>Glaske16\_gp98\_(56773-57150 bp)  
MALAGEAKREYQRQWRANRRAAWFAGKACVRCGSDEDLELDHVDPTLKVTNAVWSWSQERRDVELAKCQVLCNACHKAKTISQTVITIGLKAYRHGTCSMYEHHRCRCGLCRLWARNKKRRQRAAZ

From the yellow highlighted sequence above, we note that it has H-N-N-H in a 35 aa span (not exactly HNH), whereas the Official Function List states that HNH endonuclease “Must have H-N-H over a 30 aa span.” Since many previous annotators have called it HNH (Glaske16 gp98 at position 56773-57150 bp has more than 60 hits to HNH endonuclease in phagesDB!), could it help to state that every HNH endonuclease, “Must have H-N-H within a span of not more than 30 aa,” besides clarifying whether H-N-N-H could also be acceptable if it is within a 30 aa span?

This will help because in HHPRED, this same sequence matches the same hit 5H0M\_A in PDB with the same everything as the HNH reference sequences in the Official Function list, and high probability (98%), alignment 52.4%, albeit with not as great an e value (0.000029). See data below:

A screenshot of a computer code

Description automatically generated with low confidence

A screenshot of a computer

Description automatically generated with medium confidence