gln	Arg	
	450					455					460					
Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu	
465					470					475					480	
His	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Asn	Gly	His	Asp	Lys	
			485					490					495			
Val	Val	Gln	Leu	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His	
			500					505					510			
Asn	Gly	Trp	Thr	Ala	Leu	His	His	Ala	Ser	Met	Gly	Gly	Tyr	Thr	Gln	
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Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu	
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Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His	
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Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu	
			565					570					575			
Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg	
			580					585					590			
Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys	
		595					600					605				
Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr	
	610					615					620					
Glu	Met	Ile	Glu	Tyr	Leu	Pro	Glu	Cys	Met	Lys	Val	Leu	Leu	Asp	Phe	
625					630					635					640	
Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile	
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Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys	
		660						665					670			
Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala	
		675					680					685				
Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys	
	690					695					700					
Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met	
705					710					715					720	
Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu	
			725					730					735			
Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile	
		740						745					750			
Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr	
		755					760					765				
Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly	
	770					775					780					
Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe	
785					790					795					800	

Met Asp Ile Ser Asn Val Leu Glu Trp Ile Ile Tyr Thr Thr Gly Ile
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 Ile Phe Val Leu Pro Leu Phe Val Glu Ile Pro Ala His Leu Gln Trp
 820 825 830
 Gln Cys Gly Ala Ile Ala Val Tyr Phe Tyr Trp Met Asn Phe Leu Leu
 835 840 845
 Tyr Leu Gln Arg Phe Glu Asn Cys Gly Ile Phe Ile Val Met Leu Glu
 850 855 860
 Val Ile Leu Lys Thr Leu Leu Arg Ser Thr Val Val Phe Ile Phe Leu
 865 870 875 880
 Leu Leu Ala Phe Gly Leu Ser Phe Tyr Ile Leu Leu Asn Leu Gln Asp
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 Pro Phe Ser Ser Pro Leu Leu Ser Ile Ile Gln Thr Phe Ser Met Met
 900 905 910
 Leu Gly Asp Ile Asn Tyr Arg Glu Ser Phe Leu Glu Pro Tyr Leu Arg
 915 920 925
 Asn Glu Leu Ala His Pro Val Leu Ser Phe Ala Gln Leu Val Ser Phe
 930 935 940
 Thr Ile Phe Val Pro Ile Val Leu Met Asn Leu Leu Ile Gly Leu Ala
 945 950 955 960
 Val Gly Asp Ile Ala Glu Val Gln Lys His Ala Ser Leu Lys Arg Ile
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 Ala Met Gln Val Glu Leu His Thr Ser Leu Glu Lys Lys Leu Pro Leu
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 Trp Phe Leu Arg Lys Val Asp Gln Lys Ser Thr Ile Val Tyr Pro Asn
 995 1000 1005
 Lys Pro Arg Ser Gly Gly Met Leu Phe His Ile Phe Cys Phe Leu Phe
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 Cys Thr Gly Glu Ile Arg Gln Glu Ile Pro Asn Ala Asp Lys Ser Leu
 1025 1030 1035 1040
 Glu Met Glu Ile Leu Lys Gln Lys Tyr Arg Leu Lys Asp Leu Thr Phe
 1045 1050 1055
 Leu Leu Glu Lys Gln His Glu Leu Ile Lys Leu Ile Ile Gln Lys Met
 1060 1065 1070
 Glu Ile Ile Ser Glu Thr Glu Asp Asp Asp Ser His Cys Ser Phe Gln
 1075 1080 1085
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 transmembrane domains protein 1 (ANKTM1), transformation
 sensitive protein p120

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Asn	Phe	Asn	Lys	Gln	Lys	Lys	Leu	Lys	Arg	Cys	Asp	Asp	Met	Asp	Thr
	50					55					60				
Phe	Phe	Leu	His	Tyr	Ala	Ala	Ala	Glu	Gly	Gln	Ile	Glu	Leu	Met	Glu
65					70					75					80
Lys	Ile	Thr	Arg	Asp	Ser	Ser	Leu	Glu	Val	Leu	His	Glu	Met	Asp	Asp
				85					90					95	
Tyr	Gly	Asn	Thr	Pro	Leu	His	Cys	Ala	Val	Glu	Lys	Asn	Gln	Ile	Glu
			100					105					110		
Ser	Val	Lys	Phe	Leu	Leu	Ser	Arg	Gly	Ala	Asn	Pro	Asn	Leu	Arg	Asn
		115					120					125			
Phe	Asn	Met	Met	Ala	Pro	Leu	His	Ile	Ala	Val	Gln	Gly	Met	Asn	Asn
	130					135					140				
Glu	Val	Met	Lys	Val	Leu	Leu	Glu	His	Arg	Thr	Ile	Asp	Val	Asn	Leu
145					150					155					160
Glu	Gly	Glu	Asn	Gly	Asn	Thr	Ala	Val	Ile	Ile	Ala	Cys	Thr	Thr	Asn
				165					170					175	
Asn	Ser	Glu	Ala	Leu	Gln	Ile	Leu	Leu	Asn	Lys	Gly	Ala	Lys	Pro	Cys
			180					185					190		
Lys	Ser	Asn	Lys	Trp	Gly	Cys	Phe	Pro	Ile	His	Gln	Ala	Ala	Phe	Ser
		195				200						205			
Gly	Ser	Lys	Glu	Cys	Met	Glu	Ile	Ile	Leu	Arg	Phe	Gly	Glu	Glu	His
	210					215					220				
Gly	Tyr	Ser	Arg	Gln	Leu	His	Ile	Asn	Phe	Met	Asn	Asn	Gly	Lys	Ala
225					230					235					240
Thr	Pro	Leu	His	Leu	Ala	Val	Gln	Asn	Gly	Asp	Leu	Glu	Met	Ile	Lys
				245					250					255	
Met	Cys	Leu	Asp	Asn	Gly	Ala	Gln	Ile	Asp	Pro	Val	Glu	Lys	Gly	Arg
			260					265					270		
Cys	Thr	Ala	Ile	His	Phe	Ala	Ala	Thr	Gln	Gly	Ala	Thr	Glu	Ile	Val
		275					280					285			
Lys	Leu	Met	Ile	Ser	Ser	Tyr	Ser	Gly	Ser	Val	Asp	Ile	Val	Asn	Thr
	290					295					300				
Thr	Asp	Gly	Cys	His	Glu	Thr	Met	Leu	His	Arg	Ala	Ser	Leu	Phe	Asp
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His	His	Glu	Leu	Ala	Asp	Tyr	Leu	Ile	Ser	Val	Gly	Ala	Asp	Ile	Asn
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Lys	Ile	Asp	Ser	Glu	Gly	Arg	Ser	Pro	Leu	Ile	Leu	Ala	Thr	Ala	Ser
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Ala	Ser	Trp	Asn	Ile	Val	Asn	Leu	Leu	Leu	Ser	Lys	Gly	Ala	Gln	Val
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Asp	Ile	Lys	Asp	Asn	Phe	Gly	Arg	Asn	Phe	Leu	His	Leu	Thr	Val	Gln
	370					375					380				
Gln	Pro	Tyr	Gly	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Phe	Met	Gln	Met	Gln
385					390					395					400
Gln	Ile	Lys	Glu	Leu	Val	Met	Asp	Glu	Asp	Asn	Asp	Gly	Cys	Thr	Pro
				405					410					415	
Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu
			420					425					430		
Leu	Gly	Phe	Asn	Val	Ser	Ile	His	Ser	Lys	Ser	Lys	Asp	Lys	Lys	Ser
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Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu
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Val	Val	Gln	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His	
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Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu		
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Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His		
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Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu		
				565					570					575			
Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg		
			580					585					590				
Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys		
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Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr		
		610				615					620						
Glu	Met	Ile	Glu	Tyr	Leu	Pro	Glu	Cys	Met	Lys	Val	Leu	Leu	Asp	Phe		
625					630					635					640		
Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile		
				645					650					655			
Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys		
			660				665						670				
Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala		
		675					680					685					
Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys		
		690				695					700						
Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met		
705					710					715					720		
Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu		
				725					730					735			
Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile		
		740					745						750				
Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr		
		755					760					765					
Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly		
		770				775					780						
Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe		
785					790					795					800		
Met	Asp	Ile	Ser	Asn	Val	Leu	Glu	Trp	Ile	Ile	Tyr	Thr	Thr	Gly	Ile		
				805					810					815			
Ile	Phe	Val	Leu	Pro	Leu	Phe	Val	Glu	Ile	Pro	Ala	His	Leu	Gln	Trp		
			820					825					830				
Gln	Cys	Gly	Ala	Ile	Ala	Val	Tyr	Phe	Tyr	Trp	Met	Asn	Phe	Leu	Leu		
		835					840					845					
Tyr	Leu	Gln	Arg	Phe	Glu	Asn	Cys	Gly	Ile	Phe	Ile	Val	Met	Leu	Glu		
		850				855					860						
Val	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Ser	Thr	Val	Val	Phe	Ile	Phe	Leu		
865					870					875					880		
Leu	Leu	Ala	Phe	Gly	Leu	Ser	Phe	Tyr	Ile	Leu	Leu	Asn	Leu	Gln	Asp		
				885					890					895			
Pro	Phe	Ser	Ser	Pro	Leu	Leu	Ser	Ile	Ile	Gln	Thr	Phe	Ser	Met	Met		
			900					905					910				
Leu	Gly	Asp	Ile	Asn	Tyr	Arg	Glu	Ser	Phe	Leu	Glu	Pro	Tyr	Leu	Arg		
		915					920					925					
Asn	Glu	Leu	Ala	His	Pro	Val	Leu	Ser	Phe	Ala	Gln	Leu	Val	Ser	Phe		
					930		935				940						
Thr	Ile	Phe	Val	Pro	Ile	Val	Leu	Met	Asn	Leu	Leu	Ile	Gly	Leu	Ala		
945					950					955					960		
Val	Gly	Asp	Ile	Ala	Glu	Val	Gln	Lys	His	Ala	Ser	Leu	Lys	Arg	Ile		
				965					970					975			
Ala	Met	Gln	Val	Glu	Leu	His	Thr	Ser	Leu	Glu	Lys	Lys	Leu	Pro	Leu		
			980					985					990				

Trp Phe Leu Arg Lys Val Asp Gln Lys Ser Thr Ile Val Tyr Pro Asn
 995 1000 1005
 Lys Pro Arg Ser Gly Gly Met Leu Phe His Ile Phe Cys Phe Leu Phe
 1010 1015 1020
 Cys Thr Gly Glu Ile Arg Gln Glu Ile Pro Asn Ala Asp Lys Ser Leu
 1025 1030 1035 1040
 Glu Met Glu Ile Leu Lys Gln Lys Tyr Arg Leu Lys Asp Leu Thr Phe
 1045 1050 1055
 Leu Leu Glu Lys Gln His Glu Leu Ile Lys Leu Ile Ile Gln Lys Met
 1060 1065 1070
 Glu Ile Ile Ser Glu Thr Glu Asp Asp Ser His Cys Ser Phe Gln
 1075 1080 1085
 Asp Arg Phe Lys Lys Glu Gln Met Glu Gln Arg Asn Ser Arg Trp Asn
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 Thr Val Leu Arg Ala Val Lys Ala Lys Thr His His Leu Glu Pro
 1105 1110 1115

<210> 6

<211> 1119

<212> PRT

<213> Homo sapiens

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<222> (1)...(1119)

<223> transient receptor potential cation channel subfamily A member 1
 (TRPA1), familial episodic pain syndrome 1 (FEPS1), VAR_069737,
 ankyrin-like with transmembrane domains protein 1 (ANKTM1),
 transformation sensitive protein p120

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 Pro Gln Gly Val Val Tyr Glu Asp Val Pro Asp Asp Thr Glu Asp Phe
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 Lys Glu Ser Leu Lys Val Val Phe Glu Gly Ser Ala Tyr Gly Leu Gln
 35 40 45
 Asn Phe Asn Lys Gln Lys Lys Leu Lys Arg Cys Asp Asp Met Asp Thr
 50 55 60
 Phe Phe Leu His Tyr Ala Ala Ala Glu Gly Gln Ile Glu Leu Met Glu
 65 70 75 80
 Lys Ile Thr Arg Asp Ser Ser Leu Glu Val Leu His Glu Met Asp Asp
 85 90 95
 Tyr Gly Asn Thr Pro Leu His Cys Ala Val Glu Lys Asn Gln Ile Glu
 100 105 110
 Ser Val Lys Phe Leu Leu Ser Arg Gly Ala Asn Pro Asn Leu Arg Asn
 115 120 125
 Phe Asn Met Met Ala Pro Leu His Ile Ala Val Gln Gly Met Asn Asn
 130 135 140
 Glu Val Met Lys Val Leu Leu Glu His Arg Thr Ile Asp Val Asn Leu
 145 150 155 160
 Glu Gly Glu Asn Gly Asn Thr Ala Val Ile Ile Ala Cys Thr Thr Asn
 165 170 175
 Asn Ser Glu Ala Leu Gln Ile Leu Leu Lys Lys Gly Ala Lys Pro Cys
 180 185 190
 Lys Ser Asn Lys Trp Gly Cys Phe Pro Ile His Gln Ala Ala Phe Ser
 195 200 205
 Gly Ser Lys Glu Cys Met Glu Ile Ile Leu Arg Phe Gly Glu Glu His
 210 215 220

Gly	Tyr	Ser	Arg	Gln	Leu	His	Ile	Asn	Phe	Met	Asn	Asn	Gly	Lys	Ala	
225					230				235						240	
Thr	Pro	Leu	His	Leu	Ala	Val	Gln	Asn	Gly	Asp	Leu	Glu	Met	Ile	Lys	
				245					250					255		
Met	Cys	Leu	Asp	Asn	Gly	Ala	Gln	Ile	Asp	Pro	Val	Glu	Lys	Gly	Arg	
			260					265					270			
Cys	Thr	Ala	Ile	His	Phe	Ala	Ala	Thr	Gln	Gly	Ala	Thr	Glu	Ile	Val	
		275					280					285				
Lys	Leu	Met	Ile	Ser	Ser	Tyr	Ser	Gly	Ser	Val	Asp	Ile	Val	Asn	Thr	
	290					295					300					
Thr	Asp	Gly	Cys	His	Glu	Thr	Met	Leu	His	Arg	Ala	Ser	Leu	Phe	Asp	
305					310					315					320	
His	His	Glu	Leu	Ala	Asp	Tyr	Leu	Ile	Ser	Val	Gly	Ala	Asp	Ile	Asn	
				325					330					335		
Lys	Ile	Asp	Ser	Glu	Gly	Arg	Ser	Pro	Leu	Ile	Leu	Ala	Thr	Ala	Ser	
			340					345					350			
Ala	Ser	Trp	Asn	Ile	Val	Asn	Leu	Leu	Leu	Ser	Lys	Gly	Ala	Gln	Val	
		355					360					365				
Asp	Ile	Lys	Asp	Asn	Phe	Gly	Arg	Asn	Phe	Leu	His	Leu	Thr	Val	Gln	
	370					375					380					
Gln	Pro	Tyr	Gly	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Phe	Met	Gln	Met	Gln	
385					390					395					400	
Gln	Ile	Lys	Glu	Leu	Val	Met	Asp	Glu	Asp	Asn	Asp	Gly	Cys	Thr	Pro	
				405					410					415		
Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu	
			420					425					430			
Leu	Gly	Phe	Asn	Val	Ser	Ile	His	Ser	Lys	Ser	Lys	Asp	Lys	Lys	Ser	
		435					440					445				
Pro	Leu	His	Phe	Ala	Ala	Ser	Tyr	Gly	Arg	Ile	Asn	Thr	Cys	Gln	Arg	
	450					455					460					
Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu	
465					470					475					480	
His	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Asn	Gly	His	Asp	Lys	
				485					490					495		
Val	Val	Gln	Leu	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His	
				500					505				510			
Asn	Gly	Trp	Thr	Ala	Leu	His	His	Ala	Ser	Met	Gly	Gly	Tyr	Thr	Gln	
		515					520					525				
Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu	
	530					535					540					
Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His	
545					550					555					560	
Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu	
				565					570					575		
Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg	
				580					585				590			
Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys	
		595					600					605				
Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr	
	610					615					620					
Glu	Met	Ile	Glu	Tyr	Leu	Pro	Glu	Cys	Met	Lys	Val	Leu	Leu	Asp	Phe	
625					630					635					640	
Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile	
				645					650					655		
Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys	
			660					665					670			
Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala	
		675					680					685				
Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys	
	690					695					700					

Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met	705		710		715		720
Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu		725		730		735	
Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile		740		745		750	
Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr		755		760		765	
Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly		770		775		780	
Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe		785		790		800	
Met	Asp	Ile	Ser	Ser	Val	Leu	Glu	Trp	Ile	Ile	Tyr	Thr	Thr	Gly	Ile		805		810		815	
Ile	Phe	Val	Leu	Pro	Leu	Phe	Val	Glu	Ile	Pro	Ala	His	Leu	Gln	Trp		820		825		830	
Gln	Cys	Gly	Ala	Ile	Ala	Val	Tyr	Phe	Tyr	Trp	Met	Asn	Phe	Leu	Leu		835		840		845	
Tyr	Leu	Gln	Arg	Phe	Glu	Asn	Cys	Gly	Ile	Phe	Ile	Val	Met	Leu	Glu		850		855		860	
Val	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Ser	Thr	Val	Val	Phe	Ile	Phe	Leu		865		870		875	
Leu	Leu	Ala	Phe	Gly	Leu	Ser	Phe	Tyr	Ile	Leu	Leu	Asn	Leu	Gln	Asp		885		890		895	
Pro	Phe	Ser	Ser	Pro	Leu	Leu	Ser	Ile	Ile	Gln	Thr	Phe	Ser	Met	Met		900		905		910	
Leu	Gly	Asp	Ile	Asn	Tyr	Arg	Glu	Ser	Phe	Leu	Glu	Pro	Tyr	Leu	Arg		915		920		925	
Asn	Glu	Leu	Ala	His	Pro	Val	Leu	Ser	Phe	Ala	Gln	Leu	Val	Ser	Phe		930		935		940	
Thr	Ile	Phe	Val	Pro	Ile	Val	Leu	Met	Asn	Leu	Leu	Ile	Gly	Leu	Ala		945		950		955	
Val	Gly	Asp	Ile	Ala	Glu	Val	Gln	Lys	His	Ala	Ser	Leu	Lys	Arg	Ile		965		970		975	
Ala	Met	Gln	Val	Glu	Leu	His	Thr	Ser	Leu	Glu	Lys	Lys	Leu	Pro	Leu		980		985		990	
Trp	Phe	Leu	Arg	Lys	Val	Asp	Gln	Lys	Ser	Thr	Ile	Val	Tyr	Pro	Asn		995		1000		1005	
Lys	Pro	Arg	Ser	Gly	Gly	Met	Leu	Phe	His	Ile	Phe	Cys	Phe	Leu	Phe		1010		1015		1020	
Cys	Thr	Gly	Glu	Ile	Arg	Gln	Glu	Ile	Pro	Asn	Ala	Asp	Lys	Ser	Leu		1025		1030		1035	
Glu	Met	Glu	Ile	Leu	Lys	Gln	Lys	Tyr	Arg	Leu	Lys	Asp	Leu	Thr	Phe		1045		1050		1055	
Leu	Leu	Glu	Lys	Gln	His	Glu	Leu	Ile	Lys	Leu	Ile	Ile	Gln	Lys	Met		1060		1065		1070	
Glu	Ile	Ile	Ser	Glu	Thr	Glu	Asp	Asp	Asp	Ser	His	Cys	Ser	Phe	Gln		1075		1080		1085	
Asp	Arg	Phe	Lys	Lys	Glu	Gln	Met	Glu	Gln	Arg	Asn	Ser	Arg	Trp	Asn		1090		1095		1100	
Thr	Val	Leu	Arg	Ala	Val	Lys	Ala	Lys	Thr	His	His	Leu	Glu	Pro			1105		1110		1115	

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<211> 1119

<212> PRT

<213> Homo sapiens

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 <222> (1)...(1119)
 <223> transient receptor potential cation channel subfamily A member 1
 (TRPA1), variant rs959976, VAR_020663, ankyrin-like with
 transmembrane domains protein 1 (ANKTM1), transformation
 sensitive protein p120

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			20					25					30		
Lys	Glu	Ser	Leu	Lys	Val	Val	Phe	Glu	Gly	Ser	Ala	Tyr	Gly	Leu	Gln
		35					40					45			
Asn	Phe	Asn	Lys	Gln	Lys	Lys	Leu	Lys	Arg	Cys	Asp	Asp	Met	Asp	Thr
	50					55					60				
Phe	Phe	Leu	His	Tyr	Ala	Ala	Ala	Glu	Gly	Gln	Ile	Glu	Leu	Met	Glu
65					70					75					80
Lys	Ile	Thr	Arg	Asp	Ser	Ser	Leu	Glu	Val	Leu	His	Glu	Met	Asp	Asp
			85						90					95	
Tyr	Gly	Asn	Thr	Pro	Leu	His	Cys	Ala	Val	Glu	Lys	Asn	Gln	Ile	Glu
			100					105					110		
Ser	Val	Lys	Phe	Leu	Leu	Ser	Arg	Gly	Ala	Asn	Pro	Asn	Leu	Arg	Asn
		115					120					125			
Phe	Asn	Met	Met	Ala	Pro	Leu	His	Ile	Ala	Val	Gln	Gly	Met	Asn	Asn
	130					135					140				
Glu	Val	Met	Lys	Val	Leu	Leu	Glu	His	Arg	Thr	Ile	Asp	Val	Asn	Leu
145					150					155					160
Glu	Gly	Glu	Asn	Gly	Asn	Thr	Ala	Val	Ile	Ile	Ala	Cys	Thr	Thr	Asn
			165						170					175	
Asn	Ser	Glu	Ala	Leu	Gln	Ile	Leu	Leu	Lys	Lys	Gly	Ala	Lys	Pro	Cys
			180					185					190		
Lys	Ser	Asn	Lys	Trp	Gly	Cys	Phe	Pro	Ile	His	Gln	Ala	Ala	Phe	Ser
		195					200					205			
Gly	Ser	Lys	Glu	Cys	Met	Glu	Ile	Ile	Leu	Arg	Phe	Gly	Glu	Glu	His
	210					215					220				
Gly	Tyr	Ser	Arg	Gln	Leu	His	Ile	Asn	Phe	Met	Asn	Asn	Gly	Lys	Ala
225					230					235					240
Thr	Pro	Leu	His	Leu	Ala	Val	Gln	Asn	Gly	Asp	Leu	Glu	Met	Ile	Lys
			245						250					255	
Met	Cys	Leu	Asp	Asn	Gly	Ala	Gln	Ile	Asp	Pro	Val	Glu	Lys	Gly	Arg
		260						265					270		
Cys	Thr	Ala	Ile	His	Phe	Ala	Ala	Thr	Gln	Gly	Ala	Thr	Glu	Ile	Val
		275					280					285			
Lys	Leu	Met	Ile	Ser	Ser	Tyr	Ser	Gly	Ser	Val	Asp	Ile	Val	Asn	Thr
	290					295					300				
Thr	Asp	Gly	Cys	His	Glu	Thr	Met	Leu	His	Arg	Ala	Ser	Leu	Phe	Asp
305					310					315					320
His	His	Glu	Leu	Ala	Asp	Tyr	Leu	Ile	Ser	Val	Gly	Ala	Asp	Ile	Asn
			325						330					335	
Lys	Ile	Asp	Ser	Glu	Gly	Arg	Ser	Pro	Leu	Ile	Leu	Ala	Thr	Ala	Ser
			340					345					350		
Ala	Ser	Trp	Asn	Ile	Val	Asn	Leu	Leu	Leu	Ser	Lys	Gly	Ala	Gln	Val
		355					360					365			
Asp	Ile	Lys	Asp	Asn	Phe	Gly	Arg	Asn	Phe	Leu	His	Leu	Thr	Val	Gln
	370					375					380				
Gln	Pro	Tyr	Gly	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Phe	Met	Gln	Met	Gln
385					390					395					400
Gln	Ile	Lys	Glu	Leu	Val	Met	Asp	Glu	Asp	Asn	Asp	Gly	Cys	Thr	Pro
			405						410					415	

Leu	His	Tyr	Ala	Cys	Arg	Gln	Gly	Gly	Pro	Gly	Ser	Val	Asn	Asn	Leu	420	425	430
Leu	Gly	Phe	Asn	Val	Ser	Ile	His	Ser	Lys	Ser	Lys	Asp	Lys	Lys	Ser	435	440	445
Pro	Leu	His	Phe	Ala	Ala	Ser	Tyr	Gly	Arg	Ile	Asn	Thr	Cys	Gln	Arg	450	455	460
Leu	Leu	Gln	Asp	Ile	Ser	Asp	Thr	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Leu	465	470	475
His	Gly	Met	Thr	Pro	Leu	His	Leu	Ala	Ala	Lys	Asn	Gly	His	Asp	Lys	485	490	495
Val	Val	Gln	Leu	Leu	Leu	Lys	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asp	His	500	505	510
Asn	Gly	Trp	Thr	Ala	Leu	His	His	Ala	Ser	Met	Gly	Gly	Tyr	Thr	Gln	515	520	525
Thr	Met	Lys	Val	Ile	Leu	Asp	Thr	Asn	Leu	Lys	Cys	Thr	Asp	Arg	Leu	530	535	540
Asp	Glu	Asp	Gly	Asn	Thr	Ala	Leu	His	Phe	Ala	Ala	Arg	Glu	Gly	His	545	550	555
Ala	Lys	Ala	Val	Ala	Leu	Leu	Leu	Ser	His	Asn	Ala	Asp	Ile	Val	Leu	565	570	575
Asn	Lys	Gln	Gln	Ala	Ser	Phe	Leu	His	Leu	Ala	Leu	His	Asn	Lys	Arg	580	585	590
Lys	Glu	Val	Val	Leu	Thr	Ile	Ile	Arg	Ser	Lys	Arg	Trp	Asp	Glu	Cys	595	600	605
Leu	Lys	Ile	Phe	Ser	His	Asn	Ser	Pro	Gly	Asn	Lys	Cys	Pro	Ile	Thr	610	615	620
Glu	Met	Ile	Glu	Tyr	Leu	Pro	Glu	Cys	Met	Lys	Val	Leu	Leu	Asp	Phe	625	630	635
Cys	Met	Leu	His	Ser	Thr	Glu	Asp	Lys	Ser	Cys	Arg	Asp	Tyr	Tyr	Ile	645	650	655
Glu	Tyr	Asn	Phe	Lys	Tyr	Leu	Gln	Cys	Pro	Leu	Glu	Phe	Thr	Lys	Lys	660	665	670
Thr	Pro	Thr	Gln	Asp	Val	Ile	Tyr	Glu	Pro	Leu	Thr	Ala	Leu	Asn	Ala	675	680	685
Met	Val	Gln	Asn	Asn	Arg	Ile	Glu	Leu	Leu	Asn	His	Pro	Val	Cys	Lys	690	695	700
Glu	Tyr	Leu	Leu	Met	Lys	Trp	Leu	Ala	Tyr	Gly	Phe	Arg	Ala	His	Met	705	710	715
Met	Asn	Leu	Gly	Ser	Tyr	Cys	Leu	Gly	Leu	Ile	Pro	Met	Thr	Ile	Leu	725	730	735
Val	Val	Asn	Ile	Lys	Pro	Gly	Met	Ala	Phe	Asn	Ser	Thr	Gly	Ile	Ile	740	745	750
Asn	Glu	Thr	Ser	Asp	His	Ser	Glu	Ile	Leu	Asp	Thr	Thr	Asn	Ser	Tyr	755	760	765
Leu	Ile	Lys	Thr	Cys	Met	Ile	Leu	Val	Phe	Leu	Ser	Ser	Ile	Phe	Gly	770	775	780
Tyr	Cys	Lys	Glu	Ala	Gly	Gln	Ile	Phe	Gln	Gln	Lys	Arg	Asn	Tyr	Phe	785	790	795
Met	Asp	Ile	Ser	Asn	Val	Leu	Glu	Trp	Ile	Ile	Tyr	Thr	Thr	Gly	Ile	805	810	815
Ile	Phe	Val	Leu	Pro	Leu	Phe	Val	Glu	Ile	Pro	Ala	His	Leu	Gln	Trp	820	825	830
Gln	Cys	Gly	Ala	Ile	Ala	Val	Tyr	Phe	Tyr	Trp	Met	Asn	Phe	Leu	Leu	835	840	845
Tyr	Leu	Gln	Arg	Phe	Glu	Asn	Cys	Gly	Ile	Phe	Ile	Val	Met	Leu	Glu	850	855	860
Val	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Ser	Thr	Val	Val	Phe	Ile	Phe	Leu	865	870	875
Leu	Leu	Ala	Phe	Gly	Leu	Ser	Phe	Tyr	Ile	Leu	Leu	Asn	Leu	Gln	Asp	885	890	895

Pro	Phe	Ser	Ser	Pro	Leu	Leu	Ser	Ile	Ile	Gln	Thr	Phe	Ser	Met	Met
			900					905					910		
Leu	Gly	Asp	Ile	Asn	Tyr	Arg	Glu	Ser	Phe	Leu	Glu	Pro	Tyr	Leu	Arg
		915					920					925			
Asn	Glu	Leu	Ala	His	Pro	Val	Leu	Ser	Phe	Ala	Gln	Leu	Val	Ser	Phe
	930					935					940				
Thr	Ile	Phe	Val	Pro	Ile	Val	Leu	Met	Asn	Leu	Leu	Ile	Gly	Leu	Ala
945					950					955					960
Val	Gly	Asp	Ile	Ala	Glu	Val	Gln	Lys	His	Ala	Ser	Leu	Lys	Arg	Ile
			965						970					975	
Ala	Met	Gln	Val	Glu	Leu	His	Thr	Ser	Leu	Glu	Lys	Lys	Leu	Pro	Leu
			980					985					990		
Trp	Phe	Leu	Arg	Lys	Val	Asp	Gln	Lys	Ser	Thr	Ile	Val	Tyr	Pro	Asn
	995						1000					1005			
Lys	Pro	Arg	Ser	Gly	Gly	Met	Leu	Phe	Arg	Ile	Phe	Cys	Phe	Leu	Phe
	1010					1015				1020					
Cys	Thr	Gly	Glu	Ile	Arg	Gln	Glu	Ile	Pro	Asn	Ala	Asp	Lys	Ser	Leu
1025					1030					1035					1040
Glu	Met	Glu	Ile	Leu	Lys	Gln	Lys	Tyr	Arg	Leu	Lys	Asp	Leu	Thr	Phe
			1045					1050					1055		
Leu	Leu	Glu	Lys	Gln	His	Glu	Leu	Ile	Lys	Leu	Ile	Ile	Gln	Lys	Met
			1060					1065					1070		
Glu	Ile	Ile	Ser	Glu	Thr	Glu	Asp	Asp	Asp	Ser	His	Cys	Ser	Phe	Gln
	1075						1080					1085			
Asp	Arg	Phe	Lys	Lys	Glu	Gln	Met	Glu	Gln	Arg	Asn	Ser	Arg	Trp	Asn
	1090					1095				1100					
Thr	Val	Leu	Arg	Ala	Val	Lys	Ala	Lys	Thr	His	His	Leu	Glu	Pro	
1105					1110					1115					