BLAST database setup example (using FASTA file):

makeblastdb -in VR1.txt -dbtype nucl -out VR1

BLASTN search command example:

blastn -query 2337c-4120Ftrimmed.txt -db VR1 -out 2337cF\_VR1 -num\_descriptions 1 -num\_alignments 1

Note: files must in same directory where the command is made, unless a full unix-valid address is provided.

|  |  |  |
| --- | --- | --- |
| SEQUENCE | SEARCH | VLS MATCHES |
| AZLZY | VR1 | 15 |
| B5HW8 | VR1 | 5 (100) |
| CEMNN | VR1 | 5 (100) |
| COE93 | VR1 | 5 (100) |
| CSV5W | VR1 | 5 (100) |
| EAX75 | VR1 | 5 |
| C0GYQ | VR1 | 6 (100) |
| CECTZ | VR1 | 6 (100) |
| AKLDM | VR2 | 3,12,9,13 |
| CSV5W | VR2 | **5**, 4, 14, 13 |
| D9FVQ | VR2 | **4,** 5, 14, 13 |
| DCR6V | VR2 | **6** (100), 5, 4, 1 |
| BKVYR | VR2 | 3 (87.9), 12, 9 |
| BW863 | VR2 | 12, 9, 3, 6 |
| BWCEZ | VR2 | 6 (93.5), 1, 12, 9 |
| DOESE | VR2 | 12,9,3,6 |
| CT4VR | VR2 | 6 (95.3),13,1,3 |
| AUEAF | VR4 | 13,3 (VR1 VLS3 (100)) |
| CB09Q | VR4 | 7,8 |

VR3, VR5 too short for standard criteria; need to adjust criteria