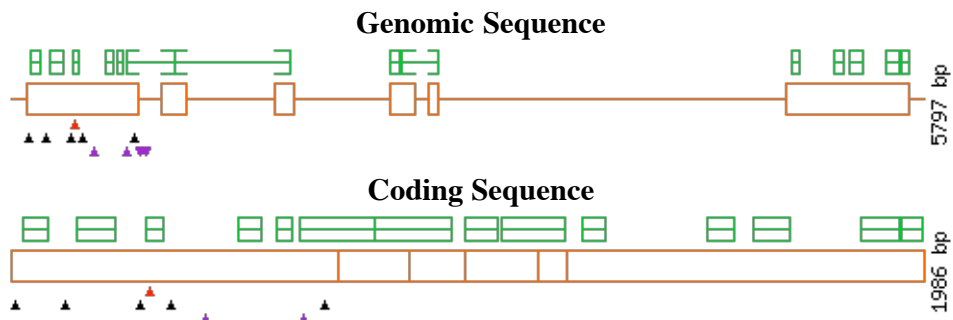


eomes

IPB001699, IPB002070, IPB003846, and User BLOCKs



For help interpreting these results, view the [PARSENP Introduction](#) page.

#	View On Sequence	Nucleotide Change	Effect	Restriction Enzyme Differences from REBASE		PSSM Difference	SIFT Score	Description	Zygoty
				Gained in Variant	Lost from Reference				
1	G C	A109T	L3F				0.00	7093	Homo
2	G C	A219G	Q40R	FinI			0.19	1027	Homo
3	G C	T381C	L94P	MnII	AluI , BseSI , HgiAI , SacI		0.10	4990	Homo
4	G C	C400A	Y100*					5345	Homo
5	G C	A447T	Q116L				0.21	6815	Homo
6	G C	G523A	S141=		TaqI			4453	Homo
7	G C	T736C	V212=					1257	Homo
8	G C	A780C	Q227P	FokI , MmeI		13.0	0.01	7767	Homo
9	G	A822T	Intron	AvaIII , CviRI , SfaNI	TspDTI			5447	Homo
10	G	A853T	Intron		BspHI , Hinfl , Hpy178III , Tfil			4242	Homo

[Download Tab-Separated table](#)

[View Variants on 3D Structure](#)

No [protein homology model](#) was submitted. You may add one using any or all of the fields below.

Blocks Families:

Blocks File: no file selected

Sequence Alignment: no file selected

-OR-

Genomic Sequence

ggtaagctgcggggcgcacggagccgcgtcctggtgtgatctacttgatctccgccttgctttccactgat 0
 72

User BLOCK 1 (4.6e-19) IC 2.73
 M Q L E S I L P G A S 11
 cctcatccctttatcagcacagtgaaga atg cag tta gaa agc atc ctc cct ggc gca tct 133
 tL3F[1]

V N L P K T F Y N L S S S S E S T N 29
 gta aac tta ccc aag acc ttc tac aac ctg tcc tca tcc tcc gaa agc acc aat 187

N S P G S T Q I D F Q D M D R T D S 47
 aat agc ccg ggg tca acg cag atc gac ttt cag gac atg gac cgg acg gat tcg 241
 gQ40R[2]

User BLOCK 2 (2.6e-20) IC 2.46
 E O S S G A K K F L M D D A D S E S 65
 gag cag agt tct ggt gcc aag aag ttt ctg atg gat gat gct gac agt gag agc 295

F T G T K A A A A A T A A P D A R K 83
 ttt acc ggg act aaa gca gca gca gca gcc acc gcc gca ccg gac gcg cgt aaa 349

User BLOCK 3 (5.7e-11) IC 2.17
 S S P V I G A D D E L S S T R R Y N 101
 agt tct ccg gtg atc ggc gcg gat gat gag ctc tcc agc acc cgc aga tac aac 403
 cL94P[3] aY100*[4]

I D D L G T D R Y F I S S S Q P S S 119
 atc gat gat ctg ggc act gat cga tac ttc ata tcg tcc tct caa ccg agt tct 457
 tQ116L[5]

D V A N P C S L F P Y G G Q T G S V 137
 gac gtg gcc aac cct tgc tct ctg ttc ccg tac gga ggg cag acc ggg tcg gtg 511

Y S G S N G S R Y S S S L H Y G S V 155
 tac agc ggc tcg aat ggc tcc ccg tat tcg tcg tct ctg cat tac ggt tcg gtt 565
 aS141=[6]

User BLOCK 4 (1.3e-16) IC 2.38
 L P P A G F S S A V C A S R S O F G 173
 ctt cca ccc gcc ggg ttc tca tcc gcc gtg tgc gcc agc agg agt cag ttt ggg 619

G G Y O F G O G P G C L Y P S Y P G 191
 ggt ggt tat cag ttc gga cag ggt ccc ggg tgt ctg tac ccg tcc tat ccc ggt 673

User BLOCK 5 (9.2e-10) IC 2.33
 P G S S L S S M P I P G S G S A A R 209
 cca ggc tcc agt ctc agc tcg atg ccc att cca ggt tcg ggc tcc gcg gcg cgg 727

User BLOCK 6 (7.7e-67) IC 4.24

A O V Y L C N R P L W L K F H R H O 227
gcg cag gtt tac ctg tgc aac aga ccg ctg tgg ctc aaa ttt cac cgc cat caa 781
cV212=[7] cQ227P[8]

T E M I I T K O G R 237
act gag atg atc ata act aaa cag ggc ag gtaagaaatgaagcattacaaatattttaaact 843
t[9]

gagatcatgattcaaacattgaataaaattgtttagcagaagtgcgtaacgaatattaattttccttcagt 237
t[10] 915

R M F P F L S 244
gcgtaatggaattttaatggtttaaattgtgtattcccag g cga atg ttc ccc ttt ctg agt 977

F N I T G L N L T A H Y N V F V E I 262
ttt aat atc act gga ctg aac ctg act gcg cat tat aat gtg ttt gtg gag att 1031

User BLOCK 7 (7.7e-73) IC 4.32
V L A D P N H W R F O G G K W V T C 280
gtt ctg gcc gat ccg aac cac tgg aga ttt cag ggc gga aag tgg gtg acc tgc 1085

G K A D N N M O G 289
ggg aaa gcg gac aac aac atg caa g gtgagagaattaaatgtaaataatttgagcaaata 1148

289
aaacagcctgtaaacactgtgtcaaattgtttcatctccgacaaagactgtattaaattaaattgtttaa 1220

289
aacaatttaataaaacgaaaatctaagttggatattcgattttaattttcgttcgatgcttttattgataat 1292

289
cgaagtaaataattaaattaacatcgaagatttttttagttttaatacaaacgaaatgcacaaactgaaacg 1364

289
aatttttttattagattaaaacttgaatgtcgggatccgaaaatacttttagatgcgcaaaattgtttgttt 1436

289
aataaattcgatgttttttaaaatccctgacatgtcattcggtttaaaaatgagtttcatttaaaacgcaag 1508

289
cgatctgcagagatgacacctgacagcgcgggggtggatgtgttattttcctttaagtattagaattaatct 1580

289
aaacaaatcttcttagtcatgatgcatctgttttagtttttctaattgatattttcactggacgggtgtttaag 1652

N K V Y V H P E S P N 300
ttcatcgatgcattttttctttcag ga aac aag gtg tat gtt cac cca gag tca cca aac 1712

T G A H W M R O E I S F G K L K L T 318
act gga gcg cac tgg atg aga caa gaa ata tct ttc gga aaa ctg aag cta acc 1766

<u>N</u> N K G A N N N N T Q	329
aac aac aaa gga gca aat aac aac aat act cag gtaaacaattaatatagcagcaatgctc	1827
	329
attgtttaaatgtaagccatgtttaatttagcgggtgttgatggagaaaatagttataaatgcacaaacatg	1899
	329
agctcttggtgtttttggtttattgcactttttttcaatttaagcagacttttaattatgttaatgtagtaa	1971
	329
tatttaatttctaattctaaaaagccacacagatgatctaaatgtaaagcagaacgtttaaacggtgtagg	2043
	329
ttgatttgaaatgttaaaaatatttagatttttcaatatatttaactcaatattggcttgaacaagccagca	2115
	329
tttttagagtggtctattttctacggttcacttgattttcttcttacacagaaagctctttgtgattgtgatat	2187
	329
atgtgctgttacaagaactgatgcctcttgcacatttttaagataaagatgagtggtgaggtgggtaga	2259
	329
agtgtgtgtgtgtgtagaaacttccagtcactcctcaaaggccttcgggtgtggctttgacacctctaactgcaa	2331
	User BLOCK 8 (4.8e-31) IC 3.90
gtgctggcctgaactctgcaaactcatatgtgtctctctctctgtgtgtgtgtgtgttaaaacag atg	2402
	<u>M</u> 330
	2402
<u>I V L O S L H K Y O P R L H I V E V</u>	348
att gtc ctg cag tcc ctg cat aag tac cag cct cgg ctt cac att gtg gag gtg	2456
	User BLOCK 9 (6.9e-56) IC 4.32
<u>T E D G V</u> E D M <u>S S E A K T O T F T</u>	366
act gag gac ggt gtg gag gac atg agc agc gaa gct aaa aca cag acc ttc act	2510
<u>F P E N O F I A V T A Y O N T D</u>	382
ttc cct gaa aac cag ttc atc gct gta acg gct tac caa aac aca gac gtaagcag	2566
	382
aacgtcctccacaacacacacttgcacacacacttctgcatttgagccgcttctgagatcctgctgtttttg	2638
	396
tgtttaattgcag atc aca cag ctc aag atc gac cac aac ccc ttt gca aaa ggc	2693
	403
<u>F R D N Y D</u> S	403
ttc agg gac aat tat gat tc gtaagtgcatttccgagaacttccggaacgtccgaatgatgcacgt	2758
	403
ttctttacatttataagcagcaaaatgttagaactttgagaattaatgcgcaaccattatcatcatgcatgc	2830
	403
attgatattcaacaatgcaatgttttgaagctgtctgttgataagtctgactatttactatatttgtaata	2902

tagcaagtgtaagttagttaatgcattacctaataattgagctattatTTTTTTattaatacaaatgcaactgt	403 2974
tgcaaaatacaacaattattgcatcagttgaaataaaaaaaaaactaagttatataactaataatgcacaca	403 3046
aaagcatactcattagctctcaagtgcctgctcaatataatTTTtatataataaaaaatgaaaaacaatata	403 3118
tatgagaagagttcagacacagaagcctcttcattcaacataaattaaaatttactcgaactaaacataaaa	403 3190
taaatgctcattttagaagatTTTTTTTTgtgtgcacttggaggcaatacaaaaagaaaagtgctttagtata	403 3262
taataaatattgaagaaattactttctcatttcagttcatgcacacaaaagcagcacatcagtctcaagt	403 3334
gggtgctcaataaaatggtaaaatttcagttcttgtaatgaataattaacttgactaatgggactTTTT	403 3406
tgctgtattacgaacaatagtcctgcacttatataacatatagtcctgcatattgcattgctgtatataaat	403 3478
gcaggccagatgaaaagtgctcatgcaaaacaaatgcttTTTTTTTTggctctcatttaagaactgaaatga	403 3550
tctgaaatcctaaaagctaattaattcccttgctgatggtgaagctggtgtgattaggtttgaagtgagct	403 3622
aataatgaacagttgcattaactataaatgaggatttaattggttactatattaatacaaatgcaactgttc	403 3694
attattactttacatcagctcaggtttaatgaacaacagcttcaagatctgctaaatttatagatTTTTat	403 3766
aagtattgattaagattcatctgacatgcattaatatgcaacaatgcattgcttcaattcttttgtgcaatt	403 3838
acaggactatttactatataaataacaggtcctgttagtgcaagttatttaaatgcattaataaaaactgaac	403 3910
agtatatttattttatcaatttatatttggtatcaagcaccatttgagactgatgtgcatgcttttgtgtg	403 3982
catgagctaaaattgagtaggtaatttgcttctatatctttatacaaatcaactgttatacaaatgcaact	403 4054
aactaatgcagtggttctcaaactgtggtacgtgtaccacaagtggtacggaggcttcttttagtggtacgc	403 4126

ggaggaatgaaatatgtcatgtacatgctacacacatttataaaatgtatcaaaaatgatggatataatatgc 403
 4198

 catatatgacatatagcctatatttctgaggtaatctgccacgtttttttaactgtgcagagttgtagctgc 403
 4270

 tttattgggcctacgacgctactttatttcaatactgctcattttgggtggtacttggagaaacaattttttt 403
 4342

 ctgaggtggtacttggatgaaaaaagtttgagaaccactgaactaatgcattatatacatacactggtttggg 403
 4414

 tatatatatatatatatatatatatatatatatacacacacatagatatgtatgtacgtatgtgtgtgta 403
 4486

 tatatatatacacataaatacacacacacacacaccctatataaatatatatatatatatatatatatatat 403
 4558

 atatataatgcaaaggcaatgtaataaatgcaactaattattgcaaactaacaattacaatttcaaattg 403
 4630

 caaacattttgcaactaaaaatattgtgtgtgtgcatatatatgtatatttatattagtctgcaacgtacta 403
 4702

 taataaccacttgag 403
 4774

 agactgatgtacatgcttttgtgtgcataaattaatttgccttatatattaactaacacaaatgcaaatca 403
 4846

 gttcaataaccaagagcttcataaacatgcaagactcctcaagcccctcacagtgtgctttttttccccctca 403
 4918

 IPB002070E (4.7e-05) IC 0.90
 M Y T A P E S D R L T P S P T D S 420
 g g atg tac aca gct cca gag agc gac aga ctg acg ccc tct cct act gac tct 4971

P R S H Q I V P G A R Y A M Q P F F 438
 ccg cgg tcg cac cag att gtc ccc ggc gcc cgc tac gca atg cag ccc ttc ttc 5025

 Q D Q F V N N L P Q N H R F Y G S E 456
 caa gac caa ttt gtc aac aac ctt ccc caa aac cac cga ttc tac ggc agc gag 5079

 R A V P Q T N G L L S P Q S E D S A 474
 cgc gcc gtt ccc caa acc aac ggc ctg ctg tct cct cag agc gaa gat tcg gcc 5133

 A G S A S A Q R W F V G P V Q Q S G 492
 gcg gcc tcg gcg tca gct cag cgc tgg ttt gtg ggg ccg gtg caa caa agt ggt 5187

 User BLOCK 1 (1.1e-05) IC 2.73
 A T T K L D L S Y D S E Y S A S S L 510

gcg acc acc aaa ctg gat ctg tcc tat gac agt gag tac tct gcc tcc agt ctg 5241

L P Y G I K P L P L O S P H A L G Y 528
ctt ccc tac ggc atc aaa cca ctg ccg ctc cag agt cca cat gca ctc ggc tac 5295

User BLOCK 10 (4.4e-28) IC 2.69
Y P D S A F A S M A A G W S S R S S 546
tat cct gat tct gca ttc gca tct atg gca gcc gga tgg agc agc aga agt tcc 5349

Y O R K M T T G L P W S P R P S P P 564
tac cag aga aaa atg acc acc ggc ctg ccg tgg tca ccc cga cca agc cct ccg 5403

A Y T D D L L S S K D K L Q D E N S 582
gca tac acc gat gac ctg ctg tcc tcc aaa gac aag ctg cag gat gaa aac tcc 5457

T A A P T A A S T G P W M E A P P V 600
aca gcg gcc cct acg gct gcc agc aca ggc ccc tgg atg gag gca cct ccg gtg 5511

User BLOCK 11 (2.8e-26) IC 3.16
L K S V D S G D T S G Y S M A C K R 618
ctg aaa agc gtg gat tca ggc gac acc agc ggt tac tcc atg gcc tgt aag ccg 5565

R R V S P G G S S T D A S P T I K C 636
cgg cgt gtt tcg cct gga ggc tcc agt aca gac gct tca ccc act ata aag tgt 5619

User BLOCK 12 (7.6e-19) IC 3.45
E D L S S E E Y N K E S H K A M G Y 654
gag gac ttg agc tct gag gag tac aac aaa gag agc cat aaa gcc atg ggt tat 5673

Y A F Y T S P * 662
tac gcc ttc tac acc agc cct taa gaactgcttttcaagatcctttatcaatccattcattctc 5737

tctatctctctatctggttttattttcttttaaagtgatcttgctcatgttgtgttttaaa 662
5797

Coding Sequence

User BLOCK 1 (4.6e-19) IC 2.73
M Q L E S I L P G A S V N L P K T F 18
atg cag tta gaa agc atc ctc cct ggc gca tct gta aac tta ccc aag acc ttc 54
tL3F[1]

Y N L S S S S E S T N N S P G S T Q 36
tac aac ctg tcc tca tcc tcc gaa agc acc aat aat agc ccg ggg tca acg cag 108

User BLOCK 2 (2.6e-20) IC 2.46
I D F Q D M D R T D S E O S S G A K 54
atc gac ttt cag gac atg gac ccg acg gat tcg gag cag agt tct ggt gcc aag 162
gQ40R[2]

K F L M D D A D S E S F T G T K A A 72
aag ttt ctg atg gat gat gct gac agt gag agc ttt acc ggg act aaa gca gca 216

A A A T A A P D A R K S S P V I G A 90
gca gca gcc acc gcc gca ccg gac gcg cgt aaa agt tct ccg gtg atc ggc gcg 270

User BLOCK 3 (5.7e-11) IC 2.17

D D E L S S T R R Y N I D D L G T D 108
gat gat gag ctc tcc agc acc cgc aga tac aac atc gat gat ctg ggc act gat 324
cL94P[3] aY100*[4]

R Y F I S S S Q P S S D V A N P C S 126
cga tac ttc ata tcg tcc tct caa ccg agt tct gac gtg gcc aac cct tgc tct 378
tQ116L[5]

L F P Y G G Q T G S V Y S G S N G S 144
ctg ttc ccg tac gga ggg cag acc ggg tcg gtg tac agc ggc tcg aat ggc tcc 432
aS141=[6]

R Y S S S L H Y G S V L P P A G F S 162
cgg tat tcg tcg tct ctg cat tac ggt tcg gtt ctt cca ccc gcc ggg ttc tca 486

User BLOCK 4 (1.3e-16) IC 2.38

S A V C A S R S O F G G G Y O F G O 180
tcc gcc gtg tgc gcc agc agg agt cag ttt ggg ggt ggt tat cag ttc gga cag 540

User BLOCK 5 (9.2e-10) IC 2.33

G P G C L Y P S Y P G P G S S L S S 198
ggt ccc ggg tgt ctg tac ccg tcc tat ccc ggt cca ggc tcc agt ctc agc tcg 594

User BLOCK 6 (7.7e-67) IC 4.24

M P I P G S G S A A R A O V Y L C N 216
atg ccc att cca ggt tcg ggc tcc gcg gcg cgg gcg cag gtt tac ctg tgc aac 648
cV212=[7]

R P L W L K F H R H O T E M I I T K 234
aga ccg ctg tgg ctc aaa ttt cac cgc cat caa act gag atg atc ata act aaa 702
cQ227P[8]

O G R | R M F P F L S F N I T G L N 251
cag gcc ag | g cga atg ttc ccc ttt ctg agt ttt aat atc act gga ctg aac 753

User BLOCK 7 (7.7e-73) IC 4.32

L T A H Y N V F V E I V L A D P N H 269
ctg act gcg cat tat aat gtg ttt gtg gag att gtt ctg gcc gat ccg aac cac 807

W R F O G G K W V T C G K A D N N M 287
tgg aga ttt cag ggc gga aag tgg gtg acc tgc ggg aaa gcg gac aac aac atg 861

O G | N K V Y V H P E S P N T G A H 304
caa g | ga aac aag gtg tat gtt cac cca gag tca cca aac act gga gcg cac 912

W M R O E I S F G K L K L T N N K G 322
tgg atg aga caa gaa ata tct ttc gga aaa ctg aag cta acc aac aac aaa gga 966

User BLOCK 8 (4.8e-31) IC 3.90

A N N N N T Q | M I V L O S L H K Y 339
gca aat aac aac aat act cag | atg att gtc ctg cag tcc ctg cat aag tac 1017

User BLOCK 9 (6.9e-56) IC 4.32

O P R L H I V E V T E D G V E D M S 357
cag cct ccg ctt cac att gtg gag gtg act gag gac ggt gtg gag gac atg agc 1071

S E A K T O T F T F P E N O F I A V 375

agc gaa gct aaa aca cag acc ttc act ttc cct gaa aac cag ttc atc gct gta 1125

T A Y O N T D | I T O L K I D H N P 392
acg gct tac caa aac aca gac | atc aca cag ctc aag atc gac cac aac ccc 1176

F A K G F R D N Y D S | M Y T A P E 409
ttt gca aaa ggc ttc agg gac aat tat gat tc | g atg tac aca gct cca gag 1227

IPB002070E (4.7e-05) IC 0.90

S D R L T P S P T D S P R S H O I V 427
agc gac aga ctg acg ccc tct cct act gac tct ccg cgg tcg cac cag att gtc 1281

P G A R Y A M Q P F F Q D Q F V N N 445
ccc ggc gcc cgc tac gca atg cag ccc ttc ttc caa gac caa ttt gtc aac aac 1335

L P Q N H R F Y G S E R A V P Q T N 463
ctt ccc caa aac cac cga ttc tac ggc agc gag cgc gcc gtt ccc caa acc aac 1389

G L L S P Q S E D S A A G S A S A Q 481
ggc ctg ctg tct cct cag agc gaa gat tcg gcc gcg ggc tcg gcg tca gct cag 1443

R W F V G P V Q Q S G A T T K L D L 499
cgc tgg ttt gtg ggg ccg gtg caa caa agt ggt gcg acc acc aaa ctg gat ctg 1497

User BLOCK 1 (1.1e-05) IC 2.73

S Y D S E Y S A S S L L P Y G I K P 517
tcc tat gac agt gag tac tct gcc tcc agt ctg ctt ccc tac ggc atc aaa cca 1551

L P L O S P H A L G Y Y P D S A F A 535
ctg ccg ctc cag agt cca cat gca ctc ggc tac tat cct gat tct gca ttc gca 1605

User BLOCK 10 (4.4e-28) IC 2.69

S M A A G W S S R S S Y O R K M T T 553
tct atg gca gcc gga tgg agc agc aga agt tcc tac cag aga aaa atg acc acc 1659

G L P W S P R P S P P A Y T D D L L 571
ggc ctg ccg tgg tca ccc cga cca agc cct ccg gca tac acc gat gac ctg ctg 1713

S S K D K L Q D E N S T A A P T A A 589
tcc tcc aaa gac aag ctg cag gat gaa aac tcc aca gcg gcc cct acg gct gcc 1767

S T G P W M E A P P V L K S V D S G 607
agc aca ggc ccc tgg atg gag gca cct ccg gtg ctg aaa agc gtg gat tca ggc 1821

User BLOCK 11 (2.8e-26) IC 3.16

D T S G Y S M A C K R R R V S P G G 625
gac acc agc ggt tac tcc atg gcc tgt aag cgg cgg cgt gtt tcg cct gga ggc 1875

S S T D A S P T I K C E D L S S E E 643
tcc agt aca gac gct tca ccc act ata aag tgt gag gac ttg agc tct gag gag 1929

User BLOCK 12 (7.6e-19) IC 3.45

Y N K E S H K A M G Y Y A F Y T S P 661
tac aac aaa gag agc cat aaa gcc atg ggt tat tac gcc ttc tac acc agc cct 1983

*
taa

662
1986