GEPHE SUMMARY

Gephebase Gene
opsin - rhodopsin (MWS=duplicate of LWS) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^opsin - rhodopsin (MWS=duplicate of LWS)^#gephebase-summary-title)

GepheID
GP00000778

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Color vision (green-shift) (https://www.gephebase.org/search-criteria?/and+Trait=^Color vision (green-shift)^#gephebase-summary-title)

Trait State in Taxon A
Other primates

Trait State in Taxon B
Catarrhines; Homo sapiens

Ancestral State
Data not curated

Taxonomic Status
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intergeneric or Higher^#gephebase-summary-title)

Taxon A

Latin Name
Primates (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Primates^#gephebase-summary-title)

Common Name
-

Synonyms
Primata; Primates Linnaeus, 1758

Rank
order

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires

Parent
Euarchontoglires () - (Rank: superorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 314146)

NCBI Taxonomy ID
9443 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9443)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Catarrhini (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Catarrhini^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
parvorder

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes

Parent
Simiiformes () - (Rank: infraorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 314293)

NCBI Taxonomy ID
9526 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9526)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
OPN1MW

Synonyms
GCP; GOP; OPN1MW

String
-

Sequence Similarities
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.

GO - Molecular Function
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)
GO:0009881 : photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0009881)

GO - Biological Process
GO:0007186 : G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007186)

UniProtKB Homo sapiens
P04001 (http://www.uniprot.org/uniprot/P04001)

GenebankID or UniProtKB
BAB88652 (https://www.ncbi.nlm.nih.gov/nuccore/BAB88652)

GO:0001523 : retinoid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0001523)
GO:0018298 : protein-chromophore linkage
(https://www.ebi.ac.uk/QuickGO/term/GO:0018298)
GO:0007601 : visual perception (https://www.ebi.ac.uk/QuickGO/term/GO:0007601)
GO:0071482 : cellular response to light stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0071482)
GO:0007602 : phototransduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007602)
GO:0032467 : positive regulation of cytokinesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0032467)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0001750 : photoreceptor outer segment
(https://www.ebi.ac.uk/QuickGO/term/GO:0001750)
GO:0097381 : photoreceptor disc membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0097381)

Mutation #1

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ser	Tyr	116

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

Asenjo AB; Rim J; Oprian DD

Abstract

The human red and green color vision pigments are identical at all but 15 of their 364 amino acids, and yet their absorption maxima differ by 31 nm. In an extensive mutagenesis study, including a set of 28 chimeric proteins modeled after pigments in the color-deficient human population and an additional 30 single and multiple point mutants, the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser116-->Tyr, Ser180-->Ala, Ile230-->Thr, Ala233-->Ser, Tyr277-->Phe, Thr285-->Ala, and Tyr309-->Phe.

Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

Mutation #2

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ser	Ala	180

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

Asenjo AB; Rim J; Oprian DD

Abstract

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Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

Mutation #3

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ile	Thr	230

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

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Abstract

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Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

Mutation #4

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ala	Ser	233

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

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Abstract

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Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

Mutation #5

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Tyr	Phe	277

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

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Abstract

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Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

Mutation #6

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Thr	Ala	285

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

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Abstract

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Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

Mutation #7

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S116Y; S180A; I230T; A233S/T; Y277F; T285A; Y309F
according to an extensive mutagenesis study including a set of 28 chimeric proteins and an additional 30 single and multiple point mutants the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser 116Tyr Ser 180Ala Ile 230Thr Ala233Ser Tyr277Phe Thr285Ala and Tyr309Phe.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Tyr	Phe	309

Main Reference

Molecular determinants of human red/green color discrimination. (1994) (https://pubmed.ncbi.nlm.nih.gov/8185948)

Authors

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Abstract

The human red and green color vision pigments are identical at all but 15 of their 364 amino acids, and yet their absorption maxima differ by 31 nm. In an extensive mutagenesis study, including a set of 28 chimeric proteins modeled after pigments in the color-deficient human population and an additional 30 single and multiple point mutants, the spectral difference between these 2 pigments is shown to be determined by 7 and only 7 amino acid residues. In going from the red pigment to the green pigment, the 7 residues are Ser116-->Tyr, Ser180-->Ala, Ile230-->Thr, Ala233-->Ser, Tyr277-->Phe, Thr285-->Ala, and Tyr309-->Phe.

Additional References

Molecular evolution of trichromacy in primates. (1998) (https://pubmed.ncbi.nlm.nih.gov/9893841)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect