

Mutations *Aspergillus nidulans*

Allele	Nucleotide change ¹	Mutation type	Predicted mutant fungal HGO protein ²	Equivalence of mutated residue(s) to human HGO residue(s)
<i>hmgA2</i>	C1206G	Nonsense	1→ 302*	1→ 297*
<i>hmgA3</i>	879insA	Frameshift	1→ 194fs	1→ 190fs
<i>hmgA5</i>	ΔG1657	Frameshift	1→ 437fs	1→ 430fs
<i>hmgA6</i>	C1188G	Missense	His297Gln	His292
<i>hmgA8</i>	G875C	Missense	Arg193Pro	Ser189
<i>hmgA9</i>	G198T	Missense	Met1Ile	
<i>hmgA10</i>	C1315T	Missense	His340Tyr	His335
<i>hmgA11</i>	ΔA523fs	Frameshift	1→ 94fs	1→ 86fs
<i>hmgA12</i>	Δ(A1414→C1416)	Deletion	Δ Ile373	Δ Thr367
<i>hmgA13</i>	A310T	Splicing	?	
<i>hmgA14</i>	C238T	Nonsense	1→ 14*	1→ 5*
<i>hmgA15</i>	C504G	Nonsense	1→ 86*	1→ 78*
<i>hmgA16</i>	C1318G	Missense	Arg341Gly	Arg336
<i>hmgA17</i>	G763C	Missense	Gly174Arg	Gly170
<i>hmgA18</i>	G1647A	Nonsense	1→ 433*	1→ 426*
<i>hmgA19</i>	393ins26nts	Frameshift	1→ 50fs	1→ 44fs
<i>hmgA20</i>	G816C	Splicing	?	
<i>hmgA21</i>	Δ(G1473→G1569)	Deletion	Δ (Lys393→Ser408)	Δ (Ala387→ Thr395)
<i>hmgA22</i>	T770G	Missense	Leu176Trp	Met172
<i>hmgA23</i>	609ins7nts	Frameshift	1→ 122fs	1→ 118fs
<i>hmgA24</i>	T743C	Missense	Leu167Pro	Leu163
<i>hmgA25</i>	G264T	Splicing	?	

1) Nucleotide 1 is the first base of the published *A. nidulans* cDNA sequence: U30797.

2) Asterisk denotes an stop codon; fs indicates mutant frameshifted amino acid sequence after the indicated wild type residue

(AKUdatabase; <http://www.alkaptonuria.cib.csic.es/>)