

LOGO

Sequence analysis of protein MB21D1

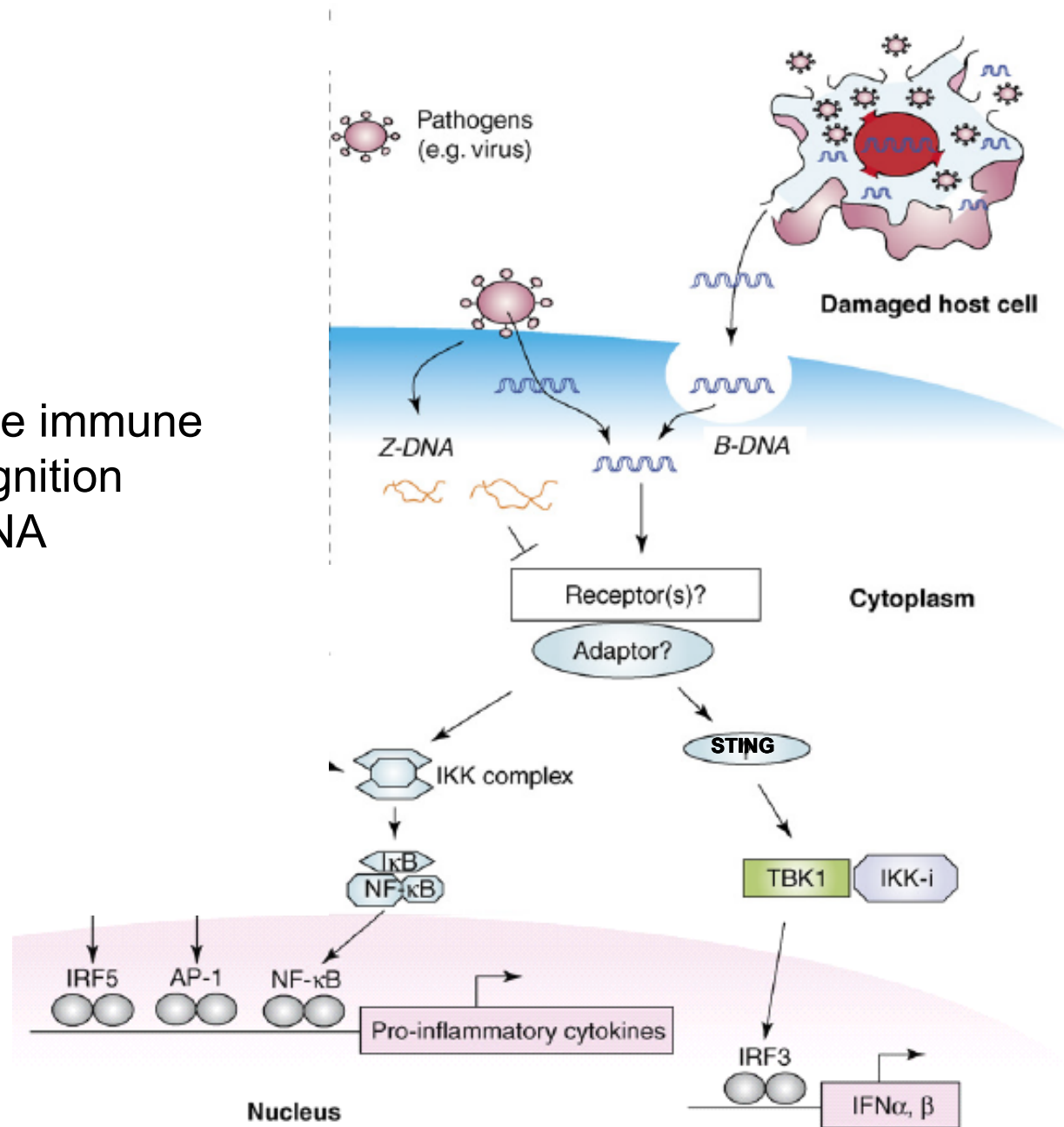
组别: **G5**

组员: 杨永康 高居一 王帅 鲁慧因

报告人: 高居一

2013-1-11

Innate immune recognition of DNA



Cyclic GMP-AMP Synthase Is a Cytosolic DNA Sensor That Activates the Type I Interferon Pathway

Lijun Sun,^{1,2*} Jiayi Wu,^{1*} Fenghe Du,^{1,2} Xiang Chen,^{1,2} Zhijian J. Chen^{1,2†}

1 MEDP~~RRRTTA~~ PRAKKPSAKR APTQPSRTRA HAESCGPQ~~RG~~ ARS~~RR~~AERDG
51 ~~DTTEKPRAPG~~ PRVHPARATE LTKDAQPSAM DAAGATARPA VRVPQQQAIL
101 ~~DP~~ELPAVREP QPPADPEAR~~K~~ VVRG~~PSHRRG~~ ARSTGQPRAP RGS~~RKE~~PD~~KL~~
151 KKVLDKLR~~LK~~ RKDISEAAET VNKVVERLLR RMQKRESEFK GVEQLNTGSY
201 YEHVKISAPN EFDVMFKLEV PRIELQ~~EYYE~~ TGAFYLVKFK RIPRGNPLSH
251 FLEGEVLSAT KMLSKFRKII KEEVKEIKDI DVSVEKEKPG SPAVTL~~LIRN~~
301 PEEISVDIIL ALESKGSWPI STKEGLPIQG WLGTKV~~RTNL~~ RREP~~FY~~LV~~PK~~
351 NAKD~~GNSFQG~~ ETWRLSFSHT EKYILNNHGI EKTCC~~SSGA~~ KCCRKECLKL
401 MKYLLEQLKK EFQELDAFCS YHVKTAIFHM WTQDPQDSQW DPRNLSSCFD
451 KLLAFFLECL RTEKLDHYFI PKFNLF~~SQEL~~ IDRKSKEFLS KKIEYERNNG
501 FPIFDKL

**Amino acid sequence of mouse MB21D1 protein (E330016A19).
Peptides identified by mass spectrometry are shown in red.**

ProtParam tool

ProtParam ([References](#) / [Documentation](#)) is a tool which allows the computation for a user entered sequence. The computed parameters include the molecular half-life, instability index, aliphatic index and grand average of hydropathicity.

Please note that you may only fill out **one** of the following fields at a time.

Enter a Swiss-Prot/TrEMBL accession number (AC) (for example **P05130**)

Or you can paste your own sequence in the box below:

```
MQPWHGKAMQRASEAGATAPKASARNARGAPMDPTESPAAPEAALPKAGKFGPARKSGSR
QKKSAPDTQERPPVRATGARAKKAPQRAQDTQPSDATSAPGAEGLEPPAAREPALSRAGS
CRQRGARCSTKPRPPPGPWVPSGLPVSAPILVRRDAAPGASKLRVLEKLSRDDIS
TAAGMVKGVVDHLLLRLKDSAFRGVLLNTGSYYEHVKISAPNEFDVMFKLEVPRIQLE
EYSNTRAYYFVKFKRNPKENPLSQFLEGEILSASKMLSKFRKIIKEEINDIKDQVIMKR
KRGGSPAVTLLISEKISVDITLALESKSSWPASTQEGLRIQNWLSAKVRKQLRLKPFYLV
PKHAKGNGFQEETWRLSFSHIEKEILNNHGKSKTCCENKEEKCCRKDCLKMKYLLEQL
KERFKDKKHLDFSSYHVKTAFHVCTQNPQDSQWDRKDLGLCFDNCVTTYFLQCLRTEKL
ENYFIFEFNLFSSNLIDKRSKEFLTKQIEYERNNEFPVFDEF
```

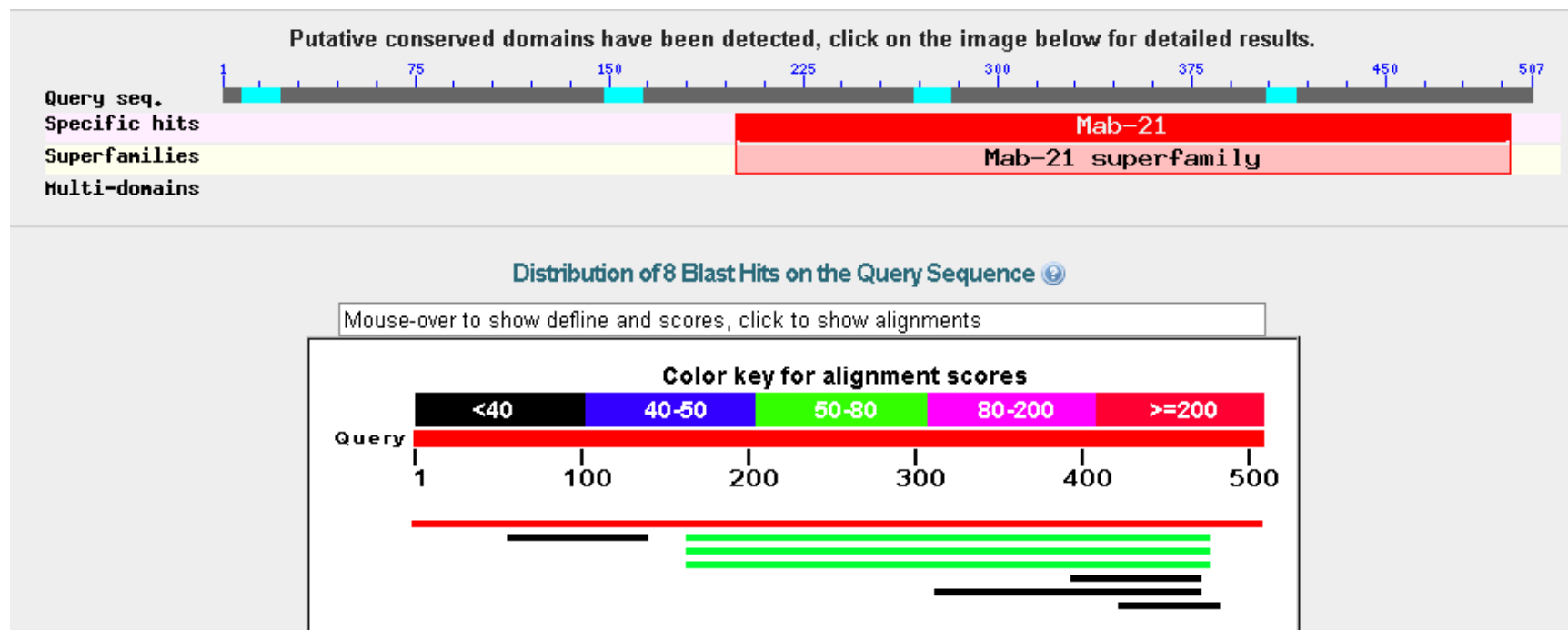
RESET

Compute parameters

Number of amino acids: 522

Molecular weight: 58814.4

Theoretical pI: 9.54



MB21D1 belongs to *Mab-21* family

UniProt > UniProtKB

Search Blast Align Retrieve ID Mapping *

Search in Protein Knowledgebase (UniProtKB) Query family:Mab-21 Search

1 - 25 of 30 results for **family:Mab-21** in UniProtKB sorted by **score** descending

nucleotidyltransferase

Search

 Keyword
 Family
 Clan
 Gene

Below are the results of your search for

- keyword = *nucleotidyltransferase*

ID	Name	Type	Description	# Aligned Sequences	Alignment length in AA
PF01909	NTP_transf_2	family	Nucleotidyltransferase domain	122	155
PF03445	DUF294	family	Putative nucleotidyltransferase DUF294	5	333
PF03726	PNPase	domain	Polyribonucleotide nucleotidyltransferase, RNA binding domain	25	90

MB21D1 may function as a nucleotidyltransferase

Alignment

Download: AA align

The **seed** alignment for this family in the [PANDIT database](#) contains **122** aligned sequences:

[CCA_ARCFU/24-133](#)
[CCA_MET1A/31-147](#)
[CCA_METTH/25-141](#)
[CCA_SULSH/20-129](#)
[CID1_SCHPO](#)
[GLND_KLEOX/61-166](#)
[GLND_RHIME/83-183](#)
[GLND_RHITR/82-178](#)
[GLND_SALTY/70-169](#)
[GLND_YIBI](#)
[O26508_METTH/2-97](#)
[O26564_METTH/17-113](#)
[O26650_METTH/160-253](#)
[O27299_METTH/109-195](#)
[O28300_ARCFU/44-135](#)
[O28312_ARCFU/97-191](#)
[O28500_ARCFU/437-531](#)
[O28587_ARCFU/3-100](#)
[O29314_ARCFU/10-94](#)
[O29641_ARCFU/1-90](#)
[O29943_ARCFU/1-101](#)
[O29980_ARCFU/3-88](#)
[O3023](#)
[O57773_PYRHO/28-110](#)
[O58140_PYRHO/3-102](#)
[O58159_PYRHO/174-266](#)
[O58160_PYRHO/23-123](#)
[O66796_AQUAE/82-173](#)
[O73987_PYRHO/19-110](#)
[O74081_PYRHO/60-152](#)
[O74326_SCHPO/68-179](#)
[O87229_9LACT/24-161](#)
[O97205_LEIMA/1065-1163](#)
[OAS1_RAT/34-140](#)
[OAS2_HUMAN/368-474](#)

The **full** alignment for this family in the [Pfam database](#) contains **4119** aligned sequences [↗](#)

There were **1** matches in SMART for your query *NTP_transf_2*. Results are sorted based on relevance.

Page 1 of 1

[NTP_transf_2](#)

Pfam domain

A small region that overlaps with a nuclear localization signal and binds to the RNA primer...

Family: *NTP_transf_2* (PF01909)

96 arch

Summary

Domain organisation

Clan

Alignments

HMM logo

Trees

Curation & model

Summary: Nucleotidyltransferase domain

Pfam includes annotations and additional family information from a range of dif

No Wikipedia article

Pfam

Interpro

This tab holds the annotation information that is stored in the Pfam database, this tab will be gradually replaced by the Wikipedia tab.

Nucleotidyltransferase domain

Add annotation

Pfam Clan

This family is a member of clan [NTP_transf](#) (CL0260), which contains the following 19 members:

[Adenyl_cycl_N](#)

[DUF925](#)

[Mmp37](#)

[UPF0157](#)

[Adenyl_transf](#)

[DZE](#)

[NTP_transf_2](#)

[DUF1693](#)

[GlnE](#)

[Nuc-transf](#)

[DUF1814](#)

[LicD](#)

[PolyA_pol](#)

[DUF2204](#)

[Mab-21](#)

[Pox_polyA_pol](#)

[DUF294](#)

[MdcG](#)

[RelA_SpoT](#)

Nucleotidyltransferase (NTase) family includes adenylate cyclase, poly[A] polymerase and DNA polymerases , and is relative to Mab-21 family.

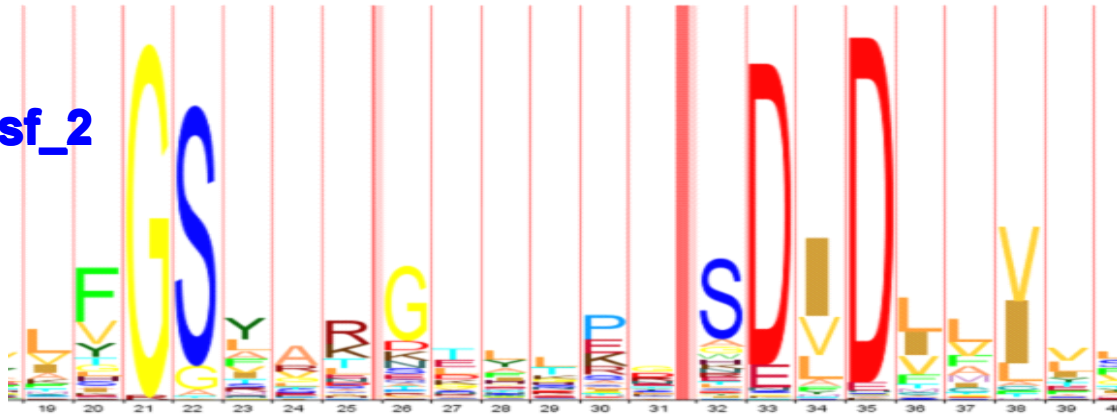
Results [Customize](#)

> Show only [reviewed \(4\)](#) ★ (UniProtKB/Swiss-Prot) or [unreviewed \(1\)](#) ★ (UniProtKB/TrEMBL) entries

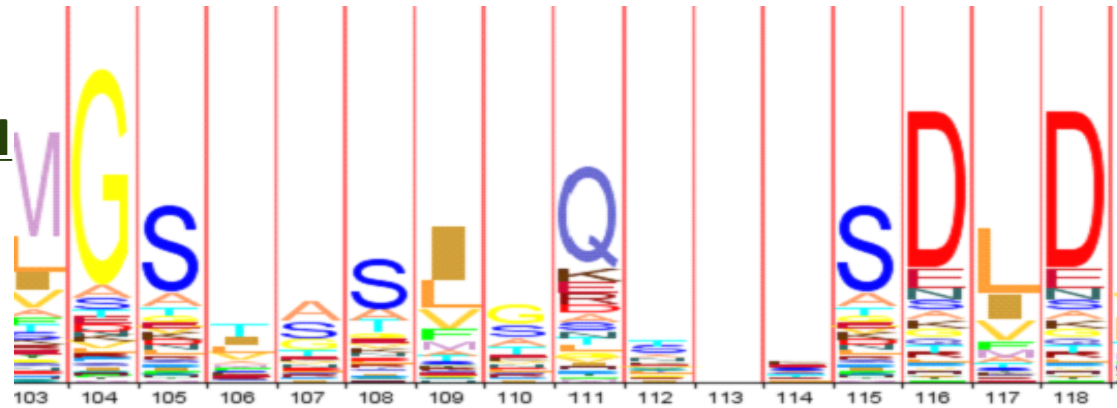
<input type="checkbox"/>	Entry	Entry name	Status	Protein names
<input type="checkbox"/>	Q8N884	M21D1_HUMAN	★	Protein MB21D1
<input type="checkbox"/>	Q8C6L5	Q8C6L5_MOUSE	★	Protein E330016A19Rik
<input type="checkbox"/>	Q5XG87	PAPD7_HUMAN	★	DNA polymerase sigma
<input type="checkbox"/>	P29728	OAS2_HUMAN	★	2'5'-oligoadenylate synthase 2
<input type="checkbox"/>	P04053	TDT_HUMAN	★	DNA nucleotidylexotransferase



NTP_transf_2

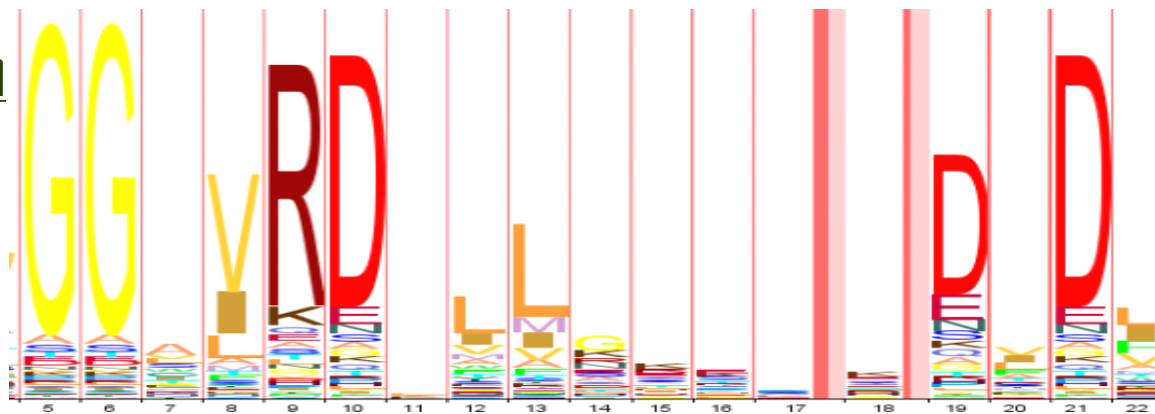


Adenyl_cycl_N



PolyA_pol

**This superfamily has a
G[G/S]₉₋₁₃[E/D]h[E/D]h
motif.**



LOGO

THX^{^^}