

Alignment of wildtype and knockout cDNA sequences

NM_022290.2 = NCBI reference sequence
ORF = Open reading frame
= Serine

NM_022290.2	CCGCCAGCGAGAACTCTGGTCTTTAAAGGATGAAGAACTCAATGCTGGAGGCTGCGTCC	300
ORF	-----ATGAAGAACTCAATGCTGGAGGCTGCGTCC	30
wildtype_cDNA	-----ATGAAGAACTCAATGCTGGAGGCTGCGTCC	30
Knockout_cDNA	-----ATGAAGAACAGT-TGCTGGAGGCTGCGTCC	29
	*****###*****	

NM_022290.2	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	360
ORF	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	90
wildtype_cDNA	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	90
Knockout_cDNA	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	89

NM_022290.2	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGGTGACGTG	420
ORF	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGGTGACGTG	150
wildtype_cDNA	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGGTGACGTG	150
Knockout_cDNA	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGGTGACGTG	149

NM_022290.2	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTG	480
ORF	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTG	210
wildtype_cDNA	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTG	210
Knockout_cDNA	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTG	209

NM_022290.2	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	540
ORF	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	270
wildtype_cDNA	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	270
Knockout_cDNA	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	269

NM_022290.2	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	600
ORF	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	330
wildtype_cDNA	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	330
Knockout_cDNA	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	329

NM_022290.2	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	660
ORF	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	390
wildtype_cDNA	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	390
Knockout_cDNA	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	389

NM_022290.2	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	720
ORF	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	450
wildtype_cDNA	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	450
Knockout_cDNA	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	449

NM_022290.2	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	780
ORF	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	510
wildtype_cDNA	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	510
Knockout_cDNA	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	509

NM_022290.2	GGCTCTCCTATCAGTCCGCAAGGCTGAGAAGTTTACGAGACTGTGAAGATACTCATTCTGT	840
ORF	GGCTCTCCTATCAGTCCGCAAGGCTGAGAAGTTTACGAGACTGTGAAGATACTCATTCTGT	570
wildtype_cDNA	GGCTCTCCTATCAGTCCGCAAGGCTGAGAAGTTTACGAGACTGTGAAGATACTCATTCTGT	570
Knockout_cDNA	GGCTCTCCTATCAGTCCGCAAGGCTGAGAAGTTTACGAGACTG-----	552

NM_022290.2	GATCAGAGAAGTTGTCTTGCTTCAGTGTCTTGGGATTAGTGTCTATTATCTACACAGGC	900
ORF	GATCAGAGAAGTTGTCTTGCTTCAGTGTCTTGGGATTAGTGTCTATTATCTACACAGGC	630
wildtype_cDNA	TGCTGTGGGTGTCA-----	584
Knockout_cDNA	-----	552

Alignment of wildtype cDNA sequences using forward and reverse primers

NM_022290.2 = NCBI reference sequence
ORF = Open reading frame

ORF	-----ATGAAGAACTCAATGCTGGAGGCTGCGTCC	30
NM_022290.2	CCGCCAGCGAGAACTCTGGTCTTTAAAGGATGAAGAACTCAATGCTGGAGGCTGCGTCC	300
wildtype_cDNA_forward	-----ATGAAGAACTCAATGCTGGAGGCTGCGTCC	30
wildtype_cDNA_reverse	-----ATGAAGAACTCAATGCTGGAGGCTGCGTCC	30

ORF	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTTCAAGATCTTTAGCGTGTGCGCCCCG	90
NM_022290.2	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTTCAAGATCTTTAGCGTGTGCGCCCCG	360
wildtype_cDNA_forward	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTTCAAGATCTTTAGCGTGTGCGCCCCG	90
wildtype_cDNA_reverse	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTTCAAGATCTTTAGCGTGTGCGCCCCG	90

ORF	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	150
NM_022290.2	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	420
wildtype_cDNA_forward	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	150
wildtype_cDNA_reverse	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	150

ORF	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	210
NM_022290.2	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	480
wildtype_cDNA_forward	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	210
wildtype_cDNA_reverse	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	210

ORF	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	270
NM_022290.2	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	540
wildtype_cDNA_forward	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	270
wildtype_cDNA_reverse	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	270

ORF	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	330
NM_022290.2	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	600
wildtype_cDNA_forward	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	330
wildtype_cDNA_reverse	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	330

ORF	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	390
NM_022290.2	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	660
wildtype_cDNA_forward	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	390
wildtype_cDNA_reverse	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	390

ORF	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	450
NM_022290.2	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	720
wildtype_cDNA_forward	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	450
wildtype_cDNA_reverse	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	450

ORF	CTGACCCCCTACAGCCTACTGTGGAACAACCTTGTGACCTACTGCAGATAC	510
NM_022290.2	CTGACCCCCTACAGCCTACTGTGGAACAACCTTGTGACCTACTGCAGATAC	780
wildtype_cDNA_forward	CTGACCCCCTACAGCCTACTGTGGAACAACCTTGTGACCTACTGCAGATAC	510
wildtype_cDNA_reverse	CTGACCCCCTACAGCCTACTGTGGA-----	475

ORF	GGCTCTCCTATCAGTCCGCGAGGCTGAGAAGTTTACGAGACTGTGAAGATACTCATTTCGT	570
NM_022290.2	GGCTCTCCTATCAGTCCGCGAGGCTGAGAAGTTTACGAGACTGTGAAGATACTCATTTCGT	840
wildtype_cDNA_forward	GGCTCTCCTATCAGTCCGCGAGGCTGAGAAGTTTACGAGACTGTGAAGAGAGCCGTA	570
wildtype_cDNA_reverse	-----	475

ORF	GATCAGAGAAGTTGTCTTGCTTCAGCTGTCTTGGGATTAGTGTCTATTATCTACACAGGC	630
NM_022290.2	GATCAGAGAAGTTGTCTTGCTTCAGCTGTCTTGGGATTAGTGTCTATTATCTACACAGGC	900
wildtype_cDNA_forward	TGCTGTGGGTGTCA-----	584
wildtype_cDNA_reverse	-----	475

Alignment of knockout cDNA sequences using forward and reverse primers

NM_022290.2 = NCBI reference sequence
ORF = Open reading frame
= Serine

NM_022290.2	CCGCCAGCGAGAAACTCTGGTCTTTAAAGGATGAAGAACTCAATGCTGGAGGCTGCGTCC	300
ORF	-----ATGAAGAACTCAATGCTGGAGGCTGCGTCC	30
Knockout_cDNA_forward	-----ATGAAGAACAGT-TGCTGGAGGCTGCGTCC	28
Knockout_cDNA_reverse	-----ATGAAGAACAGT-TGCTGGAGGCTGCGTCC *****###*****	29
NM_022290.2	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	360
ORF	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	90
Knockout_cDNA_forward	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG	88
Knockout_cDNA_reverse	CTCCTTCTGGAGAAGCTGCTCCTTATTTCCAACCTCAAGATCTTTAGCGTGTGCGCCCCG *****	89
NM_022290.2	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	420
ORF	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	150
Knockout_cDNA_forward	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG	148
Knockout_cDNA_reverse	GGAGGAGGCACAGGGAAGAAACATCCCTATGAAATCAACTCTTTTCTCCGGGTGACGTG *****	149
NM_022290.2	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	480
ORF	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	210
Knockout_cDNA_forward	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC	208
Knockout_cDNA_reverse	TTGGAAGTGTACGGACCCATTTTACCCACTATGGGATCTACCTGGGGGACAACCGTGTC *****	209
NM_022290.2	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	540
ORF	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	270
Knockout_cDNA_forward	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG	268
Knockout_cDNA_reverse	GCCCATCTAATGCCTGACATCCTGTTGGCCCTGACCAGTGACAAGGAACGCACTCAGAAG *****	269
NM_022290.2	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	600
ORF	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	330
Knockout_cDNA_forward	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG	328
Knockout_cDNA_reverse	GTGGTCTCCAACAAGCGTCTCCTCCCAGGAGTCATTTGCAAGGTGGCCAGCATCCGTGTG *****	329
NM_022290.2	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	660
ORF	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	390
Knockout_cDNA_forward	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT	388
Knockout_cDNA_reverse	GACACAGTAGAGGACTTTGCCTATGGAGCGGACATCCTCGTCAATCACCTAGACGAGACT *****	389
NM_022290.2	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	720
ORF	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	450
Knockout_cDNA_forward	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG	448
Knockout_cDNA_reverse	CTCAAGAAGAAGTCCTTGCTCAATGAGGAGGTGGCACGCAGAGCAGAGCAGCAGTTGGGG *****	449
NM_022290.2	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	780
ORF	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	510
Knockout_cDNA_forward	CTGACCCCCTACAGCCTACTGTGGAACAACCTGCGAACACTTTGTGACCTACTGCAGATAC	508
Knockout_cDNA_reverse	CTGACCCCCTACAGCCTACTGTG----- *****	473
NM_022290.2	GGCTCTCCTATCAGTCCGCGAGGCTGAGAAGTTTCACGAGACTGTGAAGATACTCATTCGT	840
ORF	GGCTCTCCTATCAGTCCGCGAGGCTGAGAAGTTTCACGAGACTGTGAAGATACTCATTCGT	570
Knockout_cDNA_forward	GGCTCTCCTATCAGTCCGCGAGGCTGAGAAGTTTCACGAGACTGA-----	552
Knockout_cDNA_reverse	-----	473

Alignment of the wildtype human and rat Lrat ORF nucleotide sequences

LRAT_human	ATGAAGAACCCCATGCTGGAGGTGGTGTCTTTACTACTGGAGAAGCTGCTCCTCATCTCC	60
Lrat_rat	ATGAAGAACTCAATGCTGGAGGCTCGTCCCTCCTTCTGGAGAAGCTGCTCCTTATTTCC	60
	***** * ***** * ** * * ***** ** **	
LRAT_human	AACTTCACGCTCTTTAGTTCGGGCGCCGGGCGAAGACAAAGGGAGGAACAGTTTTTAT	120
Lrat_rat	AACTTCAAGATCTTTAGCGTGTGCGCCCCGGGAGGAGGCACAGGAAGAAACATCCCTAT	120
	***** * ***** * ***** ** * * * ***** ** * **	
LRAT_human	GAAACCAGCTCTTTCCACCGAGGCGACGTGCTGGAGGTGCCCCGGACCCACCTGACCCAC	180
Lrat_rat	GAAATCAACTCTTTTCTCGGGGTGACGTGTTGGAAGTGTACGGACCCATTTTACCCAC	180
	**** * ***** * ** * * ***** ** * * ***** * *****	
LRAT_human	TATGGCATCTACCTAGGAGACAACCGTGTGCCACATGATGCCCCGACATCCTGTTGGCC	240
Lrat_rat	TATGGGATCTACCTGGGGGACAACCGTGTGCGCCATCTAATGCCTGACATCCTGTTGGCC	240
	***** ***** * ***** ***** * ***** *****	
LRAT_human	CTGACAGACGACATGGGGCGCAGCAGAAAGTGGTCTCCAACAAGCGTCTCATCCTGGGC	300
Lrat_rat	CTGACCAGTGACAAGGAACGCACTCAGAAAGTGGTCTCCAACAAGCGTCTCCTCCCAGGA	300
	***** ** * * ***** ***** ***** ** *	
LRAT_human	GTTATTGTCAAAGTGGCCAGCATCCGCTGGACACAGTGGAGGACTTCGCCTACGGAGCT	360
Lrat_rat	GTCATTTGCAAGGTGGCCAGCATCCGTGTGGACACAGTAGAGGACTTTGCCTATGGAGCG	360
	** * * * * ***** ***** ***** ***** *****	
LRAT_human	AACATCCTGGTCAATCACCTGGACGAGTCCCTCCAGAAAAAGGCACTGCTCAACGAGGAG	420
Lrat_rat	GACATCCCTGTCATCACCTAGACGAGACTCTCAAGAAGAAGTCCTTGCTCAATGAGGAG	420
	***** ***** ***** * * * * * * * * *****	
LRAT_human	GTGGCGCGGAGGGCTGAAAAGCTGCTGGGCTTTACCCCTACAGCCTGCTGTGGAACAAC	480
Lrat_rat	GTGGCACGCAGAGCAGAGCAGAGTTGGGGTGACCCCTACAGCCTACTGTGGAACAAC	480
	***** * * * * * * * * * * ***** ***** *****	
LRAT_human	TGCGAGCACTTCGTGACCTACTGCAGATATGGCACCCCGATCAGTCCCAGTCCGACAAG	540
Lrat_rat	TGCGAACACTTTGTGACCTACTGCAGATACGGCTCTCCTATCAGTCCGAGGCTGAGAAG	540
	***** ***** ***** ***** * * * * ***** ** * * *	
LRAT_human	TTTTGTGAGACTGTGAAGATAATTATTCGTGATCAGAGAAGTGTTCTTGCTTCAGCAGTC	600
Lrat_rat	TTTCACGAGACTGTGAAGATACTCATTCGTGATCAGAGAAGTTGTCTTGCTTCAGCTGTC	600
	*** ***** * ***** ***** ***** ***** **	
LRAT_human	TTGGGATTGGCGTCTATAGTCTGTACGGGCTTGGTATCATACACTACCTTCCTGCAATT	660
Lrat_rat	TTGGGATTAGTGTCTATTATCTACACAGGCCCTGGCATCATATATGACCTTCCTGCAGTC	660
	***** * ***** ** * * * * * * * * * * ***** *	
LRAT_human	TTTATTCATTCTTCCTATGGAT---GGCTGGCTAA	693
Lrat_rat	TGCATCCCGTTCTGCTTGTGGATGATGCTGGCTAG	696
	* * * * * * * * * * * * * * * * *	

Alignment of the wildtype human and rat LRAT ORF amino acid sequences

* = The same amino acid
: = Indicates conservation between groups of strongly similar properties
. = Indicates conservation between groups of weakly similar properties

LRAT_human	MKNPMLLEVSLLEKLLISNFTLFSSGAAGEDKGRNSFYETSSFHRGDVLEVPRTLTH	60
Lrat_rat	MKNSMLEAASLLLEKLLISNFKIFSVCAPGGGTGKKHPYEINSFLRGDVLEVSRTHTH	60
	*** **_.*****.:** ** _.:** ** ***** **_.**	
LRAT_human	YGIYLGDNRAHMPDILLALTDDMGRTQKVVSNNKRLILGVIVKVASIRVDTVDFAYGA	120
Lrat_rat	YGIYLGDNRAHMLPDILLALTSKERTQKVVSNNKRLPGVICKVASIRVDTVDFAYGA	120
	*****.*****.* *****.*** *****	
LRAT_human	NILVNHLDLQKALLNEEVARRAEKLLGFTPYSLWNNCEHFVTCRYGTPISPQSDK	180
Lrat_rat	DILVNHLDLTKKSLNEEVARRAEQLGLTPYSLWNNCEHFVTCRYGSPISPQAEK	180
	:*****.:.:**.*****.:.**.******.*****.*****.:.*	
LRAT_human	FCETVKIIRDQRSVLASAVLGLASIVCTGLVSYTTLPAIFIPFFLWMAG-	230
Lrat_rat	FHETVKILIRDQRSCLASAVLGLVSIYTGSLASYMTLPAVCIPFCLWMMSG	231
	* *****.***** *****.:.**.* ** *****.*** ** *	

Alignment of the mutant human and rat LRAT ORF nucleotide sequences

LRAT_human	ATGAAGAACCATGCTGGAGGTGGTGTCTTTACTACTGGAGAAGCTGCTCCTCATCTCCA	60
Lrat_rat	ATGAAGAACTCATGCTGGAGGTGCGTCCCTCCTTCTGGAGAAGCTGCTCCTTATTCCA	60
	***** ***** * ** * ** ***** ***** ** *	
LRAT_human	ACTTCACGCTCTTTAGTTCGGGCGCCGCGGGCGAAGACAAAGGGAGGAACAGTTTTATG	120
Lrat_rat	ACTTCAAGATCTTTAGCGTGTGCGCCCGGGAGGAGGCACAGGGAAGAAACATCCCTATG	120
	***** * ***** * ***** ***** * ** * ** ***** ***** * *****	
LRAT_human	AAACCAGCTCTTTCCACCGAGGCGACGTGCTGGAGGTGCCCCGGACCCACCTGA-----	174
Lrat_rat	AAATCAACTCTTTCTCCGGGGTGACGTGTTGGAAGTGTCACGGACCCATTTACCCACT	180
	*** ** ***** * ** * ** ***** ***** ***** * ***** * *	
LRAT_human	-----	174
Lrat_rat	ATGGGATCTACCTGGGGGACAACCGTGTGCCCCATCTAA	219

Alignment of the mutant human and rat LRAT theoretic ORF amino acid sequences

* = The same amino acid
: = Indicates conservation between groups of strongly similar properties
. = Indicates conservation between groups of weakly similar properties

LRAT_human	MKNPCWRWCLYYWRSCSSSPTSRSLSVRAPRAKTKGGTVFMKPALSTEATCWRCPGPT---	57
LRAT_rat	MKNSCWRLRPSFWRSCSLFPTSRLACAPREEAQGRNIPMKSTLFSGVTCWKCHGPILPT	60
	*** ** :***** *****. *** ::* .: ** :* :.***:* **	
LRAT_human	-----	57
LRAT_rat	MGSTWGTTVSPI	72