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🌐 IgG sequencing of rat hybridoma

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dx.doi.org/10.17504/protocols.io.x54v9ppw1g3e/v1

```
acgcaggagcccagtcctgg  
tgcacagactactcaccatg  
aagggtgccagtgagggtg  
ggtcctgaaactctcctgt  
gggtccgcccaggctcaaag  
gtggcacttactatggagac  
aaagcaccctgtacctgcaa  
gtgcaagacagggcaacctc  
tctcctcagcccaacaaca  
ncaaccagctncca
```

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<https://dx.doi.org/10.17504/protocols.io.x54v9ppw1g3e/v1>

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Protocol status: Working

We use this protocol and it's working

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Abstract

The purpose of this protocol is to amplify IgG antibody variable regions derived from rat hybridoma RNA, using RT-PCR and Sanger sequencing.

Materials needed:

- RNA extraction: Qiagen RNEasy mini kit (74104)
- Reverse Transcription Kit: SMARTScribe Reverse Transcriptase (639537)
- DNA Polymerase: Invitrogen Platinum SuperFi II PCR Master Mix (12368010)
- Invitrogen's PureLink™ PCR Purification Kit #K310001

The layout of this protocol was adapted from a protocol composed by Andrew McGuire's laboratory at the Fred Hutchinson Cancer Center, which in turn was adapted from Meyer et al 2019 "A simplified workflow for monoclonal antibody sequencing." See attachment for the respective manuscript.

For this protocol, rat-specific primers were designed, as the immunization campaign was executed in rats. See attachment for the primer design strategy.

Attachments



[Meyer et al 2019 A s...](#) [20211119 primer desi...](#)

1.6MB



1.9MB

Troubleshooting



Primers

- 1 TS pF is ordered as RNA oligo; the remainder as DNA oligo

universal TS pF AAGCAGTGGTATCAACGCAGAGTACATrGrGrG

ISPCR pF aagcagtggatatcaacgcagag

rat IGHG RT pR GGACAGGGCTCCAGAGTTCC

rat IGHG PCR pR GACTGGCTCAGGGAAATAGCC

rat IGKC RT pR CTGATCAGTAACACTGTCCAGGAC

rat IGKC PCR pR CACTGATGTCTCTGGGATAGAAGTTG

rat IGLC1 RT pR GGGAGATAGGTGCACCATTTGC

rat IGLC1 PCR pR GGCCACTTCCACATCACTCG

rat IGLC2 RT pR TCCACACCCTGAGTGATAGGG

rat IGLC2 PCR pR CTTCCAGACCACTGTCATAACACC

Procedure

- 2 **RNA extraction:** Extract RNA from the hybridoma sample using RNeasy total RNA kit, according to the manufacturer's instructions.
- 3 **Reverse Transcription:** On ice, prepare the 1st reaction mix in PCR tubes for gamma chain and kappa chain (or lambda chain) cDNA synthesis according to the following recipe:

3.1 Gamma

Component	Volume per rxn
IGHG RT pR (10 uM)	1 uL
dNTP (10 mM)	1 uL



RNA sample (50 ng/uL)	2 uL
Total volume	4 uL

3.2 Kappa

Component	Volume per rxn
IGKC RT pR (10 uM)	1 uL
dNTP (10 mM)	1 uL
RNA sample (50 ng/uL)	2 uL
Total volume	4 uL

3.3 Lambda (include later if Kappa does not amplify)

A	B
Component	Volume per rxn
IGLC1 (or C2) RT pR (10 uM)	1 uL
dNTP (10 mM)	1 uL
RNA sample (50 ng/uL)	2 uL
Total volume	4 uL

3.4 On ice, prepare a 2nd mastermix in Eppendorf tubes. This recipe is for one reaction regardless of chain type. *Scale up for the number of samples as needed.*

2nd reaction mix

A	B
Component	Volume per rxn
5x SMARTScribe buffer	2 uL



A	B
DTT (20 mM)	1 uL
Universal TS pR (100 uM)	0.3 uL
H ₂ O	1.70 uL
Total volume	5.00 uL

3.5 After preparing the 2nd mastermix, incubate each of the 1st reaction mixes in a thermocycler for **3 minutes at 72°C**.

3.6 While the incubation reaction is proceeding, add the following to the 2nd reaction mix:

A	B
Component	Vol. per rxn
RNAse inhibitor (40 U/uL)	0.50 uL
SMARTScribe Rev. Transcriptase (100 U/uL)	0.50 uL
Total volume	1.00 uL

3.7 Once the incubation of the 1st reaction mix (from step 3.5) finishes, add 6 uL of the 2nd reaction mix to each tube of the 1st reaction mix.

3.8 With the 2 reaction mixes now combined, incubate each according to the following conditions:

A	B	C
Temperature	Time	Cycles
42°C	60 min	1
70°C	5 min	1
4°C	hold	-

Proceed to PCR amplification step immediately after incubation has finished (once samples reach 4°C hold step).



- 4 **PCR amplification:** Prepare mastermix for PCR reaction according to following 2-step recipe:

- 4.1 Add the following components to each PCR tube.

Gamma

A	B
Component	Volume per rxn
Platinum SuperFi II PCR MM	25 uL
ISPCR pF (10 uM)	2.5 uL
IGHG PCR pR (10 uM)	2.5 uL
cDNA from RT step (5-100ng)	3 uL
Water, nuclease-free	17 uL
Total volume	50 uL

- 4.2 **Kappa**

A	B
Component	Volume per rxn
Platinum SuperFi II PCR MM	25 uL
ISPCR pF (10 uM)	2.5 uL
IGK PCR pR (10 uM)	2.5 uL
cDNA from RT step (5-100ng)	3 uL
Water, nuclease-free	17 uL
Total volume	50 uL

- 4.3 **Lambda** (*if Kappa doesn't amplify*)

A	B
Component	Volume per rxn



A	B
Platinum SuperFi II PCR MM	25 uL
ISPCR pF (10 uM)	2.5 uL
IGLC1 (or C2) PCR pR (10 uM)	2.5 uL
cDNA from RT step (5-100ng)	3 uL
Water, nuclease-free	17 uL
Total volume	50 uL

- 4.4 Cap each tube, then mix and briefly centrifuge the PCR tubes.
Place PCR tubes in thermocycler, and run according to the following conditions:

Gamma

A	B	C
Temperature	Time	Cycles
98°C	30 sec	1
98°C	15 sec	35
63°C	30 sec	
72°C	25 sec	
72°C	5 min	1
4°C	hold	-

Kappa/Lambda

A	B	C
Temperature	Time	Cycles
98°C	30 sec	1
98°C	15 sec	35
56°C	30 sec	
72°C	25 sec	
72°C	5 min	1
4°C	hold	-

5 **Verify the gel bands**

After PCR reaction completes, set up 1% agarose gel according to the following conditions:

In a flask, add the following components:

0.5 g – Agarose powder

50 mL – 1X TAE buffer

Put flask, with added reagents, in microwave and heat up until all the powder is fully dissolved (about 1 minute).

After microwaving is finished, remove flask with hot pad; add 5 uL of Sybrsafe to flask, swirl to mix. Pour into a tray with appropriate plastic comb, preferably one with wells that accommodate 20uL volumes.

Prepare a fraction of each PCR products to verify the band size on the gel. Aliquot 5 uL from each PCR tube into a new PCR strip, and add 1 uL of DNA Loading Dye to each sample.

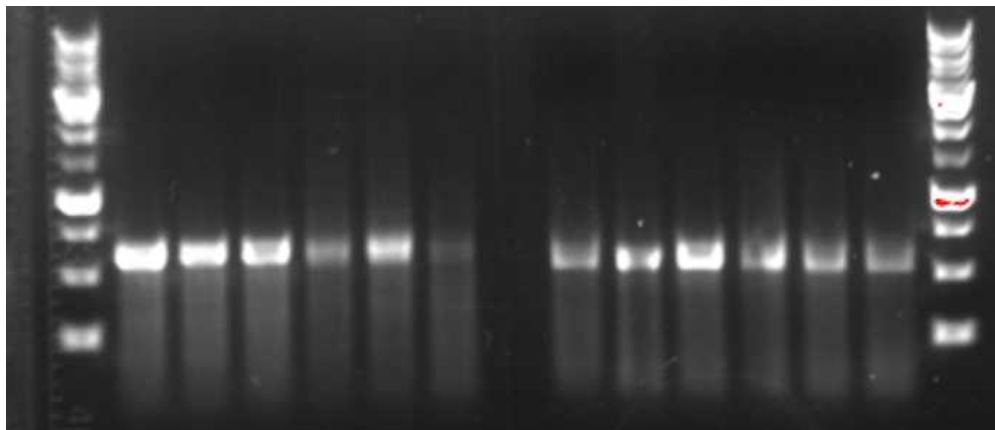
Load the gel and run it for 25-30 minutes at 110 V. *Modify these settings if needed.*

Remove gel, image, and save an image copy for the records.

Note: There should be a gamma chain, and either a kappa or lambda chain.

Amplified rat antibody products: 550-600 bp.

A significant majority of mouse antibody light chains will be kappa; if kappa not present, repeat with IGLC1 and IGLC2 samples.



6 **PCR cleanup**



PCR samples that produce a band of the expected size can then be finalized using a PCR purification kit (e.g. Invitrogen's PureLink™ PCR Purification Kit #K310001), and eluted in 25 uL volume. Verify cDNA concentration by nanodrop.

7 **Sanger sequencing** should be performed (e.g. GeneWiz or Genomic Core).

8 **Analyze the antibody nucleotide sequence**

Open the website: https://www.imgt.org/IMGT_vquest/vquest

Copy and paste sequence into the IMGT webpage, in the section "sequence submission".

Select "Rattus norvegicus" for species, and "IGH" as receptor type or locus.

Click on "Start".

Your selection

Species **Receptor type or locus**

Sequence submission

☒ Type (or copy/paste) your nucleotide sequence(s) in [FASTA](#) or in [FASTQ](#) format

>1G7 GH|

```
NNNNNNNTGGNAGCTGTTGNANCACNACATCCNGGAGCCAGTGGATAGACAGATGGGGCTGTTGTTTGGGCTGAGGAGACAGTGAAGCT
CCTTGACCCAGGAGCTATAACATAGAGTTGCCCTGTCTTGGACAATAAAGTGGCCGTGTCTCAGACTTCAGACTGTTCAATTTGCAGGTACAGG
GTGCTTTTTGCATTATCTCTGGAGATAGTGAATCGGCCCTTCACGGAGTCTCCATAGTAAGTGGCCACCCTCATGACTAATGGATGCGACCACTCC
AGACCCTTTTGGAGCCTGGCGGACCCAGGCCATGTAATAGTCACTGAAAGTGAATCCTGAGACTGCACAGGAGAGTTTACGGGACCGTCCAGGCT
GTAAGCCTCCCCAGACTCCACAGCTGCACCTCAGACTGGACACCTTTATGAAAAGGACAAGGAAAACCAAGCTGAGCCTGGTGTCCATGGTG
AGTAGTCTGTGCACTGCTGCACTACTGATTACTGAGTGGGAGAGCCTCAGAGTCCAGGACTGGGCTCCTGCGTCCCCANGNACTCTGCNNNNN
```

☐ Or give the path access to a local file containing your sequence(s) in [FASTA](#) or in [FASTQ](#) format

no file selected

A. Detailed results for the IMGT/V-QUEST analysed sequences

Number of analysed sequences: **1**

1. 1G7_GH

 This release of IMGT/V-QUEST uses **IMGT/JunctionAnalysis** for the analysis of the JUNCTION

 Hyphens (-) show nucleotide identity, dots (.) represent gaps

Sequence: 1 1G7_GH

Nb of 5' trimmed-n: 8.

Nb of 3' trimmed-n: 5.

Analysed sequence length: 570.

Sequence analysis category: 3 (complementary reverse, no indel search).

Complementary reverse sequence compared with the [Rattus norvegicus \(Norway rat\) IG set](#) from the [IMGT reference directory](#) (set: F+ORF+ in-frame P)

>1G7_GH (complementary reverse)

```
gcagagtcnctggggagcgaggagccagtcctggactctgaggtctccactcagta
atcagtcactgcagcactgcacagactactcaccatggacaccaggtcagcttggttttc
cttgctcttttcataaaaggtgtccagtggtgaggtgcagctggaggagctctggggaggc
ttagtacagcttgagctgctgaaactctctgtgagtcacagattcactttcagtc
gactattacatggcctgggtccgcaggctccaaagaaggctcggagtggtcgcatcc
attagtcagagggtgggtggcacttactatggagactccgtgaaggccgattcactatc
tccagagataatgcaaaagcaccctgtactctgcaaatgaacagctctgaagctgaggac
acggccacttattatgtgcaagacaagggaacctctatgttatgactgcctggggtaa
ggagcttcagtcactgtctctcagcccaacaacagcccatctgtctatccactggct
ccnggatgtgngtgncaaccagctncca
```

Result summary: 1G7_GH	Productive IGH rearranged sequence (no stop codon and in-frame junction)		
V-GENE and allele	Ratnor.IGHV5-22*01 F	score = 1359	identity = 96.88% (279/288 nt)
J-GENE and allele	Ratnor.IGHJ4*01 F	score = 225	identity = 90.74% (49/54 nt)
D-GENE and allele by IMGT/JunctionAnalysis	Ratnor.IGHD3-4*01 F	D-REGION is in reading frame 2	
FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	[25,17,38,11]	[8,8,11]	CARQGNLYVMTAW
JUNCTION length (in nt) and decryption	39 nt = (11)0(3)-15(5)-3(1)-4(19)	(3)V(3)(N1)S(D)3(N2)S(5)J	