HFI Mutations

(As of September 1, 1999 there were 23 published HFI mutations)

Exon	Trivial Name[a] (recommended)	Codon[b]	Nucleotide change[c]	Codon change[d]	Systematic (cDNA based)[e]	Systematic (Genomic based)[f]	Other Names[g]	Consequence	Other Comment
2	**M-1T**	-1	ATG A**C**G	Met Thr	c.2T>C	g.2T>C	M1T	missense	initiation codon
2	**R3op**	3	C **C**GA C **T**GA	Arg Opal	c.10C>T	g.10C>T	R3X; R3ter	nonsense	CpG dinucleotic opal stop codon
2	**Q20A**	20	C[**A**]G CG	Gln Arg (fs)	c.62delA	g.62delA	A20	frameshift	
3	**IVS2-14**	37-38	a[**gGT A]**C aC			g.922delGGTA	G12/3; IVS2-1del GGTA; 4IVS2-E3	splicing defect	3'-end IVS2 acceptor splice site, frameshift
3	**R59op**	59	**C**GA **T**GA	Arg Opal	c.178C>T	g.987C>T	R59X; R59ter	nonsense	CpG dinucleotic opal stop codon
3	**1123ins12**	104	GT[GGGGATCGTGGT]GG		c.314^315ins12	g.1123^1124insGGGGATCGTGGT	12E3; V104+GIVV	insertion of 4 amino acids	
4	**4E4**	118-120	C[**A AAC]**A C A		c.357delAAAC	g.2397delAAAC	4, MD4	frameshift	frameshift
4-5	**E4-E5**		cc[tg....CC]AG ccAG			g.1701^3356del	F13/4,5	large deletion	1649 bp deletior from IVS3 to pa of E5
5	**C134R**	134	**T**GT **C**GT	Cys Arg	c.403T>C	g.3279T>C		missense	expression showed alterations in activity
5	**W147R**	147	**T**GG **C**GG	Trp Arg	c.442T>C	g.3318T>C		missense	
5	**A149P**	149	**G**CT **C**CT	Ala Pro	c.448G>C	g.3324G>C		missense	
5	**A174D**	174	G**C**C G**A**C	Ala Asp	c.524C>A	g.3400C>A		missense	
6-7	**E6-E7**		tc[tc....gc]ac tcac			g.4105^5028del	G10/6,7	large deletion	~1.4 kbp deletio from IVS5 to IV
I5	**IVS5+1G>C**		Ggt Gct			g.3417G>C	G C, 5'intron 5; IVS5nt1	splicing defect	
6	**Y203oc**	203	TA**T** TA**A**	Tyr Ochre	c.612T>A	g.4329T>A	Y203X; Y203ter	nonsense	ochre stop codor

I6	**IVS6-1 G>A**		agG aaG			g.4620G>A	G A, 3'intron 6; IVS6sas	splicing defect	3'-end of IVS6 acceptor splice site
7	**C239op**	239	TG**C** TG**A**	Cys Opal	c.720C>A	g.4716C>A	M240; C239X; C239ter	nonsense	opal stop codon
7	**L256P**	256	CTC CCC	Leu Pro	c.770T>C	g.4766T>C		missense	
8	**L288C**	288	[**C**]TT TT	Leu Phe (fs)	c.865delC	g.5272delC	L288delC	frameshift	
8	**R303W**	303	**C**GG **T**GG	Arg Trp	c.910C>T	g.5317C>T		missense	CpG dinucleotic
I8	**7+1**	333-334	ta[**gGCT AAC**]TGC taTG[**G**]C			[g.8343delGGCTAAC; g.8351^8352insG]		slicing defect	3'-end of IVS8 acceptor splice site and codons 333-334 deletec plus G insertion codon 335, expression of RNA showed splicing defect
9	**N334K**	334	AA**C** AA**G**	Asn Lys	c.1005C>G	g.8349C>G		missense	
9	**A337V**	337	G**C**G G**T**G	Ala Val	c.1013C>T	g.8357C>T		missense	CpG dinucleotic expression showed alterations in activity

Polymorphisms in the Human Aldolase B Gene

Exon	Trivial Name[a]	Nucleotide change[c]	Systematic Name[f] (Genomic based)	Other Names[g]	Consequence	Comments	Reference
I8	**IVS8nt84; IVS8nt105**	tcg ttg; caa cga	[g.5490C>T;g.5511A>G]		SNP	CpG dinucleotide,	Brooks an 1993
I8	**IVS8nt1410**	?	g.6817^6822?		RFLP	loss of *Pvu* II site	Paolella 1987
9	**g.8508T>C**	CTA CCA	g.8508T>C	3UTnt69	SNP		Chi and T unpublish
-	**g.9442Msp**	?	g.9442?	3FLnt570	RFLP	*Msp* I site	Sadakane Hori, 199

[a] The names of the HFI mutations are derived from the original literature citations or comply with the recommended nomenclature described by Antonarakis et al., 1998. names are recommended and intended to minimize confusion in the literature. The Trivial Names recommended were changed from the original description in the literatu underlined names in "Other Names" column) only in such cases for consistency with other mutations of the same type (i.e., Q20A and L288C), to be consistent with rec

(Ali et al., 1998 and Tolan, 1995) (e.g., □4E4 and C239op), or shortened to compl;y with the recommended nomenclature (e.g., IVS5+1G>C instead of G□ C, 5'intron 5). Th for stop codons; **op**, **oc**, or **am** (TGA, TAA, or TAG in the DNA, respectively) are used here rather than the alternate designation 'X', and is suggested for general use. Th (X) is inappropriate because it means 'unspecified amino acid' as defined by the IUPAC one-letter code for amino acids (IUPAC-IUB, 1985). These designations are in ge the HFI mutations described (Ali et al., 1994b; Brooks and Tolan, 1994).

[b] Numbering of codons corresponds to that described by Tolan et al. (1984). It does not count condon #1 as methionine because it is well established that the amino-term human aldolase B protei is alanine. Re-naming the condons will confuse genetic studies with those of the enzyme's structure and function.

[c] **Bold** indicates mutated bases. The capital letters denote nucleotide bases encoded in exons, small letters denote nucleotides encoded in introns or flanking regions. Bra bases involved in insertions or deletions.

[d] Reference sequence for the cDNA of human aldolase B is from Besmond et al., 1983 and Tolan et al., 1984. GenBank accession number **K01177**. Base #1 is base c.1 in t nomenclature.

[e] Reference sequence for the human aldolase B gene (aldoB) is from Tolan and Penhoet, 1986. GenBank accession numbers **M15656** & **M15657**. Base #5817 in M15567 i this nomenclature, until g.4424 which is base #1 in M15656. This two-part GenBank reference is necessary due to ca. 500 bp missing sequence from intron 6. When this complete the HFI mutations in exons 7-9 (IVS6-1 G>A, C239op, L256P, L288□C, R303W, □7+1, N334K, & A337V) will have a different genomic sytematic name.

[f] <u>Underline</u> indicates the name of a mutation not listed unter the Trivial Name that was originally used in the publication where it was first described.

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