

	Gephebase Gene	GepheID
Sulfotransferase-OXA-Resistance (SULT-OR) (<a +sulfotransferase-oxa-resistance+(sult-or)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Sulfotransferase-OXA-Resistance+(SULT-OR)+"#gephebase-summary-title)	GP00001470	Main curator
Published	Prigent	
	Entry Status	

Trait Category	Trait	Trait State in Taxon A	Trait State in Taxon B	Ancestral State	Taxonomic Status
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)					
Xenobiotic resistance (oxamniquine) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (oxamniquine)^#gephebase-summary-title)					
Human blood fluke OXA-sensitive (wild-type)					
Human blood fluke laboratory-selected OXA-resistant (500-fold reduction in drug sensitivity)					
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)					

GENOTYPIC CHANGE

SULT-OR	Generic Gene Name	G4VLE5 (http://www.uniprot.org/uniprot/G4VLE5)	UniProtKB Schistosoma mansoni
Smp_089320	Synonyms	KU952091 (https://www.ncbi.nlm.nih.gov/nuccore/KU952091)	GenebankID or UniProtKB
-	String		
-	Sequence Similarities		
-	GO - Molecular Function		
	GO:0016740 : transferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016740)		
-	GO - Biological Process		
-	GO - Cellular Component		
	No (<a +no`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?and+Presumptive+Null=">https://www.gephebase.org/search-criteria?and+Presumptive+Null="+No`#gephebase-summary-title)		Presumptive Null
			Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding~#gephebase-summary-title)	Aberration Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Deletion~#gephebase-summary-title)	Deletion Size
1-9 bp	Molecular Details of the Mutation
E142del	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	Main Reference
Genetic and molecular basis of drug resistance and species-specific drug action in schistosome parasites. (2013) (https://pubmed.ncbi.nlm.nih.gov/24263136)	Authors
Valentim CL; Cioli D; Chevalier FD; Cao X; Taylor AB; Holloway SP; Pica-Mattoccia L; Guidi A; Basso A; Tsai IJ; Berriman M; Carvalho-Queiroz C; Almeida M; Aguilar H; Frantz DE; Hart PJ; LoVerde PT; Anderson TJ	Abstract
Oxamniquine resistance evolved in the human blood fluke (<i>Schistosoma mansoni</i>) in Brazil in the 1970s. We crossed parental parasites differing ~500-fold in drug response, determined drug sensitivity and marker segregation in clonally derived second-generation progeny, and identified a single quantitative trait locus (logarithm of odds = 31) on chromosome 6. A sulfotransferase was identified as the causative gene by using RNA interference knockdown and biochemical complementation assays, and we subsequently demonstrated independent origins of loss-of-function mutations in field-derived and laboratory-selected resistant parasites. These results demonstrate the utility of linkage mapping in a human helminth parasite, while crystallographic analyses of protein-drug interactions illuminate the mode of drug action and provide a framework for rational design of oxamniquine derivatives that kill both <i>S. mansoni</i> and <i>S. haematobium</i>, the two species responsible for >99% of schistosomiasis cases worldwide.	
	Additional References

RELATED GEPHE

No matches found.	Related Genes
2 (https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~Sulfotransferase-OXA-Resistance+(SULT-OR)~/and+Taxon+ID=~6183~/or+Gene+Gephebase=~Sulfotransferase-OXA-Resistance+(SULT-OR)~/and+Taxon+ID=~6183~#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS

identified as the causative gene using RNAi knockdown and biochemical complementation assays