



Maybe Scrolly?

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Er....guys...

Why is there an 861bp sequence in the vaccine RNA that maps to a mouse GM-CSF gene?

@Ducky68257909 @Daoyu15 @Fynnderella1

**Expression vector GM-C79, partial sequence**

GenBank AF474411.1  
FASTA | GBrowse

[Go to:](#)

LOCUS AF474411 7857 bp DNA linear SYN 27-NOV-2004  
DEFINITION Expression vector GM-C79, partial sequence.  
ACCESSION AF474411  
VERSION AF474411.1  
KEYWORDS  
SOURCE Expression vector GM-C79  
ORGANISM Expression vector:GM-C79  
other sequences; artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 7957)  
AUTHORS Burke,B., Pringle,A., Harraghy,N., Collick,A., Brown,J. and Hickey,M.J.  
TITLE Transgenic mice showing inflammation-inducible overexpression of granulocyte macrophage colony-stimulating factor  
JOURNAL Clin. Diagn. Lab. Immunol. 11 (3), 588-598 (2004)  
PUBMED 15138187  
REFERENCE 2 (bases 1 to 7957)  
AUTHORS Burke,B., Harraghy,N. and Mitchell,T.J.  
TITLE Direct Submission  
JOURNAL Submitted (24-10-2002) Division of Infection & Immunity, University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK  
LOCATION/Qualifiers  
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CDS

> Clin Diagn Lab Immunol. 2004 May;11(3):588-98. doi: 10.1128/CDLI.11.3.588-598.2004.

**Transgenic mice showing inflammation-inducible overexpression of granulocyte macrophage colony-stimulating factor**

B Burke<sup>1</sup>, A Pridmore, N Harraghy, A Collick, J Brown, T Mitchell

Affiliations + expand  
PMID: 15138187 PMCID: PMC404575 DOI: 10.1128/CDLI.11.3.588-598.2004  
Free PMC article

**Abstract**

We used the promoter of the human C-reactive protein (CRP) gene to drive inflammation-inducible overexpression of the cytokine granulocyte-macrophage colony-stimulating factor (GM-CSF) in transgenic mice. Transgenic mice carrying a CRP/GM-CSF fusion gene show a >150-fold increase in circulating levels of GM-CSF within 6 h of intraperitoneal inoculation with 25 microg of lipopolysaccharide. However, some of the transgenic mice also display relatively high basal levels of GM-CSF in the absence of any obvious inflammatory stimulus. Raised basal levels of GM-CSF are associated with a number of pathological changes, including enlarged and histologically abnormal livers and spleens and with increases in the number and activation state of macrophages and granulocytes in the peripheral blood. Despite problems associated with the expression of such a potent pleiotropic cytokine as GM-CSF, the principle of inflammation-inducible expression of chimeric constructs has been shown to be feasible. Inducible expression systems such as that described here could be of potential use in the study of the role of cytokines in health and disease and in the development of disease-resistant strains of livestock.

Links:

[ncbi.nlm.nih.gov/nucleotide/MP5...](https://ncbi.nlm.nih.gov/nucleotide/MP5...)

[ncbi.nlm.nih.gov/nucleotide/AF4...](https://ncbi.nlm.nih.gov/nucleotide/AF4...)

Here's the match of the full spike vaccine mRNA. The first 84% matches to patent WO2021094282

Then there is a bit left over before the PolyA tail...

Your results are filtered to match records with percent identity between 99 and 100.

**Filter Results**

Organization: only top 20 hit appear

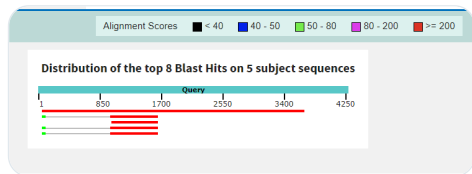
Type: common, name, biosource, based on group, name

Percent Identity: 99-100

E value: [ ] Query Coverage: [ ]

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Description	Identity Name	Max	Total	Query	E	Per	Acc
		Score	Score	Cover	Value	cent	Ident
Sequences.BI from Patent WO2021094282	ncbi.nlm.nih.gov	1447	1239	100%	0.0	99.99%	100.00000000000001
Sequences.76 from Patent WO2021094282	ncbi.nlm.nih.gov	1190	1239	100%	0.0	99.99%	100.00000000000001
Sequences.72 from Patent WO2021094282	ncbi.nlm.nih.gov	1190	1190	100%	0.0	100.00%	100.00000000000001
Sequences.71 from Patent WO2021094282	ncbi.nlm.nih.gov	1190	1239	100%	0.0	99.99%	100.00000000000001
Sequences.81 from Patent WO2021094282	ncbi.nlm.nih.gov	1190	1239	100%	0.0	99.99%	100.00000000000001



What does this match to?

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A mutant measles chimaeric SARS2 virus. Of course. Because we really need another experimental vaccine platform!

And guess who's on the creators list?

[ncbi.nlm.nih.gov/nucleotide/MWo...](https://ncbi.nlm.nih.gov/nucleotide/MWo...)

@OfComforts @Ducky68257909

**Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome**  
 Sequence ID: MW090971.1 Length: 19800 Number of Matches: 1

Score	Expect	Identities	Gaps	Strand
309 bits(342)	1e-79	198(215(92%))	2(215(0%))	Plus/Plus
Query 1	6TACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTTATC	60		
Sbjct 12872	GTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTTATC	12931		
Query 61	GATGGTCAACATCATGCTGTGCTGATGACAGCTGCTGAGT	120		
Sbjct 12932	GATGGTCAACATCATGCTGTGCTGATGACAGCTGCTGAGT	12991		
Query 121	TAGCTGTGGCAGCTGCTGCAAGTTCGACGAGGACGATT	180		
Sbjct 12992	CAGCTGTGGCAGCTGCTGCAAGTTCGACGAGGACGATT	13051		
Query 181	GAACCTGCACCTACAC--ATGATGACTCGAGCTGGT	213		
Sbjct 13052	GAACCTGCACCTACACCTAAGACCTCTGGACTGAT	13086		

**Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome**  
 GenBank: MW090971.1

LOCUS MW090971 19800 bp cDNA linear SYN 02-NOV-2020  
 DEFINITION Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome.  
 ACCESSION MW090971  
 VERSION MW090971.1  
 KEYWORDS Measles morbillivirus  
 ORGANISM Measles morbillivirus  
 Viruses; Riboviria; Orthornavirae; Negarnaviricota; Haploviricotina; Morbillivirales; Monomegavirales; Paramyxoviridae; Orthoparamyxovirinae; Morbillivirus.  
 REFERENCE 1 (bases 1 to 19800)  
 Hoerner,C., Schumann,C., Auste,A., Ebenig,A., Muralidharan,S., Dimon,K.H. III, Scholz,T., Herrmann,H., Schierle,B., Baric,R.S. and Muehlebach,M.O.  
 TITLE A Highly Immunogenic and Effective Measles Virus-based Thi-biased COVID-19 vaccine  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 19800)  
 Hoerner,C., Schumann,C., Auste,A., Ebenig,A., Muralidharan,S., Dimon,K.H. III, Scholz,T., Herrmann,H., Schierle,B., Baric,R.S. and Muehlebach,M.O.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-OCT-2020) Abteilung Veterinärmedizin, Paul-Ehrlich-Institut, Paul-Ehrlich-Str. 61-69, Langen, Hessa 63225, Germany  
 COMMENT ##Assembly-Data-START##  
 Assembly Method :: BWA mem v. v 0.7.12-r1039  
 Sequencing Technology :: Illumina  
 ##Assembly-Data-END##  
 FEATURES Location/Qualifiers

Source for full sequence: [berthub.eu/articles/posts...](https://berthub.eu/articles/posts...)

With link to the document file: [berthub.eu/articles/11889...](https://berthub.eu/articles/11889...)

Reverse Engineering the source code of the BioNTech/Pfizer SARS-CoV-2 Va...  
 Translations: ελληνικά / العربية / 中文 (Weixin video, Youtube video) / 粵文 / bahasa Indonesia / český / Català / český / Deutsch / Español / 2فارسی / فارسی / Français / ...  
<https://berthub.eu/articles/posts/reverse-engineering-source-code-of-the-biontech-pfi...>

Thanks to @Ducky68257909 here is the sequence with Pseudo-U changed to T for ease of pasting into BLAST

[files.catbox.moe/7yf2ke.txt](https://files.catbox.moe/7yf2ke.txt)

(or if link doesn't work copy and paste this into an OCR)

Let us know if you spot any errors

```

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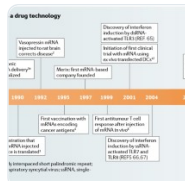
```

Oh crap.  
[@Ducky68257909](#) check the first author.  
 2014.  
[nature.com/articles/nrd42...](https://www.nature.com/articles/nrd42...)  
[@Fynnderella1](#) [@Daoyu15](#)

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naked mRNA alone led to the induction of a T helper 2 (T<sub>H</sub>2)-type antigen-specific immune response. By contrast, a strong shift towards a T<sub>H</sub>1-type response was accomplished by co-delivering adjuvants such as granulocyte-macrophage colony-stimulating factor (GM-CSF)<sup>119</sup> or complexing the IVT mRNA with protamine<sup>120</sup>. Early clinical trials with protamine-complexed IVT mRNA as well as mRNA combined with GM-CSF revealed that intradermal vaccination with these compounds is feasible, safe and can lead to the induction of antigen-specific antibody and T cell immune responses<sup>17,92</sup>. This approach was



mRNA-based therapeutics — developing a new class of drugs – Nature Review...  
The therapeutic potential of in vitro-transcribed mRNA (IVT mRNA) extends from prophylactic and therapeutic vaccines to applications such as protein replacement an...  
<https://www.nature.com/articles/nrd4278?fbclid=IwAR0B8wG6qI3QCvTOPYSOAdIU6GiiM...>

And of interest, the furin cleavage site fragment in the vaccine version loses the CGGCGG repeat.

It is now unique.