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

Select \*

From Enacen.rna

Where (“timestamp” > ‘2008-12-31 00:00:00’) AND (rna.len > 12)

Limit 500

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

Select count (distinct rrp.id)

From enacen.rnc\_rna\_precomputed rrp

Where rrp.update\_date < ’2022-01-01’ AND (rrp.is\_active = true)

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

Select count(rrp.id)

From rnacen.rnc\_rna\_precomputed rrp

Where rrp.rna\_type IN (‘snoRNA’, ‘tRNA’) AND extract (YEAR FROM rrp.update\_date) IN (2011, 2014. 2016, 2020)

Query 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 Distinct rrp.databases

From enacen.rnc\_rna\_precomputed rrp

Join enacen.rna ON rrp.upi

Where rna.len NOT IN (100, 200, 300, 400, 500)

Query 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 center, east and north using the name you set for your column?

Select rsra.id, rsra.chromosome, rsra.exon\_count, rsra.region\_name as myregions

From rnacen.rnc\_sequence\_regions\_active rsra

Limit 500