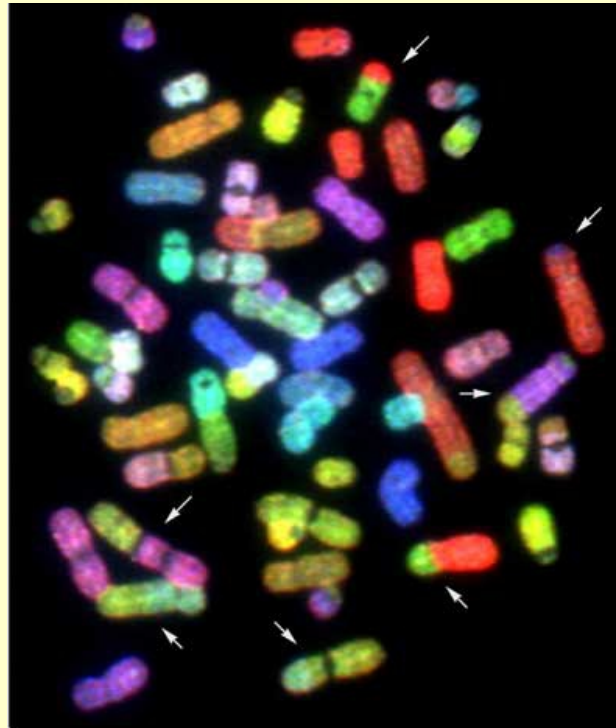


Genome Databases

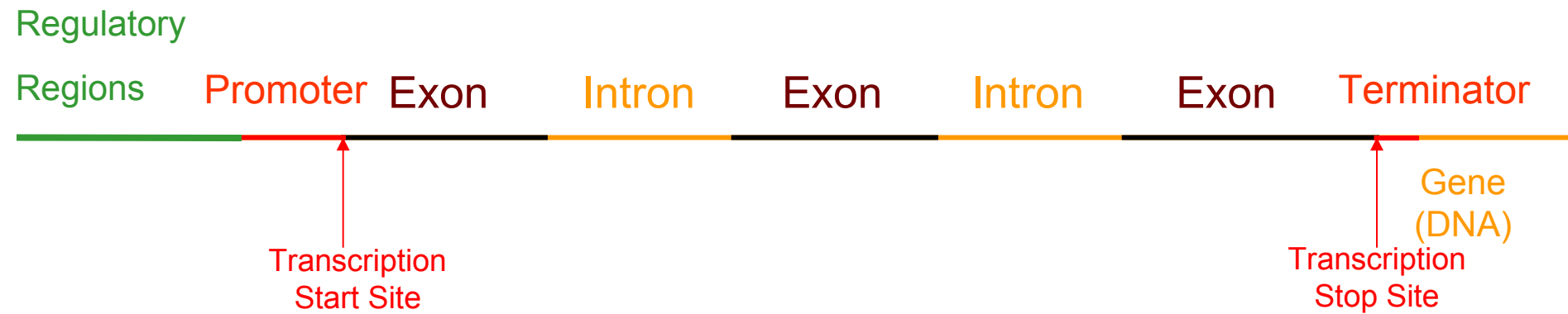
Genomics & Medicine

<http://biochem118.stanford.edu/>

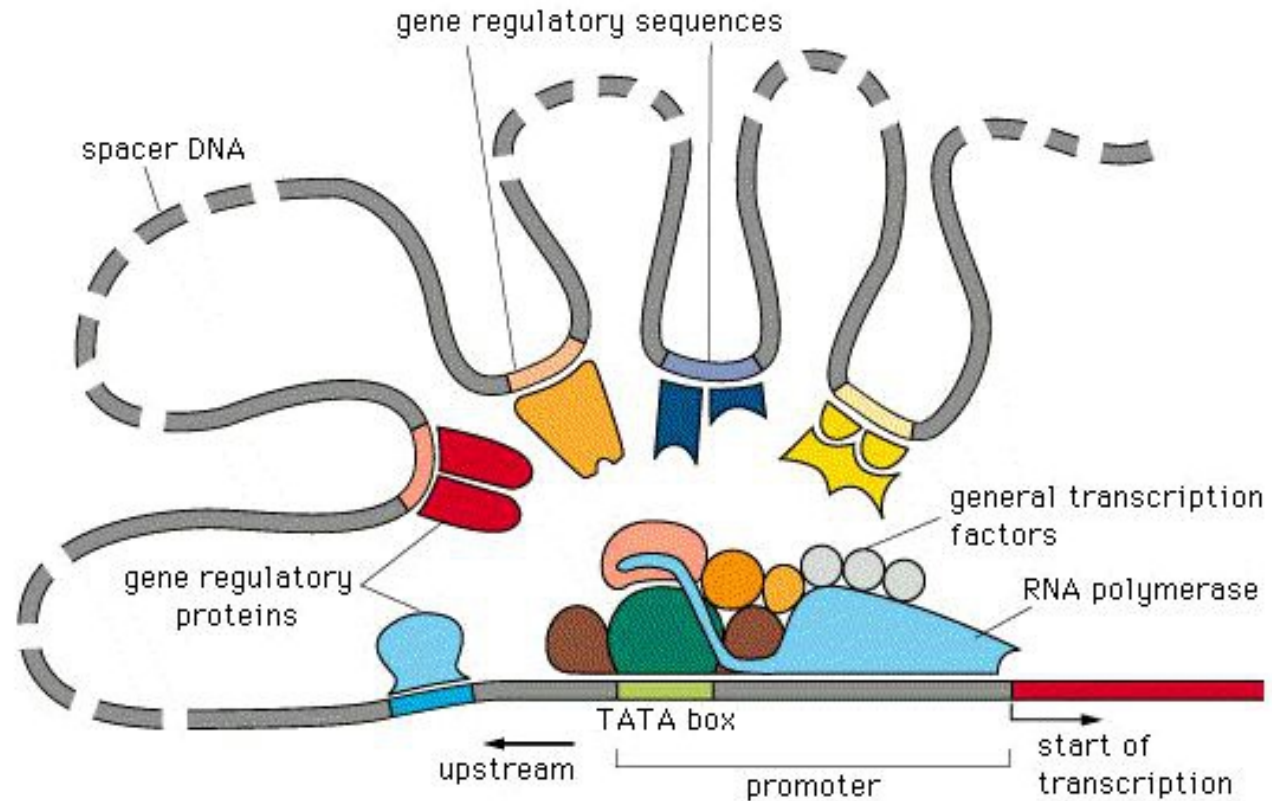


Doug Brutlag, Professor Emeritus
of Biochemistry & Medicine (by courtesy)
Stanford University School of Medicine

Components of a Typical Human Gene

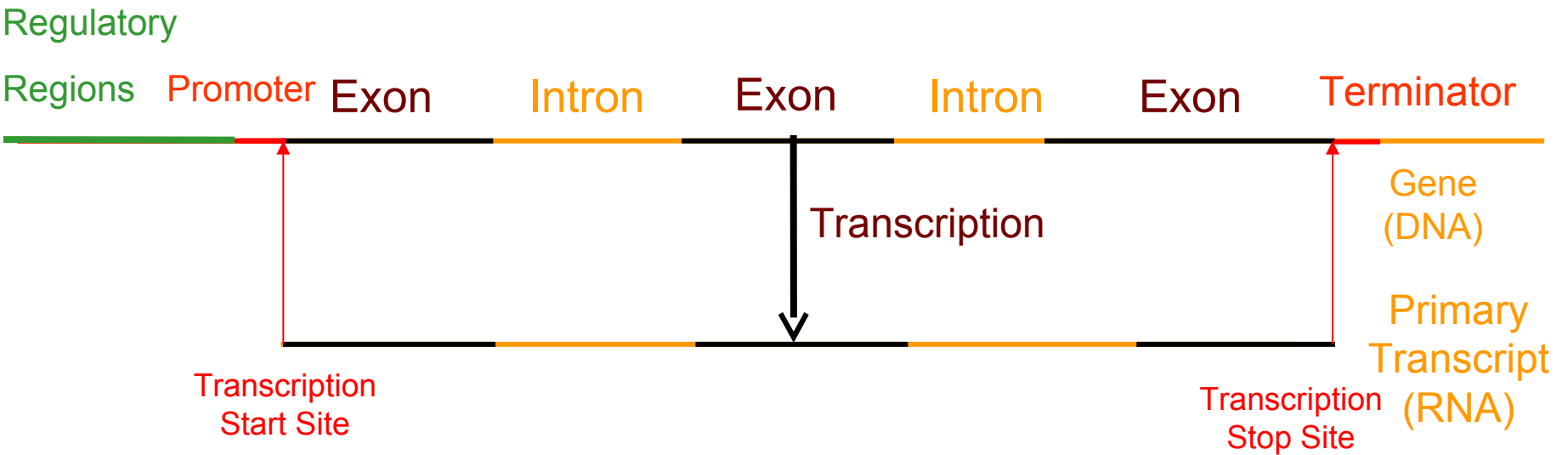


Multiple Enhancer Sequences

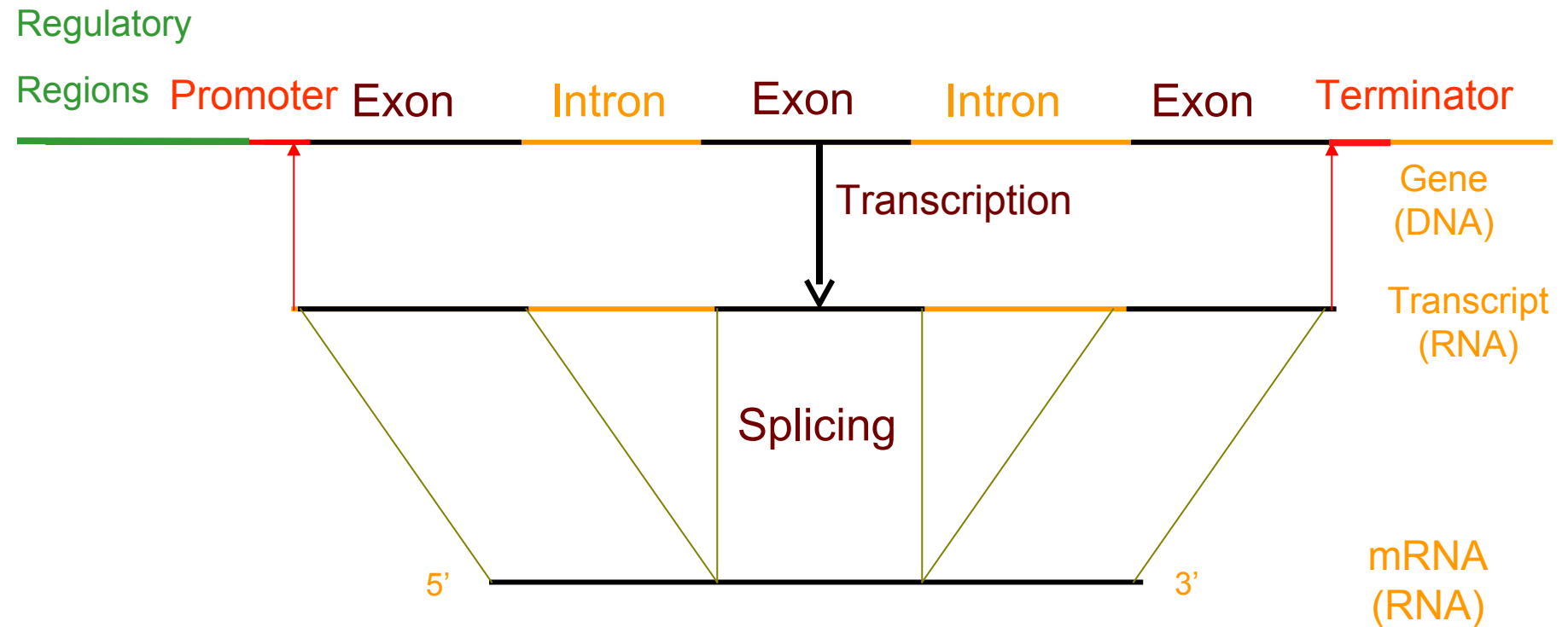


©1996 GARLAND PUBLISHING

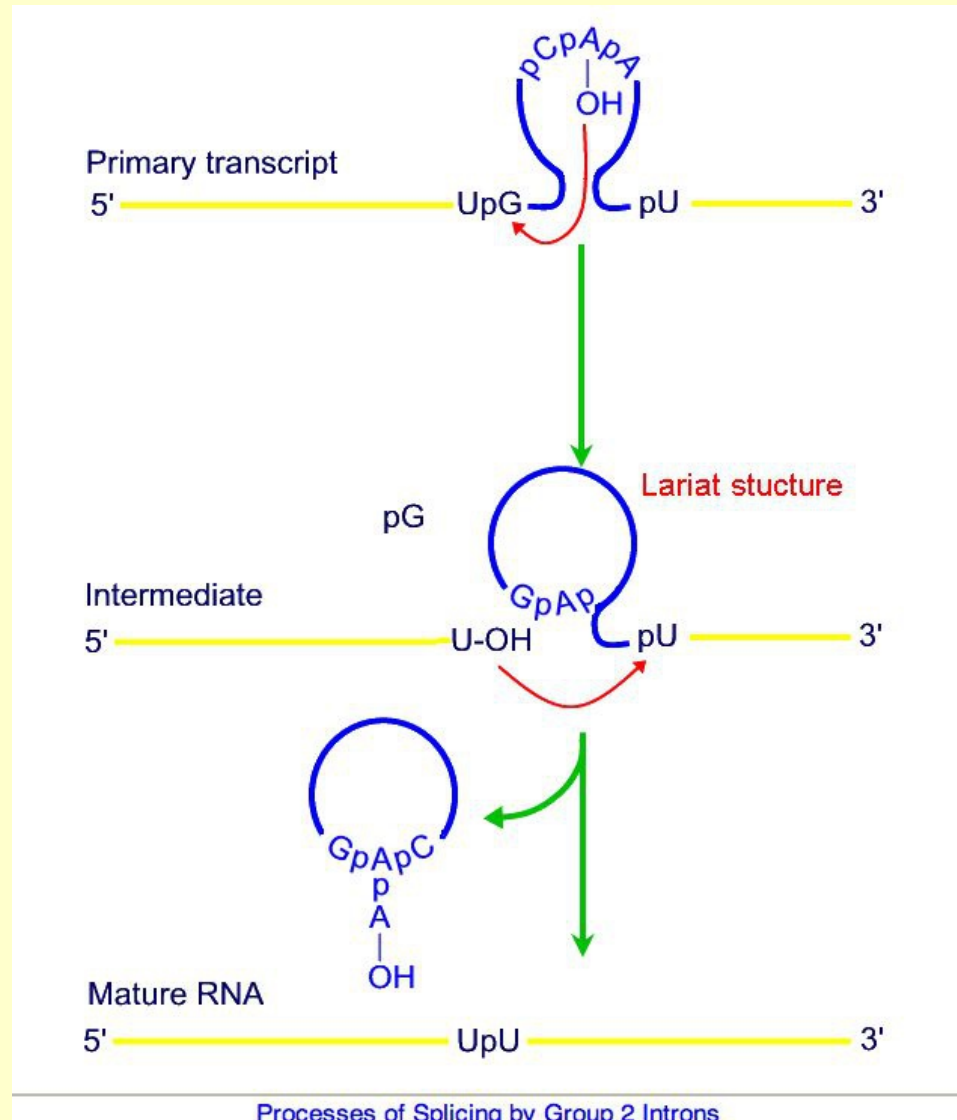
Active Genes are Transcribed into RNA



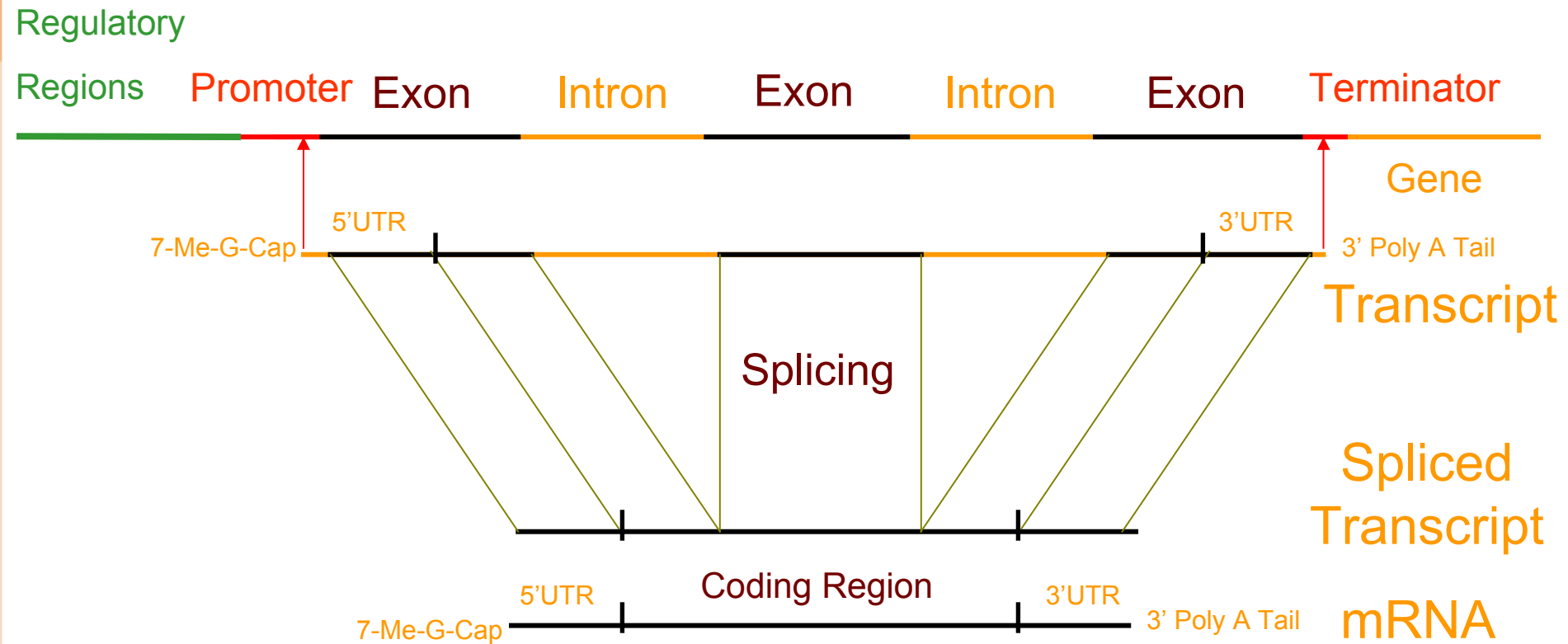
Splicing Transcript Yields Mature mRNA



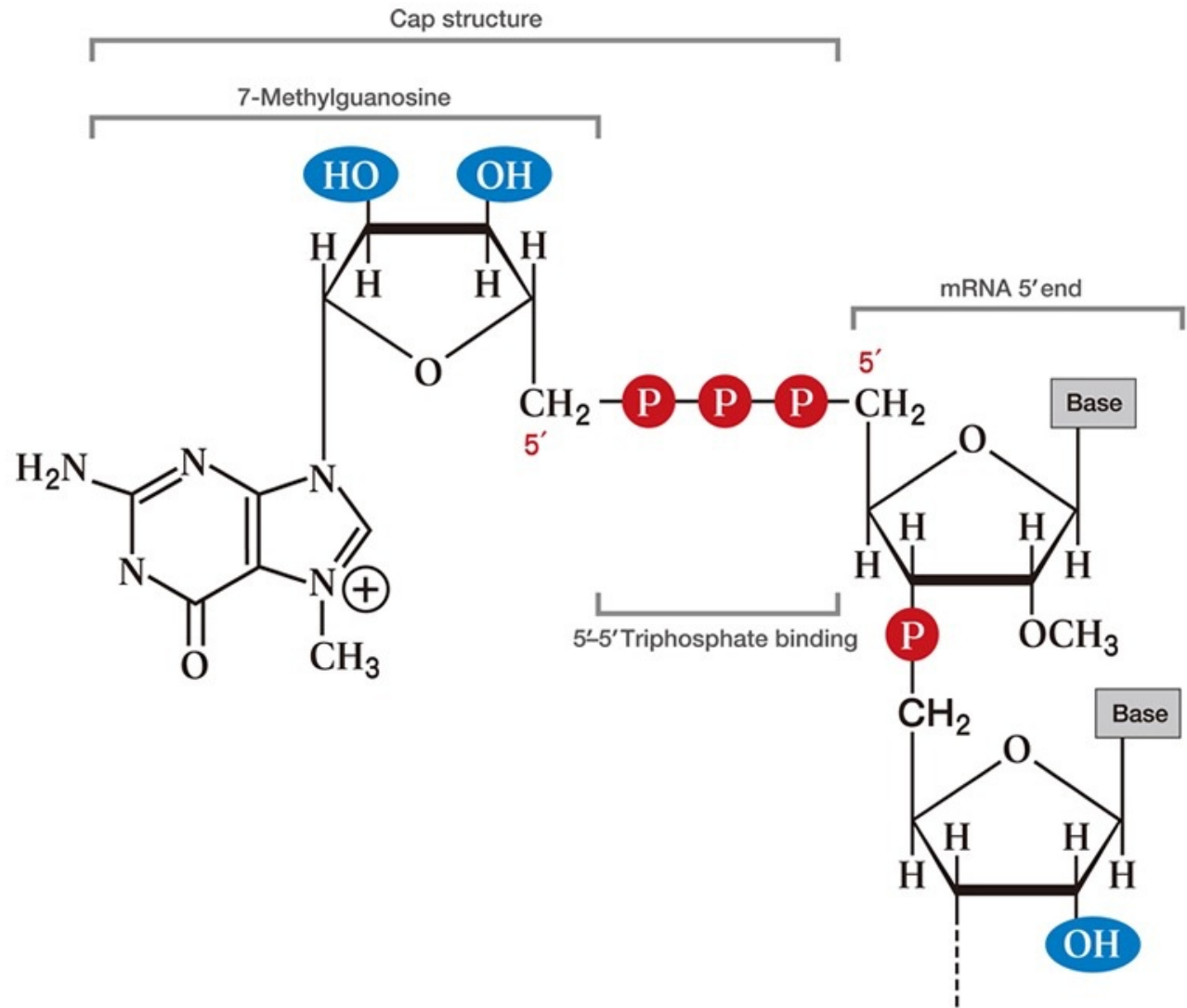
Intron Splicing Mechanism



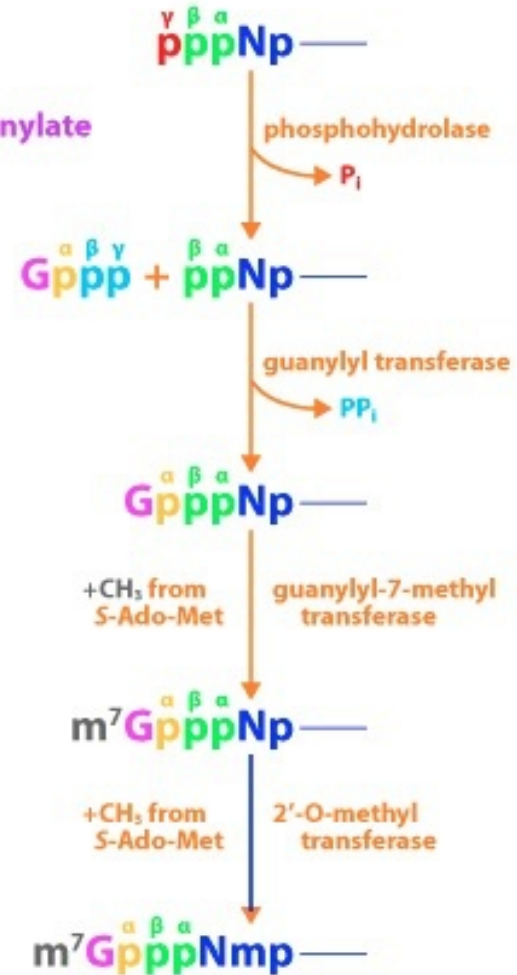
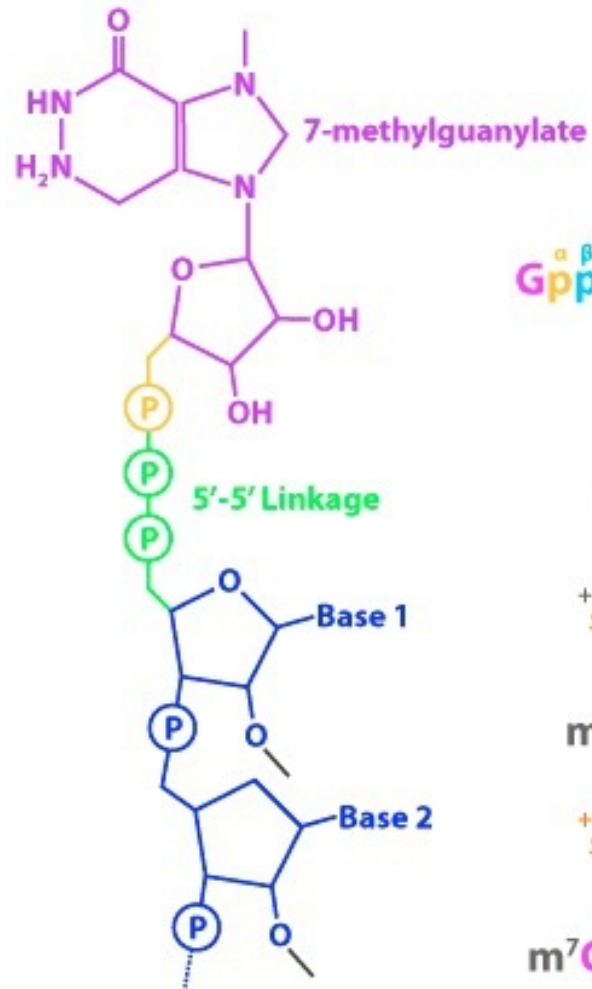
Mature mRNA contains 7-Methyl-Guanylate 5' Cap and 3' Poly A Tail



Mature mRNA contains 7-Methyl-Guanylate 5' Cap

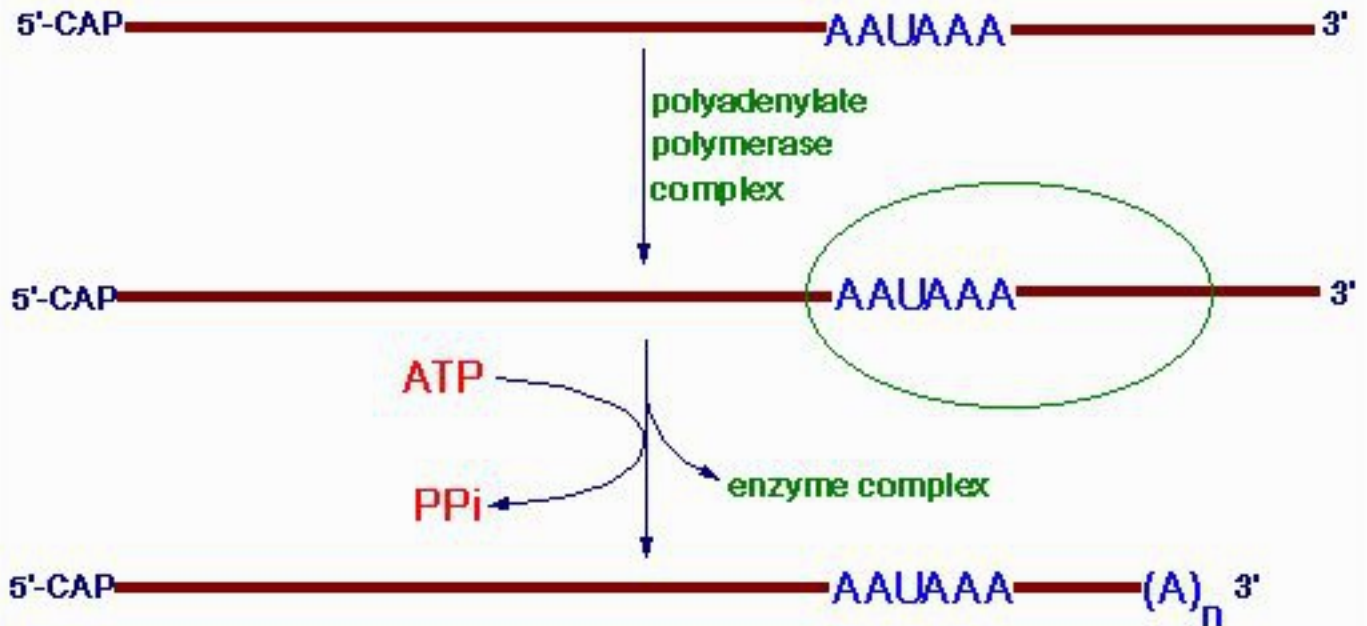


Mature mRNA contains 7-Methyl-Guanylate 5' Cap



PolyAdenylation of mRNAs

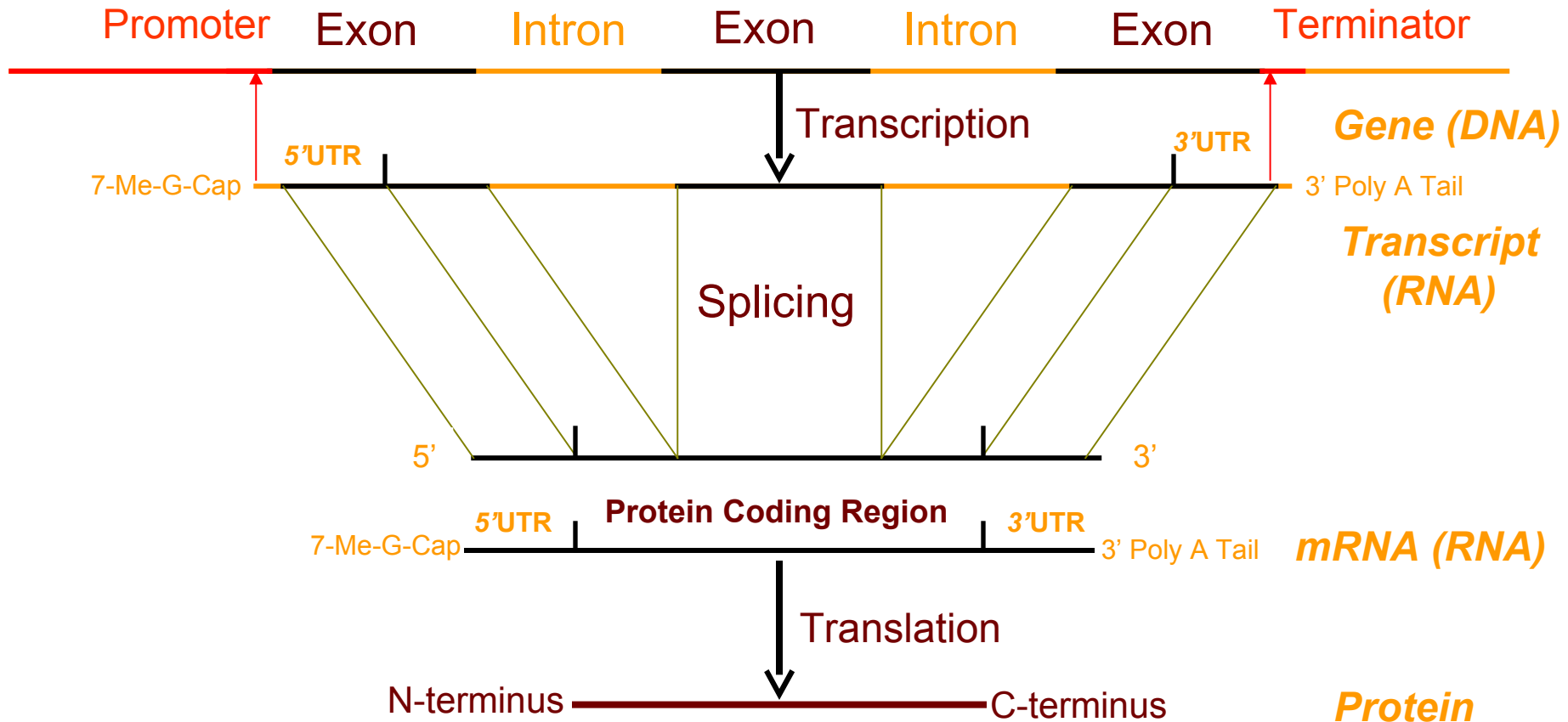
Polyadenylation of mRNAs



copyright 1996 M.W.King

Processes of Polyadenylation

Mature mRNA contains Coding Region and 5' and 3' Untranslated Regions

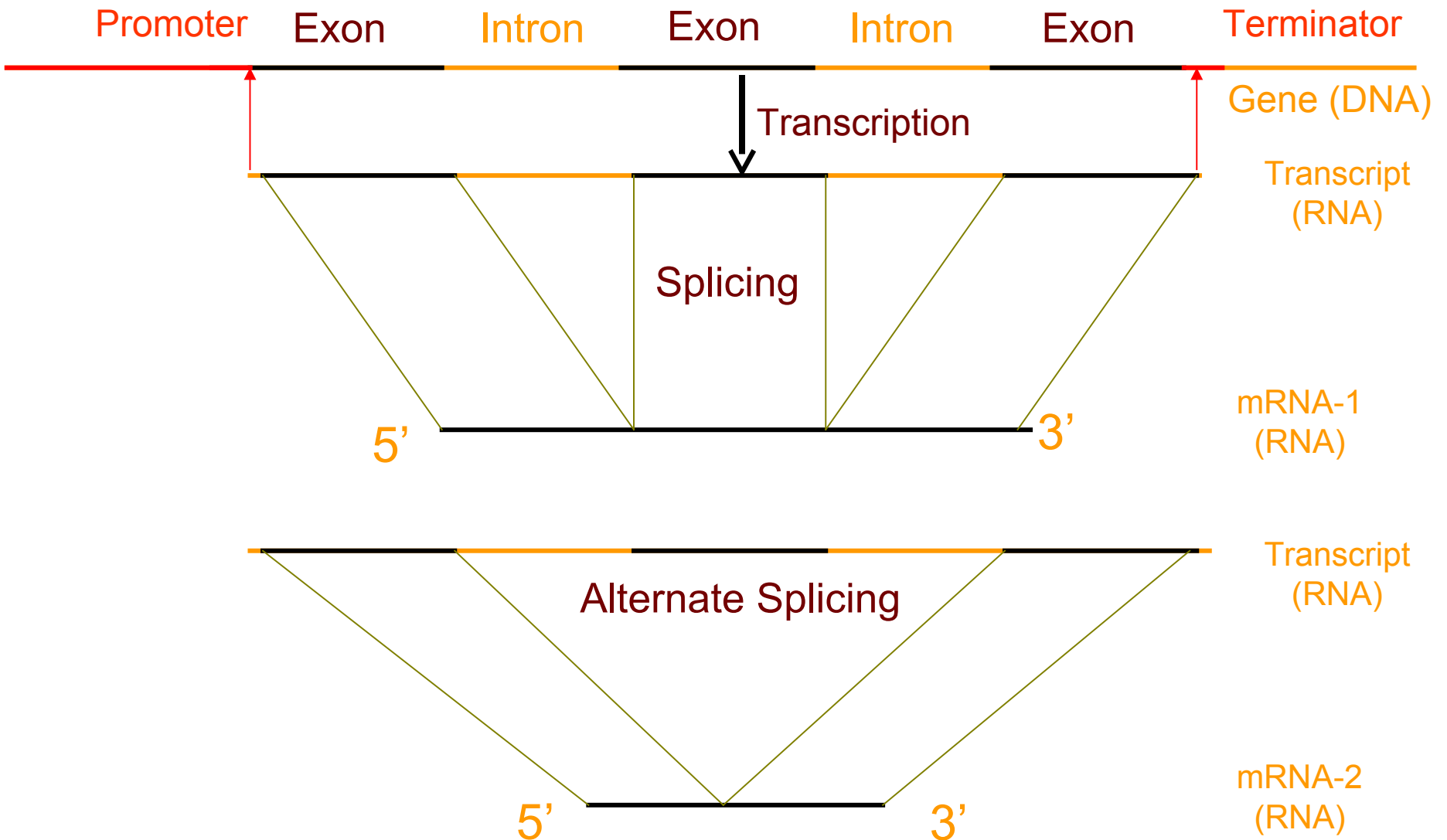




		Second Letter				
		T	C	A	G	
First Letter	T	TTT } Phe TTC } TTA } Leu TTG }	TCT } TCC } Ser TCA } TCG }	TAT } Tyr TAC } TAA } Stop TAG } Stop	TGT } Cys TGC } TGA } Stop TGG } Trp	T C A G
	C	CTT } CTC } Leu CTA } CTG }	CCT } CCC } Pro CCA } CCG }	CAT } His CAC } CAA } Gln CAG }	CGT } CGC } Arg CGA } CGG }	T C A G
	A	ATT } ATC } Ile ATA } ATG } Met	ACT } ACC } Thr ACA } ACG }	AAT } Asn AAC } AAA } Lys AAG }	AGT } Ser AGC } AGA } Arg AGG }	T C A G
	G	GTT } GTC } Val GTA } GTG }	GCT } GCC } Ala GCA } GCG }	GAT } Asp GAC } GAA } Glu GAG }	GGT } GGC } Gly GGA } GGG }	T C A G

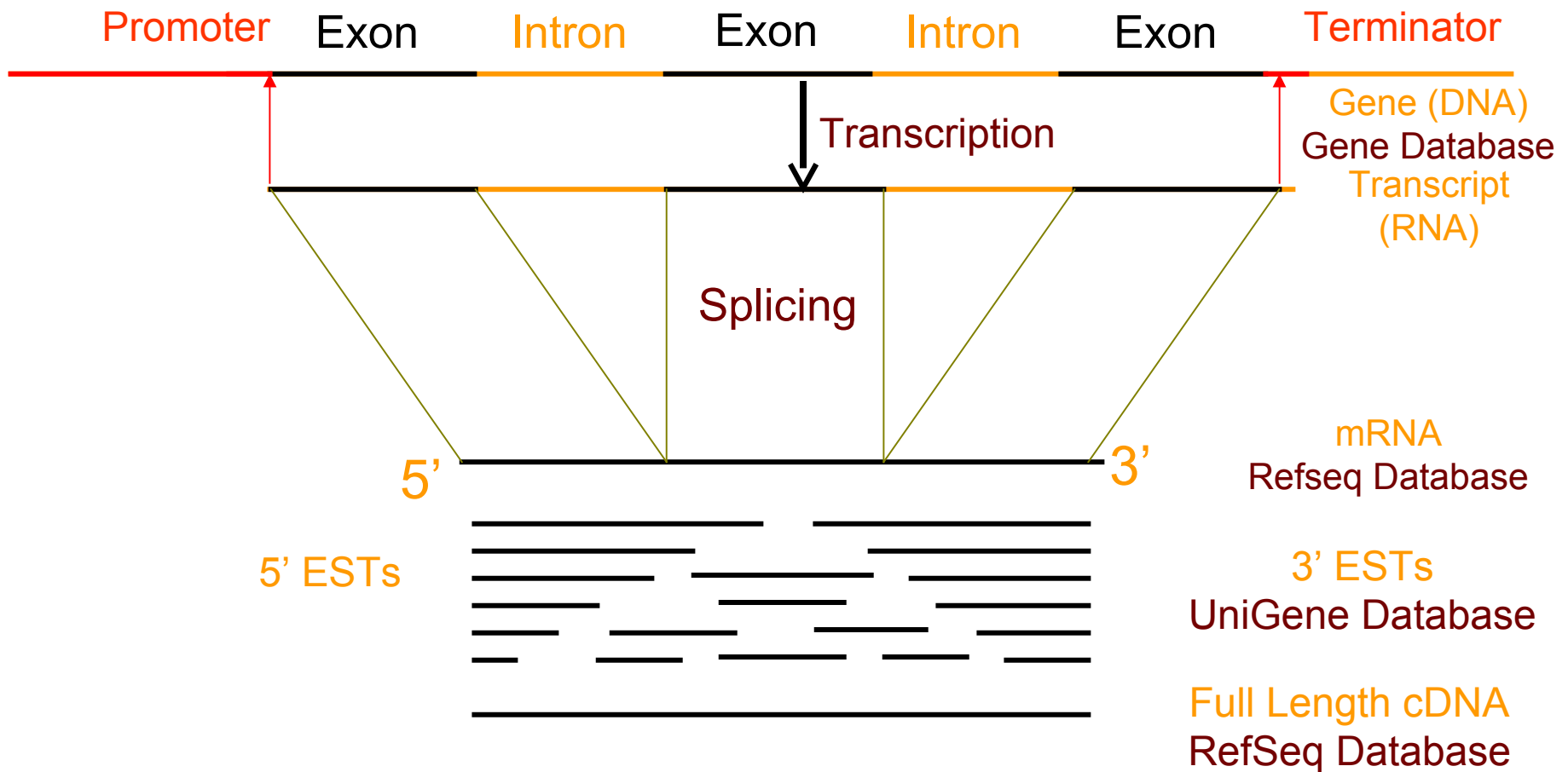
The Genetic Code

Alternative Splicing Generates Distinct Proteins in Different Tissues

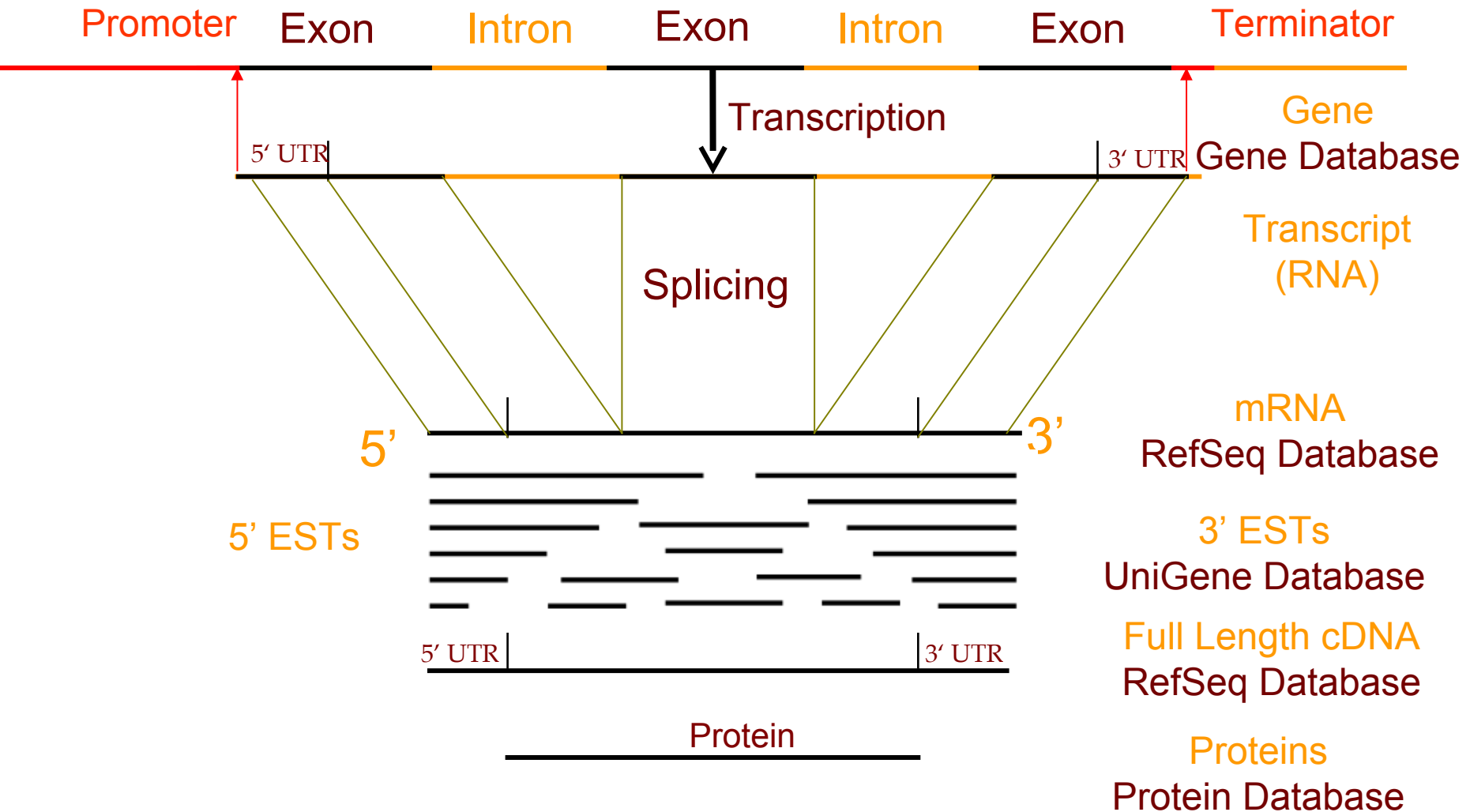


Messenger RNA (mRNA) Databases

ESTs UniGene & Full Length cDNA RefSeq



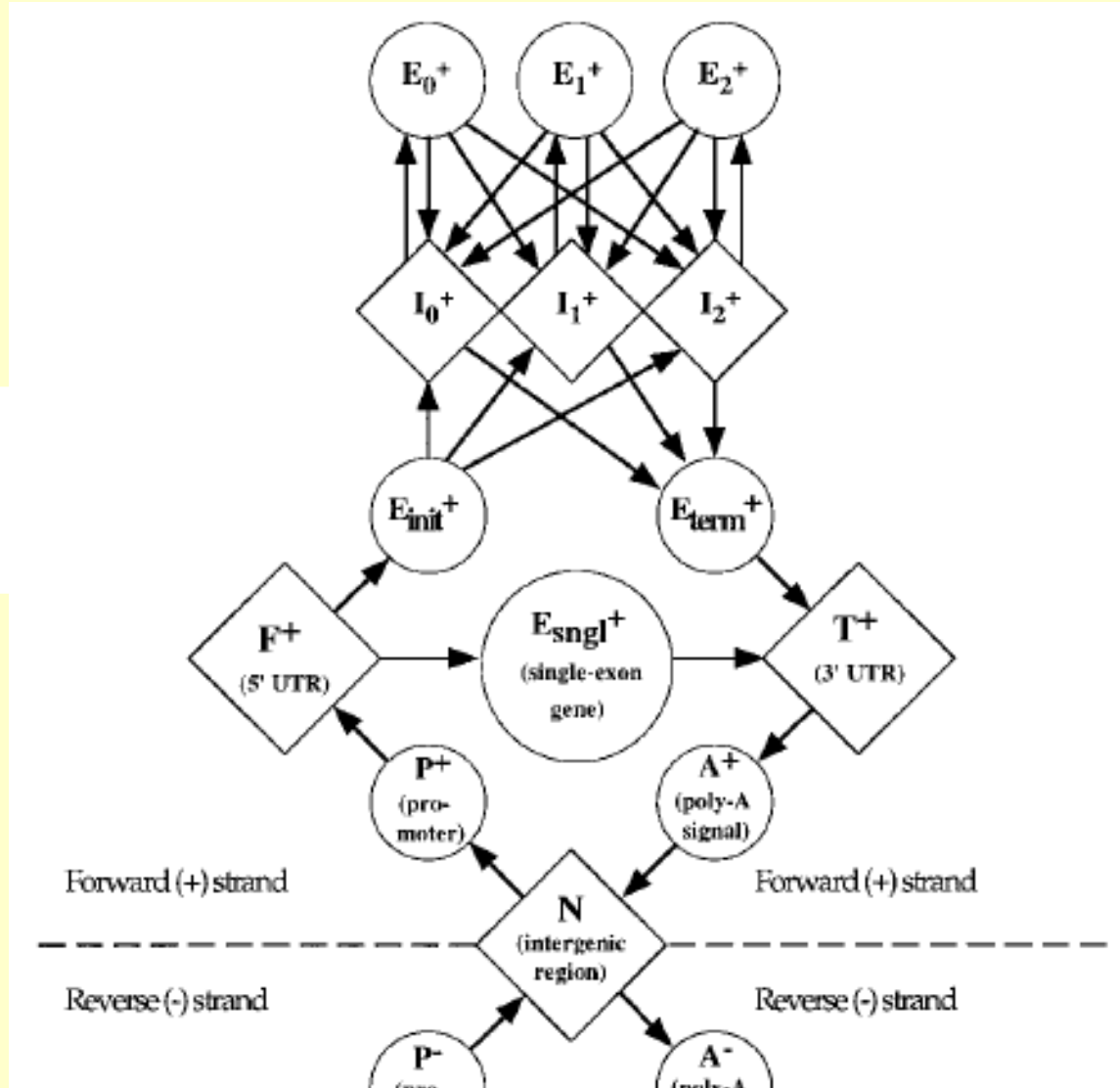
ESTs, Full Length cDNA UniGene & RefSeq Databases



GENSCAN Gene Model

<http://genes.mit.edu/GENSCAN.html>

Hidden Markov models of gene structure



Genome Databases

Assembled contigs

A Mapping

uniSTS

dbSNP

B Gene Prediction

GrailEXP

GenScan

FGENESH

FGENESH+

GeneMark

C Expression Data

Human ESTs

UniGene Human

RefSeq Human

Ensembl cDNA

Mouse ESTs

Entrez Gene Mouse

RefSeq Mouse

D Protein Similarity

NCBI Proteins

UniProt

E Additional Data

Promoters

F Summary

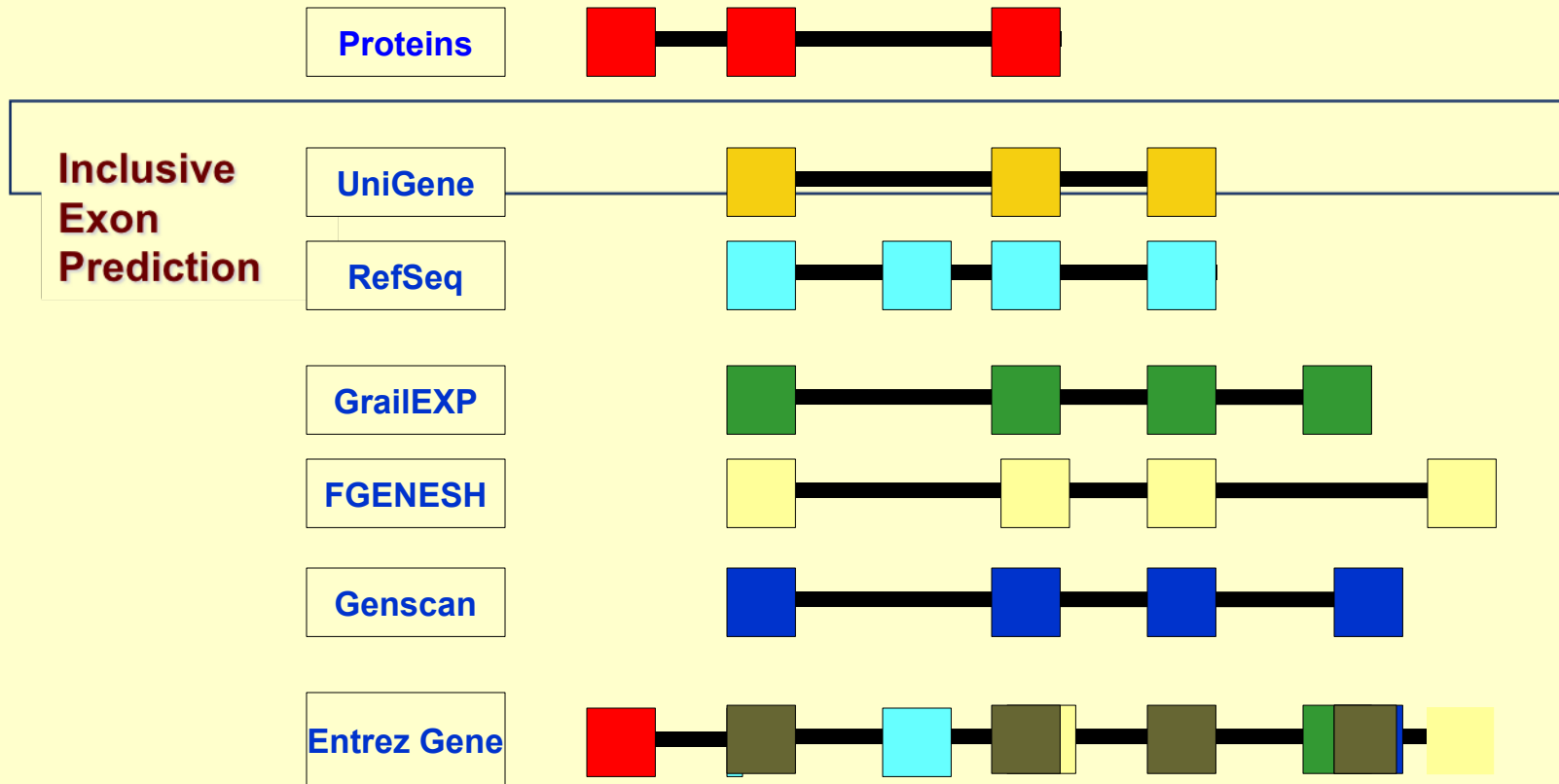
Entrez Gene

UCSC Browser

Ensembl

Entrez Gene Loci

<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>



Genome

Genome ▾

dog



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Genome

This resource organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations.

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Genome Annotation and Analysis

[Eukaryotic Genome Annotation](#)

[Prokaryotic Genome Annotation](#)

[PASC \(Pairwise Sequence Comparison\)](#)

[TaxPlot \(3-way Genome Comparison\)](#)

External Resources

[GOLD - Genomes Online Database](#)

[Ensembl Genome Browser](#)

[Bacteria Genomes at Sanger](#)

[Large-Scale Genome Sequencing \(NHGRI\)](#)

Canis lupus familiaris Genome

<http://www.ncbi.nlm.nih.gov/genome/85>

Display Settings: Overview

Send to:

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Canis lupus familiaris (dog)

Model organism that is notable for its extensive genetic diversity and morphological variation

Lineage: [Eukaryota\[2439\]](#); [Metazoa\[952\]](#); [Chordata\[393\]](#); [Craniata\[386\]](#); [Vertebrata\[385\]](#); [Euteleostomi\[377\]](#); [Mammalia\[147\]](#); [Eutheria\[143\]](#); [Laurasiatheria\[56\]](#); [Carnivora\[14\]](#); [Caniformia\[11\]](#); [Canidae\[3\]](#); [Canis\[3\]](#); [Canis lupus\[2\]](#); [Canis lupus familiaris\[1\]](#)

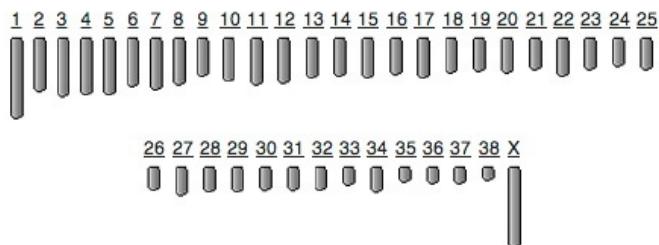
The dog, *Canis lupus familiaris*, is a useful model organism for medical research due to extensive genetic diversity and morphological variation within the species and to aggressive breeding practices that have resulted in inbred populations of dogs. Many breeds of dog are particularly susceptible to inherited diseases that are also common in [More...](#)

Representative

Reference genome:

[Canis lupus familiaris CanFam3.1](#)

Chromosomes



Click on chromosome name to open MapViewer

Genome Sequencing Projects

Chromosomes [1] Scaffolds or contigs [2] SRA or Traces [2]

Organism	BioProject	Assembly	Status	Chrs	Organelles	Size (Mb)	GC%	Gene	Protein
Canis lupus familiaris	PRJNA12384, PRJNA13179	CanFam3.1	<input checked="" type="radio"/>	39	1	2,410.98	35.5	28,864	42,303
Canis lupus familiaris	PRJNA10628	ASM18141v1	<input type="radio"/>	-	-	1,517.48	41.1	-	-
Canis lupus familiaris	PRJNA176193	Beagle	<input type="radio"/>	-	-	2,254.63	40.7	-	-
Canis lupus familiaris	PRJNA167192	-	<input type="radio"/>	-	-	-	-	-	-
Canis lupus familiaris	PRJNA186960	-	<input type="radio"/>	-	-	-	-	-	-

See more...

Canis lupus familiaris

<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9615>



Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock

Display 3 levels using filter: none

Canis lupus familiaris

Taxonomy ID: 9615

Genbank common name: **dog**

Inherited blast name: **carnivores**

Rank: subspecies

Genetic code: [Translation table 1 \(Standard\)](#)

Mitochondrial genetic code: [Translation table 2 \(Vertebrate Mitochondrial\)](#)

Other names:

synonym: **Canis familiaris**

synonym: **Canis domesticus**

synonym: **Canis canis**

common name: **dogs**

includes: **beagle dogs**

includes: **beagle dog**


[Lineage\(full \)](#)

[cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Dipnotetrapodomorpha](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Laurasiatheria](#); [Carnivora](#); [Caniformia](#); [Canidae](#); [Canis](#); [Canis lupus](#)

Entrez records	
Database name	Direct links
Nucleotide	273,893
Nucleotide EST	382,638
Nucleotide GSS	853,938
Protein	53,600
Structure	96
Genome	1
Popset	214
SNP	3,298,379
GEO Datasets	2,478
UniGene	23,847
UniSTS	11,765
PubMed Central	2,234
Gene	39,453
HomoloGene	17,186
SRA Experiments	230
Probe	70,678
Assembly	4
Bio Project	109
Bio Sample	312
Bio Systems	1,746
dbVar	736
GEO Profiles	205,497
PubChem BioAssay	14,366
Protein Clusters	13
Taxonomy	1

Human Genome Resources

<http://www.ncbi.nlm.nih.gov/genome/guide/human/>


 NCBI • Genomic Biology • Homo sapiens
 Search for

Browse your Genome
Click on the Chromosome to show


Genes




Find A Gene

Search for
from

The NCBI Handbook

 An online guide to the use of NCBI resources. Titles of selected chapters that refer to human genome resources are shown below.

 **The Single Nucleotide Polymorphism Database (dbSNP) of Nucleotide Sequence Variation**
Adrienne Kitts and Stephen Sherry



A challenge facing researchers today is that of piecing together and analyzing the plethora of data currently being generated through the Human Genome Project and scores of smaller projects. NCBI's Web site serves an integrated, one-stop, genomic information infrastructure for biomedical researchers from around the world so that they may use these data in their research efforts. [More...](#)

Genes and Human Health

▶ Gene Database

A new database of genes and associated information is now available for searching in Entrez.

▶ dbSNP

A database of single nucleotide polymorphisms (SNPs) and other nucleotide variations.

▶ OMIM

A guide to human genes and inherited disorders maintained by Johns Hopkins University and collaborators.

▶ dbGaP

The database of Genotypes and Phenotypes (dbGaP) was developed to archive and distribute the results of studies that have investigated the interaction of genotype and phenotype.

Epigenomics

▶ NIH Epigenomics Roadmap

Reference epigenomic maps and studies on new epigenetic mechanisms and their relevance to human health.

▶ Roadmap Epigenomics Data

A comprehensive listing of all NIH Roadmap Epigenomics datasets submitted to GEO and SRA.

NCBI Entrez Gene

<http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene>

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Entrez Gene
Genes and mapped phenotypes

Search: Gene

Limits Advanced search Help

human hemoglobin beta Search Clear



Welcome to Entrez Gene

Entrez Gene maintains information about genes from genomes of interest to the RefSeq group.

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[Gene Mailing List](#)

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[Submit Correction](#)

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[Genome Workbench](#)

[Splign](#)

Other Resources

[HomoloGene](#)

[OMIM](#)

[RefSeq](#)

[RefSeqGene](#)

[UniGene](#)

[Protein Clusters](#)

Human Beta-Hemoglobin Gene Entry

<http://www.ncbi.nlm.nih.gov/gene/3043>

Gene

Genes and mapped phenotypes

Search:

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[Send to:](#)

HBB hemoglobin, beta [*Homo sapiens*]

Gene ID: 3043, updated on 14-Jan-2011

Summary

- Official Symbol** HBB provided by [HGNC](#)
- Official Full Name** hemoglobin, beta provided by [HGNC](#)
- Primary source** [HGNC:4827](#)
- See related** [Ensembl:ENSG00000223609](#); [Ensembl:ENSG00000244734](#); [HPRD:00786](#); [MIM:141900](#)
- Gene type** protein coding
- RefSeq status** REVIEWED
- Organism** [Homo sapiens](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
- Also known as** CD113t-C; beta-globin; HBB
- Summary** The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, Hb A. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon -- gamma-G -- gamma-A -- delta -- beta--3'. [provided by RefSeq]

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- [Genomic regions, transcripts, and products](#)
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- [Interactions](#)
- [General gene info](#)
- [General protein info](#)
- [Reference sequences](#)
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Links

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- [BioSystems](#)
- [Books](#)
- [CCDS](#)
- [Conserved Domains](#)
- [Full text in PMC](#)

Human Beta-Hemoglobin Gene Entry

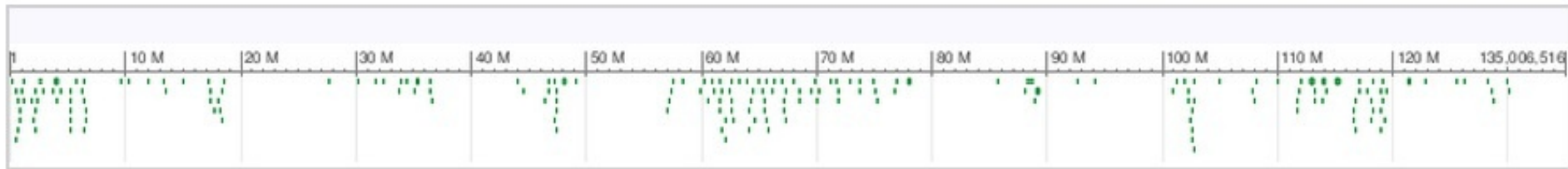
<http://www.ncbi.nlm.nih.gov/gene/3043>

Genomic regions, transcripts, and products

Genomic Sequence

[Go to reference sequence details](#)

[Go to nucleotide](#) [Graphics](#) [FASTA](#) [GenBank](#)



Genes	SNP	Clinical Channel	Cited Variants	Association Results
<p>NC_000518.4  NP_000509.1</p>				

Human Hemoglobin Gene Entry

<http://www.ncbi.nlm.nih.gov/gene/3043>

Related articles in PubMed

1. [Distribution of beta-globin haplotypes among the tribes of southern Gujarat, India.](#)
Aggarwal A, *et al.* Gene, 2013 Jun 1. PMID 23500448.
2. [Self-catalytic DNA depurination underlies human \$\beta\$ -globin gene mutations at codon 6 that cause anemias and thalassemias.](#)
Alvarez-Dominguez JR, *et al.* J Biol Chem, 2013 Apr 19. PMID 23457306.
3. [Sistani population: a different spectrum of \$\beta\$ -thalassemia mutations from other ethnic groups of Iran.](#)
Miri-Moghaddam E, *et al.* Hemoglobin, 2013. PMID 23437895.
4. [Association in cis of the mutations +20 \(C>T\) in the 5' untranslated region and IVS-II-745 \(C>G\) on the \$\beta\$ -globin gene.](#)
Ropero P, *et al.* Hemoglobin, 2013. PMID 23425204.
5. [Identification and molecular characterization of a novel 55-kb deletion recurrent in southern Italy: the Italian \(G\) \$\gamma\$ \(\(A\) \$\gamma\delta\beta\$ \)^o-thalassemia.](#)
Lacerra G, *et al.* Eur J Haematol, 2013 Mar. PMID 23281611.

[See all \(600\) citations in PubMed](#)

[See citations in PubMed for homologs of this gene provided by HomoloGene](#)

GeneRIFs: Gene References Into Functions [What's a GeneRIF?](#)

1. [The beta-globin distribution pattern of various haplotypes was consistent with the global pattern.](#)
2. [analysis of the contact region between CD163 and its high affinity ligand Hp-Hb reveals a mechanism of Ca²⁺-dependent coupling and uncoupling of ligand](#)
3. [Data indicate association of the +20 and IVS-II-745 mutations of beta-globin beta-thalassemia \(beta-thal\). Read More: <http://informahealthcare.com/doi/full/10.3109/03630269.2013.766620>](#)
4. [Data indicate twenty-one beta-globin mutations were identified in beta-thalassemia \(beta-thal\), of which the most frequent ones were IVS-I-5 \(G>C\), followed by codon 15 G>A codon -88 \(C>T\), IVS-II-1 \(G>A\), codons 8/9 \(+G\) and IVS-I-1 \(G>T\).](#)
5. [Data show that Hgb-alpha and Hgb-beta are expressed in carcinoma cells of several types of solid tumors.](#)
6. [analysis of a mouse model of the human beta-globin locus](#)

Human Beta-Hemoglobin Phenotypes

<http://www.ncbi.nlm.nih.gov/gene/3043>

Phenotypes

[Find tests for this gene in the NIH Genetic Testing Registry \(GTR\)](#)

[Review eQTL and phenotype association data in this region using PheGenI](#)

Associated conditions

Description	Tests
<p>beta Thalassemia</p> <p>MedGen: C0005283, OMIM: 613985, GeneReviews: Beta-Thalassemia</p>	Compare labs
<p>Beta thalassemia, dominant inclusion body type</p> <p>MedGen: C1858990, OMIM: 603902, GeneReviews: Not available</p>	Compare labs
<p>Fetal hemoglobin quantitative trait locus 1</p> <p>MedGen: C1841621, OMIM: 141749, GeneReviews: Not available</p>	Compare labs
<p>Hb SS disease</p> <p>MedGen: C0002895, OMIM: 603903, GeneReviews: Sickle Cell Disease</p>	Compare labs
<p>Heinz body anemias</p> <p>MedGen: C0700299, OMIM: 140700, GeneReviews: Not available</p>	Compare labs
<p>Susceptibility to malaria</p> <p>MedGen: C1970028, OMIM: 611162, GeneReviews: Not available</p>	not available

Human Beta-Hemoglobin Phenotypes

<http://www.ncbi.nlm.nih.gov/gene/3043>

NHGRI GWAS Catalog

Description

A genome-wide association scan on the levels of markers of inflammation in Sardinians reveals associations that underpin its complex regulation.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

Genome-wide and fine-resolution association analysis of malaria in West Africa.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

Genome-wide association study indicates two novel resistance loci for severe malaria.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

Genome-wide association study shows BCL11A associated with persistent fetal hemoglobin and amelioration of the phenotype of beta-thalassemia.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

GWAS of blood cell traits identifies novel associated loci and epistatic interactions in Caucasian and African-American children.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

HbA2 levels in normal adults are influenced by two distinct genetic mechanisms.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

Hemoglobin Interactions

<http://www.ncbi.nlm.nih.gov/gene/3043>

Interactions



Items 1 - 25 of 31 < Prev Page 1 of 2 Next >

Products	Interactant	Other Gene	Complex	Source	Pubs	Description
NC_000011.8	NP_006181.1	ORC2		BIND	PubMed	Orc2 interacts with beta-globin origin.
NC_000011.8	NP_000928.1	POLR2A		BIND	PubMed	Beta-globin interacts with pol II.
NC_000011.8	NP_066964.1	XRCC5		BIND	PubMed	Ku80 interacts with beta-globin origin.
P68871	Hemoglobin alpha 2	HBA2		HPRD	PubMed	
P68871	P69905	HBA2		HPRD	PubMed	
P68871	P68871	HBB		HPRD	PubMed	
P68871	P69892	HBG2		HPRD	PubMed	
P68871	P02008	HBZ		HPRD	PubMed	
P68871	P00738	HP		HPRD	PubMed	
P68871	Selenoprotein T	SELT		HPRD	PubMed	
BioGRID:109293	BioGRID:106710	AKT1		BioGRID	PubMed	Affinity Capture-MS
BioGRID:109293	BioGRID:107452	CDK2		BioGRID	PubMed	Affinity Capture-MS
BioGRID:109293	BioGRID:108102	DMWD		BioGRID	PubMed	Affinity Capture-MS
BioGRID:109293	BioGRID:115119	EIF4A3		BioGRID	PubMed	Affinity Capture-RNA
BioGRID:109293	BioGRID:119934	GDAP1		BioGRID	PubMed	Co-fractionation
BioGRID:109293	BioGRID:109289	HBA1		BioGRID	PubMed	Co-crystal Structure; Two-hybrid

Display Settings: Full Report

Send to:

HBB hemoglobin, beta [*Homo sapiens*]

Gene ID: 3043, updated on 14-Jan-2011

Summary

Official Symbol HBB provided by [HGNC](#)

Official Full Name hemoglobin, beta provided by [HGNC](#)

Primary source [HGNC:4827](#)

See related [Ensembl:ENSG00000223609](#); [Ensembl:ENSG00000244734](#); [HPRD:00786](#); [MIM:141900](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Homo sapiens](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

Also known as CD113t-C; beta-globin; HBB

Summary The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, Hb A. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon -- gamma-G -- gamma-A -- delta -- beta--3'. [provided by RefSeq]

Genomic regions, transcripts, and products

Go to [reference sequence details](#)

Genomic Sequence

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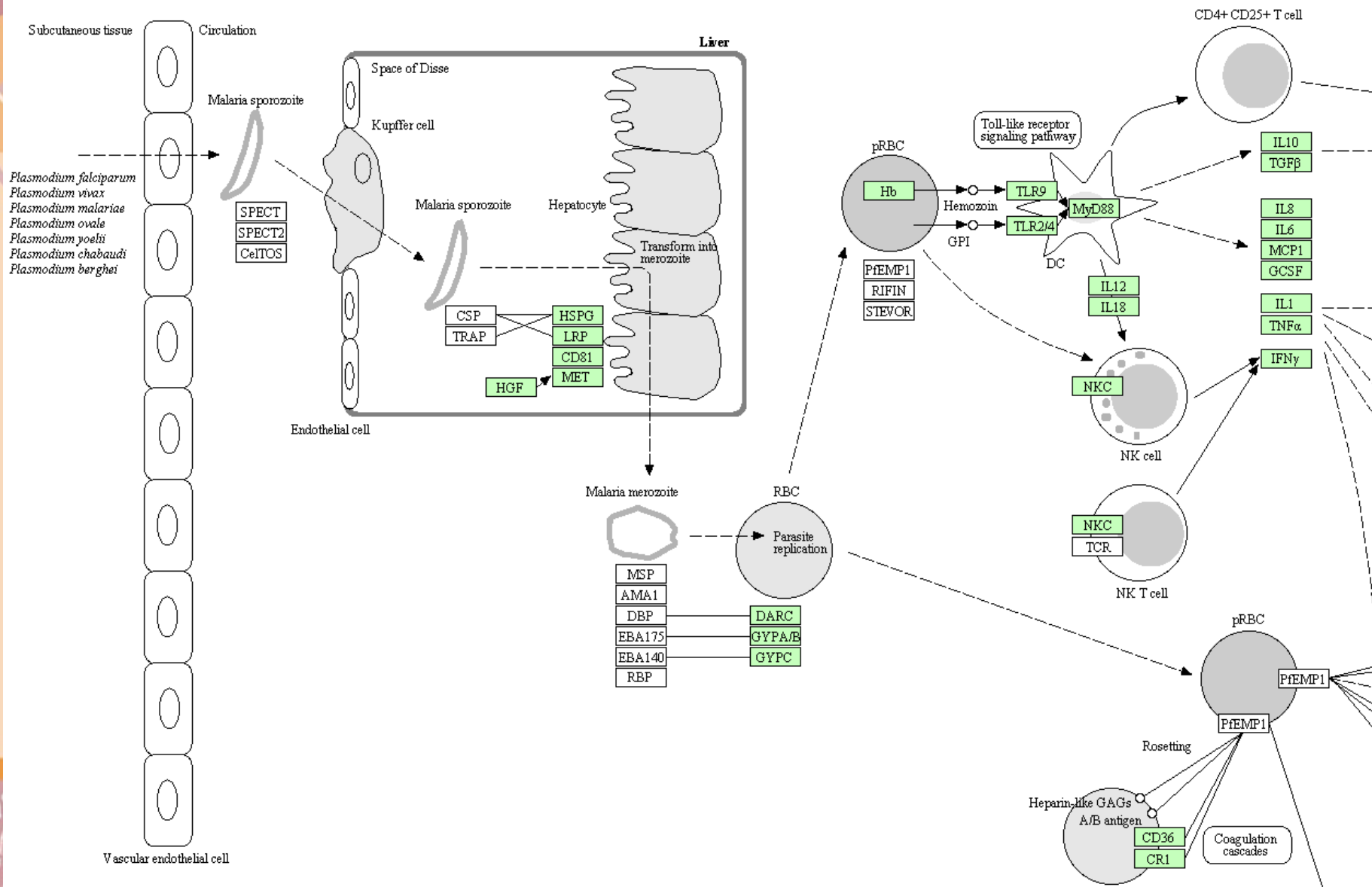
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- BioSystems
- Books
- CCDS
- Conserved Domains
- Full text in PMC
- GEO Profiles
- Genome
- HomoloGene
- Map Viewer

Human Beta-Hemoglobin Biosystems

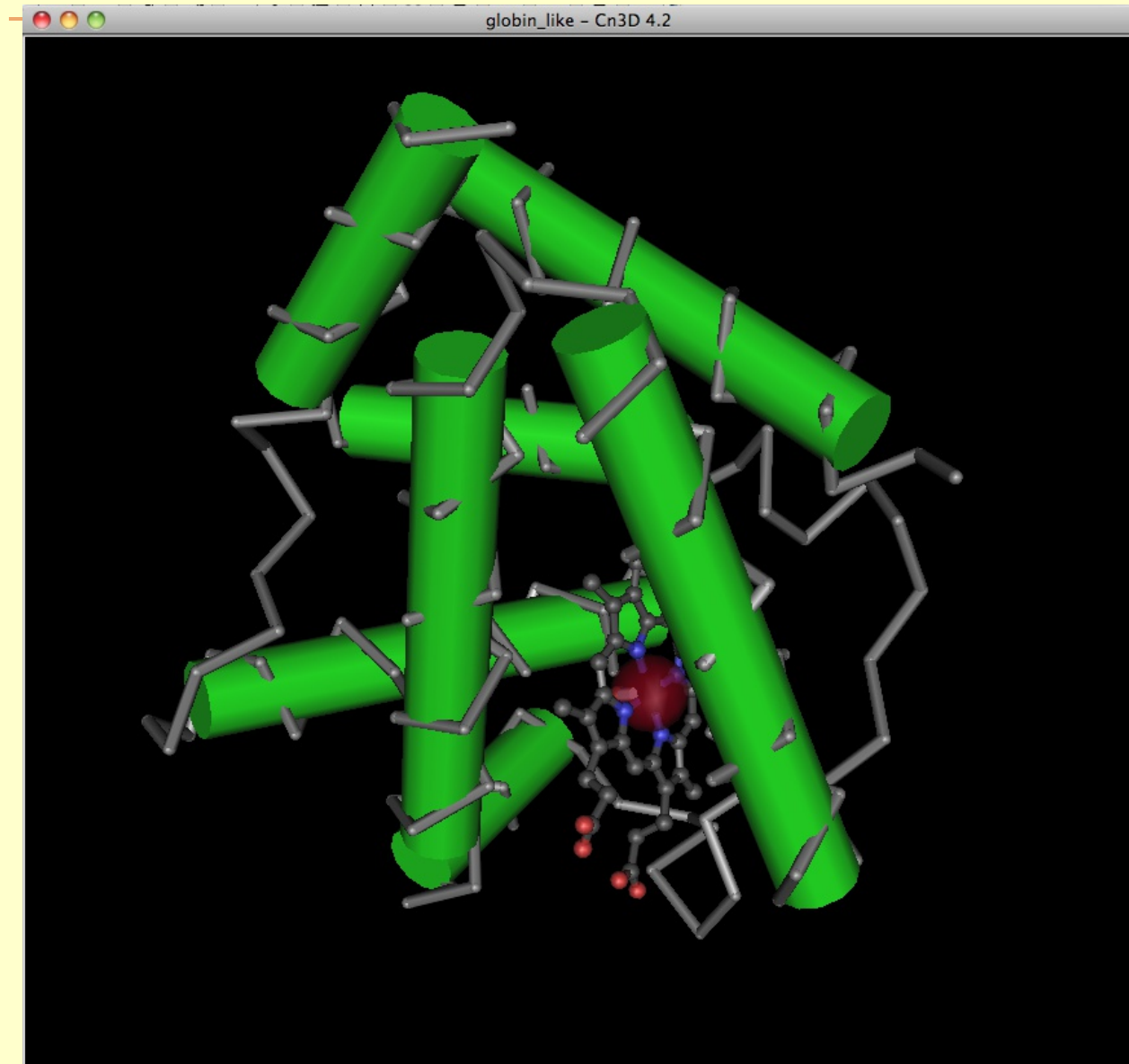
<http://www.ncbi.nlm.nih.gov/biosystems/152665>

MALARIA



Human Beta-Hemoglobin Conserved Domain

http://www.ncbi.nlm.nih.gov/cdd?LinkName=gene_cdd&from_uid=3043



Human Beta-Hemoglobin Homologene

http://www.ncbi.nlm.nih.gov/homologene?LinkName=gene_homologene&from_uid=3043h

Display Settings: HomoloGene

HomoloGene:68066. Gene conserved in Eutheria
















Genes

Genes identified as putative homologs of one another during the construction of HomoloGene.

- HBB, *H.sapiens*
hemoglobin, beta
- HBB, *P.troglodytes*
hemoglobin, beta
- HBB, *M.mulatta*
hemoglobin, beta
- LOC609402, *C.lupus*
hemoglobin subunit beta-like
- LOC480784, *C.lupus*
hemoglobin subunit beta-like
- HBD, *C.lupus*
hemoglobin, delta
- LOC100337028, *B.taurus*
hemoglobin fetal subunit beta-like
- HBB, *B.taurus*
hemoglobin, beta
- LOC781674, *B.taurus*
hemoglobin fetal subunit beta-like
- Beta-s, *M.musculus*
hemoglobin subunit beta-1-like
- Hbb-b1, *M.musculus*
hemoglobin, beta adult major chain
- Hbb-b1, *R.norvegicus*
hemoglobin, beta adult major chain
- LOC689064, *R.norvegicus*
beta-globin
- Hbb, *R.norvegicus*
hemoglobin, beta
- LOC100134871, *R.norvegicus*
beta globin minor gene

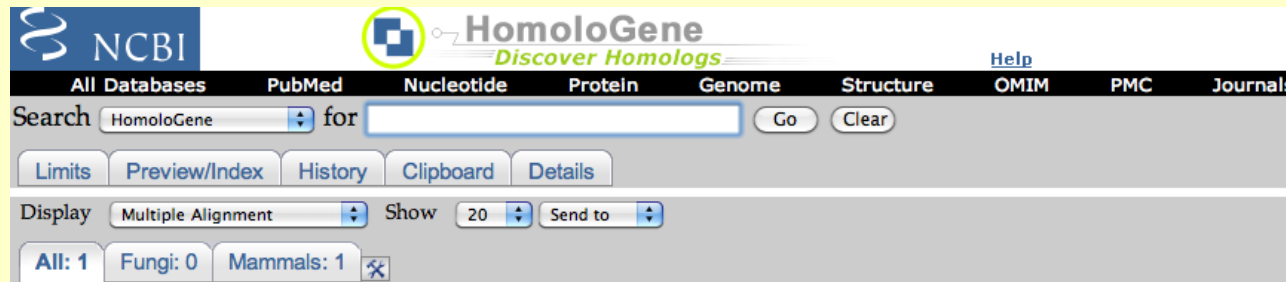
Proteins

Proteins used in sequence comparisons and their conserved domain architectures.

- NP_000509.1 
147 aa
- XP_508242.1 
147 aa
- NP_001157900.1 
147 aa
- XP_862442.1 
162 aa
- XP_003433067.1 
147 aa
- XP_534029.2 
147 aa
- XP_002693271.1 
145 aa
- NP_776342.1 
145 aa
- XP_003587018.1 
145 aa
- NP_001188320.1 
147 aa
- NP_032246.2 
147 aa
- NP_942071.1 
147 aa
- NP_001104739.1 
147 aa
- NP_150237.1 
147 aa
- NP_001106694.1 
147 aa

Human Beta-Hemoglobin Homologene

http://www.ncbi.nlm.nih.gov/homologene?LinkName=gene_homologene&from_uid=3043h



NCBI HomoloGene Discover Homologs

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journal

Search HomoloGene for Go Clear

Limits Preview/Index History Clipboard Details

Display Multiple Alignment Show 20 Send to

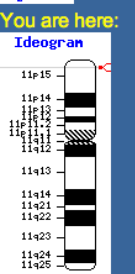
All: 1 Fungi: 0 Mammals: 1

1: HomoloGene:68066. Gene conserved in Eutheria [Download](#) , [Links](#)

Multiple Sequence Alignment

Generated by MUSCLE [\[see reference\]](#) version 3.6 (using option: -maxiters 2).

NP_000509.1	1	MVHLTPEEKSAVTALWGKVNVDVGGGALGRLLVVYPWTPQRFESFGDLS	50
XP_508242.1	1	MVHLTPEEKSAVTALWGKVNVDVGGGALGRLLVVYPWTPQRFESFGDLS	50
XP_850823.1	1	MVHLTAEKSLIVSGLWGKVNVDVGGGALGRLLIVYPWTPQRFESFGDLS	50
XP_534029.2	1	MVHLTAEKSLISSMWGKVNVDVGGGALGRLLIVYPWTPQRFESFGDLS	50
XP_537902.1	1	MVHLTAEKSLIVSGLWGKVNVDVGGGALGRLLIVYPWTPQRFESFGDLS	50
XP_001249460.2	1	--MLSAEKA AVTSLFAKVKVDVGGGALGRLLVVYPWTPQRFESFGDLS	48
NP_001014902.1	1	--MLSAEKA AVTSLFAKVKVDVGGGALGRLLVVYPWTPQRFESFGDLS	48
XP_001252211.2	1	--MLSAEKA AVTSLFAKVKVDVGGGALGRLLVVYPWTPQRFESFGDLS	48
XP_001250142.2	1	--MLSAEKA AVTSLFAKVKVDVGGGALGRLLVVYPWTPQRFESFGDLS	48
NP_001103979.1	1	--MLSAEKA AVTSLFAKVKVDVGGGALGRLLVVYPWTPQRFESFGDLS	48
NP_776342.1	1	--MLTAEKA AVTAFWGKVKVDVGGGALGRLLVVYPWTPQRFESFGDLS	48
NP_032246.2	1	MVHLTDAEKA AVSGLWGKVNADVGGGALGRLLVVYPWTPQRYFDSFGDLS	50
NP_150237.1	1	MVHLTDAEKA AVNGLWGKVNPDVGGGALGRLLVVYPWTPQRYFDSFGDLS	50
XP_001069372.1	1	MVHLTDAEKATV SGLWGKVNADNVGAEALGRLLVVYPWTPQRYFSKFGDLS	50
NP_942071.1	1	MVHLTDAEKATV NGLWGKVNPEI GAESLASLLIVYPWTPQRYFSKFGDLS	50
NP_000509.1	51	TPDAVMGNPKVKAHGKKV LGA FSDGLAHL DNLKGT FATLSELHCDKLHVD	100
XP_508242.1	51	TPDAVMGNPKVKAHGKKV LGA FSDGLAHL DNLKGT FATLSELHCDKLHVD	100
XP_850823.1	51	TPDAVMSNAKVKAHGKKV LNS FSDGLK NLDNLKGT FAKLSELHCDKLHVD	100
XP_534029.2	51	TPDAVMSNAKVKAHGKKV LNS FSDGLK NLDNLKGT FAKLSELHCDKLHVD	100
XP_537902.1	51	TPDAVMSNAKVKAHGKKV LNS FSDGLK NLDNLKGT FAKLSELHCDKLHVD	100
XP_001249460.2	49	SADAILGNPKVKAHGKKV LDS FCEGLK QLDDLKGA FASLSELHCDKLHVD	98
NP_001014902.1	49	SADAILGNPKVKAHGKKV LDS FCEGLK QLDDLKGA FASLSELHCDKLHVD	98
XP_001252211.2	49	SADAILGNPKVKAHGKKV LDS FCEGLK QLDDLKGA FASLSELHCDKLHVD	98
XP_001250142.2	49	SADAILGNPKVKAHGKKV LDS FCEGLK QLDDLKGA FASLSELHCDKLHVD	98
NP_001103979.1	49	SADAILGNPKVKAHGKKV LDS FCEGLK QLDDLKGA FASLSELHCDKLHVD	98
NP_776342.1	49	TADAVMNNPKVKAHGKKV LDS FSNGMKHL DDLKGTFAALSELHCDKLHVD	98
NP_032246.2	51	SASAIMGNAKVKAHGKKV ITAFNDGLNHLDSLKGTFA LSELHCDKLHVD	100
NP_150237.1	51	SASAIMGNPKVKAHGKKV INAFNDGLKHL DNLKGTFAHLSELHCDKLHVD	100
XP_001069372.1	51	SASAIMGNPQVKAHGKKV INAFNDGLKHL DNLKGTFAHLSELHCDKLHVD	100
NP_942071.1	51	SVASAIMGNPQVKAHGK VINA FDDGLKHL DNLKGTFA LSELHCDKLHVD	100



NCBI Map Viewer

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

[Search](#)

Homo sapiens (human) Build 37.2 (Current)

[BLAST The Human Genome](#)

Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) | [11](#) | [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [X](#) [Y](#) [MT](#)

Query: 3043[[gene_id](#)] [\[clear\]](#)

Master Map: Genes On Sequence

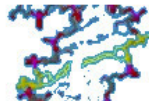
[Summary of Maps](#)

[Maps & Options](#)

Region Displayed: 5,180K-5,315K bp

[Download/View Sequence/Evidence](#)

Model	Hs UniG	ensGenes	RefSeq	RNA	Genes_seq	Symbol	Links	E	Cyto	Description
						OR51A1P	HGNC sv prd lev mm	sts		best RefSeq 11p15.4 olfactory receptor, family 51, s
						OR5221P	HGNC sv prd lev mm	sts		best RefSeq 11p15.4 olfactory receptor, family 52, s
						OR52A1				
						OR51V1	HGNC sv prd lev mm	hm sts	SNP	best RefSeq 11p15.4 hCG_1647060
						HBB	OMIM HGNC sv prd lev mm	hm sts	SNP	best RefSeq 11p15.5 hCG_21979
						HBD	OMIM HGNC sv prd lev mm	sts	SNP	best RefSeq 11p15.5 hCG_1641001
						HBBP1	HGNC sv	d lev mm	sts	best RefSeq 11p15.5 hemoglobin, beta pseudogene
						HBG1	OMIM HGNC sv prd lev mm	hm sts	SNP	best RefSeq 11p15.5 hCG_28329
						HBG2	OMIM HGNC sv prd lev mm	hm sts	SNP	best RefSeq 11p15.5 hemoglobin, gamma G
						HBE1	OMIM HGNC sv prd lev mm	hm sts	SNP	best RefSeq 11p15.5 hCG_1640999



PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Books SNP

Search for SNP on NCBI Reference Assembly

Search Entrez for

BUILD 132

Have a question about dbSNP? Try searching the SNP FAQ Archive!

GENERAL

HUMAN VARIATION

Search, Annotate, Submit NEW

Annotate and Submit Batch Data with Clinical Impact NEW

SNP SUBMISSION

DOCUMENTATION

SEARCH

RELATED SITES

SNP linked to Gene HBB(geneID:3043) Via Contig Annotation

rs# on all gene models to Batch Query all rs# to file.

Gene Model (mRNA alignment) information from genome sequence

Total gene model (contig mRNA transcript):				1		
mRNA	transcript	protein	mRNA orientation	Contig	Contig Label	List SNP
NM_000518.4	plus strand	NP_000509.1	forward	NT_009237.18	GRCh37	<- currently shown

Include clinically associated in gene region cSNP has frequency double hit

gene model	Contig Label	Contig	mRNA	protein	mRNA orientation	transcript	snp count
(contig mRNA transcript):	GRCh37	NT_009237.18	NM_000518.4	NP_000509.1	forward	plus strand	15, coding

Region	Chr. position	mRNA pos	dbSNP rs# cluster id	Heterozygosity	Validation	3D	Linkout	Function	dbSNP allele	Protein residue	Codon pos	Amino acid pos	PubMed
	5246854	465	rs41405449	N.D.		Yes		frame shift			1	139	
								frame shift	AGC	Ser [S]	1	139	
								contig reference	GCTA	[AN]	1	139	
	5246870	452	rs113082294	N.D.		Yes		synonymous	C	Val [V]	3	134	
								contig reference	G	Val [V]	3	134	
	5246876	430	rs41511744	N.D.		Yes		frame shift			2	127	
								frame shift (15bp)	[QAAYQ]		2	127	
								contig reference (17bp)	[VQAAYQ]		2	127	
	5246958	365	rs71811954	N.D.				frame shift			3	105	
								frame shift (15bp)			3	105	
								contig reference	G	Arg [R]	3	105	
	5247800	309	rs41539866	N.D.				frame shift			1	87	
								frame shift (17bp)			1	87	
								contig reference	G	Ala [A]	1	87	
	5247855	317	rs11549405	N.D.		Yes		synonymous	C	Leu [L]	3	89	
								contig reference	G	Leu [L]	3	89	
	5247878	294	rs11549406	0.005		Yes		missense	G	Val [V]	1	82	
								contig reference	C	Leu [L]	1	82	
	5247915	257	rs112287010	N.D.		Yes		synonymous	T	Leu [L]	3	69	
								contig reference	C	Leu [L]	3	69	
	5247969	203	rs17850156	N.D.		Yes		synonymous	C	Thr [T]	3	51	
								contig					

HBB Variation Viewer [Download report](#) (86948 bytes)

Gene	HBB; hemoglobin, beta
Description	beta globin chain hemoglobin beta chain hemoglobin subunit beta Also known as: CD113t-C, beta-globin
Species	Homo sapiens
Cyto	11p15.5

Gene Reference Sequences	NG_000007.3 genomic NM_000518.4 transcript NP_000509.1 protein <i>variation locations are based on these acc</i>
Links	HGMD , Panther , Gene , OMIM

Observed Variation | Page 3 of 45 | Displaying results 41 - 60 of 883

Var Class	Genomic	Transcript	Protein	Clinical interpretation	Test status	Freq	Pub...	MIM AI Var	Orig
SNC	g.70610C>G	c.16C>G	p.Pro6Ala			5	5			141900.0451	G
SNC	g.70611C>G	c.17C>G	p.Pro6Arg			3	3			141900.0296	G
DIP	g.70612delT	c.18delT	p.Pro6=fs			2	2				
DIP	g.70612delTins...	c.18delTinsCT	p.Pro6?fs			2	2				
SNC	g.70613G>A	c.19G>A	p.Glu7Lys	probable-pathogenic		18	18		1	141900.0010...	G
SNC	g.70613G>C	c.19G>C	p.Glu7Gln	probable-pathogenic		18	18		1	141900.0010...	G
MIX	g.70614A>C	c.20A>C	p.Glu7Ala			34	34	Q	8	141900.0039...	
MIX	g.70614A>T	c.20A>T	p.Glu7Val			34	34	Q	8	141900.0039...	
DIP	g.70614delA	c.20delA	p.Glu7Glyfs			1	1				
SNC	g.70614A>G	c.20A>G	p.Glu7Gly	pathogenic		7	7	Q		141900.0085...	G
MIX	g.70614delA	c.20delA	p.Glu7Glyfs			34	34	Q	8	141900.0039...	
MIX	g.70614A>C	c.20A>C	p.Glu7Ala			34	34	Q	8	141900.0039...	
MIX	g.70614A>G	c.20A>G	p.Glu7Gly			34	34	Q	8	141900.0039...	
MIX	g.70614A>T	c.20A>T	p.Glu7Val			34	34	Q	8	141900.0039...	
SNC	g.70614A>T	c.20A>T	p.Glu7Val	pathogenic		7	7	Q		141900.0085...	G
DIP	g.70616_7061...	c.22_24delGAG	p.Glu8delGlu			1	1			141900.0156	

Search: for

e.g. **BRCA2** or **rat X:100000..200000** or **coronary heart disease**

Browse a Genome

The Ensembl project produces genome databases for vertebrates and other eukaryotic species, and makes this information freely available online.

Popular genomes



Human
GRCh37



Mouse
GRCm38



Zebrafish
Zv9

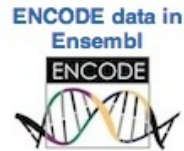
★ [Log in to customize this list](#)

All genomes

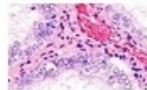
-- Select a species --

[View full list of all Ensembl species](#)

Other species are available in [Ensembl Pre!](#) and [EnsemblGenomes](#)



Gene expression in different tissues



Find SNPs and other variants for my gene

```

GTTATACATTC
CRTRAAAGTCTT
CTTCTAAATTCT
GTAACATTTTCC
    
```

Retrieve gene sequence

```

GCGTGACTCCGSETGG;
GGGCTTGTGGCGGAGC;
GGGCTCTGCTGCGCCT;
AGGGACAGATTGTGAG;
CACCTCTGGAGCGGTT;
CCAGTCCAGCGTGGCG;
    
```

Compare genes across species



Use my own data in Ensembl



Learn about a disease or phenotype



What's New in Release 73 (September 2013)

- [New search engine using Solr](#)
- [New species: Duck \(Anas platyrhynchos\) and Flycatcher \(Ficedulla albicollis\)](#)
- [Updated patches for the human assembly \(GRCh37.p12\)](#)

[Full details of this release](#)

[More release news on our blog →](#)

Latest blog posts

- 24 Sep 2013: [Pre! update: vervet monkey, naked mole-rat, aardvark, dolphin and pika](#)
- 16 Sep 2013: [Ensembl at #ASHG2013](#)
- 12 Sep 2013: [Ensembl Genomes release 20 is out!](#)

[Go to Ensembl blog →](#)

Did you know...?

It's free- take our [browser workshop](#) online!



Human (GRCh37) ▾



Human

Homo sapiens

Search all categories ▾ Search Human...

e.g. BRCA2 or 6:133017695-133161157 or osteoarthritis

Genome assembly: GRCh37 (GCA_000001405.13)

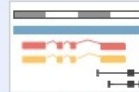
- More information and statistics
- Download DNA sequence (FASTA)
- Convert your data to GRCh37 coordinates
- Display your data in Ensembl

Other assemblies

- NCBI36 (Ensembl release 54)



View karyotype

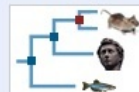


Example region

Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

- More about comparative analysis
- Download alignments (EMF)



Example gene tree

Regulation

What can I find? DNA methylation, transcription factor binding sites, histone modifications, and regulatory features such as enhancers and repressors, and microarray annotations.

- More about the Ensembl regulatory build and microarray annotation
- Download all regulatory features (GFF)



Example regulatory feature



ENCODE data in Ensembl

What's New in Human release 73

- Update to Ensembl-Havana GENCODE gene set (release 18)
- Human: assembly updated to GRCh37.p12
- Human: updated RefSeq gene import

[More news...](#)

Gene annotation

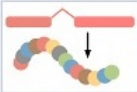
What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

- More about this genebuild
- Download genes, cDNAs, ncRNA, proteins (FASTA)
- Update your old Ensembl IDs

Additional manual annotation can be found in Vega



Example gene



Example transcript

Variation

What can I find? Short sequence variants and longer structural variants; disease and other phenotypes

- More about variation in Ensembl
- Download all variants (GVF)
- Variant Effect Predictor



Example variant



Example phenotype



Example structural variant

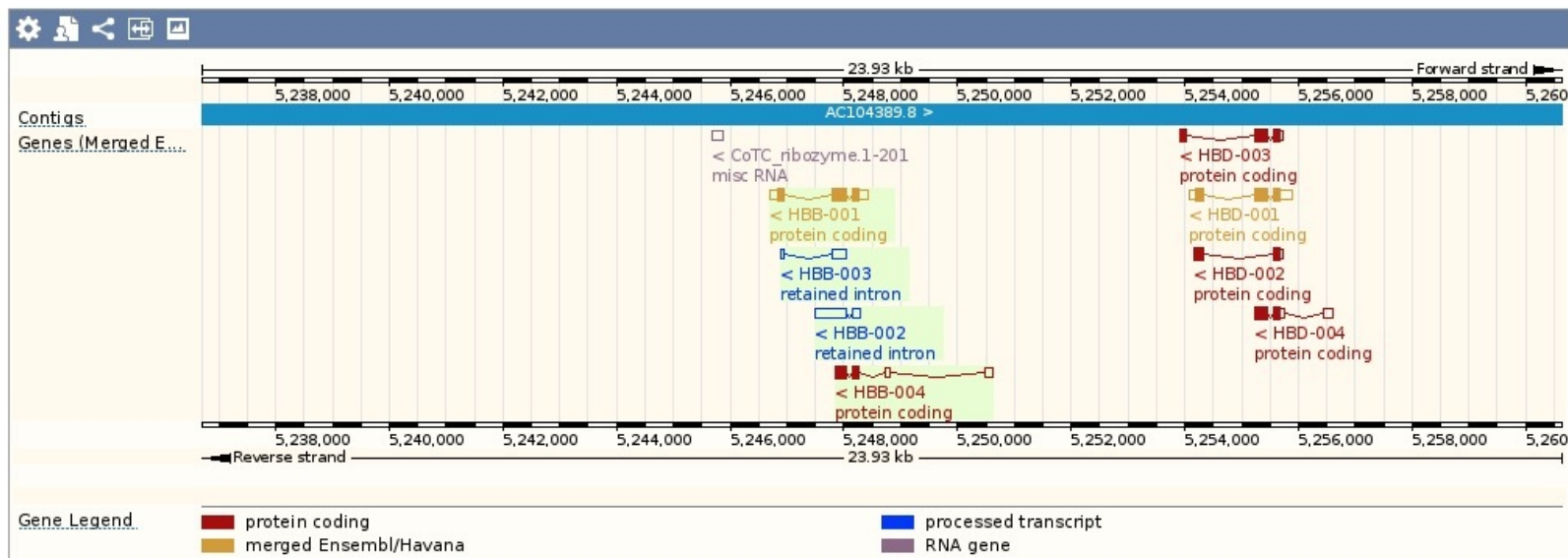
Gene: HBB ENSG00000244734

Description hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
Location [Chromosome 11: 5,246,694-5,250,625](#) reverse strand.
INSDC coordinates chromosome:GRCh37:CM000673.1:5246694:5250625:1
Transcripts This gene has 4 transcripts (splice variants) [Show transcript table](#)

Gene summary ⓘ

Name [HBB](#) (HGNC Symbol)
Synonyms beta-globin, CD113t-C, HBD [To view all Ensembl genes linked to the name [click here.](#)]
CCDS This gene is a member of the Human CCDS set: [CCDS7753](#)
Ensembl version ENSG00000244734.1
Gene type Known protein coding
Prediction Method Annotation for this gene includes both automatic annotation from Ensembl and [Havana](#) manual curation, see [article](#).
Alternative genes **This gene corresponds to the following database identifiers:**
Havana gene: [OTTHUMG00000066678](#) (version 2)

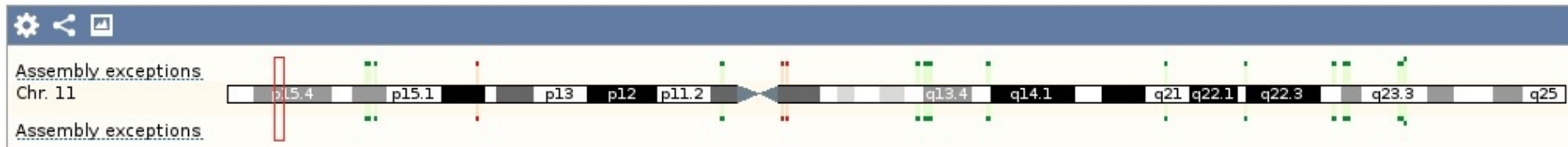
[Go to Region in Detail](#) for more tracks and navigation options (e.g. zooming)



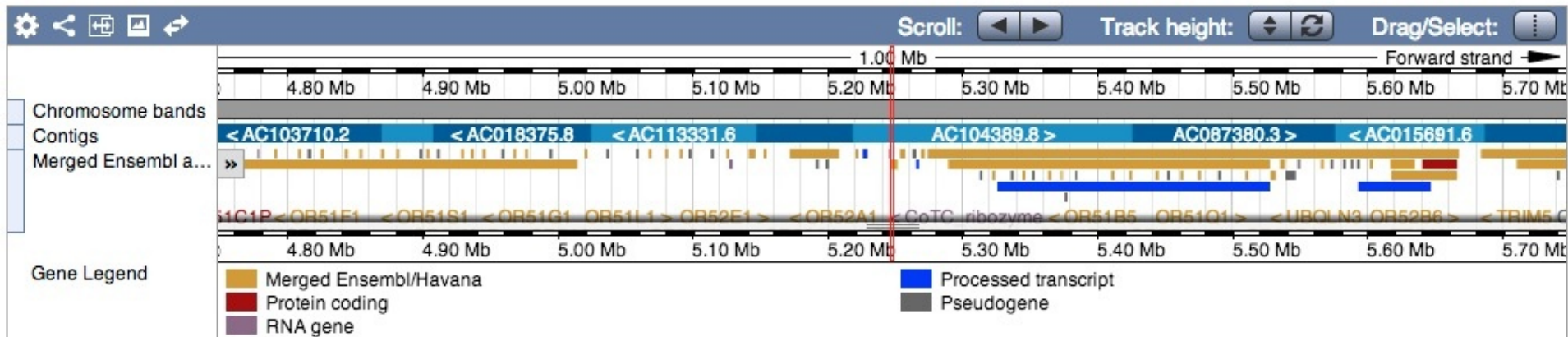
Ensembl Human HBB Gene

http://uswest.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000244734;r=11:5246694-5250625

Chromosome 11: 5,246,116-5,250,047



Region in detail



Location:

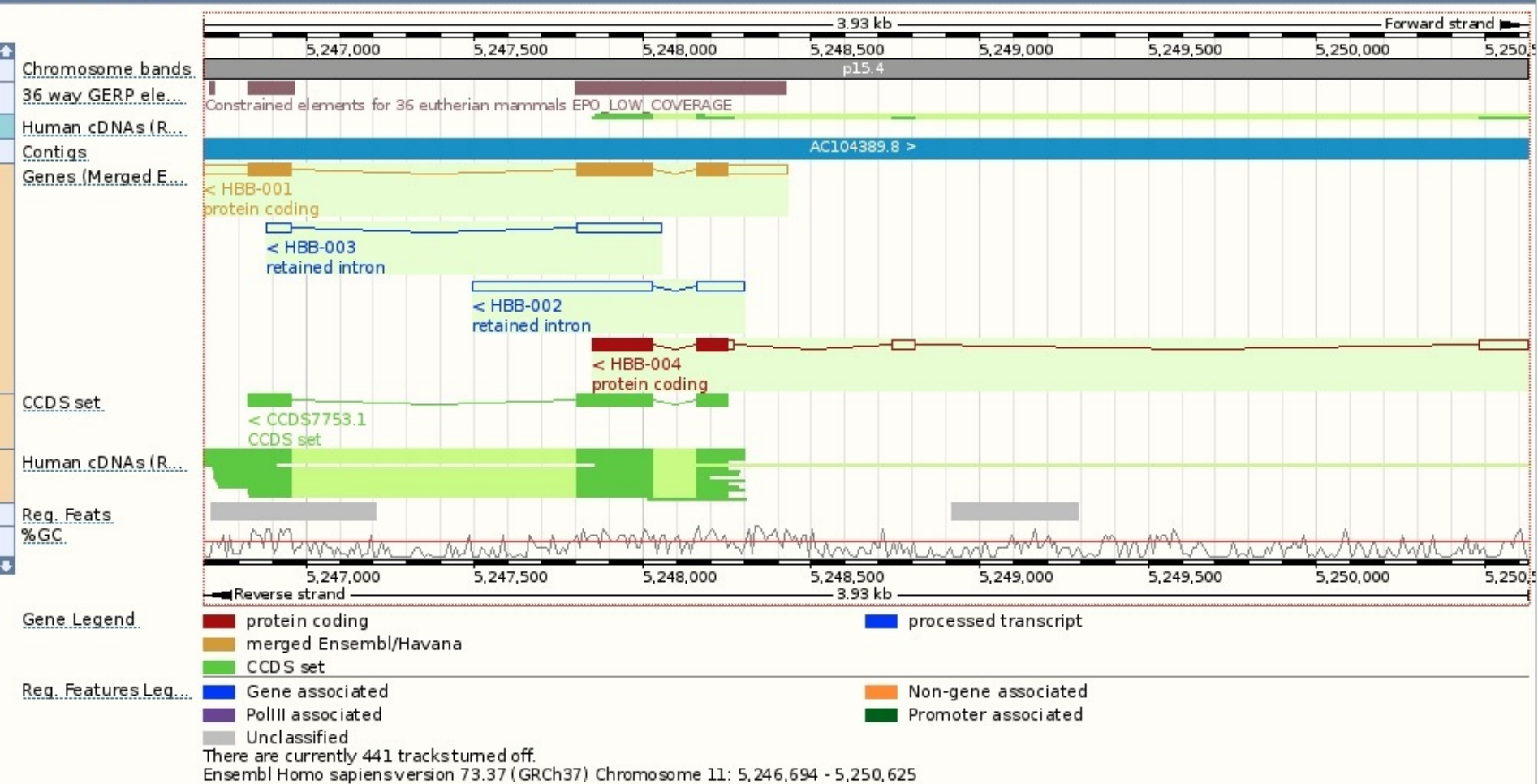
Gene:

Navigation controls: << < + slider - > >>



Ensembl Human HBB Gene Transcripts

http://uswest.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000244734;r=11:5246694-5250625

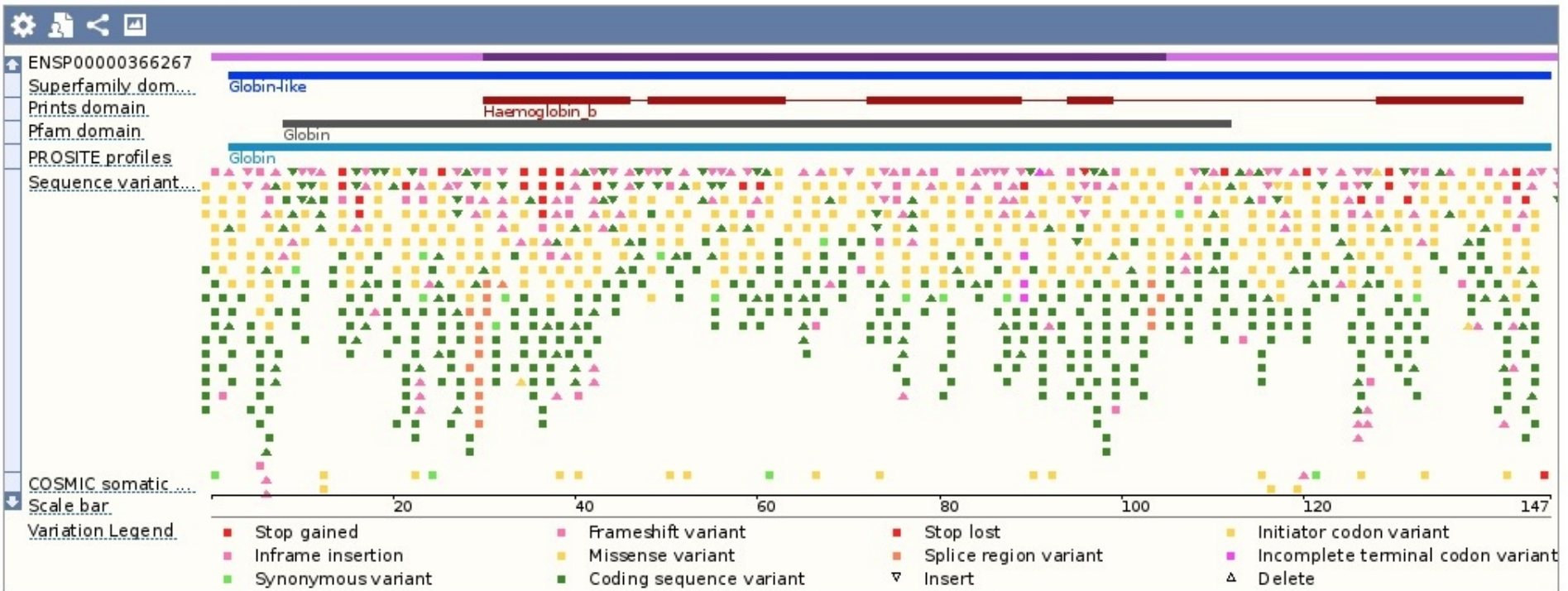


Ensembl Human HBB Protein Summary

http://uswest.ensembl.org/Homo_sapiens/Transcript/ProteinSummary?db=core;g=ENSG00000244734;r=11:52

Protein summary

Protein domains for ENSP00000333994.3



Statistics

Ave. residue weight: 108.833 g/mol
 Charge: 3.5
 Isoelectric point: 7.3230
 Molecular weight: 15,998.41 g/mol
 Number of residues: 147 aa

Ensembl Tutorials

<http://uswest.ensembl.org/info/website/tutorials/index.html>



Ensembl Tutorials and Worked Examples

Online tutorials

- [Introduction to Browsing Chordate Genomes](#) - a 3-hour comprehensive interactive tutorial aimed at beginners

Video tutorials

The tutorials listed below are Flash animations of some of our training presentations. We are gradually adding to the list, so please check back regularly.



Note that we are now hosting all our tutorials on [YouTube](#) (and [优酷网](#) for users in China) for ease of maintenance. A selection of tutorials is also available on the [EBI E-Video website](#).

Title	Running time (minutes)
The Ensembl Genome Browser	10:00
EnsemblGenomes - Extending Ensembl across the taxonomic space	4:54
Comparative Genomics	9:58
SNPs and other Variations - 1 of 2	7:06
SNPs and other Variations - 2 of 2	6:30
Introduction to BioMart	4.27
BioMart: Variation IDs to HGNC Symbols	2:58
Clip: Exons and Introns	1:12
Clip: Export Sequence	1:08
Clip: Genome Variation	0:37
Clip: Transcriptomics (ArrayExpress)	1:12
Clip: View Conserved Sequence	1:26
Clip: View External Data (DAS)	1:53

UCSC Genome Bioinformatics

[Genomes](#) - [Blat](#) - [Tables](#) - [Gene Sorter](#) - [PCR](#) - [VisiGene](#) - [Session](#) - [FAQ](#) - [Help](#)[Genome Browser](#)[ENCODE](#)[Neandertal](#)[Blat](#)[Table Browser](#)[Gene Sorter](#)[In Silico PCR](#)[Genome Graphs](#)

About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides portals to the [ENCODE](#) and [Neandertal](#) projects.

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering ([CBSE](#)) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#).

Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
Software Copyright (c) The Regents of the University of California. All rights reserved.

group	genome	assembly	position	search term
Mammal	Human	Feb. 2009 (GRCh37/hg19)	chr11:4,444,499-6,050,498	enter position, gene symbol or search term: <input type="button" value="submit"/>

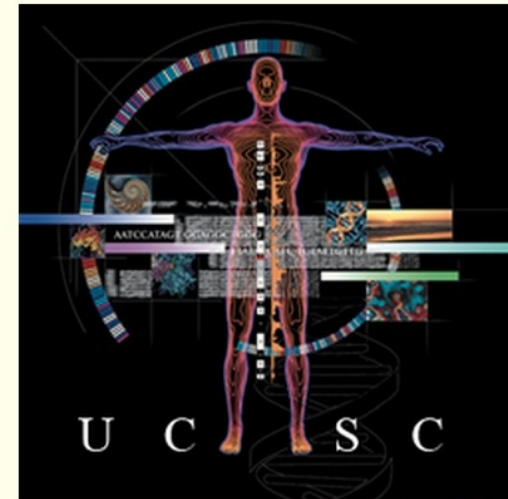
[Click here to reset](#) the browser user interface settings to their defaults.

Human Genome Browser – hg19 assembly ([sequences](#))

The February 2009 human reference sequence (GRCh37) was produced by the [Genome Reference Consortium](#). For more information about this assembly, see [GRCh37](#) in the NCBI Assembly database.

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the [User's Guide](#) for more information.



Homo sapiens
(Graphic courtesy of [CBSE](#))

UCSC Genes

[HBB \(uc001mae.1\) at chr11:5246696-5248301](#) - Homo sapiens hemoglobin, beta (HBB), mRNA.
[HBD \(uc001maf.1\) at chr11:5254059-5255858](#) - Homo sapiens hemoglobin, delta (HBD), mRNA.
[RBM17 \(uc010gav.2\) at chr10:6131309-6159422](#) - Homo sapiens RNA binding motif protein 17
[RBM17 \(uc001ijb.3\) at chr10:6130949-6159422](#) - Homo sapiens RNA binding motif protein 17
[HBA1 \(uc002cfx.1\) at chr16:226679-227520](#) - Homo sapiens hemoglobin, alpha 1 (HBA1), mRNA
[HBA2 \(uc002cfv.4\) at chr16:222846-223709](#) - Homo sapiens hemoglobin, alpha 2 (HBA2), mRNA
[HBBP1 \(uc001mag.3\) at chr11:5263185-5264822](#) - Homo sapiens hemoglobin, beta pseudogene 1
[TMEM158 \(uc011baf.2\) at chr3:45265956-45267814](#) - Homo sapiens transmembrane protein 158

RefSeq Genes

[HBB at chr11:5246696-5248301](#) - (NM_000518) hemoglobin subunit beta
[HBBP1 at chr11:5263185-5264822](#) - (NR_001589)

Non-Human RefSeq Genes

[hbb at chr11:5247810-5275746](#) - (NM_001201019) hemoglobin subunit beta
[HBB at chr11:5246810-5248260](#) - (NM_001164428) hemoglobin subunit beta
[HBB at chr11:5246828-5248251](#) - (NM_001168847) hemoglobin subunit beta
[HBB at chr11:5254194-5255663](#) - (NM_001164018) hemoglobin subunit beta
[HBB at chr11:5246828-5248251](#) - (NM_001164018) hemoglobin subunit beta
[HBB at chr11:5246828-5248301](#) - (NM_001144841) hemoglobin subunit beta

UCSC HBB Gene in the UCSC Genome Browser

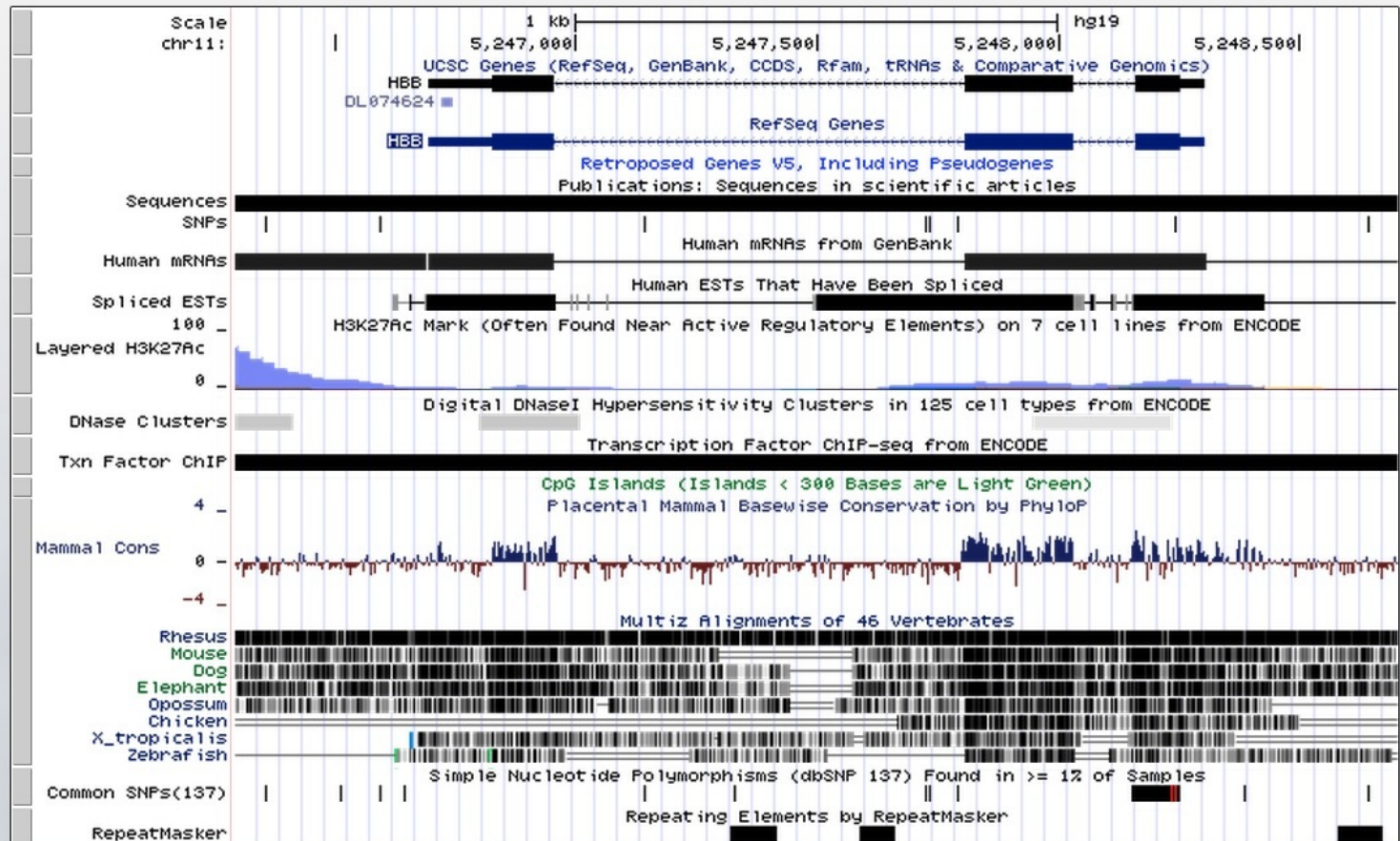
<http://genome.ucsc.edu/cgi-bin/hgTracks?position=chr11:5246696-5248301&hgid=349247439&refGene=pack&>

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

chr11:5,246,295-5,248,703 2,409 bp.

chr11 (p15.4) p 5.4 p13 p12 q14.1 21 22.3 23.3 25





Mapping and Sequencing Tracks

[refresh](#)

Base Position <input type="text" value="dense"/>	Chromosome Band <input type="text" value="hide"/>	STS Markers <input type="text" value="hide"/>	18 FISH Clones <input type="text" value="hide"/>	Recomb Rate <input type="text" value="hide"/>	18 deCODE Recomb <input type="text" value="hide"/>
X ENCODE Pilot <input type="text" value="hide"/>	Map Contigs <input type="text" value="hide"/>	Assembly <input type="text" value="hide"/>	GRC Map Contigs <input type="text" value="hide"/>	INSDC <input type="text" value="hide"/>	Gap <input type="text" value="hide"/>
BAC End Pairs <input type="text" value="hide"/>	18 Fosmid End Pairs <input type="text" value="hide"/>	GC Percent <input type="text" value="hide"/>	GRC Patch Release <input type="text" value="hide"/>	Hg18 Diff <input type="text" value="hide"/>	GRC Incident <input type="text" value="hide"/>
Hi Seq Depth <input type="text" value="hide"/>	Wiki Track <input type="text" value="hide"/>	X BU ORChID <input type="text" value="hide"/>	X Mapability <input type="text" value="hide"/>	Short Match <input type="text" value="hide"/>	Restr Enzymes <input type="text" value="hide"/>

Phenotype and Disease Associations

[refresh](#)

18 GAD View <input type="text" value="hide"/>	DECIPHER <input type="text" value="hide"/>	OMIM AV SNPs <input type="text" value="hide"/>	OMIM Genes <input type="text" value="hide"/>	OMIM Pheno Loci <input type="text" value="hide"/>	COSMIC <input type="text" value="hide"/>
LOVD Variants <input type="text" value="hide"/>	HGMD Variants <input type="text" value="hide"/>	UniProt Variants <input type="text" value="hide"/>	GWAS Catalog <input type="text" value="hide"/>	ISCA <input type="text" value="hide"/>	Coriell CNVs <input type="text" value="hide"/>
18 RGD Human QTL <input type="text" value="hide"/>	18 RGD Rat QTL <input type="text" value="hide"/>	18 MGI Mouse QTL <input type="text" value="hide"/>	GeneReviews <input type="text" value="hide"/>		

Genes and Gene Prediction Tracks

[refresh](#)

UCSC Genes <input type="text" value="pack"/>	GENCODE... <input type="text" value="hide"/>	Old UCSC Genes <input type="text" value="hide"/>	UCSC Alt Events <input type="text" value="hide"/>	CCDS <input type="text" value="hide"/>	RefSeq Genes <input type="text" value="pack"/>
Other RefSeq <input type="text" value="hide"/>	MGC Genes <input type="text" value="hide"/>	ORFome Clones <input type="text" value="hide"/>	TransMap... <input type="text" value="hide"/>	Vega Genes <input type="text" value="hide"/>	Pfam in UCSC Gene <input type="text" value="hide"/>
Retroposed Genes <input type="text" value="pack"/>	Ensembl Genes <input type="text" value="hide"/>	AceView Genes <input type="text" value="hide"/>	SIB Genes <input type="text" value="hide"/>	N-SCAN <input type="text" value="hide"/>	SGP Genes <input type="text" value="hide"/>
Geneid Genes <input type="text" value="hide"/>	Genscan Genes <input type="text" value="hide"/>	Exoniphy <input type="text" value="hide"/>	Yale Pseudo60 <input type="text" value="hide"/>	tRNA Genes <input type="text" value="hide"/>	H-Inv 7.0 <input type="text" value="hide"/>
17 EvoFold	sno/miRNA	IKMC Genes Mapped	lincRNAs...		

mRNA and EST Tracks refresh

Human mRNAs dense ▾	Spliced ESTs dense ▾	Human ESTs hide ▾	Other mRNAs hide ▾	Other ESTs hide ▾	18 H-Inv hide ▾
UniGene hide ▾	Gene Bounds hide ▾	SIB Alt-Splicing hide ▾	18 Poly(A) hide ▾	PolyA-Seq hide ▾	18 CGAP SAGE hide ▾
Human RNA Editing hide ▾					

Expression refresh

Affy Exon Array hide ▾	Affy GNF1H hide ▾	<input checked="" type="checkbox"/> Affy RNA Loc hide ▾	Affy U133 hide ▾	Affy U133Plus2 hide ▾	Affy U95 hide ▾
Allen Brain hide ▾	Burge RNA-seq hide ▾	<input checked="" type="checkbox"/> CSHL Small RNA-seq hide ▾	<input checked="" type="checkbox"/> ENC Exon Array... hide ▾	<input checked="" type="checkbox"/> ENC ProtGeno... hide ▾	<input checked="" type="checkbox"/> ENC RNA-seq... hide ▾
<input checked="" type="checkbox"/> GIS RNA PET hide ▾	GNF Atlas 2 hide ▾	18 Illumina WG-6 hide ▾	qPCR Primers hide ▾	<input checked="" type="checkbox"/> RIKEN CAGE Loc hide ▾	18 Sestan Brain hide ▾

Regulation refresh

<input checked="" type="checkbox"/> ENCODE Regulation... show ▾	18 CD34 DnaseI hide ▾	CpG Islands pack ▾	<input checked="" type="checkbox"/> ENC Chromatin... hide ▾	<input checked="" type="checkbox"/> ENC DNA Methyl... hide ▾	<input checked="" type="checkbox"/> ENC DNase/FAIRE... hide ▾
<input checked="" type="checkbox"/> ENC Histone... hide ▾	<input checked="" type="checkbox"/> ENC RNA Binding... hide ▾	<input checked="" type="checkbox"/> ENC TF Binding... hide ▾	<input checked="" type="checkbox"/> FSU Repli-chip hide ▾	18 ORegAnno hide ▾	<input checked="" type="checkbox"/> Stanf Nucleosome hide ▾
<input checked="" type="checkbox"/> SUNY SwitchGear hide ▾	17 SwitchGear TSS hide ▾	TFBS Conserved hide ▾	TS miRNA sites hide ▾	UMMS Brain Hist hide ▾	<input checked="" type="checkbox"/> UW Repli-seq hide ▾
Vista Enhancers hide ▾	18 NKI Nuc Lamina... hide ▾	18 UCSF Brain Methyl hide ▾			

Comparative Genomics refresh

Conservation full	18 Cons Indels MmCf hide	GERP hide	18 Evo Cpg hide	Primate Chain/Net hide	Placental Chain/Net hide
Vertebrate Chain/Net hide					

Neandertal Assembly and Analysis refresh

18 H-C Coding Diffs hide	18 Sel Swp Scan (S) hide	18 5% Lowest S hide	18 S SNPs hide	18 Cand. Gene Flow [No data-chr11]	Neandertal Seq hide
18 Neandertal Mito [No data-chr11]					

Denisova Assembly and Analysis refresh

Variation and Repeats refresh

Common SNPs(137) dense	Flagged SNPs(137) hide	Mult. SNPs(137) hide	All SNPs(137) hide	Common SNPs(135) hide	Flagged SNPs(135) hide
Mult. SNPs(135) hide	All SNPs(135) hide	Common SNPs(132) hide	Flagged SNPs(132) hide	Mult. SNPs(132) hide	All SNPs(132) hide
SNPs (131) hide	1000G Ph1 Vars hide	1000G Ph1 Accsbl hide	<input checked="" type="checkbox"/> GIS DNA PET hide	<input checked="" type="checkbox"/> HAIB Genotype hide	SNP/CNV Arrays hide
HGDP Allele Freq hide	18 HapMap SNPs hide	DGV Struct Var hide	Segmental Dups hide	RepeatMasker dense	Interrupted Rpts hide
Simple Repeats hide	Microsatellite hide	Self Chain hide	18 Genome Variants hide	NumtS Sequence hide	

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Genome Browser User Guide

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Search the Genome Browser help pages:

Search the Genome mailing list archives:

See also the [Open Helix tutorial and training materials](#).

[Questions and feedback are welcome.](#)

What does the Genome Browser do?