

La traduzione

Introduction

Key-components during translation

- tRNAs
- Aminoacil-tRNA sintetasi
- Ribosoma

The process of translation

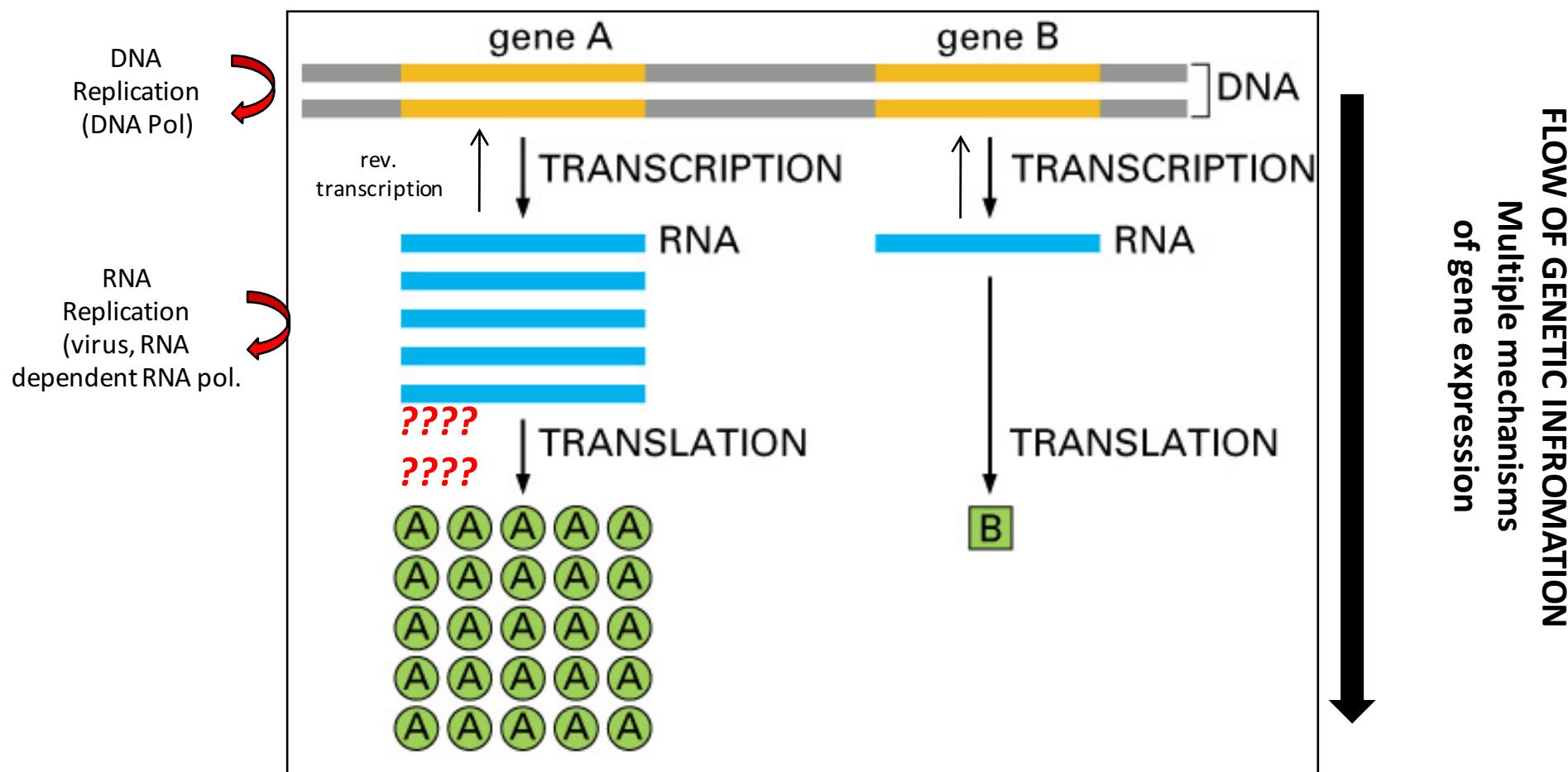
- Iniziazione
- Allungamento
- Terminazione

Il codice genetico

“IL DOGMA CENTRALE”

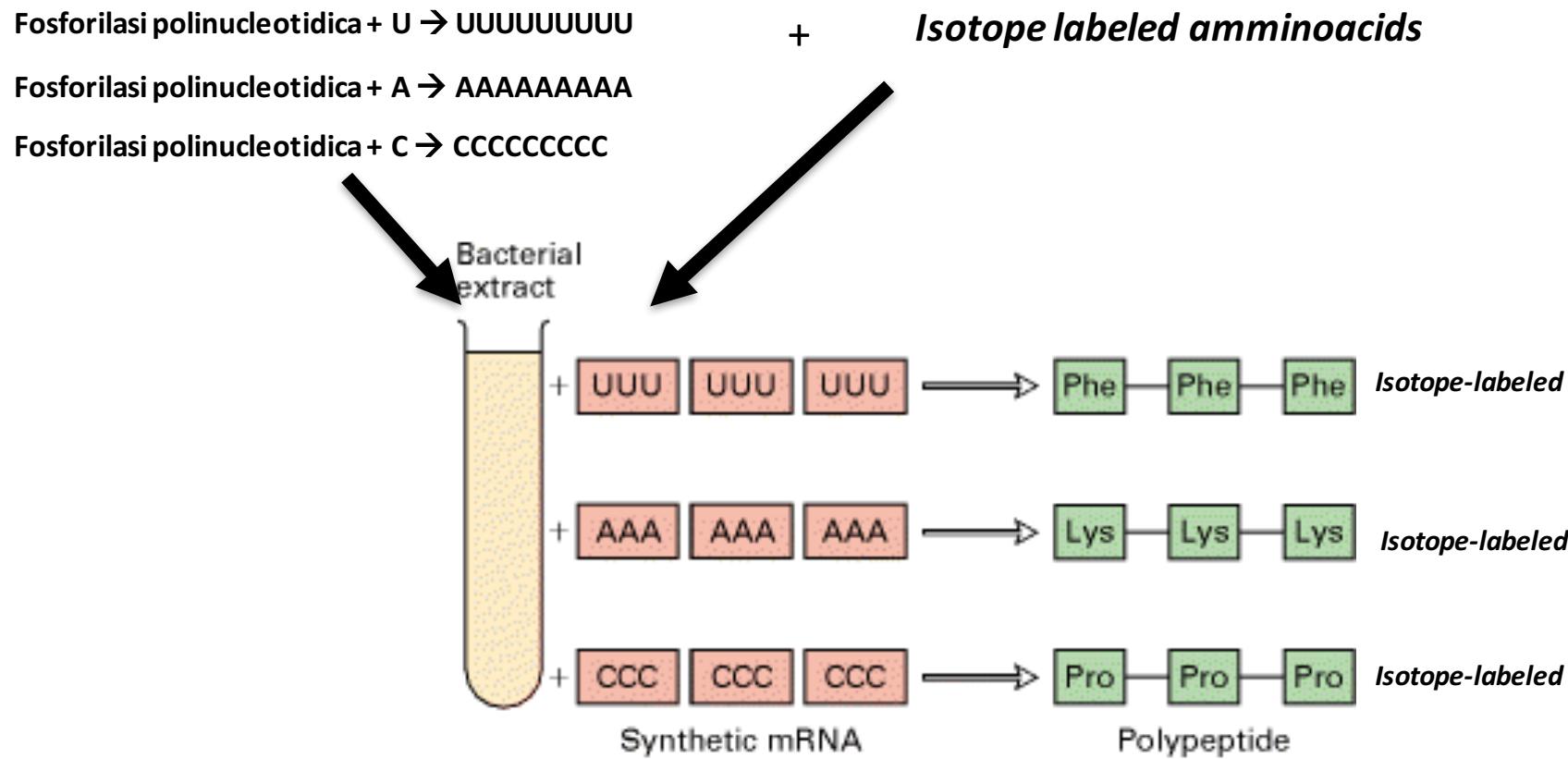
DNA → RNA → PROTEIN

Crick, F (1970). "Central dogma of molecular biology.". Nature 227 (5258):
The central dogma of molecular biology deals with the detailed residue-by-residue transfer of sequential information. It states that such information cannot be transferred back from protein to either protein or nucleic acid.



Come il codice genetico venne decodificato (1960ies)

1. Fosforilasi polinucleotidica: degrades RNA, but at high nucleosid diphosphate concentrations
polynucleotide phosphorylase reaction reverses: synthesis of RNA molecules



2.: mixing nucleotides: Inoltre sintesi di poliribonucleotidi a sequenza casuale di due monomeri in proporzione diversa, ad es. G e U in rapporto 3:1,
 GGUGGGGUGUGGUUGGGGUUUGGGGUUGGGGUGUGGGUGGGGGGUUGGUUGGUUGGGUGGGGG...
 il codone più frequente era GGG e l' amminoacido più abbondante nel polipeptide era la glicina, dunque GGG codificava per la glicina, ecc..

3. STEP: controlled synthesis of oligo-ribonucleotides: verification of all 64 codons

Il codice genetico e degenerato

		AGA									
		AGG									
GCA		CGA									
GCC		CGC									
GCG		CGG	GAC	AAC	UGC	GAA	CAA	GGA	GGC	GGG	AUA
GCU		CGU	GAU	AAU	UGU	GAG	CAG	GGU	CAC	CAU	AUC
											AUU
			Ala	Arg	Asp	Asn	Cys	Glu	Gln	Gly	His
			A	R	D	N	C	E	Q	G	H
											I
		UUA					AGC				
		UUG					AGU				
		CUA			CCA	UCA	ACA				
		CUC			CCC	UCC	ACC				
		CUG	AAA	UUC	CCG	UCG	ACG		GUA		
		CUU	AAG	AUG	CCU	UCU	ACU	UAC	GUC	GUG	UAA
				UUU			UGG	UAU	GUU		UAG
											UGA
			Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr
			L	K	M	F	P	S	T	W	Y
											V
											stop

- Il codice è basato su triplette = 64 combinazioni.
- È degenerato – 1 aa can be encoded by more then one type of codon
- SINONIMI/codon synonym: condos that encode for same aminoacid

Human (2013): 497 tRNA genes
324 tRNA pseudogenes

Il codice genetico e degenerato

mRNA

seconda posizione				terza posizione (estremità 3')			
U		C		A		G	
U	UUU	Phe	UCU	UAA	Tyr	UGU	Cys
	UUC		UCC	UAC	stop	UGC	
	UUA		UCA	UAG*	stop	UGA*	stop
	UUG	Leu	UCG			UGG	Trp
C	CUU		CCU	CAU	His	CGU	
	CUC	Leu	CCC	CAC		CGC	
	CUA		CCA	CAA	Gln	CGA	Arg
	CUG		CCG	CAG		CGG	
A	AUU		ACU	AAU	Asn	AGU	
	AUC	Ile	ACC	AAC		AGC	Ser
	AUA		ACA	AAA	Lys	AGA	
	AUG†	Met	ACG	AAG		AGG	Arg
G	GUU		GCU	GAU	Asp	GGU	
	GUC	Val	GCC	GAC		GGC	
	GUA		GCA	GAA	Glu	GGA	Gly
	GUG		GCG	GAG		GGG	

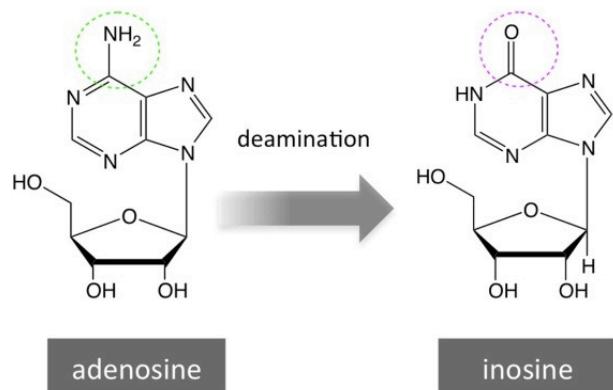
Tentennamento dell'anticodon

“wobbling” of the 3° position of codon-anticodon

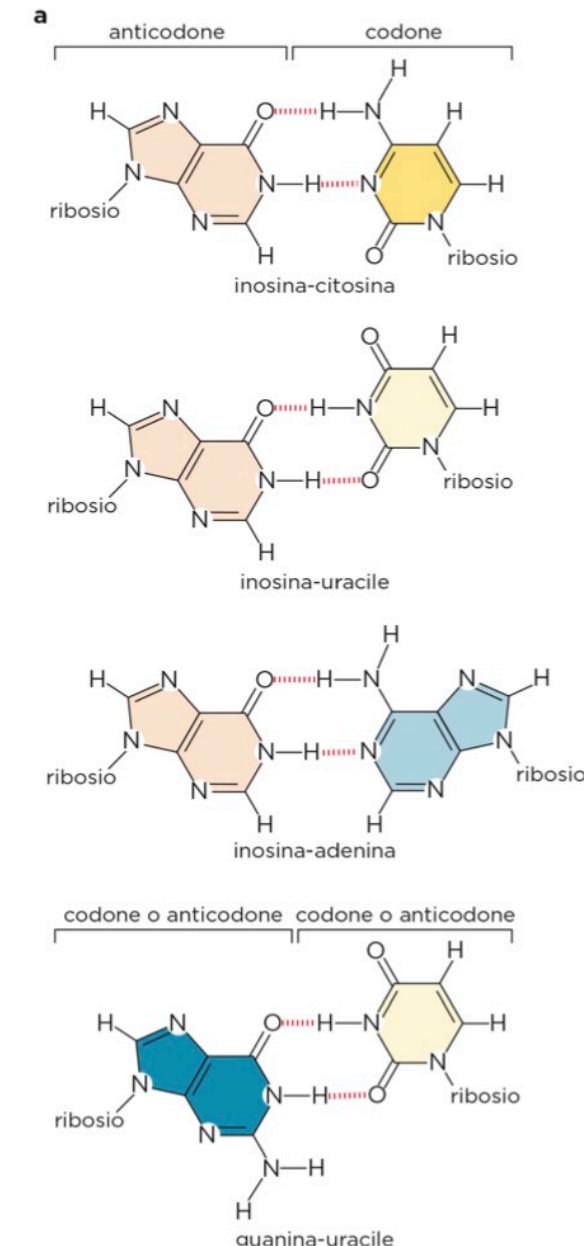
Francis Crick 1966

Observation:

- 1 tRNA anticodon can recognize more than one codon
- nucleotide in anticodon can be INOSINE
- U and I allow additional combination of base pairing



Base dell'anticodone	Base del codone
G	U o C
C	G
A	U
U	A o G
I	A, U o C



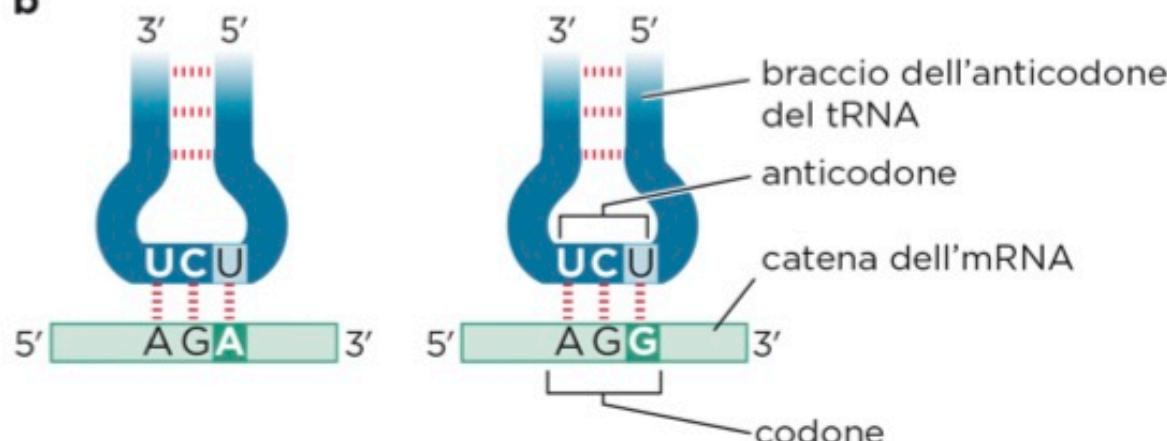
Tentennamento dell'anticodon

“wobbling” of the 3° position of codon-anticodon

A	G
AU AC AA* AG*	Tyr stop stop
UGU UGC UGA* UGG	Cys stop Trp
UC A G	
AU AC	His
AA AG	Gln
AG	
AU AC	Asn
AA AG	Lys
GAU GAC GAA GAG	Asp Ser Arg
GGU GGC GGA GGG	Gly
U G A G	

terza posizione (estremità 3')

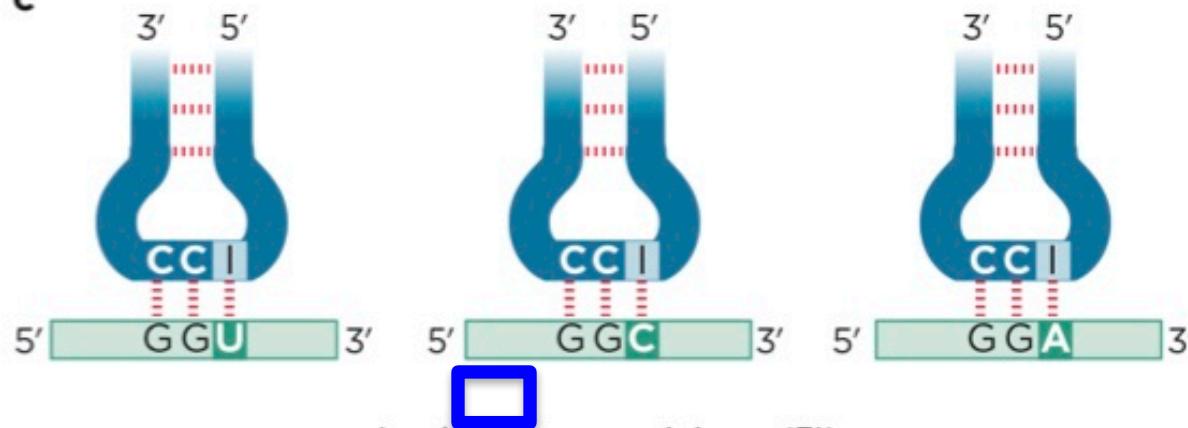
b



both codons encode for Arg

U nella prima posizione (5') dell'anticodone può appaiarsi con A o G

c



all three codons encode for Gly

I nella prima posizione (5') dell'anticodone può appaiarsi con U, C o A

Il codice genetico e degenerato

	AGA										
	AGG										
GCA	CGA										
GCC	CGC										
GCG	CGG	GAC	AAC	UGC	GAA	CAA	GGA				
GCU	CGU	GAU	AAU	UGU	GAG	CAG	GGC				
							GGG				
							GGU				
							CAC	AUA			
							CAU	AUC			
							AUU				
Ala	Arg	Asp	Asn	Cys	Glu	Gln	Gly	His	Ile		
A	R	D	N	C	E	Q	G	H	I		
UUA					AGC						
UUG					AGU						
CUA				CCA	UCA	ACA				GUA	
CUC				CCC	UCC	ACC				GUC	
CUG	AAA			CCG	UCG	ACG				GUG	
CUU	AAG	AUG	UUC	CCU	UCU	ACU	UGG	UAC	UAU	GUU	
			UUU								UAA
											UAG
											UGA
Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val		
L	K	M	F	P	S	T	W	Y	V		

SERINE: 6 codons and min. 3 tRNAs

LEUCINE and **ARGININE**: more then one tRNA

Il codice genetico

- I codoni con pirimidine (U/C) in 2° posizione → aa idrofobici
 - I codoni con purine (G/A) in 2° posizione → aa polari

		U	C	A	G	
		UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
U		UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
		UUU Leu	UCA Ser	UAA TER	UGA TER	A
		UUG Leu	UCG Ser	UAG TER	UGG Trp	G
		CUU Leu	CCU Pro	CAU His	CGU Arg	U
C		CUC Leu	CCC Pro	CAC His	CGC Arg	C
		CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
		CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
		AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
A		AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
		AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
		AUG Met	ACG Thr	AAG Lys	AGG Arg	G
		GUU Val	GCU Ala	GAU Asp	GGU Gly	U
G		GUC Val	GCC Ala	GAC Asp	GGC Gly	C
		GUA Val	GCA Ala	GAA Glu	GGA Gly	A
		GUG Val	GCG Ala	GAG Glu	GGG Gly	G

3 basic rules of the genetic code

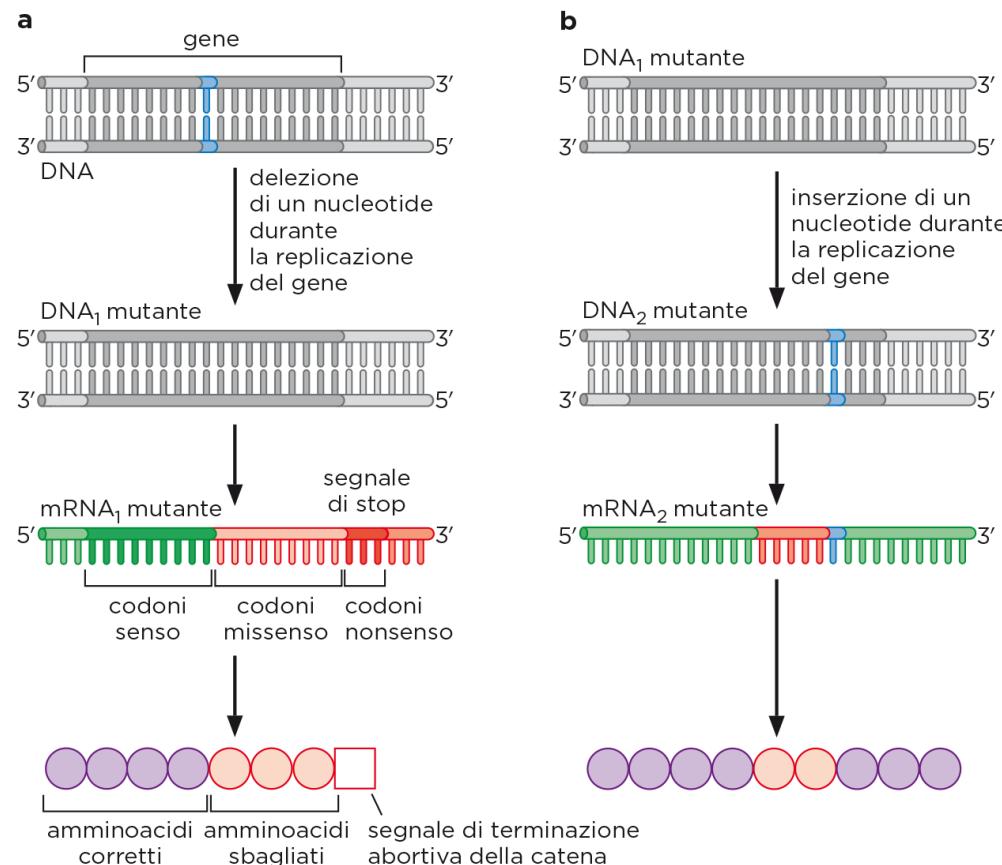
1. mRNA codons are read from 5' → 3' orientation
→ This results a protein in NH₂-aa-aa-aa-COOH orientation
2. Codons do not overlap,; there are not interruptions
3. Each ORF is a defined sequence of codons defined by the start codon

3 basic mutations of the genetic code

1. **MISSENSE:** mutation of codon results in another aa
Example: UUU=Phe; UCU=Ser
2. **FRAMESHIFT:** insertion or deletion of one or two nucleotides Inside an ORF causes a shift in the reading frame
Example: **UUU/UCU=Phe/Ser**; **UUU/UUC/U=Phe/Phe/etc**
3. **NONSENSE or STOP MUTATION:** insertion or deletion of Nucleotides that result in a premature stop-codon
Example: **UUU/UCU=Phe/Ser**; **UUU/UAA/U=Phe/STOP**

Suppressor mutations can rescue mutant ORFs

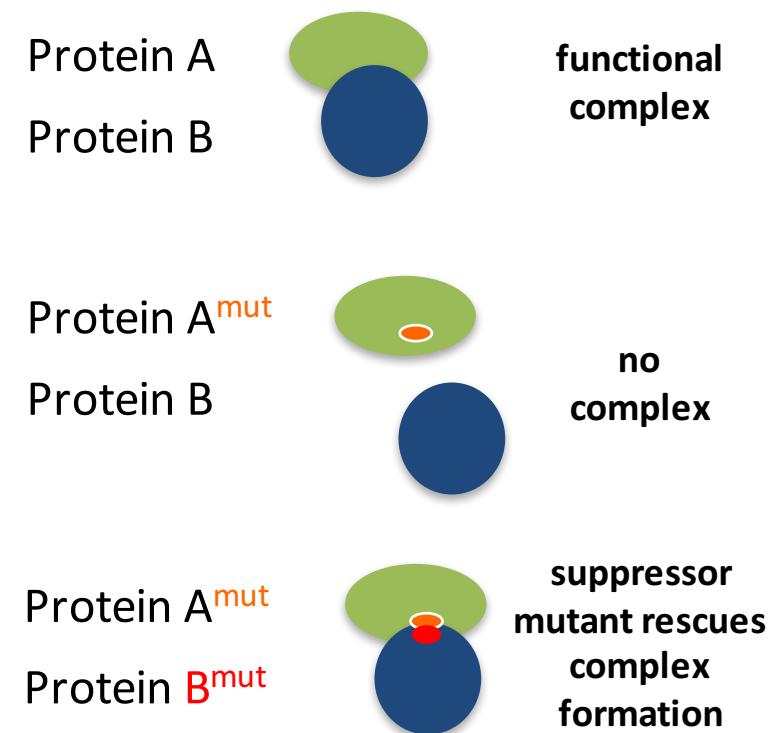
INTRAGENIC SUPPRESSOR MUTANT



Deletion=event1
Causes frameshift, leading
to the usage of a premature
Stop codon
→ Protein is not functional!

Insertion=event2
Causes another frameshift, that
Prevents the use of the premature
stop codon
→ Protein function (partially) rescued

INTERGENIC SUPPRESSOR MUTANTS



functional
complex

no
complex

suppressor
mutant rescues
complex
formation

Different codon usage in mitochondria

Pro/Eucaryotes

seconda posizione				terza posizione (estremità 3')												
				prima posizione (estremità 5')												
U		C		A		G		U		C		A		G		
U	UUU	Phe	UCU	UAA*	Tyr	UGU	Cys	UCA	G	UCC	Ser	UAC	stop	UGC	UAG*	stop
	UUC		UCC	UAA*	stop	UGC		UAG		UUA	Leu	UAC	stop	UGG	Trp	
	UUA		UCA							UUG						
	UUG	Leu	UCG													
C	CUU		CCU	CAU	His	CGU		UCA	G	CUC	Leu	CCC	Pro	CGC	Arg	UCA
	CUC		CCC	CAC		CGC		UAG		CUA	(UAA)	CCA		CGA		UAG
	CUA	Leu	CCA	CAA	Gln	CGA				CUG		CCG		CGG		
	CUG		CCG	CAG		CGG										
A	AUU		ACU	AAU	Asn	AGU		UCA	G	AUC		ACC	Thr	AAC	Ser	UCA
	AUC	Ile	ACCA	AAC		AGC		UAG		AUA		ACA		AAA	Lys	UAG
	AUA		ACA	AAA	Lys	AGA				AUG†	Met	ACG		AAG	Arg	UAG
	AUG†	Met		AAC		AGG										
G	GUU		GCU	GAU	Asp	GGU		UCA	G	GUC		GCC		GGA	Gly	UCA
	GUC		GCC	GAC		GGC		UAG		GUA	Val	GCA		GGA		UAG
	GUA	Val	GCA	GAA	Glu	GGA				GUG		GCG		GGG		
	GUG		GCG	GAG		GGG										

Mitochondria

seconda posizione				terza posizione (estremità 3')												
				prima posizione (estremità 5')												
U		C		A		G		U		C		A		G		
U	UUU	Phe (GAA)†	UCU	UAA	Tyr (GUA)	UGU	Cys (GCA)	UCA	G	UUC	Ser (UGA)	UCC	stop	UGC	Trp (UCA)	UCA
	UUC		UCC	UAA	Leu (UAA)	UCA		UAG		UUA		UAC	stop	UAG		
	UUA		UCA							UUG						
	UUG		UCG													
C	CUU		CCU	CAU	His (GUG)	CGU	Arg (UCG)	CGU	G	CUC	Leu (UAG)	CCC	Pro (UGG)	CAC	Arg (UCC)	UCA
	CUC		CCC	CAC		CGC		CAA		CUA	(UAG)	CCA		CAG	(UUG)	CGG
	CUA	Leu	CCA	CAA	Lys	CGA		CAA		CUG		CCG		CAG		CGG
	CUG		CCG	CAG		CGG										
A	AUU		ACU	AAU	Asn (GUU)	AGU	Asn (GUU)	AAU	G	AUC	Ile (GAU)	ACC	Thr (UGU)	ACA	Ser (GCU)	UCA
	AUC	Ile	ACC	AAC		AGC		ACC		AUA	Met (CAU)‡	ACA		AAA	Lys (UUU)	UAG
	AUA		ACA	AAA	Lys	AGA		ACA		AUG	Met (CAU)‡	ACG		AAG	Arg (UUC)	UAG
	AUG†	Met	ACG	AAG		AGG		ACG						AGA	stop	UAG
G	GUU		GCU	GAU	Asp (GUC)	GGU	Asp (GUC)	GAU	G	GUC	Val (UAC)	GCC	Ala (UGC)	GCA	Gly (UCC)	UCA
	GUC		GCC	GAC		GGC		GCU		GUA	(UAC)	GCG		GGA		GGU
	GUA	Val	GCA	GAA	Glu	GGA		GCG		GUG		GCG		GAG		GGC
	GUG		GCG	GAG		GGG										GGG

Mitochondria have transferred a part of their tRNA genes to the nucleus of the eukaryotic cell

THEORY GOES INTO PRACTICE

Your task in a project:

DESIGN:

- 1- siRNAs that target RAD51
- 2- design PCR primers to PCR amplify RAD51 for the purpose of generating a RAD51 overexpression vector in pcDNA3.1(+)
- 3- design PCR primers to measure RAD51 mRNA in diverse tumorsamples by real-time PCR

FIRST WE NEED TO STUDY THE RAD51 mRNA SEQEUNCE!

ENSEMBL – a collection of annotated genes/transcripts

Search for human RAD51

Ensembl Genome Browser

http://www.ensembl.org/index.html

Concorsi, gar...i di Trieste Oncogene – ...ancer cells Webmail Unit...i di Trieste DiePresse.com Abolishment ...rly Mitosis derStandard... in Echtzeit Library Gene...fic Articles GMX – E-Mail...ing–Portal LEO-DICT

Mail :: Inbox Zimbra: Fwd: Application Returne... Ensembl Genome Browser How to take a screenshot on your... Login/Register

e!Ensembl BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors Rad51

Search: Human for Rad51 Go

e.g. BRCA2 or rat 5:62797383-63627669 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 GRCh38.p2 Mouse GRCm38.p3

Zebrafish Zv9

[★ Log in to customize this list](#)

All genomes

-- Select a species --

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

ENCODE data in Ensembl

Variant Effect Predictor

Gene expression in different tissues

Find SNPs and other variants for my gene

Retrieve gene sequence

Compare genes across species

Use my own data in Ensembl

Learn about a disease or phenotype

What's New in Ensembl Release 79 (March 2015)

- Update to Ensembl-Havana GENCODE gene set (release 22)
- RefSeq-to-Ensembl model comparison
- Query hit distribution image on BLAST/BLAT results page

[Full details](#) | [All web updates, by release](#) | [More news on our blog](#)

Latest blog posts

- 16 Apr 2015: [What's coming in Ensembl release 80](#)
- 09 Apr 2015: [dbSNP 142 and 1000 Genomes Phase 3](#)
- 07 Apr 2015: [Say hello to the new Regulation mart](#)

[Go to Ensembl blog →](#)

Recent tweets from @ensembl

Ensembl supports data from external projects through Trackhubs

ENSEMBL – a collection of annotated genes/transcripts

PICK THE CORRECT ENTRY

The screenshot shows the Ensembl genome browser interface for Homo sapiens (GRCh38.p2). The search term "Rad51" has been entered into the search bar, resulting in 23716 matches. The results are categorized by type: Gene, Transcript, Variation, Somatic Mutation, GeneTree, Clones & Regions, ProbeFeature, Protein Domain, and Protein Family. The first result listed is RAD51 (Human Gene), which is associated with ENSG0000051180. Other results include RAD51 antisense RNA 1, RAD51-AS1, RAD51-001, and RAD51-009.

Ensembl genome browser 79: Homo sapiens – Results Summary – Ensembl text search

http://www.ensembl.org/Human/Search/Results?q=Rad51;site=ensembl;facet_species=Human

Concorsi, gar...i di Trieste Oncogene – ...ancer cells Webmail Unit...i di Trieste DiePresse.com Abolishment ...rly Mitosis derStandard... in Echtzeit Library Gene...fic Articles GMX – E-Mai...ing-Portal LEO-DICT

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Human (GRCh38.p2) ▾

Current selection: < all Species Only searching Human

Restrict category to:

Gene	20
Transcript	102
Variation	22843
Somatic Mutation	583
GeneTree	7
Clones & Regions	2
ProbeFeature	134
Protein Domain	3
Protein Family	22

Per page: 10 25 50 100

Layout: Standard Table

Only searching Human Rad51

23716 results match Rad51 when restricted to species: Human

RAD51 (Human Gene)
ENSG0000051180 15:40694774-40732339:1
RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:9817]

RAD51 (Vega gene) is associated with Gene ENSG0000051180
Variation table • Phenotypes • Location • External Refs. • Regulation • Orthologues • Gene tree

RAD51-AS1 (Human Gene)
ENSG00000245849 15:40686724-40695107:-1
RAD51 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:HGNC:48621]

RAD51-AS1 (EntrezGene record with a description of RAD51 antisense RNA 1 (head to head)) is associated with Gene ENSG00000245849
Variation table • Phenotypes • Location • External Refs. • Regulation • Orthologues • Gene tree

RAD51-001 (Human Transcript)
ENST00000267868 15:40695160-40732339:1
RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:9817]

RAD51-001 (Vega transcript) is associated with Transcript ENST00000267868
Location • External Refs. • cDNA seq. • Variation table • Protein seq. • Population • Protein

RAD51-009 (Human Transcript)
ENST00000382643 15:40695174-40731593:1
RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:9817]

RAD51-009 (Vega transcript) is associated with Transcript ENST00000382643
Location • External Refs. • cDNA seq. • Variation table • Protein seq. • Population • Protein

RAD51-002 (Human Transcript)

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PAGE OPENS WITH ALL KNOWN RAD51 TRANSCRIPTS

Part 1: annotated transcripts---- WHICH TYPES OF RNAs CAN YOU IDENTIFY??

Mail :: Inbox Zimbra: Fwd: Application Returne... Ensembl genome browser 79: Ho... How to take a screenshot on your... Login/Register

e!Ensembl BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors Human (GRCh38.p2) ▾ Location: 15:40,694,774-40,732,339 Gene: RAD51

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Supporting evidence
- Gene alleles
- Sequence
 - └ Secondary Structure
 - External references
 - Regulation
- Comparative Genomics
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
 - Ensembl protein families
- Phenotype
- Genetic Variation
 - Variation table
 - Variation image
 - Structural variation
- External data
 - └ Personal annotation
- ID History
 - └ Gene history

Gene: RAD51 ENSG00000051180

Description RAD51 recombinase [Source:HGNC Symbol;Acc:[HGNC:9817](#)]

Synonyms BRCC5, HsRad51, HsT16930, RAD51A, RECA

Location [Chromosome 15: 40,694,774-40,732,339](#) forward strand.

INSDC coordinates chromosome:GRCh38:CM000677.2:40694774:40732339:1

About this gene This gene has 10 transcripts ([splice variants](#)), [65 orthologues](#), [3 paralogues](#), is a member of [4 Ensembl protein families](#) and is associated with [5 phenotypes](#).

Transcripts [Hide transcript table](#)

Show/hide columns (1 hidden)

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
RAD51-001	ENST00000267968	2449	339aa	Protein coding	CCDS10062	Q06609	NM_002875 NP_002866	TSL:1 GENCODE basic APPRIS PI1
RAD51-002	ENST00000423169	1611	280aa	Protein coding	CCDS53932	Q06609	NM_001164270 NP_001157742	TSL:1 GENCODE basic
RAD51-009	ENST00000382643	1588	340aa	Protein coding	CCDS53931	Q06609	NM_001164269 NP_001157741	TSL:2 GENCODE basic
RAD51-008	ENST00000532743	1515	340aa	Protein coding	CCDS53931	Q06609	NM_133487 NP_597994	TSL:2 GENCODE basic
RAD51-003	ENST00000557850	1397	242aa	Protein coding	-	Q06609	-	TSL:2 GENCODE basic
RAD51-006	ENST00000526763	625	75aa	Protein coding	-	Q9NZG9	-	CDS 3' incomplete TSL:3
RAD51-007	ENST00000527860	566	172aa	Protein coding	-	E9PNT5	-	CDS 3' incomplete TSL:4
RAD51-004	ENST00000525066	1545	151aa	Nonsense mediated decay	-	E9PJ30	-	TSL:5
RAD51-010	ENST00000531277	658	100aa	Nonsense mediated decay	-	E9PI54	-	TSL:3
RAD51-013	ENST00000533741	425	65aa	Nonsense mediated decay	-	H0YD61	-	CDS 5' incomplete TSL:1

Summary ⓘ

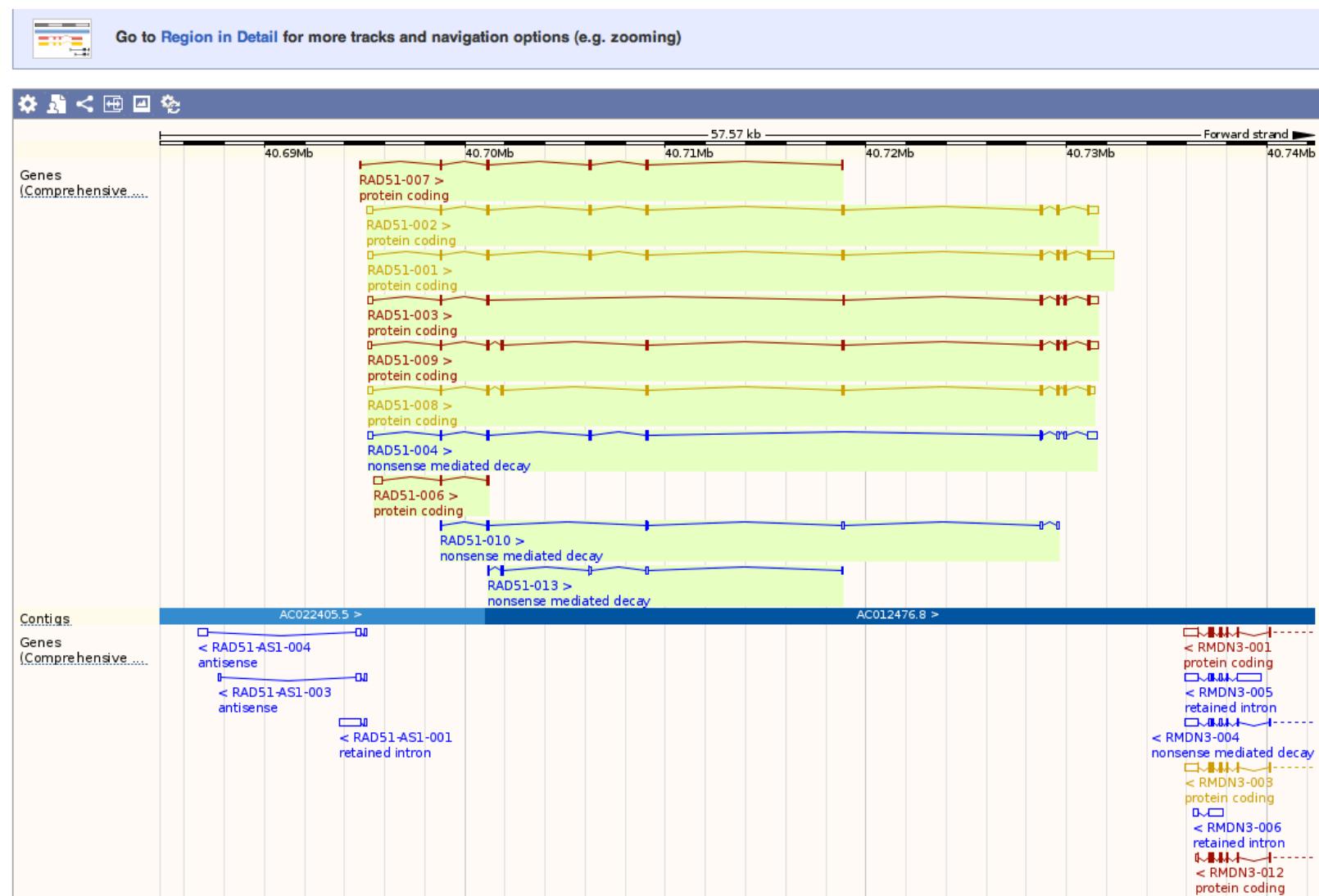
Name [RAD51](#) (HGNC Symbol)
CCDS This gene is a member of the Human CCDS set: [CCDS10062.1](#), [CCDS53931.1](#), [CCDS53932.1](#)

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PAGE OPENS WITH ALL KNOWN RAD51 TRANSCRIPTS

Part 2: mapping transcripts against genomic DNA
---- WHICH TYPES OF RNAs CAN YOU IDENTIFY??



ENSEMBL – a collection of annotated genes/transcripts

PICK RAD51 transcript 009

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Human (GRCh38.p2) ▾ Location: 15:40,694,774-40,732,339 Gene: RAD51 Transcript: RAD51-009

Search Human...

Transcript-based displays

- Summary
- Supporting evidence
- Sequence
 - Exons
 - cDNA
 - Protein
- External References
 - General identifiers
 - Oligo probes
- Ontology
 - GO graph
 - GO table
- Genetic Variation
 - Variation table
 - Variation image
 - Population comparison
 - Comparison image
- Protein Information
 - Protein summary
 - Domains & features
 - Variations
- External data
 - Personal annotation
- ID History
 - Transcript history
 - Protein history

Transcript: RAD51-009 ENST00000382643

Description RAD51 recombinase [Source:HGNC Symbol;Acc:[HGNC:9817](#)]

Synonyms BRCC5, HsRad51, HsT16930, RAD51A, RECA

Location Chromosome 15: 40,695,174-40,731,593 forward strand.

About this transcript This transcript has [10 exons](#), is annotated with [12 domains and features](#), is associated with [67 variations](#) and maps to [13 oligo probes](#).

Gene This transcript is a product of gene [ENSG00000051180](#) [Hide transcript table](#)

Show/hide columns (1 hidden)

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
RAD51-001	ENST00000267868	2449	339aa	Protein coding	CCDS10062	Q06609	NM_002875 NP_002866	TSL:1 GENCODE basic APPRIS PI1
RAD51-002	ENST00000423169	1611	280aa	Protein coding	CCDS53932	Q06609	NM_001164270 NP_001157742	TSL:1 GENCODE basic
RAD51-009	ENST00000382643	1588	340aa	Protein coding	CCDS53931	Q06609	NM_001164269 NP_001157741	TSL:2 GENCODE basic
RAD51-008	ENST00000532743	1515	340aa	Protein coding	CCDS53931	Q06609	NM_133487 NP_597994	TSL:2 GENCODE basic
RAD51-003	ENST00000557850	1397	242aa	Protein coding	-	Q06609	-	TSL:2 GENCODE basic
RAD51-006	ENST00000526763	625	75aa	Protein coding	-	Q9NZG9	-	CDS 3' incomplete TSL:3
RAD51-007	ENST00000527860	566	172aa	Protein coding	-	E9PNT5	-	CDS 3' incomplete TSL:4
RAD51-004	ENST00000525066	1545	151aa	Nonsense mediated decay	-	E9PJ30	-	TSL:5
RAD51-010	ENST00000531277	658	100aa	Nonsense mediated decay	-	E9PI54	-	TSL:3
RAD51-013	ENST00000533741	425	65aa	Nonsense mediated decay	-	H0YD61	-	CDS 5' incomplete TSL:1

Summary

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Codons	Alternating codons	Alternating codons
Exons	Alternating exons	Alternating exons
Variations	3 prime UTR	5 prime UTR
Other	UTR	

1 AATTCTGAAAGCCGCTGGCGGACCGGCGCAGCGGCCAGAGACCGGCCCTAAGGAGGT
.....
61 CGGGCGCTTCCCAGGGCGTCAGCTGGARACTGCAACTCATTCGGTTGTGCCAGAACCG
.....
121 CTGGGGCAAGCGAGTAGAGAAAGTGGAGCTAATGCAATGCAGATGCAGCTTGAAGCAAAT
..... ATGGCAATGCAGATGCAGCTTGAAGCAAAT
..... -M--A--M--Q--M--Q--L--E--A--N--

181 GCAGATATTCAGTGGAAAGAAGAAAGCTTGGCCCACAACCCATTCACGGTTAGAGC
31 GCAGATATTCAGTGGAAAGAAGAAAGCTTGGCCCACAACCCATTCACGGTTAGAGC
11 -A--D--T--S--V--E--E--S--F--G--P--Q--P--I--S--R--L--E--Q--

241 TGTGGCATAAATGCCAACGATGTGAAGAAATTGGAAGAAGCTGGATTCCCATACTGTGGAG
91 TGTGGCATAAATGCCAACGATGTGAAGAAATTGGAAGAAGCTGGATTCCCATACTGTGGAG
31 -C--G--I--N--A--N--D--V--K--K--L--E--E--A--G--F--H--T--V--E--

301 GCTGTTGCTATGCGCAAGAGGAGGCTATAATTAGGGATTATGTGAGCAA
151 GCTGTTGCCTATGCGCAAGAGGAGGCTATAATTAGGGATTATGTGAGCAA
51 -A--V--A--Y--A--P--K--K--E--L--I--N--I--K--G--I--S--E--A--K--

361 GCTGATAAAATCTGACGAGTCTCGCTTGTTGGCAGGCTGAGTGCAATAGCGTGAT
211 GCTGATAAAATCTGACGGGAGTCTCGCTTGTTGGCAGGCTGAGTGCAATAGCGTGAT
71 -A--D--K--I--L--T--E--S--R--S--V--A--R--L--E--C--N--S--V--I--

421 TTGGTCTATGCACCTCGCTCTCAGGTTTCAGTGATTCTCCGA
271 TTGGTCTATGCACCTCGCTCTCAGGTTTCAGTGATTCTGCTCCGA
91 -L--V--Y--C--T--L--R--L--S--G--S--S--D--S--P--A--S--A--S--R--

1. cDNA sequence

note:

The 7meG cap is

Not part of the cDNA

Sequeunce!!!!

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Navigation sidebar:

- Oligo probes
- Ontology
 - GO graph
 - GO table
- Genetic Variation
 - Variation table
 - Variation image
 - Population comparison
 - Comparison image
- Protein Information
 - Protein summary
 - Domains & features
 - Variations
- External data
 - Personal annotation
- ID History
 - Transcript history
 - Protein history

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- Add your data
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Gene table:

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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
RAD51-001	ENST00000267868	2449	339aa	Protein coding	CCDS10062	Q06609	NM_002875 NP_002866	TSL:1 GENCODE basic APPRIS P1
RAD51-002	ENST00000423169	1611	280aa	Protein coding	CCDS53932	Q06609	NM_001164270 NP_001157742	TSL:1 GENCODE basic
RAD51-009	ENST00000382643	1588	340aa	Protein coding	CCDS53931	Q06609	NM_001164269 NP_001157741	TSL:2 GENCODE basic
RAD51-008	ENST00000532743	1515	340aa	Protein coding	CCDS53931	Q06609	NM_133487 NP_597994	TSL:2 GENCODE basic
RAD51-003	ENST00000557850	1397	242aa	Protein coding	-	Q06609	-	TSL:2 GENCODE basic
RAD51-006	ENST00000526763	625	75aa	Protein coding	-	Q9NZG9	-	CDS 3' incomplete TSL:3
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RAD51-013	ENST00000533741	425	65aa	Nonsense mediated decay	-	H0YD61	-	CDS 5' incomplete TSL:1

Protein sequence:

Download sequence BLAST this sequence

Exons Alternating exons Alternating exons Residue overlap splice site

MAMQMQLLEANADTSVEEESFGPQPISRLQCQGINANDVKKLEEAGFHTVEAVAYAPKKEL
INIKGISEAKADKILTESRSVARLCNSVILVYCTRLSGSSDSPASASRVGTTGCIGET
GSITEMFGEFRTGKTOICHTLAVTCQLPIDRGGGEGKAMYIDTEGTRPERLLAVAEERYG
LSGSVDLNDNVAYARAFTDHQTOOLYQASAMMVESEYALLIVDSATALYRTDYSRGELS
ARQMHLARFLRLRLADEFGVAVVITNQVVAQVDGAAMFAADPKPIGGNIIIAHASTTR
LYLRKGRRGETRICKIYDSPCLPEAEAMFAINADGVGDARD

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2. Protein sequence

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3. EXONS

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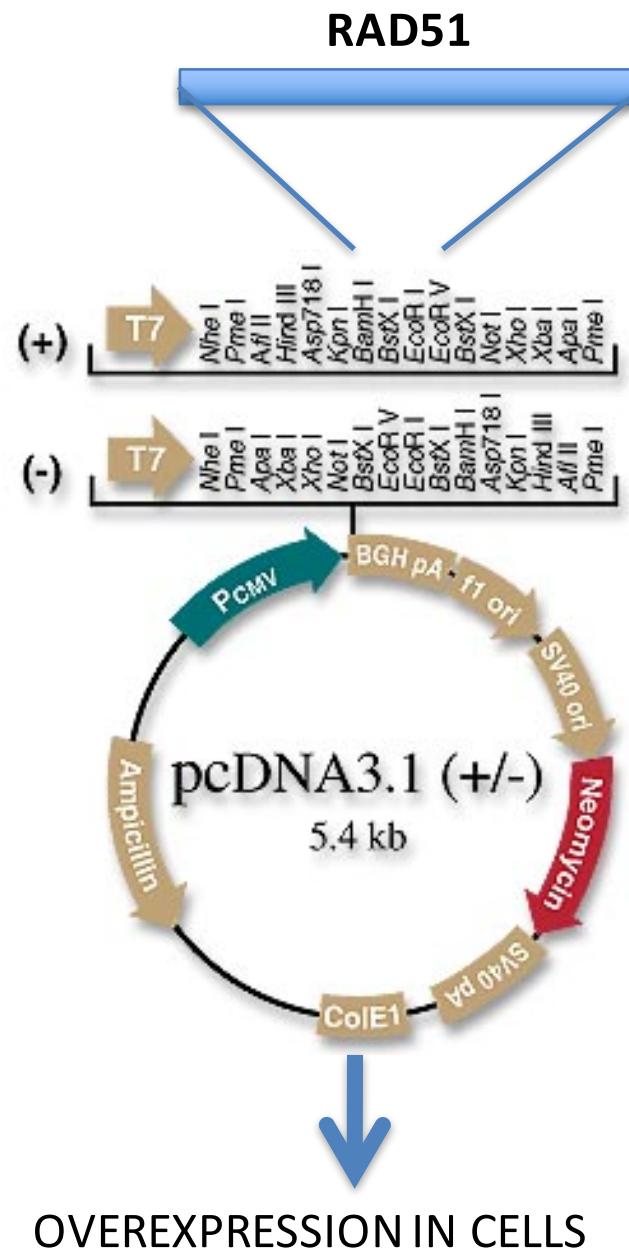
3. EXONS

ENSEMBL – a collection of annotated genes/transcripts

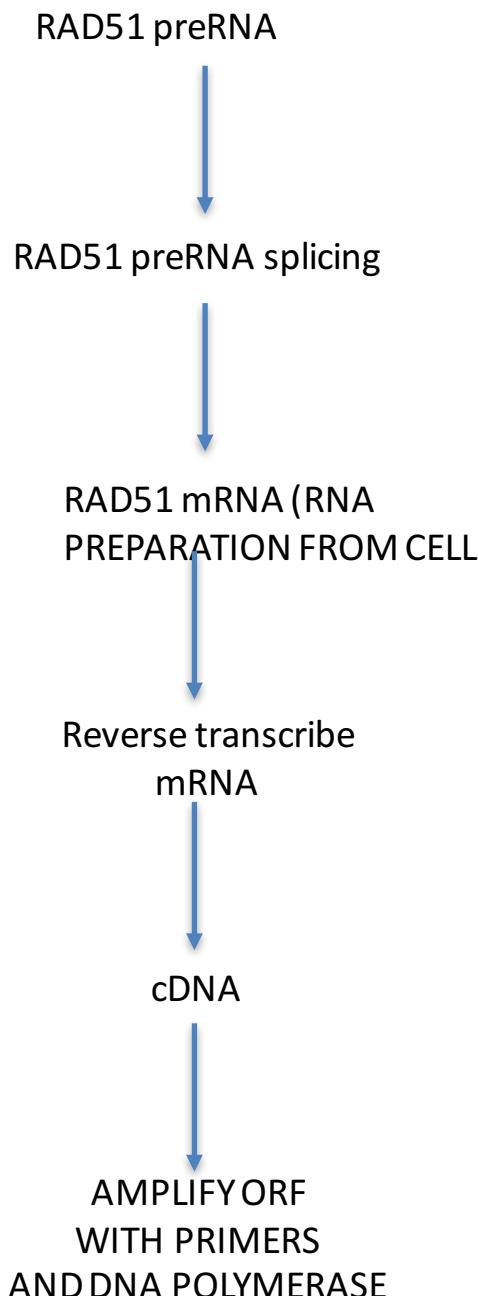
3' END

			Exons/ Translated sequence	Flanking sequence	Intron sequence	UTR
	Intron 4-5	40,709,117	CTCCGCCCTCTCAGGGTCAAGTGATTCTCTGCCTCAGGCTCCCCGAGTAGTTGGGACTACA			at.....gagttatttcttatcgcttttag
5	ENSE00003614784	40,718,805	Introns			CACAGAAATGTTGGAGAATTCCGAACGGAAAGACCC CACCTGCCAG
	Intron 5-6	40,709,117 40,718,804		9,688	gtgagctgtgggctatacgtaat.....	ctactgtgtttgttctatag
6	ENSE00003635979	40,718,805 40,718,899	0	2 95	CTTCCCATTGACCGGGGTGGAGGTGAAGGAAAGGCCATGTACATTGACACTGAGGGTACC TTTAGGCCAGAACCGCTGCTGGCAGTGGCTGAGAG	
	Intron 6-7	40,718,900 40,728,710		9,811	gtaggtaactggtttagataagaga.....	aaaaatgttcttcctctcatag
7	ENSE00003596640	40,728,711 40,728,824	2	2 114	GTATGGTCTCTGGCAGTGTGTCCTGGATAATGTAGCATATGCTCGAGCGTTAACAC AGACCACCAAGCCAGCTCCTTATCAAGCATCAGCCATGATGGTAAATCTAG	
	Intron 7-8	40,728,825 40,729,504		680	gtatgttcaagtataagacaccaa.....	ttcagagaatcctgtttctgtag
8	ENSE00003571456	40,729,505 40,729,634	2	0 130	GTATGCACTGCTTATTGTAGACAGTGCACCCGCCCTTACAGAACAGACTACTCGGGTCG AGGTGAGCTTCAGCCAGGCAGATGCACTGCCAGGTTCTGCGGATGCTCTGCGACT CGCTGATGAG	
	Intron 8-9	40,729,635 40,729,852		218	gtaagttgtggataggacagaga.....	ttgacatttacccatccccatcag
9	ENSE00003540252	40,729,853 40,729,974	0	2 122	TTTGGTGTAGCAGTGGTAATCACTAACGAGGTGGTAGCTCAAGTGGATGGAGCAGCGATG TTTGCTGCTGATCCCAAAACCTATTGGAGGAAATATCATGCCCATGCATCAACAACC AG	
	Intron 9-10	40,729,975 40,731,054		1,080	gtaaggttgtatggatcaggttct.....	gctttggctgtgtctttgggtcag
10	ENSE00002170856	40,731,055 40,731,593	2	- 539	ATTGTATCTGAGGAAAGGAAGAGGGAAACCAGAACTGCAAATCTACGACTCTCCCTG TCTTCCCTGAAGCTGAAGCTATGTCGCCATTAATGCAGATGGAGTGGGAGATGCCAAAGA CTGAATCATGGGTTTCTCTACAGGCCTCTCCTGTTAAAGTGTGCTGCAGCCTAATGAGAGTGC ACTGCTCCCTGGGTTCTACAGGCCTCTCCTGTTGGTAGTGTGCTGCAGCCTAATGAGAGTGC GGGAAACAGCTATTATATCAGCTTCTGATGGTATAAACAGGGAGACAGGTCAAGTAGTC ACAAACTGATCTAAAATGTTATTCCCTCTGTTAGTGTATTAAATCTCTGTTGGGTT GGTTTGGAGGAGGGTATGAAGTATCTTGACATGGCCTTAGGAATGACTTGGGTT ACAAACTGTCAGTGGACAATCTTATGTTCCAAGAGAACTAAAGCTGGAGAGACCTGA CCCTCTCTCACTCTAAATGGTAAAATAAATGCCCTCAGCTATGTAGCAAAGGG	
	3' downstream sequence				aatgggtctgcacagattctttttctgtcagtaaaactctcaagcagg.....	

DESIGN: 2. PCR oligos to subclone RAD51 into a mammalian expression vector



DESIGN: 2. PCR oligos to subclone RAD51 into a mammalian expression vector



DESIGN PRIMERS FOR AMPLIFICATION OF RAD51 ORF

RAD51:

5' end: 5'-TTTGTATTTTCAGTA**ATG**GCAATGCAGATGC-3'

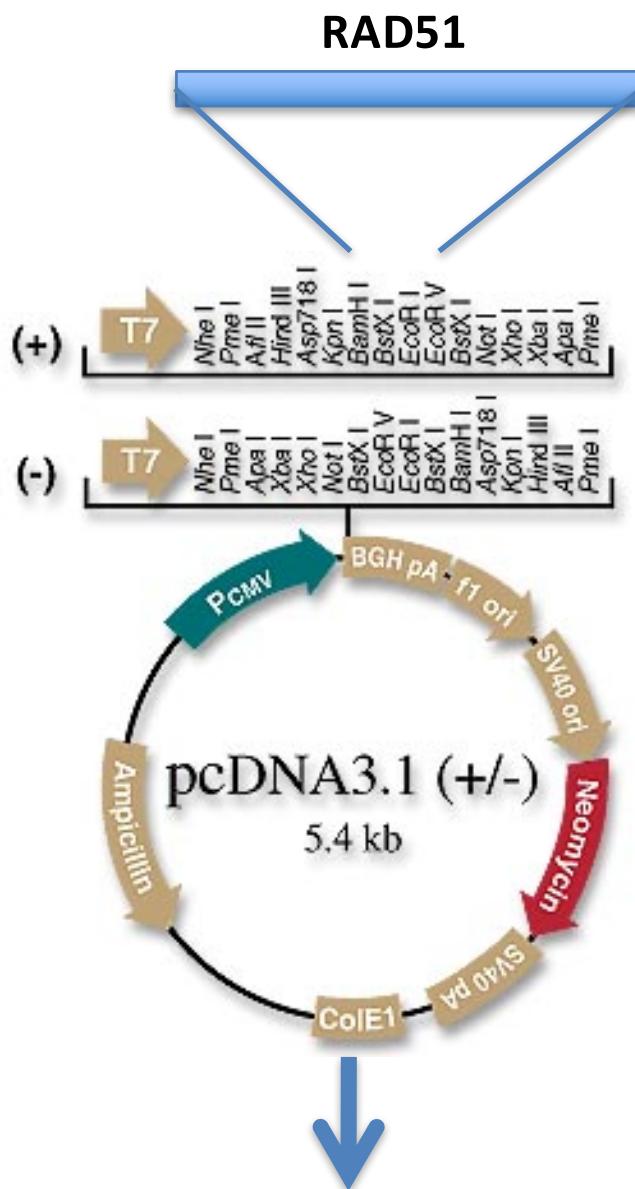
Oligo: 5'-GTA**ATG**GCAATGCAGATGC-3'

3' end: 5' AAAGAC**UGA**ATCATTGGGTTTCCT 3

Oligo: 3'-**ACT**TAGTAACCCAAAAAGGA-5'

KOZAK sequence: 5'-G/A^NNAUGG-3'

DESIGN: 2. PCR oligos to subclone RAD51 into a mammalian expression vector



GTAATGGCAATGCAGATGCAGCTGAAGCAAATGCAGATACTCAGTGGAAAGAAGAAAGCTTGGC
CCACAACCCATTACGGTTAGAGCAGTGTGGCATAAATGCCAACGATGTGAAGAAATTGGAAGAA
GCTGGATTCCATACTGTGGAGGCTGTGCCTATGCCCAAAGAAGGAGCTAATAAATATTAGGGAA
TTAGTGAAGCCAAGCTGATAAAAATTCTGACGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAATAG
CGTGATCTTGGTCTACTGCACCCCTCCGCCTCAGGTTCAAGTGAATTCTCCTGCCTCAGCCTCCGAGT
AGTTGGGACTACAGGTGGAATTGAGACTGGATCTACAGAAAATGTTGGAGAATTCCGAACCTGG
GAAGACCCAGATCTGTACATGACACTGAGGGTACCTTAGGCCAGAACGGCTGCTGGCAGTGGCTGAG
GGAAAGGCCATGTACATTGACACTGAGGGTACCTTAGGCCAGAACGGCTGCTGGCAGTGGCTGAG
AGGTATGGTCTCTGGCAGTGATGTCCTGGATAATGTAGCATATGCTGAGCGTTCAACACAGACCA
CCAGACCCAGCTCTTATCAAGCATCAGCCATGATGGTAGAATCTAGGTATGCACTGCTTATTGAGA
CAGTGCCACCGCCCTTACAGAACAGACTACTGGGTCGAGGTGAGCTTCAGCCAGGCAGATGCAC
TTGGCCAGGTTCTCGGGATGCTCTGCAGCTGCTGATGAGTTGGTAGCAGTGGTAATCACTAA
TCAGGTGGTAGCTCAAGTGGATGGAGCAGCGATGTTGCTGCTGATCCCACACCTATTGGAGG
AAATATCATGCCCATGCATCAACAACCAGATTGTATCTGAGGAAAGGAAGAGGGAAACCAGAAC
TGCAAAATCTACGACTCTCCCTGCTTCCCTGAAGCTGAAGCTATGTTGCCATTAAATGCAGATGGAGT
GGGAGATGCCAAAGACTGAATCATTGGGTTTTCCT

OVEREXPRESSION IN CELLS