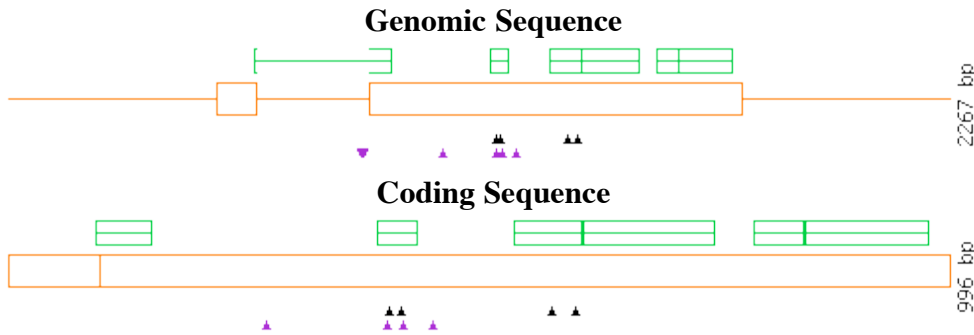


# pou4f3

**IPB013847, IPB000327, IPB003350, IPB012502, IPB000747, IPB003106, IPB002877, and IPB001686**



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	Zygoticity
				Gained in Variant	Lost from Reference				
1	<a href="#">G</a>	A848T	Intron		<a href="#">NdeI</a>			7394	Homo
2	<a href="#">G</a>	G854T	Intron		<a href="#">BsePI</a> , <a href="#">Cac8I</a> , <a href="#">FnuDII</a>			4589	Homo
3	<a href="#">G</a> <a href="#">C</a>	C1044T	H91=	<a href="#">FokI</a>	<a href="#">HphI</a> , <a href="#">TaqII</a> , <a href="#">TstI</a>			4937	Homo
4	<a href="#">G</a> <a href="#">C</a>	G1173T	V134=		<a href="#">HphI</a>			4907	Homo
5	<a href="#">G</a> <a href="#">C</a>	A1174G	M135V	<a href="#">BstEII</a> , <a href="#">MaeIII</a> , <a href="#">Tsp45I</a>		-2.2	0.57	7977	Homo
6	<a href="#">G</a> <a href="#">C</a>	G1186A	A139T		<a href="#">CviJI</a>	0.5	0.03	3127	Homo
7	<a href="#">G</a> <a href="#">C</a>	C1188T	A139=	<a href="#">AluI</a> , <a href="#">HphI</a>				6014	Homo
8	<a href="#">G</a> <a href="#">C</a>	C1221T	H150=		<a href="#">BsiYI</a> , <a href="#">PflMI</a>			7217	Homo
9	<a href="#">G</a> <a href="#">C</a>	T1346A	I192K			20.7	0.00	7007	Homo
10	<a href="#">G</a> <a href="#">C</a>	T1371A	D200E		<a href="#">FokI</a> , <a href="#">Hin4I</a>	17.6	0.18	4045	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

attatttacagaattacacttctgtctacagtttaccatccgatttcctatntttggcatttgaaaacaaaga	0 72
catttaataaattttgcattgctattatcagattaaaaactgatctgcattttaatatgttaaataaaaaat	0 144
ataaattattacattttttaattaattaattaataatcaatttatttatttaatacaacgtcaataaaatcatt	0 216
agttttattattatgctaaatatgtcaatatttatttttttttaaatcacttcggtgaaataactgggt	0 288
taaataacctacgaaatcccacgcgtgagtgtcagaccagtttgccacttgatccccgagtagatggaggcg	0 360
ggagggcagtgtagtttggggtggggggagaaccctgagggcgtgccaatggaaactgaacacacacgag	0 432
gagcgtcgagccagagcgcgcggtttcctccatgtcaggtccactcacctgcaaggtgcgcaacgaag atg	M 1 503
M T M N G K Q H F S M H P A L H P S atg acc atg aac ggc aag cag cac ttc tcc atg cac cct gcg ctg cac ccg agc	19 557
S E G M R R V C L P A P <u>O</u> tcc gag ggc atg cgg cgg gtg tgc cta cct gcc ccg cag gtacgtctcacgctaaactc	IPB001686A (6.9e-05) IC 4.32 32 616
ctcgtattgttaccattctgtcactttgaagtgttttgagttgctccagcatccattcatccctccctocca	32 688
acttctcctttctttactcttgactctctctctcctaccacatgcctatccaagcaaagctgctgctttca	32 760

tattaatTTTTatgacctgtgctttgaggagggtgcttgggaatgttctttaatccagagttgacacaattc 32  
 832

L O G N I F S G F 41  
 cccactgacttccatatgCGCGctcttgcctgcag ctc cag ggc aat ata ttc agc ggc ttt 894  
 t[1] t[2]

D E S L L A R A E A L A A A D I V S 59  
 gat gag agt ctg ctg gcc cgc gct gaa gct ctg gcg gcg gct gac atc gtg tct 948

H G K S H P F K T D V T Y H T M S S 77  
 cac ggc aag agt cac cct ttc aag acg gac gtc acc tac cat acc atg agc agc 1002

V P C T S S S S T V P I S H P S S N 95  
 gtg ccc tgc acc tcc tct tcg tcc aca gtg ccc ata tct cac cca tca tcc aac 1056  
 tH91=[3]

L P S H H H H H L S H Q T L E G D L 113  
 ctc ccg tcg cat cat cac cac cac ctc agc cac cag acc ctg gag ggg gac cta 1110

IPB003106F (9.3e-05) IC 2.17  
 L D H I S S S L S V S G M G A P P D 131  
 ctc gac cac att tcc tcg agt tta tcg gtc agc ggc atg ggg gcg ccg ccg gat 1164

P S V M T T O A H O H H L Q M G H L 149  
 cca tcg gtg atg acc aca caa gcc cac cag cat cac ctg caa atg ggt cac tta 1218  
 tV134=[4] aA139T[6]  
 gM135V[5] tA139=[7]

H Q A M A M G H P H T L S V H N G M 167  
 cac caa gca atg gcg atg ggc cac ccg cac acc ctg tcg gtc cac aac ggc atg 1272  
 tH150=[8]

IPB013847A (5.0e-25) IC 1.79  
 A C V N D V E S D P R E L E A F A E 185  
 gcg tgc gtc aac gac gtc gag tcc gat cca aga gag ctg gag gcg ttc gcg gag 1326

R F K O R R I K L G V T O A D V G S 203  
 agg ttc aag cag cgg agg ata aag tta gga gtg acc cag gcg gat gtg ggc tct 1380  
 aI192K[9] aD200E[10]

IPB000327A (6.5e-35) IC 1.61  
A L A N L K I P G V G S L S O S T I 221  
 gct ctc gcc aac ctg aag ata ccg ggg gtc ggc tcg ctg agc caa agc acc atc 1434

C R F E S L T L S H N N M I A L K P 239  
 tgc agg ttc gag tcc tta aca ctt tca cac aac aac atg atc gcc ctc aaa ccc 1488

V L O A W L E E A E A A Y R E K N G 257

gtc ctc caa gct tgg ctg gag gaa gct gaa gct gct tac cgg gag aaa aac ggg 1542

IPB000327B (4.1e-13) IC 1.50

K P D L F N G N E R K R K R T S I A 275  
 aaa ccg gac ctt ttc aat ggg aac gag agg aaa cga aag cgt acg tcc atc gca 1596

IPB000327C (1.5e-35) IC 2.66

A P E K R S L E A Y F A I O P R P S 293  
 gct ccg gag aag cga tcg ctc gag gca tat ttt gca atc cag ccg cga ccg tcg 1650

S E K I A A I A E K L D L K K N V V 311  
 tcg gaa aaa atc gcg gct atc gcg gag aag ttg gat cta aag aag aac gtg gtt 1704

R V W F C N O R O K O K R M K Y S A 329  
 cgg gtt tgg ttc tgt aat caa cgg caa aaa cag aaa agg atg aag tat tca gca 1758

V H \* 332  
 gtg cac taa tactggttagagcaaagtagacatthtttaggaacaccacagggatctaaatctttcccccc 1827

ctcataattataagcctataatathtttcacatcgccctcagactggtgaaactgtgcgaattattccagga 332  
 1899

cgtctgtaacctttataaagcattgatgccctctthaaaatgtcataacatatctgtcataccaaatctgt 332  
 1971

gtgttatatgaggcatgtagtctgagtathtttaacatgtgggtacatgcaaagttcaacagcctttcaaac 332  
 2043

gatttagcaatcacaaaagttcattaagtcctgtatgactttgtaaatcaaagtaacagtagttgcttgagc 332  
 2115

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 2187

gcagtgcggcaaagggccattattcatttattaattcattattattggctcgagataagtgtaaactattt 332  
 2259

atctcgaa 332  
 2267

### Coding Sequence

M M T M N G K Q H F S M H P A L H P 18  
 atg atg acc atg aac ggc aag cag cac ttc tcc atg cac cct gcg ctg cac ccg 54

IPB001686A (6.9e-05) IC 4.32

S S E G M R R V C L P A P O | L O G 35  
 agc tcc gag ggc atg cgg cgg gtg tgc cta cct gcc ccg cag | ctc cag ggc 105

N I F S G F D E S L L A R A E A L A 53  
aat ata ttc agc ggc ttt gat gag agt ctg ctg gcc cgc gct gaa gct ctg gcg 159

A A D I V S H G K S H P F K T D V T 71  
gcg gct gac atc gtg tct cac ggc aag agt cac cct ttc aag acg gac gtc acc 213

Y H T M S S V P C T S S S S T V P I 89  
tac cat acc atg agc agc gtg ccc tgc acc tcc tct tcg tcc aca gtg ccc ata 267

S H P S S N L P S H H H H H L S H Q 107  
tct cac cca tca tcc aac ctc ccg tcg cat cat cac cac cac ctc agc cac cag 321  
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T L E G D L L D H I S S S L S V S G 125  
acc ctg gag ggg gac cta ctc gac cac att tcc tcg agt tta tcg gtc agc ggc 375

IPB003106F (9.3e-05) IC 2.17

M G A P P D P S V M T T O A H O H H 143  
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tV134=[4] aA139T[6]  
gM135V[5] tA139=[7]

L Q M G H L H Q A M A M G H P H T L 161  
ctg caa atg ggt cac tta cac caa gca atg gcg atg ggc cac ccg cac acc ctg 483  
tH150=[8]

IPB013847A (5.0e-25) IC 1.79

S V H N G M A C V N D V E S D P R E 179  
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L E A F A E R F K O R R I K L G V T 197  
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IPB000327A (6.5e-35) IC 1.61

Q A D V G S A L A N L K I P G V G S 215  
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aD200E[10]

L S O S T I C R F E S L T L S H N N 233  
ctg agc caa agc acc atc tgc agg ttc gag tcc tta aca ctt tca cac aac aac 699

M I A L K P V L O A W L E E A E A A 251  
atg atc gcc ctc aaa ccc gtc ctc caa gct tgg ctg gag gaa gct gaa gct gct 753

IPB000327B (4.1e-13) IC 1.50

Y R E K N G K P D L F N G N E R K R 269  
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IPB000327C (1.5e-35) IC 2.66

K R T S I A A P E K R S L E A Y F A 287

aag cgt acg tcc atc gca gct ccg gag aag cga tcg ctc gag gca tat ttt gca 861

I O P R P S S E K I A A I A E K L D 305  
 atc cag ccg cga ccg tcg tcg gaa aaa atc gcg gct atc gcg gag aag ttg gat 915

L K K N V V R V W F C N O R O K O K 323  
 cta aag aag aac gtg gtt cgg gtt tgg ttc tgt aat caa cgg caa aaa cag aaa 969

R M K Y S A V H \* 332  
 agg atg aag tat tca gca gtg cac taa 996