

Multi-Query Sequence Analysis From CDRs to Constructs

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I have a LOT of sequences to search

....and I need combinations and variations! HELP!

Or

I have a due diligence search to perform over the IP portfolio of a company we're considering acquiring, and they have hundreds of sequences....

Or

I need to do a quick screen on early-stage research candidate sequences-a lot of them! Or...I want my researchers to do the initial screen.

Or

I need to share my results with colleagues so they can also view and analyze my searches

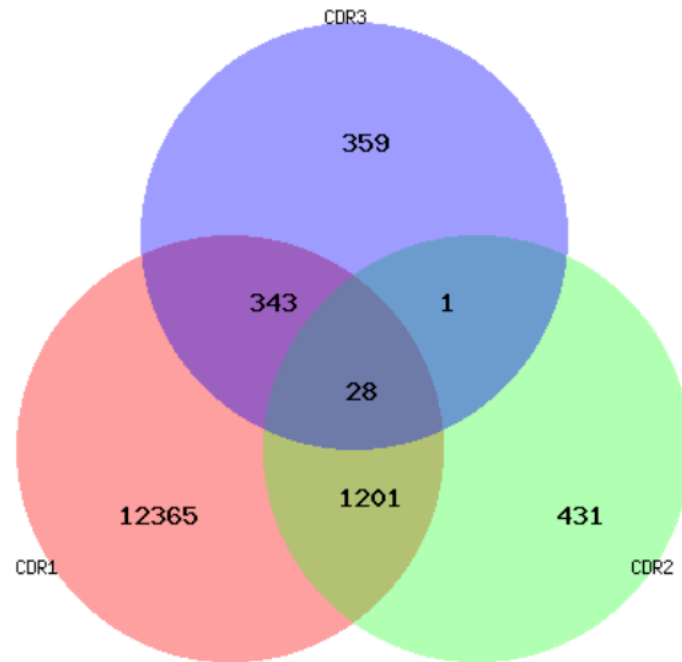
So what can GenomeQuest do for me?

- Search & analyze as many as 250 sequences simultaneously
 - Apply saved (or newly-created) filters & views and create workflows that can be applied by non-expert users
 - Flexible filters, grouping and views allow interaction with specific sequence(s)
 - For the more detailed analysis or special projects, create a library of saved analysis parameters, methods and views.
- Create reports or extract sequences in multiple formats
 - Standard report formats (Word, Excel, Bizint) facilitate information exchange
 - Live result sharing and saved view formats enable real-time collaboration
 - Export sequences in standard interchange formats for use in your choice of sequence analysis software (FASTA, EMBL, Genbank)

Patent Documents with Different Query Combinations

VENN DIAGRAM


This is a Venn diagram of your 3 queries with hits to patents. The clickable numbers are the number of patents 1, 2 or 3 queries hit.



This Venn is available on the “intermediate page” when you search two or three query sequences. By clicking on the numbers on each intersection, you can filter for PNs containing the specified combination of hits.











Group by Query

For each query sequence, immediately see the hit count and best hit.













 Quick Launch ▾ Ellen Sherin ▾ Help ▾

[Home](#) > [49 sequence search](#) > [Full aln results of workflow 49 sequence search](#) Help on this page

Result View Export Applications 0 results selected [x]

 Filtering ▾  Grouping ▾  Sorting ▾  Sharing ▾  Family Portrait  Family Portrait (Java)  Export PN List ▾  LifeQuest  Browse with GQ Discover  Browse with GQ Discover (Java)

Grouped by Query << First < Previous Query 1-49 of 49 Next > Last >> 4,900 Results

	Query Identifier	Identifier	Patent Family ID	Patent Number	Query % Id ▾	Subj. % Id	Align % Id	Align. Length	Query % Align. Cov.	Query Start Pos.	Query Stop Pos.	Subj. Start Pos.	Subj. Stop Pos.	Length	Legal Status
	MN938385 1-1 of 100 [View all 100 Results]														
	MN938385	EP2178897-0052	40259266	EP2178897	91.29	15.38	94.93	276	96.17	1	276	904	1,179	1,703	Application
	MN938386 1-1 of 100 [View all 100 Results]														
	MN938386	EP2178897-0052	40259266	EP2178897	91.29	15.38	94.93	276	96.17	1	276	904	1,179	1,703	Application
	MN975263 1-1 of 100 [View all 100 Results]														
	MN975263	EP2178897-0052	40259266	EP2178897	91.29	15.38	94.93	276	96.17	1	276	904	1,179	1,703	Application
	MN975264 1-1 of 100 [View all 100 Results]														
	MN975264	EP2178897-0052	40259266	EP2178897	91.29	15.38	94.93	276	96.17	1	276	904	1,179	1,703	Application
	MN975265 1-1 of 100 [View all 100 Results]														
	MN975265	EP2178897-0052	40259266	EP2178897	91.29	15.38	94.93	276	96.17	1	276	904	1,179	1,703	Application
	MN938387 1-1 of 100 [View all 100 Results]														

Or in GQ Discover...

- ▼ Query Sequence ID
 - ☐ repOrigin (5,475)
 - ☐ oriT (5,051)
 - ☐ regulatory1 (16,342)
 - ☐ regulatory2 (1,387)
 - ☐ lacZ (100,000)
 - ☐ parE (52)
 - ☐ parD (86)
 - ☐ parC (27)
 - ☐ parB (25)
 - ☐ parA (25)
 - ☐ aph (16,342)
 - ☐ trfA (4,320)
 - ☐ kanamycin_PPT (24,995)

- Track the hit count for each query sequence
- Very visible if a query sequence is filtered out

- ▼ Query Sequence ID
 - ☐ HC-Ebola (74,100)
 - ☐ LC-Ebola (914,028)
 - ☐ HCDR1 (961,786)
 - ☐ HCDR2 (25,540)
 - ☐ HCDR3 (21)
 - ☐ LCDR1 (464,801)
 - ☐ LCDR2 (1,000,000)
 - ☐ LCDR3 (444,158)

Grouping

Group by Query and show 1 result per group.

Show only Ungrouped

Group size Subject than or equal to

US20200045-0001

US20200040065 100.00 14.84 100.00

Query Identifier

Keywords

Patent Id

Normalized Patent Assignee

Unique Family Sequence ID

Patent family ID

Application number

Grouping filters



Result View Export Applications

Filtering Grouping Sorting Sharing

Grouped by Patent family ID

	Query Identifier	Identifier	Patent Family ID	Patent Number	Query % Id	Subj. % Id
<input type="checkbox"/>	US10517941	1-1 of 24	[View all 24 Results]			
<input type="checkbox"/>	CA2868330-0002	US10517941-0047	US10517941	US10517941	94.70	94.87

And combine grouping with filtering

Group by Subject and show 3 results per group.

Show only groups with Subjects comprising 3 CDRs

Query Identifier	one member matches	*CDR1
Query Identifier	one member matches	*CDR2
Query Identifier	one member matches	*cdr3

Random Tip

Select Families with Grouping & Date Filters

Group by Patent family ID ▾ and show 3 ▾ results per group.

New families since 1/1/20

Show only groups with

Date of entry ▾ earliest date is after ▾ 2020 ▾ January ▾ 1 ▾

Group by Patent family ID ▾ and show 1 ▾ result per group.

Families with new member(s) since 1/2/20

Show only groups with

Date of entry ▾ earliest date is before ▾ 2020 ▾ January ▾ 1 ▾ - +
Date of entry ▾ latest date is later than ▾ 2020 ▾ January ▾ 2 ▾ - +

Patent Statistics Report

PN Level

Home > 6_CDR_GP_80 > Full aIn results of work

Result
View
Export
Applications

Filtering
Gr

Numeric: * - Grouped by Subj
Filter Applied

Query Identifier
Pat

EMBOSS
Extract
Geneious
Patent Statistics
Launch New Search
Bizint Smart Charts
Clustalw
Vector NTI

Also helpful as a way to regenerate the Venn if you started with >3 query sequences and then narrowed.

13 1-3 of 3
29 documents match 6 of the 6 queries

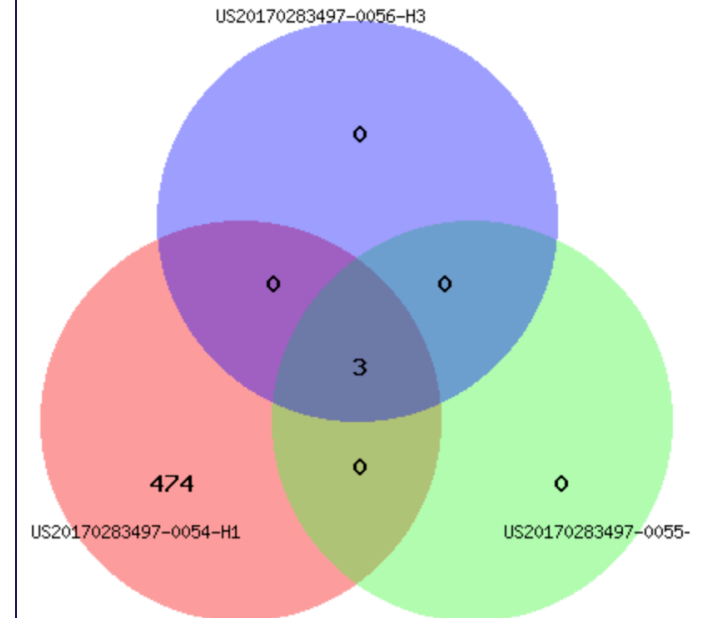
PATENT NUMBER	NB QUERIES	QUERY 1	QUERY 2	QUERY 3	QUERY 4	QUERY 5	QUERY 6	PATTERN
CA2754113	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
CA2851737	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
CA2856866	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
EP2408816	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2012520679	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2014140372	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2015214563	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2015505822	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP5498566	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP5980384	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP6203740	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
KR1020110128948	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
KR1020130067314	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
KR20130067314	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20100254975	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20120177662	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20120183561	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20130302354	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20140322209	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20150086563	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20170275365	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8444981	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8454961	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8454962	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8871490	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US9499620	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
WO2010107752	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
WO2013078375	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
WO2017180587	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY

Excel export

Global Statistics

There were original queries of which 3 have hits
There are 1266 hits to the patent databanks.
There is a total of 477 patent documents from 204 INPADOC patent families.
The earliest priority date is : IN249086 20050202

Venn Diagram of the number of document by matching queries



Number of documents per query

Spreadsheet of all hits classified by patents.

3 documents match 3 of the 3 queries

Workshop Searches Here



IP Search | Keyword Search | More ▾

- + My Data
- + Reference Data
- Data Shared With Me
 - + sub
 - + StandardDemo Searches
 - + STD TESTS
 - + PIUG Practice Datasets



May also have been run in your student account.



Quick Start

Launch IP Search

Run IP sequence searches with a simple launch page.



News

Practice: Grouping & Patent Statistics

Basic: PIUG Practice Ebola LC CDRs 10k (vm)

1. Enter search results by clicking on search name
2. Use Venn to pre-select for PNs comprising all three CDRs
3. Use grouping & filtering to narrow to chains comprising all three CDRs

Group by Subject and show All results per group.



Show only groups with

Query Identifier	one member matches	*CDR1*
Query Identifier	one member matches	*cdr2*
Query Identifier	one member matches	*cdr3



Advanced: PIUG Practice Ebola 6 CDR short name (vm)

1. Go directly to search results
2. Create your own grouping filter to narrow to chains comprising all 3 HC CDRs, then chains comprising all 3 LC CDRs.
3. Experiment with Patent Statistics to find PNs with all 6 CDRs

Home > PIUG Practice Ebola 6 CDR short name (vm) > Full a

Result	View	Export	Applications
 Filtering	 Gro		EMBOSS Extract Geneious Patent Statistics Launch New Search Bizint Smart Charts Clustalw Vector NTI

CDR: - Grouped by Subject

	Query Identifier	
		
	2811	1-1 of 1

If you like, try out the new family/new members grouping method as well.

How about filtering for coordinates?

Find CDR hits to my chain that cover specific coordinates

Results must meet ☐ all conditions ☐ at least one condition ☒ custom

PIUG CDRs align to chain & c

f1 and f2 and ((f3 and f4) or (f5 and f6) or (f7 and f8))

Gaps removed separately

	Field	Operator	Value	Result	Buttons
F1	Subject Sequence Length	less than or equal	25		<div>+</div> <div>-</div>
F2	Diff. Count	less than or equal	3		<div>+</div> <div>-</div>
F3	Query Start Position	less than or equal	24		<div>+</div> <div>-</div>
F4	Query Stop Position	more than or equal	34		<div>+</div> <div>-</div>
F5	Query Start Position	less than or equal	50		<div>+</div> <div>-</div>
F6	Query Stop Position	more than or equal	55		<div>+</div> <div>-</div>
F7	Query Start Position	less than or equal	89		<div>+</div> <div>-</div>
F8	Query Stop Position	more than or equal	97		<div>+</div> <div>-</div>

Narrow to CDRs

Claimed # mismatches

CDR coordinates

Clear All

Cancel

Overwrite Existing My Filter

Multiple Query Sequence Analysis Working with Chains & CDRs

Methods – Query Sequence is Chain

To narrow results to just CDRs or just chains, add a subject length (or % subject coverage) filter.
Use query coordinate filters to select for subsequence alignments (e.g. CDR2 only)

Match to only chains

Show results that

Query number of gaps	less than or equal to	0
Subj. number of gaps	less than or equal to	0
Length	greater than	50

Match to only CDRs

Show results that



Query number of gaps	less than or equal to	0
Subj. number of gaps	less than or equal to	0
Length	less than	40

The key is the length field
This means “length of hit sequence”

Practice – Query Sequence is Chain

PIUG Practice HC full chain (vm)

Click REDO on this search twice; the first time set it as 80% ID over query; the second time, set it as 80% ID over query or subject. Set a maximum of 10k hits both times. How many results do you get for each set of parameters?

	Name	Type	
	PIUG ebola HC chain practice [Full aln results]	IP	

Be aware of these settings – query only will omit CDR hits.

Search Strategy ?

GenePAST Blast Fragment Search

Percent identity 80
Over the length of query or subject

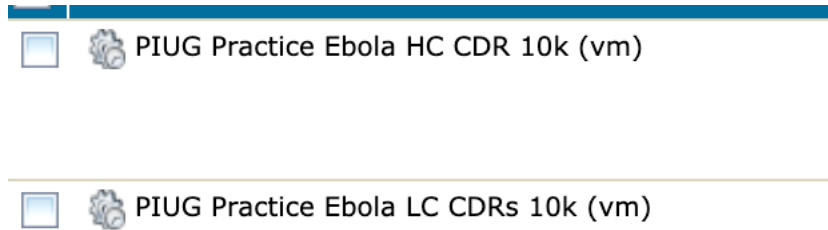
Additional Strategy Parameters

Limit subject length from 6 to 1000 residues

Keep a maximum of 30000 results (per query)

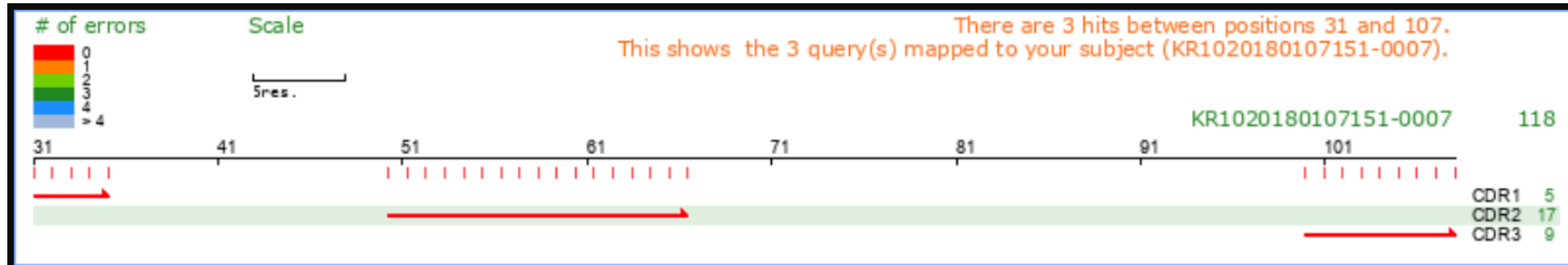
Let's get some CDR searches going

Click REDO for the following searches:



You are welcome to change the parameters, or just leave them alone for now. We'll use them later.

Visualizing CDRs

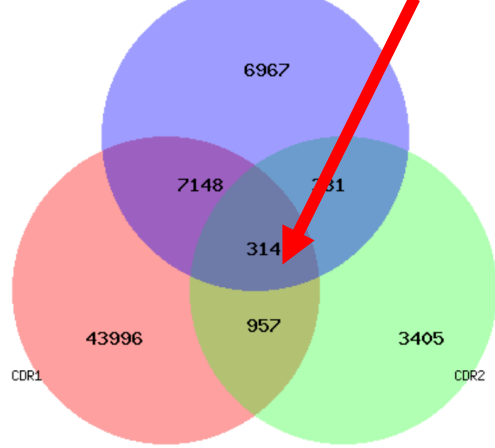


☐ HCDR3 EP3525813-0001 61905948 EP3525813

Alignment Patent Subject Annotation Subject Sequence Query Sequence Report data issue

☐ See all subjects mapped to this query
☐ See all queries mapped to this subject

1. Venn: Detect PNs comprising all three CDRs;
any combination of Chain/CDR hits



CDR Searching Review GQ Classic Methods

3. Select for CDR:CDR hits only

Show results that

Subj. % align. cov.

Can potentially be a bit lower, depending on CDR length

2. Select for CDRs hitting chain only

Show results that

Subj. % align. cov.

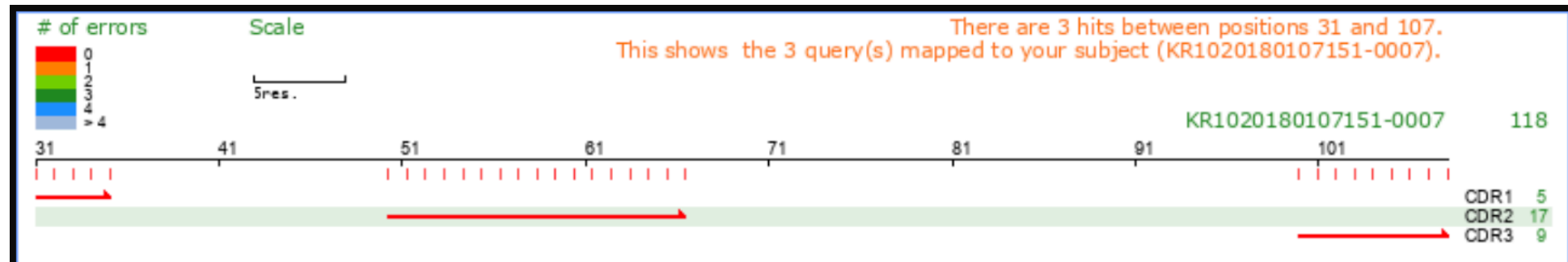
Arbitrary
Can also use subject length

Group by and show results per group.

Show only groups with

Query Identifier	one member matches	cdr1	[+]	-	+
Query Identifier	one member matches	cdr2	[+]	-	+
Query Identifier	one member matches	cdr3	[+]	-	+

Detect chain sequences comprising all three query CDRs



Search 3 CDRs, select for chains as a result PNs comprising all 3 CDRs

Show results that meet all conditions

Subj. % align. cov. less than 30

Increase subj % align coverage to $\geq \sim 90\%$ to select for CDR hits instead. For this method, group by PN to find hits in each PN, or use Venn.

Home > CIPO Generic 3 CDR search (vm) > Full aln results of workflow CIPO Generic 3 CDR search (vm) Help on this page

Result View Export Applications 0 results selected [x]

Filtering

Grouping

Sorting

Sharing

Family Portrait

Family Portrait (Java)

Export PN List

LifeQuest

Browse with GQ Discover

Browse with GQ Discover (Java)

StandardView: * - Grouped by Patent number Filter Applied << First < Previous Patent number 1-3 of 5 Next > Last >> 90 Results

	Identifier	Query Identifier	Length	Query % Id	Subj. % Id	Subj. Start Pos.	Subj. Stop Pos.
<input type="checkbox"/> CA3012294 1-18 of 18							
<input type="checkbox"/>	CA3012294-0007	CDR1	118	100.00	4.24	31	35
<input type="checkbox"/>	CA3012294-0007	CDR2	118	100.00	14.41	50	66
<input type="checkbox"/>	CA3012294-0007	CDR3	118	100.00	7.63	99	107
<input type="checkbox"/>	CA3012294-0009	CDR1	448	100.00	1.12	31	35
<input type="checkbox"/>	CA3012294-0009	CDR2	448	100.00	3.79	50	66
<input type="checkbox"/>	CA3012294-0009	CDR3	448	100.00	2.01	99	107
<input type="checkbox"/>	CA3012294-0027	CDR1	118	100.00	4.24	31	35
<input type="checkbox"/>	CA3012294-0027	CDR2	118	100.00	14.41	50	66
<input type="checkbox"/>	CA3012294-0027	CDR3	118	100.00	7.63	99	107
<input type="checkbox"/>	CA3012294-0029	CDR1	448	100.00	1.12	31	35
<input type="checkbox"/>	CA3012294-0029	CDR2	448	100.00	13.56	50	66
<input type="checkbox"/>	CA3012294-0029	CDR3	448	100.00	7.63	99	107
<input type="checkbox"/>	CA3012294-0087	CDR1	118	100.00	4.24	31	35
<input type="checkbox"/>	CA3012294-0087	CDR2	118	94.12	13.56	50	66
<input type="checkbox"/>	CA3012294-0087	CDR3	118	100.00	7.63	99	107
<input type="checkbox"/>	CA3012294-0089	CDR1	448	100.00	1.12	31	35
<input type="checkbox"/>	CA3012294-0089	CDR2	448	94.12	13.56	50	66
<input type="checkbox"/>	CA3012294-0089	CDR3	448	100.00	7.63	99	107

Query = CDR1, 2 and 3

For same PN hits, group by PN, group contains all 3 CDRs

Variant chain?

Q: 1 WIDPGQSNTRYSPSFQG 17
S: 50 WIDPGTSNTRYSPSFQG 66

Search for PNs comprising all 6 Query CDRs

Result View Export Applications 0 results selected [x]

Filtering ▾ Grouping ▾ Sorting ▾ Sharing ▾ Family Portrait Family Portrait (Java) Export PN List ▾ LifeQuest Browse with GQ Discover Browse with GQ Discover (Java)

Grouped by Patent number Filter Applied << First < Previous Patent number 1-4 of 4 Next > Last >> 64 Results

Query Identifier	Identifier	Patent Family ID	Patent Number	Query % Id ▾	Subj. % Id	Align % Id	Align. Length	Comments
EP3525813 1-1 of 16 [View all 16 Results]								
LCDR1	EP3525813-0006	61905948	EP3525813	100.00	100.00	100.00	11	Copyright (c) GQ Life Sciences, Inc. 2020
CN110087677 1-1 of 16 [View all 16 Results]								
LCDR1	CN110087677-0006	61905948	CN110087677	100.00	100.00	100.00	11	Copyright (c) GQ Life Sciences, Inc. 2020
WO2018071345 1-1 of 16 [View all 16 Results]								
LCDR1	WO2018071345-0006	61905948	WO2018071345	100.00	100.00	100.00	11	Copyright (c) GQ Life Sciences, Inc. 2020
US20200040065 1-1 of 16 [View all 16 Results]								
LCDR1	US20200040065-0006	US20200040065	US20200040065					

<< First < Prev

Group by Patent number ▾ and show 1 ▾ result per group.

Show only groups with

Query Identifier ▾	one member matches ▾	hcdr1	[+]	-	+
Query Identifier ▾	one member matches ▾	hcdr2	[+]	-	+
Query Identifier ▾	one member matches ▾	hcdr3	[+]	-	+
Query Identifier ▾	one member matches ▾	lcdr1	[+]	-	+
Query Identifier ▾	one member matches ▾	lcdr2	[+]	-	+
Query Identifier ▾	one member matches ▾	lcdr3	[+]	-	+

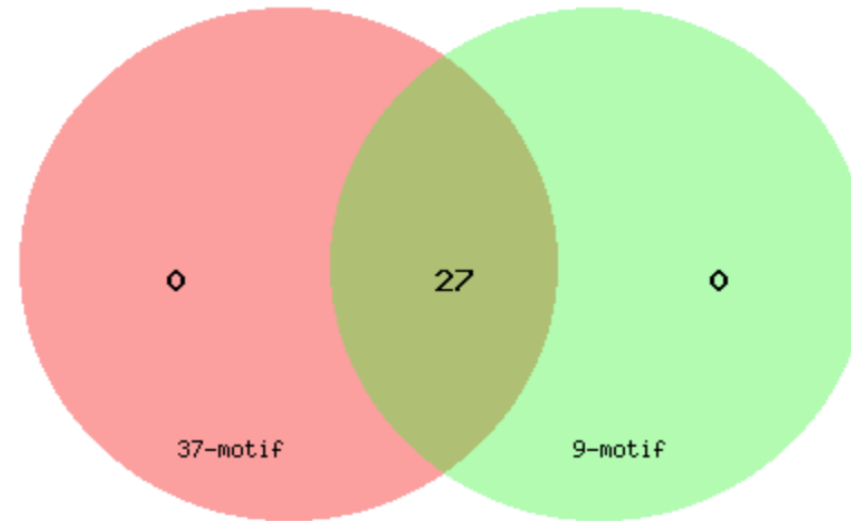
Use hit sequence length or subject % ID/coverage to further narrow to just CDR hits or just chain hits if desired.

Same method works for just 3 CDRs

Searching for chains comprising all three CDRs

Method 1: MOTIF on Full Length Chain

Direct Strike



This is the method Danie Kolker from the USPTO talked about yesterday – concatenating all three CDRs.

The long sequence gives hits comprising all three CDRs in **the specific order provided, with 100% identity to each CDR (or variations as specified)**. **.*** Represents “any number of unspecified residues, including zero”.

>37-motif

DLSIH.*GFDPQDGETIYAQKFQG.*GSSSSWFDP

>9-motif

RA[ST]QGISSWLA.*GASNLES.*QQANSFPWT

>37-CDR1

DLSIH

>37-CDR2

GFDPQDGETIYAQKFQG

>37-CDR3

GSSSSWFDP

Method 2: Group & Filter, GQ Classic (Review)

Show results that **Remove gaps**

Query number of gaps

Subj. number of gaps

Select for subjects comprising all three CDRs (or a subset of CDRs) or for CDR:CDR matches instead (or sequentially).

Grouping

Group by and show result per group.

Show only groups with **Subjects comprising 3 CDRs**

Query Identifier

Query Identifier

Query Identifier

Show results that

CDR:CDR matches

Subj. % align. cov.

Method 3: 3 click analysis in GQ Discover

Navigation bar with icons for back, chart, list, and image. A dropdown menu shows "Current Page Unannotated". Sort: Highest %Id. Query. View: 20,021 Alignments.

Multiple Query Sequence Analysis

- matching all 3 query seqs:
- [2 Patent Families](#)
 - [4 Patent Numbers](#)
 - [2 Unique Sequences](#)
- matching 2 out of 3 query seqs:
- [159 Patent Families](#)
 - [818 Patent Numbers](#)
 - [7 Unique Sequences](#)
- matching 1 out of 3 query seqs:
- [1,428 Patent Families](#)
 - [5,764 Patent Numbers](#)
 - [4,203 Unique Sequences](#)

Total

- matching at least one query seq
- [1,589 Patent Families](#)
 - [6,586 Patent Numbers](#)
 - [4,212 Unique Sequences](#)

Reset

1. Open search results
2. [Browse with GQ Discover](#)
3. Click on "Matching all 3 query seqs" gives chains comprising all three CDRs.

Optionally apply filters:

Gaps, % ID/differences count, Query Sequence ID, etc

Advanced Filters

☐ Create New Filter

Sample Filters

- ☐ % id simple Boolean
- ☐ Query comprises subject
- ☒ Remove gapped hits

My Filters

- ☒ diff<=1

Query Sequence ID

- ☐ HCDR1 (10,000)
- ☐ HCDR2 (10,000)
- ☐ HCDR3 (21)
- ☐ LCDR1 (10,000)
- ☐ LCDR2 (10,000)
- ☐ LCDR3 (10,000)

What are “Unique Sequences”?

▶ Simple Unique Family Sequence ID 61905948-5

▶ Patent Family 61905948

<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR1	WO2018071345-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR2	WO2018071345-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR3	WO2018071345-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR1	EP3525813-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR2	EP3525813-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR3	EP3525813-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR1	CN110087677-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR2	CN110087677-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR3	CN110087677-0001	Query 100.0%	SEQ ID NO 1

- This is the UFS we use regularly
- It is the identical sequence, segregated by patent family.

▶ Simple Unique Family Sequence ID US20200040065-5

▶ Patent Family US20200040065

<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR1	US20200040065-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR2	US20200040065-0001	Query 100.0%	SEQ ID NO 1
<input type="checkbox"/> ★★★★★ <input type="checkbox"/> ▶ HCDR3	US20200040065-0001	Query 100.0%	SEQ ID NO 1

Our upcoming release....

One click finds the needle in >1 million result haystack....

My Column Groups

- Select Displayed Columns
- Saved Views

Highlight Text

Highlight all text

Filter Text

Search all text

Query Sequence ID

- ☐ HCDR1 (300,000)
- ☐ HCDR2 (25,529)
- ☐ HCDR3 (21)
- ☐ LCDR1 (300,000)
- ☐ LCDR2 (300,000)
- ☐ LCDR3 (300,000)

- Patent Numbers
- Sequence Databases
- Annotation Filters
- Patent Authorities
- Extended Legal Status
- Patent Sequence Location
- Advanced Filters

GQ Power Tools

- Sequence Variation Discovery
- Variation Filters
 - Create New Variation Filter
 - Global Filters
 - Result-specific Filters
- Variation Landscape

Current Page Unannotated

Sort: Highest %Id. Query

View: 1,225,550 Alignments

Multiple Query Sequence Analysis

matching all 6 query seqs:	<ul style="list-style-type: none"> 2 Patent Families 4 Patent Numbers
matching 5 out of 6 query seqs:	<ul style="list-style-type: none"> 223 Patent Families 1,013 Patent Numbers
matching 4 out of 6 query seqs:	<ul style="list-style-type: none"> 812 Patent Families 3,346 Patent Numbers 1 Unique Sequences
matching 3 out of 6 query seqs:	<ul style="list-style-type: none"> 2,558 Patent Families 11,187 Patent Numbers 99 Unique Sequences
matching 2 out of 6 query seqs:	<ul style="list-style-type: none"> 4,880 Patent Families 21,509 Patent Numbers 5,837 Unique Sequences
matching 1 out of 6 query seqs:	<ul style="list-style-type: none"> 18,019 Patent Families 66,441 Patent Numbers 270,480 Unique Sequences

Total	<ul style="list-style-type: none"> 26,494 Patent Families 103,500 Patent Numbers 276,417 Unique Sequences
matching at least one query seq	

Reset

View: 1,225,550 Alignments

From 1.2 million to 64 results



My Column Groups

- ⊕ Select Displayed Columns
- Saved Views

Highlight Text

Highlight all text

Filter Text

Search all text

▼ Query Sequence ID

- ☐ HCDR1 (8)
- ☐ HCDR2 (12)
- ☐ HCDR3 (8)
- ☐ LCDR1 (12)
- ☐ LCDR2 (8)
- ☐ LCDR3 (16)
- Patent Numbers
- Sequence Databases
- Annotation Filters
- Patent Authorities
- Extended Legal Status



☐ ★★☆☆

Sort: Highest %Id. Query ▾

View: 64 Alignments ▾

?

Multiple Query Sequence Analysis

matching all 6 query seqs:	<ul style="list-style-type: none">• 2 Patent Families• 4 Patent Numbers
matching 5 out of 6 query seqs:	
matching 4 out of 6 query seqs:	
matching 3 out of 6 query seqs:	<ul style="list-style-type: none">• 4 Unique Sequences
matching 2 out of 6 query seqs:	<ul style="list-style-type: none">• 2 Unique Sequences
matching 1 out of 6 query seqs:	<ul style="list-style-type: none">• 16 Unique Sequences

Total	<ul style="list-style-type: none">• 2 Patent Families• 4 Patent Numbers• 22 Unique Sequences
matching at least one query seq	

Reset

3 CDR Report Creation

GQ Classic



Home > PIUG Practice HC full chain (vm) > Full alignment results of workflow PIUG Practice HC full chain (vm)

Result View Export Applications

Filtering

Document: Current View
Table: Current View

Sorting

Sharing

Family Portrait

Family Portrait (Java)

Export PN List

CDRview: - Grouped
Filter Applied

54156 1-3 of 3

US10273530-0055 CA3025536-0004_VLCDR3

US10273530-0055 CA3025536-0003_VLCDR2

US10273530-0055 CA3025536-0002_VLCDR1

15101 1-3 of 3

US20170204454-0055 CA3025536-0004_VLCDR3

US20170204454-0055 CA3025536-0003_VLCDR2

US20170204454-0055 CA3025536-0002_VLCDR1

Table: Current View

You are about to export the top 3 results per subject (limited to 10000).

Selections

☐ All 10,662 results

☒ Top 3 results per subject (10,662 total)

Options

Format

XLS

You could even make group size =1, then export top 1 result/subject, given that each subject comprises the three CDRs

Practice Finding CDRs

Use either PIUG practice Ebola HC CDR 10k search or LC CDR 10k search you started earlier

1. Use the Venn diagram as an entry point to your results. Note how many PNs contain all three CDRs
2. Move to GQ Discover. Does the MQSA show the same PN count?
3. Click on your choice of PNs or Unique Sequences containing all 3 query sequences.
4. Group by patent family, sort by Subject Sequence ID for a clear view. You may want to make some column selections to better understand your data.

◀

📈

☰

🖼️

📊 ⭐⭐⭐ ☐ Current Page Unannotated

Sort: A-Z Subject Sequence ID ▾

View: 2 Patent Families ▾

Multiple Query Sequence Analysis

matching all 3 query seqs:

- [2 Patent Families](#)
- [4 Patent Numbers](#)
- [2 Unique Sequences](#)

matching 2 out of 3 query seqs:

matching 1 out of 3 query seqs:

Total

matching at least one query seq

- 2 Patent Families
- 4 Patent Numbers
- 2 Unique Sequences

Reset

Part 2 – going back

Check your result count on PIUG Practice HC full chain (vm) for the two different methods (we did this REDO earlier).

What did you see?

Moving on to some claims

HC Analysis

wherein the VH comprises heavy chain complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein CDRH1 comprises SEQ ID NO: 3 or SEQ ID NO: 3 with one or two single amino acid substitutions, wherein the substitutions are at positions XI and/or X2 of G-Y-Y-X1-W-X2 (SEQ ID NO: 9); wherein CDRH2 comprises SEQ ID NO: 4, or SEQ ID NO: 4 with one, two, or three single amino acid substitutions; and wherein CDRH3 comprises SEQ ID NO: 5 or SEQ ID NO: 5 with one, two, or three single amino acid substitutions, wherein the substitutions are at positions XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI₁, and/or X12 of D-X1-G-X2-T-I-F-X3-X4-X5-I-X6-X7-W-X8-X9-X10-D-X12 (SEQ ID NO: 10); and

How painful is it to interpret and write the query for SID 9 or 10? Let's start off simple...

Custom Boolean Replacement Count and Query Identifier

Results must meet ☐ all conditions ☐ at least one condition ☒ custom

PIUG complex HC CDR

(f1 and f2) or ((f3 or f4) and f5)

HC-CDR1: up to 2 replacements

HC-CDR2 & 3: up to 3 replacements

F1	Query Sequence ID	contains	HCDR1*	-	+
F2	Diff. Count	less than or equal	2	-	+
F3	Query Sequence ID	contains	hcdr2*	-	+
F4	Query Sequence ID	contains	hcdr3*	-	+
F5	Diff. Count	less than or equal	3	-	+

Comprising all three

We dodged a bullet!



Multiple Query Sequence Analysis

matching all 3 query seqs:

- 2 Patent Families
- 4 Patent Numbers
- 2 Unique Sequences

matching 2 out of 3 query seqs:

matching 1 out of 3 query seqs:

Total

matching at least one query seq

- 2 Patent Families
- 4 Patent Numbers
- 2 Unique Sequences

▶ US20200040065

- ☐ ★★★★★ ▶ HCDR1-WO2018071345-0003
- ☐ ★★★★★ ▶ HCDR2-WO2018071345-0004
- ☐ ★★★★★ ▶ HCDR3-WO2018071345-0005

Query 100.0% US20200040065-0001
Query 100.0% US20200040065-0001
Query 100.0% US20200040065-0001

▶ EP3525813

- ☐ ★★★★★ ▶ HCDR1-WO2018071345-0003
- ☐ ★★★★★ ▶ HCDR2-WO2018071345-0004
- ☐ ★★★★★ ▶ HCDR3-WO2018071345-0005

Query 100.0% EP3525813-0001
Query 100.0% EP3525813-0001
Query 100.0% EP3525813-0001

▶ CN110087677

- ☐ ★★★★★ ▶ HCDR1-WO2018071345-0003
- ☐ ★★★★★ ▶ HCDR2-WO2018071345-0004
- ☐ ★★★★★ ▶ HCDR3-WO2018071345-0005

Query 100.0% CN110087677-0001
Query 100.0% CN110087677-0001
Query 100.0% CN110087677-0001

▶ WO2018071345

- ☐ ★★★★★ ▶ HCDR1-WO2018071345-0003
- ☐ ★★★★★ ▶ HCDR2-WO2018071345-0004
- ☐ ★★★★★ ▶ HCDR3-WO2018071345-0005

Query 100.0% WO2018071345-0001
Query 100.0% WO2018071345-0001
Query 100.0% WO2018071345-0001

If mismatches were found, however....

wherein the VH comprises heavy chain complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein CDRH1 comprises SEQ ID NO: 3 or SEQ ID NO: 3 with one or two single amino acid substitutions, wherein the substitutions are at positions XI and/or X2 of G-Y-Y-X1-W-X2 (SEQ ID NO: 9); wherein CDRH2 comprises SEQ ID NO: 4, or SEQ ID NO: 4 with one, two, or three single amino acid substitutions; and wherein CDRH3 comprises SEQ ID NO: 5 or SEQ ID NO: 5 with one, two, or three single amino acid substitutions, wherein the substitutions are at positions XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI1, and/or X12 of D-X1-G-X2-T-I-F-X3-X4-X5-I-X6-X7-W-X8-X9-X10-D-X12 (SEQ ID NO: 10); and

8. The antibody or fragment thereof of claim 6 or claim 7, wherein any one amino acid at position XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI1, or X12 of SEQ ID NO: 10 is substituted with alanine, any two amino acids at positions XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI1, or X12 of SEQ ID NO: 10 are substituted with alanine, or any three amino acids at positions XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI1, or X12 of SEQ ID NO: 10 are substituted with alanine.

Even though there are some very specific variation claims, because we filtered by number of differences and found nothing >0 differences, we don't have to go any further.

Had there been any hits with variations, GQ's Sequence Variation Discovery Module would have enabled quick determination of the presence of the recited substitutions...**which would have been very simple because only alanine is stated.**

We'll use light chain as an example to illustrate this method

WO2018071345

LC Claim Section, Claim 6

wherein the VL comprises light chain complementarity determining regions CDRL1, CDRL2, and CDRL3, wherein CDRL1 comprises SEQ ID NO: 6, or SEQ ID NO: 6 with one, two, or three single amino acid substitutions; wherein CDRL2 comprises SEQ ID NO: 7, or SEQ ID NO: 7 with one, two, or three single amino acid substitutions; and wherein CDRL3 comprises SEQ ID NO: 8, or SEQ ID NO: 8 with one, two, or three single amino acid substitutions.

Translation: filter for CDRL1-3 with number of differences ≤ 3

Show results that

First the regular search....

<input type="text" value="No. diff"/>	<input type="text" value="less than or equal to"/>	<input type="text" value="3"/>
<input type="text" value="Subj. number of gaps"/>	<input type="text" value="equals"/>	<input type="text" value="0"/>
<input type="text" value="Query number of gaps"/>	<input type="text" value="equals"/>	<input type="text" value="0"/>

GQ Discover

How to Identify Variations



Multiple Query Sequence Analysis

matching all 3 query seqs:

- [3 Patent Families](#)
- [11 Patent Numbers](#)
- [4 Unique Sequences](#)

matching 2 out of 3 query seqs:

matching 1 out of 3 query seqs:

Total

matching at least one query seq

- [3 Patent Families](#)
- [11 Patent Numbers](#)
- [4 Unique Sequences](#)

Reset

- Use MQSA to find chains comprising all three CDRs, then export a variation landscape.
- Prefilter as appropriate (diffs, query ID, etc)

GQ Power Tools

- ▼ Sequence Variation Discovery ⓘ
 - ▶ Variation Filters
 - ▼ Variation Landscape
 - ▶ LCDR1-WO2018071345-0006 (35)
[create](#)
 - ▶ LCDR2-WO2018071345-0007 (30)
[create](#)
 - ▶ LCDR3-WO2018071345-0008 (35)
[create](#)

Variation Landscape Overview

Narrow Resultset

RASQSI>NNL A

LC-CDR1

Query position	Variation type	Description
11	Replacement	A11N (14)

AASNLA

LC-CDR2

Query position	Variation type	Description
----------------	----------------	-------------

No variations found

QQHNTLPLT

LC-CDR3

Query position	Variation type	Description
3	Replacement	H3S (14)
6	Replacement	L6S (14)

This output shows variations in individual CDR positions when all three are present on a single chain.

- This was created by using MQSA to identify chains comprising all three CDRs.
- Remove the requirement for all 3 CDRs to be present to study CDR variations in isolation
- Use filters to limit to just CDR:CDR matches if preferred.
- Create virtual database of CDR results and search chain against that for chain variations in CDR regions.

The above output is from three separate Variation Landscape Reports,
available with GQ's Sequence Variation Discovery Module

Let's take it further – Let's create a landscape for our three CDR regions.

Use chain as query here

Create vDB from CDR Search Hits

Home > PIUG Ebola LC 3 CDR CAS short name > Full aln results of workflow PIUG

The screenshot shows the Apteian interface with a search results table. The 'Applications' menu is open, showing options like EMBOS, Extract, Geneious, Patent Statistics, Launch New Search, Bizint Smart Charts, Clustalw, and Vector NTI. The 'Extract' option is highlighted, and a sub-menu is visible with 'Queries that did not hit', 'Query Sequences', and 'Subject Sequences'. The table below has columns for Query Identifier, Identity, Query ID, Patent Number, and Query % Id.

If you want to follow along, the database already exists in our shared data folder.

Create virtual database of CDR results and search chain against that for chain variations in CDR regions.

Why vDB? Just to have a narrow resultset to search chain against



In “my data”

The screenshot shows the 'Databases' panel in the Apteian interface. It lists three databases: 'PIUG Ebola LC chain vs my 3CDR db', 'PIUG LC 3 cdr db', and 'PIUG Ebola HC CDR short name CAS (vm) [Full aln results]'. The 'PIUG LC 3 cdr db' is highlighted.

Normal GQ Search vs vDB

Result Name

☐ Send E-mail on completion

☐ Compare to both nucleotide and protein databases

☒ Include variation analysis capability

Search Strategy ?

GenePASTBlastFragment Search

Percent identity

Over the length of

Additional Strategy Parameters

Limit subject length from to residues

Keep a maximum of results (per query)

Subject Databases ?

Apply filters to subject databases

- Nucleotides
- ☒ Patents
- ☒ Reference Data
- ☒ Data Shared With Me
- ☒ My Data

- Proteins
- ☒ Patents
- ☒ Reference Data
- ☒ My Data
- ☒ BGN
- ☐ ebola CDR nogap vdb
- ☐ ebolaWTvdb
- ☐ piug ebola comprise all 3
- ☒ PIUG Biotech
- ☒ PIUG LC 3 cdr db
- ☐ PIUG WO2018071345 HC full chain only
- ☐ PIUG WO2018071345 LC full chain

Use GQ view to identify CDR positions for next step

Identifier	Query Start Pos.	Query Stop Pos.
WO2018071345-0006	24	34
WO2018071345-0008	89	97
WO2018071345-0007	50	55

vDB shows up in My Data or Data Shared with Me

GQ Discover:

Filter to Create Tightly-Targeted Variation Report

Results must meet ☐ all conditions ☐ at least one condition ☒ custom

PIUG CDRs align to chain & c

f1 and f2 and ((f3 and f4) or (f5 and f6) or (f7 and f8))

Optionally limit to hits covering CDR coordinates

F1	Subject Sequence Length	less than or equal	25	-	+
F2	Diff. Count	less than or equal	3	-	+
F3	Query Start Position	less than or equal	24	-	+
F4	Query Stop Position	more than or equal	34	-	+
F5	Query Start Position	less than or equal	50	-	+
F6	Query Stop Position	more than or equal	55	-	+
F7	Query Start Position	less than or equal	89	-	+
F8	Query Stop Position	more than or equal	97	-	+

Create landscape

CDR coordinates

Clear All

Cancel

Overwrite Existing My Filter

Create & Export Variation Landscape

- ☐ PIUG <=5 diff LC
- ☒ PIUG CDRs align to chain & con
- ☐ PIUG complex HC CDR
- ☐ PIUG Ebola chain query
- ☐ PIUG Ebola LC query
- ☐ subtilase cas family dedupe
- ☐ WO2010056640-subtl demo

GQ Power Tools

- ▼ Sequence Variation Discovery ⓘ
 - ▼ Variation Filters
 - ⊕ Create New Variation Filter
 - ▶ Global Filters
 - ▶ Result-specific Filters
 - ▼ Variation Landscape
 - ▶ LC-Ebola (43,052) [create](#)

Variation Landscape Summary Table



Query position	Variation type	Description
24	Replacement	R24K(11), R24Q(354)
25	Replacement	A25P(4), A25T(2)
26	Replacement	S26N(16), S26Q(9)
27	Replacement	Q27E(31), Q27H(5), Q27K(3), Q27P(10), Q27R(11)
28	Replacement	S28A(76), S28D(517), S28G(2841), S28N(17), S28P(6), S28R(15), S28T(62), S28V(44), S28Y(14)
29	Replacement	I29L(19), I29M(27), I29S(16), I29V(2707), I29W(1), I29X(10)
30	Replacement	S30A(32), S30F(43), S30G(186), S30H(4), S30I(24), S30K(64), S30L(6), S30N(127), S30R(111), S30T(19), S30V(10), S30W(1), S30Y(85)
31	Replacement	N31A(4), N31D(71), N31E(16), N31F(31), N31G(50), N31H(66), N31I(30), N31K(18), N31R(333), N31S(10307), N31T(295), N31V(28), N31Y(79), N31Z(3)
32	Replacement	N32A(60), N32C(6), N32D(263), N32F(3959), N32G(2), N32H(150), N32I(2), N32L(109), N32Q(92), N32R(79), N32S(340), N32T(14), N32W(5671), N32Y(3378)
33	Replacement	L33V(52)
34	Replacement	A34G(11), A34H(828), A34I(5), A34L(14), A34N(977), A34Q(27), A34S(37), A34T(2), A34V(31), A34X(3)
35	Replacement	W35I(18), W35Z(16)
39	DIQMTQSPSS LSASVGDVT ITCRASQSI S NNLAWYQQRP RRAPQLLIYA ASNLASGVPS RFSGSGSGTD FTLTISSLQA EDFAAAYYCQQ HNTLPLTFGG GTKVEI	R39K(17)
46		L46A(1), L46P(111), L46R(1), L46S(1), L46T(1)
47		L47A(1), L47K(4), L47W(119)
48		I48A(4), I48L(1), I48S(4), I48V(24)
49	Replacement	Y49A(18), Y49D(3), Y49F(2), Y49G(8), Y49H(1), Y49I(8), Y49K(1), Y49N(9), Y49P(15), Y49Q(1), Y49S(7), Y49V(4)
50	Replacement	A50D(186), A50G(483), A50H(3), A50K(78), A50L(68), A50Q(164), A50R(418), A50S(182), A50T(39), A50V(12), A50W(3)
51	Replacement	A51C(2), A51D(2), A51E(2), A51F(2), A51G(4), A51H(5), A51I(26), A51K(3), A51L(2), A51M(2), A51N(2), A51P(367), A51Q(2), A51R(2), A51S(39), A51T(1828), A51V(8), A51W(2), A51X(1), A51Y(2)
52	Replacement	S52A(12), S52F(52), S52I(1), S52K(9), S52M(36), S52R(34), S52T(1046)
53	Replacement	N53D(30), N53F(43), N53G(3), N53I(8), N53K(90), N53L(34), N53P(36), N53R(10), N53S(50), N53T(165), N53Y(9)
54	Replacement	L54E(3), L54G(3), L54I(3), L54N(3), L54Q(5), L54R(98), L54T(6), L54V(7)
55	Replacement	A55D(132), A55E(8012), A55G(61), A55H(64), A55I(21), A55K(101), A55P(6), A55Q(1074), A55R(59), A55S(3), A55T(1), A55X(7), A55Y(37)
56	Repl:	S56A(58), S56C(2), S56D(1358), S56E(17), S56F(141), S56H(2), S56I(17), S56K(19), S56L(5), S56M(2), S56N(25), S56P(26), S56Q(6), S56R(39), S56
57	Repl:	
58	Repl:	
60	Repl:	
88	Repl:	
89	Repl:	
91	Replacement	H91A(141), H91F(17), H91G(5713), H91L(66), H91R(9), H91S(181), H91T(82), H91V(4), H91W(4), H91Y(204)
92	Replacement	N92D(87), N92E(10), N92F(17), N92H(11), N92K(33), N92S(11), N92Y(131)
93	Replacement	T93A(9), T93E(401), T93H(12), T93K(15), T93N(135), T93S(84), T93V(4), T93Y(2)
94	Replacement	L94A(6), L94D(73), L94F(64), L94H(3), L94I(33), L94N(73), L94P(4), L94S(68), L94T(105), L94W(116), L94Y(551)
96	Replacement	L96A(8), L96F(98), L96H(8), L96I(12), L96P(236), L96R(45), L96W(1174), L96X(3), L96Y(4067)
98	Replacement	F98I(4)
100	Replacement	G100S(5)
102	Replacement	T102C(8)

Remember the ALA in HC claims 7 & 8? We'd look for A in any of the recited positions; if found we'd build appropriate variation filters

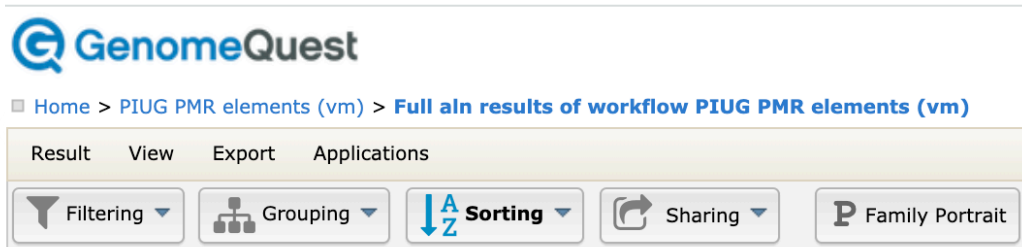
Multiple Query Sequence Analysis

Combinations of Components

Constructs & Elements

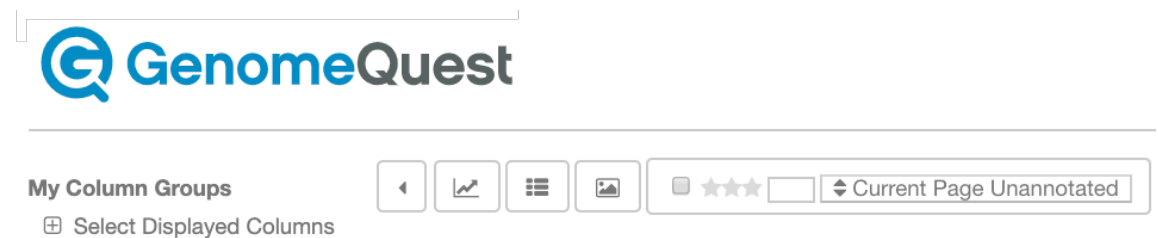
Find Component Combinations Interactively in GenomeQuest

GQ Classic



- PN level combinations via Patent Statistics
- Or use grouping and grouping filters to narrow to subjects comprising multiple specific components

GQ Discover



- Use Query Identifier checkboxes to narrow to specific subject combinations, followed by MQSA for drilldown.
- MQSA single-click identification of subjects or PNs comprising multiple query sequences.

Export from either browser into Excel and use pivot table to get quick & easy component combination analysis

GQ Classic

13 Query Sequences

Components: * - Grouped by Query

<< First < Previous Query 1-13 of 13 Next > Last >>

174,127 Results

▼	Query Identifier	Identifier	Patent Family ID	Patent Number	Query % Id	Subj. % Id	Align % Id	Align. Length	Query Start Pos.	Query Stop Pos.	Subj. Start Pos.	Subj. Stop Pos.	Patent SEQ ID NO	Patent Sequence Location	Title
<input type="checkbox"/>	parE	1-1 of 52 [View all 52 Results]													
<input type="checkbox"/>	parE	US20190348154-153544	56014840	US20190348154	100.00	100.00	100.00	312	1	312	1	312	153,544	claim: 1; 4	STABLE PAN-GENOMES AND THEIR USE
<input type="checkbox"/>	parD	1-1 of 86 [View all 86 Results]													
<input type="checkbox"/>	parD	US20190348154-153543	56014840	US20190348154	100.00	100.00	100.00	252	1	252	1	252	153,543	claim: 1; 4	STABLE PAN-GENOMES AND THEIR USE
<input type="checkbox"/>	parC	1-1 of 27 [View all 27 Results]													
<input type="checkbox"/>	parC	US20190348154-153542	56014840	US20190348154	100.00	100.00	100.00	294	1	294	1	294	153,542	claim: 1; 4	STABLE PAN-GENOMES AND THEIR USE
<input type="checkbox"/>	trfA	1-1 of 4,320 [View all 4,320 Results]													
<input type="checkbox"/>	trfA	US20190348154-54020	56014840	US20190348154	100.00	100.00	100.00	1,149	1	1,149	1	1,149	54,020	claim: 1; 4	STABLE PAN-GENOMES AND THEIR USE
<input type="checkbox"/>	parB	1-1 of 25 [View all 25 Results]													
<input type="checkbox"/>	parB	US20190348154-153541	56014840	US20190348154	100.00	100.00	100.00	534	1	534	1	534	153,541	claim: 1; 4	STABLE PAN-GENOMES AND THEIR USE
<input type="checkbox"/>	lacZ	1-1 of 100,000 [View all 100,000 Results]													
<input type="checkbox"/>	lacZ	JP6011759-0015	48187192	JP6011759	100.00	100.00	100.00	21	1	21	1	21	15	probable disclosure (not found by automated parsing)	Silencing suppressor and method for obtaining the

Identify sequences comprising specific query sequence combinations, either at patent number or sequence level

GQ Classic

Group & Filter – Direct Strike (What we did with CDR searches)

Group by and show result per group.

Show only groups with

<input type="text" value="Query Identifier"/>	<input type="text" value="one member matches"/>	<input type="text" value="lacZ"/>	[+]	<input type="button" value="-"/>	<input type="button" value="+"/>
<input type="text" value="Query Identifier"/>	<input type="text" value="one member matches"/>	<input type="text" value="oriT"/>	[+]	<input type="button" value="-"/>	<input type="button" value="+"/>
<input type="text" value="Query Identifier"/>	<input type="text" value="one member matches"/>	<input type="text" value="regulatory1"/>	[+]	<input type="button" value="-"/>	<input type="button" value="+"/>
<input type="text" value="Query Identifier"/>	<input type="text" value="one member matches"/>	<input type="text" value="trfA"/>	[+]	<input type="button" value="-"/>	<input type="button" value="+"/>

Reset

Apply

Works perfectly and is highly specific. Excellent for CDRs

GQ Classic

Broader Search (Pivot Setup)



Home > PIUG PMR elements (vm) > Full all results of workflow PIUG PMR elements (vm)

Result View Export Applications

Filtering Grouping Sorting Sharing Family Portrait Family Portrait (Java) Export PN List LifeQuest

Components: * - Group Filter Applied

Query Identifier

136368 1-1 of 2 regulatory

136369 1-1 of 2 regulatory

4364 1-1 of 2 [View all 2 Results]

5623 1-1 of 2 [View all 2 Results]

90714 1-1 of 2 [View all 2 Results]

92963 1-1 of 2 [View all 2 Results]

13666 1-1 of 2 [View all 2 Results]

Group by Subject and show 1 result per group.

Show only groups with

Group size greater than 1

Reset Apply

Subj. Start Pos.	Subj. Stop Pos.
12	61
10	59

parE	JP2018537123-0055	56889219	JP2018537123	100.00	38.95	100.00	312	1	312	434	745
parE	JP2018527931-0055	56896792	JP2018527931	100.00	38.95	100.00	312	1	312	434	745
parE	US20190078106-0055	56889219	US20190078106	100.00	38.95	100.00	312	1	312	434	745
parE	US20180216123-0055	56896792	US20180216123	100.00	38.95	100.00	312	1	312	434	745
parE	WO2017078836-0055	56889219	WO2017078836	100.00	38.95	100.00	312	1	312	434	745

Here we are just filtering by group size, not specific query sequences comprised by a subject.

Next step (after filtering for % identity or any other attributes), is to export as Excel, and then prepare a pivot table.

GQ Discover

Multiple Query Sequence Analysis

Select query sequences to combine, click MQSA button

- ▼ Query Sequence ID
- ☐ repOrigin (2,696)
 - ☐ oriT (3,896)
 - ☐ regulatory1 (16,089)
 - ☐ regulatory2 (1,332)
 - ☐ lacZ (88,318)
 - ☐ parE (47)
 - ☐ parD (77)
 - ☐ parC (26)
 - ☐ parB (23)
 - ☐ parA (0)
 - ☐ aph (16,089)
 - ☐ trfA (4,304)
 - ☐ kanamycin_PPT (18,752)

Previously filtered out

◀

📈

☰

🖨

OFF

★ ★ ★

Current Page Unannotated

Sort: Highest %Id. Alignment

View: 826,569 Alignments

?

Multiple Query Sequence Analysis

matching all 6 query seqs:	<ul style="list-style-type: none">1 Patent Families3 Patent Numbers
matching 5 out of 6 query seqs:	<ul style="list-style-type: none">172 Patent Families747 Patent Numbers
matching 4 out of 6 query seqs:	<ul style="list-style-type: none">549 Patent Families2,003 Patent Numbers1 Unique Sequences
matching 3 out of 6 query seqs:	<ul style="list-style-type: none">1,807 Patent Families7,583 Patent Numbers52 Unique Sequences
matching 2 out of 6 query seqs:	<ul style="list-style-type: none">3,900 Patent Families16,765 Patent Numbers2,997 Unique Sequences
matching 1 out of 6 query seqs:	<ul style="list-style-type: none">15,981 Patent Families56,798 Patent Numbers179,582 Unique Sequences
Total matching at least one query seq	<ul style="list-style-type: none">22,410 Patent Families83,899 Patent Numbers182,632 Unique Sequences

Reset

View: 826,569 Alignments

Pivot Table Component Analysis

Subject Sequence Level Analysis

Settings Selection Slicer Timeline Connections Data Source Pivot Table Items, & Sets List Buttons Headers																		
A4	Row Labels																	
Count of Query Identifier	Column Labels																	
Row Labels	aph	lacZ	oriT	parB	parC	parD	parE	regulatory1	regulatory2	repOrigin	trfA	Grand Total						
AU2016203675-0056		1		1				1			1	5						
AU2016203675-0064		1		1				1			1	5						
AU2016203675-0065		1		1				1			1	5						
AU2016203675-0066		1		1														
AU2016203675-0067		1		1														
AU2016203675-0068		1		1														
AU2016203675-0071		1		1														
AU2016236175-0048		1	1	1														
CA2413022-0001		2																
CA2417246-0005		1		1				1			1	4						
CA2435081-0020		1		1				1			1	5						
CA2435081-0021		1		1				1			1	5						
CA2435081-0022		1		1				1			1	5						
CA2435081-0023		1		1				1			1	5						
CA2435081-0024		1		1				1			1	5						
CA2435081-0025		1		1				1			1	5						
CA2435081-0028		1		1				1			1	5						
CA2435091-0020		1		1				1			1	5						
CA2435091-0021		1		1				1			1	5						
CA2435091-0022		1		1				1			1	5						
CA2435091-0023		1		1				1			1	5						
CA2435091-0024		1		1				1			1	5						
CA2435091-0025		1		1				1			1	5						
CA2435091-0028		1		1				1			1	5						
CA2484001-0036		1		1				1			1	5						
CA2485060-0038		1		1				1			1	5						
CA2485060-0039		1		1				1			1	5						

SEQ ID NO level
Find hit sequences comprising multiple queries (aka elements or components)

Use filters to quickly drill down to desired combinations

PivotTable Fields

FIELD NAME

☒ Identifier
☒ Query Identifier
☐ Query % Id
☐ Subj. % Id
☐ Align % Id

Filters

Columns

: Query Identifier

Rows

: Identifier

Values

: Count of Query Id...

Summary

- GQ gives you the ability to search and analyze resultsets with multiple query sequences
 - Drill down to a specific subset, then back up to the full set or a different subset
 - Analyze and report on various groupings or all
 - Saving views and filters makes life easier for both experienced and inexperienced users
- Variation searches are tedious and painful!
 - Use the variation landscape for a high-level overview

Thank You!

Questions?

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Bill.Perkins@aptean.com

Stephen.Allen@aptean.com

Ellen.Sherin@aptean.com



WO2018071345A1

wherein the VH comprises heavy chain complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein CDRH1 comprises SEQ ID NO: 3 or SEQ ID NO: 3 with one or two single amino acid substitutions, wherein the substitutions are at positions XI and/or X2 of G-Y-Y-X1-W-X2 (SEQ ID NO: 9); wherein CDRH2 comprises SEQ ID NO: 4, or SEQ ID NO: 4 with one, two, or three single amino acid substitutions; and wherein CDRH3 comprises SEQ ID NO: 5 or SEQ ID NO: 5 with one, two, or three single amino acid substitutions, wherein the substitutions are at positions XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI1, and/or X12 of D-X1-G-X2-T-I-F-X3-X4-X5-I-X6-X7-W-X8-X9-X10-D-X12 (SEQ ID NO: 10); and

wherein the VL comprises light chain complementarity determining regions CDRL1, CDRL2, and CDRL3, wherein CDRL1 comprises SEQ ID NO: 6, or SEQ ID NO: 6 with one, two, or three single amino acid substitutions; wherein CDRL2 comprises SEQ ID NO: 7, or SEQ ID NO: 7 with one, two, or three single amino acid substitutions; and wherein CDRL3 comprises SEQ ID NO: 8, or SEQ ID NO: 8 with one, two, or three single amino acid substitutions.

7. The antibody or fragment thereof of claim 6, wherein the amino acid at position XI of SEQ ID NO: 9 is substituted with alanine, the amino acid at position X2 of SEQ ID NO: 9 is substituted with alanine, or the amino acids at positions XI and X2 of SEQ ID NO: 9 are substituted with alanine.

1. Search chains & CDRs GenePast, 65% over query
2. Group/MQW for chains comprising all 3 (first filter for subj seq length >40 to get chains, q seq length <40 to get CDRs.
3. HC first query id contains *HC*– comprises all 3
4. Annotate all 3 red
5. Filter SID3, pos 4 or 6 for ala; annotate 1 star (red and 1 star means has variant SID3. Generate landscape report.
6. Red & 1 star
7. Filter SID 4 broad, mark 2 star

WO2018071345A1 plan b

wherein the VH comprises heavy chain complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein CDRH1 comprises SEQ ID NO: 3 or SEQ ID NO: 3 with one or two single amino acid substitutions, wherein the substitutions are at positions XI and/or X2 of G-Y-Y-X1-W-X2 (SEQ ID NO: 9); wherein CDRH2 comprises SEQ ID NO: 4, or SEQ ID NO: 4 with one, two, or three single amino acid substitutions; and wherein CDRH3 comprises SEQ ID NO: 5 or SEQ ID NO: 5 with one, two, or three single amino acid substitutions, wherein the substitutions are at positions XI, X2, X3, X4, X5, X6, X7, X8, X9, X10, XI1, and/or X12 of D-X1-G-X2-T-I-F-X3-X4-X5-I-X6-X7-W-X8-X9-X10-D-X12 (SEQ ID NO: 10); and

wherein the VL comprises light chain complementarity determining regions CDRL1, CDRL2, and CDRL3, wherein CDRL1 comprises SEQ ID NO: 6, or SEQ ID NO: 6 with one, two, or three single amino acid substitutions; wherein CDRL2 comprises SEQ ID NO: 7, or SEQ ID NO: 7 with one, two, or three single amino acid substitutions; and wherein CDRL3 comprises SEQ ID NO: 8, or SEQ ID NO: 8 with one, two, or three single amino acid substitutions.

7. The antibody or fragment thereof of claim 6, wherein the amino acid at position XI of SEQ ID NO: 9 is substituted with alanine, the amino acid at position X2 of SEQ ID NO: 9 is substituted with alanine, or the amino acids at positions XI and X2 of SEQ ID NO: 9 are substituted with alanine.

1. Search chains & CDRs GenePast, 65% over query
2. Group for chains comprising all 3, make vdb
3. Search against these chains and do vm analysis. Since they already comprise all 3 I don't have to annotate them, so I can do the variants and not out the ones with non-specified mismatches.
4. The goal is less about finding the ones in scope than it is notting out the ones out of scope.
5. I wonder if for sid5 I'd be better off to fix the stated residues, and do a query % ID cutoff for the rest.19 residues/3 mismatches 84.2% QID and just fix pos 1,3,5,6,7,

Additional CDR Methods

Results Pre & Post filtering

Patent-Level Grouping

1MM sequences



Filter



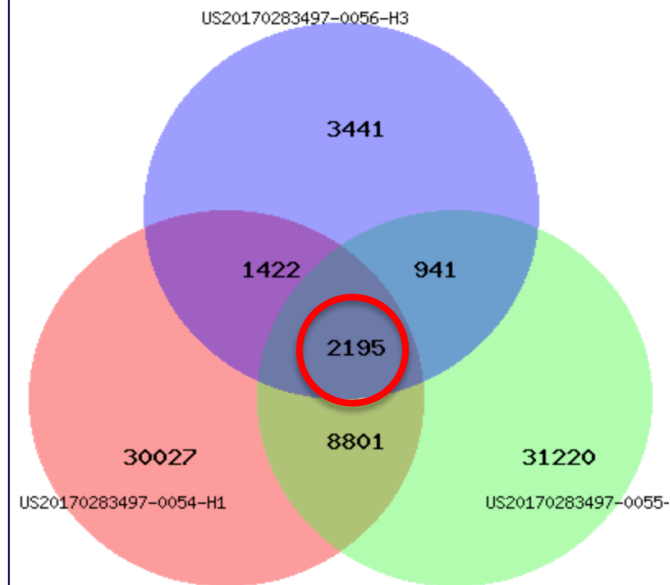
1.3K sequences

BROWSE

Browse [1029988](#) results, [1029988](#) patent only results, or [0](#) non patent results.

VENN DIAGRAM

This is a Venn diagram of your 3 queries with hits to patents. The clickable numbers



Intermediate Page

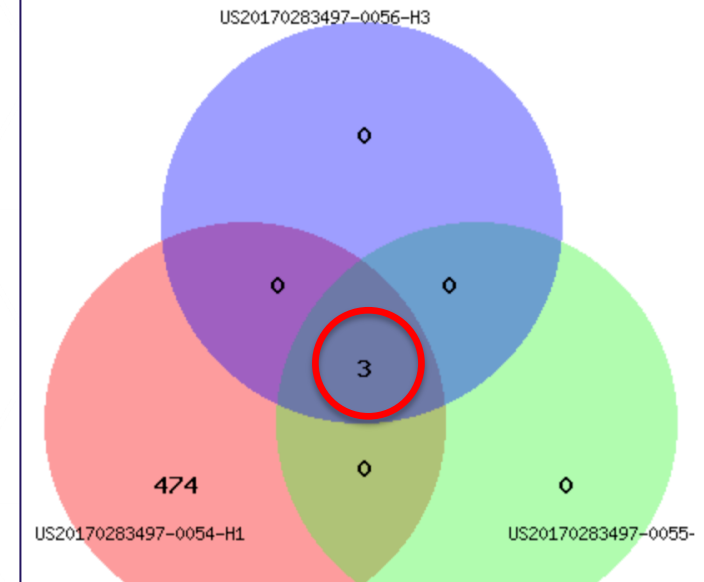
STATISTICS

Total number of hits: 1,029,988
Number of hits where a query is identical to a subject: 1,200

Global Statistics

There were original queries of which 3 have hits
There are 1266 hits to the patent databanks.
There is a total of 477 patent documents from 204 INPADOC patent families.
The earliest priority date is : IN249086 20050202

Venn Diagram of the number of document by matching queries



Patent Statistics Page

Number of documents per query

[Spreadsheet](#) of all hits classified by patents.

3 documents match 3 of the 3 queries

[Link to Results](#)

Motif – Targeted Results



Result View Export Applications0 results selected [x]

Filtering ▾

Grouping ▾

Sorting ▾

Sharing ▾

Family Portrait

Export PN List ▾

LifeQuest

Try Out New Interface

1_GP_view: - Grouped by Patent family ID

<< First < Previous Patent family ID 1-31 of 31 Next > Last >>

322 Results

Query % Id	Subj. % Id	Align % Id	Align. Length	Query % Align. Cov.	Subj. % Align. Cov.	Query Identifier	Identifier	Description / Title	Extended Legal Status	Earliest Priority Date	Normalized Parent	Patent Number	PDF Link	Patent Family ID
39144327 1-1 of 33 [View all 33 Results]														
100.00	17.48	100.00	82	100.00	17.48	US20180099045-0007_HC_Motif	JP6223771-0001	Anti-KIR Antibody, Formulation, and Uses Thereof	GRANTED	11-Jan-2007	ノヴォ ノルディスク アクティーゼルスカブ ; ノヴォ ノルディスク アクティーゼルスカブ	JP6223771	PDF	39144327
54478990 1-1 of 10 [View all 10 Results]														
100.00	66.67	100.00	82	100.00	66.67	US20180099045-0007_HC_Motif	WO2016069589-0001	TREATMENT OF PEDIATRIC BCP-ALL PATIENTS WITH AN ANTI-KIR ANTIBODY	LAPSED	28-Oct-2014	UNIV CHILDREN S HOSPITAL TÜBINGEN [DE];	WO2016069589	PDF	54478990
WO2018093907 1-1 of 2 [View all 2 Results]														
100.00	18.22	100.00	82	100.00	18.22	US20180099045-0007_HC_Motif	WO2018093907-0022	COMBINATION IMMUNOTHERAPIES FOR TREATMENT OF CANCER	UNKNOWN	16-Nov-2016	PRIMEVAX IMMUNO-ONCOLOGY, INC.;	WO2018093907	PDF	WO2018093907
US20180117147 1-1 of 4 [View all 4 Results]														
100.00	18.22	100.00	82	100.00	18.22	US20180099045-0007_HC_Motif	US20180117147-0001	COMBINATION OF ANTI-KIR AND ANTI-CTLA-4 ANTIBODIES TO TREAT CANCER	PENDING	n/a	BRISTOL-MYERS SQUIBB COMPANY; INNATE PHARMA	US20180117147	PDF	US20180117147

- Alignment
- Patent
- Subject Annotation
- Subject Sequence
- Query Sequence
- Report data issue



- See all subjects mapped to this query
- See all queries mapped to this subject

A part of your query matches a part of this sequence. GQ subject-centric view.

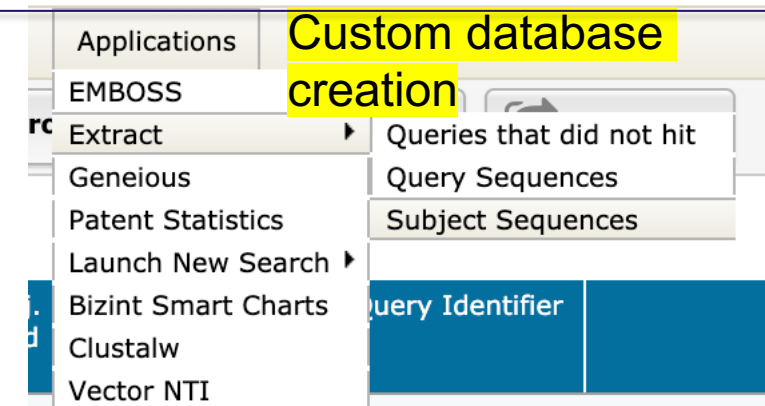
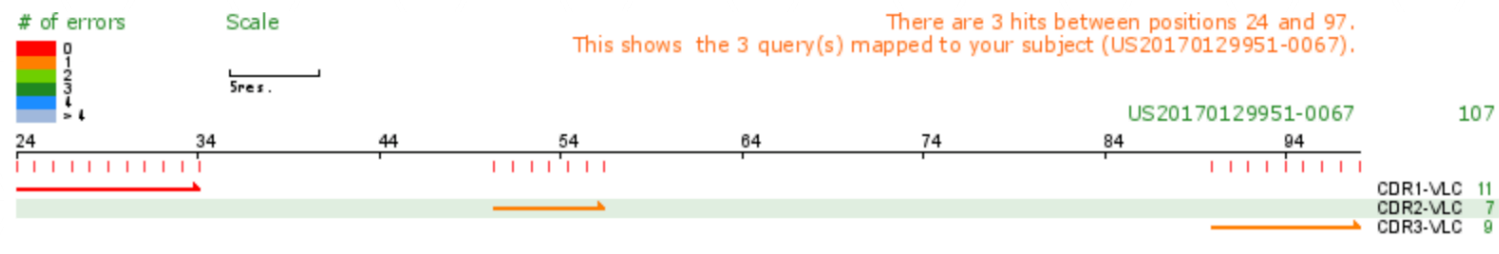
Align len= 82 aa, , Identity= 100%, Similarity= 100%
Query (US20180099045-0007_HC_Motif) len= 39 unk, pos= 1-82 aa (fw), Identity query= 100%, Nb gaps query= 0, Alignment coverage query= 100%
Subject (US20180117147-0001) len= 450 aa, pos= 31-112 aa , Identity subject= 18.22%, Nb gaps subject= 0, Alignment coverage subject= 18.22%

Q: 1 FYAISWVRQAPGQGLEWMGGFIPIFGAANYAQKFGQGRVTITADESTSTAYMELSSLRSD 60
S: 31 FYAISWVRQAPGQGLEWMGGFIPIFGAANYAQKFGQGRVTITADESTSTAYMELSSLRSD 90

Q: 61 TAVYYCARIPSGSYYYDYDMDV 82
S: 91 TAVYYCARIPSGSYYYDYDMDV 112

Method 3 Search within Hits (Use for Huge Resultsets)

1. Search just LC and HC full length
2. Filter for 80% (or appropriate) query identity, zero gaps, which will only return full length hits and omit CDR and non-specific short hits.
3. Export filtered results to custom database (optionally separate LC from HC; this would result in two custom databases if desired-filter first for query id=LC, extract, then filter for query id=HC, extract)
4. Search all 3 (or 6) corresponding CDRs against appropriate custom db
5. Filter for desired % ID/# of differences
6. Use group by subject, filter for query identifier = method shown earlier



GQ Patent Statistics

Grouping on Steroids



Table of Contents

[Global Statistics](#)

[Number of documents per query](#)

[Number of documents by authority](#)

Global Statistics

There were original queries of which 11 have hits

There are 90985 hits to the patent databanks.

There is a total of 16128 patent documents from 4806 INPADOC patent families.

The earliest priority date is : EP134242 19830128

Number of documents per query

[Spreadsheet](#) of all hits classified by patents.

[2](#) documents match 7 of the 11 queries

[50](#) documents match 6 of the 11 queries

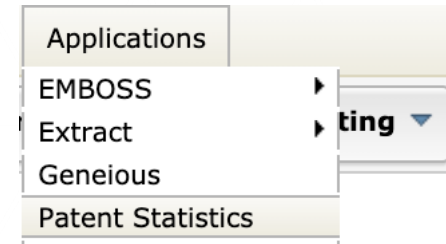
[165](#) documents match 5 of the 11 queries

[171](#) documents match 4 of the 11 queries

[1627](#) documents match 3 of the 11 queries

[3104](#) documents match 2 of the 11 queries

[11009](#) documents match 1 of the 11 queries



This is on the patent number level...a little later we will talk about identifying hit sequences comprising different combinations of query sequences

Patent Statistics Report

PN Level

Home > 6_CDR_GP_80 > Full aIn results of work

Result View Export Applications

Filtering

Numeric: * - Grouped by Sub Filter Applied

Query Identifier

13 1-3 of 3

EMBOSS
Extract
Geneious
Patent Statistics
Launch New Search
Bizint Smart Charts
Clustalw
Vector NTI

29 documents match 6 of the 6 queries

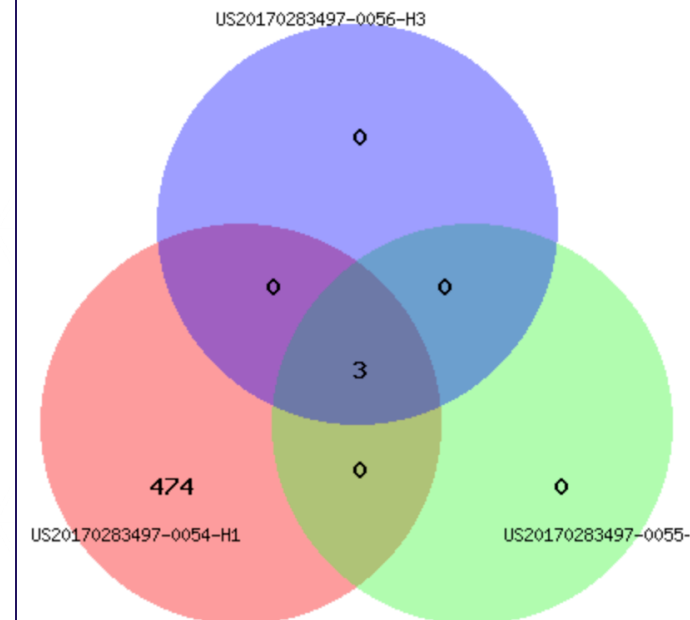
PATENT NUMBER	NB QUERIES	QUERY 1	QUERY 2	QUERY 3	QUERY 4	QUERY 5	QUERY 6	PATTERN
CA2754113	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
CA2851737	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
CA2856866	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
EP2408816	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2012520679	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2014140372	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2015214563	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP2015505822	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP5498566	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP5980384	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
JP6203740	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
KR1020110128948	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
KR1020130067314	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
KR20130067314	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20100254975	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20120177662	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20120183561	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20130302354	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20140322209	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20150086563	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US20170275365	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8444981	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8454961	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8454962	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US8871490	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
US9499620	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
WO2010107752	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
WO2013078375	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY
WO2017180587	6	37-CDR1	37-CDR2	37-CDR3	9-CDR1	9-CDR2	9-CDR3	YYYYYY

Excel export

Global Statistics

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The earliest priority date is : IN249086 20050202

Venn Diagram of the number of document by matching queries



Number of documents per query

Spreadsheet of all hits classified by patents.

3 documents match 3 of the 3 queries

US 8106170 B2

CLAIMS

1. A composition comprising at least two immunoglobulins that are capable of specifically binding to Spike (S) protein of Severe Acute Respiratory Syndrome Coronavirus (SARS-Co-V) and neutralizing **SARS-CoV**, wherein the first immunoglobulin comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 4 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 8, and wherein the second immunoglobulin comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 6 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 10, and wherein the relative amounts of the at least two immunoglobulins are such that they exhibit a synergistic neutralizing activity.
2. The composition of claim 1, wherein the immunoglobulins are capable of reacting with different, non-competing epitopes of the S protein of **SARS-CoV**.
3. The composition of claim 2, wherein the immunoglobulins are capable of reacting with different, non-competing epitopes of amino acids 318-510 of the S protein (SEQ ID NO:115) of **SARS-CoV**.
4. The composition of claim 1, wherein at least one of the immunoglobulins is capable of reacting with an animal SARS-like CoV at a region corresponding to amino acids 318-510 of the S protein (SEQ ID NO: 115) of **SARS-CoV**.

- A composition comprising at least two immunoglobulins that are capable of specifically binding to Spike (S) protein of Severe Acute Respiratory Syndrome Coronavirus (SARS-Co-V) and neutralizing **SARS-CoV**, wherein the first immunoglobulin comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 4 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 8, and wherein the second immunoglobulin comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 6 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 10, and wherein the relative amounts of the at least two immunoglobulins are such that they exhibit a synergistic neutralizing activity.