

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=9; day=18; hr=8; min=1; sec=24; ms=657;]

=====

Application No: 12100088

Version No: 2.1

Input Set:

Output Set:

Started: 2009-09-18 07:59:14.046

Finished: 2009-09-18 07:59:24.617

Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 571 ms

Total Warnings: 0

Total Errors: 75

No. of SeqIDs Defined: 221

Actual SeqID Count: 221

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 300	Invalid codon found Thr SEQID (3) POS: 193
E 300	Invalid codon found Tyr SEQID (3) POS: 196
E 300	Invalid codon found Ile SEQID (3) POS: 199
E 300	Invalid codon found Ser SEQID (3) POS: 202
E 300	Invalid codon found Asn SEQID (3) POS: 205
E 300	Invalid codon found Ser SEQID (3) POS: 208
E 300	Invalid codon found Asp SEQID (3) POS: 211
E 300	Invalid codon found Leu SEQID (3) POS: 214
E 300	Invalid codon found Gln SEQID (3) POS: 217
E 300	Invalid codon found Arg SEQID (3) POS: 220
E 300	Invalid codon found Cys SEQID (3) POS: 223
E 300	Invalid codon found Val SEQID (3) POS: 226
E 300	Invalid codon found Asn SEQID (3) POS: 229
E 300	Invalid codon found Leu SEQID (3) POS: 232
E 300	Invalid codon found Gln SEQID (3) POS: 235
E 300	Invalid codon found Ala SEQID (3) POS: 238
E 323	Invalid/missing amino acid numbering SEQID (3) POS (244)
E 355	Empty lines found between the amino acid numbering and the

Input Set:

Output Set:

Started: 2009-09-18 07:59:14.046
Finished: 2009-09-18 07:59:24.617
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 571 ms
Total Warnings: 0
Total Errors: 75
No. of SeqIDs Defined: 221
Actual SeqID Count: 221

Error code	Error Description
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 300	Invalid codon found Arg SEQID (3) POS: 961
E 300	Invalid codon found Phe SEQID (3) POS: 964
E 300	Invalid codon found Tyr SEQID (3) POS: 967
E 300	Invalid codon found Leu SEQID (3) POS: 970 This error has occurred more than 20 times, will not be displayed
E 323	Invalid/missing amino acid numbering SEQID (3) POS (1009)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 323	Invalid/missing amino acid numbering SEQID (3) POS (1789)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (33)

SEQUENCE LISTING

<110> Hardiman, Gerard T.
 Rock, Fernando L.
 Bazan, J. Fernando
 Kastelein, Robert A.
 Ho, Stephen W.K.
 Liu, Yong-Jun

<120> HUMAN DNAX TOLL-LIKE RECEPTOR 4 PROTEINS, RELATED REAGENTS AND METHODS

<130> DX0724XK1D

<140> 12/100,088
 <141> 2008-04-09

<150> 11/844,179
 <151> 2007-08-23

<150> 10/975,909
 <151> 2004-10-28

<150> 09/950,041
 <151> 2001-09-10

<150> 09/728,540
 <151> 2000-11-28

<150> 60/207,558
 <151> 2000-05-25

<150> 09/073,363
 <151> 1998-05-06

<150> 60/076,947
 <151> 1998-03-05

<150> 60/072,212
 <151> 1998-01-22

<150> 60/044,293
 <151> 1997-05-07

<160> 221

<170> PatentIn version 3.3

<210> 1
 <211> 2367
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2358)

<220>

<221> mat_peptide

<222> (67)..()

<400> 1

atg act agc atc ttc cat ttt gcc att atc ttc atg tta ata ctt cag	48
Met Thr Ser Ile Phe His Phe Ala Ile Ile Phe Met Leu Ile Leu Gln	
-20 -15 -10	

atc aga ata caa tta tct gaa gaa agt gaa ttt tta gtt gat agg tca	96
Ile Arg Ile Gln Leu Ser Glu Glu Ser Glu Phe Leu Val Asp Arg Ser	
-5 -1 1 5 10	

aaa aac ggt ctc atc cac gtt cct aaa gac cta tcc cag aaa aca aca	144
Lys Asn Gly Leu Ile His Val Pro Lys Asp Leu Ser Gln Lys Thr Thr	
15 20 25	

atc tta aat ata tcg caa aat tat ata tct gag ctt tgg act tct gac	192
Ile Leu Asn Ile Ser Gln Asn Tyr Ile Ser Glu Leu Trp Thr Ser Asp	
30 35 40	

atc tta tca ctg tca aaa ctg agg att ttg ata att tct cat aat aga	240
Ile Leu Ser Leu Ser Lys Leu Arg Ile Leu Ile Ile Ser His Asn Arg	
45 50 55	

atc cag tat ctt gat atc agt gtt ttc aaa ttc aac cag gaa ttg gaa	288
Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu	
60 65 70	

tac ttg gat ttg tcc cac aac aag ttg gtg aag att tct tgc cac cct	336
Tyr Leu Asp Leu Ser His Asn Lys Leu Val Lys Ile Ser Cys His Pro	
75 80 85 90	

act gtg aac ctc aag cac ttg gac ctg tca ttt aat gca ttt gat gcc	384
Thr Val Asn Leu Lys His Leu Asp Leu Ser Phe Asn Ala Phe Asp Ala	
95 100 105	

ctg cct ata tgc aaa gag ttt ggc aat atg tct caa cta aaa ttt ctg	432
Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu	
110 115 120	

ggg ttg agc acc aca cac tta gaa aaa tct agt gtg ctg cca att gct	480
Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala	
125 130 135	

cat ttg aat atc agc aag gtc ttg ctg gtc tta gga gag act tat ggg	528
His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly	
140 145 150	

gaa aaa gaa gac cct gag ggc ctt caa gac ttt aac act gag agt ctg	576
Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu	
155 160 165 170	

cac att gtg ttc ccc aca aac aaa gaa ttc cat ttt att ttg gat gtg	624
His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val	
175 180 185	

tca gtc aag act gta gca aat ctg gaa cta tct aat atc aaa tgt gtg	672
Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val	
190 195 200	
cta gaa gat aac aaa tgt tct tac ttc cta agt att ctg gcg aaa ctt	720
Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu	
205 210 215	
caa aca aat cca aag tta tca agt ctt acc tta aac aac att gaa aca	768
Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr	
220 225 230	
act tgg aat tct ttc att agg atc ctc caa cta gtt tgg cat aca act	816
Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr	
235 240 245 250	
gta tgg tat ttc tca att tca aac gtg aag cta cag ggt cag ctg gac	864
Val Trp Tyr Phe Ser Ile Ser Asn Val Lys Leu Gln Gly Gln Leu Asp	
255 260 265	
ttc aga gat ttt gat tat tct ggc act tcc ttg aag gcc ttg tct ata	912
Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile	
270 275 280	
cac caa gtt gtc agc gat gtg ttc ggt ttt ccg caa agt tat atc tat	960
His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr	
285 290 295	
gaa atc ttt tcg aat atg aac atc aaa aat ttc aca gtg tct ggt aca	1008
Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr	
300 305 310	
cgc atg gtc cac atg ctt tgc cca tcc aaa att agc ccg ttc ctg cat	1056
Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His	
315 320 325 330	
ttg gat ttt tcc aat aat ctc tta aca gac acg gtt ttt gaa aat tgt	1104
Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys	
335 340 345	
ggg cac ctt act gag ttg gag aca ctt att tta caa atg aat caa tta	1152
Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu	
350 355 360	
aaa gaa ctt tca aaa ata gct gaa atg act aca cag atg aag tct ctg	1200
Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu	
365 370 375	
caa caa ttg gat att agc cag aat tct gta agc tat gat gaa aag aaa	1248
Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys	
380 385 390	
gga gac tgt tct tgg act aaa agt tta tta agt tta aat atg tct tca	1296
Gly Asp Cys Ser Trp Thr Lys Ser Leu Leu Ser Leu Asn Met Ser Ser	
395 400 405 410	
aat ata ctt act gac act att ttc aga tgt tta cct ccc agg atc aag	1344

Asn Ile Leu Thr Asp Thr Ile Phe Arg Cys Leu Pro Pro Arg Ile Lys	
415 420 425	
gta ctt gat ctt cac agc aat aaa ata aag agc att cct aaa caa gtc	1392
Val Leu Asp Leu His Ser Asn Lys Ile Lys Ser Ile Pro Lys Gln Val	
430 435 440	
gta aaa ctg gaa gct ttg caa gaa ctc aat gtt gct ttc aat tct tta	1440
Val Lys Leu Glu Ala Leu Gln Glu Leu Asn Val Ala Phe Asn Ser Leu	
445 450 455	
act gac ctt cct gga tgt ggc agc ttt agc agc ctt tct gta ttg atc	1488
Thr Asp Leu Pro Gly Cys Gly Ser Phe Ser Ser Leu Ser Val Leu Ile	
460 465 470	
att gat cac aat tca gtt tcc cac cca tca gct gat ttc ttc cag agc	1536
Ile Asp His Asn Ser Val Ser His Pro Ser Ala Asp Phe Phe Gln Ser	
475 480 485 490	
tgc cag aag atg agg tca ata aaa gca ggg gac aat cca ttc caa tgt	1584
Cys Gln Lys Met Arg Ser Ile Lys Ala Gly Asp Asn Pro Phe Gln Cys	
495 500 505	
acc tgt gag ctc gga gaa ttt gtc aaa aat ata gac caa gta tca agt	1632
Thr Cys Glu Leu Gly Glu Phe Val Lys Asn Ile Asp Gln Val Ser Ser	
510 515 520	
gaa gtg tta gag ggc tgg cct gat tct tat aag tgt gac tac ccg gaa	1680
Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys Cys Asp Tyr Pro Glu	
525 530 535	
agt tat aga gga acc cta cta aag gac ttt cac atg tct gaa tta tcc	1728
Ser Tyr Arg Gly Thr Leu Leu Lys Asp Phe His Met Ser Glu Leu Ser	
540 545 550	
tgc aac ata act ctg ctg atc gtc acc atc gtt gcc acc atg ctg gtg	1776
Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val	
555 560 565 570	
ttg gct gtg act gtg acc tcc ctc tgc atc tac ttg gat ctg ccc tgg	1824
Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr Leu Asp Leu Pro Trp	
575 580 585	
tat ctc agg atg gtg tgc cag tgg acc cag acc cgg cgc agg gcc agg	1872
Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg Arg Ala Arg	
590 595 600	
aac ata ccc tta gaa gaa ctc caa aga aat ctc cag ttt cat gca ttt	1920
Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe	
605 610 615	
att tca tat agt ggg cac gat tct ttc tgg gtg aag aat gaa tta ttg	1968
Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu	
620 625 630	
cca aac cta gag aaa gaa ggt atg cag att tgc ctt cat gag aga aac	2016
Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn	

635	640	645	650	
ttt gtt cct ggc aag agc att gtg gaa aat atc atc acc tgc att gag				2064
Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr Cys Ile Glu				
655		660	665	
aag agt tac aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag agt				2112
Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser				
670	675		680	
gaa tgg tgc cat tat gaa ctc tac ttt gcc cat cac aat ctc ttt cat				2160
Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His				
685	690		695	
gaa gga tct aat agc tta atc ctg atc ttg ctg gaa ccc att ccg cag				2208
Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln				
700	705		710	
tac tcc att cct agc agt tat cac aag ctc aaa agt ctc atg gcc agg				2256
Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg				
715	720	725	730	
agg act tat ttg gaa tgg ccc aag gaa aag agc aaa cgt ggc ctt ttt				2304
Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe				
735	740		745	
tgg gct aac tta agg gca gcc att aat att aag ctg aca gag caa gca				2352
Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala				
750	755		760	
aag aaa tagtctaga				2367
Lys Lys				

<210> 2
 <211> 786
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Thr Ser Ile Phe His Phe Ala Ile Ile Phe Met Leu Ile Leu Gln
-20 -15 -10

Ile Arg Ile Gln Leu Ser Glu Glu Ser Glu Phe Leu Val Asp Arg Ser
-5 -1 1 5 10

Lys Asn Gly Leu Ile His Val Pro Lys Asp Leu Ser Gln Lys Thr Thr
15 20 25

Ile Leu Asn Ile Ser Gln Asn Tyr Ile Ser Glu Leu Trp Thr Ser Asp
30 35 40

Ile	Leu	Ser	Leu	Ser	Lys	Leu	Arg	Ile	Leu	Ile	Ile	Ser	His	Asn	Arg	45	50	55
Ile	Gln	Tyr	Leu	Asp	Ile	Ser	Val	Phe	Lys	Phe	Asn	Gln	Glu	Leu	Glu	60	65	70
Tyr	Leu	Asp	Leu	Ser	His	Asn	Lys	Leu	Val	Lys	Ile	Ser	Cys	His	Pro	75	80	85
Thr	Val	Asn	Leu	Lys	His	Leu	Asp	Leu	Ser	Phe	Asn	Ala	Phe	Asp	Ala	95	100	105
Leu	Pro	Ile	Cys	Lys	Glu	Phe	Gly	Asn	Met	Ser	Gln	Leu	Lys	Phe	Leu	110	115	120
Gly	Leu	Ser	Thr	Thr	His	Leu	Glu	Lys	Ser	Ser	Val	Leu	Pro	Ile	Ala	125	130	135
His	Leu	Asn	Ile	Ser	Lys	Val	Leu	Leu	Val	Leu	Gly	Glu	Thr	Tyr	Gly	140	145	150
Glu	Lys	Glu	Asp	Pro	Glu	Gly	Leu	Gln	Asp	Phe	Asn	Thr	Glu	Ser	Leu	155	160	165
His	Ile	Val	Phe	Pro	Thr	Asn	Lys	Glu	Phe	His	Phe	Ile	Leu	Asp	Val	175	180	185
Ser	Val	Lys	Thr	Val	Ala	Asn	Leu	Glu	Leu	Ser	Asn	Ile	Lys	Cys	Val	190	195	200
Leu	Glu	Asp	Asn	Lys	Cys	Ser	Tyr	Phe	Leu	Ser	Ile	Leu	Ala	Lys	Leu	205	210	215
Gln	Thr	Asn	Pro	Lys	Leu	Ser	Ser	Leu	Thr	Leu	Asn	Asn	Ile	Glu	Thr	220	225	230
Thr	Trp	Asn	Ser	Phe	Ile	Arg	Ile	Leu	Gln	Leu	Val	Trp	His	Thr	Thr	235	240	245
Val	Trp	Tyr	Phe	Ser	Ile	Ser	Asn	Val	Lys	Leu	Gln	Gly	Gln	Leu	Asp	255	260	265

Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile
270 275 280

His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr
285 290 295

Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr
300 305 310

Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His
315 320 325 330

Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys
335 340 345

Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu
350 355 360

Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu
365 370 375

Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys
380 385 390

Gly Asp Cys Ser Trp Thr Lys Ser Leu Leu Ser Leu Asn Met Ser Ser
395 400 405 410

Asn Ile Leu Thr Asp Thr Ile Phe Arg Cys Leu Pro Pro Arg Ile Lys
415 420 425

Val Leu Asp Leu His Ser Asn Lys Ile Lys Ser Ile Pro Lys Gln Val
430 435 440

Val Lys Leu Glu Ala Leu Gln Glu Leu Asn Val Ala Phe Asn Ser Leu
445 450 455

Thr Asp Leu Pro Gly Cys Gly Ser Phe Ser Ser Leu Ser Val Leu Ile
460 465 470

Ile Asp His Asn Ser Val Ser His Pro Ser Ala Asp Phe Phe Gln Ser
475 480 485 490

Cys Gln Lys Met Arg Ser Ile Lys Ala Gly Asp Asn Pro Phe Gln Cys

495

500

505

Thr Cys Glu Leu Gly Glu Phe Val Lys Asn Ile Asp Gln Val Ser Ser
510 515 520

Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys Cys Asp Tyr Pro Glu
525 530 535

Ser Tyr Arg Gly Thr Leu Leu Lys Asp Phe His Met Ser Glu Leu Ser
540 545 550

Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val
555 560 565 570

Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr Leu Asp Leu Pro Trp
575 580 585

Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg Arg Ala Arg
590 595 600

Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe
605 610 615

Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu
620 625 630

Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn
635 640 645 650

Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr Cys Ile Glu
655 660 665

Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser
670 675 680