

**Plasmid Information: human peroxisome proliferator activated receptor alpha A/B domain deletion (aa101-468) *Escherichia coli* pTrcHisA expression construct**

---

DNA nucleotide sequence of the synthetic gene:

GGTACCTCGAGGAATGCCGTATTTGCGGCGATAAAGCGAGCGGCTATCATT  
ATGGCGTGTCATGCGTGCGAAGGCTGCAAAGGCTTTTTTCGTTCGTACCATTCGT  
CTGAAACTGGTGTACGATAAATGCGATCGCAGCTGCAAAATCCAGAAAAAAA  
ACCGCAACAAATGCCAGTATTGCCGCTTTCATAAATGCCTGAGCGTGGGCAT  
GAGCCATAACGCGATTTCGTTTTGGCCGTATGCCGCGTAGCGAAAAAGCGAAA  
CTGAAAGCGGAAATTCTGACCTGCGAACACGATATTGAAGATAGCGAAACCG  
CGGATCTGAAAAGCCTGGCCAAACGTATTTATGAAGCGTATCTGAAAAACTT  
CAACATGAACAAAGTGAAAGCGCGTGTGATTCTGAGCGGCAAAGCGAGCAA  
CAATCCGCCGTTTGTGATTCATGATATGGAAACCCTGTGCATGGCGGAAAAA  
ACCCTGGTGGCGAAACTGGTGGCGAACGGCATTTCAGAACAAAGAAGCGGAA  
GTTTCGCATTTTTTCATTGCTGCCAGTGCACCAGCGTGGAACCGTGACCGAGCT  
GACCGAATTTGCGAAAGCGATTCCGGGCTTTGCGAACCTGGATCTGAACGAT  
CAGGTGACCCTGCTGAAATATGGCGTGTATGAAGCGATTTTTGCGATGCTGA  
GCAGCGTGATGAACAAAGATGGCATGCTGGTTGCGTATGGCAACGGCTTTAT  
TACCCGCGAATTTCTGAAATCTCTGCGTAAACCGTTTTGCGATATCATGGAAC  
CGAAATTCGATTTTCGCGATGAAATTTAACGCGCTGGAGCTGGATGATAGCGA  
TATTAGCCTGTTTGTGGCGGCGATTATTTGCTGCGGCGATCGTCCGGGCCTGC  
TGAACGTGGGCCATATTGAAAAAATGCAGGAAGGCATTGTTACGTTCTGCG  
TCTGCATCTGCAGAGCAACCATCCGGATGATATTTTCTGTTCCCGAAACTGC  
TGCAGAAAATGGCGGATCTGCGTCAGCTGGTGACCGAACATGCGCAGCTGGT  
GCAGATTATCAAAAAAACCGAAAGCGATGCGGCGCTGCATCCGCTGCTGCAG  
GAAATTTATCGCGATATGTAC**TGA**GGAATTCGAGCTC

---

DNA sequencing results from the pTrcHisA BamHI/KpNI sub-cloned synthetic gene:

GGATCCGAATGCCGTATCTGCGGTGACAAAGCTTCTGGTTACCACTACGGTGT  
TCACGCTTGCGAAGGTTGCAAAGGTTTCTTCCGTCGTACCATCCGTCTGAAAC  
TGTTTTACGACAAATGCGACCGTTCTTGCAAAATCCAGAAAAAAAACCGTAA  
CAAATGCCAGTACTGCCGTTTCCACAAATGCCTGTCTGTTGGTATGTCTCACA  
ACGCTATCCGTTTCCGGTCGTATGCCGCGTTCTGAAAAAGCTAAACTGAAAGCT  
GAAATCCTGACCTGCGAACACGACATCGAAGACTCTGAAACCGCTGACCTGA  
AATCTCTGGCTAAACGTATCTACGAAGCTTACCTGAAAAACTTCAACATGAA

CAAAGTTAAAGCTCGTGTTATCCTGTCTGGTAAAGCTTCTAACAACCCGCCGT  
TCGTTATCCACGACATGGAAACCCTGTGCATGGCTGAAAAAACCTGGTTGC  
TAAACTGGTTGCTAACGGTATCCAGAACAAAGAAGCTGAAGTTCGTATCTTC  
CACTGCTGCCAGTGCACCTCTGTTGAAACCGTTACCGAACTGACCGAATTCGC  
TAAAGCTATCCCGGGTTTCGCTAACCTGGACCTGAACGACCAGGTTACCCTG  
CTGAAATACGGTGTTTACGAAGCTATCTTCGCTATGCTGTCTTCTGTTATGAA  
CAAAGACGGTATGCTGGTTGCTTACGGTAACGGTTTCATCACCCGTGAATTCC  
TGAAATCTCTGCGTAAACCGTTCTGCGACATCATGGAACCGAAATTCGACTTC  
GCTATGAAATTCAACGCTCTGGAACCTGGACGACTCTGACATCTCTCTGTTCTG  
TGCTGCTATCATCTGCTGCGGTGACCGTCCGGGTCTGCTGAACGTTGGTCACA  
TCGAAAAAATGCAGGAAGGTATCGTTCACGTTCTGCGTCTGCACCTGCAGTCT  
AACCACCCGGACGACATCTTCCTGTTCCCGAAACTGCTGCAGAAAATGGCTG  
ACCTGCGTCAGCTGGTTACCGAACACGCTCAGCTGGTTCAGATCATCAAAAA  
AACCGAATCTGACGCTGCTCTGCACCCGCTGCTGCAGGAAATCTACCGTGAC  
ATGTACTAGGGTACC

Size of synthetic gene fragment=1119bp

020406GE0601 sequencing primers(3'-5'):

020406GE0601 W286 R1 CAGCAGGGTAACCTGGTC from 616 to 633

020406GE0601 sequencing primers(5'-3'):

020406GE0601 W286 F1 CCAGAACAAAGAAGCTG from 495 to 500

020406GE0601 W286 F2 GACCTGAAATCTCTGGC from 310 to 326

Translation of the [5'3' Frame 1](#) of the above nucleotide sequencing data

GSECRICGDKASGYHYGVHACEGCKGFFRRTIRLKLVD  
KCDRSCKIQKKNRNKCQYCRFKCLSVGMSHNAIRFGM  
PRSEKAKLKAEILTCEHDIEDSETADLKSLAKRIYEAYLK  
NFMNKKVKARVILSGKASNNPPFVIHDMETLCMAEKT  
LVAKL VANGIQNKEAEVRIFHCCQCTSVETVTELEFAKA  
IPGFANLDLNDQVTLLKYGVYEAI FAMLSSVMNKDGM  
LVAYGNGFITREFLKSLRKPFCDIMPKFDFAMKFNALE  
LDDSDISLFVAAIICCGDRPGLLNVGHIKMQEGIVHVL  
RLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQ  
IIKKTESDAALHPLLQEIYRDMY **Stop** GT

---

PPAR $\alpha$  $\Delta$ AB [Homo sapiens]: Amino acid sequence of translation product with un-cleaved [His]<sub>6</sub> tag

MGGSHHHHHHGMASMTGGQQMGR~~TL~~YDDDDKDRWGS~~ECRICGDKASGYHYGVHACEGCKGFFRRTIRLKL~~V  
YDKCDRSCKIQKKNRNKCQYCRFHKCLSVGM~~SHNAIRFGRMPRSEKAKL~~KAEILTC~~EHDI~~EDSETADLKSL  
AKRIYEAYLKNFNMNKKV~~KARVILSGKASNNPPFVIHDMETLCMAE~~KT~~LVAKLVANGIQNKEAEVRIFHCCQ~~  
CTSVETVTELTEFAKAI~~PGFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNGFITREFLKSLR~~  
KPFCDIMEPKFDFAMKFNALELDDSDISL~~FVA~~AIICCGDRPGLLN~~VGHIEKMQEGIVHVLRLHLQSNHPDD~~  
IFLFPKLLQKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQE~~IYRDMY~~

GREEN=Extra residues from plasmid to maintain correct reading frame.

BLUE=[His]<sub>6</sub> tag

RED=Enterokinase cleavage site

**Molecular weight: 45938.2 Da**

**Theoretical pI: 8.35**

PPAR $\alpha$  $\Delta$ AB [Homo sapiens]: Amino acid sequence of translation product with cleaved [His]<sub>6</sub> tag

DRWGS~~ECRICGDKASGYHYGVHACEGCKGFFRRTIRLKL~~VYDKCDRSCKIQKKNRNKCQYCRFHKCLSVGM  
SHNAIRFGRMPRSEKAKL~~KAEILTC~~EHDI~~EDSETADLKSLAKRIYEAYLKNFNMNKKV~~KARVILSGKASNNP  
PFVIHDMETLCMAEKT~~LVAKLVANGIQNKEAEVRIFHCCQ~~CTSVETVTELTEFAKAI~~PGFANLDLNDQVTLL~~  
KYGVYEAIFAMLSSVMNKDGMLVAYGNGFITREFLKSLR~~KPFCDIMEPKFDFAMKFNALELDDSDISL~~FV  
AAIICCGDRPGLLN~~VGHIEKMQEGIVHVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKT~~  
ESDAALHPLLQE~~IYRDMY~~

GREEN=Extra residues from plasmid to maintain correct reading frame.

**Molecular weight: 42523.5 Da**

**Theoretical pI: 8.56**

-

---

Amino acid sequence alignment of full length human PPAR $\alpha$  VS the translated amino acid sequence derived from the nucleotide sequencing data of the pTrcHisA *Bam*HI and *Kpn*I sub-cloned PPAR $\alpha$  $\Delta$ AB(aa101-468) synthetic gene VS the translated amino acid sequence derived from the theoretical nucleotide sequence of the PPAR $\alpha$  $\Delta$ AB(aa101-468) synthetic gene

requested for synthesis:

NucleotideSequenceData	1	-----
FullLengthHumanPPARalpha	1	MVDTESPLCPLSPLEAGDLESPLSEEFLLQEMGNIQEISQSIGEDSSGSFG
SyntheticGeneRequested	1	-----
consensus	1	

NucleotideSequenceData	1	-----GS-----
FullLengthHumanPPARalpha	51	FTEYQYLGSCP <del>GS</del> DGSVITDTLSPASSPSSVTYPVVPGSVDESPGALNI
SyntheticGeneRequested	1	-----GT-----LE
consensus	51	*.

NucleotideSequenceData	3	ECRICGDKASGYHYGVHACEGCKGFFRRTIRLKLVDKCDRSCKIQKKNR
FullLengthHumanPPARalpha	101	ECRICGDKASGYHYGVHACEGCKGFFRRTIRLKLVDKCDRSCKIQKKNR
SyntheticGeneRequested	5	ECRICGDKASGYHYGVHACEGCKGFFRRTIRLKLVDKCDRSCKIQKKNR
consensus	101	*****

NucleotideSequenceData	53	NKCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEHDIEDSET
FullLengthHumanPPARalpha	151	NKCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEHDIEDSET
SyntheticGeneRequested	55	NKCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEHDIEDSET
consensus	151	*****

NucleotideSequenceData	103	ADLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFVIHDMETLCMA
FullLengthHumanPPARalpha	201	ADLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFVIHDMETLCMA
SyntheticGeneRequested	105	ADLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFVIHDMETLCMA
consensus	201	*****

NucleotideSequenceData	153	EKTLVAKLVANGIQNKEAEVRIFHCCQCTSVETVTELTEFAKAIPGFANL
FullLengthHumanPPARalpha	251	EKTLVAKLVANGIQNKEAEVRIFHCCQCTSVETVTELTEFAKAIPGFANL
SyntheticGeneRequested	155	EKTLVAKLVANGIQNKEAEVRIFHCCQCTSVETVTELTEFAKAIPGFANL
consensus	251	*****

NucleotideSequenceData	203	DLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNNGFITREFLKSRLKP
FullLengthHumanPPARalpha	301	DLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNNGFITREFLKSRLKP
SyntheticGeneRequested	205	DLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNNGFITREFLKSRLKP
consensus	301	*****

NucleotideSequenceData	253	FCDIMEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIKEM
FullLengthHumanPPARalpha	351	FCDIMEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIKEM
SyntheticGeneRequested	255	FCDIMEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIKEM
consensus	351	*****

NucleotideSequenceData	303	QEGIVHVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKT
FullLengthHumanPPARalpha	401	QEGIVHVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKT
SyntheticGeneRequested	305	QEGIVHVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKT
consensus	401	*****

NucleotideSequenceData	353	ESDAALHPLLQEIYRDMY
FullLengthHumanPPARalpha	451	ESDAALHPLLQEIYRDMY
SyntheticGeneRequested	355	ESDAALHPLLQEIYRDMY
consensus	451	*****

---

---