

SEQUENCE LISTING

<110> Takasago International Corporation

<120> Citrus-like flavor composition, citrus flavored beverage

<130> P2551

<160> 4

<210> 1

<211> 945

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(945)

<400> 1

atg gct gaa agg aat tac acc gta gtg acg gag ttc ttc ctt act gca	48
Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala	
1 5 10 15	

ttt act gaa cat ctc cag tgg agg gtt cct ctc ttc ctc ata ttt ttg	96
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Phe Leu	
20 25 30	

agt ttc tat ctt gcc act atg tta ggg aac aca ggc atg atc ctc ctg	144
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu	
35 40 45	

atc cgt ggc gat cgt cgg ctc cac acc ccg atg tac ttc ttc ctc agc	192
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser	
50 55 60	

cac ctt tcc ttg gtg gac atc tgc tac tcg tcc gcc atc atc cct cag	240
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln	
65 70 75 80	

atg ctg gct gtg ctg tgg gag cac ggc aca acc atc tcc cag gct cgc	288
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg	
85 90 95	

tgt gca gct cag ttc ttc ctc ttc acc ttc ttt gcc tcc atc gac tgc	336
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys	
100 105 110	

tac ctt ctg gcc atc atg gcc tat gac cgc tac acg gcc gtg tgc cag	384
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Tyr	Leu	Leu	Ala	Ile	Met	Ala	Tyr	Asp	Arg	Tyr	Thr	Ala	Val	Cys	Gln		
115																120	125
ccc Pro	ctg Leu	ctt Leu	tat Tyr	gtc Val	acc Thr	atc Ile	ata Ile	acc Thr	gag Glu	aag Lys	gcc Ala	cgc Arg	tgg Trp	ggc Gly	cta Leu	432	
130																135	140
gtc Val	act Thr	ggg Gly	gct Ala	tac Tyr	gtt Val	gct Ala	ggg Gly	ttt Phe	ttc Phe	agt Ser	gcc Ala	ttt Phe	gtt Val	cga Arg	acg Thr	480	
145																150	155
gtc Val	aca Thr	gcc Ala	ttc Phe	act Thr	ctc Leu	tcc Ser	ttt Phe	tgt Cys	gga Gly	aac Asn	aat Asn	gag Glu	atc Ile	aac Asn	ttc Phe	528	
165																170	175
att Ile	ttc Phe	tgt Cys	gac Asp	ctc Leu	cct Pro	cct Pro	cta Leu	tta Leu	aaa Lys	ctc Leu	tcc Ser	tgt Cys	ggg Gly	gac Asp	agc Ser	576	
180																185	190
tac Tyr	act Thr	cag Gln	gaa Glu	gtg Val	gtg Val	att Ile	att Ile	gtg Val	ttt Phe	gct Ala	ctt Leu	ttc Phe	gtc Val	atg Met	cct Pro	624	
195																200	205
gcc Ala	tgt Cys	atc Ile	ttg Leu	gtg Val	atc Ile	ttg Leu	gta Val	tcc Ser	tac Tyr	ctg Leu	ttt Phe	atc Ile	att Ile	gtg Val	gcc Ala	672	
210																215	220
atc Ile	ctg Leu	cag Gln	atc Ile	cac His	tct Ser	gct Ala	gga Gly	ggc Gly	cgg Arg	gcc Ala	aag Lys	acc Thr	ttc Phe	tcc Ser	acc Thr	720	
225																230	235
tgc Cys	gcc Ala	tcc Ser	cac His	ctc Leu	act Thr	gcc Ala	gtc Val	gct Ala	ctt Leu	ttc Phe	ttt Phe	ggc Gly	acc Thr	ctc Leu	atc Ile	768	
245																250	255
ttc Phe	atg Met	tac Tyr	ctg Leu	cga Arg	gac Asp	aac Asn	aca Thr	ggc Gly	cag Gln	tcc Ser	tcc Ser	gag Glu	gga Gly	gac Asp	cga Arg	816	
260																265	270
gtg Val	gtg Val	tct Ser	gtg Val	ctc Leu	tac Tyr	acg Thr	gtg Val	gtg Val	acc Thr	cca Pro	atg Met	ctg Leu	aat Asn	ccc Pro	ctt Leu	864	
275																280	285
atc Ile	tat Tyr	agc Ser	ctg Leu	aga Arg	aac Asn	aag Lys	gag Glu	gta Val	aaa Lys	gag Glu	gcc Ala	act Thr	agg Arg	aaa Lys	gcc Ala	912	
290																295	300
ctg Leu	agc Ser	aaa Lys	tca Ser	aag Lys	cct Pro	gct Ala	aga Arg	aga Arg	ccc Pro	taa							945
305																310	

<210> 2
<211> 314
<212> PRT
<213> Homo sapiens

<400> 2

Met	Ala	Glu	Arg	Asn	Tyr	Thr	Val	Val	Thr	Glu	Phe	Phe	Leu	Thr	Ala
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Phe	Thr	Glu	His	Leu	Gln	Trp	Arg	Val	Pro	Leu	Phe	Leu	Ile	Phe	Leu
			20					25					30		
Ser	Phe	Tyr	Leu	Ala	Thr	Met	Leu	Gly	Asn	Thr	Gly	Met	Ile	Leu	Leu
		35					40					45			
Ile	Arg	Gly	Asp	Arg	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
His	Leu	Ser	Leu	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Ala	Ile	Ile	Pro	Gln
65					70					75					80
Met	Leu	Ala	Val	Leu	Trp	Glu	His	Gly	Thr	Thr	Ile	Ser	Gln	Ala	Arg
				85					90					95	
Cys	Ala	Ala	Gln	Phe	Phe	Leu	Phe	Thr	Phe	Phe	Ala	Ser	Ile	Asp	Cys
			100					105					110		
Tyr	Leu	Leu	Ala	Ile	Met	Ala	Tyr	Asp	Arg	Tyr	Thr	Ala	Val	Cys	Gln
		115					120					125			
Pro	Leu	Leu	Tyr	Val	Thr	Ile	Ile	Thr	Glu	Lys	Ala	Arg	Trp	Gly	Leu
	130					135					140				
Val	Thr	Gly	Ala	Tyr	Val	Ala	Gly	Phe	Phe	Ser	Ala	Phe	Val	Arg	Thr
145					150					155					160
Val	Thr	Ala	Phe	Thr	Leu	Ser	Phe	Cys	Gly	Asn	Asn	Glu	Ile	Asn	Phe
				165					170					175	
Ile	Phe	Cys	Asp	Leu	Pro	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Gly	Asp	Ser
			180					185					190		
Tyr	Thr	Gln	Glu	Val	Val	Ile	Ile	Val	Phe	Ala	Leu	Phe	Val	Met	Pro
		195					200					205			

Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
210 215 220

Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
225 230 235 240

Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
245 250 255

Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
260 265 270

Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
290 295 300

Leu Ser Lys Ser Lys Pro Ala Arg Arg Pro
305 310

<210> 3
<211> 1057
<212> DNA
<213> Bos taurus

<220>
<221> CDS
<222> (1)..(1047)

<400> 3
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acg ggc gtg gtg cgc agc ccc ttc gag gcc ccg cag tac tac ctg gcg 96
Thr Gly Val Val Arg Ser Pro Phe Glu Ala Pro Gln Tyr Tyr Leu Ala
20 25 30

gag cca tgg cag ttc tcc atg ctg gcc gcc tac atg ttc ctg ctg atc 144
Glu Pro Trp Gln Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile
35 40 45

atg ctt ggc ttc ccc atc aac ttc ctc acg ctg tac gtc aca gtc cag 192
Met Leu Gly Phe Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln
50 55 60

cac aag aag ctg cgc aca ccc ctc aac tac atc ctg ctc aac ctg gcc	240
His Lys Lys Leu Arg Thr Pro Leu Asn Tyr Ile Leu Leu Asn Leu Ala	
65 70 75 80	
gtg gcc gac ctc ttc atg gtc ttc ggg ggc ttc acc acc acc ctc tac	288
Val Ala Asp Leu Phe Met Val Phe Gly Gly Phe Thr Thr Thr Leu Tyr	
85 90 95	
acc tct ctg cac gga tac ttc gtc ttt ggg ccc acg ggc tgc aac ctg	336
Thr Ser Leu His Gly Tyr Phe Val Phe Gly Pro Thr Gly Cys Asn Leu	
100 105 110	
gag ggc ttc ttt gcc acc ctg ggc ggt gaa att gca ctg tgg tcc ttg	384
Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp Ser Leu	
115 120 125	
gtg gtc ctg gcc atc gag cgg tac gtg gtg gtg tgc aag ccc atg agc	432
Val Val Leu Ala Ile Glu Arg Tyr Val Val Val Cys Lys Pro Met Ser	
130 135 140	
aac ttc cgc ttc ggg gag aac cac gcc atc atg ggc gtc gcc ttc acc	480
Asn Phe Arg Phe Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr	
145 150 155 160	
tgg gtc atg gct ctg gcc tgt gcc gcg ccc ccc ctc gtc ggc tgg tcc	528
Trp Val Met Ala Leu Ala Cys Ala Ala Pro Pro Leu Val Gly Trp Ser	
165 170 175	
agg tac atc ccg gag ggc atg cag tgc tcg tgc ggg att gac tac tac	576
Arg Tyr Ile Pro Glu Gly Met Gln Cys Ser Cys Gly Ile Asp Tyr Tyr	
180 185 190	
acg ccc cac gag gag acc aac aat gag tcg ttc gtc atc tac atg ttc	624
Thr Pro His Glu Glu Thr Asn Asn Glu Ser Phe Val Ile Tyr Met Phe	
195 200 205	
gtg gtc cac ttc atc atc ccc ctg att gtc ata ttc ttc tgc tac ggg	672
Val Val His Phe Ile Ile Pro Leu Ile Val Ile Phe Phe Cys Tyr Gly	
210 215 220	
cag ctg gtg ttc acc gtc aag gag gcg gct gcc cag cag cag gag tcg	720
Gln Leu Val Phe Thr Val Lys Glu Ala Ala Ala Gln Gln Gln Glu Ser	
225 230 235 240	
gcc acc act cag aag gcc gag aag gag gtc acc cgc atg gtg atc atc	768
Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Ile Ile	
245 250 255	
atg gtc atc gct ttc cta atc tgc tgg ctg ccc tac gct ggg gtg gcg	816
Met Val Ile Ala Phe Leu Ile Cys Trp Leu Pro Tyr Ala Gly Val Ala	

260	265	270	
ttc tac atc ttc acc cat cag ggc tct gac ttt ggc ccc atc ttc atg			864
Phe Tyr Ile Phe Thr His Gln Gly Ser Asp Phe Gly Pro Ile Phe Met			
275	280	285	
acc atc ccg gct ttc ttt gcc aag act tct gcc gtc tac aac ccc gtc			912
Thr Ile Pro Ala Phe Phe Ala Lys Thr Ser Ala Val Tyr Asn Pro Val			
290	295	300	
atc tac atc atg atg aac aag cag ttc cgg aac tgc atg gtc acc act			960
Ile Tyr Ile Met Met Asn Lys Gln Phe Arg Asn Cys Met Val Thr Thr			
305	310	315	320
ctc tgc tgt ggc aag aac ccg ctg ggt gac gac gag gcc tcc acc acc			1008
Leu Cys Cys Gly Lys Asn Pro Leu Gly Asp Asp Glu Ala Ser Thr Thr			
325	330	335	
gtc tcc aag aca gag acc agc cag gtg gcg cct gcc taa gccctccag			1057
Val Ser Lys Thr Glu Thr Ser Gln Val Ala Pro Ala			
340	345		

<210> 4
 <211> 348
 <212> PRT
 <213> Bos taurus

<400> 4

Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys
1 5 10 15

Thr Gly Val Val Arg Ser Pro Phe Glu Ala Pro Gln Tyr Tyr Leu Ala
20 25 30

Glu Pro Trp Gln Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile
35 40 45

Met Leu Gly Phe Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln
50 55 60

His Lys Lys Leu Arg Thr Pro Leu Asn Tyr Ile Leu Leu Asn Leu Ala
65 70 75 80

Val Ala Asp Leu Phe Met Val Phe Gly Gly Phe Thr Thr Thr Leu Tyr
85 90 95

Thr Ser Leu His Gly Tyr Phe Val Phe Gly Pro Thr Gly Cys Asn Leu
100 105 110

Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp Ser Leu
115 120 125

Val Val Leu Ala Ile Glu Arg Tyr Val Val Val Cys Lys Pro Met Ser
130 135 140

Asn Phe Arg Phe Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr
145 150 155 160

Trp Val Met Ala Leu Ala Cys Ala Ala Pro Pro Leu Val Gly Trp Ser
165 170 175

Arg Tyr Ile Pro Glu Gly Met Gln Cys Ser Cys Gly Ile Asp Tyr Tyr
180 185 190

Thr Pro His Glu Glu Thr Asn Asn Glu Ser Phe Val Ile Tyr Met Phe
195 200 205

Val Val His Phe Ile Ile Pro Leu Ile Val Ile Phe Phe Cys Tyr Gly
210 215 220

Gln Leu Val Phe Thr Val Lys Glu Ala Ala Ala Gln Gln Gln Glu Ser
225 230 235 240

Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Ile Ile
245 250 255

Met Val Ile Ala Phe Leu Ile Cys Trp Leu Pro Tyr Ala Gly Val Ala
260 265 270

Phe Tyr Ile Phe Thr His Gln Gly Ser Asp Phe Gly Pro Ile Phe Met
275 280 285

Thr Ile Pro Ala Phe Phe Ala Lys Thr Ser Ala Val Tyr Asn Pro Val
290 295 300

Ile Tyr Ile Met Met Asn Lys Gln Phe Arg Asn Cys Met Val Thr Thr
305 310 315 320

Leu Cys Cys Gly Lys Asn Pro Leu Gly Asp Asp Glu Ala Ser Thr Thr
325 330 335

Val Ser Lys Thr Glu Thr Ser Gln Val Ala Pro Ala
340 345