

1. Write a query to get data having length of Rna structures more than 12 with them being added after 2008.

SELECT *

FROM rna

WHERE rna.len >12

AND EXTRACT (YEAR FROM rna. timestamp) > 2008

LIMIT 1000;

Query

Query History

1

SELECT *

2

FROM rna

3

WHERE rna.len > 12

4

AND EXTRACT(YEAR FROM rna.timestamp) > 2008

5

LIMIT 1000;

6

Data Output

Messages

Notifications

<

2. How many pre computed RNA are present that are still active and got their last release update before 2022

```
SELECT COUNT (*) AS Active_Release_Before_2022  
FROM rnc_rna_precomputed  
WHERE is_active = true  
AND last_release < 2022;
```

Query		Query History		Scratch Pad	
1	SELECT	COUNT(*)	AS Active_Release_Before_2022		
2	FROM	rnc_rna_precomputed			
3	WHERE	is_active = true			
4	AND	last_release < 2022;			
5					

Data Output		Messages		Notifications	
active_release_before_2022	bigint				
1	70886776				

3. How many total pre computed RNA records for snoRNA and tRNA were recorded in 2011, 2016, 2014, and 2020.

```
SELECT EXTRACT (YEAR FROM update_date) AS year, rna_type, COUNT (*)
FROM rnc_rna_precomputed
WHERE rna_type IN('snoRNA','tRNA')
AND EXTRACT (YEAR FROM update_date) IN (2011, 2014, 2016, 2020)
GROUP BY year, rna_type
ORDER BY year, rna_type
LIMIT 1000;
```

Query

Query History

Scratch Pad

1

SELECT EXTRACT(YEAR FROM update_date) AS year, rna_type, COUNT(*)

2

FROM rnc_rna_precomputed

3

WHERE rna_type IN ('snoRNA', 'tRNA')

4

AND EXTRACT(YEAR FROM update_date) IN (2011, 2014, 2016, 2020)

5

GROUP BY year, rna_type

6

ORDER BY year, rna_type

7

LIMIT 1000;

Data Output

Messages

Notifications

+

SQL

year

double precision

rna_type

character varying (500)

count

bigint

1

2020

snoRNA

70872

2

2020

tRNA

844505

4. Can you give me the names of all databases built for RNA with minimum length other than 100, 200, 300, 400, and 15?

SELECT display_name

FROM rnc_database

WHERE min_length NOT IN (100,200,300,400,15)

LIMIT 1000;



The screenshot shows a SQL query editor interface. The query editor has tabs for 'Query' and 'Query History'. The query text is as follows:

```
1 SELECT display_name
2 FROM rnc_database
3 WHERE min_length NOT IN (100, 200, 300, 400, 15)
4 LIMIT 1000;
5
```

Below the query editor is a 'Data Output' tab, which is currently active. It shows a table with the following data:

	display_name character varying (60)
1	ENA
2	GENCODE
3	MGnify
4	GeneCards
5	RDP
6	snoRNA Database
7	Rfam
8	TAIR
9	PSICOIIC

5. Can you get complete 500 records of sequences for active regions and name your column as myregions in which you are getting the region name column value. Then tell me what different chromosomes with exon_count we have for regions including centre, east and north using the name you set for your column.

```
SELECT region_name AS myregions
FROM rnc_sequence_regions
WHERE region_name IS NOT NULL
LIMIT 500;

SELECT DISTINCT chromosome, exon_count
FROM rnc_sequence_regions
WHERE region_name IN ('center', 'east', 'north')
LIMIT 1000;
```

Query	Query History
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1	▼	SELECT region_name AS myregions
2		FROM rnc_sequence_regions
3		WHERE region_name IS NOT NULL
4		LIMIT 500;
5	▼	SELECT DISTINCT chromosome, exon_count
6		FROM rnc_sequence_regions
7		WHERE region_name IN ('center', 'east', 'north')
8		LIMIT 1000;