

1.) Vzameš podano zaporedje in ga daš v BLASTp.

select all 100 clusters selected

GenPept Graphics Distance tree of results Multiple alignment MSA Viewer

	Cluster Composition ▲ Click the ⊞ to see the cluster contents	Cluster Ancestor ▼	Cluster Representative Sequence	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<input checked="" type="checkbox"/>	⊞35 member(s), 1 organism(s)	viruses	G1 and G2 sur...	1095	1095	100%	0.0	100.00%	1138	NP_604472.1
<input checked="" type="checkbox"/>	⊞3 member(s), 1 organism(s)	viruses	glycoprotein G...	1095	1095	100%	0.0	99.25%	677	QQN67568.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein pr...	1015	1015	99%	0.0	89.85%	569	WNR62051.1
<input checked="" type="checkbox"/>	⊞26 member(s), 5 organism(s)	viruses	glycoprotein pr...	1011	1011	100%	0.0	89.72%	1138	WNR62050.1
<input checked="" type="checkbox"/>	⊞20 member(s), 2 organism(s)	viruses	glycoprotein pr...	998	998	100%	0.0	87.48%	1138	WZH56200.1
<input checked="" type="checkbox"/>	⊞5 member(s), 2 organism(s)	viruses	glycoprotein pr...	946	946	94%	0.0	89.50%	1133	XGD07570.1
<input checked="" type="checkbox"/>	⊞5 member(s), 5 organism(s)	viruses	glycoprotein pr...	929	929	100%	0.0	83.74%	1138	AFV36409.1
<input checked="" type="checkbox"/>	⊞6 member(s), 1 organism(s)	viruses	glycoprotein pr...	924	924	99%	0.0	84.06%	904	YBO61619.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein [N...	922	922	100%	0.0	79.63%	1138	YP_009666010.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	envelope glyco...	904	904	100%	0.0	78.32%	1138	YP_009362281.1
<input checked="" type="checkbox"/>	⊞6 member(s), 2 organism(s)	viruses	envelope glyco...	880	880	100%	0.0	76.26%	1138	WPS68785.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein pr...	865	865	100%	0.0	79.07%	787	YBP05222.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein pr...	861	861	99%	0.0	80.19%	1133	XGD07568.1
<input checked="" type="checkbox"/>	⊞5 member(s), 2 organism(s)	viruses	glycoprotein pr...	787	787	99%	0.0	66.98%	1141	YP_009505597.1
<input checked="" type="checkbox"/>	⊞49 member(s), 5 organism(s)	viruses	glycoprotein pr...	786	786	100%	0.0	69.96%	1140	NP_941974.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	RecName: Full...	784	784	100%	0.0	66.73%	1141	P0DTJ0.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	envelope glyco...	779	779	87%	0.0	76.92%	806	XZG99835.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein pr...	776	776	100%	0.0	66.42%	1139	YP_009361843.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein pr...	768	768	97%	0.0	65.83%	1138	YP_009362100.1
<input checked="" type="checkbox"/>	⊞6 member(s), 2 organism(s)	viruses	glycoprotein pr...	763	763	100%	0.0	65.80%	1141	WWS34654.1
<input checked="" type="checkbox"/>	⊞3 member(s), 3 organism(s)	viruses	glycoprotein pr...	761	761	100%	0.0	68.66%	1139	BAK08526.1
<input checked="" type="checkbox"/>	⊞1 member(s), 1 organism(s)	viruses	glycoprotein pr...	731	731	91%	0.0	74.13%	742	YBO61630.1

Vidiš, da so organizmi virusi. Torej je odgovor virus.

Na BLASTu kliknem na prvih par zadetkov, ki pod organizem vrnejo Orthohantavirus andesense, Juquitiba virus, Necocli virus, ... Torej iz navadnega blasta ne mormo sklepati. Zato spremenimo zbirko po kateri iščemo na SWISS-Prot. Tu večina zadetkov kaže na Orthohantavirus.

### Nucleotide Advanced Search Builder

Filters activated: genomic DNA/RNA [Clear all](#)

(Orthohantavirus refseq) AND 6562[Sequence Length]

[Edit](#)

[Clear](#)

#### Builder

All Fields

Orthohantavirus refseq

[Show index list](#)

AND

Sequence Length

6562

[Show index list](#)

AND

All Fields

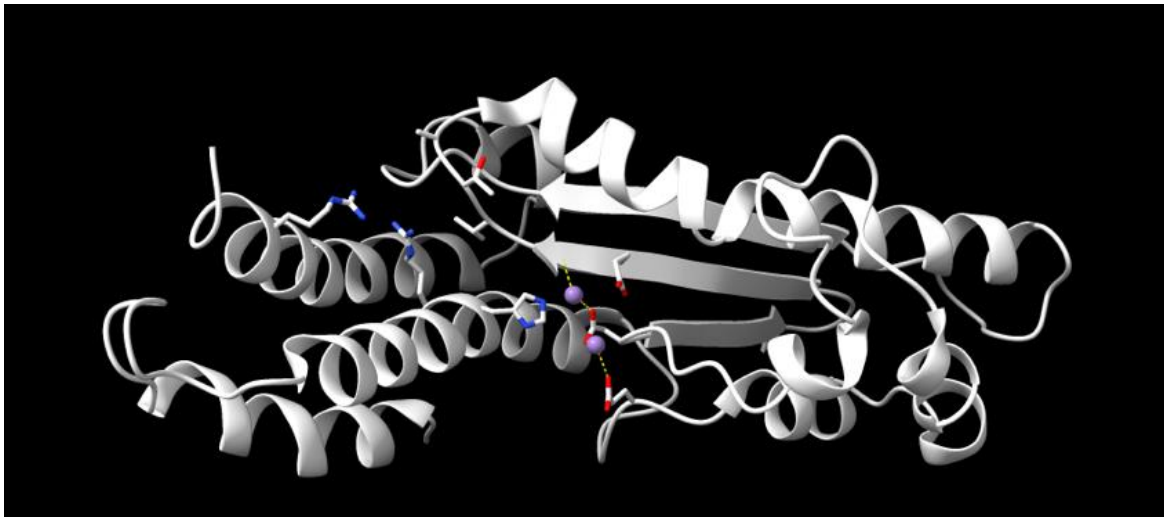
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Po genbank pogledaš za referenčno zaporedje podanih dolžin in najdeš, da gre za Orthohantavirus andesense (Andes virus). Imena segmentov so L, M, S.

- 2.) L kodira RNA polimerazo, M kodira G1 in G2 prekursor površinskega glikoproteina, S kodira nukleokapsidni protein in predvideni nestrukturni protein. Najbolj verjetni tarči sta RNA polimeraza in nukleokapsidni protein.

3.1.)

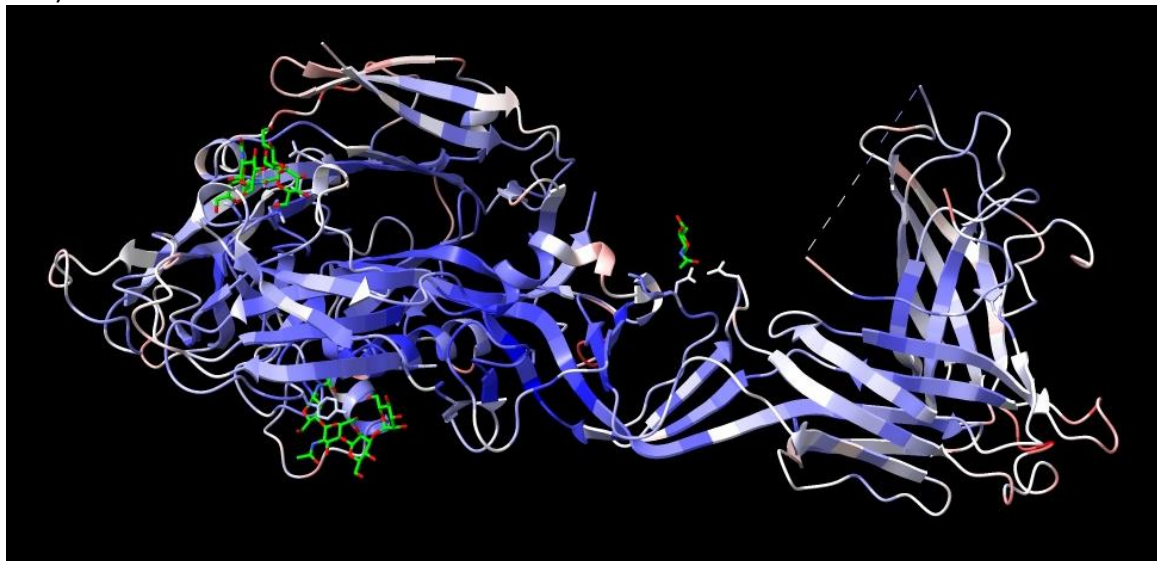


6q99 (RNA polimeraza).

Pri RNA polimerazi sta 2 liganda, in sicer Manganova iona. Tvoril naj bi kontakte z Val 111, Asp 97, Glu 54. Kontakt z Val 111 ni smiseln, bolj bi bil smiseln z Glu 110, ki se nahaja v bližini in ima pravi naboj.

Kot artefakt sta prisotna glicerol in voda.

3.2.)



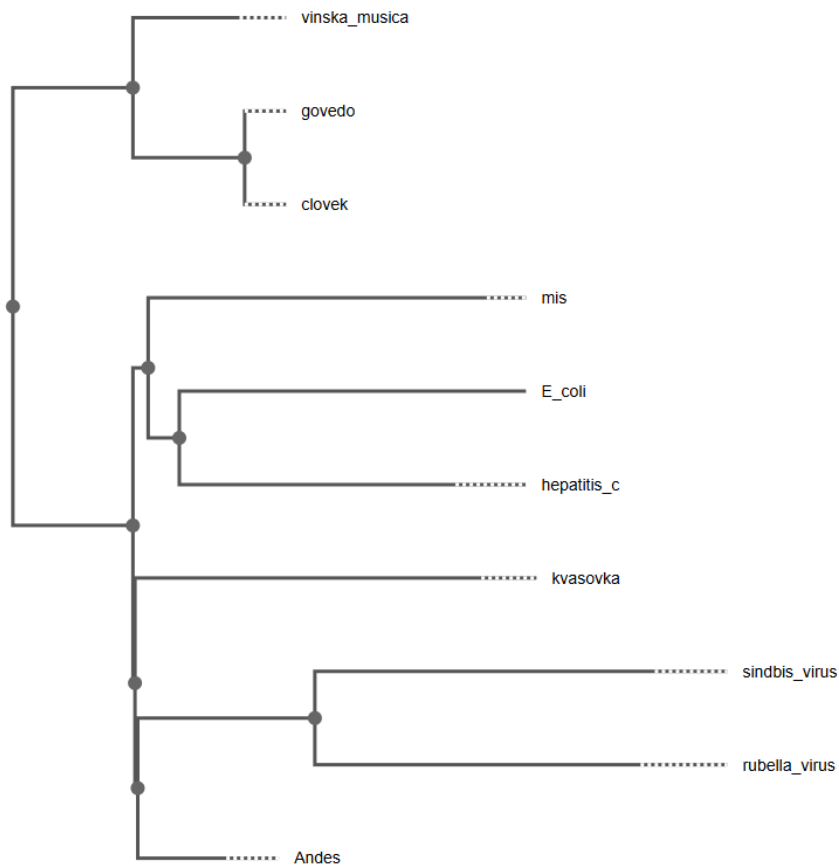
6Y5F (predfuzijski kompleks). Greš iz PDB na UniProt in najdeš alternativna imena: glikoprotein G1 = glikoprotein N, glikoprotein G2 = glikoprotein C.

Ni zmodeliran celoten kompleks. V ChimeriX pogledaš, da manjkajo ostanki 1063-1076, na PDB pogledaš kaj so te ostanki. Manjkajo fenilalanin 1063 do serin 1076.

Da, v modelu se nahajata še dva oligosaharida  $\alpha$ -D-mannopyranose-(1-3)- $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose in en N-acetilglikozamin. Smiselno je, da se nahajajo v modelu saj gre za glikoprotein. Pričakoval bi pa, da se stikajo s proteinom.

Položaj proteina je večinoma zanesljiv, saj vidimo veliko modre in bele barve.

4.)



(če se pri poravnavi nisem zmotil) Posebej izstopa, da je RNA polimeraza hepatitisa c bližje E. coli in miši kot drugim virusom. Prav tako izstopa, da RNA polimeraza miši ni ob drugih živalskih RNA polimerazah.

Inhibitor bi iskal pri virusoma Sindbis in Rubella, morda bi bila zanimiva tudi kvasovka. (Pogledaš kateri organizmi so blizu Andes viusa in hkrati niso blizu človeka)