

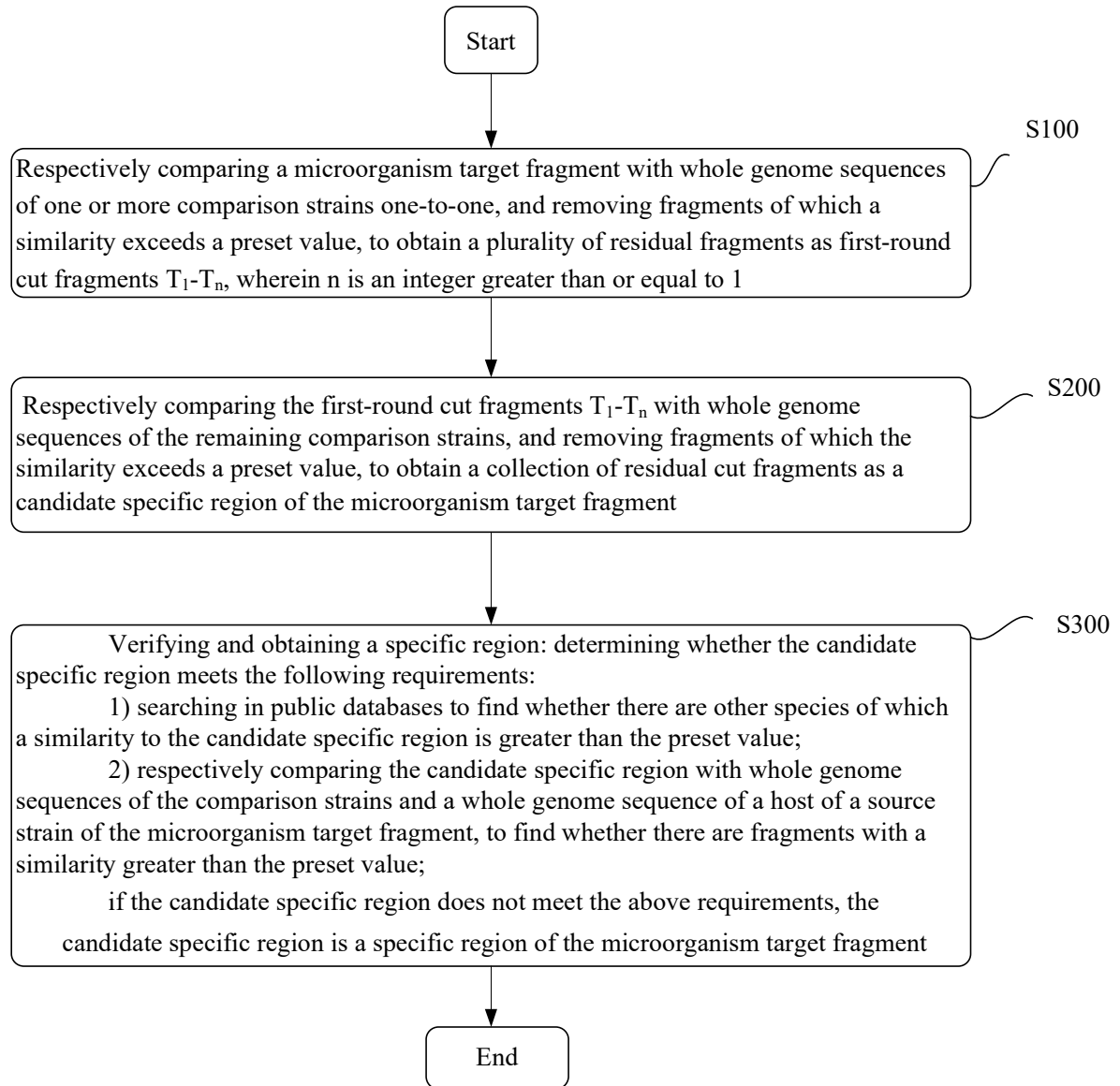


FIG. 1

Sequence 1	Sequence 2	Sequence matching rate	Alignment length	Mismatch length	Length of gap	Starting value of sequence 1	End value of sequence 1	Starting value of sequence 2	End value of sequence 2	e-value	Score
Query id	Subject id	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
A	B	98.4	187	3	0	1	187	1170	1356	1.90E-98	356
Sequence coverage rate = (alignment length / (end value of sequence 1 - starting value of sequence 1 + 1))											
Similarity = sequence coverage rate * sequence matching rate											

FIG. 1-1

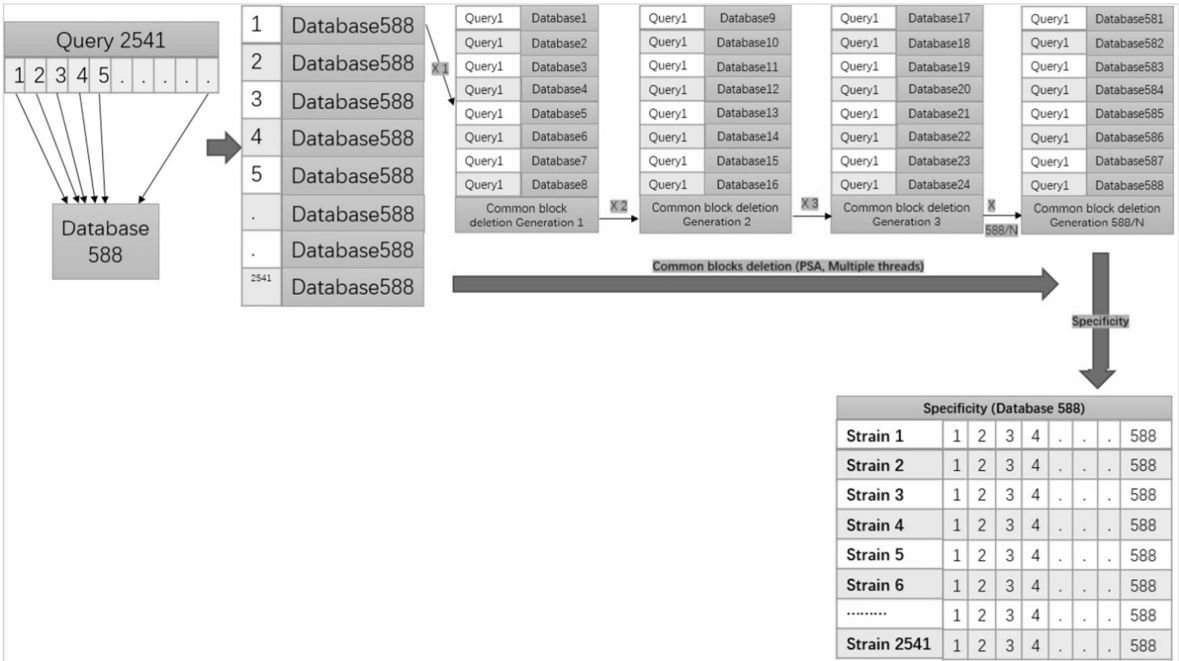


FIG. 1-2



FIG. 1-3

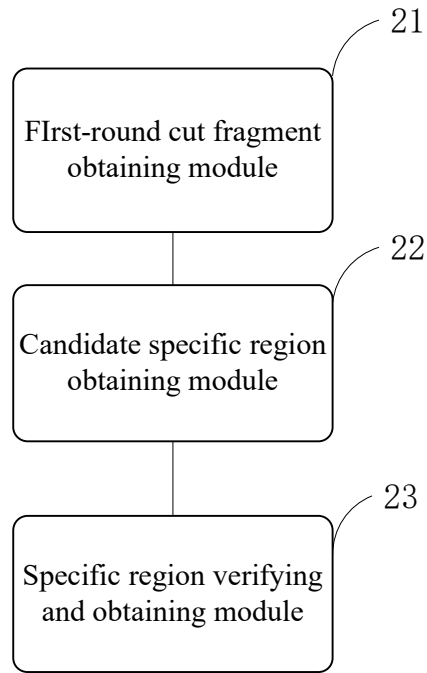


FIG. 2

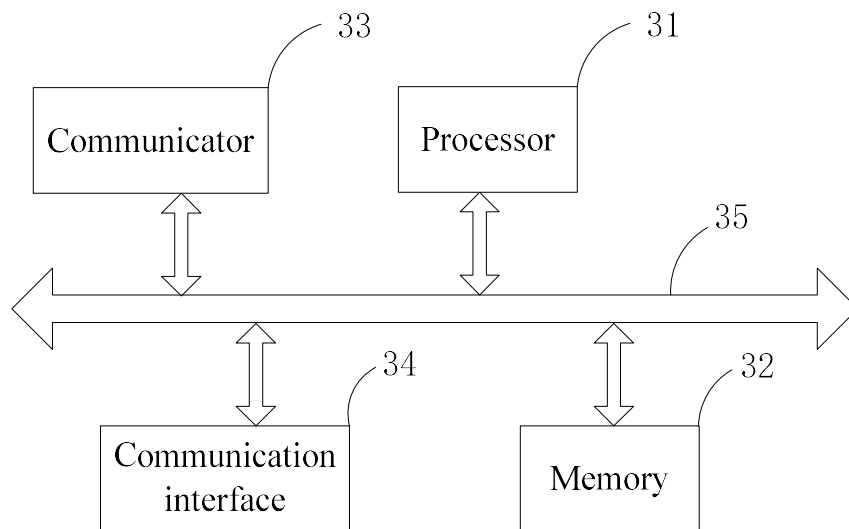


FIG. 3