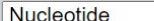


1. Select A **HUMAN GENE** OF YOUR INTEREST WITH AN **ENTRY IN PDB** DATABASE (<https://www.rcsb.org/>) Introduce the general information available about “your gene” (5 points).
2. Find the genomic region of “your gene.” In which chromosomal band and clone or contig in the genomic assembly is your gene of interest located? Comment on the gene structure/model, possible mRNA and protein products, and their function? (10 points)
3. Comment about the supporting evidence for the annotation of the gene. **Is it a well-determined gene or not? Why?** Compare the experimental data and automated annotations. (10 points)
4. Find out if any of the following species has proteins homologous to “your protein/gene of interest.” *M. musculus*, *G. gallus*, *O. lapites*, *A. mellifera*, *C. elegans*, *S. cerevisiae*. Make multiple alignments and phylogenetic tree using **only three of the homologous protein sequences**. Do you see any clusters on the phylogenetic tree which are different from the tree of life? Next, build the phylogenetic tree with all the sequences, describe any differences you have observed and, discuss possible effects of adding more sequences to the phylogenetic analysis. (20 points)

5. Find the mouse genomic region **syntenic** to this locus. Get the list of genes in those syntenic regions. Is there a human gene in this list without a mouse homolog, name if any? **Suggest few reasons for not observing a homolog gene on a syntenic region between the genomes of 2 organisms.** (15 points)
  
6. Find the protein sequence and which protein family or superfamily it belongs to. How many predicted or known proteins are there in the same family? Are there any conserved motifs, patterns, domains in this family; mark these features on a multiple sequence alignment? (10 points)
  
7. Show the main secondary structures on the sequence. Display the 3D structure of the protein and label the regions with different colors with **helical and/or b-sheet** conformation. **Also, identify the one great turn/loop/bend or break in the helix on the 3D structure. Label the amino acid residues that are mainly responsible for this structure and discuss their role.** (20 points)

 NCBI Resources  How To 

Nucleotide  Nucleotide  Advanced Help

**COVID-19 Information** 

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

GenBank  Send to:  Change region shown

 Due to the large size of this record, sequence and annotated features are not shown. Use the "Customize view" panel to change the display.

## Homo sapiens chromosome 16, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC\_000016.10

[FASTA](#) [Graphics](#)

[Go to: !\[\]\(84605d36fdd34af39a387412552dd1b3\_img.jpg\)](#)

LOCUS NC\_000016 90338345 bp DNA linear CON 22-NOV-2021

DEFINITION Homo sapiens chromosome 16, GRCh38.p13 Primary Assembly.

ACCESSION NC\_000016

VERSION NC\_000016.10

DBLINK BioProject: PRJNA168  
Assembly: [GCF\\_000001405.39](#)

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

**Analyze this sequence**   
Run BLAST  
Pick Primers  
Highlight Sequence Features  
Show in Genome Data Viewer

**Related information**   
Assembly  
BioProject

Chromosome 16 is an autosomal chromosome, meaning it carries both maternal and paternal genes. Genes containing about 3 percent of the total DNA in a human cell are located on this chromosome. It contains about 800 to 900 genes and these genes are used in the construction of various proteins with different functions in the body. [1]

This chromosome contains the highest levels of segmentally duplicated sequence relative to other human autosomes. This chromosome contains 880 protein-coding genes confirmed by 1,670 aligned transcripts, 19 transfer RNA genes, 341 pseudogenes and three RNA pseudogenes. [2]

# chromosomal conditions for chromosome 16: [1]

## Health Conditions Related to Chromosomal Changes

The following chromosomal conditions are associated with changes in the structure or number of copies of chromosome 16.

16p11.2 deletion syndrome

16p11.2 duplication

16p12.2 microdeletion

Alveolar capillary dysplasia with misalignment of pulmonary veins

Core binding factor acute myeloid leukemia

Rubinstein-Taybi syndrome

Cancers

Other chromosomal conditions

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## Related Health Topics

Genetic Disorders

## MEDICAL ENCYCLOPEDIA

Chromosome

## Related Medical Tests

Karyotype Genetic Test

## Understanding Genetics

What is a chromosome?

How many chromosomes do people have?

Can changes in the number of chromosomes affect health and development?

Can changes in the structure of chromosomes affect health and

# A GENE PRODUCT from CH16: - NM\_000485.3 -mrna:

**COVID-19 Information**

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

GenBank ▾ Send to: ▾ Change region shown ▾

**Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, mRNA**

NCBI Reference Sequence: NM\_000485.3

[FASTA](#) [Graphics](#)

Go to: ▾

LOCUS NM\_000485 931 bp mRNA linear PRI 27-JUN-2021

DEFINITION Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, mRNA.

ACCESSION NM\_000485

VERSION NM\_000485.3

KEYWORDS RefSeq; MANE Select.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 931)

AUTHORS Haenig C, Atias N, Taylor AK, Mazza A, Schaefer MH, Russ J, Riechers SP, Jain S, Coughlin M, Fontaine JF, Freibaum BD, Brusendorf L, Zenkner M, Porras P, Stroedicke M, Schnoegl S, Arnsburg K, Boeddrich A, Pigazzini L, Heutink P, Taylor JP,

Customize view ▾

Analyze this sequence ▾

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Show in Genome Data Viewer

Articles about the APRT gene ▾

SARS-CoV-2-host proteome interactions for antiviral drug discovery. [Mol Syst Biol. 2021]

A proximity-dependent biotinylation map of a human cell. [Nature. 2021]

Dual proteome-scale networks reveal cell-specific remodeling of the human inte [Cell. 2021]

NM\_000485.3 -mrna is updated version of the mrna, the previous version of this mrna is NM\_000485.2 and NM\_000485.1

Nucleotide Nucleotide  Search Advanced Help

**COVID-19 Information**  
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GenBank ▾ Send to: ▾ Change region shown ▾  
Customize view ▾

**Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, mRNA**

NCBI Reference Sequence: NM\_000485.2  
⚠ This sequence has been updated. See current version.

[FASTA](#) [Graphics](#)

Go to:

Locus: NM\_000485 807 bp mRNA linear PRI 04-MAY-2019  
Definition: Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, mRNA.  
Accession: NM\_000485  
Version: NM\_000485.2  
Keywords: RefSeq; RefSeq Select.  
Source: Homo sapiens (human)  
Organism: *Homo sapiens*  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
Reference: 1 (bases 1 to 807)  
Authors: Hiramine S, Sugiyama M, Furusyo N, Uto H, Ido A, Tsubouchi H, Watanabe H, Ueno Y, Korenaga M, Murata K, Masaki N, Hayashi J, Thomas DL and Mizokami M.  
Title: A thymine-adenine dinucleotide repeat polymorphism near IL28B is associated with spontaneous clearance of hepatitis C virus  
Journal: *J Gastroenterol* 50 (10) 1069-1077 (2015).

Analyze this sequence Run BLAST Pick Primers Highlight Sequence Features Find in this Sequence

LinkOut to external resources  
LSBio APRT Nucleic Acids [LifeSpan BioSciences, Inc.]  
LSBio APRT Elisa Kits [LifeSpan BioSciences, Inc.]  
LSBio APRT Proteins [LifeSpan BioSciences, Inc.]

Recent activity Turn Off Clear

NM\_000485.3 -mrna is updated version of the mrna, the previous version of this mrna is NM\_000485.2 and NM\_000485.1

Nucleotide Nucleotide Advanced Search Help

**COVID-19 Information**  
[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

GenBank ▾ Send to: ▾ Change region shown ▾

**Homo sapiens adenine phosphoribosyltransferase (APRT), mRNA**

NCBI Reference Sequence: NM\_000485.1

**⚠ This sequence has been updated. See current version.**

[FASTA](#) [Graphics](#)

Go to: ▾

LOCUS NM\_000485 841 bp mRNA linear PRI 22-APR-2005  
DEFINITION Homo sapiens adenine phosphoribosyltransferase (APRT), mRNA.  
ACCESSION NM\_000485  
VERSION NM\_000485.1  
KEYWORDS RefSeq.  
SOURCE Homo sapiens (human)  
ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 841)  
AUTHORS Taniguchi,A., Tsuchida,S., Kuno,S., Mita,M., Machida,T.,  
Ioritani,N., Terai,C., Yamanaka,H. and Kamatani,N.  
TITLE Identification of two novel mutations in adenine  
phosphoribosyltransferase gene in patients with  
2,8-dihydroxyadenine urolithiasis  
JOURNAL Nucleosides Nucleotides Nucleic Acids 23 (8-9), 1141-1145 (2004)

Analyze this sequence Run BLAST  
Pick Primers  
Highlight Sequence Features  
Find in this Sequence

Recent activity Turn Off Clear

[Homo sapiens adenine phosphoribosyltransferase \(APRT\), Nucleotide](#)  
[Homo sapiens adenine phosphoribosyltransferase \(APRT\), Nucleotide](#)  
[Phenotype and Genotype Characterization of Adenine Phosphoribosyltransferase Def...](#)  
[Structure for Protein \(Select 4502171\) \(10\)](#)

In this assignment, the latest version of the mRNA seq (NM\_000485.1) was used. The related sequence of mRNA is derived from:

REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [BM423481.1](#), [BU507629.1](#) and [AC092384.5](#).

APRT is an enzyme encoded by the APRT gene encoded on human chromosome 16. This enzyme belongs to the purine/pyrimidine phosphoribosyltransferase family. Transcript variant is the name given to different mRNA variants synthesized by the same gene. Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, is an APRT mRNA transcript variant whose mRNA is NCBI Reference Sequence: NM\_000485.3. [3] , [4].

Two transcript variants encoding different isoforms have been found for this gene.

# refSeq PROTEIN PRODUCT:

GenPept ▾

Send to: ▾

Change region shown

## adenine phosphoribosyltransferase isoform a [Homo sapiens]

NCBI Reference Sequence: NP\_000476.1

[Identical Proteins](#) [FASTA](#) [Graphics](#)

Go to:

LOCUS NP\_000476 180 aa linear PRI 27-JUN-2021

DEFINITION adenine phosphoribosyltransferase isoform a [Homo sapiens].

ACCESSION NP\_000476

VERSION NP\_000476.1

DBSOURCE REFSEQ: accession [NM\\_000485.3](#)

KEYWORDS RefSeq; MANE Select.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

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

REFERENCE 1 (residues 1 to 180)

AUTHORS Haenig C, Atias N, Taylor AK, Mazza A, Schaefer MH, Russ J,  
Riechers SP, Jain S, Coughlin M, Fontaine JF, Freibaum BD,  
Brusendorf L, Zenkner M, Porras P, Stroedicke M, Schnoegl S,  
Arnsburg K, Boeddrich A, Pigazzini L, Heutink P, Taylor JP,  
Kirstein J, Andrade-Navarro MA, Sharan R and Wanker EE.

TITLE Interactome Mapping Provides a Network of Neurodegenerative Disease  
Proteins and Uncovers Widespread Protein Aggregation in Affected  
Brains

JOURNAL [Cell Rep 32 \(7\), 108050 \(2020\)](#)

PUBMED [32814053](#)

REFERENCE 2 (residues 1 to 180)

AUTHORS Luck K, Kim DK, Lambourne L, Spirohn K, Begg BE, Bian W, Brignall

Customize view

### Analyze this sequence

Run BLAST

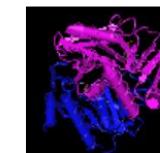
Identify Conserved Domains

Highlight Sequence Features

Find in this Sequence

Show in Genome Data Viewer

### Protein 3D Structure



Crystal Structure of Human  
APRT wild type in complex  
with GMP

PDB: 6HGS

Source: Homo sapiens

Method: X-ray Diffraction

Resolution: 1.55 Å

[See all 10 structures...](#)

### Articles about the APRT gene

Structural basis for substrate selectivity and  
nucleophilic substitution mediated by APRT

APRT proteins are in charge of the purine salvage pathway, in this pathway nucleotides are synthesized from their own degrageted intermediate products or products similar to them. Naturally, this pathway recovers bases and nucleosides. Mutations in these genes cause problems affecting the urinary tract and kidneys [5].

protein summary [10]:

[treatment information \(HHS\)](#) | [Español](#)

## 6HGS: Crystal Structure of Human APRT wild type in complex with GMP

**Citation:** [\[?\]](#)  
**Structural basis for substrate selectivity and nucleophilic substitution mechanisms in human adenine phosphoribosyltransferase catalyzed reaction**  
Ozeir M, Huyet J, Burgevin MC, Pinson B, Chesney F, Remy JM, Siddiqi AR, Lupoli R, Pinon G, Saint-Marc C, Gibert JF, Morales R, Ceballos-Picot I, Barouki R, Daignan-Fornier B, Olivier-Bandini A, Augé F, Nioche P  
*J Biol Chem* (2019) **294** p.11980-11991

**Abstract**  
The reversible adenine phosphoribosyltransferase enzyme (APRT) is essential for purine homeostasis in prokaryotes and eukaryotes. In humans, APRT (hAPRT) is the only enzyme known to produce AMP in cells from dietary adenine. APRT can also process adenine analogs, which are involved in plant development or neuronal homeostasis. However, the molecular mechanism underlying substrate...  
[read more](#)

**PDB ID:** 6HGS [Download](#) [\[?\]](#)  
**MMDB ID:** 177932 [\[?\]](#)  
**PDB Deposition Date:** 2018/8/23 [\[?\]](#)  
**Updated:** 2018/8/23, 10:18 [\[?\]](#)  
**Experimental Method:** x-ray diffraction [\[?\]](#)  
**Resolution:** 1.55 Å [\[?\]](#)  
**Source Organism:** Homo sapiens [\[?\]](#)  
**Similar Structures:** [VAST+](#) [\[?\]](#)  
[Download sequence data](#) [\[?\]](#)

[PDB](#) [All Biological Units](#) (2) [Asymmetric Unit](#) [\[?\]](#)

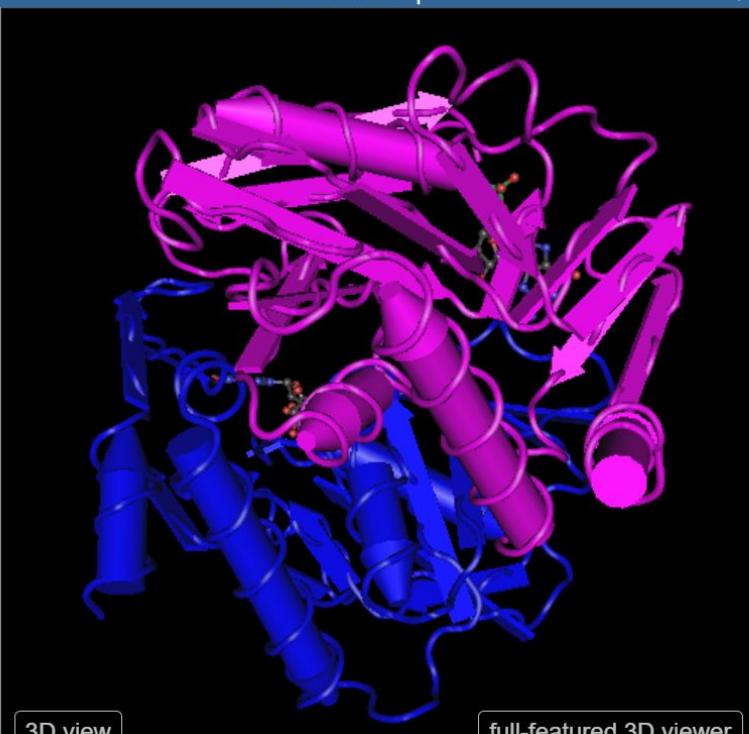
[rcsb.org/pdb/explore/explore.do?structureId=6HGS](https://www.rcsb.org/pdb/explore/explore.do?structureId=6HGS)

## PROTEIN 3D:

6HGS: Crystal Structure of Human APRT wild type in complex with GMP

Biological Unit for 6HGS: dimeric; determined by author and by software (PISA) [?](#)

Molecular Graphic [?](#)



full-featured 3D viewer

Interactions [?](#)

A → B

1

Drag symbols to move  
Double click symbols to explore molecules

Download Stucture Data [?](#)

Download

Format: ASN.1 (Cn3D) [?](#)

Data Set: Single 3D structure [?](#)

# PROTEIN ENTRY IN PDB:

rcsb.org/structure/6HGS

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... StatQuest: Principa... » Diğer yer işaretleri Okuma listesi

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Biological Assembly 1 ?

6HGS

Crystal Structure of Human APRT wild type in complex with GMP

DOI: [10.22110/pdb6HGS/pdb](https://doi.org/10.22110/pdb6HGS/pdb)

Classification: TRANSFERASE

Organism(s): Homo sapiens

Expression System: Escherichia coli BL21(DE3)

Mutation(s): No ⓘ

Deposited: 2018-08-23 Released: 2019-07-31

Deposition Author(s): Nioche, P., Huyet, J., Ozeir, M.

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 1.55 Å

R-Value Free: 0.177

R-Value Work: 0.158

R-Value Observed: 0.158

wwPDB Validation ⓘ

3D Report Full Report

Metric	Percentile Ranks	Value
Rfree	Worse	0.187
Clashscore	5	5
Ramachandran outliers	0	0
Sidechain outliers	0	0
RSRZ outliers	Better	2.6%

Worse Better

Percentile relative to all X-ray structures

Percentile relative to X-ray structures of similar resolution

3D View: Structure | Electron Density | Validation Report | Ligand Interaction

Global Symmetry: Cyclic - C2 ⓘ (3D View)

Global Stoichiometry: Homo 2-mer - A2 ⓘ

Contact Us

the genomic location of APRT gene  
in ch-16 from:  
<https://www.genecards.org/cgi-bin/carisp.pl?gene=APRT>

Size: 2,590 bases Orientation: Minus strand

#### Genomic View for APRT Gene

Genes around APRT on UCSC Golden Path with GeneCards custom track

Cytogenetic band: 16q24.3 by HGNC 16q24.3 by Entrez Gene 16q24.3 by Ensembl

APRT Gene in genomic location: bands according to Ensembl, locations according to GeneLoc (and/or Entrez Gene and/or Ensembl if different)

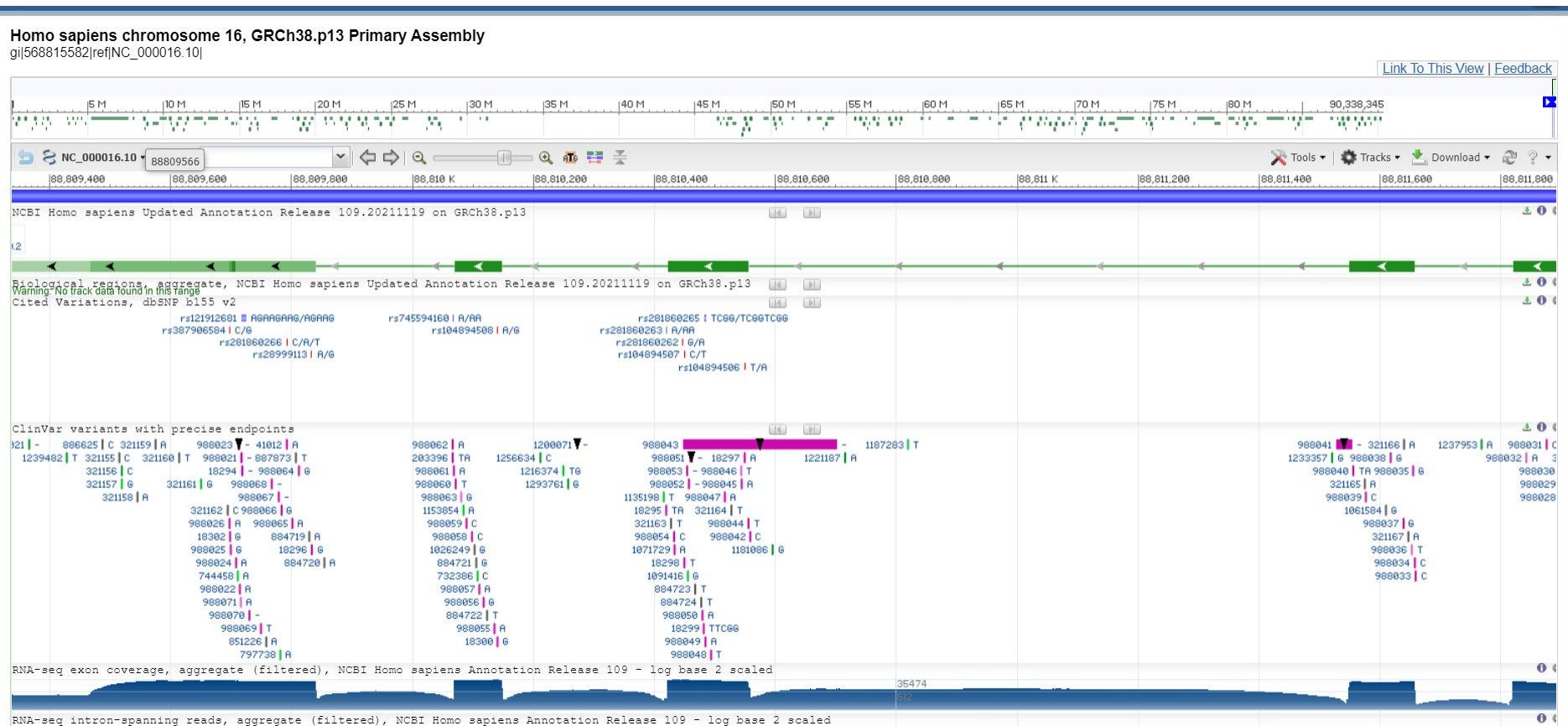


 GeneLoc Genomic Neighborhood • Exon Structure • Gene Density

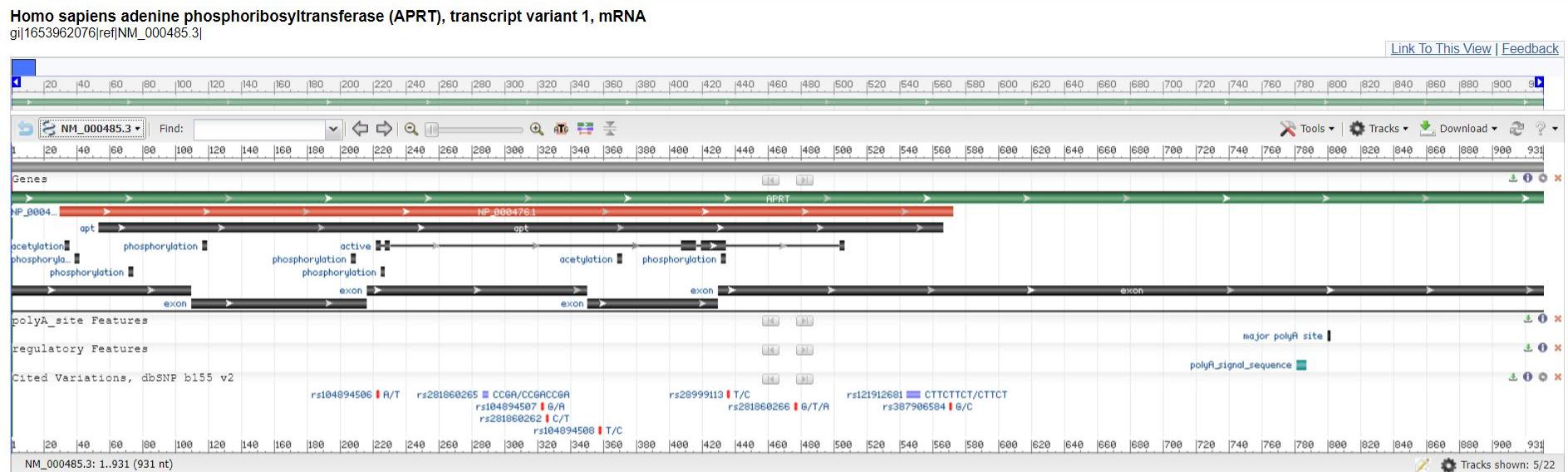
#### RefSeq DNA sequence for APRT Gene

NC\_000016.10

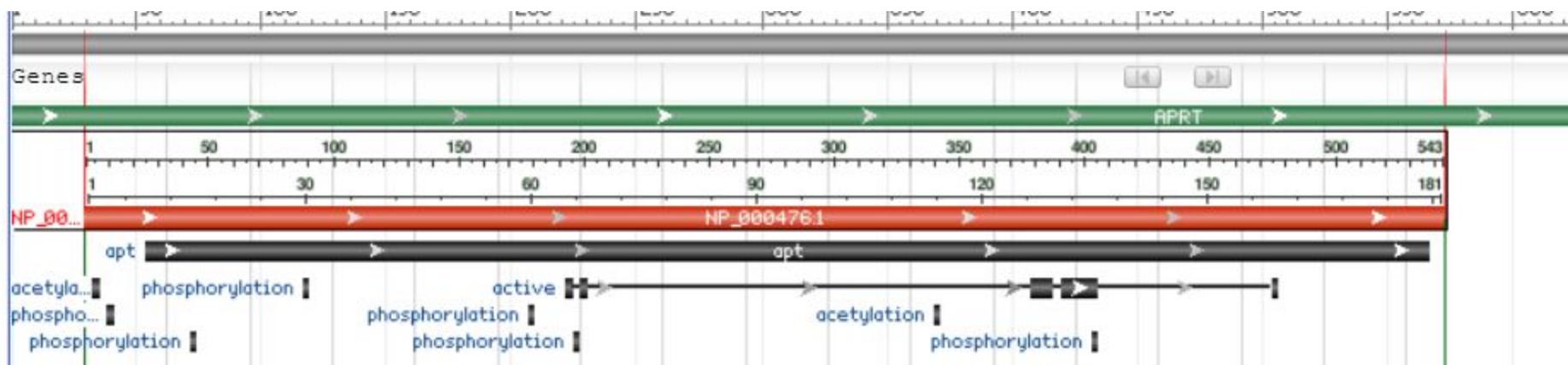
ch 16:



# APRT gene: green, mRNA variant 1 prudction of the protein -: red



The protein seq under the APRT gene:



## position information

NM\_000485.3 ▾ Find:  ↺ ↻ 🔎 ↻

1 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320

Genes

NP\_0004... NP\_000476.1

acetylation phosphoryla... phospho...

polyA\_sit regulator

Cited Var

1 20 NM\_000485.3

**NP\_000476.1**

CDS: NP\_000476.1  
Name: adenine phosphoribosyltransferase isoform a  
Comment: isoform a is encoded by transcript variant 1  
Location: 30..572  
[Length]  
Span on NM\_000485.3: 543 nt  
Protein length: 180 aa  
[Positional Info]  
NM\_000485.3 position: 30  
CDS position: 1  
Protein position: 1  
Protein sequence: [M]ADSELQLVQRIRS

Download FASTA: [NP\\_000476.1](#)

Links & Tools  
CCDS: [CCDS32511.1](#)

Contact | National Cent 8600 Rockville

BLAST Protein: [NP\\_000476.1](#)  
BLAST nr: [NM\\_000485.3 \(30..572\)](#)  
BLAST to Genome: [NM\\_000485.3 \(30..572\)](#)  
NP\_000476.1  
FASTA record: [NM\\_000485.3 \(30..572\)](#)  
[NP\\_000476.1](#)  
GenBank record: [NM\\_000485.3 \(30..572\)](#)  
[NP\\_000476.1](#)  
Graphical View: [NP\\_000476.1](#)

31860265 ■ CCGA/CCGACCE  
rs104894507 | G/F  
rs281860262 | C/  
rs1041

260 280 300 320

## sequence view

Sequence View (positive strand)

Prev Page | Next Page | Flip Strands | Annotated | Go To Position

1 2345678901234567890123456789012345678901234567890123456789012345678901234567890  
**1 GGGCTGCCGCTGGCTCTCGCACGCCATGGCCGACTCCGAGCTGCAGCTGGTGTGAGCAGCGGATCCCGCAGCTCCCCGACTTCCCCA**

M A D S E L Q V E Q R I R S F P D F P

91 **CCCCAGGGCGTGGTATTCA**GGGACATCTCGCCCCTGAAGGACCCCCGGCTCTTCCGC~~GGCC~~CATCGGCCTCTGGCGCAGACCTGA  
 T P G V V F R D I S P V L K D P A S F R A A I G L L A R H L

181 **AGGCGACCCACGGGGGCC**CATCGACTACATCGCAGGCCCTAGACTCCCGAGGCTTCCCTCTTTGGCCCTCCCTGGCCAGGAGCTGGAC  
 K A T H G G R I D Y I A G L D S R G F L F G P S L A Q E L G

271 **TGGGCTGCGTGC**TCACTCCGAAAGCGGGGGAAAGCTGCCAGGCCACTCTGTGGGCTCCTATTCCCTGGAGTACGGGAAGGCTGAGCTGG  
 L G C V L I R K R G K L P G P T L W A S Y S L E Y G K A E L

361 **AGATTCA**GAAAGACGCCCTGGAGCCAGGGACAGAGGGTGGTCGTGATGATCTGCTGGCCACTGGTGGAACCATGAACGCTGCCTGTG  
 E I Q K D A L E P G Q R V V V D D L L A T G G T M N A A C

451 **AGCTGCTGGGCC**CTGCAGGCTGAGGCTCTGGAGTGCCTGGAGCTGCCACTCGCTTAAGGGCAGGGAGAAGCTGGCACCTG  
 E L L G R L Q A E V L E C V S L V E L T S L K G R E K L A P

541 **TACCCCTCTTCTCTCTCG**AGTATGAGTGACCAACAGGGCCTCCCAGCCAAACATCTCCAGCTGGATCCCAGGGAAATATCAGCCTTGG  
 V P F F S L L Q Y E \*

631 **GCAACTGCAGT**GACCAGGGCACCGGGTGCCACAGGGAACACATTCCCTTGCTGGGTTCAAGCGCCTCTCTGGGCTGGAAGTGCCAA

721 **AGCCTGGGGCAA**AGCTGTGTTCAGCCACACTGAACCCAATTACACACAGCGGGAGAACCGCAGTAAACAGCTTCCCACAAGAGCCGTCT

811 **CCTGTCCTC**CTGGTCCCCAGGGCAGGGAGCCCCCAGGACAACACCAGACTTCAGCTGTACTGTGGCATGTGCTGCTTGGCGTATGCCCA

901 **GCAGAACCTGT**CCTGGTTCTCACCTCAGGAG

the sequence is referred 10 times in different articles, and as mentioned previously, the sequence updated 3 times by NCBI staff using RefSeq, therefore it can be said that this gene is well determined gene. ,  
[https://www.ncbi.nlm.nih.gov/nuccore/NM\\_000485.3/](https://www.ncbi.nlm.nih.gov/nuccore/NM_000485.3/)

REFERENCE	10 (bases 1 to 931)
AUTHORS	Johnson,L.A., Gordon,R.B. and Emmerson,B.T.
TITLE	Adenine phosphoribosyltransferase: a simple spectrophotometric assay and the incidence of mutation in the normal population
JOURNAL	Biochem Genet 15 (3-4), 265-272 (1977)
PUBMED	<a href="#">869896</a>

##Evidence-Data-START##

Transcript exon combination :: SRR7410570.627404.1,  
SRR7410570.627401.1 [ECO:0000332]  
RNAseq introns :: single sample supports all introns  
SAMEA1965299, SAMEA1966682  
[ECO:0000348]

##Evidence-Data-END##

##RefSeq-Attributes-START##

MANE Ensembl match :: ENST00000378364.8/ ENSP00000367615.3  
RefSeq Select criteria :: based on conservation, expression,  
longest protein

##RefSeq-Attributes-END##

COMPLETENESS: complete on the 3' end.

Since the gen product is collected under RefSeq -which provides a stable reference for genome annotation, gene identification and characterization- the annotated seq. is trustable.  
see for more information about RefSeq::  
<https://www.ncbi.nlm.nih.gov/refseq/about/>

some remarks from the publications (experimental evidences):

GeneRIF: binding to hAPRT is substrate shape-specific in the forward reaction, whereas it is base-specific in the reverse reaction. The forward reaction is mainly a nucleophilic substitution of type 2 (SN2) with a mix of SN1-type molecular mechanism. Based on our structural analysis, a magnesium-assisted SN2-type mechanism would be involved in the reverse reaction.

DOI: 10.1074/jbc.RA119.009087

GeneRIF: A long TA repeat in the promoter region of IL28B was associated with spontaneous HCV clearance. DOI:  
10.1007/s00535-015-1056-1

GeneRIF: We found large differences between tumour types and individual tumours in their expression of XDH and APRT Variations in locus-specific DNA methylation and gene copy number correlated with the expression levels of XDH and APRT in human tumours respectively  
DOI: 10.1042/BSR20171716

general theoretical summary from the gene annotation information

Summary: Adenine phosphoribosyltransferase belongs to the purine/pyrimidine phosphoribosyltransferase family. A conserved feature of this gene is the distribution of CpG dinucleotides. This enzyme catalyzes the formation of AMP and inorganic pyrophosphate from adenine and 5-phosphoribosyl-1-pyrophosphate (PRPP). It also produces adenine as a by-product of the polyamine biosynthesis pathway. A homozygous deficiency in this enzyme causes 2,8-dihydroxyadenine urolithiasis. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008].

Transcript Variant: This variant (1) represents the longer transcript and encodes the longer isoform (a).

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

# finding homologous for desired proteins

NCBI Resources How To Sign in to NCBI

HomoloGene HomoloGene Search Limits Advanced Help

## COVID-19 Information

Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

Display Settings: HomoloGene Send to:

**HomoloGene:413. Gene conserved in Eukaryota**

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

APRT, *H.sapiens*  
adenine phosphoribosyltransferase  
APRT, *Ptroglodytes*  
adenine phosphoribosyltransferase  
APRT, *M.mulatta*  
adenine phosphoribosyltransferase  
APRT, *C.lupus*  
adenine phosphoribosyltransferase  
APRT, *B.taurus*  
adenine phosphoribosyltransferase  
Aprt, *M.musculus*  
adenine phosphoribosyl transferase  
Aprt, *R.norvegicus*  
adenine phosphoribosyl transferase  
APRT, *G.gallus*  
adenine phosphoribosyltransferase  
aprt, *X.tropicalis*  
adenine phosphoribosyltransferase  
aprt, *D.rerio*

**Proteins**  
Proteins used in sequence comparisons and their conserved domain architectures.

NP\_000476.1 — 180 aa  
XP\_003952966.1 — 180 aa  
XP\_001089867.1 — 180 aa  
XP\_536752.2 — 180 aa  
NP\_001020505.1 — 180 aa  
NP\_033828.2 — 180 aa  
NP\_001013079.1 — 180 aa  
NP\_001264576.1 — 179 aa  
NP\_001007941.1 — 180 aa  
NP\_956962.1 — 177 aa

Download , Links

the whole list  
for homology:

M. musculus  
& G.gallus &  
S.cerevisiae  
→ found  
homologs;

no homology  
for →  
O.lapites,  
A.mellifera,  
C.elegans

Genes	Proteins
Genes identified as putative homologs of one another during the construction of HomoloGene.	Proteins used in sequence comparisons and their conserved domain architectures.
APRT, <i>H.sapiens</i>	NP_000476.1 180 aa
adenine phosphoribosyltransferase	XP_003952966.1 180 aa
APRT, <i>P.troglodytes</i>	XP_001089867.1 180 aa
adenine phosphoribosyltransferase	XP_536752.2 180 aa
APRT, <i>M.mulatta</i>	NP_001020505.1 180 aa
adenine phosphoribosyltransferase	NP_033828.2 180 aa
APRT, <i>C.lupus</i>	NP_001013079.1 180 aa
adenine phosphoribosyltransferase	NP_001264576.1 179 aa
APRT, <i>B.taurus</i>	NP_001007941.1 180 aa
adenine phosphoribosyltransferase	NP_956962.1 177 aa
Aprt, <i>M.musculus</i>	NP_476637.1 182 aa
adenine phosphoribosyl transferase	XP_315739.4 187 aa
Aprt, <i>R.norvegicus</i>	NP_491663.1 185 aa
adenine phosphoribosyl transferase	NP_013690.1 187 aa
APRT, <i>G.gallus</i>	KLLA0B01309g, <i>K.lactis</i> XP_451589.1 187 aa
adenine phosphoribosyl transferase	KLLA0B01309g NP_985181.1 187 aa
apt, <i>X.tropicalis</i>	AGOS_AER325W, <i>E.gossypii</i> NP_594433.1 188 aa
adenine phosphoribosyl transferase	apt, <i>D.reio</i> MGG_17399, <i>M.orzae</i> XP_003718359.1 216 aa
apt, <i>D.melanogaster</i>	T19B4.3 NCU02090, <i>N.crassa</i> XP_963727.2 171 aa
Adenine phosphoribosyltransferase	APT1, <i>S.cerevisiae</i> APT1 NP_564284.1 243 aa
AgaP_AGAP005723, <i>A.gambiae</i>	apt1, <i>S.pombe</i> Os12g0589100, <i>O.sativa</i> NP_001067164.1 240 aa
AgaP_AGAP005723	apt1
T19B4.3	MGG_17399
APT1, <i>S.cerevisiae</i>	NCU02090
APT1	APT1, <i>A.thaliana</i>
KLLA0B01309g, <i>K.lactis</i>	Os12g0589100
KLLA0B01309g	Os12g0589100
AGOS_AER325W, <i>E.gossypii</i>	
AGOS_AER325W	
apt1, <i>S.pombe</i>	
apt1	
MGG_17399, <i>M.orzae</i>	
MGG_17399	
NCU02090, <i>N.crassa</i>	
NCU02090	
APT1, <i>A.thaliana</i>	
APT1	
Os12g0589100, <i>O.sativa</i>	
Os12g0589100	

in Ensembl for searching orthologs:

ensembl.org/Homo\_sapiens/Gene/Compara\_Ortholog?db=core;g=ENSG00000198931;r=16:87830023-88811937

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... StatQuest: Principal... » Diğer yer işaretleri Okuma li

Login/Register

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Human (GRCh38.p13) ▾

Location: 16:87,830,023-88,811,937 Gene: APRT

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles

Sequence

- Secondary Structure

Comparative Genomics

- Genomic alignments
- Gene tree
- Gene gain/loss tree

Orthologues

- Paralogues
- Ensembl protein families

**Gene: APRT ENSG00000198931**

Description adenine phosphoribosyltransferase [Source:HGNC Symbol;Acc:[HGNC:626](#)]

Location Chromosome 16: 88,809,339-88,811,937 reverse strand.  
GRCh38:CM000678.2

About this gene This gene has 11 transcripts ([splice variants](#)), [207 orthologues](#) and is associated with [2 phenotypes](#).

Transcripts [Show transcript table](#)

**Orthologues** ?

[Show transcript table](#)

## Orthologues

[!\[\]\(c7774dea93eb10ead3ed0542c77a8534\_img.jpg\) Download orthologues](#)

### Summary of orthologues of this gene [Hide](#)

Click on 'Show details' to display the orthologues for one or more groups of species. Alternatively, click on 'Configure this page' to choose a custom list of species.

Species set	Show details	With 1:1 orthologues	With 1:many orthologues	With many:many orthologues	Without orthologues
<b>Primates (26 species)</b> Humans and other primates	<input type="checkbox"/>	21	1	0	<a href="#">4</a>
<b>Rodents and related species (32 species)</b> Rodents, lagomorphs and tree shrews	<input type="checkbox"/>	18	4	0	<a href="#">10</a>
<b>Laurasiatheria (43 species)</b> Carnivores, ungulates and insectivores	<input type="checkbox"/>	27	2	0	<a href="#">14</a>
<b>Placental Mammals (106 species)</b> All placental mammals	<input type="checkbox"/>	69	7	0	<a href="#">30</a>
<b>Sauropsida (69 species)</b> Birds and Reptiles	<input type="checkbox"/>	24	1	0	<a href="#">44</a>
<b>Fish (86 species)</b> Ray-finned fishes	<input type="checkbox"/>	53	11	0	<a href="#">22</a>
<b>All (278 species)</b> All species, including invertebrates	<input checked="" type="checkbox"/>	161	19	0	<a href="#">98</a>

### Selected orthologues [Hide](#)

[Show All !\[\]\(4754fc919b2e8116c30595fd4b918f00\_img.jpg\) entries](#)[Show/hide columns](#)[Filter](#)



## COVID-19 Information

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## adenine phosphoribosyltransferase isoform 1 [Gallus gallus]

NCBI Reference Sequence: NP\_001264576.1

[GenPept](#) [Identical Proteins](#) [Graphics](#)

```
>NP_001264576.1 adenine phosphoribosyltransferase isoform 1 [Gallus gallus]
MSEERLRAVRDRVRSPDFPVPGVLFRDISPLLKDPVAFKALIDLLEDHLRASFPRIDVIAGLDSRGFLI
GPSLAQRLGVGFVLIRKKGKLPGPTESISYALEYGKAELIQSDAVEAGQKVVVDDLLATGGTMRAACE
LLVRLKADILECLVVIELKALGGAAKLEAIPFHSLLQYD
```

FASTA ▾

## adenine phosphoribosyltransferase [Mus musculus]

NCBI Reference Sequence: NP\_033828.2

[GenPept](#) [Identical Proteins](#) [Graphics](#)

>NP\_033828.2 adenine phosphoribosyltransferase [Mus musculus]  
MSEPEKLVARRIRSFPDFPIPGVLFRDISPLLKDPSFRASIRLLASHLKSTHSGKIDYIAGLDSRGFL  
FGPSLAQELGVGCVLIRKQGKLPGPTVSASYSLEYGKAELEIQKDALEPGQRVVIVDDLLATGGTMFAAC  
DLLHQQLRAEVVECVSLVELTSKGGRERLGPPIPFFSLLQYD

FASTA ▾

## adenine phosphoribosyltransferase isoform a [Homo sapiens]

NCBI Reference Sequence: NP\_000476.1

[GenPept](#) [Identical Proteins](#) [Graphics](#)

>NP\_000476.1 adenine phosphoribosyltransferase isoform a [Homo sapiens]

MADSELQLVEQRIRSFPDFPTPGVVFRDISPVLKDPASFRAAIGLLARHLKATHGGRIDYIAGLDSRGFL  
FGPSLAQELGLGCVLIRKRGKLPGPTLWASYSLEYGKAELEIQKDALEPGQRVVVDDLLATGGTMNAAC  
ELLGRLQAEVLECVSLVELTSLKGREKLAPVPFFSLLQYE

# Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

## Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between **three or more** sequences. For the alignment of two sequences please instead use our [pairwise sequence alignment tools](#).

**Important note:** This tool can align up to 4000 sequences or a maximum file size of 4 MB.

### STEP 1 - Enter your input sequences

Enter or paste a set of

PROTEIN

sequences in any supported format:

```
>NP_03382.2 adenine phosphoribosyltransferase [Mus musculus]
MSEPELKLVARRIRSRFPDFIPGVLFRDISPLKDPDSFRASIRLLASHLKKSTHSGKIDYIAGLDSRGFL
FGPSLAQELGVGCVLIRKQGKLPGPTVSASYSLYEYGKAELIQKDALEPGQRVIVDDLLATGGTMFAAC
DLLHQLRAEVVECVLVELTSLGKRERLGPPIPFFSLLQYD
>NP_000476.1 adenine phosphoribosyltransferase isoform a [Homo sapiens]
MADSELQLVEQRIRSRFPDFPTPGVVFRDIPSPVLPKDPASFRAAIGLLARHLKATHGGRIDYIAGLDSRGFL
FGPSLAQELGLGCVLIRKRGKLPGPTLWASYSLEYGKAELIQKDALEPGQRVIVDDLLATGGTMNAAC
ELLGRLQAEVLECVSLLVELTSLGKREKLAPVPFSSLLQYE
```

Or, upload a file:  Dosya seçilmedi

[Use a example sequence](#) | [Clear sequence](#) | [See more example inputs](#)

# Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20220109-131824-0157-62459849-p2m

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CLUSTAL O(1.2.4) multiple sequence alignment

NP_001264576.1	MSEERLRAVRDRVRSFPDFPVPGVLFRDISPLLKDPWAKFALKIDLLEDHLRASF-PRIDV	59
NP_033828.2	MSEPELKLVARRIRSFPDFPIPVGVLFRDISPLLKDPDSFRASIRLLASHLKSTHSGKIDY	60
NP_000476.1	MADSELQLVEQRIRSFPPDFPTPGVVFRRDISPVLKDPSFRAAIGLLARHLKATHGGRIDY	60
	*** . *: * *:***** ***:***** ,*** :*: * * ** ***:*. ;**	
NP_001264576.1	IAGLDSRGFLIGPSLAQRLGVGFVLIRKKGKLPGPTESISYALEYGKAELIQSDAVEAG	119
NP_033828.2	IAGLDSRGFLFGPSLAQELGVGCVLIRKQGKLPGPTVSASYSLYEYGKAELIQKDALEPG	120
NP_000476.1	IAGLDSRGFLFGPSLAQELGLGCVLIRKRGKLPGPTLWASYSLYEYGKAELIQKDALEPG	120
	*****:*****.*;* ****:***** ***:***** .***,* *	
NP_001264576.1	QKVVVVDLLATGGTMRAACELLVRLKADILECLVVIELKALGGAAKLEAIPFHSLQYD	179
NP_033828.2	QRVVIVDDLLATGGTMAAACDLHQQLRAEVVECVSVELTSKGRRERLGPPIPFFSSLQYD	180
NP_000476.1	QRVVVVDLLATGGTMRAACELLGRLOAEVLECVSVELTSKGREKLAPVFFSSLQYE	180
	*;*****:***** ***;* :*;*:*** : ;***.;* * ;* ;* .*****:	

*PLEASE NOTE: Showing colors on large alignments is slow.*

# Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-I20220109-131824-0157-62459849-p2m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Guide Tree Data](#)

### Phylogram

Branch length:  Cladogram  Real



NP\_001264576.1 0.163408  
NP\_033828.2 0.0861111  
NP\_000476.1 0.0861111

### Guide Tree

```
(  
NP_001264576.1:0.163408  
,  
(  
NP_033828.2:0.0861111  
,  
NP_000476.1:0.0861111  
):0.0772967  
)  
;
```

The phylogenetic trees of the alignments had a common branch, meaning that each protein emerged from the same origin.

# Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20220109-131824-0157-62459849-p2m

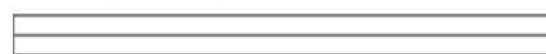
[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real



NP\_0012645/6.1 0.22394  
NP\_033828.2 0.08332  
NP\_000476.1 0.0889

### Tree Data

```
(  
NP_001264576.1:0.22394,  
NP_033828.2:0.08332,  
NP_000476.1:0.0889);
```

## Results for job clustalo-l20220109-131824-0157-62459849-p2m

[Alignments](#)[Result Summary](#)[Guide Tree](#)[Phylogenetic Tree](#)[Results Viewers](#)[Submission Details](#)[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real

```
graph TD; Root --- Node1["NP_001264576.1:0.22394"]; Root --- Node2["NP_033828.2:0.08332"]; Root --- Node3["NP_000476.1:0.08890"];
```

### Tree Data

```
(  
NP_001264576.1:0.22394,  
NP_033828.2:0.08332,  
NP_000476.1:0.08890);
```

Since t-coffe is suitable for shorter alignments, t-coffe alignment was also performed with clustal omega.

## T-Coffee

Consistency-based MSA tool that attempts to mitigate the pitfalls of progressive alignment methods. Suitable for small alignments.

 [Launch T-Coffee](#)

## Clustal Omega

New MSA tool that uses seeded guide trees and HMM profile-profile techniques to generate alignments. Suitable for medium-large alignments.

 [Launch Clustal Omega](#)

# multiple alignment except for S.cerevisiae (including: homo sapines, M.musculus, G.gallus) - in t-coffe

Tools > Multiple Sequence Alignment > T-Coffee

## Results for job tcoffee-I20220109-132314-0179-91848131-p2m

Alignments Result Summary Guide Tree Phylogenetic Tree Results Viewers Submission Details  
Download Alignment File Show Colors

CLUSTAL W (1.83) multiple sequence alignment

NP\_000476.1 MADSELQLVEQRIRSRFPDFPTPGVVFRDISPVLKDPASFRAAIGLLARHL  
NP\_001264576.1 MSEERLRAVRDRVRSRFPDFPVPGVLFRDISPLLKDPVAFKALIDLLEDHL  
NP\_033828.2 MSEPELKLVARRIRSRFPDFPTPGVLFRDISPLLKDPDSFRASIRLLASHL  
\*::: .\*: \* \*:\*\*\*\*\* \* \*:\*\*\*\*\*:\*\*\*\*\* ;\*: \* \*\* \*\* \*

NP\_000476.1 KATHGGRIDYIAGLDSRGFLFGPSLAQELGLGCVLIRKGKLPGPTLWAS  
NP\_001264576.1 RASF-PRIDVIAGLDSRGFLIGPSLAQRLGVGFVLIRKKGKLPGPTESIS  
NP\_033828.2 KSTHSGKIDYIAGLDSRGFLFGPSLAQELGVGCVLIRKQGKLPGPTVSAS  
::: .\*\*\* \*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*.\*\*\*.\* \*\*\*\*\*:\*\*\*\*\* \*

NP\_000476.1 YSLEYGKAELEIQKDALEPGQRVWWDDLLATGGTMNAACELLGRLQAEV  
NP\_001264576.1 YALEYGKAELEIQSDAVEAQGKVVVDDLLATGGTMRAACELLVRLKADI  
NP\_033828.2 YSLEYGKAELEIQKDALEPGQRVIVDDLLATGGTMFAACDLLHQQLRAEV  
\*:\*\*\*\*\*:\*\*\*,\*:\*\*\*:\*\*\*\*\*:\*\*\*:\*\*\*:\*\*\*:\*\*\*:\*\*\*:

NP\_000476.1 LECVSLVELTSKGREKLAPVFFSLLQYE  
NP\_001264576.1 LECLVIELKALGGAAKLEATPFHSSLQYD  
NP\_033828.2 VECVSLVELTSKGRERLGPITPFFSLLQYD  
;\*\*\*: :\*\*\*: :\* \* \* :\* .\*\*\*:\*\*\*\*\*:

PLEASE NOTE: Showing colors on large alignments is slow.

## Results for job tcoffee-I20220109-132314-0179-91848131-p2m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Guide Tree Data](#)

### Phylogram

Branch length:  Cladogram  Real



NP\_000476.1:0.04000  
NP\_001264576.1:0.15000  
NP\_033828.2:0.05000

### Guide Tree

(NP\_000476.1:0.04000,NP\_001264576.1:0.15000,NP\_033828.2:0.05000);

When only 3 sequences were used, only 1 cluster was formed and it could not be determined which sequence was more closely related to the other. (in both clustal omega and t-coffe)

Tools > Multiple Sequence Alignment > T-Coffee

## Results for job tcoffee-l20220109-132314-0179-91848131-p2m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real



NP\_000476.1:0.0889  
NP\_001264576.1:0.22394  
NP\_033828.2:0.08332

### Tree Data

```
(  
NP_000476.1:0.08890,  
NP_001264576.1:0.22394,  
NP_033828.2:0.08332);
```

the phylogenetic real time tree is same as the clustal-o, the G.gallus has the longest branch length and homo sapiens and m.musculus has same branch lengths.

Tools > Multiple Sequence Alignment > T-Coffee

## Results for job tcoffee-l20220109-132314-0179-91848131-p2m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real

└ NP\_000476.1 0.0889  
  NP\_001264576.1 0.22394  
  NP\_033828.2 0.08332

### Tree Data

```
(  
NP_000476.1:0.08890,  
NP_001264576.1:0.22394,
```

adding the remained sequence for multiple alignment:



## COVID-19 Information

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Change region shown

## adenine phosphoribosyltransferase APT1 [Saccharomyces cerevisiae S288C]

NCBI Reference Sequence: NP\_013690.1

[GenPept](#) [Identical Proteins](#) [Graphics](#)

>NP\_013690.1 adenine phosphoribosyltransferase APT1 [Saccharomyces cerevisiae S288C]  
MSIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEEAFFPEVKIDYIVGLESRG  
FLFGPTLALALGVGFVPRKAGKLPGECFKATYEKEYGSDLFEIQKNAIPAGSNVIIVDDIIATGGSAAA  
AGELVQELEANLLEYNFVMEFLDKGRSKLNAPFTLLNAQKEALKK

Analyze this sequence

Run BLAST

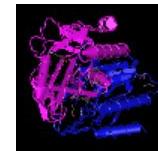
Identify Conserved Domains

Highlight Sequence Features

Find in this Sequence

Show in Genome Data Viewer

Protein 3D Structure



Crystal Structure of Adenine Phosphoribosyltransferase from Saccharomyces

PDB: 5VJP

Source: Saccharomyces cerevisiae

Method: X-ray Diffraction

# Clustal Omega

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Tools &gt; Multiple Sequence Alignment &gt; Clustal Omega

## Results for job clustalo-I20220109-133051-0639-92961921-p1m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)[Download Alignment File](#) [Show Colors](#)

CLUSTAL O(1.2.4) multiple sequence alignment

NP_013690.1	MISIAYAQEKLKALAHQYPNIPFSEGLILFEFLPLIFRNGLFOKLIDAFKLHLLEAFPEVKI	60
NP_001264576.1	MS-EERLRAVRDRVRSFPDFPVPGVLFRDISPLLKDPVAFKALIDLLEDHLRASF--PRI	57
NP_033828.2	MS-EPELKLKARRIRSRSPDFPIPGVLFRDISPLLKDPDSFRASIRLASHLHKSTH-SGKI	58
NP_000476.1	MA-DSELQLVEQRIRSFPDFPTPGVFRD1SPVLPDKPASFRAAIGLLARHLKATH-GGRI	58
	* : ; : ; : ; * : * ; : ; : ; * ; * : * : * . . ; *	
NP_013690.1	DYIVGLESRGFLFPGPTLALALGVGFVPRKAGKLPGECFKATYEKEYGSDLFIEIQKNAIP	120
NP_001264576.1	DVIAGLDSRGFLFPGPSLAQRLGVGFVLIRKKGKLPGPCTESIYALEYGKAELIQSDAVE	117
NP_033828.2	DVIAGLDSRGFLFPGPSLAQELGVGCVLIRKQKLPGPCTVSAYSLEYGKAELIQKDALE	118
NP_000476.1	DVIAGLDSRGFLFPGPSLAQELGLGCVLIRKRKGKLPGPTLWAYSLEYGKAELIQKDALE	118
	* .***:*****:***:***: * ;***:***** ;* ***. ;***:*	
NP_013690.1	AGSNVIIVDDIIATGGSAAAAGELVEQLLEANLLEYNFMELDFLKGRSKLNAPVF-TLLN	179
NP_001264576.1	AGQKVVVVDDLLATGGTIRAACELLVRLKADILECLVIEALKLGGAAKLEAIPFHSSLQ	177
NP_033828.2	PGQRVVIVDDLLATGGTMAACDLLHQLRAEVCEVSLVELTSLKGRERLGPPIPFFSLLQ	178
NP_000476.1	PGQRVVVVDDLLATGGTMAACCELLGRLQAEVLECVSLVELTSLKGRERLAPVFFSLLQ	178
	*..*:;***:;*****: ** :*.*:;* ;***: * * ;* * ;***:	
NP_013690.1	AQKEALKK 187	
NP_001264576.1	YD----- 179	
NP_033828.2	YD----- 180	
NP_000476.1	YE----- 180	
	:	

PLEASE NOTE: Showing colors on large alignments is slow.

When an extra sequence was added to the previous 3 sequences, clusters were formed and it was determined which sequences would be more closely related to the other.

# Clustal Omega

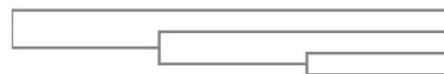
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Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20220109-133051-0639-92961921-p1m

[Alignments](#)[Result Summary](#)[Guide Tree](#)[Phylogenetic Tree](#)[Results Viewers](#)[Submission Details](#)[Download Guide Tree Data](#)

### Phylogram

Branch length:  Cladogram  Real

NP\_013690.1 0.286903  
NP\_001264576.1 0.163408  
NP\_033828.2 0.0861111  
NP\_000476.1 0.0861111

### Guide Tree

```
(  
NP_013690.1:0.286903  
,  
(  
NP_001264576.1:0.163408  
,  
(  
NP_033828.2:0.0861111  
,  
NP_000476.1:0.0861111  
);
```

By providing only an extra sequence, the algorithm was able to detect which of the three sequences were closer to the field and which were farther away.

Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20220109-133051-0639-92961921-p1m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real



NP\_013690.1:0.38977  
NP\_001264576.1:0.14955  
NP\_033828.2:0.08332  
NP\_000476.1:0.0889

### Tree Data

```
(  
(  
NP_013690.1:0.38977,  
NP_001264576.1:0.14955)  
:0.07439,  
NP_033828.2:0.08332,  
NP_000476.1:0.0889);
```

real time phylogenetic tree for the evolutionary history: Generally, close relatives show more resemblance and distant relatives show less resemblance when forming phylogenetic trees. Therefore, adding an extra sequence created a data entry to see which sequences showed more similarity within themselves.

TOOLS > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20220109-133051-0639-92961921-p1m

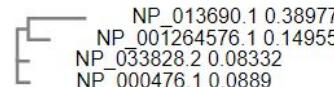
[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real



### Tree Data

```
(  
(  
NP_013690_1:0.38977,  
NP_001264576_1:0.14955  
:0.07439,  
NP_033828_2:0.08332,  
NP_000476_1:0.0889);
```

# T-Coffee

[Input form](#)[Web services](#)[Help & Documentation](#)[Bioinformatics Tools FAQ](#)[Tools](#) > [Multiple Sequence Alignment](#) > T-Coffee

## Results for job tcoffee-I20220109-133053-0641-39837190-p2m

[Alignments](#)[Result Summary](#)[Guide Tree](#)[Phylogenetic Tree](#)[Results Viewers](#)[Submission Details](#)[Download Alignment File](#)[Show Colors](#)

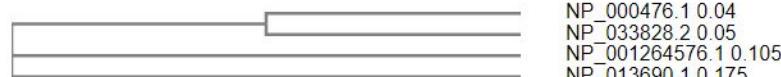
CLUSTAL W (1.83) multiple sequence alignment

NP_000476.1	MADSE-LQLVEQRIRSFDPDFTPGVFRDISPVLKDPASFRAAIGLLRHH
NP_001264576.1	MSEER-LRAVRDRVRSPDFPVPVGVLFRDISPLLKDPVAFKALIDLLEDH
NP_013690.1	MSIASYAQELKLAHQYPNFPSEGILFEDLPFIRNPGLFOQLIDAFKLH
NP_033828.2	MSEPE-LKLVARRIRSFDPPIPVGVLFRDISPLLKDPDSFRASIRLLASH
	*: : : . .: ** * : ; : * : * : * : * : *
NP_000476.1	LKATHG-GRIDYIAGLDSRGFLFGPSLAQEGLLGCVLIRKRGKLPGPTLW
NP_001264576.1	LRASF--PRIDVIAGLDSRGFLFGPSLAQRLGVGFVLIRKKGKLPGPTE
NP_013690.1	LEEAFFPEVKIDYIVGLESRGFLFGPTLALALGVGFVPPRKAGKLPGECKF
NP_033828.2	LKSTHS-GKIDYIAGLDSRGFLFGPSLAQEGLGVCVLIRKQGKLPGPTVS
	*. . . : ** * . ** . **** . ** : ** *** : * : *** ****
NP_000476.1	ASYSLEYGKAELEIQKDALLEPGQRVVVDDLLATGGTMNAACELLGRLQA
NP_001264576.1	ISYALEYGKAELEIQSDAVEAGQKVVVVDDLLATGGTMRAACELLVRLKA
NP_013690.1	ATYEKEYGSDLFEIQKNAIPAGSNVIIIVDDIIATGGSAAAAGELVEQLEA
NP_033828.2	ASYSLEYGKAELEIQKDALLEPGQRVVIVDDLLATGGTMFAACDLLHQQLRA
	: * *** . : *** . : . * . * ; *** : * : * : * : *
NP_000476.1	EVLECVSLSVELTSLKGREKLAPEVFPSLLQYE-----
NP_001264576.1	DILECLVIELKALGGAAKLEAIPFHSSLQYD-----
NP_013690.1	NLLEYNFVMEFLDFLKGRSKLNA-PVFTLNAQKEALKK
NP_033828.2	EVVECVSLSVELTSLKGRERLGPPIPFFSLLQYD-----
	: . * . : ** * * : * . * . : *** : *

## Results for job tcoffee-l20220109-133053-0641-39837190-p2m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)[Download Guide Tree Data](#)

### Phylogram

Branch length:  Cladogram  Real

### Guide Tree

```
((NP_000476.1:0.04000,NP_033828.2:0.05000):0.04500,NP_001264576.1:0.10500,NP_013690.1:0.17500);
```

# T-Coffee

[Input form](#)[Web services](#)[Help & Documentation](#)[Bioinformatics Tools FAQ](#)

Tools &gt; Multiple Sequence Alignment &gt; T-Coffee

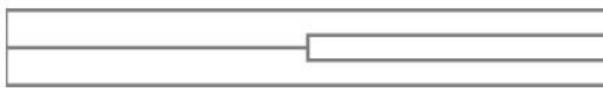
## Results for job tcoffee-I20220109-133053-0641-39837190-p2m

[Alignments](#)[Result Summary](#)[Guide Tree](#)[Phylogenetic Tree](#)[Results Viewers](#)[Submission Details](#)[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real



NP\_000476.1 0.0903  
NP\_001264576.1 0.15095  
NP\_013690.1 0.38838  
NP\_033828.2 0.08192

### Tree Data

```
(  
NP_000476.1:0.09030,  
(
```

The phylogenetic tree results of T-coffe and clustal-o are almost identical. Possibly, if the data set were larger, clustal omega and t-coffe results would favor clustal omega, because clustal omega is algorithmically more successful in medium-large alignments than t-coffe (uses HMM).

Tools > Multiple Sequence Alignment > T-Coffee

## Results for job tcoffee-I20220109-133053-0641-39837190-p2m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Branch length:  Cladogram  Real

```
NP_000476.1 0.0903
NP_001264576.1 0.15095
NP_013690.1 0.38838
NP_033828.2 0.08192
```

### Tree Data

```
(  
NP_000476.1:0.09030,  
(  
NP_001264576.1:0.15095  
NP_013690.1:0.38838  
NP_033828.2:0.08192
```

getting the position for this locus from homo sapiens from MGI: human synthesize this gene in chr 16 whereas for mouse the ch is 8

Guvenni degili | informatics.jax.org/nomology/marker/MGI:88061

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... StatQuest: Principa... » Diğer yer işaretleri Okuma listesi

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Keywords, Symbols, or IDs Quick Search

ALLIANCE of GENOME RESOURCES FOUNDING MEMBER

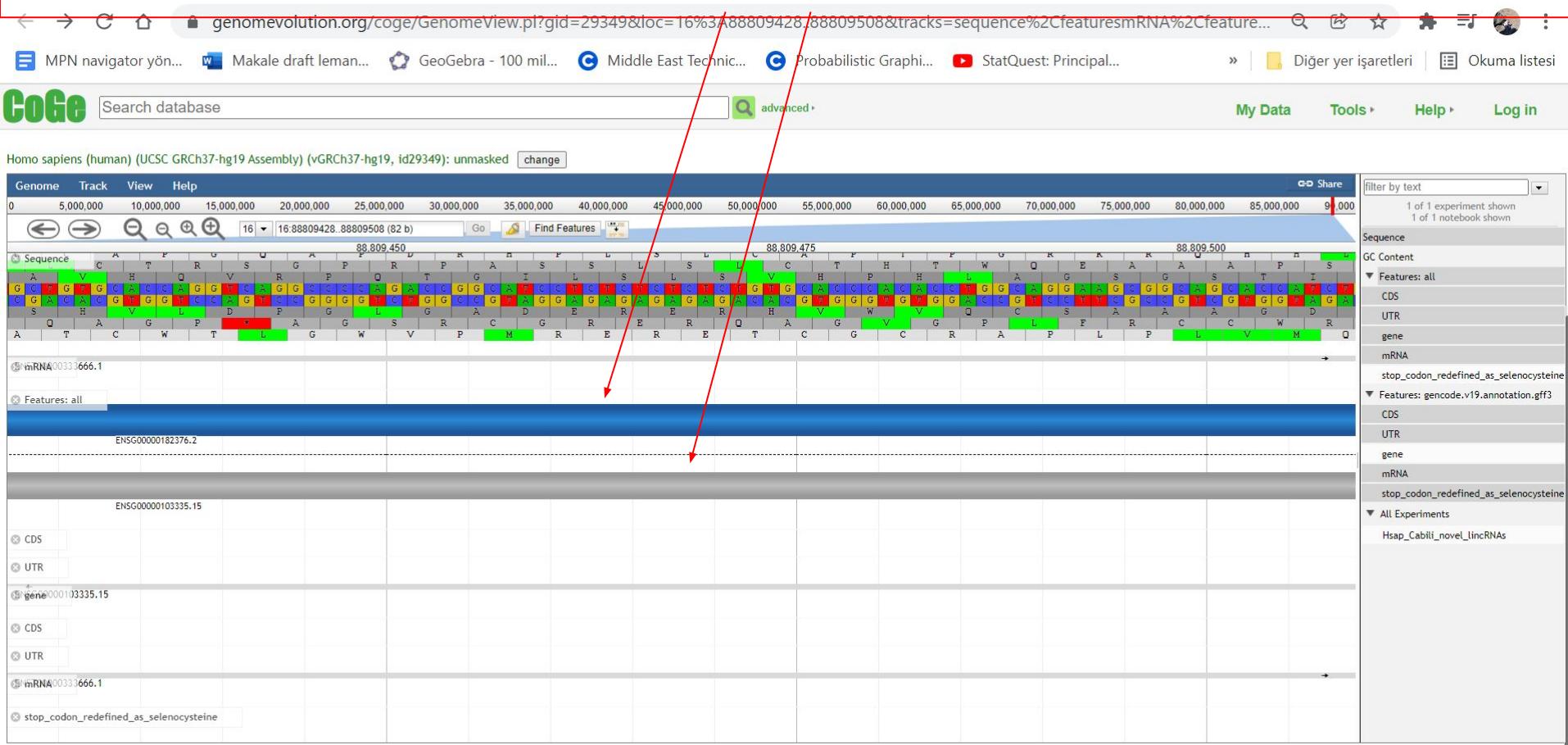
## Vertebrate Homology

Source: Alliance of Genome Resources

Comparative GO Graph (mouse, human, rat, zebrafish) Multiple Genome Viewer Alliance Homology Information

Species	Symbol	Gene Links	Genetic Location	Genome Coordinates (mouse and human only)	Associated Human Diseases	Sequences
human	APRT	HGNC:626 ( <a href="#">HGNC</a> ) 353 ( <a href="#">Entrez Gene</a> ) 102600 ( <a href="#">OMIM</a> ) APRT ( <a href="#">Alliance of Genome Resources</a> )	Chr16 q24.3	Chr16:88809469-88811934 (-) GRCh38.p7	adenine phosphoribosyltransferase deficiency	<input type="checkbox"/> P07741 ( <a href="#">UniProt</a>   <a href="#">EBI</a> ) <input type="checkbox"/> NM_001030018 ( <a href="#">RefSeq</a> )
mouse	Aprt	MGI:88061 ( <a href="#">MGI</a> ) 11821 ( <a href="#">Entrez Gene</a> ) <a href="#">Gene Tree</a> Aprt ( <a href="#">Alliance of Genome Resources</a> )	Chr8 71.91 cM	Chr8:123301376-123303646 (-) GRCm39	adenine phosphoribosyltransferase deficiency	<input type="checkbox"/> 11821 ( <a href="#">NCBI Gene Model</a> ) <input type="checkbox"/> P08030 ( <a href="#">UniProt</a>   <a href="#">EBI</a> ) <input type="checkbox"/> NM_009698 ( <a href="#">RefSeq</a> )
rat	Aprt	RGD:1307758 ( <a href="#">Rat Genome Database</a> ) 292072 ( <a href="#">Entrez Gene</a> ) Aprt ( <a href="#">Alliance of Genome Resources</a> )	Chr19 q12			<input type="checkbox"/> P36972 ( <a href="#">UniProt</a>   <a href="#">EBI</a> ) <input type="checkbox"/> NM_001013061 ( <a href="#">RefSeq</a> )
zebrafish	aprt	ZDB-GENE-040426-1492 ( <a href="#">Zebrafish Model Organism Database</a> ) 393641 ( <a href="#">Entrez Gene</a> ) aprt ( <a href="#">Alliance of Genome Resources</a> )	Chr7			<input type="checkbox"/> NP_956962 ( <a href="#">RefSeq</a> ) <input type="checkbox"/> NM_200668 ( <a href="#">RefSeq</a> )

finding the position in CoGO: in the bottom the gene and mrna product representations can be seen as lines , this lines not found in mouse (in the next slides)



# M. musculus genome for : Chr16:88809469-88811934 (-)



Search database

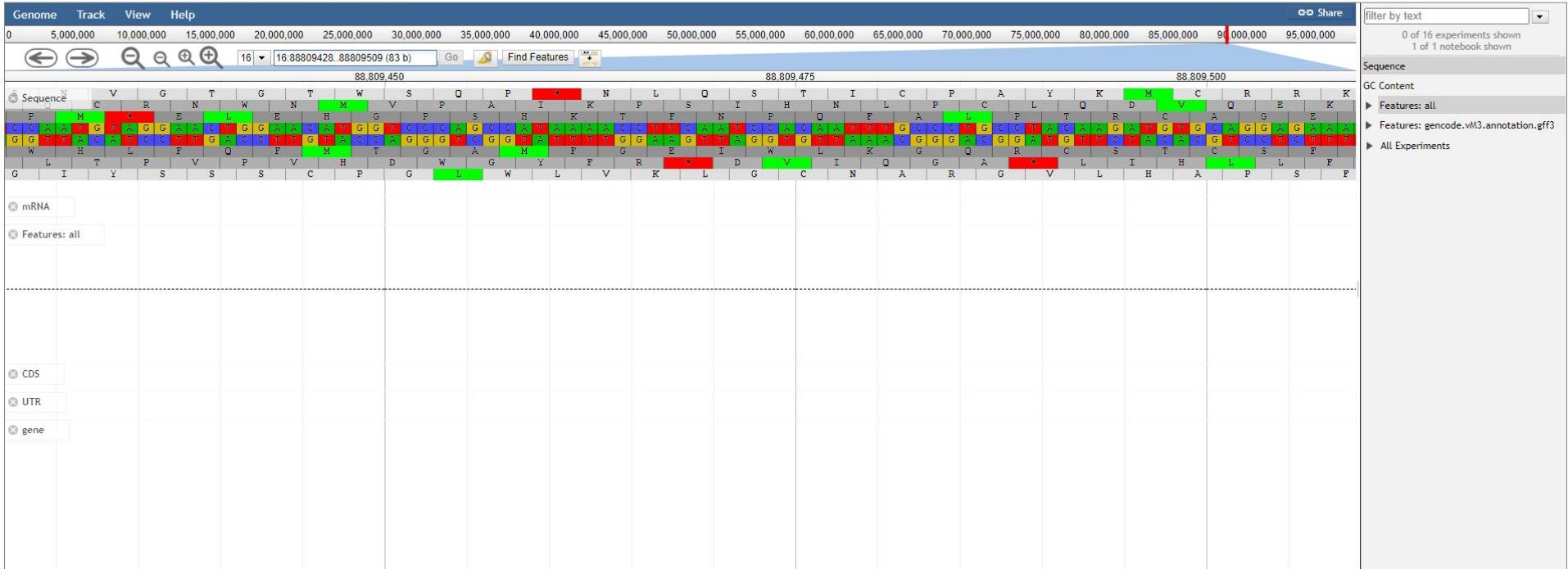
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Mus musculus (house mouse) (vGRCh38.p5, id34107): unmasked change

there is no mrna product from a gene in this region in mouse

## synteny view in ensembl:

genes that lie on the same chromosome: **syntenic genes**

ensembl.org/Human/Search/Results?q=APRT;site=ensembl;facet\_species=Human

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... StatQuest: Principa... Diğer yer işaretleri Okuma listesi

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New Search

Current selection:  
Only searching Human

Only searching Human

Restrict category to:  
Gene Transcript Variant Phenotype GeneTree

Per page:  
10 25 50 100

Layout:  
Standard Table

Tip:  
Help and Documentation can be searched from the homepage! Just type in a term you want to know more about, like non-synonymous SNP.

Only searching Human APRT

15 results match APRT when restricted to species: Human

APRT (Human Gene)  
**ENSG00000198931** 16:88809339-88811937-1  
Adenine phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:626]  
ADENINE PHOSPHORIBOSYLTRANSFERASE DEFICIENCY; APRTD [#614723] (MIM morbid record;  
description: ADENINE PHOSPHORIBOSYLTRANSFERASE DEFICIENCY; APRTD; APRT  
DEFICIENCY; UROLITHIASIS, 2,8-@DIHYDROXYADENINE; UROLITHIASIS,  
DHA; NEPHROLITHIASIS, DHA.) is an external reference matched to Gene ENSG00000198931  
Variant table • Phenotypes • Location • External Refs. • Regulation • Orthologues • Gene tree

APRT-203 (Human Transcript)  
**ENST00000562464** 16:88809736-88811880-1  
Adenine phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:626].  
Location • External Refs. • cDNA seq. • Exons • Variant table • Population

APRT-204 (Human Transcript)  
**ENST00000563655** 16:88809472-88811920-1  
Adenine phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:626].  
Location • External Refs. • cDNA seq. • Exons • Variant table • Protein seq. • Population • Protein summary

APRT-205 (Human Transcript)  
**ENST00000564858** 16:88811174-88811920-1  
Adenine phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:626].  
Location • External Refs. • cDNA seq. • Exons • Variant table • Population

APRT-206 (Human Transcript)  
**ENST00000567057** 16:88809469-88810268-1  
Adenine phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:626].

Best gene match

Human Gene Human APRT HGNC Symbol; Acc:HGNC:626

Protein coding gene adenine phosphoribosyltransferase

10kb 16:88809339-88811937-1

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Search Human...



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Human (GRCh38.p13) ▾

Location: 16:88,809,339-88,811,937

Gene: APRT

## Location-based displays

- Whole genome
- Chromosome summary
- Region overview

## Region in detail

- Comparative Genomics
- Synteny
- Alignments (image)
- Alignments (text)
- Region Comparison

- Genetic Variation
- Variant table
- Resequencing
- Linkage Data

## Markers

- Other genome browsers
- UCSC
- NCBI
- Ensembl GRCh37

Configure this page

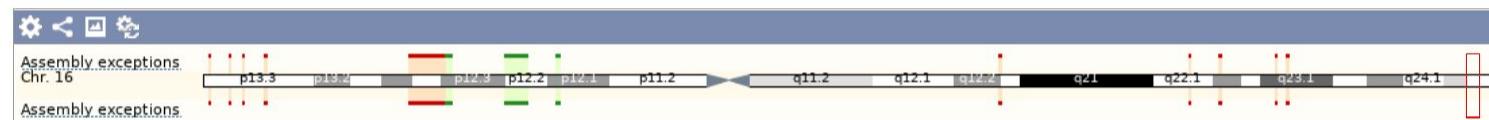
Custom tracks

Export data

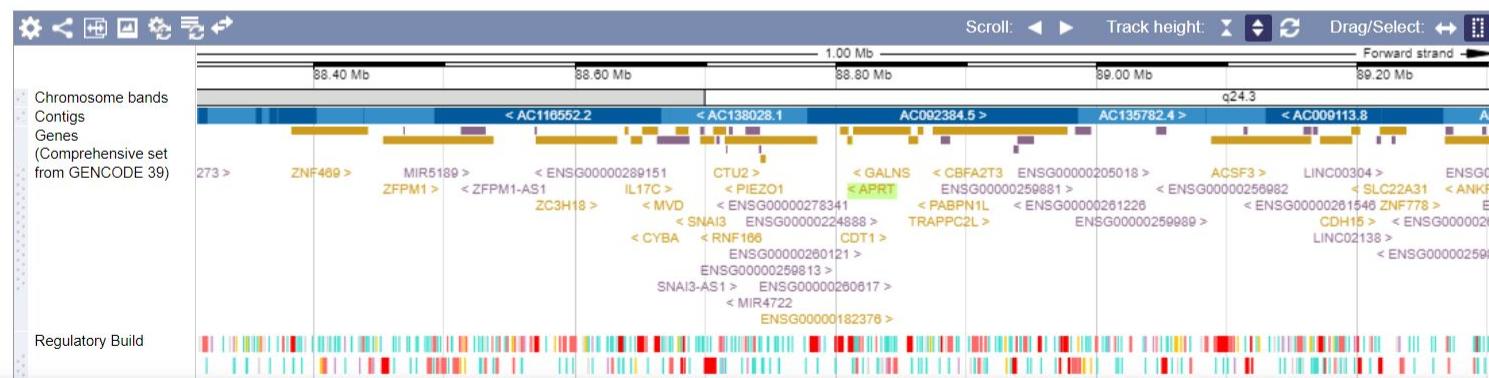
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## Chromosome 16: 88,809,339-88,811,937



## Region in detail ?

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Human (GRCh38.p13) ▾

Location: 16:88,809,339-88,811,937 Gene: APRT

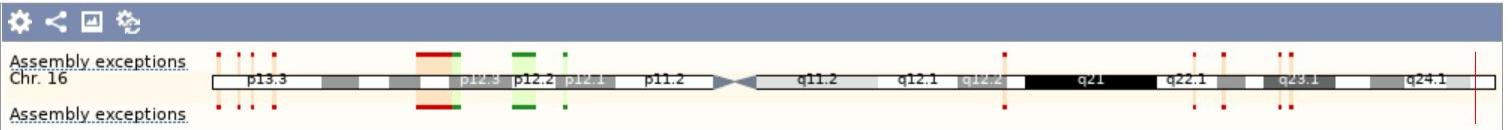
Location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail
- Comparative Genomics
- Synteny**
- Alignments (image)
- Alignments (text)

**Chromosome 16: 88,809,339-88,811,937**

Assembly exceptions Chr. 16 p13.3 p12.3 p12.2 p12.1 p11.2 q11.2 q12.1 q12.2 q21 q22.1 q23.1 q24.1

Assembly exceptions



- Alignments (image)
- Alignments (text)
- Region Comparison
- Genetic Variation
  - Variant table
  - Resequencing
  - Linkage Data
- Markers
- Other genome browsers
  - UCSC
  - NCBI
  - Ensembl GRCh37

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## Assembly exceptions

### Synteny

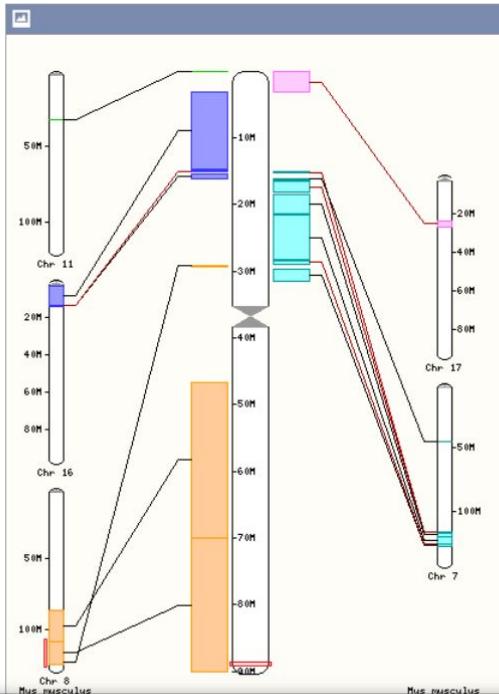
Synteny between Human chromosome 16 and Mouse

Change species:

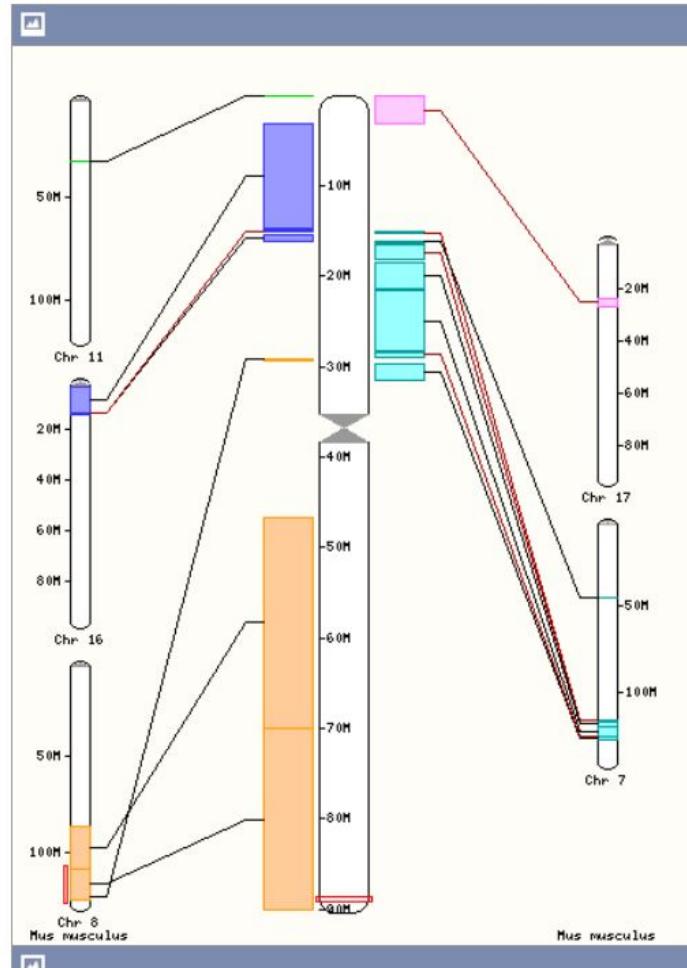
Mouse

Change chromosome:

16



## Synteny between Human chromosome 16 and Mouse



in ensembl, the homologous regions for the gene for humans and mouse

The screenshot shows a comparison of the APRT gene across two species. On the left, under 'Homo sapiens genes', the APRT gene (ENSG00000198931) is shown with its location at 16:88809339-88811937. On the right, under 'Mus musculus homologues', the homologous gene is labeled 'Aprt' (ENSMUSG0000006589) with its location at 8:123301374-123303648. A 'Region Comparison' link is also present. Navigation links for '15 upstream genes' and '15 downstream genes' are at the top, along with a 'Centre on gene APRT' button. A 'Show/hide columns' button and a 'Filter' input field are also visible.

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Preserved co-localization of genes can be caused by synteny. This means that at the same time, there are chromosome rearrangements in the evolutionary timeline. Synteny can be disrupted by chromosomal rearrangement processes such as translocation, inversion, chromosome fusion, and breakage, gene, segment, and chromosomal duplication and loss. In such a case, homologs can be found by prediction and tracking of syntenic blocks.

APRTs are Phosphoribosyltransferases which belongs to the Transerases

Biological Assembly 1 ?



3D View: Structure | Electron Density | Validation Report | Ligand Interaction

Global Symmetry: Cyclic - C2 (3D View)  
Global Stoichiometry: Homo 2-mer - A2

# 6HGS

Crystal Structure of Human APRT wild type in complex with GMP

DOI: [10.2210/ndb/6HGS/ndb](https://doi.org/10.2210/ndb/6HGS/ndb)

Classification: TRANSFERASE

Organism(s): Homo sapiens

Expression System: Escherichia coli BL21(DE3)

Mutation(s): No ⓘ

Deposited: 2018-08-23 Released: 2019-07-31

Deposition Author(s): Nioche, P., Huyet, J., Ozeir, M.

## Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 1.55 Å

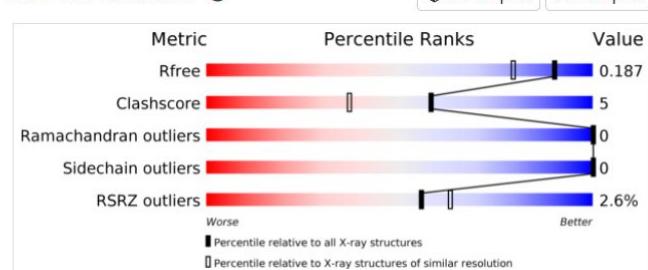
R-Value Free: 0.177

R-Value Work: 0.158

R-Value Observed: 0.158

## wwPDB Validation ⓘ

[3D Report](#) [Full Report](#)



# searching interpro:

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... StatQuest: Principal... » Diğer yer işaretleri Okuma listesi

## InterPro Classification of protein families

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/ Search / Text / Adenine Phosphoribosyltransferase

### Search InterPro

by sequence by text by domain architecture

Search families, domains, proteins, keywords or GO terms

Adenine phosphoribosyltransferase

e.g. IPR020422, kinase, O00167, PF02932, GO:0007165, 1t2v, UP000005640

Powered by EBI search

Search Clear

1 - 20 of 21 entries

ACCESSION	NAME	SOURCE DATABASE	DESCRIPTION
TIGR01090	adenine phosphoribosyltransferase	TIGRFAMs	...ng only tentative predictions of adenine phosphoribosyltransferase function for this lineage. The trusted cutoff score is made high for this reason. Most proteins scoring between the trusted and noise...
IPR000836	Phosphoribosyltransferase domain	InterPro	... and salvage pathways, including adenine phosphoribosyltransferase [intenz:2.4.2.7], hypoxanthine-guanine-xanthine phosphoribosyltransferase, hypoxanthine phosphoribosyltransferase [intenz:2.4.2.8], r...

H Export

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# taxonomy search for APRT in interpro

Home / Browse / By Entry / TIGRFams / TIGR01090 / Taxonomy / Uniprot

## TIGRFams adenine phosphoribosyltransferase TIGR01090

TIGRFams entry 

Overview Proteins 28k Taxonomy 20k Proteomes 6k Structures 33 Signature



The taxonomy information is available for both Key species and all organisms. The below tables are shown based on the preference in InterPro settings. If you wish to change it, please do in the [Settings](#) page 

### ▼ Hide Key Species

TAX ID	NAME	PROTEIN COUNT	ACTIONS
 10090	Mus musculus (Mouse)	1	   
 284812	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	1	   
 3702	Arabidopsis thaliana (Mouse-ear cress)	16	   
 39947	Oryza sativa subsp. japonica (Rice)	14	   
 559292	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	1	   

superfamily:

COVID-19 Information

Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

TIGR01090: apt

adenine phosphoribosyltransferase

A phylogenetic analysis suggested omitting the bi-directional best hit homologs from the spirochetes from the seed for this model and making only tentative predictions of adenine phosphoribosyltransferase function for this lineage. The trusted cutoff score is made high for this reason. Most proteins scoring between the trusted and noise cutoffs are likely to act as adenine phosphotransferase. [Purines, pyrimidines, nucleosides, and nucleotides, Salvage of nucleosides and nucleotides]

Links

Source: tigr  
Taxonomy: cellular organisms  
Protein: Representatives  
Specific Protein  
Related Protein  
Related Structure  
Architectures  
Superfamily: cl00309

TIGR01090 is a member of the superfamily cl00309.

Statistics



conserved compositions are red in the MSA:

Structure		?		
Sequence Alignment		■ include consensus sequence ?		
Reformat	Format: Hypertext	Row Display: up to 5	Color Bits: 2.0 bit	Type Selection: the most diverse members
1ORE_A	9 VEQRIRSFPDFPTPGVFRDISPVLKDPASFRAAIGLLARHLKATHggr-idYIAGLDSRGFLFGPSLAQEGLGCVLIR	87	human	
P07672	11 LKNSIKSIQDYPKPGILFRDVTSLLEDPKAYALSIDLLVERYKNAGi---tKVVGTEARGFLFGAPVALGLGVGFVPVR	86	Escherichia coli	
AAF94212	9 IKSSIKSIPDYPKKGILFRDVTSLLEDAQAYQATIQLLVEKYKDMGf---tKVVGTEARGFLFGAPLAELGVGFVPVR	84	Vibrio cholerae...	
P73935	3 LKALIRDIPDFPKPGIMFRDITLLNSPEGLRTIDSLSVQCESQelv--pdHVGMESRGFLFGMPPLAYQMNAGFIPVR	80	Synechocystis s...	
025296	9 LLQSIREVKDYPKKGILFKDITLLNYPKLFNKLIIDLTKKRYALALNi---dFIVGIEARGFILGSALAYALGVGFVPVR	84	Helicobacter py...	
CAB73184	12 LLDSIRIIIPDFPKKGIIIFRDITLLNNKEALNFLLKHLKERYKDYNl---dFIAGTESRGFIFASMICAKLNLPFVPVR	87	Campylobacter j...	
Q9JYB4	13 LADKIRKIEPNPQKGILFHDIITPQSAEYFRLLVLDLVRQYMDQKi---dIVAGLDARGFIIGAALAYQLNVGFVPVR	88	Neisseria menin...	
AAAS1769	9 VEQRIRSFPDFPTPGVFRDISPVLKDPASFRAAIGLLARHLKATHggr-idYIAGLDSRGFLFGPSLAQEGLGCVLIR	87	human	
P49435	10 LKLAHQYPNPFSEGLFEDFLPLIFRNPGLFQKLIDAFKLHLEAFpevkidYIVGLESRGFLFGPTLALALGVGFVPVR	89	Saccharomyces c...	
WP_010874751	8 LDRAIKRFNDPFTPGILFYDITPIFLNSELFEVLEQMAQFIQEVKa---dGIVCPEARGFIFGGALASKTKLPLVLR	83	Mycoplasma pneu...	
1ORE_A	88 KRGKLPGPTLWASYSLLEYKA-ELEIQKDALE--PGQRVVVDDLLATGGTMNAACELLGRQLQAEVLECVSLVELTSLK	164	human	
P07672	87 KPGKLPRETISETYDLEYTD-QLEIHVDIAK--PGDKVLVVDLLATGGTIEATVKLIRRLGEVADAIFIINLFDLGG	163	Escherichia coli	
AAF94212	85 KPGKLPRTQVQSYELEYTD-TLEIHVDIAK--PGDKVLVVDLLATGGTIEATVKLIRRLGEVHEAAVINLPEIGG	161	Vibrio cholerae...	
P73935	81 KPGKLPAPVHRVEYDLEYKD-SLEIHQDAVA--PHHRVLVVDLLATGGTAKATAELLTKLGCEVLGFAFIIELAALNG	157	Synechocystis s...	
025296	85 KKGKLPAPHTLSQSYSLEYGSD-SIEHSDAFArqiKGVRVLLIDDLATGGTALASLELIKALQACECIEACFLIGLKLPG	163	Helicobacter py...	
CAB73184	88 KPGKLPFETFSCEYDLEYGSD-KVELHKDAFKnqNARVLLVDDLIATGGTAIASYELIQKAGAKCVEACFLINLKDLNG	166	Campylobacter j...	
Q9JYB4	89 KKGKLPFETVSQSYALEYGE-AVEIHTDAVK--LGSRVLVLLDDLIATGGTMAGLELIRKLKGGEVIEAAALIEFTDLQG	165	Neisseria menin...	
AAAS1769	88 KRGKLPGPTLWASYSLLEYKA-ELEIQKDALE--PGQRVVVDDLLATGGTMNAACELLGRQLQAEVLECVSLVELTSLK	164	human	
P49435	90 KAGKLPGECFKATYEKEYGSD-LFEIQKNAIP--AGSNVIIVDDIIATGGSAAAAGELVQELEANLLEYNFVMEIDFLKG	166	Saccharomyces c...	
WP_010874751	84 KPHKLSGELARETYDLEYRQNsILEMRVDALE--NCKRCVIVDDLLATAGTVAAIDKLIARLGSQTGYCFIELQKLHG	161	Mycoplasma pneu...	
1ORE_A	165 REKLAP--VPFFSLLQY	179	human	
P07672	164 EQRLEKqgITSYSLVPF	180	Escherichia coli	
AAF94212	162 DKRLEGlglLQVYSICEF	178	Vibrio cholerae O1 biovar El Tor str. N16961	
P73935	158 RQCLPD--LPIISLVEY	172	Synechocystis sp. PCC 6803 substr. Kazusa	
025296	164 -IQLLeerVKTFCCLLC	179	Helicobacter pylori 26695	
CAB73184	167 -ANKLEkltSVSYVLEI	182	Campylobacter jejuni subsp. jejuni NCTC 11168	
Q9JYB4	166 GKNIRAsgAPLFTLLQN	182	Neisseria meningitidis MC58	
AAAS1769	165 REKLAP--VPFFSLLQY	179	human	
P49435	167 RSKLNA--PVFTLLNA	180	Saccharomyces cerevisiae S288c	
WP_010874751	162 KAKLQPn-VATKILLHY	177	Mycoplasma pneumoniae	



10°C Parçalı bulutlu



19:21

9.01.2022

Conserved domain was found among these homologs when searched for homologs via NCBI.

## Conserved Domains

*Conserved Domains from CDD found in protein sequences by rpsblast searching.*

### PRTases\_typeI (cl00309)

- Phosphoribosyl transferase (PRT)-type I domain.



HOME | SEARCH | SITE MAP

Entrez

## Conserved Protein Domain Family *PRTases\_typeI*

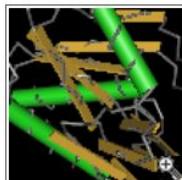
Structure

Protein

Help

### cl00309: PRTases\_typeI Superfamily

?



#### Phosphoribosyl transferase (PRT)-type I domain

Phosphoribosyl transferase (PRT) domain. The type I PRTases are identified by a conserved PRPP binding motif which features two adjacent acidic residues surrounded by one or more hydrophobic residue. PRTases catalyze the displacement of the alpha-1'-pyrophosphate of 5-phosphoribosyl-alpha1-pyrophosphate (PRPP) by a nitrogen-containing nucleophile. The reaction products are an alpha-1 substituted ribose-5'-phosphate and a free pyrophosphate (PP). PRPP, an activated form of ribose-5-phosphate, is a key metabolite connecting nucleotide synthesis and salvage pathways. The type I PRTase family includes a range of diverse phosphoribosyl transferase enzymes and regulatory proteins of the nucleotide synthesis and salvage pathways, including adenine phosphoribosyltransferase EC:2.4.2.7., hypoxanthine-guanine-xanthine phosphoribosyltransferase, hypoxanthine phosphoribosyltransferase EC:2.4.2.8., ribose-phosphate pyrophosphokinase EC:2.7.6.1., amidophosphoribosyltransferase EC:2.4.2.14., orotate phosphoribosyltransferase EC:2.4.2.10., uracil phosphoribosyltransferase EC:2.4.2.9., and xanthine-guanine phosphoribosyltransferase EC:2.4.2.22.

Links

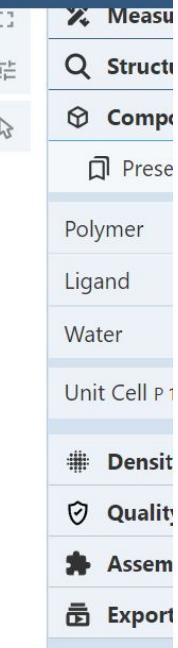
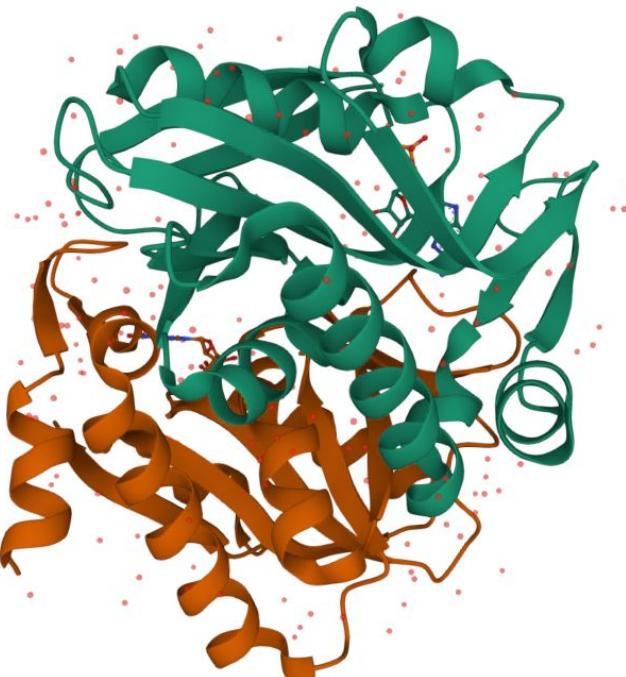
?

Superfamily

investigating the protein in the PDB and other sources:

electron density as whole [9]

Beta sheets are planar alpha helices are circular in helix shape.

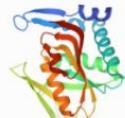


2 identical  
macromolecules in the  
protein::A,B

## Macromolecules

Find similar proteins by: [Sequence](#) (by identity cutoff) | [Structure](#)

Entity ID: 1

Molecule	Chains	Sequence Length	Organism	Details	Image
Adenine phosphoribosyltransferase	A, B	178	<a href="#">Homo sapiens</a>	Mutation(s): 0 ⓘ Gene Names: <a href="#">APRT</a> EC: <a href="#">2.4.2.7</a>	

## UniProt & NIH Common Fund Data Resources

Find proteins for [P07741](#) (*Homo sapiens*)

Explore [P07741](#) ⓘ

Go to UniProtKB: [P07741](#)

PHAROS: [P07741](#)

GTEX: [ENSG00000198931](#)

all ligands and ions  
information: only 1 unique  
ligand

## Small Molecules

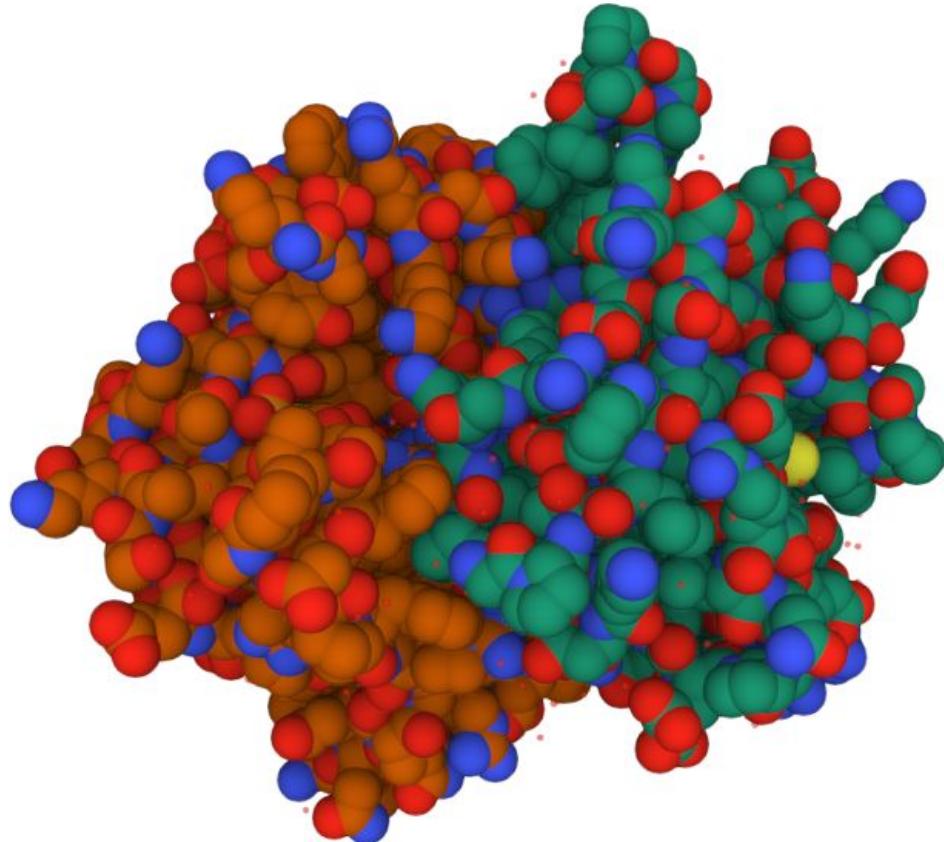
### Ligands 1 Unique

ID	Chains <small>i</small>	Name / Formula / InChI Key	2D Diagram	3D Interactions
5GP (Subject of Investigation/LOI) <a href="#">Query on 5GP</a>	C [auth A], D [auth B]	<b>GUANOSINE-5'-MONOPHOSPHATE</b> C <sub>10</sub> H <sub>14</sub> N <sub>5</sub> O <sub>8</sub> P RQFCJASXJCIDSX-UUOKFMHZSA-N		<a href="#">Ligand Interaction</a>

### Binding Affinity Annotations

ID	Source	Binding Affinity
5GP	Binding MOAD: <a href="#">6HGS</a>	Ki: 1.70e+5 (nM) from 1 assay(s)

spacefill  
representation  
of the  
molecule in  
PDB



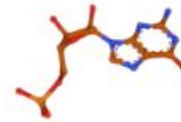
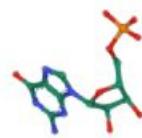
nine beta-strands and six alpha-helices with 2 identical subunits



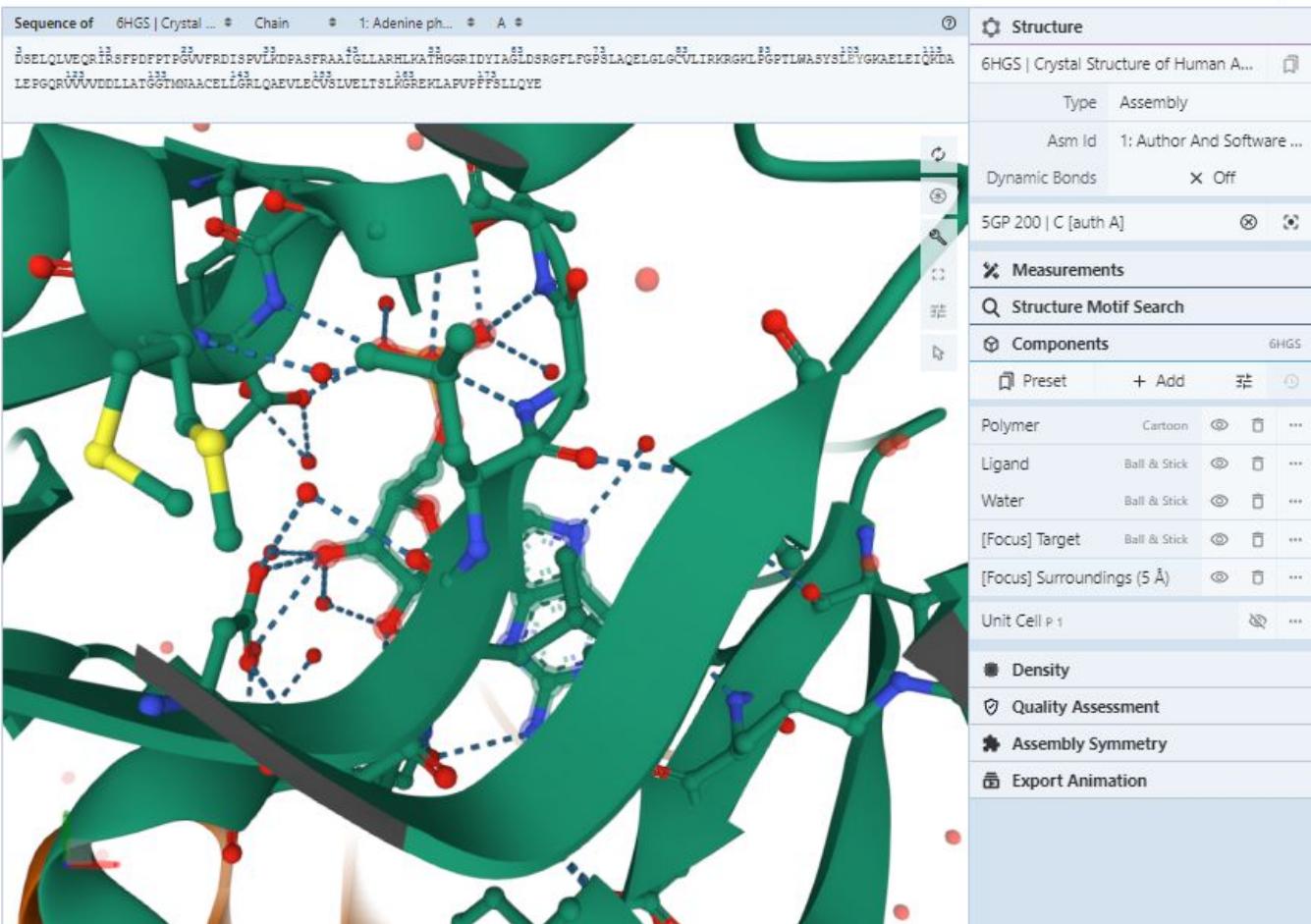
n-terminal

c terminal

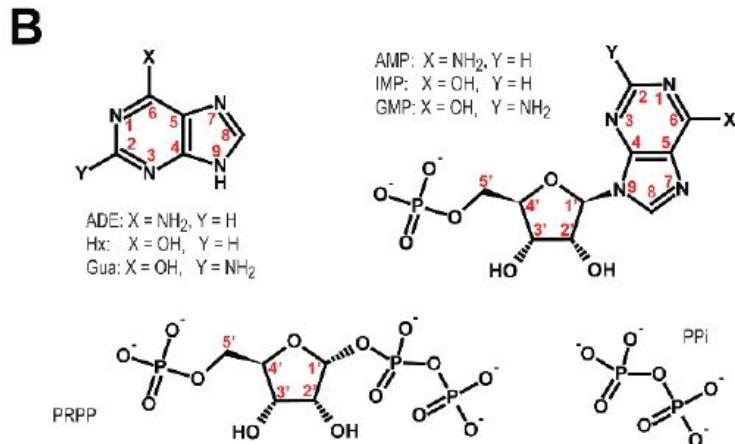
ligand binding  
sites:PDB



## detailed ligand interactions:PDB



The ligand binding sites detailed information [8]



**Figure 1. Reversible enzymatic reactions by human adenine phosphoribosyltransferase (hAPRT).** (A) Magnesium ion is necessary for the transformation of ADE and PRPP into AMP and PPi, and *vice versa*. (B) Chemical structures of the hAPRT substrates (ADE, AMP, PRPP, PPi) and analogs (Hx, Gua, IMP, GMP) tested. Atom numbering is indicated in red.

The responsible residues for the structure and the function : Leu159 & Ala151: responsible for base specificity[8]

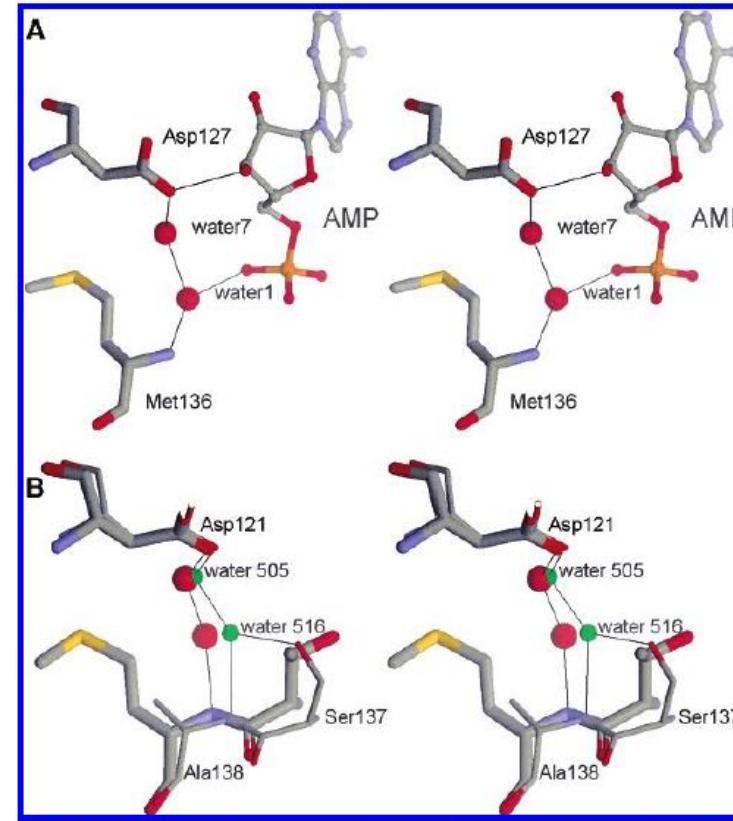
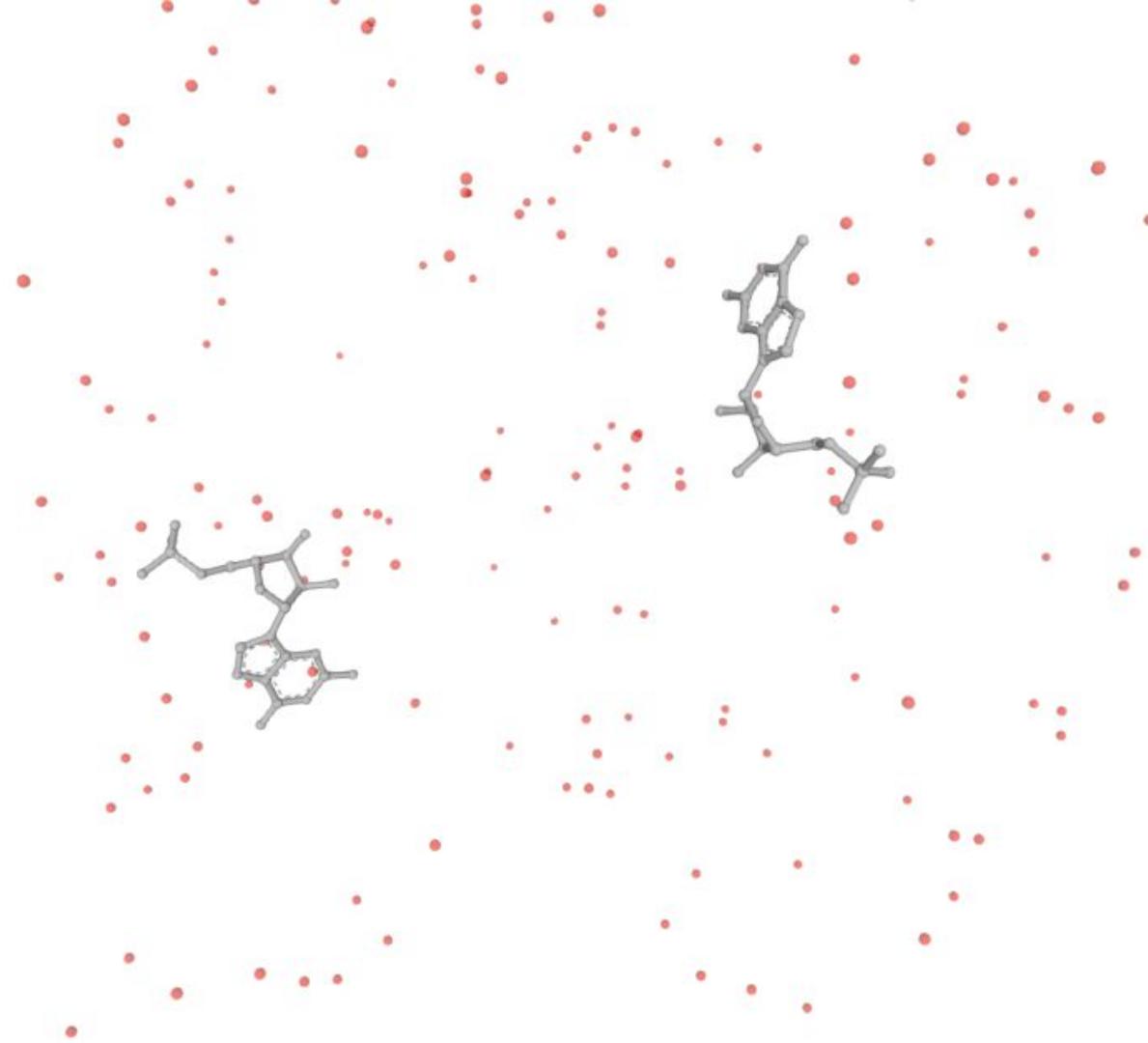


FIGURE 6: (A) Stereoview of selected residues and water molecules of the hAPRT active site. In the human APRT structure, the water1 and water7 molecules participate in a hydrogen bond network (shown as lines) involving especially the 5'-phosphate moiety of PRPP (or AMP), the Met136 backbone nitrogen, and a  $\delta$ -oxygen atom of the conserved Asp127 residue. Water1 must be an important element for PRPP binding, and perhaps the Met136Thr mutation favors competition of the hydroxyl group with the backbone nitrogen atom of the same Thr136 residue for this water, shifting this molecule closer to the threonine residue and, consequently, disfavoring the bond to the 5'-phosphate group. (B) Stereoview of selected residues and water molecules of superimposed hAPRT and *S. cerevisiae* APRT structures. In the *S. cerevisiae* APRT structure (residues labeled and shown as thick cylinders), which does not contain either a PRPP or a AMP bound, the equivalent water 516 (water1 in hAPRT) forms a hydrogen bond to Ser137 (Thr135 in hAPRT) and, as opposed to water505 (water7 in hAPRT), is shifted compared to the positions of the equivalent waters of the three other structures, which bind PRPP or AMP. All the hydrogen bonds are shown as lines.

ligands are colored as their interaction type:  
no difference in  
interaction  
profile btw  
ligands in PDB



# the ligand information detail in pdb

RCSB PDB Deposit Search Visualize Analyze Download Learn More Documentation Careers MyPDB



Structure Summary 3D View Annotations Experiment Sequence Genome Ligands Versions

## 6HGS

5GP

### 5GP: GUANOSINE-5'-MONOPHOSPHATE

5GP is a Ligand Of Interest in 6HGS designated by the Author

Display Files Download Files

Ligand Definition and Summary of 5GP

Help



◆ Best-fitted instance in this entry

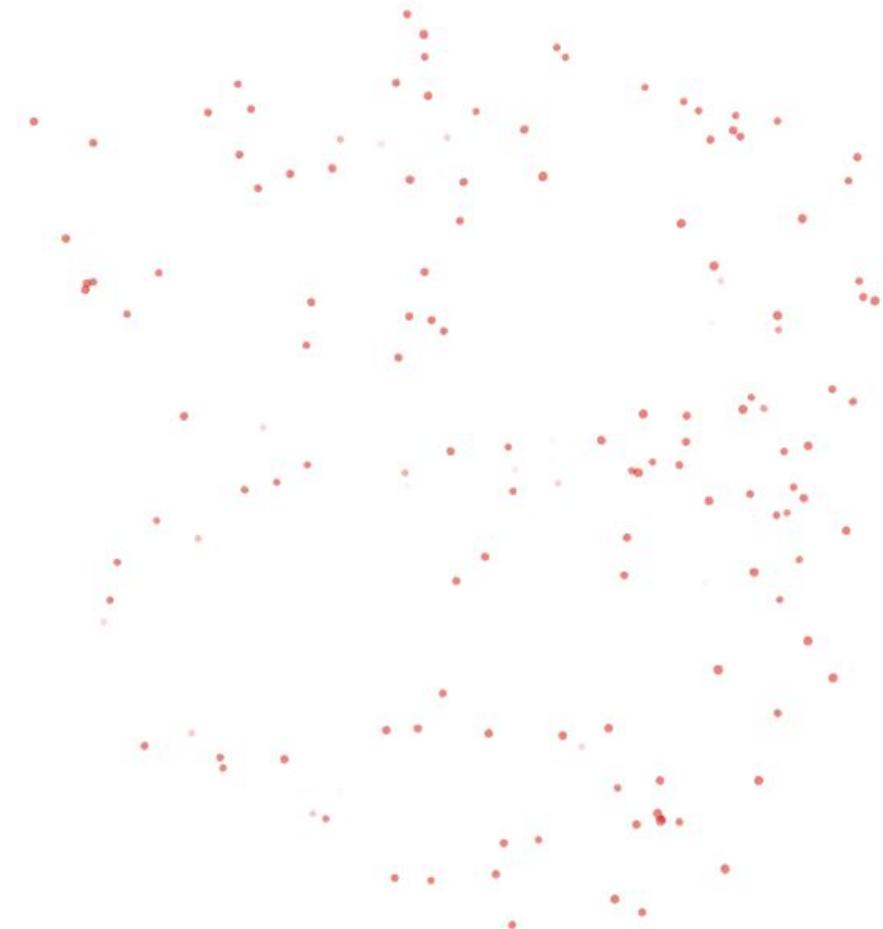
● Other instances in this entry



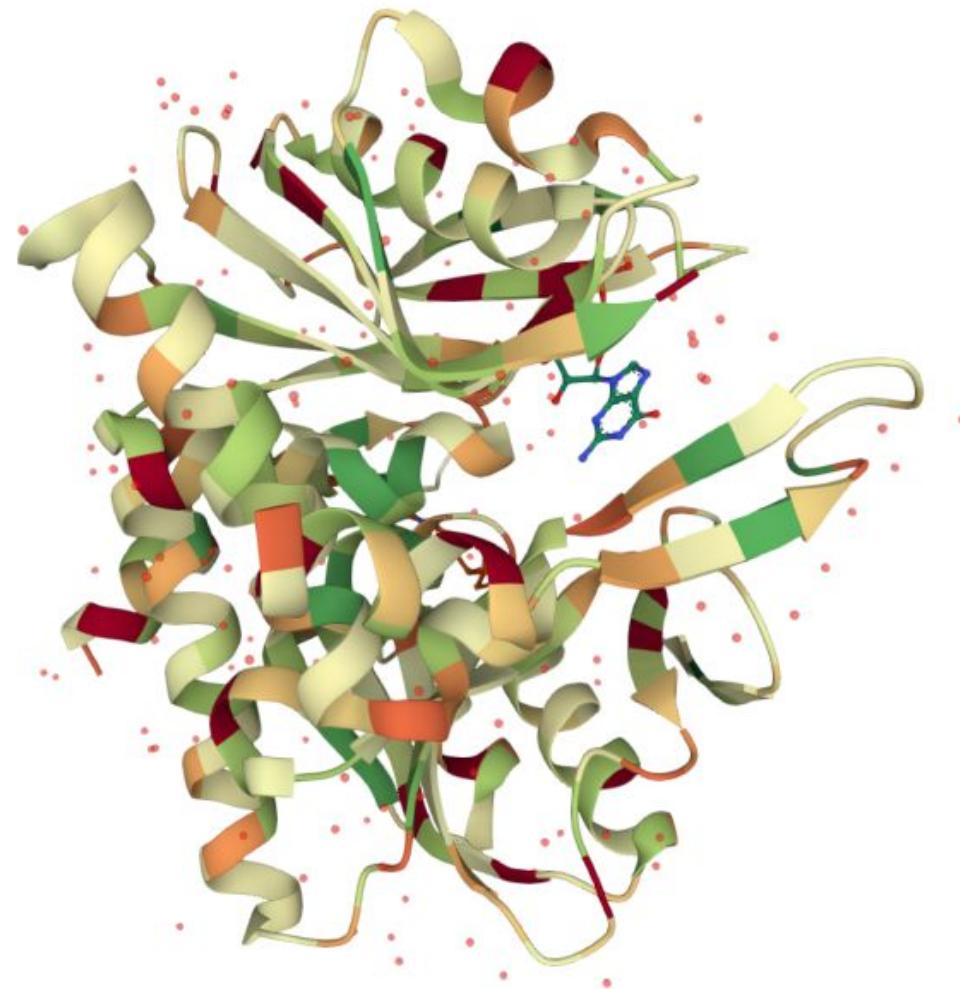
◆ Best-fitted instance in this entry

● Best-fitted PDB instances (top 5)

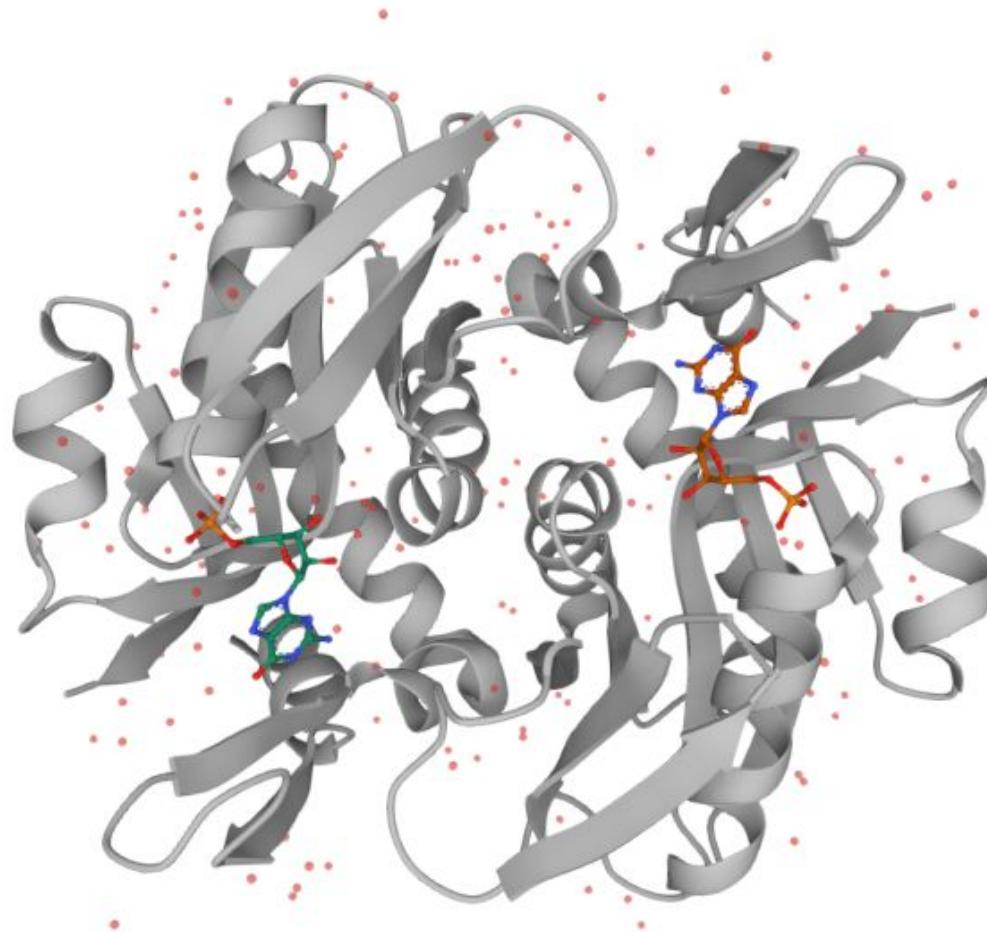
water  
molecules  
distributions:  
PDB



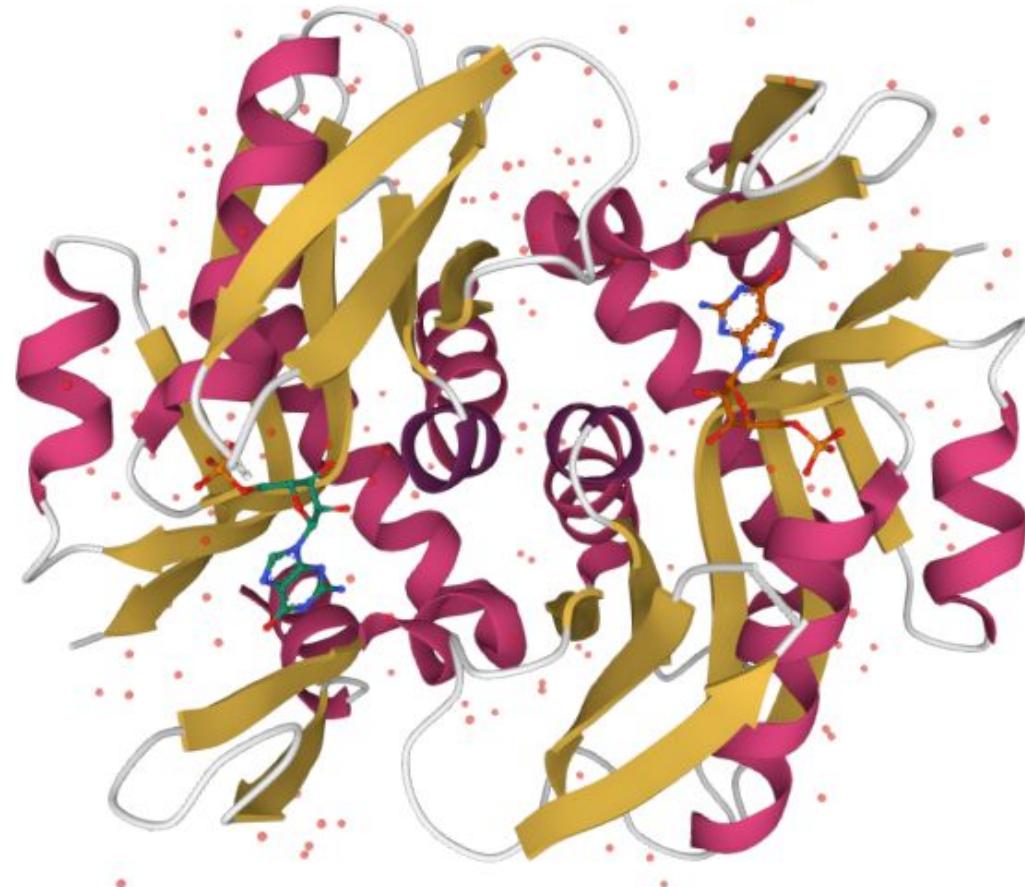
residues characterized  
by their hydrophilic  
characteristics



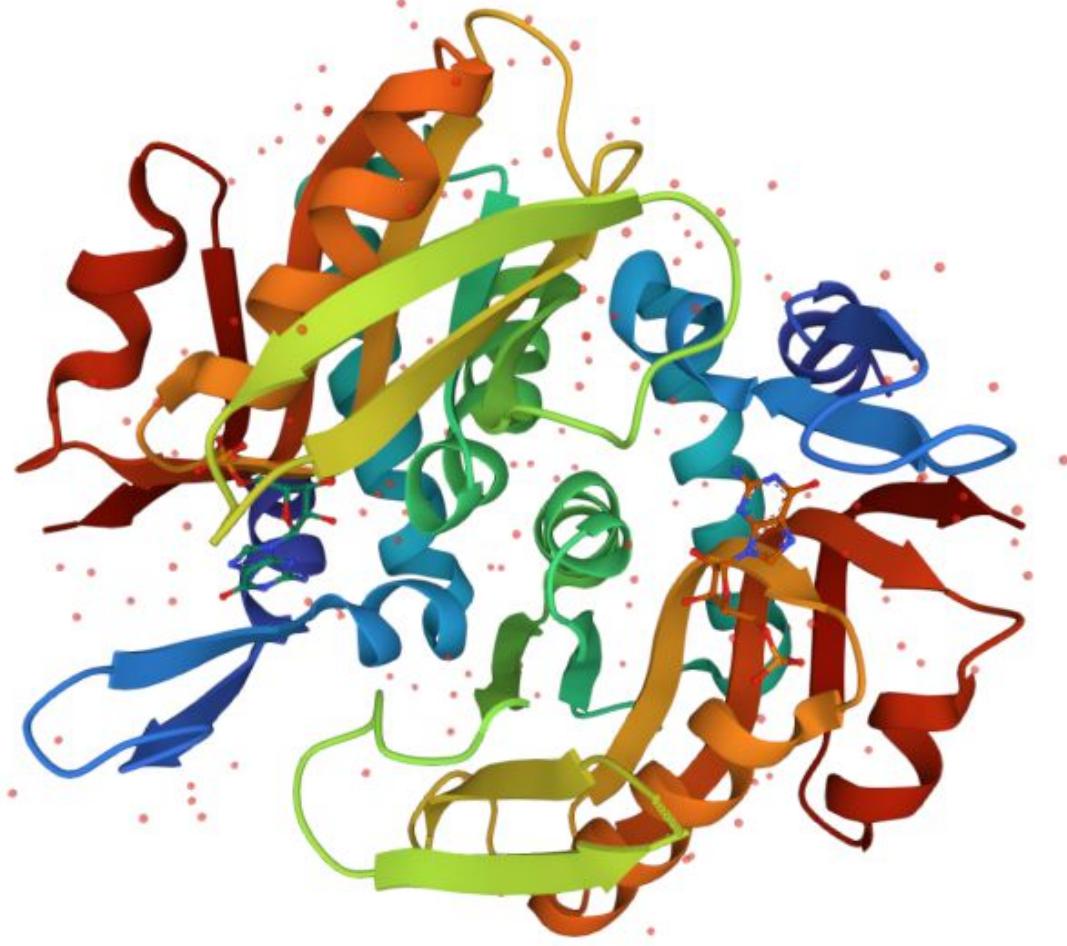
residues colored by their interaction properties: only ligands are colorfull, this means the remained alpha helices and beta sheets are not interact with other molecules, they are composed to make the general structure and do not go interaction with other molecules except each other to make structural stability



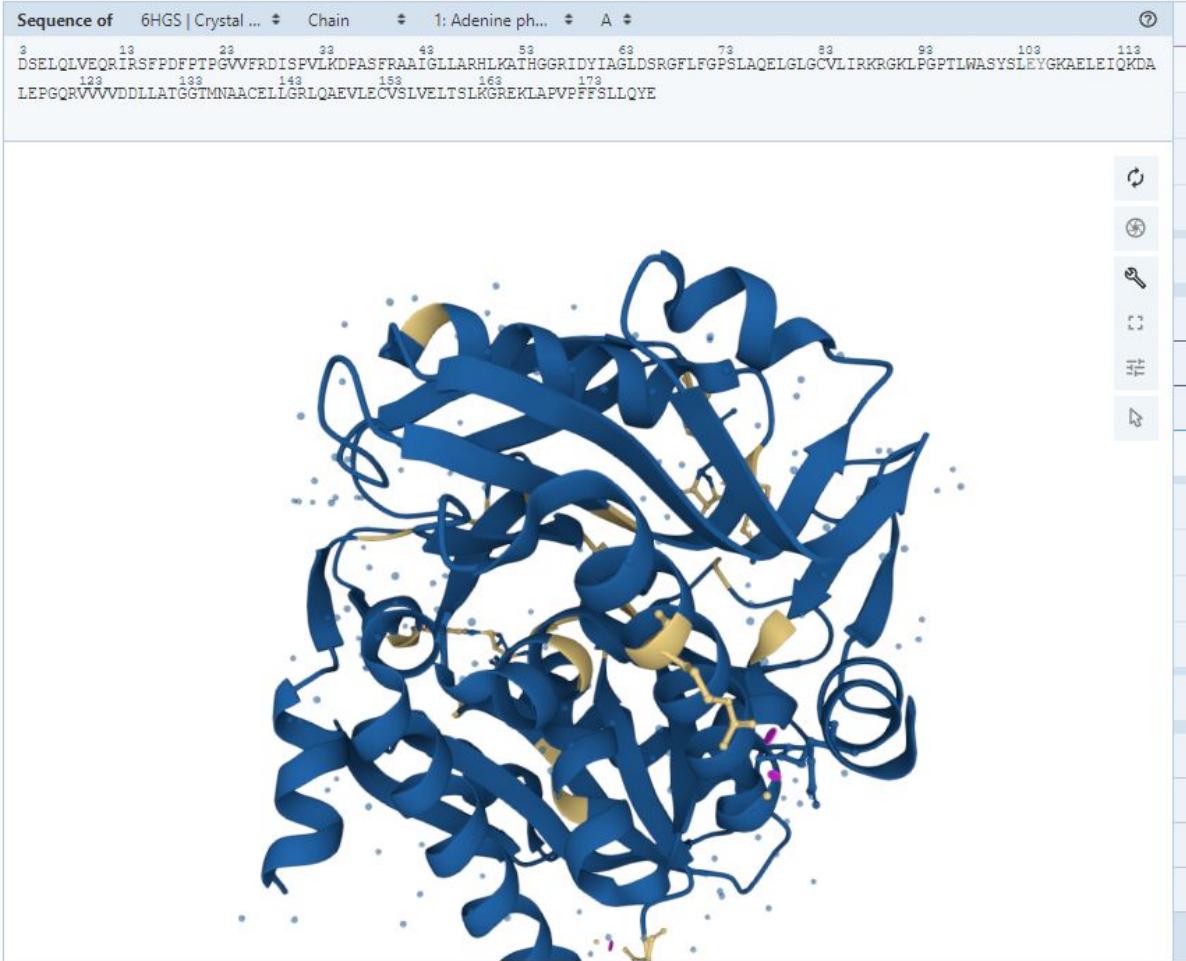
residues colored as their secondary structure as alpha helices as pink and yellows for beta sheets



all sub-seq.s are  
colored as their  
seq. ids



validation report  
(global quality  
score//correctness of  
the protein entry in  
PDB):PDB



# secondary structure summary information in interpro:

Google X | BIN 50 X | NCBI N X | Google X | adenin X | Human X | PDB 1e X | PDB 1e X | 3D Vie X | Sci-Hu X | + | ▾ | - | ☰ | X

Güvenli değil | ebi.ac.uk/interpro/structure/PDB/1ore/

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... StatQuest: Principal... » Diğer yer işaretleri Okuma listesi

## InterPro Classification of protein families

Home Search Browse Results Release notes Download Help About

Chain A (P07741)

Domains on protein ①

A PDB chain 1 - 180 Options

1 20 40 60 80 100 120 140 160 180

50 150

MADSELQLVEQRIRSRFPDFPTPGVVFRDISPVLKDPAFRAAIGLLARHLKATHGGRIDYIAGLDSRGFLFGPSL... GKAELIQQDALEPGQRRVVVDDLLATGGTMIAACELLGRLOAEVLECVSLSVELTSLSKGREKLAPVFFSLQYE

Chain

Secondary Structure

Entries

Chain A

H IPR029057  
SS53271  
GSDSA3.40.50.2020  
F IPR005764  
TIGR01090  
MF\_00004  
D IPR000836  
PF00156  
cd06223  
PTHR32315

Detailed description: The screenshot shows a protein structure analysis page. At the top, there's a navigation bar with various links like Google, BIN 50, NCBI, etc. The main title is 'Classification of protein families'. Below it, a menu bar includes Home, Search, Browse, Results, Release notes, Download, Help, and About. The 'About' tab is currently selected. The main content area is titled 'Chain A (P07741)'. It features a sequence alignment with residues 1-180. A callout box highlights the 'PDB chain' section, showing the sequence from 1 to 180. Below the sequence are tracks for 'Chain' (purple bar), 'Secondary Structure' (red arrows for alpha-helices and green arrows for beta-sheets), and 'Entries' (multiple colored bars representing different protein families or domains). On the right side, there's a sidebar with detailed information for several entries, including IPR029057, IPR005764, IPR000836, PF00156, cd06223, and PTHR32315.

searching the related protein in  
PDBe:

EMBL-EBI

 Protein Data Bank in Europe  
Bringing Structure to Biology

PROTEIN DATA BANK 

Examples: [hemoglobin](#), [B](#)

## PDBe > 1ore

### Human Adenine Phosphoribosyltransferase

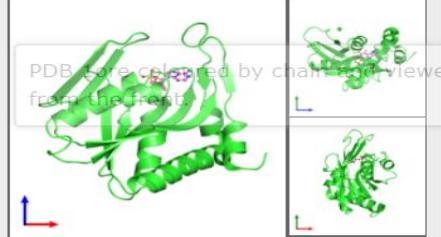
**Source organism:** *Homo sapiens*

**Primary publication:**  
 Three-dimensional structure of human adenine phosphoribosyltransferase and its relation to DHA-uroolithiasis.  
Silva M, Silva CH, Iulek J, Thiemann OH  
*Biochemistry* **43** 7663-71 (2004)  
PMID: 15196008 

**X-ray diffraction  
2.1 Å resolution**

**Released:** 30 Mar 2004  
**DOI:** [10.2210/pdb1ore/pdb](https://doi.org/10.2210/pdb1ore/pdb)

Model geometry Fit model/data 

PDB core colored by chain, viewed from the front. 

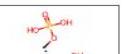
#### Function and Biology

**Reaction catalysed:**

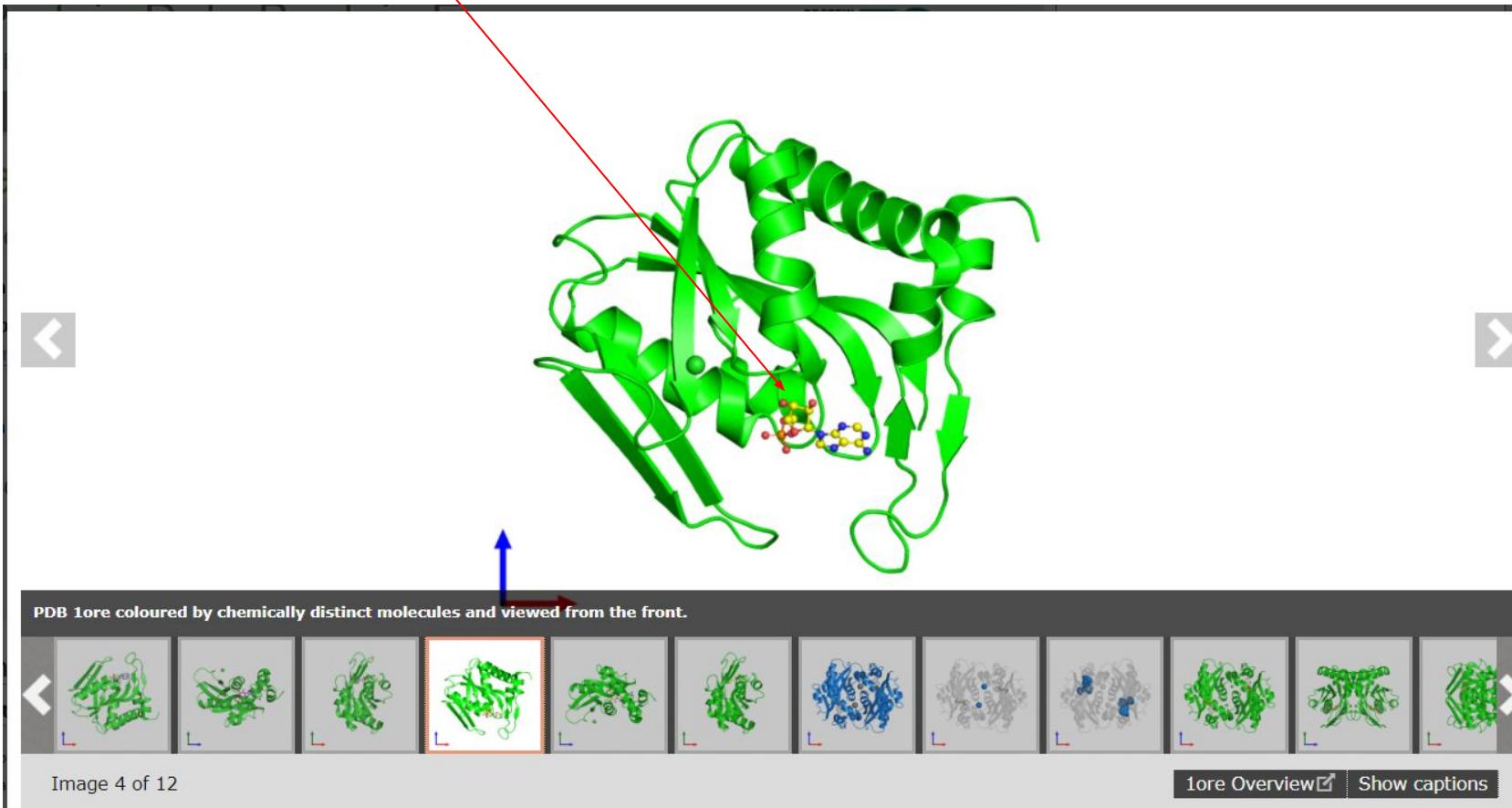
AMP + diphosphate = adenine + 5-phospho-alpha-D-ribose 1-diphosphate

#### Details

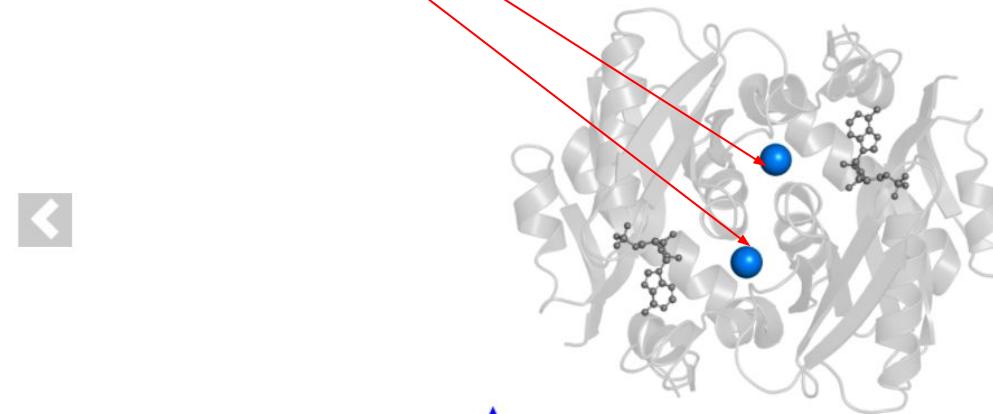
#### Ligands and Environments

**2 bound ligands:**  

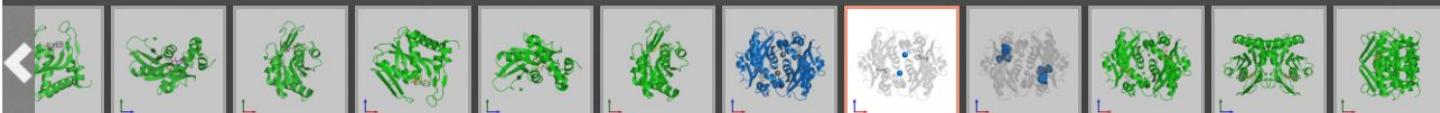
chemically distinct molecules

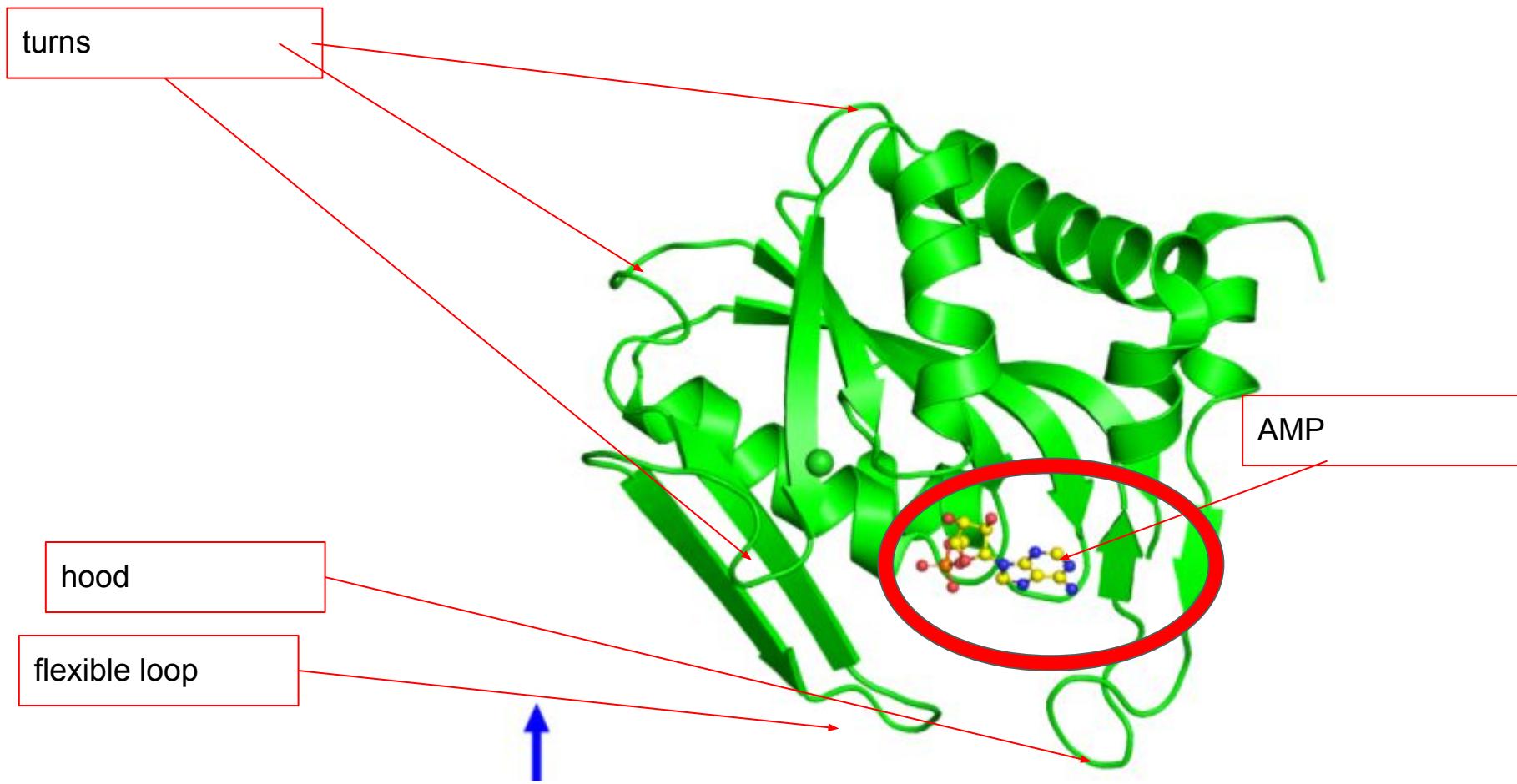


chloride ions



PDB 1ore contains 2 copies of CHLORIDE ION in assembly 1. This small molecule is highlighted and viewed from the front.





# references

- [1]: <https://medlineplus.gov/genetics/chromosome/16/#conditions>
- [2]: Martin, J., Han, C., Gordon, L. et al. The sequence and analysis of duplication-rich human chromosome 16. *Nature* 432, 988–994 (2004). <https://doi.org/10.1038/nature03187>
- [3]: [https://www.ncbi.nlm.nih.gov/nuccore/NM\\_000485.3/](https://www.ncbi.nlm.nih.gov/nuccore/NM_000485.3/)
- [4]: <https://www.biostars.org/p/125079/>
- [5]: <https://medlineplus.gov/genetics/gene/aprt/>
- [6]: <https://www.genecards.org/cgi-bin/carddisp.pl?gene=APRT>
- [7]: Ghiurcuta, C. G., & Moret, B. M. (2014). Evaluating synteny for improved comparative studies. *Bioinformatics* (Oxford, England), 30(12), i9–i18. <https://doi.org/10.1093/bioinformatics/btu259>
- [8]: Ozeir M, Huyet J, Burgevin MC, Pinson B, Chesney F, Remy JM, Siddiqi AR, Lupoli R, Pinon G, Saint-Marc C, Gibert JF, Morales R, Ceballos-Picot I, Barouki R, Daignan-Fornier B, Olivier-Bandini A, Augé F, Nioche P. Structural basis for substrate selectivity and nucleophilic substitution mechanisms in human adenine phosphoribosyltransferase catalyzed reaction. *J Biol Chem.* 2019 Aug 9;294(32):11980-11991. doi: 10.1074/jbc.RA119.009087. Epub 2019 Jun 3. PMID: 31160323; PMCID: PMC6690681.
- [9]: <https://pdb101.rcsb.org/learn/videos/exploring-pdb-structures-in-3d-with-molstar>
- [10]: [https://www.youtube.com/watch?v=QIZ8QH6JcC8&ab\\_channel=TheNationalLibraryofMedicine](https://www.youtube.com/watch?v=QIZ8QH6JcC8&ab_channel=TheNationalLibraryofMedicine)