

به نام خدا

پروژه مبانی بیوانفورماتیک

گرد آورنده :شادی اسدی سامانی
شماره دانشجویی:40013330507048

سکشن:سه شنبه 10-12

نام استاد مربوطه:سید حسین خادم حسینی

نام ژن:ATM

پاییز 1403

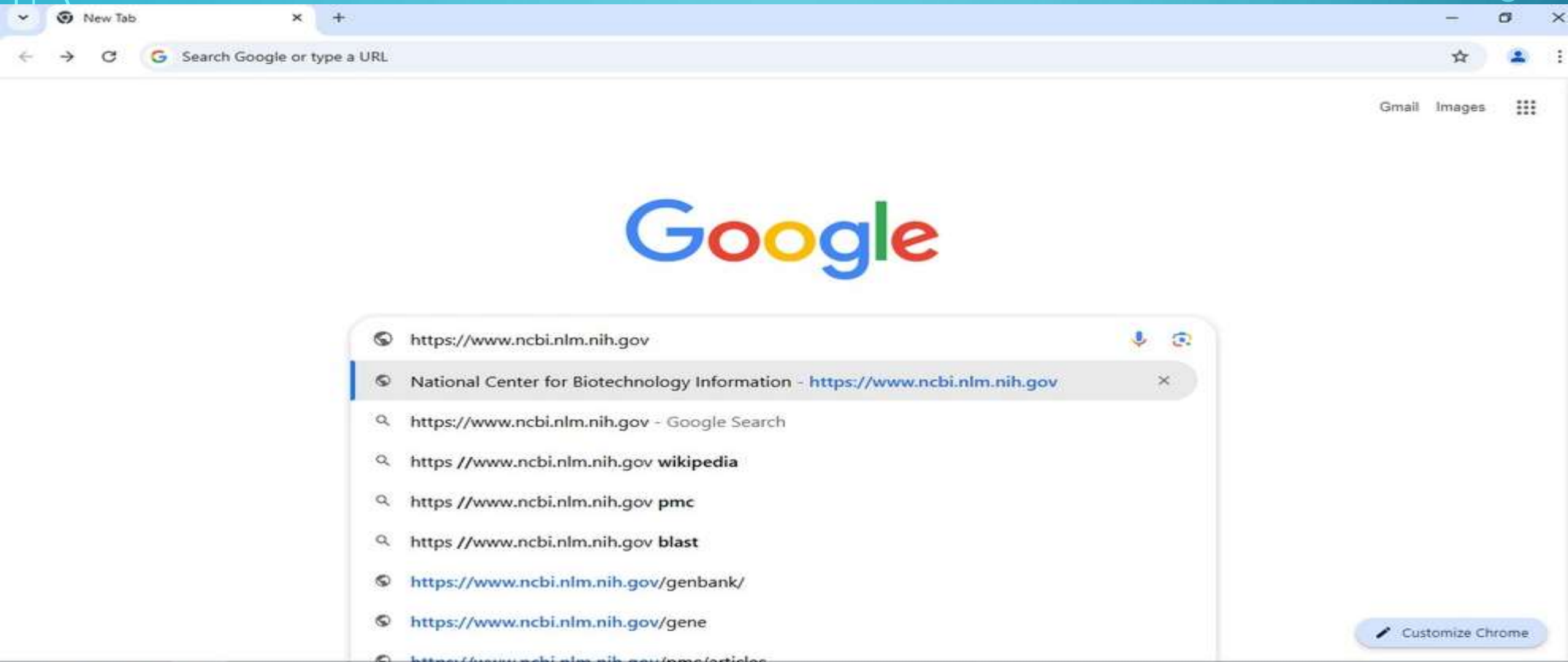
معرفی ژن ATM

The protein encoded by this gene belongs to the PI3/PI4-kinase family. This protein is an important cell cycle checkpoint kinase that phosphorylates; thus, it functions as a regulator of a wide variety of downstream proteins, including tumor suppressor proteins p53 and BRCA1, checkpoint kinase CHK2, checkpoint proteins RAD17 and RAD9, and DNA repair protein NBS1. This protein and the closely related kinase ATR are thought to be master controllers of cell cycle checkpoint signaling pathways that are required for cell response to DNA damage and for genome stability. Mutations in this gene are associated with ataxia telangiectasia, an autosomal recessive disorder.

پروتئین کدگذاری شده توسط این ژن متعلق به خانواده PI3/PI4-kinase است. این پروتئین یک کیناز بازرسی چرخه سلولی مهم است که فسفریله می شود. بنابراین، به عنوان تنظیم کننده طیف گسترده ای از پروتئین های پایین دستی، از جمله پروتئین های سرکوب کننده تومور p53 و BRCA1، نقطه بازرسی کیناز CHK2، پروتئین های نقطه بازرسی RAD17 و RAD9، و پروتئین ترمیم DNA NBS1 عمل می کند. تصور می شود که این پروتئین و ATR کیناز نزدیک به آن، کنترل کننده های اصلی مسیرهای سیگنال دهی نقطه بازرسی چرخه سلولی هستند که برای پاسخ سلولی به آسیب DNA و پایداری ژنوم مورد نیاز هستند. جهش در این ژن با آتاکسی تلانژکتازی، یک اختلال اتوزومال مغلوب مرتبط است.

ارائه شده در اگوست 2010

مرکز ملی اطلاعات بیوتکنولوژی آمریکا : NCBI



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04 Dec 2024

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Homo sapiens (633)

Mus musculus (191)

Anopheles merus (38)

Trichomonas vaginalis G3 (37)

Choloepus didactylus (32)

All other taxa (4177)

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ATM[All Fields] AND alive[prop]

GENE

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ATM – ATM serine/threonine kinase

[Homo sapiens \(human\)](#)

Also known as: AT1, ATA, ATC, ATD, ATDC, ATE, TEL1, TELO1

Gene ID: 472

Orthologs

Genome Data Viewer

RefSeq transcripts and proteins

RefSeq Sequences



Search results

یعنی این ژن در انسان است

نام های دیگر قابل جست و جو
برای این ژن

در این صفحه وجود ژن مورد نظر (ATM) در انسان و سایر گونه‌ها را ما مشاهده میکنیم

گزینه اول مربوط به انسان و سایر موارد متعلق به سایر گونه‌ها است
گزینه انتخابی ما گزینه اول یعنی مربوط به انسان است

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Name/Gene ID	Description	Location	Aliases	MIM
☐ ATM ID: 472	ATM serine/threonine kinase [<i>Homo sapiens</i> (human)]	Chromosome 11, NC_000011.10 (108223067..108369102)	AT1, ATA, ATC, ATD, ATDC, ATE, TEL1, TELO1	607585
☐ Atm ID: 11920	ataxia telangiectasia mutated [<i>Mus musculus</i> (house mouse)]	Chromosome 9, NC_000075.7 (53348422..53448125, complement)	C030026E19Rik	
☐ Atm ID: 300711	ATM serine/threonine kinase [<i>Rattus norvegicus</i> (Norway rat)]	Chromosome 8, NC_086026.1 (62724939..62829040, complement)		
☐ ATM ID: 823975	Serine/Threonine-kinase ATM-like protein [<i>Arabidopsis thaliana</i> (thale cress)]	Chromosome 3, NC_003074.8 (17801289..17828553)	AT3G48190, ARABIDOPSIS THALIANA ATAXIA-TELANGIECTASIA MUTATED, ATATM, PIG1, ataxia-telangiectasia mutated, pcd in male gametogenesis 1	
☐ atm ID: 403064	ATM serine/threonine kinase [<i>Danio rerio</i> (zebrafish)]	Chromosome 15, NC_007126.7 (6514964..6651137, complement)		
☐ ATM ID: 100101922	ATM serine/threonine kinase [<i>Sus scrofa</i> (pig)]	Chromosome 9, NC_010451.4 (36620656..36759555)		
☐ ATM ID: 479450	ATM serine/threonine kinase [<i>Canis lupus familiaris</i> (dog)]	Chromosome 5, NC_051809.1 (24211375..24326057, complement)		

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ATM AND (alive[prop]) (5108)

Gene

Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA
Nucleotide

Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA
Nucleotide

ATM ATM serine/threonine kinase [Homo sapiens]
Gene

Homo sapiens hemoglobin subunit beta (HBB), mRNA
Nucleotide

See more...

ATM ATM serine/threonine kinase [*Homo sapiens* (human)]

Gene ID: 472, updated on 3-Dec-2024

[Download Datasets](#)

Summary

- 1 Official Symbol **ATM** provided by [HGNC](#)
 - 2 Official Full Name **ATM serine/threonine kinase** provided by [HGNC](#)
Primary source [HGNC:HGNC:795](#)
See related [Ensembl:ENSG00000149311](#) [MIM:607585](#) [AllianceGenome:HGNC:795](#)
 - 3 Gene type protein coding
 - 4 RefSeq status REVIEWED
 - 5 Organism [Homo sapiens](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
 - 6 Also known as AT1; ATA; ATC; ATD; ATE; ATDC; TEL1; TELO1
- Summary** The protein encoded by this gene belongs to the PI3/PI4-kinase family. This protein is an important cell cycle checkpoint kinase that phosphorylates; thus, it functions as a regulator of a wide variety of downstream proteins, including tumor suppressor proteins p53 and BRCA1, checkpoint kinase CHK2, checkpoint proteins RAD17 and RAD9, and DNA repair protein NBS1. This protein and the closely related kinase ATR are thought to be master controllers of cell cycle checkpoint signaling pathways that are required for cell response to DNA damage and for genome stability. Mutations in this gene are associated with ataxia telangiectasia, an autosomal recessive disorder. [provided by RefSeq, Aug 2010]
- Expression** Ubiquitous expression in lymph node (RPKM 15.4), spleen (RPKM 9.5) and 25 other tissues [See more](#)
- Orthologs** [mouse](#) [all](#)
- NEW** Try the new [Gene table](#)
Try the new [Transcript table](#)

Table of contents

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[Pathways from PubChem](#)

[Interactions](#)

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[Markers, Clone Names, Homology, Gene Ontology](#)

[General protein information](#)

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Genome Browsers

1-نماد ژن

2-نام کامل ژن

3-نوع ژن

4-ارگانیسم مد نظر

5-نامهای دیگر این ژن

6-خلاصه ای راجب
این ژن

Expression Ubiquitous expression in lymph node (RPKM 15.4), spleen (RPKM 9.5) and 25 other tissues [See more](#)

Orthologs [mouse](#) [all](#)

NEW

Try the new [Gene table](#)

Try the new [Transcript table](#)

q: بازوی بلند
P: بازوی کوتاه

Genomic context

Location: 11q22.3

Exon count: 67

جایگاه قرار گیری ژن در کروموزوم
این ژن بر روی بازوی بلند کروموزوم شماره ۱۱. باند
اصلی ۲۲. زیرباند ۳ قرار دارد

See ATM in [Genome Data Viewer](#)

Annotation release	Status	Assembly	Chr	Location
RS_2024_08	current	GRCh38.p14 (GCF_000001405.40)	11	NC_000011.10 (108223067..108369102)
RS_2024_08	current	T2T-CHM13v2.0 (GCF_009914755.1)	11	NC_060935.1 (108230362..108376596)
RS_2024_09	previous assembly	GRCh37.p13 (GCF_000001405.25)	11	NC_000011.9 (108093794..108239829)

Additional links

Locus-specific Databases

Genome Browsers

Genome Data Viewer

Variation Viewer (GRCh37.p13)

Variation Viewer (GRCh38)

Ensembl

UCSC

Related information

3D structures

BioAssay by Target (List)

BioAssay by Target (Summary)

BioAssay, by Gene target

BioAssays, RNAi Target, Active

BioAssays, RNAi Target, Tested

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Conserved Domains

Chromosome 11 - NC_000011.10



ژنهای همسایه ژن مورد
پژوهش

Go to [reference sequence details](#)

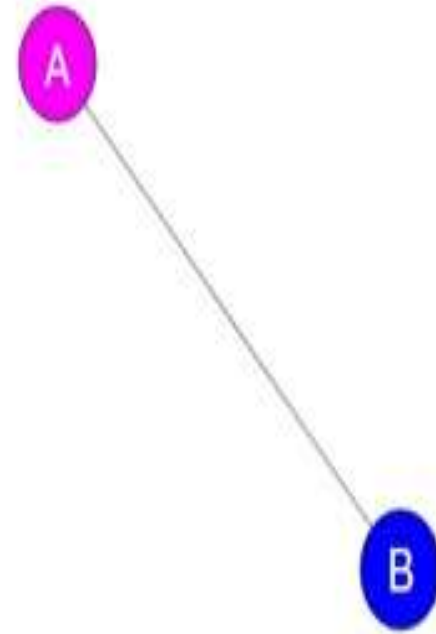
Molecular Graphic?



3D view

full-featured 3D viewer

Interactions?



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Format: ASN.1 (Cn3D) ▼

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ساختر سه بعدی پروتئین های ژن ATM

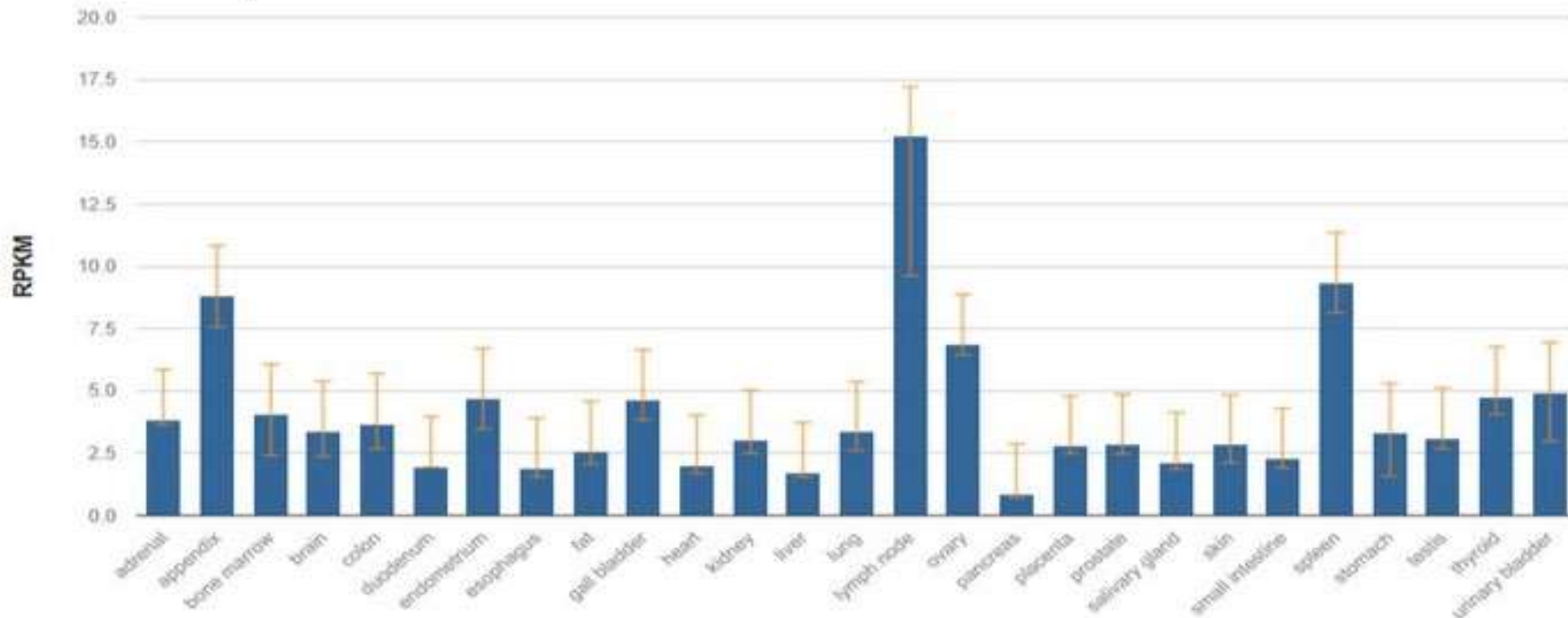
این جا اگزون ها را با خطوطی پررنگ میبینیم که شماره دسترسی هم کنار ان قرار دارد



نمودار ایجاد شده توسط ژن در ایجاد بیماری و سایر موجودات در سن های مختلف

HPA RNA-seq normal tissues

- Project title: HPA RNA-seq normal tissues
- Description: RNA-seq was performed of tissue samples from 95 human individuals representing 27 different tissues in order to determine tissue-specificity of all protein-coding genes
- BioProject: [PRJEB4337](#)
- Publication: [PMID 24309898](#)
- Analysis date: Wed Apr 4 07:08:55 2018



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ATM ATM serine/threonine kinase [Homo sapiens]
Gene

ATM AND (alive[prop]) (5108)
Gene

Homo sapiens ATM serine/threonine kinase (ATM),
transcript variant 1, mRNA
Nucleotide

Homo sapiens ATM serine/threonine kinase (ATM),
transcript variant 2, mRNA
Nucleotide

Homo sapiens hemoglobin subunit beta (HBB),
mRNA
Nucleotide

See more...

NCBI Reference Sequences (RefSeq)

NEW Try the new [Transcript table](#)

RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds. [Explain](#)

Genomic

1. NG_009830.1 RefSeqGene

Range 5001..151268

Download [GenBank](#), [FASTA](#), [Sequence Viewer \(Graphics\)](#), [LRG_135](#)

شناسه و کد اختصاصی این ژن در NCBI که با نماد NG نشان داده شده است.

mRNA and Protein(s)

1. [NM_000051.4](#) → [NP_000042.3](#) serine-protein kinase ATM isoform a

[See identical proteins and their annotated locations for NP_000042.3](#)

Status: REVIEWED

Description	Transcript Variant. This variant (2) differs in the 5' UTR compared to variant 1. Variants 1 and 2 both encode the same isoform (a).
Source sequence(s)	AP001925 , AP005718 , U26455 , U33841 , X91196
Consensus CDS	CCDS31669.1
UniProtKB/Swiss-Prot	B2RNX5 , Q15429 , Q12758 , Q13315 , Q16551 , Q93007 , Q9NP02 , Q9UCX7
UniProtKB/TrEMBL	A0AAQ5BH37
Related	ENSP00000501606.1 , ENST00000675843.1

Conserved Domains (4) [summary](#)

cd05171	PIKKc_ATM, Catalytic domain of Ataxia Telangiectasia Mutated
Location:2683 → 2962	
pfam02259	FAT, FAT domain
Location:2097 → 2489	
pfam02260	FATC, FATC domain
Location:3026 → 3055	
pfam11640	TAN, Telomere-length maintenance and DNA damage repair
Location:8 → 165	

2. [NM_001351834.2](#) → [NP_001338763.1](#) serine-protein kinase ATM isoform a

Status: REVIEWED

Description	Transcript Variant. This variant (1) represents the longest transcript and encodes the longer isoform. Variants 1 and 2 both encode the same isoform (a).
Source sequence(s)	AP001925 , AP005718 , U33841
Consensus CDS	CCDS31669.1
UniProtKB/Swiss-Prot	B2RNX5 , Q15429 , Q12758 , Q13315 , Q16551 , Q93007 , Q9NP02 , Q9UCX7
UniProtKB/TrEMBL	A0AAQ5BH37
Related	ENSP00000388058.2 , ENST00000452508.7

Conserved Domains (4) [summary](#)

این ژن ۴ واریانت دارد
که ما دو مورد از واریانتها را مورد
بررسی قرار میدهم.. واریانت
شماره ۱ و ۲

NM:
نماد کدهای توالی
نوکلئوتیدی است

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Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

NCBI Reference Sequence: NM_001351834.2

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>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

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 TCAATAATGAAATGGCTCTTATTCTATCAGTTAGAGGGTGACTTAGAAAAATAGCACAGAAGTGCCTCCAA
 TCTGTCAGCTAATTTTGGTCACTCTGACTGCAAAATGCTGCTGACTGCACTATGCAAAAGCTCTA

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ATM inhibition exploits checkpoint defects and ATM-dependent double stra [Nat Commun. 2024]

MECP2 directly interacts with RNA polymerase II to modulate transcription in human [Neuron. 2024]

REV7-p53 interaction inhibits ATM-mediated DNA damage signaling. [Cell Cycle. 2024]

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Reference sequence information ▴

RefSeq alternative splicing

See 31 reference mRNA sequence splice variants for the ATM gene.

RefSeq protein product

See the reference protein sequence for serine-protein kinase ATM isoform a (NP_001338763.1).

طرح گرافیکی قرار گرفتن اگزون ها در واریانت ۱ ژن ATM

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ATM inhibition exploits checkpoint defects and ATM-dependent double strand break re [Nat Commun. 2024]

MECP2 directly interacts with RNA polymerase II to modulate transcription in human neuron [Neuron. 2024]

REV7-p53 interaction inhibits ATM-mediated DNA damage signaling [Cell Cycle. 2024]

See all

Reference sequence information ▾

RefSeq alternative splicing

See 31 reference mRNA sequence splice variants for the ATM gene.

RefSeq protein product

See the reference protein sequence for serine-protein kinase ATM isoform a (NP_001338763.1).

More about the ATM gene ▾

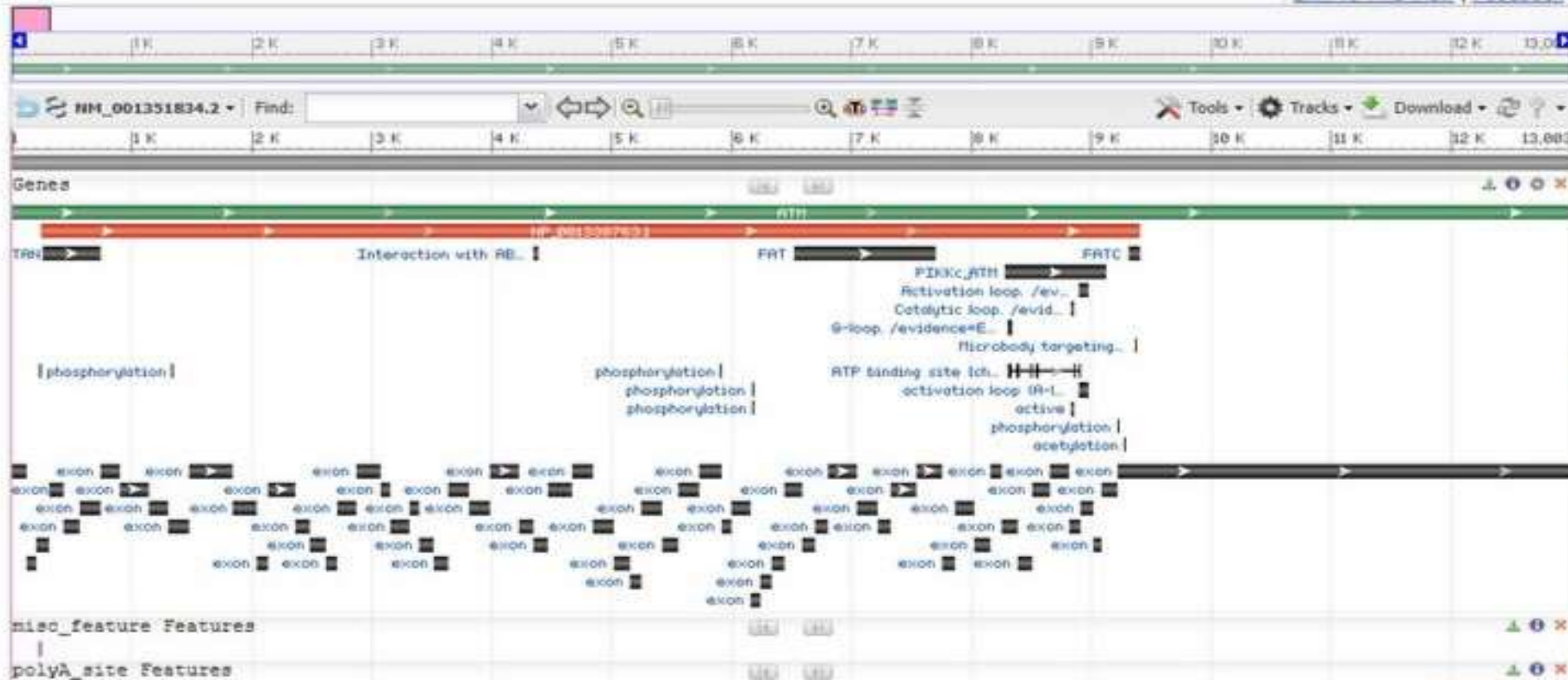
The protein encoded by this gene belongs to the PI3/PI4-kinase family. This protein is an important cell cycle checkpoint kinase that phos

Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

NCBI Reference Sequence: NM_001351834.2

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ATM inhibition exploits checkpoint defects and ATM-dependent double stra [Nat Commun. 2024]

MECP2 directly interacts with RNA polymerase II to modulate transcription in human [Neuron. 2024]

REV7-p53 interaction inhibits ATM-mediated DNA damage signaling [Cell Cycle. 2024]

See all...

Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA

NCBI Reference Sequence: NM_000051.4

[GenBank](#) [Graphics](#)

>NM_000051.4 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA

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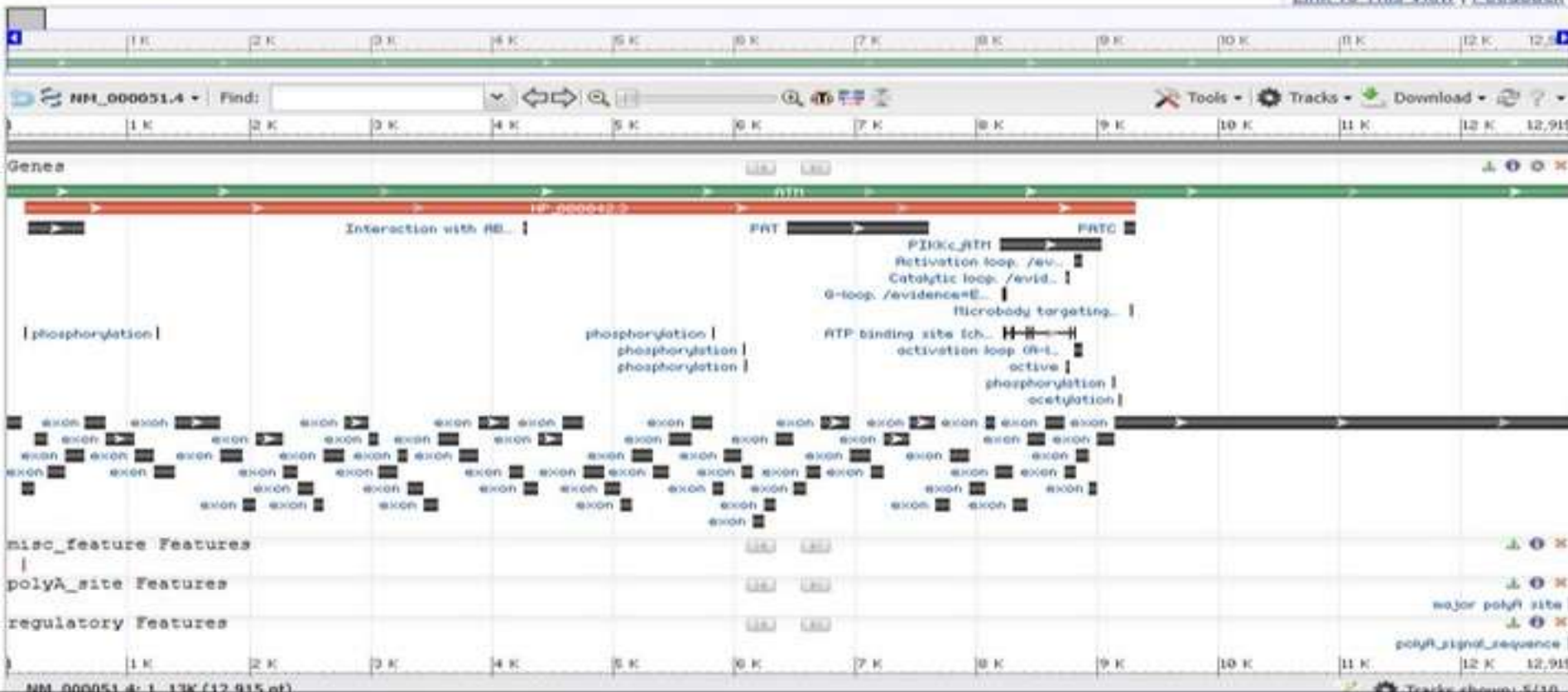

طرح گرافیکی قرار گرفتن اگزون ها در واریانت ۲ ژن ATM

Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA

NCBI Reference Sequence: NM_000051.4

[GenBank](#) [FASTA](#)

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[Show in Genome Data Viewer](#)

Articles about the ATM gene

ATM inhibition exploits checkpoint defects and ATM-dependent double strand break re [Nat Commun. 2024]

MECP2 directly interacts with RNA polymerase II to modulate transcription in human neuron [Neuron. 2024]

REV7-p53 interaction inhibits ATM-mediated DNA damage signaling [Cell Cycle. 2024]

[See all...](#)

Reference sequence information

RefSeq alternative splicing

See 31 reference mRNA sequence splice variants for the ATM gene.

RefSeq protein product

See the reference protein sequence for serine-protein kinase ATM isoform a (NP_000042.3).

More about the ATM gene

The protein encoded by this gene belongs to the PI3/PI4-kinase family. This protein is an important cell cycle checkpoint kinase that phosph...
Also Known As: AT1, ATA, ATC, ATD, ATD...

1 aggtagctgc gtggctaacc gagaaaagaa gccgtggccg cgggaggagg cgagaggagt
 61 cgggatctgc gctgcagcca ccgcccggt tgatactact ttgaccttcc gagtgcagtgc
 121 acagtgatgt gtgttctgaa attgtgaacc atgagtctag tacttaataga tctgtttatc
 181 tgctgccgtc aactagaaca tgatagagct acagaacgaa agaaagaagt tgagaaattt
 241 aagcgcctga ttcgagatcc tgaacaatt aaacatctag atcggcattc agattccaaa
 301 caaggaaaaat atttgaattg ggatgctgtt tttagatttt tacagaaata tattcagaaa
 361 gaaacagaaat gtctgagaat agcaaaacca aatgtatcag cctcaacaca agcctccagg
 421 cagaaaaaaga tgcaggaaat cagtagtttg gtcaaatact tcatcaaatg tgcaaacaga
 481 agagcaccta ggctaaaaat tcaagaactc ttaaaattata tcatggatcc agtgaaagat
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 601 tctgtgagaa aatactsgtg tgaatatctc cagcaacagt ggtagaatt gttctctgtg
 661 tacttcaggc tctatctgaa accttcacaa gatgttcata gatttttagt ggctagaata
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 1381 ccttggctac agattgcaac ccaatttaata tcaaaagtac ctgcaagttt acctaaactgt
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 1981 attcttgtga gtctcactat gaaaaactgt aaagctgcaa tgaatttttt ccaaaagcgtg
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 2101 ctatttcttc agacaacttt tgacaagatg gactttttta ccattgtgag agaattggtg

10741 ggcaaatgt tccaggacag ctacagcate agctcacata ttcaactctc tggtttttca
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 11281 tcatataaga taaacatcag ataaaaagcc acctgaaagt aaaactactg actcgtgtat
 11341 tagtgagtat aatctcttct ccctccttag gaaatgttc atcccagctg cggagattaa
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 12841 actattgaat gtattacttt actgttacct gaatttatta taaagtgttt ttgaataaat
 12901 aattctaaaa gcata

توالی نوکلئوتیدی واریانت ۱

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61 cgggatctgc gctgcagcca ccgcccgggt tgatactact ttgaccttcc gagtgcagtg
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12901 aaattatcta ttttctatag attttagtao tattgaatgt attactttac tgttaactga
12961 atttattata aagtgtttt gaataaataa ttctaaaagc ata

توالی نوکلئوتیدی واریانت ۲



برای مقایسه توالی های نوکلئوتیدی دو واریانت ژن ATM و بررسی میزان شباهت این دو واریانت از ابزار Nucleotide BLAST استفاده میکنیم.

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

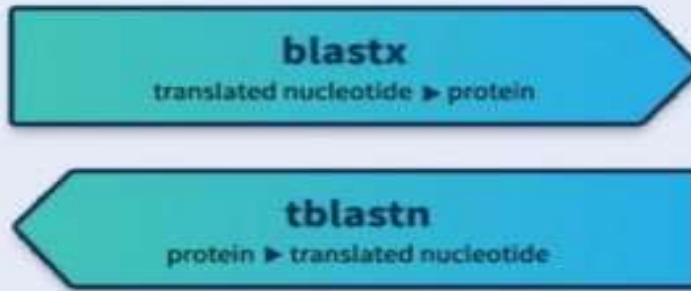
[Learn more](#)

NEWS

Non-interactive searches of nt switch to core_nt
Starting late September 2024 all non-interactive WebBLAST and PrimerBLAST searches of "nt" will
Tue, 24 Sep 2024

[More BLAST news...](#)

Web BLAST





blastn

blastp

blastx

tblastn

tblastx

Align Sequences Nucleotide BLAST

BLASTN programs search nucleotide subjects using a nucleotide query sequence

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) ? Clear

NM_001351834

Query subrange ?

From

To

Or, upload file

Choose File No file chosen ?

Job Title

NM_001351834:Homo sapiens ATM serine/threonine...

Enter a descriptive title for your BLAST search ?



Align two or more sequences ?

Enter Subject Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) ? Clear

NM_000051

Subject subrange ?

From

To

کد توالی نوکلئوتیدی (NM) را در این دو کادر وارد میکنیم.

توالی نوکلئوتیدی هر واریانت که مد نظر ما است را در این دو کادر قرار میدهیم.

نکته: واریانتی که بلندتر است را در کادر اول قرار میدهیم.

هر واریانت را میتوان ب صورت تکی بلاست انجام داد ما هر دو واریانت را باهم بلاست انجام میدهیم.

زمانی که تیک این گزینه را میزنیم دو کادر مثل تصویر به ما نشان میدهد و ما میتوانیم بلاست برای دو واریانت را انجام دهیم اما زمانی که این تیک برداشته شود به ما فقط یک کادر نشان میدهد که برای بلاست برای یک واریانت است.

Database

☒ Standard databases (nr etc.) ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus ☐ Experimental databases

Core nucleotide database (core nt) ?

Organism

Optional

Enter organism name or id—completions will be suggested ☐ exclude [Add organism](#)

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

[YouTube](#) Create custom database

Enter an Entrez query to limit search ?

Program Selection

Optimize for

- ☒ Highly similar sequences (megablast)
☐ More dissimilar sequences (discontiguous megablast)
☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm ?

1- با انتخاب این گزینه نتیجه بلاست در صفحه جدید باز میشود
2- این گزینه را انتخاب کرده و منتظر نتیجه میمانیم

2

BLAST

Search database core_nt using Megablast (Optimize for highly similar sequences)

1 ☐ Show results in a new window

+ Algorithm parameters

نتیجه بلاست (BLAST) واریانت های ژن ATM

Job Title: NM_001351834:Homo sapiens ATM serine/threonine...

RID: N8XDXM4Z114 Search expires on 12-08 23:20 pm [Download All](#)

Program: Blast 2 sequences [Citation](#)

Query ID: NM_001351834.2 (nucleic acid)

Query Descr: Homo sapiens ATM serine/threonine kinase (ATM), transc ...

Query Length: 13003

Subject ID: NM_000051.4 (nucleic acid)

Subject Descr: Homo sapiens ATM serine/threonine kinase (ATM), transc ...

Subject Length: 12915

Other reports: [MSA viewer](#)

Filter Results

Percent Identity: to E value: to Query Coverage: to

[Filter](#) [Reset](#)

Descriptions Graphic Summary Alignments Dot Plot

Sequences producing significant alignments

Download Select columns Show 100

☒ select all 1 sequences selected

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒ Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA	Homo sapiens	23630	24260	99%	0.0	100.00%	12915	NM_000051.4

عدد Score: 23630 که کیفیت هم ترازی را نشان می دهد
مقدار E-value صفر است: هم ترازی معنادار است
درصد تطابق بین 2 توالی 100% است

Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA

Sequence ID: [NM_000051.4](#) Length: 12915 Number of Matches: 4Range 1: 120 to 12915 [GenBank](#) [Graphics](#)▾ [Next Match](#) ▴ [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
23630 bits(12796)	0.0	12796/12796(100%)	0/12796(0%)	Plus/Plus
Query 208	1	ACAGTGATGTGTGTTCTGAAATTGTGAACCATGAGTCTAGTACTTAATGATCTGCTTAT	267	
Sbjct 120	2	ACAGTGATGTGTGTTCTGAAATTGTGAACCATGAGTCTAGTACTTAATGATCTGCTTAT	179	
Query 268		CTGCTGCCGTCAACTAGAACATGATAGAGCTACAGAACGAAAGAAAGAAGTTGAGAAATT	327	
Sbjct 180		CTGCTGCCGTCAACTAGAACATGATAGAGCTACAGAACGAAAGAAAGAAGTTGAGAAATT	239	
Query 328		TAAGCGCCTGATTCGAGATCCTGAAACAATTAAACATCTAGATCGGCATTGAGATTCCAA	387	
Sbjct 240		TAAGCGCCTGATTCGAGATCCTGAAACAATTAAACATCTAGATCGGCATTGAGATTCCAA	299	
Query 388		ACAAGGAAAATATTTGAATTGGGATGCTGTTTTAGATTTTACAGAAATATATTCAGAA	447	
Sbjct 300		ACAAGGAAAATATTTGAATTGGGATGCTGTTTTAGATTTTACAGAAATATATTCAGAA	359	
Query 448		AGAAACAGAATGTCTGAGAATAGCAAAACCAAATGTATCAGCCTCAACACAAGCCTCCAG	507	
Sbjct 360		AGAAACAGAATGTCTGAGAATAGCAAAACCAAATGTATCAGCCTCAACACAAGCCTCCAG	419	
Query 508		GCAGAAAAAGATGCAGGAAATCAGTAGTTTGGTCAAATACTTCATCAAATGTGCAAACAG	567	
Sbjct 420		GCAGAAAAAGATGCAGGAAATCAGTAGTTTGGTCAAATACTTCATCAAATGTGCAAACAG	479	
Query 568		AAGAGCACCTAGGCTAAAATGTCAAGAACTCTTAAATTATATCATGGATACAGTGAAAGA	627	
Sbjct 480		AAGAGCACCTAGGCTAAAATGTCAAGAACTCTTAAATTATATCATGGATACAGTGAAAGA	539	
Query 628		TTCATCTAATGGTGCTATTTACGGAGCTGATTGTAGCAACATACTACTCAAAGACATTCT	687	

Related Information

[Gene](#) - associated gene details
[PubChem BioAssay](#) - bioactivity screening
[Genome Data Viewer](#) - aligned genomic context

1: واریانت 1
2: واریانت 2

واریانت 1 از باز 208 با باز 120 واریانت 2 تطابق دارد

در بین این دو واریانت هیچ Gaps یا فاصله وجود ندارد و درصد تطابق آنها ۱۰۰٪ است.

Query	628	TTCATCTAATGGTGCTATTTACGGAGCTGATTGTAGCAACATACTACTCAAAGACATTCT	687
Sbjct	540	TTCATCTAATGGTGCTATTTACGGAGCTGATTGTAGCAACATACTACTCAAAGACATTCT	599
Query	688	TTCTGTGAGAAAATACTGGTGTGAAATATCTCAGCAACAGTGGTTAGAATTGTTCTCTGT	747
Sbjct	600	TTCTGTGAGAAAATACTGGTGTGAAATATCTCAGCAACAGTGGTTAGAATTGTTCTCTGT	659
Query	748	GTACTTCAGGCTCTATCTGAAACCTTCACAAGATGTTCATAGAGTTTTAGTGGCTAGAAT	807
Sbjct	660	GTACTTCAGGCTCTATCTGAAACCTTCACAAGATGTTCATAGAGTTTTAGTGGCTAGAAT	719
Query	808	AATTCATGCTGTTACCAAAGGATGCTGTTCTCAGACTGACGGATTAAATTCCAAATTTTT	867
Sbjct	720	AATTCATGCTGTTACCAAAGGATGCTGTTCTCAGACTGACGGATTAAATTCCAAATTTTT	779
Query	868	GGACtttttttCCAAGGCTATTCAAGTGTGCGAGACAAGAAAAGAGCTCTTCAGGTCTAAA	927
Sbjct	780	GGACTTTTTTCCAAGGCTATTCAAGTGTGCGAGACAAGAAAAGAGCTCTTCAGGTCTAAA	839
Query	928	TCATATCTTAGCAGCTCTTACTATCTTCCTCAAGACTTTGGCTGTCAACTTTCGAATTCG	987
Sbjct	840	TCATATCTTAGCAGCTCTTACTATCTTCCTCAAGACTTTGGCTGTCAACTTTCGAATTCG	899
Query	988	AGTGTGTGAATTAGGAGATGAAATCTTCCCACTTTGCTTTATATTTGGACTCAACATAG	1047
Sbjct	900	AGTGTGTGAATTAGGAGATGAAATCTTCCCACTTTGCTTTATATTTGGACTCAACATAG	959
Query	1048	GCTTAATGATTCTTTAAAAGAAGTCATTATTGAATTATTTCAACTGCAAATTTATATCCA	1107
Sbjct	960	GCTTAATGATTCTTTAAAAGAAGTCATTATTGAATTATTTCAACTGCAAATTTATATCCA	1019
Query	1108	TCATCCGAAAGGAGCCAAAACCCAAGAAAAAGGTGCTTATGAATCAACAAAATGGAGAAG	1167
Sbjct	1020	TCATCCGAAAGGAGCCAAAACCCAAGAAAAAGGTGCTTATGAATCAACAAAATGGAGAAG	1079
Query	1168	TATTTTATACAACTTATATGATCTGCTAGTGAATGAGATAAGTCATATAGGAAGTAGAGG	1227
Sbjct	1080	TATTTTATACAACTTATATGATCTGCTAGTGAATGAGATAAGTCATATAGGAAGTAGAGG	1139
Query	1228	AAAGTATTCTTCAGGATTTGTAATATTGCCGTCAAAGAAAATTTGATTGAATTGATGGC	1287

نتیجه BLAST واریانت ها



Sbjct	1080	TATTTTATACAACCTTATATGATCTGCTAGTGAATGAGATAAGTCATATAGGAAGTAGAGG	1139
Query	1228	AAAGTATTCTTCAGGATTTTCGTAATATTGCCGTCAAAGAAAATTTGATTGAATTGATGGC	1287
Sbjct	1140	AAAGTATTCTTCAGGATTTTCGTAATATTGCCGTCAAAGAAAATTTGATTGAATTGATGGC	1199
Query	1288	AGATATCTGTCACCAGGTTTTTAATGAAGATACCAGATCCTTGGAGATTTCTCAATCTTA	1347
Sbjct	1200	AGATATCTGTCACCAGGTTTTTAATGAAGATACCAGATCCTTGGAGATTTCTCAATCTTA	1259
Query	1348	CACTACTACACAAAGAGAATCTAGTGATTACAGTGTCCTTGCAAAGGAAGAAAATAGA	1407
Sbjct	1260	CACTACTACACAAAGAGAATCTAGTGATTACAGTGTCCTTGCAAAGGAAGAAAATAGA	1319
Query	1408	ACTAGGCTGGGAAGTAATAAAAGATCACCTTCAGAAGTCACAGAATGATTTTGATCTTGT	1467
Sbjct	1320	ACTAGGCTGGGAAGTAATAAAAGATCACCTTCAGAAGTCACAGAATGATTTTGATCTTGT	1379
Query	1468	GCCTTGGCTACAGATTGCAACCCAATTAATATCAAAGTATCCTGCAAGTTTACCTAACTG	1527
Sbjct	1380	GCCTTGGCTACAGATTGCAACCCAATTAATATCAAAGTATCCTGCAAGTTTACCTAACTG	1439
Query	1528	TGAGCTGTCTCCATTACTGATGATACTATCTCAGCTTCTACCCCAACAGCGACATGGGGA	1587
Sbjct	1440	TGAGCTGTCTCCATTACTGATGATACTATCTCAGCTTCTACCCCAACAGCGACATGGGGA	1499
Query	1588	ACGTACACCATATGTGTTACGATGCCTTACGGAAGTTGCATTGTGTCAAGACAAGAGGTC	1647
Sbjct	1500	ACGTACACCATATGTGTTACGATGCCTTACGGAAGTTGCATTGTGTCAAGACAAGAGGTC	1559
Query	1648	AAACCTAGAAAGCTCACAAAAGTCAGATTTATTAATACTCTGGAATAAAATTTGGTGTAT	1707
Sbjct	1560	AAACCTAGAAAGCTCACAAAAGTCAGATTTATTAATACTCTGGAATAAAATTTGGTGTAT	1619
Query	1708	TACCTTTTCGTGGTATAAGTTCTGAGCAAATACAAGCTGAAAACCTTGGCTTACTTGGAGC	1767
Sbjct	1620	TACCTTTTCGTGGTATAAGTTCTGAGCAAATACAAGCTGAAAACCTTGGCTTACTTGGAGC	1679
Query	1768	CATAATTCAGGGTAGTTTAGTTGAGGTTGACAGAGAATTCTGGAAGTTATTTACTGGGTC	1827
Sbjct	1680	CATAATTCAGGGTAGTTTAGTTGAGGTTGACAGAGAATTCTGGAAGTTATTTACTGGGTC	1739

نتیجہ BLAST واریانت ها



Query	628	TTCATCTAATGGTGTCTATTTACGGAGCTGATTGTAGCAACATACTACTCAAAGACATTCT	687
Sbjct	540	TTCATCTAATGGTGTCTATTTACGGAGCTGATTGTAGCAACATACTACTCAAAGACATTCT	599
Query	688	TTCTGTGAGAAAATACTGGTGTGAAATATCTCAGCAACAGTGGTTAGAATTGTTCTCTGT	747
Sbjct	600	TTCTGTGAGAAAATACTGGTGTGAAATATCTCAGCAACAGTGGTTAGAATTGTTCTCTGT	659
Query	748	GTACTTCAGGCTCTATCTGAAACCTTCACAAGATGTTCATAGAGTTTTAGTGGCTAGAAAT	807
Sbjct	660	GTACTTCAGGCTCTATCTGAAACCTTCACAAGATGTTCATAGAGTTTTAGTGGCTAGAAAT	719
Query	808	AATTCATGCTGTTACCAAAGGATGCTGTTCTCAGACTGACGGATTAAATTCCAAATTTTT	867
Sbjct	720	AATTCATGCTGTTACCAAAGGATGCTGTTCTCAGACTGACGGATTAAATTCCAAATTTTT	779
Query	868	GGACtttttttCCAAGGCTATTCAGTGTGCGAGACAAGAAAAGAGCTCTTCAGGTCTAAA	927
Sbjct	780	GGACTTTTTTCCAAGGCTATTCAGTGTGCGAGACAAGAAAAGAGCTCTTCAGGTCTAAA	839
Query	928	TCATATCTTAGCAGCTCTTACTATCTTCCTCAAGACTTTGGCTGTCAACTTTTGAATTTCG	987
Sbjct	840	TCATATCTTAGCAGCTCTTACTATCTTCCTCAAGACTTTGGCTGTCAACTTTTGAATTTCG	899
Query	988	AGTGTGTGAATTAGGAGATGAAATTCTTCCCACTTTGCTTTATATTTGGACTCAACATAG	1047
Sbjct	900	AGTGTGTGAATTAGGAGATGAAATTCTTCCCACTTTGCTTTATATTTGGACTCAACATAG	959
Query	1048	GCTTAATGATTCTTTAAAAGAAGTCATTATTGAATTATTTCAACTGCAAATTTATATCCA	1107
Sbjct	960	GCTTAATGATTCTTTAAAAGAAGTCATTATTGAATTATTTCAACTGCAAATTTATATCCA	1019
Query	1108	TCATCCGAAAGGAGCCAAAACCCAAGAAAAAGGTGCTTATGAATCAACAAAATGGAGAAG	1167
Sbjct	1020	TCATCCGAAAGGAGCCAAAACCCAAGAAAAAGGTGCTTATGAATCAACAAAATGGAGAAG	1079
Query	1168	TATTTTATACAACTTATATGATCTGCTAGTGAATGAGATAAGTCATATAGGAAGTAGAGG	1227
Sbjct	1080	TATTTTATACAACTTATATGATCTGCTAGTGAATGAGATAAGTCATATAGGAAGTAGAGG	1139
Query	1228	AAAGTATTCTTCAGGATTCGTAATATTGCCGTCAAAGAAAATTTGATTGAATTGATGGC	1287

نتیجه BLAST واریانت ها



Query	1768	CATAATTCAGGGTAGTTTAGTTGAGGTTGACAGAGAATTCTGGAAGTTATTTACTGGGTC	1827
Sbjct	1680	CATAATTCAGGGTAGTTTAGTTGAGGTTGACAGAGAATTCTGGAAGTTATTTACTGGGTC	1739
Query	1828	AGCCTGCAGACCTTCATGTCTGCAGTATGCTGTTTGACTTTGGCACTGACCACCAGTAT	1887
Sbjct	1740	AGCCTGCAGACCTTCATGTCTGCAGTATGCTGTTTGACTTTGGCACTGACCACCAGTAT	1799
Query	1888	AGTTCCAGGAACGGTAAAAATGGGAATAGAGCAAAATATGTGTGAAGTAAATAGAAGCTT	1947
Sbjct	1800	AGTTCCAGGAACGGTAAAAATGGGAATAGAGCAAAATATGTGTGAAGTAAATAGAAGCTT	1859
Query	1948	TTCTTTAAAGGAATCAATAATGAAATGGCTCTTATTCTATCAGTTAGAGGGTGACTTAGA	2007
Sbjct	1860	TTCTTTAAAGGAATCAATAATGAAATGGCTCTTATTCTATCAGTTAGAGGGTGACTTAGA	1919
Query	2008	AAATAGCACAGAAGTGCCTCCAATTCTTCACAGTAATTTTCCTCATCTTGACTGGAGAA	2067
Sbjct	1920	AAATAGCACAGAAGTGCCTCCAATTCTTCACAGTAATTTTCCTCATCTTGACTGGAGAA	1979
Query	2068	AATTCTTGAGTCTCACTATGAAAAACTGTAAAGCTGCAATGAATTTTTTCCAAAGCGT	2127
Sbjct	1980	AATTCTTGAGTCTCACTATGAAAAACTGTAAAGCTGCAATGAATTTTTTCCAAAGCGT	2039
Query	2128	GCCAGAATGTGAACACCACCAAAAAGATAAAGAAGAACTTTTCATTCTCAGAAGTAGAAGA	2187
Sbjct	2040	GCCAGAATGTGAACACCACCAAAAAGATAAAGAAGAACTTTTCATTCTCAGAAGTAGAAGA	2099
Query	2188	ACTATTTCTTCAGACAACCTTTTGACAAGATGGACTTTTTTAACCATTGTGAGAGAATGTGG	2247
Sbjct	2100	ACTATTTCTTCAGACAACCTTTTGACAAGATGGACTTTTTTAACCATTGTGAGAGAATGTGG	2159
Query	2248	TATAGAAAAGCACCAGTCCAGTATTGGCTTCTCTGTCCACCAGAATCTCAAGGAATCACT	2307
Sbjct	2160	TATAGAAAAGCACCAGTCCAGTATTGGCTTCTCTGTCCACCAGAATCTCAAGGAATCACT	2219
Query	2308	GGATCGCTGTCTTCTGGGATTATCAGAACAGCTTCTGAATAATTACTCATCTGAGATTAC	2367
Sbjct	2220	GGATCGCTGTCTTCTGGGATTATCAGAACAGCTTCTGAATAATTACTCATCTGAGATTAC	2279
Query	2368	AAATTCAGAAACTCTTGTCGGTGTTACGTCCTTTGGTGGGTGTCCTTGGCTGCTACTG	2427

نتیجه BLAST واریانت ها



Sbjct	2760	CGAACCTGGAGAGAGCCAAAGTACCATAGGTGCCATTAATCCTTTAGCTGAAGAATATCT	2819
Query	2908	GTCAAAGCAAGATCTACTTTTCTTAGACATGCTCAAGTTCTTGTGTTTGTGTGTAACCTAC	2967
Sbjct	2820	GTCAAAGCAAGATCTACTTTTCTTAGACATGCTCAAGTTCTTGTGTTTGTGTGTAACCTAC	2879
Query	2968	TGCTCAGACCAATACTGTGTCTTTAGGGCAGCTGATATTCGGAGGAAATTGTTAATGTT	3027
Sbjct	2880	TGCTCAGACCAATACTGTGTCTTTAGGGCAGCTGATATTCGGAGGAAATTGTTAATGTT	2939
Query	3028	AATTGATTCTAGCACGCTAGAACCTACCAAATCCCTCCACCTGCATATGTATCTAATGCT	3087
Sbjct	2940	AATTGATTCTAGCACGCTAGAACCTACCAAATCCCTCCACCTGCATATGTATCTAATGCT	2999
Query	3088	TTTAAAGGAGCTTCCTGGAGAAGAGTACCCCTTGCCAATGGAAGATGTTCTTGAACCTCT	3147
Sbjct	3000	TTTAAAGGAGCTTCCTGGAGAAGAGTACCCCTTGCCAATGGAAGATGTTCTTGAACCTCT	3059
Query	3148	GAAACCACTATCCAATGTGTGTTCTTTGTATCGTCGTGACCAAGATGTTTGTAAACTAT	3207
Sbjct	3060	GAAACCACTATCCAATGTGTGTTCTTTGTATCGTCGTGACCAAGATGTTTGTAAACTAT	3119
Query	3208	TTTAAACCATGTCCTTCATGTAGTGAAAAACCTAGGTCAAAGCAATATGGACTCTGAGAA	3267
Sbjct	3120	TTTAAACCATGTCCTTCATGTAGTGAAAAACCTAGGTCAAAGCAATATGGACTCTGAGAA	3179
Query	3268	CACAAGGGATGCTCAAGGACAGTTTCTTACAGTAATTGGAGCATTTTGGCATCTAACAAA	3327
Sbjct	3180	CACAAGGGATGCTCAAGGACAGTTTCTTACAGTAATTGGAGCATTTTGGCATCTAACAAA	3239
Query	3328	GGAGAGGAAATATATATTCTCTGTAAGAATGGCCCTAGTAAATTGCCTTAAACCTTTGCT	3387
Sbjct	3240	GGAGAGGAAATATATATTCTCTGTAAGAATGGCCCTAGTAAATTGCCTTAAACCTTTGCT	3299
Query	3388	TGAGGCTGATCCTTATTCAAAATGGGCCATTCTTAATGTAATGGGAAAAGACTTTCCTGT	3447
Sbjct	3300	TGAGGCTGATCCTTATTCAAAATGGGCCATTCTTAATGTAATGGGAAAAGACTTTCCTGT	3359
Query	3448	AAATGAAGTATTTACACAATTTCTTGCTGACAATCATACCAAGTTCGCATGTTGGCTGC	3507

نتیجه BLAST واریانت ها

Query	5248	TGTTGGAAGCTGCTTGGGAGAAGTGGGTCCTATAGATTTCTCTACCATAGCTATACAACA	5307
Sbjct	5160	TGTTGGAAGCTGCTTGGGAGAAGTGGGTCCTATAGATTTCTCTACCATAGCTATACAACA	5219
Query	5308	TAGTAAAGATGCATCTTATACCAAGGCCCTTAAGTTATTTGAAGATAAAGAACTTCAGTG	5367
Sbjct	5220	TAGTAAAGATGCATCTTATACCAAGGCCCTTAAGTTATTTGAAGATAAAGAACTTCAGTG	5279
Query	5368	GACCTTCATAATGCTGACCTACCTGAATAACACACTGGTAGAAGATTGTGTCAAAGTTTCG	5427
Sbjct	5280	GACCTTCATAATGCTGACCTACCTGAATAACACACTGGTAGAAGATTGTGTCAAAGTTTCG	5339
Query	5428	ATCAGCAGCTGTTACCTGTTTGAAAAACATTTTAGCCACAAAGACTGGACATAGTTTCTG	5487
Sbjct	5340	ATCAGCAGCTGTTACCTGTTTGAAAAACATTTTAGCCACAAAGACTGGACATAGTTTCTG	5399
Query	5488	GGAGATTTATAAGATGACAACAGATCCAATGCTGGCCTATCTACAGCCTTTTAGAACATC	5547
Sbjct	5400	GGAGATTTATAAGATGACAACAGATCCAATGCTGGCCTATCTACAGCCTTTTAGAACATC	5459
Query	5548	AAGAAAAAGTTTTTAGAAGTACCCAGATTTGACAAAGAAAACCTTTTGAAGGCCTGGA	5607
Sbjct	5460	AAGAAAAAGTTTTTAGAAGTACCCAGATTTGACAAAGAAAACCTTTTGAAGGCCTGGA	5519
Query	5608	TGATATAAATCTGTGGATTCTCTAAGTGAAAATCATGACATTTGGATAAAGACACTGAC	5667
Sbjct	5520	TGATATAAATCTGTGGATTCTCTAAGTGAAAATCATGACATTTGGATAAAGACACTGAC	5579
Query	5668	TTGTGCTTTTTTGGACAGTGGAGGCACAAAATGTGAAATTCTTCAATTATTAAGCCAAT	5727
Sbjct	5580	TTGTGCTTTTTTGGACAGTGGAGGCACAAAATGTGAAATTCTTCAATTATTAAGCCAAT	5639
Query	5728	GTGTGAAGTGAAAACCTGACTTTTGTGAGACTGTACTTCCATACTTGATTCATGATATTTT	5787
Sbjct	5640	GTGTGAAGTGAAAACCTGACTTTTGTGAGACTGTACTTCCATACTTGATTCATGATATTTT	5699
Query	5788	ACTCCAAGATACAAATGAATCATGGAGAAATCTGCTTTCTACACATGTTCAAGGGATTTTT	5847
Sbjct	5700	ACTCCAAGATACAAATGAATCATGGAGAAATCTGCTTTCTACACATGTTCAAGGGATTTTT	5759
Query	5848	CACCAGCTGTCTTCGACACTTCTCGCAAACGAGCCGATCCACAACCCCTGCAAACCTTGG	5907

نتیجه BLAST واریانت ها



Query	8548	CACAGGAACGTGCCCCATTGGTGAATTTCTTGTTAAACAATGAAGATGGTGCTCATAAAAG	8607
Sbjct	8460	CACAGGAACGTGCCCCATTGGTGAATTTCTTGTTAAACAATGAAGATGGTGCTCATAAAAG	8519
Query	8608	ATACAGGCCAAATGATTTTCAGTGCCTTTTCAGTGCCAAAAGAAAATGATGGAGGTGCaaaa	8667
Sbjct	8520	ATACAGGCCAAATGATTTTCAGTGCCTTTTCAGTGCCAAAAGAAAATGATGGAGGTGC AAAA	8579
Query	8668	aaaGTCTTTTGAAGAGAAATATGAAGTCTTCATGGATGTTTGCCAAAATTTTCAACCAGT	8727
Sbjct	8580	AAAGTCTTTTGAAGAGAAATATGAAGTCTTCATGGATGTTTGCCAAAATTTTCAACCAGT	8639
Query	8728	TTTCCGTTACTTCTGCATGGAAAAATTC TTGGATCCAGCTATTTGGTTTGAGAAGCGATT	8787
Sbjct	8640	TTTCCGTTACTTCTGCATGGAAAAATTC TTGGATCCAGCTATTTGGTTTGAGAAGCGATT	8699
Query	8788	GGCTTATACGCGCAGTGTAGCTACTTCTTCTATTGTTGGTTACATACTTGGACTTGGTGA	8847
Sbjct	8700	GGCTTATACGCGCAGTGTAGCTACTTCTTCTATTGTTGGTTACATACTTGGACTTGGTGA	8759
Query	8848	TAGACATGTACAGAATATCTTGATAAATGAGCAGTCAGCAGAACTTGACATATAGATCT	8907
Sbjct	8760	TAGACATGTACAGAATATCTTGATAAATGAGCAGTCAGCAGAACTTGACATATAGATCT	8819
Query	8908	AGGTGTTGCTTTTGAACAGGGCAAAATCCTTCCTACTCCTGAGACAGTTCCTTTTAGACT	8967
Sbjct	8820	AGGTGTTGCTTTTGAACAGGGCAAAATCCTTCCTACTCCTGAGACAGTTCCTTTTAGACT	8879
Query	8968	CACCAGAGATATTGTGGATGGCATGGGCATTACGGGTGTTGAAGGTGTCTTCAGAAGATG	9027
Sbjct	8880	CACCAGAGATATTGTGGATGGCATGGGCATTACGGGTGTTGAAGGTGTCTTCAGAAGATG	8939
Query	9028	CTGTGAGAAAACCATGGAAGTGATGAGAACTCTCAGGAACTCTGTAAACCATTGTAGA	9087
Sbjct	8940	CTGTGAGAAAACCATGGAAGTGATGAGAACTCTCAGGAACTCTGTAAACCATTGTAGA	8999
Query	9088	GGTCCTTCTATATGATCCACTCTTTGACTGGACCATGAATCCTTTGAAAGCTTTGTATTT	9147
Sbjct	9000	GGTCCTTCTATATGATCCACTCTTTGACTGGACCATGAATCCTTTGAAAGCTTTGTATTT	9059
Query	9148	ACAGCAGAGGCCGGAAGATGAAACTGAGCTTACCCTACTCTGAATGCAGATGACCAAGA	9207

نتیجه BLAST واریانت ها



Sbjct	9780	 TGCTGTGGGCCAAAATCATGCCATTGCACTCCAGCCTGGGTGACAAGAGCGAACTCCAT	9839
Query	9928	CTCaaaaaaaaaaaaaaaaaaaaaCAGAAACGTATTTGGATTTTTCTAGTAAGATCACTCA	9987
Sbjct	9840	 CTCAAAAAAAAAAAAAAAAAAAAAACAGAAACGTATTTGGATTTTTCTAGTAAGATCACTCA	9899
Query	9988	GTGTTACTAAATAATGAAGTTGTTATGGAGAACAAATTTCAAAGACACAGTTAGTGTAGT	10047
Sbjct	9900	 GTGTTACTAAATAATGAAGTTGTTATGGAGAACAAATTTCAAAGACACAGTTAGTGTAGT	9959
Query	10048	TACTAttttttAAGTGTGTATTAACCTTCTCATTCTATTCTCTTTATCTTTAAGCCC	10107
Sbjct	9960	 TACTATTTTTTAAGTGTGTATTAACCTTCTCATTCTATTCTCTTTATCTTTAAGCCC	10019
Query	10108	TTCTGTACTGTCCATGTATGTTATCTTTCTGTGATAACTTCATAGATTGCCTTCTAGTTC	10167
Sbjct	10020	 TTCTGTACTGTCCATGTATGTTATCTTTCTGTGATAACTTCATAGATTGCCTTCTAGTTC	10079
Query	10168	ATGAATTCTCTTGTCAGATGTATATAATCTCTTTTACCCTATCCATTGGGCTTCTTCTTT	10227
Sbjct	10080	 ATGAATTCTCTTGTCAGATGTATATAATCTCTTTTACCCTATCCATTGGGCTTCTTCTTT	10139
Query	10228	CAGAAATTGTTTTTCATTTCTAATTATGCATCATTTTTCAGATCTCTGTTTCTTGATGTC	10287
Sbjct	10140	 CAGAAATTGTTTTTCATTTCTAATTATGCATCATTTTTCAGATCTCTGTTTCTTGATGTC	10199
Query	10288	AtttttaatgttttttaatgttttttATGTCACCTAATTATTTTAAATGTCTGTACTTGA	10347
Sbjct	10200	 ATTTTAAATGTTTTTTAATGTTTTTATGTCACCTAATTATTTTAAATGTCTGTACTTGA	10259
Query	10348	TAGACACTGTAATAGTTCTATTAAATTTAGTTCCTGCTGTTTATATCTGTTGATTTTTGT	10407
Sbjct	10260	 TAGACACTGTAATAGTTCTATTAAATTTAGTTCCTGCTGTTTATATCTGTTGATTTTTGT	10319
Query	10408	ATTTGATAGGCTGTTTCATCCAGTTTTGTCTTTTTGAAAAGTGAGTTTATTTTCAGCAAGG	10467
Sbjct	10320	 ATTTGATAGGCTGTTTCATCCAGTTTTGTCTTTTTGAAAAGTGAGTTTATTTTCAGCAAGG	10379
Query	10468	CTTTATCTATGGGAATCTTGAGTGTCTGTTTATGTCATATTTCCAGGGCTGTTGCTGCAC	10527
Sbjct	10380	 CTTTATCTATGGGAATCTTGAGTGTCTGTTTATGTCATATTTCCAGGGCTGTTGCTGCAC	10439

نتیجه BLAST واریانت ها



Sbjct	11040	TCCACCCCTCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGCCCGGCC	11099
Query	11188	TCATTCCCCTCATTCTTTGACCGTAAGGATTTCCCCTTTCTTGTAAGTTCTGCTATGTATT	11247
Sbjct	11100	TCATTCCCCTCATTCTTTGACCGTAAGGATTTCCCCTTTCTTGTAAGTTCTGCTATGTATT	11159
Query	11248	TAAAAGAATGTTTTCTACATTTTATCCAGCATTTCTCTGTGTTCTGTTGGAAGGGAAGGG	11307
Sbjct	11160	TAAAAGAATGTTTTCTACATTTTATCCAGCATTTCTCTGTGTTCTGTTGGAAGGGAAGGG	11219
Query	11308	CTTAGGTATCTAGTTTGATACATAGGTAGAAGTGGAACATTTCTCTGTCCCCCAGCTGTC	11367
Sbjct	11220	CTTAGGTATCTAGTTTGATACATAGGTAGAAGTGGAACATTTCTCTGTCCCCCAGCTGTC	11279
Query	11368	ATCATATAAGATAAACATCAGATAAAAAGCCACCTGAAAGTAAACTACTGACTCGTGTA	11427
Sbjct	11280	ATCATATAAGATAAACATCAGATAAAAAGCCACCTGAAAGTAAACTACTGACTCGTGTA	11339
Query	11428	TTAGTGAGTATAATCTCTTCTCCATCCTTAGGAAAATGTTTCATCCCAGCTGCGGAGATTA	11487
Sbjct	11340	TTAGTGAGTATAATCTCTTCTCCATCCTTAGGAAAATGTTTCATCCCAGCTGCGGAGATTA	11399
Query	11488	ACAAATGGGTGATTGAGCTTTCTCCTCGTATTTGGACCTTGAAGGTTATATAAA	11547
Sbjct	11400	ACAAATGGGTGATTGAGCTTTCTCCTCGTATTTGGACCTTGAAGGTTATATAAATTTTT	11459
Query	11548	tCTTATGAAGAGTTGGCATTCTTTTTATTGCCAATGGCAGGCACTCATTTCATATTTGAT	11607
Sbjct	11460	TCTTATGAAGAGTTGGCATTCTTTTTATTGCCAATGGCAGGCACTCATTTCATATTTGAT	11519
Query	11608	CTCCTCACCTTCCCCTCCCCTAAAACCAATCTCCAGAACTTTTTGGACTATAAATTTCTT	11667
Sbjct	11520	CTCCTCACCTTCCCCTCCCCTAAAACCAATCTCCAGAACTTTTTGGACTATAAATTTCTT	11579
Query	11668	GGTTTGACTTCTGGAGAACTGTTTCAAGATATTACTTTGCATTTCAAATTACAACTTACC	11727
Sbjct	11580	GGTTTGACTTCTGGAGAACTGTTTCAAGATATTACTTTGCATTTCAAATTACAACTTACC	11639
Query	11728	TTGGTGTATCTTTTTCTTACAAGCTGCCTAAATGAATATTTGGTATATATTGGTAGTTTT	11787
Sbjct	11640	TTGGTGTATCTTTTTCTTACAAGCTGCCTAAATGAATATTTGGTATATATTGGTAGTTTT	11699

نتیجه BLAST واریانت ها

Sbjct	12560	AAATACATGCTGAGAGAAATCAGAAATTTGGAGAGAAATAAGTTGTCCAAAGGCCAAGAGATAGT	12559
Query	12448	AAATTATAAGTACAAGTGTAAATATGGACAGTATCTAACTTGAAAAGATTTTCAGGCGAAAA	12507
Sbjct	12360	AAATTATAAGTACAAGTGTAAATATGGACAGTATCTAACTTGAAAAGATTTTCAGGCGAAAA	12419
Query	12508	GAATCTGGGGTTTGCCAGTCAGTTGCTCAAAAGGTCAATGAAAACCAAATAGTGAAGCTA	12567
Sbjct	12420	GAATCTGGGGTTTGCCAGTCAGTTGCTCAAAAGGTCAATGAAAACCAAATAGTGAAGCTA	12479
Query	12568	TCAGAGAAGCTAATAAATTATAGACTGCTTGAACAGTTGTGTCCAGATTAAGGGAGATAA	12627
Sbjct	12480	TCAGAGAAGCTAATAAATTATAGACTGCTTGAACAGTTGTGTCCAGATTAAGGGAGATAA	12539
Query	12628	TAGCTTTCCACCCCTACTTTGTGCAGGTCATACCTCCCCAAAGTGTTTACCTAATCAGTA	12687
Sbjct	12540	TAGCTTTCCACCCCTACTTTGTGCAGGTCATACCTCCCCAAAGTGTTTACCTAATCAGTA	12599
Query	12688	GGTTCACAAACTCTTGGTCATTATAGTATATGCCTAAAATGTATGCACTTAGGAATGCTA	12747
Sbjct	12600	GGTTCACAAACTCTTGGTCATTATAGTATATGCCTAAAATGTATGCACTTAGGAATGCTA	12659
Query	12748	AAAAATTTAAATATGGTCTAAAGCAAATAAAAGCAAAGAGGAAAAAATTTGGACAGCGTAA	12807
Sbjct	12660	AAAAATTTAAATATGGTCTAAAGCAAATAAAAGCAAAGAGGAAAAAATTTGGACAGCGTAA	12719
Query	12808	AGACTAGAATAGTCTTTTAAAAAGAAAGCCAGTATATTGGTTTGAAATATAGAGATGTGT	12867
Sbjct	12720	AGACTAGAATAGTCTTTTAAAAAGAAAGCCAGTATATTGGTTTGAAATATAGAGATGTGT	12779
Query	12868	CCCAATTTCAAGTATTTTAATTGCACCTTAATGAAATTATCTATTTTCTATAGATTTTAG	12927
Sbjct	12780	CCCAATTTCAAGTATTTTAATTGCACCTTAATGAAATTATCTATTTTCTATAGATTTTAG	12839
Query	12928	TACTATTGAATGTATTACTTTACTGTTACCTGAATTTATTATAAAGTGTTTTTGAATAAA	12987
Sbjct	12840	TACTATTGAATGTATTACTTTACTGTTACCTGAATTTATTATAAAGTGTTTTTGAATAAA	12899
Query	12988	TAATTCTAAAAGCATA	13003
Sbjct	12900	TAATTCTAAAAGCATA	12915

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From

To

در این کادر توالی نوکلئوتیدی مشترک
واریانت ۱ و ۲ را وارد میکنیم

Or, upload file

[Choose File](#)

No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database

☒ Standard databases (nr etc.) ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus ☐ Experimental databases

Core nucleotide database (core nt) [?](#)

Organism

Optional

☐ exclude

[Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

Exclude

Optional

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

نتیجه صحت سنجی BLAST واریانت ها

Sequences producing significant alignments										Download	Select columns	Show	100	?
☒ select all 100 sequences selected										GenBank	Graphics	Distance tree of results	MSA Viewer	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc Len	Accession					
☒	Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA	Homo sapiens	23630	23630	100%	0.0	100.00%	13003	NM_001351834.2					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X4, mRNA	Homo sapiens	23629	23629	99%	0.0	100.00%	13953	XM_011542840.4					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X6, mRNA	Homo sapiens	23629	23629	99%	0.0	100.00%	13245	XM_047426976.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X4, mRNA	Homo sapiens	23604	23604	99%	0.0	99.97%	14156	XM_054368874.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X6, mRNA	Homo sapiens	23604	23604	99%	0.0	99.97%	13244	XM_054368876.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X1, mRNA	Homo sapiens	23468	23468	99%	0.0	99.98%	13865	XM_006718843.5					
☒	Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA	Homo sapiens	23466	23466	99%	0.0	100.00%	12915	NM_000051.4					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X3, mRNA	Homo sapiens	23466	23466	99%	0.0	100.00%	13157	XM_005271562.6					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X5, mRNA	Homo sapiens	23466	23466	99%	0.0	99.99%	13733	XM_017017790.3					
☒	Homo sapiens serine/threonine kinase ATM (ATM) mRNA, complete cds	Homo sapiens	23466	23466	99%	0.0	100.00%	12915	OM777159.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	Homo sapiens	23464	23464	99%	0.0	100.00%	13706	XM_047426975.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X1, mRNA	Homo sapiens	23446	23446	99%	0.0	99.94%	14068	XM_054368871.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X5, mRNA	Homo sapiens	23444	23444	99%	0.0	99.96%	13979	XM_054368875.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X3, mRNA	Homo sapiens	23442	23442	99%	0.0	99.97%	13156	XM_054368873.1					
☒	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	Homo sapiens	23440	23440	99%	0.0	99.97%	13705	XM_054368872.1					
☒	PREDICTED: Pan paniscus ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	Pan paniscus	22978	22978	99%	0.0	99.13%	13477	XM_055094794.2					

طراحی پرایمر

Standalone and API BLAST



Download BLAST

Get BLAST databases and executables



Use BLAST API

Call BLAST from your application



Use BLAST in the cloud

Start an instance at a cloud provider

Specialized searches

SmartBLAST



Find proteins highly similar to your query

Primer-BLAST



Design primers specific to your PCR template

Global Align



Compare two sequences across their entire span (Needleman-Wunsch)

CD-search



Find conserved domains in your sequence

IgBLAST



Search immunoglobulins and T cell receptor sequences

VecScreen



Search sequences for vector contamination

CDART



Find sequences with similar conserved domain architecture

Multiple Alignment



Align sequences using domain and protein constraints

طراحی پرایمر نقاط مشترک BLAST

Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template

Primers common for a group of sequences

[Retrieve recent results](#) [Publication](#) [Tips for finding specific primers](#)

[Save search parameters](#)

[Reset page](#)

PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) ?

[Clear](#)

Range ?

[Clear](#)

```
12661 ctcccaaaag tcttacctc atcagtaggt tcacaaactc ttggtcattc tagtatatgc
12721 ctaaaatgta tgcacttagg aatgctaaaa atttaaatat ggtctaaagc aaataaaagc
12781 aaagaggaaa aactttggac agcgtaaaaga ctagaatagt cttttaaaaa gaaagccagt
12841 atatfggttt gaaatataga gatgtgtccc aatticaagt attttaattg caccttaatg
12901 aaattatcta tttt
```

Or, upload FASTA file

[Choose File](#)

No file chosen

Forward primer

From

To

Reverse primer

در این کادر توالی نوکلئوتیدی مشترک
واریانت ۱ و ۲ را وارد میکنیم

Primer Parameters

Use my own forward primer
(5'→3' on plus strand)

?

[Clear](#)

Use my own reverse primer (5'-
→3' on minus strand)

?

[Clear](#)

PCR product size

Min

70

Max

1000

of primers to return

10

Primer melting temperatures
(T_m)

Min

57.0

Opt

60.0

Max

63.0

Max T_m difference

3

?

Primer Pair Specificity Checking Parameters

Specificity check

☒ Enable search for primer pairs specific to the intended PCR template ?

Search mode

Automatic ?

Database

Refseq mRNA ?

Exclusion

☐ Exclude predicted Refseq transcripts (accession with XM, XR prefix) ☐ Exclude uncultured/environmental sample sequences ?

Organism

Homo sapiens [Add organism](#)

Enter an organism name (or organism group name such as enterobacteriaceae, rodents), taxonomy id or select from the suggestion list as you type. ?

Entrez query (optional)

?

Primer specificity stringency

Primer must have at least total mismatches to unintended targets, including

at least mismatches within the last bps at the 3' end. ?

Ignore targets that have or more mismatches to the primer. ?

Max target amplicon size

?

Allow splice variants

☐ Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input) ?

Get Primers

☐ Show results in a new window ☒ Use new graphic view ?

- 1- با انتخاب این گزینه نتیجه پرایمر در صفحه جدید باز میشود
- 2- این گزینه را انتخاب کرده و منتظر نتیجه میمانیم

+ Advanced parameters

طراحی پرایمر نقاط مشترک BLAST

Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST)

Input PCR template |cd|Query_1

Range 1 - 12796

Your PCR template is highly similar to the following sequence(s) from the search database. To increase the chance of finding specific primers, please review the list below and select all sequences (within the given sequence ranges) that are intended or allowed targets.

Select: All None Selected:2

Accession	Title	Identity	Alignment length	Seq. start	Seq. stop
☒ NM_001351834.2	Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA	100%	12796	119	12914
☐ XM_011542840.4	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X4, mRNA	100%	12795	1070	13864
☐ XM_047426976.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X6, mRNA	100%	12795	362	13156
☐ XM_054368874.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X4, mRNA	99.97%	12795	1274	14067
☐ XM_054368876.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X6, mRNA	99.97%	12795	362	13155
☒ NM_000051.4	Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 2, mRNA	100%	12707	120	12826
☐ XM_005271562.6	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X3, mRNA	100%	12707	362	13068
☐ XM_017017790.3	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X5, mRNA	100%	12707	938	13644
☐ XM_006718843.5	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X1, mRNA	100%	12707	1070	13776
☐ XM_047426975.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	100%	12706	912	13617
☐ XM_047426975.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	100%	90	119	208
☐ XM_054368875.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X5, mRNA	99.97%	12707	1185	13890
☐ XM_054368873.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X3, mRNA	99.97%	12707	362	13067
☐ XM_054368871.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X1, mRNA	99.97%	12707	1274	13979
☐ XM_054368872.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	99.97%	12706	912	13616
☐ XM_054368872.1	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA	100%	90	119	208
☐ XM_011542844.4	PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X12, mRNA	99.82%	12269	1	12247

طرح گرافیکی پرایمر طراحی شده نقاط مشترک BLAST

National Center for Biotechnology Information

Primer-BLAST » JOB ID:LSfyRO4b47PEjfmI9Ojduo7zzIij4NeVog

Primer-BLAST Results ?

Input PCR template: Id|Query_1

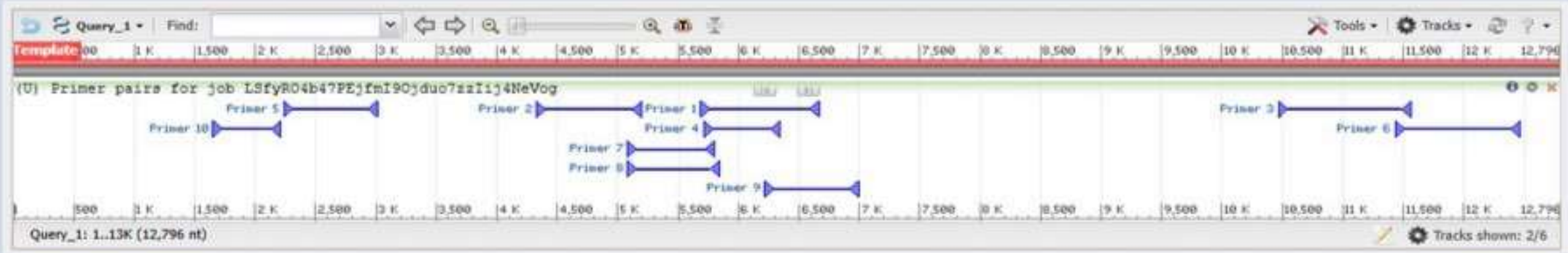
Range: 1 - 12796

Specificity of primers: Primers may **not** be specific to the input PCR template as targets were found in selected database: Refseq mRNA (Organism limited to Homo sapiens)...help on specific primers.

Other reports: [Search Summary](#)

[Edit search](#) **NEW**

— Graphical view of primer pairs



— Detailed primer reports

You can re-search for specific primers by accepting some of the unintended targets, check the box(es) next to the ones you accept and try again to re-search for specific primers

[Submit](#)

[?](#)

Download primer pairs ▾

Primer pair 1

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TCGACACTTCTCGCAAACGA	Plus	20	5742	5761	59.97	50.00	4.00	2.00
Reverse primer	AAGGCTGCGCTTACACATCT	Minus	20	6609	6590	60.04	50.00	5.00	2.00
Product length	868								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 868

Forward primer 1 TCGACACTTCTCGCAAACGA 20
Template 1648 1667

Reverse primer 1 AAGGCTGCGCTTACACATCT 20
Template 2515 2496

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 868

Forward primer 1 TCGACACTTCTCGCAAACGA 20
Template 6762 6781

Reverse primer 1 AAGGCTGCGCTTACACATCT 20
Template 7629 7610

این پرایمر مناسب نیست

طول پرایمر بین 18-25 نوکلئوتید است.
محتوای GC حدودا 40-60 درصد است.
دمای ذوب بین 55-65 درجه سانتی گراد است.
بازه عددی S.C بین 0-4 است.
بازه عددی S.3G بین 0-2 است.

Primer pair 2

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GCCATATGTGAGCAAGCAGC	Plus	20	4381	4400	59.97	55.00	6.00	3.00
Reverse primer	GCAGCTTCCAACAGCCTCTA	Minus	20	5142	5123	60.04	55.00	4.00	2.00
Product length	762								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 762

Forward primer 1 GCCATATGTGAGCAAGCAGC 20
 Template 287 306

Reverse primer 1 GCAGCTTCCAACAGCCTCTA 20
 Template 1048 1029

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 762

Forward primer 1 GCCATATGTGAGCAAGCAGC 20
 Template 5401 5420

Reverse primer 1 GCAGCTTCCAACAGCCTCTA 20
 Template 6162 6143

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 762

Forward primer 1 GCCATATGTGAGCAAGCAGC 20
 Template 4334 4353

این پرایمر مناسب نیست

Primer pair 3

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CCTTGTGCTAGTGGGCAGAA	Plus	20	10523	10542	59.96	55.00	4.00	3.00
Reverse primer	GGAGGGGAAGGTGAGGAGAT	Minus	20	11507	11488	60.03	60.00	2.00	2.00
Product length	985								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 985

```
Forward primer 1 CCTTGTGCTAGTGGGCAGAA 20
Template      6428 ..... 6447
```

```
Reverse primer 1 GGAGGGGAAGGTGAGGAGAT 20
Template      7412 ..... 7393
```

product length = 3266

```
Reverse primer 1 GGAGGGGAAGGTGAGGAGAT 20
Template      7412 ..... 7393
```

```
Reverse primer 1 GGAGGGGAAGGTGAGGAGAT 20
Template      4147 C..T..C....A.....C 4166
```

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 985

```
Forward primer 1 CCTTGTGCTAGTGGGCAGAA 20
Template      11542 ..... 11561
```

این پرایمر مناسب نیست

Primer pair 4

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TCCACAACCCCTGCAAACCTT	Plus	20	5767	5786	60.03	50.00	4.00	3.00
Reverse primer	AGGGGATTGCTGTTTCGAGG	Minus	20	6289	6270	60.04	55.00	4.00	0.00
Product length	523								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 523

Forward primer 1 TCCACAACCCCTGCAAACCTT 20
 Template 1673 1692

Reverse primer 1 AGGGGATTGCTGTTTCGAGG 20
 Template 2195 2176

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 523

Forward primer 1 TCCACAACCCCTGCAAACCTT 20
 Template 6787 6806

Reverse primer 1 AGGGGATTGCTGTTTCGAGG 20
 Template 7309 7290

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 523

Forward primer 1 TCCACAACCCCTGCAAACCTT 20

این پرایمر مناسب نیست

Primer pair 5

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GTGTCCTTGGCTGCTACTGT	Plus	20	2291	2310	59.96	55.00	3.00	3.00
Reverse primer	ATGCAGGTGGAGGGATTTGG	Minus	20	2955	2936	60.03	55.00	4.00	0.00
Product length	665								

Products on potentially unintended templates

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 665

Forward primer 1 GTGTCCTTGGCTGCTACTGT 20
 Template 3311 3330

Reverse primer 1 ATGCAGGTGGAGGGATTTGG 20
 Template 3975 3956

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 665

Forward primer 1 GTGTCCTTGGCTGCTACTGT 20
 Template 2244 2263

Reverse primer 1 ATGCAGGTGGAGGGATTTGG 20
 Template 2908 2889

☐ > XM_054368875.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X5, mRNA

product length = 665

Forward primer 1 GTGTCCTTGGCTGCTACTGT 20
 Template 3386 3405

این پرایمر مناسب نیست

Primer pair 6

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ATCTCCTCACCTTCCCCTCC	Plus	20	11488	11507	60.03	60.00	2.00	0.00
Reverse primer	CTGACTGGCAAACCCCAGAT	Minus	20	12411	12392	59.96	55.00	4.00	2.00
Product length	924								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 924

Forward primer 1 ATCTCCTCACCTTCCCCTCC 20
 Template 7393 7412

Reverse primer 1 CTGACTGGCAAACCCCAGAT 20
 Template 8316 8297

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 924

Forward primer 1 ATCTCCTCACCTTCCCCTCC 20
 Template 12507 12526

Reverse primer 1 CTGACTGGCAAACCCCAGAT 20
 Template 13430 13411

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 924

این پرایمر مناسب است

Primer pair 7

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TGGAAGCTGCTTGGGAGAAG	Plus	20	5133	5152	59.96	55.00	7.00	2.00
Reverse primer	GTGTCGAAGACAGCTGGTGA	Minus	20	5748	5729	59.97	55.00	6.00	1.00
Product length	616								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 616

Forward primer 1 TGGAAGCTGCTTGGGAGAAG 20
 Template 1039 1058

Reverse primer 1 GTGTCGAAGACAGCTGGTGA 20
 Template 1654 1635

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 616

Forward primer 1 TGGAAGCTGCTTGGGAGAAG 20
 Template 6153 6172

Reverse primer 1 GTGTCGAAGACAGCTGGTGA 20
 Template 6768 6749

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 616

این پرایمر مناسب نیست

Primer pair 8

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GGAAGCTGCTTGGGAGAAGT	Plus	20	5134	5153	59.96	55.00	7.00	1.00
Reverse primer	AAGTTTGCAGGGGTTGTGGA	Minus	20	5786	5767	60.03	50.00	4.00	0.00
Product length	653								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 653

Forward primer 1 GGAAGCTGCTTGGGAGAAGT 20
 Template 1848 1859

Reverse primer 1 AAGTTTGCAGGGGTTGTGGA 20
 Template 1692 1673

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 653

Forward primer 1 GGAAGCTGCTTGGGAGAAGT 20
 Template 6154 6173

Reverse primer 1 AAGTTTGCAGGGGTTGTGGA 20
 Template 6806 6787

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 653

Forward primer 1 GGAAGCTGCTTGGGAGAAGT 20
 Template 6887 6868

این پرایمر مناسب نیست

Primer pair 9

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CCTCGAAACAGCAATCCCCT	Plus	20	6270	6289	60.04	55.00	4.00	0.00
Reverse primer	CCCTTTCAGGGAGCTGAGTG	Minus	20	6940	6921	60.04	60.00	5.00	2.00
Product length	671								

Products on potentially unintended templates

☐ > XM_054368883.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X13, mRNA

product length = 671

Forward primer 1 CCTCGAAACAGCAATCCCCT 20
 Template 2176 2195

Reverse primer 1 CCCTTTCAGGGAGCTGAGTG 20
 Template 2846 2827

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 671

Forward primer 1 CCTCGAAACAGCAATCCCCT 20
 Template 7290 7309

Reverse primer 1 CCCTTTCAGGGAGCTGAGTG 20
 Template 7960 7941

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 671

Forward primer 1 CCTCGAAACAGCAATCCCCT 20
 Template 6223 6242

این پرایمر مناسب نیست

Primer pair 10

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GTCAGCCTGCAGACCTTCAT	Plus	20	1707	1726	60.04	55.00	6.00	2.00
Reverse primer	GCCAATACTGGACTGGTGCT	Minus	20	2157	2138	60.04	55.00	6.00	0.00
Product length	451								

Products on potentially unintended templates

☐ > XM_054368880.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X10, mRNA

product length = 451

Forward primer 1 GTCAGCCTGCAGACCTTCAT 20
 Template 2727 2746

Reverse primer 1 GCCAATACTGGACTGGTGCT 20
 Template 3177 3158

☐ > XM_054368879.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 451

Forward primer 1 GTCAGCCTGCAGACCTTCAT 20
 Template 1660 1679

Reverse primer 1 GCCAATACTGGACTGGTGCT 20
 Template 2110 2091

☐ > XM_054368875.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X5, mRNA

product length = 451

Forward primer 1 GTCAGCCTGCAGACCTTCAT 20

این پرایمر مناسب نیست

صحت سنجی پرایمر طراحی شده برای نقاط مشترک واریانت های ژن ATM در این مرحله توالی های FORWARD و REVERSE پرایمر مناسب را وارد می کنیم.

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template | Primers common for a group of sequences

Retrieve recent results | Publication | Tips for finding specific primers | Save search parameters | Reset page

PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) ?

Or, upload FASTA file No file chosen

Range ?

Forward primer From To

Reverse primer

Primer Parameters

Use my own forward primer (5'->3' on plus strand) ?

Use my own reverse primer (5'->3' on minus strand) ?

PCR product size

of primers to return

Primer melting temperatures (T_m) Max T_m difference ?

Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section ?

Exon junction span ?

Exon junction match

Minimal and maximal number of bases that must anneal to exons at the 5' or 3' side of the junction ?

>XM_054368873.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X3, mRNA

product length = 924

Forward primer	1	ATCTCCTCACCTTCCCCTCC	20
Template	11759		11778

Reverse primer	1	CTGACTGGCAAACCCAGAT	20
Template	12682		12663

>XM_054368872.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 924

Forward primer	1	ATCTCCTCACCTTCCCCTCC	20
Template	12308		12327

Reverse primer	1	CTGACTGGCAAACCCAGAT	20
Template	13231		13212

>XM_054368871.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X1, mRNA

product length = 924

Forward primer	1	ATCTCCTCACCTTCCCCTCC	20
Template	12671		12690

Reverse primer	1	CTGACTGGCAAACCCAGAT	20
Template	13594		13575

>XM_011542844.4 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X12, mRNA

product length = 924

نتیجه صحت سنجی پرایمر طراحی شده مد نظر

Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template

Primers common for a group of sequences

Retrieve recent results Publication Tips for finding specific primers

Save search parameters

Reset page

PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) ?

Clear

```
12721 ctaaaatgta tgcacttagg aatgctaaaa atttaaatat ggtctaaagc aaataaaagc
12781 aaagaggaaa aactttggac agcgtaaaga ctagaatagt ctttaaaaa gaaagccagt
12841 atattggttt gaaatataga gatgtgtccc aattcaagt atttaattg caccttaatg
12901 aaatlatcta ttttctatag attttagtac tattgaatgt attactttac tgttacctga
12961 atttattata aagtgttttt gaataaataa ttctaaaagc ata
```

Or, upload FASTA file

Choose File

No file chosen

Range ?

Clear

From

To

Forward primer

Reverse primer

توالی نوکلئوتیدی واریانت ۱ را در این
کادر وارد میکنیم

Primer Parameters

Use my own forward primer
(5'→3' on plus strand)

?

Clear

Use my own reverse primer (5'→3' on minus strand)

?

Clear

PCR product size

Min

Max

of primers to return

Primer melting temperatures

Min

Opt

Max

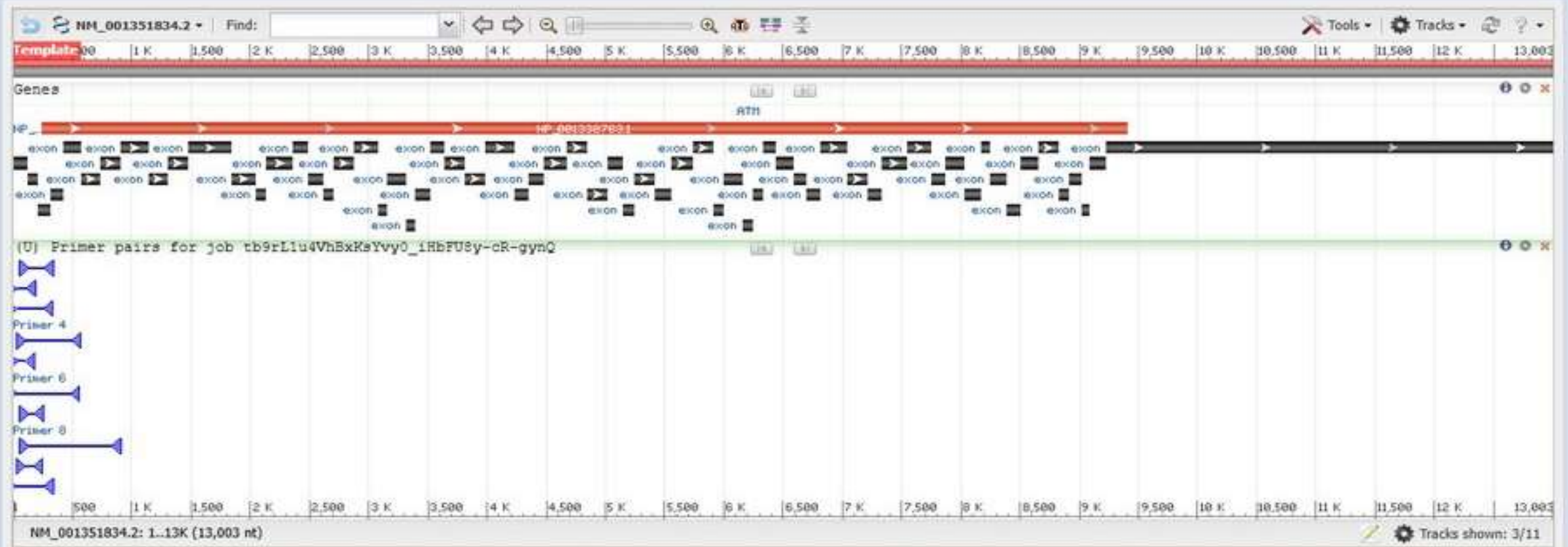
Max T_m difference

?

طرح گرافیکی پرایمرهای واریانت 1 ژن ATM

For better specificity checking, we have substituted the PCR template with the GenBank refseq record NM_001351834.2 which is identical to your input template

Graphical view of primer pairs



پرایمرهای مناسب

Primer pair 1

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CGAGTGCAGTGAGGCATACA	Plus	20	110	129	60.11	55.00	4.00	2.00
Reverse primer	TTGACGGCAGCAGATAAGCA	Minus	20	280	261	60.04	50.00	4.00	0.00
Product length	171								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 171

Forward primer 1 CGAGTGCAGTGAGGCATACA 20
Template 110 129

Reverse primer 1 TTGACGGCAGCAGATAAGCA 20
Template 280 261

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 874

Forward primer 1 CGAGTGCAGTGAGGCATACA 20
Template 110 129

Reverse primer 1 TTGACGGCAGCAGATAAGCA 20
Template 983 964

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

Primer pair 2

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TGCGTGGCTAACGGAGAAAA	Plus	20	8	27	60.25	50.00	3.00	0.00
Reverse primer	TGTATGCCTCACTGCACTCG	Minus	20	129	110	60.11	55.00	4.00	2.00
Product length	122								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 122

Forward primer 1 TGCGTGGCTAACGGAGAAAA 20
Template 8 27

Reverse primer 1 TGTATGCCTCACTGCACTCG 20
Template 129 110

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 122

Forward primer 1 TGCGTGGCTAACGGAGAAAA 20
Template 8 27

Reverse primer 1 TGTATGCCTCACTGCACTCG 20
Template 129 110

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 122

Forward primer 1 TGCGTGGCTAACGGAGAAAA 20

طول پرایمر بین 18-25 نوکلئوتید است.

محتوای GC حدوداً 40-60 درصد است.

دمای ذوب بین 55-65 درجه سانتی گراد است.

بازه عددی S.C بین 0-4 است.

بازه عددی S.3G بین 0-2 است.

Primer pair 3

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GCGTGGCTAACGGAGAAAAG	Plus	20	9	28	59.56	55.00	3.00	0.00
Reverse primer	GACGGCAGCAGATAAGCAGA	Minus	20	278	259	60.18	55.00	3.00	0.00
Product length	270								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 270

Forward primer 1 GCGTGGCTAACGGAGAAAAG 20
Template 9 28

Reverse primer 1 GACGGCAGCAGATAAGCAGA 20
Template 278 259

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 973

Forward primer 1 GCGTGGCTAACGGAGAAAAG 20
Template 9 28

Reverse primer 1 GACGGCAGCAGATAAGCAGA 20
Template 981 962

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 270

Forward primer 1 GCGTGGCTAACGGAGAAAAG 20
Template 9 28

Primer pair 5

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	ACGGAGAAAAGAAGCCGTGG	Plus	20	18	37	60.60	55.00	4.00	2.00
Reverse primer	CACTGCACTCGGAAGGTCAA	Minus	20	120	101	60.25	55.00	4.00	0.00
Product length	103								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 103

Forward primer 1 ACGGAGAAAAGAAGCCGTGG 20
Template 18 37

Reverse primer 1 CACTGCACTCGGAAGGTCAA 20
Template 120 101

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 103

Forward primer 1 ACGGAGAAAAGAAGCCGTGG 20
Template 18 37

Reverse primer 1 CACTGCACTCGGAAGGTCAA 20
Template 120 101

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 103

Forward primer 1 ACGGAGAAAAGAAGCCGTGG 20
Template 18 37

Primer pair 6

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CTGCGTGGCTAACGGAGAAA	Plus	20	7	26	60.67	55.00	4.00	0.00
Reverse primer	GAGGCTTGTGTTGAGGCTGA	Minus	20	504	485	60.25	55.00	3.00	3.00
Product length	498								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 498

Forward primer 1 CTGCGTGGCTAACGGAGAAA 20

Template 7 26

Reverse primer 1 GAGGCTTGTGTTGAGGCTGA 20

Template 504 485

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 1201

Forward primer 1 CTGCGTGGCTAACGGAGAAA 20

Template 7 26

Reverse primer 1 GAGGCTTGTGTTGAGGCTGA 20

Template 1207 1188

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 498

Forward primer 1 CTGCGTGGCTAACGGAGAAA 20

Primer pair 7

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CCGAGTGCAGTGAGGCATAC	Plus	20	109	128	60.81	60.00	4.00	2.00
Reverse primer	GTCATATCTGGGCAGCAGGG	Minus	20	199	180	60.25	60.00	4.00	0.00
Product length	91								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 91

Forward primer 1 CCGAGTGCAGTGAGGCATAC 20

Template 109 128

Reverse primer 1 GTCATATCTGGGCAGCAGGG 20

Template 199 180

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 91

Forward primer 1 CCGAGTGCAGTGAGGCATAC 20

Template 109 128

Reverse primer 1 GTCATATCTGGGCAGCAGGG 20

Template 199 180

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 91

Forward primer 1 CCGAGTGCAGTGAGGCATAC 20

Primer pair 10

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CTGCGTGGCTAACGGAGAA	Plus	19	7	25	60.08	57.89	4.00	0.00
Reverse primer	GTTGACGGCAGCAGATAAGC	Minus	20	281	262	59.62	55.00	4.00	2.00
Product length	275								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 275

```
Forward primer 1 CTGCGTGGCTAACGGAGAA 19
Template       7 ..... 25
```

```
Reverse primer 1 GTTGACGGCAGCAGATAAGC 20
Template       281 ..... 262
```

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 978

```
Forward primer 1 CTGCGTGGCTAACGGAGAA 19
Template       7 ..... 25
```

```
Reverse primer 1 GTTGACGGCAGCAGATAAGC 20
Template       984 ..... 965
```

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 275

پرایمرهای نامناسب

Primer pair 4

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CGCCGCGGTTGATACTACTT	Plus	20	82	101	60.53	55.00	6.00	0.00
Reverse primer	TTTCTGCCTGGAGGCTTGT	Minus	20	515	496	59.81	50.00	6.00	0.00
Product length	434								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 434

Forward primer 1 CGCCGCGGTTGATACTACTT 20

Template 82 101

Reverse primer 1 TTTCTGCCTGGAGGCTTGT 20

Template 515 496

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 1137

Forward primer 1 CGCCGCGGTTGATACTACTT 20

Template 82 101

Reverse primer 1 TTTCTGCCTGGAGGCTTGT 20

Template 1218 1199

☐ > XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 434

Forward primer 1 CGCCGCGGTTGATACTACTT 20

Template 82 101

Primer pair 8

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	TCCGAGTGCAGTGAGGCATA	Plus	20	108	127	60.97	55.00	4.00	2.00
Reverse primer	CCGTCAGTCTGAGAACAGCA	Minus	20	849	830	59.68	55.00	7.00	1.00
Product length	742								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 742

Forward primer 1 TCCGAGTGCAGTGAGGCATA 20

Template 108 127

Reverse primer 1 CCGTCAGTCTGAGAACAGCA 20

Template 849 830

product length = 397

Reverse primer 1 CCGTCAGTCTGAGAACAGCA 20

Template 849 830

Reverse primer 1 CCGTCAGTCTGAGAACAGCA 20

Template 453 .A.AAT.....T.... 472

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 1445

Forward primer 1 TCCGAGTGCAGTGAGGCATA 20

Template 108 127

Primer pair 9

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CGCCGCGGTTGATACTACT	Plus	19	82	100	59.93	57.89	6.00	2.00
Reverse primer	GGGCAGCAGGGTGACAATAA	Minus	20	190	171	60.32	55.00	3.00	1.00
Product length	109								

Products on intended targets

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 109

```
Forward primer 1 CGCCGCGGTTGATACTACT 19
Template      82 ..... 100
```

```
Reverse primer 1 GGGCAGCAGGGTGACAATAA 20
Template      190 ..... 171
```

Products on potentially unintended templates

☐ > XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 109

```
Forward primer 1 CGCCGCGGTTGATACTACT 19
Template      82 ..... 100
```

```
Reverse primer 1 GGGCAGCAGGGTGACAATAA 20
Template      190 ..... 171
```

☐ > XM_047426976.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 109

Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Primers for target on one template

Primers common for a group of sequences

Retrieve recent results: Publication Tips for finding specific primers

Save search parameters

Res

PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) ?

Clear

Range ?

Clear

From

To

Forward primer

Reverse primer

Or, upload FASTA file

Choose File

No file chosen

Primer Parameters

Use my own forward primer
(5'→3' on plus strand)

Use my own reverse primer (5'-
→3' on minus strand)

PCR product size

of primers to return

Primer melting temperatures

CGAGTGCAGTGAGGCATACA ?

Clear

TTGACGGCAGCAGATAAGCA ?

Clear

Min

70

Max

1000

Min

57.0

Opt

60.0

Max

63.0

Max T_m difference

3 ?

با وارد کردن توالی forward و reverse پرایمر مناسب آن را صحت سنجی میکنیم.

>XM_054368872.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 874

Forward primer	1	CGAGTGCAGTGAGGCATACA	20
Template	110		129

Reverse primer	1	TTGACGGCAGCAGATAAGCA	20
Template	983		964

>XM_047426975.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X2, mRNA

product length = 874

Forward primer	1	CGAGTGCAGTGAGGCATACA	20
Template	110		129

Reverse primer	1	TTGACGGCAGCAGATAAGCA	20
Template	983		964

>NM_001351834.2 Homo sapiens ATM serine/threonine kinase (ATM), transcript variant 1, mRNA

product length = 171

Forward primer	1	CGAGTGCAGTGAGGCATACA	20
Template	110		129

Reverse primer	1	TTGACGGCAGCAGATAAGCA	20
Template	280		261

>XM_047426978.1 PREDICTED: Homo sapiens ATM serine/threonine kinase (ATM), transcript variant X9, mRNA

product length = 171

Forward primer	1	CGAGTGCAGTGAGGCATACA	20
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نتیجه صحت سنجی پرایمر طراحی
شده مد نظر

پایان