Scatter Plot for Query Sequence q1

Trends in the Scatter Plot:
General Trends:
Most alignment scores are low (0-50).
One outlier has a high score (~200).

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
Higher density of points at shorter lengths (0-200 bp) and low scores (0-50).

Outliers:
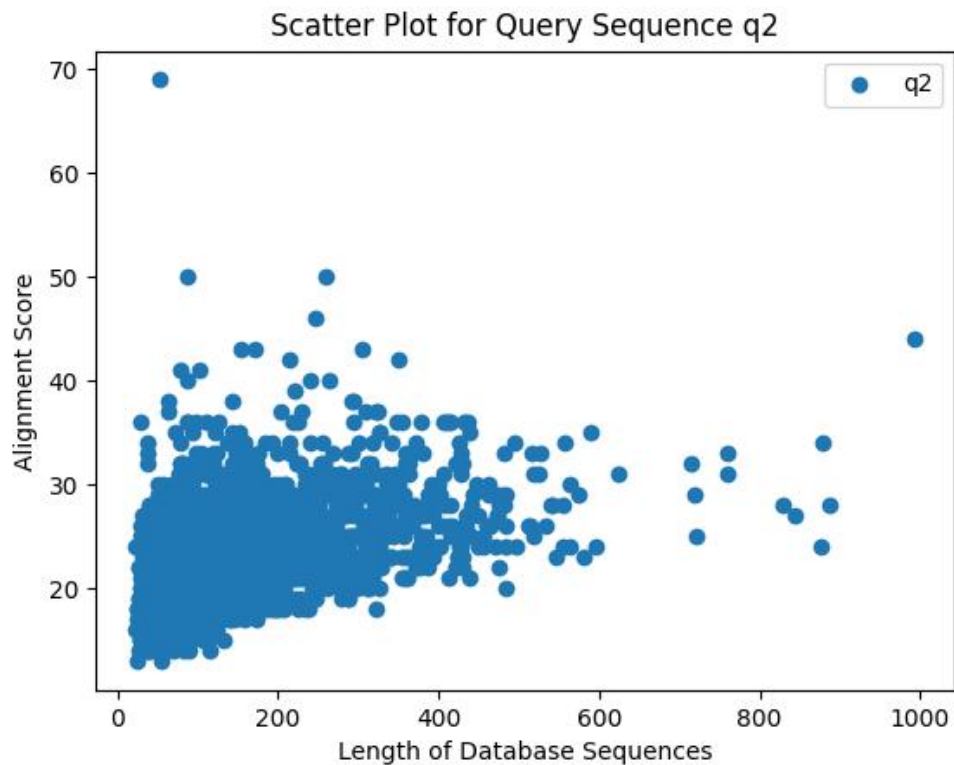One short sequence (<200 bp) has a high alignment score (~200).

Indications:
For query sequence q1:
Generally low similarity with most database sequences.
One short sequence has a very high similarity, warranting further investigation.

Future Steps:

Examine the high-scoring alignment to understand the strong match.
Explore biological significance of the matched sequence.

Scatter Plot for Query Sequence q2

Trends in the Scatter Plot for Query Sequence q2:

General Trends:
  - Most alignment scores are between 20 and 40.
  - One outlier has a score near 70.

 Sequence Lengths:
   - Database sequences range from very short to around 1000 base pairs.
   - High density of points at shorter lengths (0-300 bp) and scores (20-40).

Outliers:
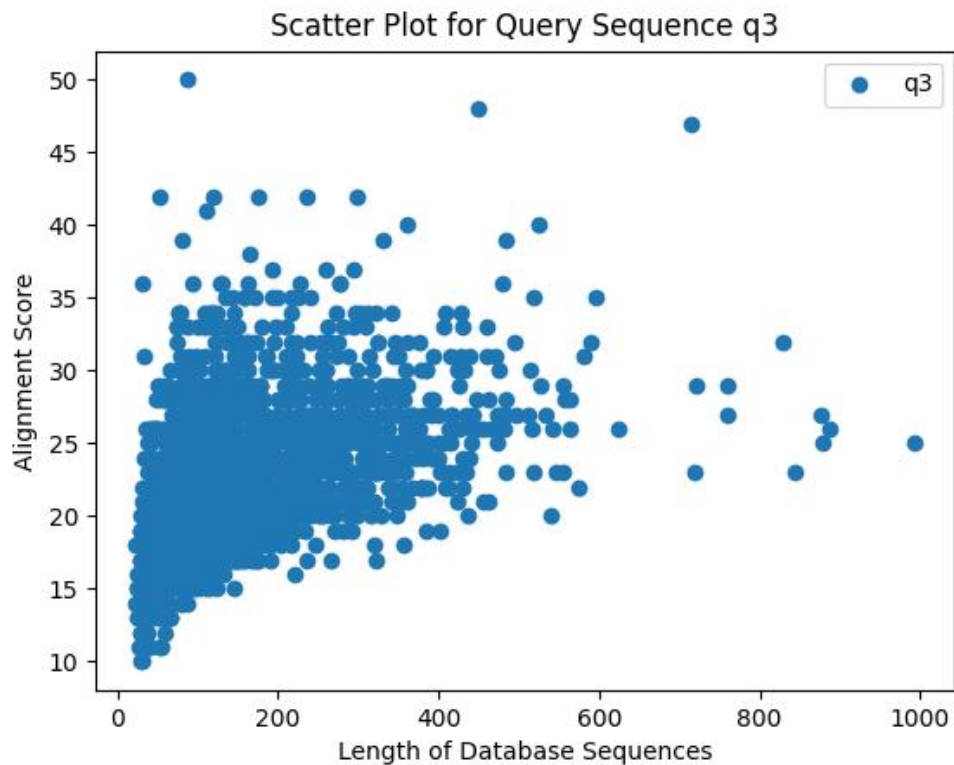   One short sequence (<100 bp) has a high alignment score (~70).

Indications:

 For query sequence q2:
  - Shows moderate similarity (scores 20-40) with many database sequences.
  - One sequence has a very high alignment score, worth further examination.

Future Steps:
  - Investigate the high-scoring alignment for its strong match.
  - Explore the biological significance of the matched sequence.

Scatter Plot for Query Sequence q3

Trends in the Scatter Plot for Query Sequence q3:

General Trends:
Most alignment scores are between 20 and 35.
A few outliers have scores between 40 and 50.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
High density of points at shorter lengths (0-300 bp) and scores (20-35).

Outliers:
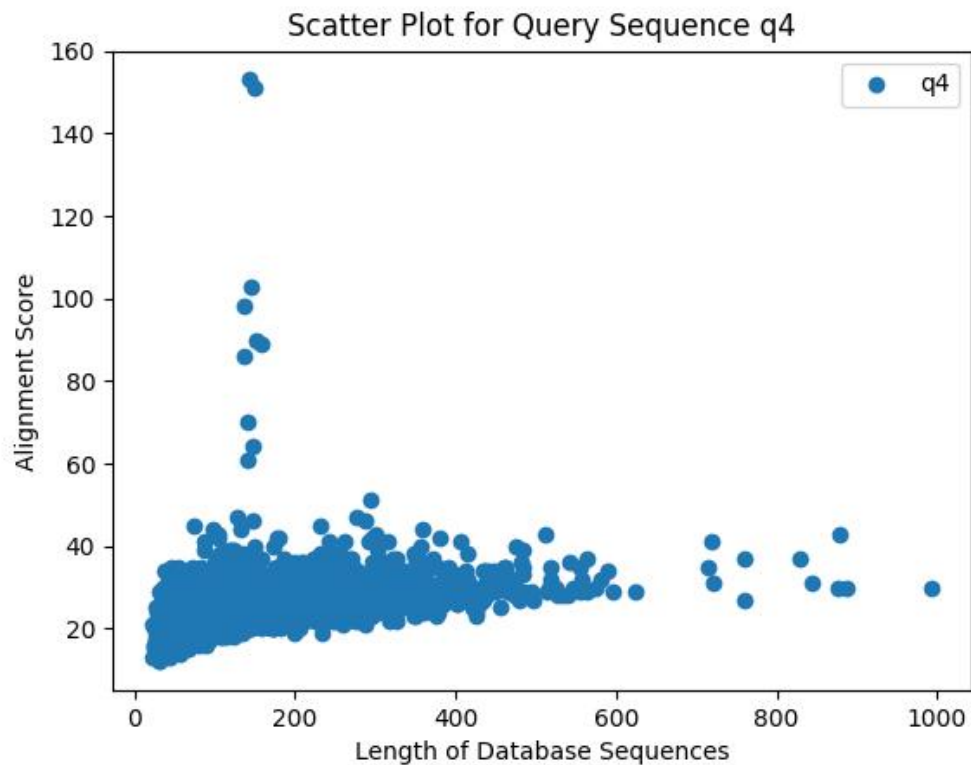A few sequences have high alignment scores (40-50), regardless of their lengths.

Indications:

For query sequence q3:
Shows moderate similarity (scores 20-35) with many database sequences.
A few sequences have very high alignment scores, suggesting strong matches.

Future Steps:
Investigate the high-scoring alignments to understand their strong matches.
Explore the biological significance of these matched sequences.

Trends in the Scatter Plot for Query Sequence q4:

General Trends:
Most alignment scores are clustered between 20 and 40.
Several high-scoring outliers exist, with scores up to 160.

Sequence Lengths:
Database sequences vary from very short to around 1000 base pairs.
High density of points at shorter lengths (0-200 bp) and scores (20-40).

Outliers:
Multiple outliers with high alignment scores (>100) are found among shorter sequences (<200 bp).

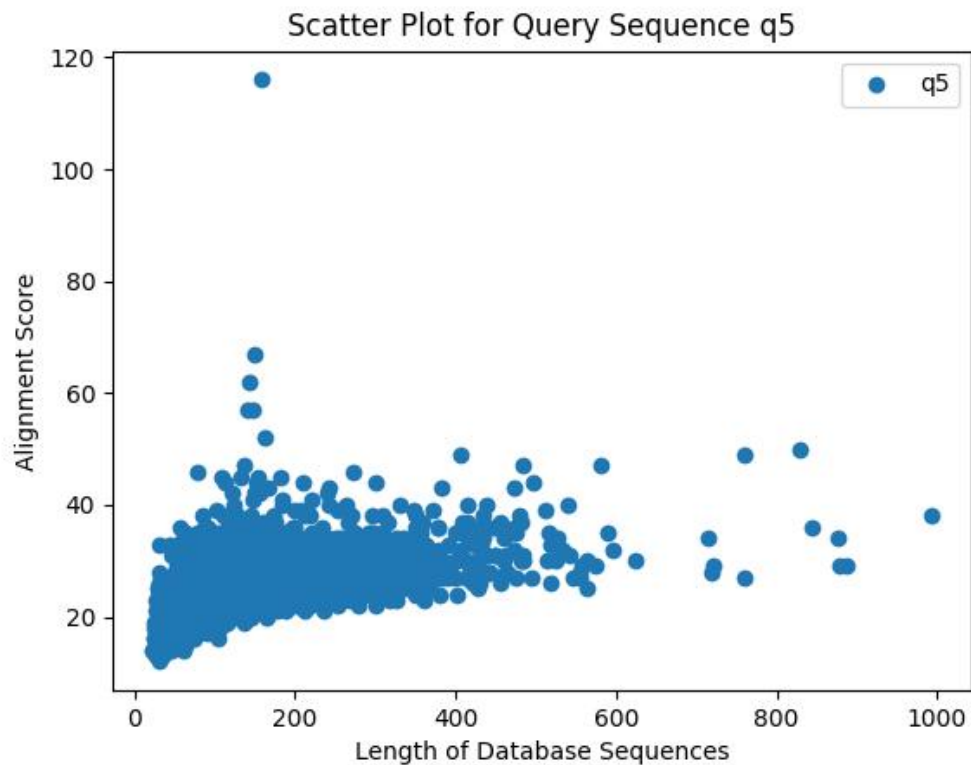**Indications:**
For query sequence q4:

Generally moderate similarity (scores 20-40) with many database sequences.
Several short sequences have very high alignment scores, indicating strong matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q5

Trends in the Scatter Plot for Query Sequence q5:

General Trends:
Most alignment scores cluster between 20 and 40.
A few outliers exist with scores reaching up to 120.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
High density of points at shorter lengths (0-200 bp) and scores (20-40).

Outliers:
Some outliers have high alignment scores (>60) and appear among shorter sequences (<200 bp).
Sparse high-scoring points scattered across longer sequence lengths.

Indications:
For query sequence q5:

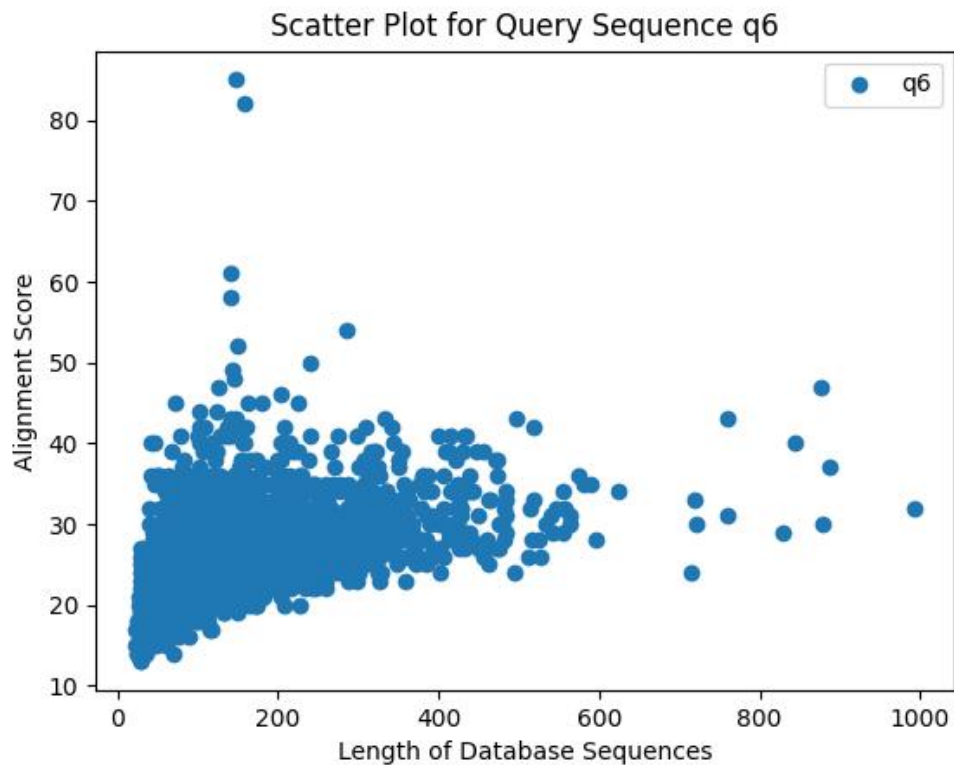Generally moderate similarity (scores 20-40) with many database sequences.
Some short sequences show very high alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q6

Trends in the Scatter Plot for Query Sequence q6:

General Trends:
Most alignment scores are clustered between 20 and 40.
A few high-scoring outliers exist, with scores up to 80.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
High density of points at shorter lengths (0-200 bp) and scores (20-40).

Outliers:
Some outliers have high alignment scores (>60), mostly among shorter sequences (<200 bp).
Few high-scoring points are scattered across longer sequence lengths.
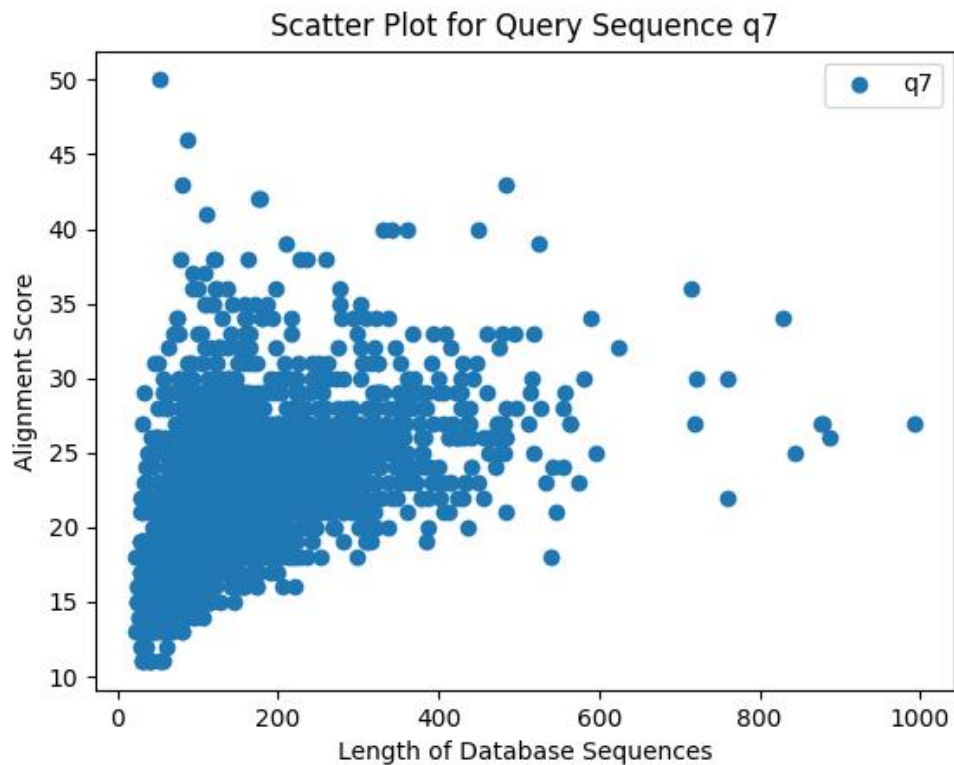
Indications:
For query sequence q6:

Generally moderate similarity (scores 20-40) with many database sequences.
Some short sequences exhibit very high alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q7

Trends in the Scatter Plot for Query Sequence q7:

General Trends:
Most alignment scores are clustered between 20 and 30.
A few high-scoring outliers exist, with scores reaching up to 50.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
High density of points at shorter lengths (0-300 bp) and scores (20-30).

Outliers:
Some outliers have high alignment scores (>40), mostly among shorter sequences (<300 bp).
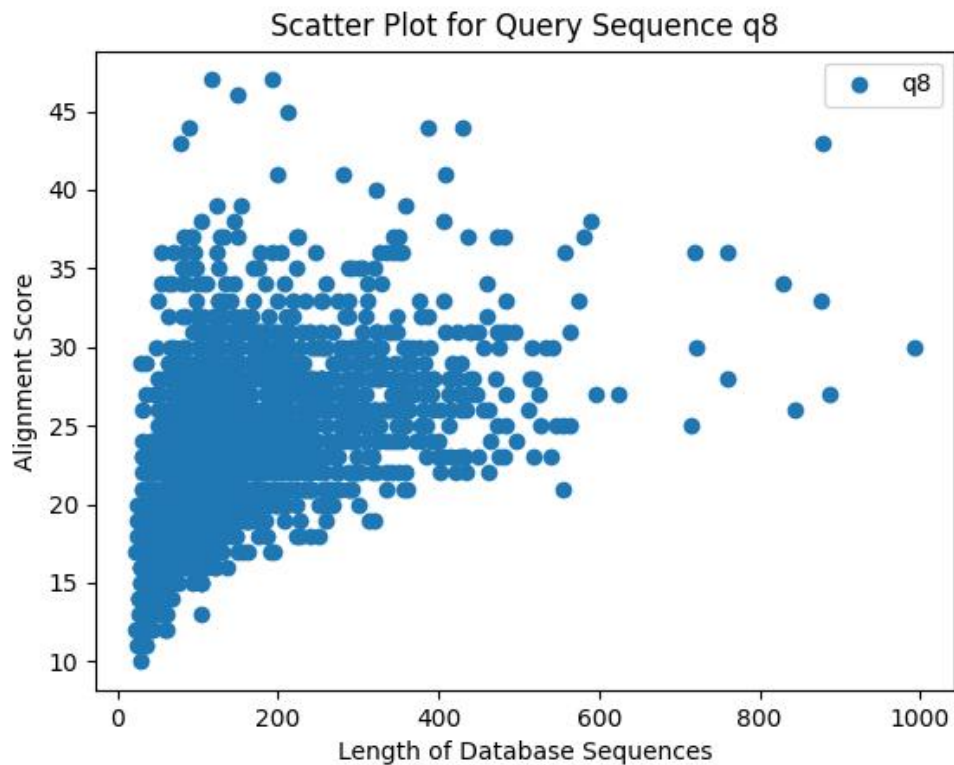Sparse high-scoring points are scattered across longer sequence lengths.

Indications:

For query sequence q7:
Generally moderate similarity (scores 20-30) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q8

Trends in the Scatter Plot for Query Sequence q8:

General Trends:
Most alignment scores are clustered between 0 and 25.
There are a few high-scoring outliers, with scores reaching up to 45.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
There is a high density of points at shorter lengths (0-300 bp) and alignment scores (0-25).

Outliers:
Some outliers have high alignment scores (>35), mostly among shorter sequences (<300 bp).
Sparse high-scoring points are scattered across longer sequence lengths.

Indications:
Generally, there is moderate similarity (scores 0-25) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
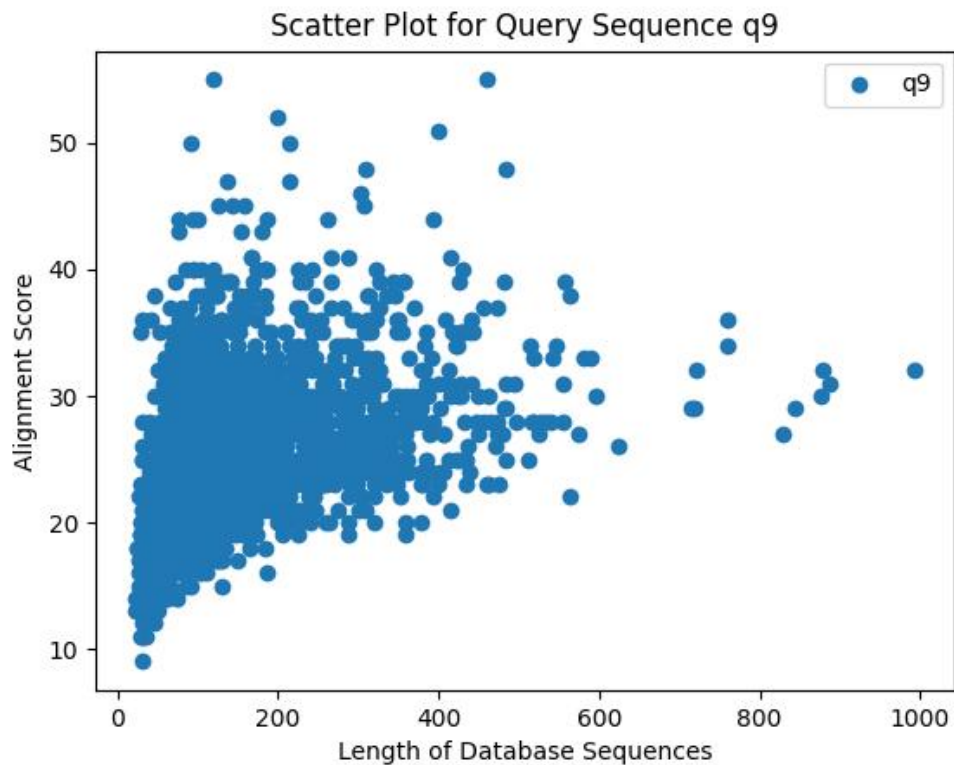Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q9

Trends in the Scatter Plot for Query Sequence q9:

General Trends:
Most alignment scores are clustered between 0 and 30.
There are a few high-scoring outliers, with scores reaching up to 60.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
There is a high density of points at shorter lengths (0-400 bp) and alignment scores (0-30).

Outliers:
Some outliers have high alignment scores (>40), mostly among shorter sequences (<400 bp).
Sparse high-scoring points are scattered across longer sequence lengths.

Indications:
Generally, there is moderate similarity (scores 0-30) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q10
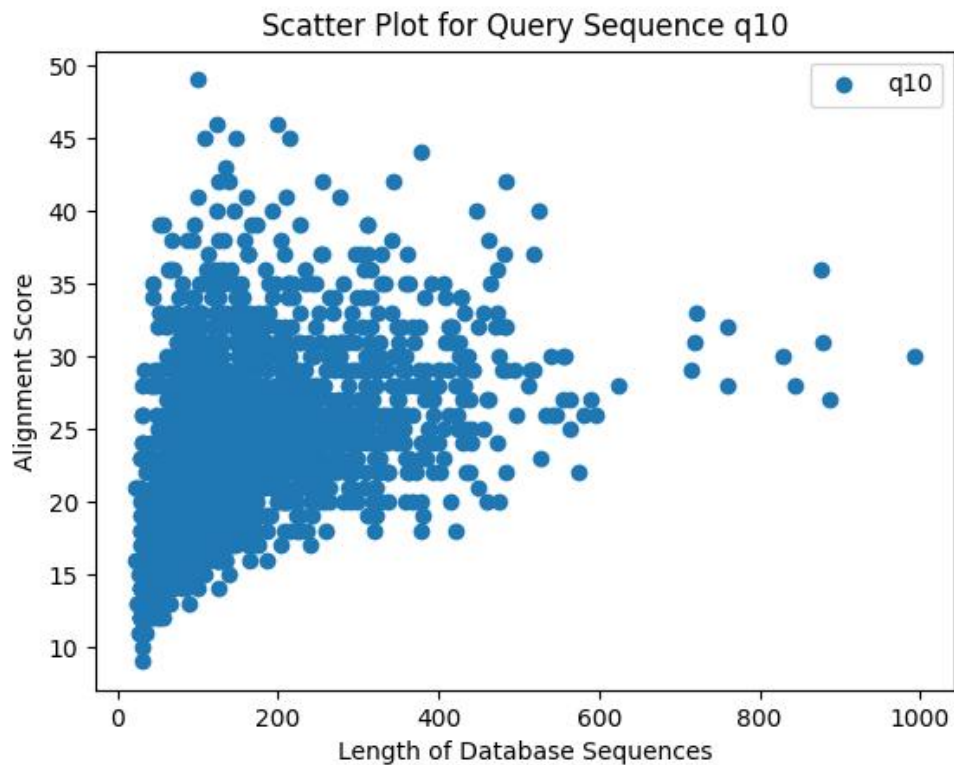
Trends in the Scatter Plot for Query Sequence q10:

General Trends:
Most alignment scores are clustered between 0 and 35.
There are a few high-scoring outliers, with scores reaching up to 50.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
There is a high density of points at shorter lengths (0-600 bp) and alignment scores (0-35).

Outliers:
Some outliers have high alignment scores (>40), mostly among shorter sequences (<600 bp).
Sparse high-scoring points are scattered across longer sequence lengths.

Indications:
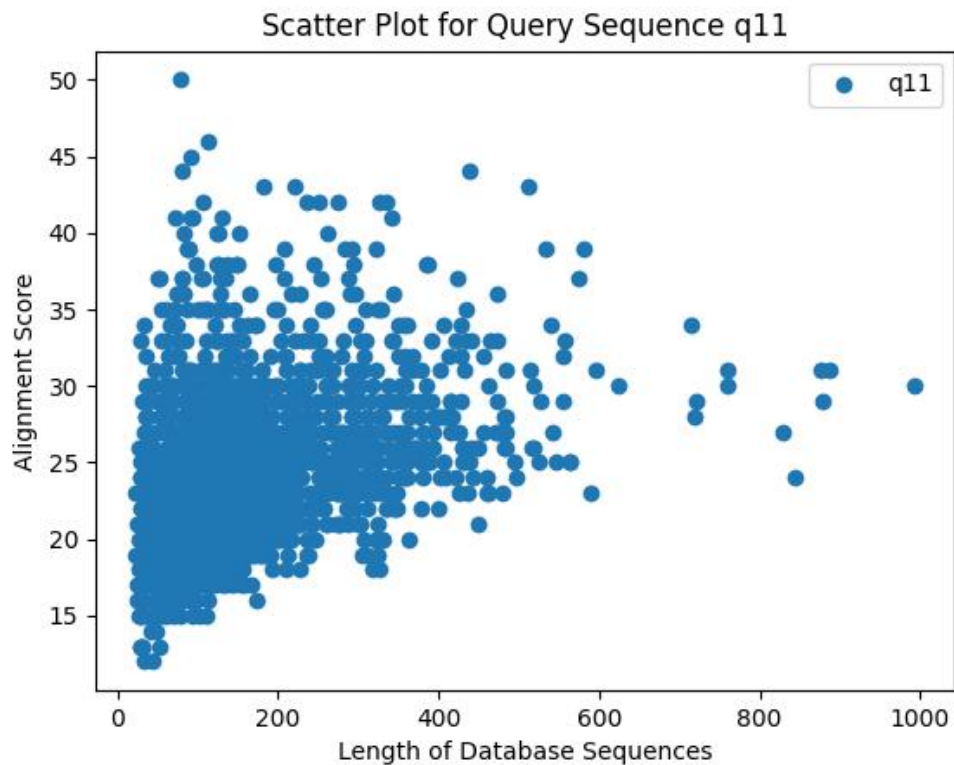Generally, there is moderate similarity (scores 0-35) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q11

Trends in the Scatter Plot for Query Sequence q11:

General Trends:
Most alignment scores are clustered between 0 and 35.
There are a few high-scoring outliers, with scores reaching up to 50.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
There is a high density of points at shorter lengths (0-600 bp) and alignment scores (0-35).

Outliers:
Some outliers have high alignment scores (>40), mostly among shorter sequences (<600 bp).
Sparse high-scoring points are scattered across longer sequence lengths.

Indications:
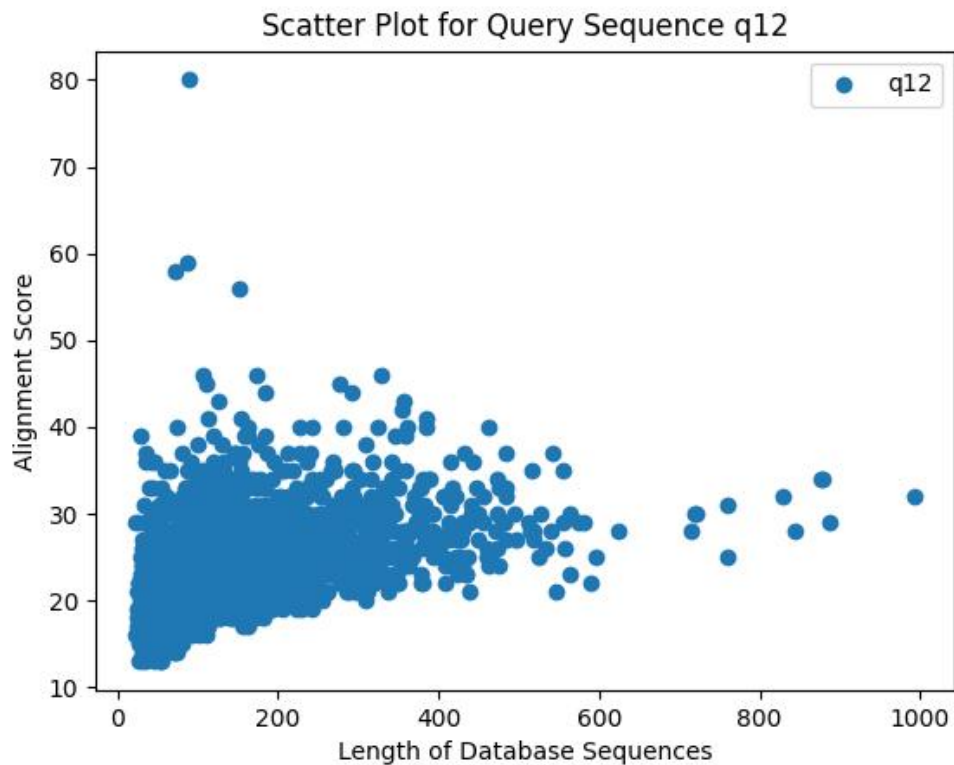Generally, there is moderate similarity (scores 0-35) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Scatter Plot for Query Sequence q12

Trends in the Scatter Plot for Query Sequence q12:

General Trends:
Most alignment scores are clustered between 0 and 35.
There are a few high-scoring outliers, with scores reaching up to 50.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
There is a high density of points at shorter lengths (0-600 bp) and alignment scores (0-35).

Outliers:
Some outliers have high alignment scores (>40), mostly among shorter sequences (<600 bp).
Sparse high-scoring points are scattered across longer sequence lengths.

Indications:
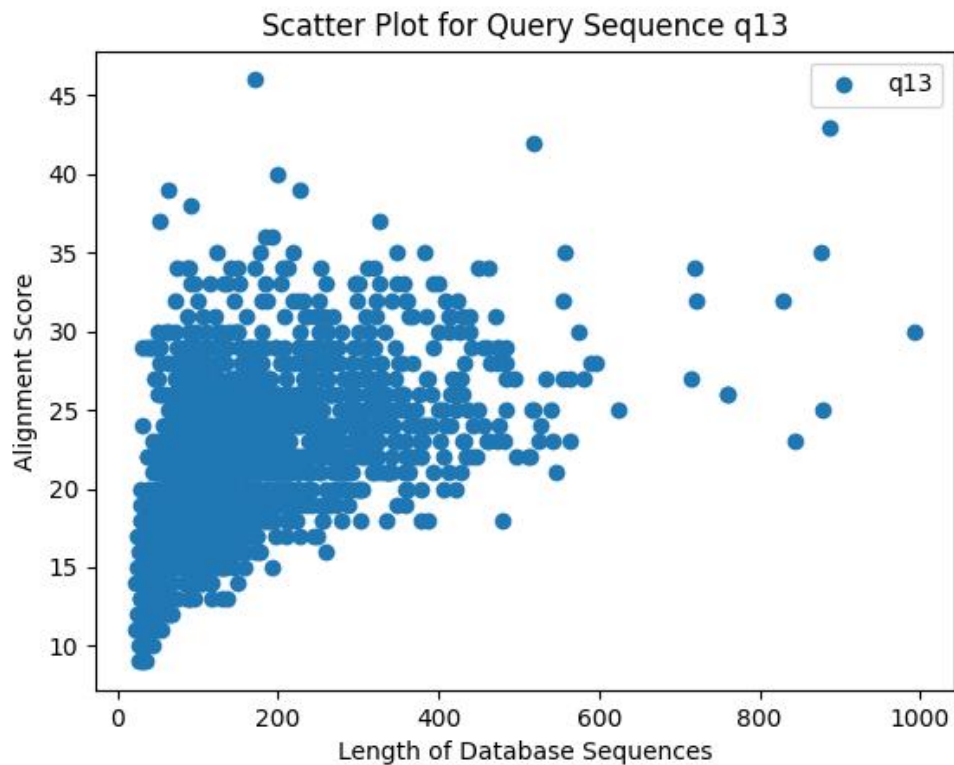Generally, there is moderate similarity (scores 0-35) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.

Trends in the Scatter Plot for Query Sequence q13:

General Trends:
Most alignment scores are clustered between 0 and 35.
There are a few high-scoring outliers, with scores reaching up to 50.

Sequence Lengths:
Database sequences range from very short to around 1000 base pairs.
There is a high density of points at shorter lengths (0-600 bp) and alignment scores (0-35).

Outliers:
Some outliers have high alignment scores (>40), mostly among shorter sequences (<600 bp).
Sparse high-scoring points are scattered across longer sequence lengths.

Indications:
Generally, there is moderate similarity (scores 0-35) with many database sequences.
Some short sequences show higher alignment scores, indicating strong matches.
Longer sequences tend to have lower or moderate alignment scores, suggesting weaker matches.

Future Steps:
Investigate high-scoring alignments to understand strong matches.
Explore the biological significance of these matched sequences.