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**Topic:** BLAST Cancer RAS Gene Project

**Summary:** Students will do a BLAST and learn about how a mutated gene will code for an abnormal protein, affecting the organism's phenotype.

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

**NGSS HS-LS1-1:** Construct an explanation based on evidence for how the structure of DNA determines the structure of proteins which carry out the essential functions of life through systems of specialized cells.

**Time Length:** 60 minutes + 30 minutes for CER

**Prerequisite Knowledge:** Protein synthesis and that mutations in the DNA can cause a change in the protein that is made. A modified protein may change the phenotype. It is highly recommended that students are introduced to the RAS protein and how the cell cycle is regulated prior to this activity.

**Materials:**

- Laptops with Internet access
- Preferred (students have a google account where two students can type on the same report at the same time)
- Handout of the project

**Procedures:**

1. You will want to demonstrate how to do a BLAST using a projector before students do a BLAST themselves.
2. Have every student do part 1, the BLAST.
3. For part 2, student will write a Claim Evidence Reasoning paragraph(s) using the following driving question "**How do scientists really know that DNA codes for proteins and those proteins are represented in our traits?**".

**Editable DOCX File and Answer Key:**

Available at [www.ngsslifescience.com](http://www.ngsslifescience.com)



# BLAST Cancer Ras Gene Project

## Part 1: Gene Look-up Direction:

1. Go to the website below to look up a gene.

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

2. In the search box, type Homo sapiens RAP1A, member of RAS oncogene family.

3. In the search results, click on the RAP1A link.

**Search results**

Items: 1 to 20 of 12721 << First < Prev Page 1 of 637 Next > Last >>

[See also 399 discontinued or replaced items.](#)

Name/Gene ID	Description	Location	Aliases	MIM
<input type="checkbox"/> <a href="#">Ras85D</a> ID: 41140	Ras oncogene at 85D [ <i>Drosophila melanogaster</i> (fruit fly)]	Chromosome 3R, NT_033777.3 (9510561..9513067, complement)	Dmel_CG9375, C-ras1, CG9375, D-Ras, D-Ras1, D-ras-1, D-ras1, DRAS1, DRas, DRas85D/Ras, Dm Ras1, DmelCG9375, Dmras85D, Dras, Dras1, Dras85D, E(faf), E(sev)3C, EC3-3, EK3-4, P08646, RAS, RAS1, RAS85D, RTK, Ras, Ras 85D, Ras-1, Ras1, Ras1/RAs85D, Ras185D, Ras85Nt, Rasl, RasV12, Ras[V12], S35097, Su(tor)3-2, dRAS1, dRas, dRas1, dRas85D, dras1, fs(3)05703, l(3)06677, l(3)s1747, p21[Ras1], ras, ras 1, ras1, ras85B, ras85D, Ras85D	
<input type="checkbox"/> <a href="#">RAN</a> ID: 5901	RAN, member RAS oncogene family [ <i>Homo sapiens</i> (human)]	Chromosome 12, NC_000012.12 (130871879..130877678)	ARA24, Gsp1, TC4	601179
<input type="checkbox"/> <a href="#">RAB11A</a> ID: 8766	RAB11A, member RAS oncogene family [ <i>Homo sapiens</i> (human)]	Chromosome 15, NC_000015.10 (65869459..65891991)	YL8	605570
<input type="checkbox"/> <a href="#">RAB5A</a> ID: 5868	RAB5A, member RAS oncogene family [ <i>Homo sapiens</i> (human)]	Chromosome 3, NC_000003.12 (19947080..19985175)	RAB5	179512
<input type="checkbox"/> <a href="#">RAP1A</a> ID: 5906	RAP1A, member of RAS oncogene family [ <i>Homo sapiens</i> (human)]	Chromosome 1, NC_000001.11 (111542223..111716695)	C21KG, G-22K, KREV-1, KREV1, RAP1, SMGP21	179520
<input type="checkbox"/> <a href="#">RAB7A</a> ID: 7879	RAB7A, member RAS oncogene family [ <i>Homo sapiens</i> (human)]	Chromosome 3, NC_000003.12 (128726136..128814798)	PRO2706, RAB7	602298



- On the RAP1A [ *Homo sapiens* (human) ] page, you will see a link in the third section down “Genomic regions, transcripts, products”. Click on the FASTA link.

**RAP1A** RAP1A, member of RAS oncogene family [ *Homo sapiens* (human) ]  
 Gene ID: 5906, updated on 26-Nov-2016

**Summary**

Official Symbol: RAP1A provided by HGNC  
 Official Full Name: RAP1A, member of RAS oncogene family provided by HGNC  
 Primary source: HGNC:HGNC:9855  
 See related: Ensembl:ENSG00000116473 HPRD:01545; MIM:179520; Vega:OTTHUMG0000011959  
 Gene type: protein coding  
 RefSeq status: REVIEWED  
 Organism: *Homo sapiens*  
 Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo  
 Also known as: RAP1; C21KG; G-22K; KREV1; KREV-1; SMGP21  
 Summary: This gene encodes a member of the Ras family of small GTPases. The encoded protein undergoes a change in conformational state and activity, depending on whether it is bound to GTP or GDP. This protein is activated by several types of guanine nucleotide exchange factors (GEFs), and inactivated by two groups of GTPase-activating proteins (GAPs). The activation status of the encoded protein is therefore affected by the balance of intracellular levels of GEFs and GAPs. The encoded protein regulates signaling pathways that affect cell proliferation and adhesion, and may play a role in tumor malignancy. Pseudogenes of this gene have been defined on chromosomes 14 and 17.  
 Alternative splicing results in multiple transcript variants. [provided by RefSeq, May 2014]  
 Orthologs: [mouse](#) [all](#)

**Genomic context**

Location: 1p13.2 See RAP1A in [Genome Data Viewer](#) [Map Viewer](#)  
 Exon count: 13

Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p7 (GCF_000001405.33)	1	NC_000001.11 (111542223..111716695)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	1	NC_000001.10 (112162405..112256800)

Chromosome 1 - NC\_000001.11

**Genomic regions, transcripts, and products**

Genomic Sequence: [NC\\_000001.11 Chromosome 1 Reference GRCh38.p7 Primary Assembly](#)

Go to reference sequence details

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

- On this page, you will see the entire gene and all of its nitrogen bases (letters). Click on the link titled “Run BLAST”. On the next page, click the BLAST button at the bottom of the screen

**Homo sapiens chromosome 1, GRCh38.p7 Primary Assembly**  
 NCBI Reference Sequence: NC\_000001.11  
[GenBank](#) [Graphics](#)

>gi|568815597:111542223-111716695 Homo sapiens chromosome 1, GRCh38.p7 Primary Assembly

TCGCGTACTGACGGAAACACTGGCGGCACATATTGAGGCCGTAATTCAGGATCAGACCTGCCGGTTCGAA  
 CACACGCGACAAAGCAAGAAAGTTAAAGAGAAGTGTCTGTGGCTCCTCCACGTGGGTGAAGGACT  
 GTGCCAGCTGAGAGGTGGTAGAGCAGGAAGCTGCCTGAGGACCTCCATTTATTTGGTGAAAACCTGGGCT  
 CCGCCCTTAAGAGAGCAAGTCGAGGGCCGTGTAGGAGTTGGAGGAGAGAAATGAAATTTTGAAGAGTCA  
 GCAGAAGGTGGAAATTTTATTTTACATTTACAGCAGTACAGACTTCATGCAGCCAAAAGTATGAATGCC  
 TTTCTTCTGTGACTTACACTGTAAAGGGAGCATTCTCTTATGTGCAAACTAACCATAGTGGACATGTTT  
 GTCTACATCCAGACAGTTCTTAGATTCAAACCTTGTCTTTGTTTTGTTTTGTTTTTTTCTTTTT  
 TTGAGATGGAGTCTCACCTGTCAACCCAGGCTGGAGTGCAGTGGTCTGTCTTGGCTCACTGAAACCTCC  
 GCCTCCGGGTTCAAGTATTCTCCTGCCTCAACCTTGGAAATAGCTGGACTACAGGCATGAACACCA  
 TGGCTGGCTAGTTTTTGCATTTTAAATAGAGATGGGTTTCAACATGTGGGCAGGCTGGTCTCCAATC  
 CTGAATCAGGTGATCTCCACTTTGGCCTCCAAAGTCTGGGATTACAAGCGTGAAGTGAAGCCATGGC  
 GCCCGGCATGATTTGTTTTATAACCATGAGAACTAAAATCAAAAGTCTATTTGTAGATTCTCCAGT  
 GGGTTATAAAATCTGGAATATTTCTGAAGAAATATTTCTGCTACACACACAGACACATACACAGAGA  
 GACACACACACAGCGCAGGTGACAGCTCTTTGGTAACTCAACTATGAAGTATAGTTTTTGAATATTTTC  
 ACTGATGAAAGATCAAACATACAGTATTCTGTGAACTCTGGTGTATGCGTGTCTGTGTGTGTG

Whole sequence  
 Selected region  
 from: 111542223 to: 111716695  
 Update View

Customize view

Analyze this sequence

Run BLAST  
 Pick Primers  
 Highlight Sequence Features  
 Find in this Sequence

Related information  
 Assembly

Run BLAST

- Type in homo sapiens for the organism and select optimized for highly similar sequences. Click the BLAST button.



blastn blastp blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

**Enter Query Sequence**

Enter accession number(s), gi(s), or FASTA sequence(s)   **Query subrange**

From  To

Or, upload file  No file selected.

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

**Choose Search Set**

Database  Human genomic + transcript  Mouse genomic + transcript  Others (nr etc.):

Organism Optional   Exclude   
 Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude Optional  Models (XM/XP)  Uncultured/environmental sample sequences

Limit to Optional  Sequences from type material

Entrez Query Optional

Enter an Entrez query to limit search [YouTube](#) [Create custom database](#)

**Program Selection**

Optimize for  Highly similar sequences (megablast)  More dissimilar sequences (discontiguous megablast)  Somewhat similar sequences (blastn)  
 Choose a BLAST algorithm

**BLAST** Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)  Show results in a new window

7. It may take a few seconds to run the DNA comparison search, but once you get to the results page, scroll down to the descriptions section. Listed here are hemoglobin genes that have been sequenced. Scroll down the list until you get to

**Homo sapiens 3 BAC RP11-200I19 (Roswell Park Cancer Institute Human BAC Library) complete sequence**

- [Homo sapiens DNA, chromosome 17, nearly complete genome](#)
- [Homo sapiens chromosome 17, clone CTD-2350C19, complete sequence](#)
- [Homo sapiens AKNA domain containing 1 \(AKNAD1\), RefSeqGene on chromosome 1](#)
- [Human DNA sequence from clone RP11-475E11 on chromosome 1, complete sequence](#)
- [Homo sapiens 3 BAC RP11-200I19 \(Roswell Park Cancer Institute Human BAC Library\) complete sequence](#)
- [Homo sapiens 3 BAC RP11-125E8 \(Roswell Park Cancer Institute Human BAC Library\) complete se](#)
- [Homo sapiens transmembrane 4 L six family member 19 \(TM4SF19\), RefSeqGene on chromosome](#)

8. Example: Look on first line Query 3473 (normal RAS) for a mutation with subject 49793 (mutated gene). A missing line represents when a nitrogen base is added or deleted



(change in the letter). When the query has a -, then a DNA base "C" was inserted as the mutation.

```

Query  3473  TCTCCGCTCACTGCAACCTCTGCCTCCCGGGTTCAAAC-AGT-T-GTGCCTCAGTCTTCC  3529
Sbjct  49793  TCTTGGCTCACTGCAACCTCTGCCTCTAGGGTTCAAACGATTCTCCTGCCTCAGCCTCCT  49852
  
```

DNA bases can change like C is changed into a T, causing a substitution mutation.

9. Try to find other mutations in the gene comparison. How many total mutations did you find? \_\_\_\_\_

10. Find seven more mutations and enter in their location and which letter was changed and the type of mutation; substitution, insertion, or deletion.

<b>Query: <u>3413</u></b> <b>Letter: <u>C</u></b> <b>Sbjct: <u>49733</u></b> <b>Letter: <u>T</u></b> <b>Mutation Type: <u>substitution</u></b>	Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____
Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____	Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____
Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____	Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____
Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____	Query: _____ Letter: ____ Sbjct: _____ Letter: ____ Mutation Type: _____

