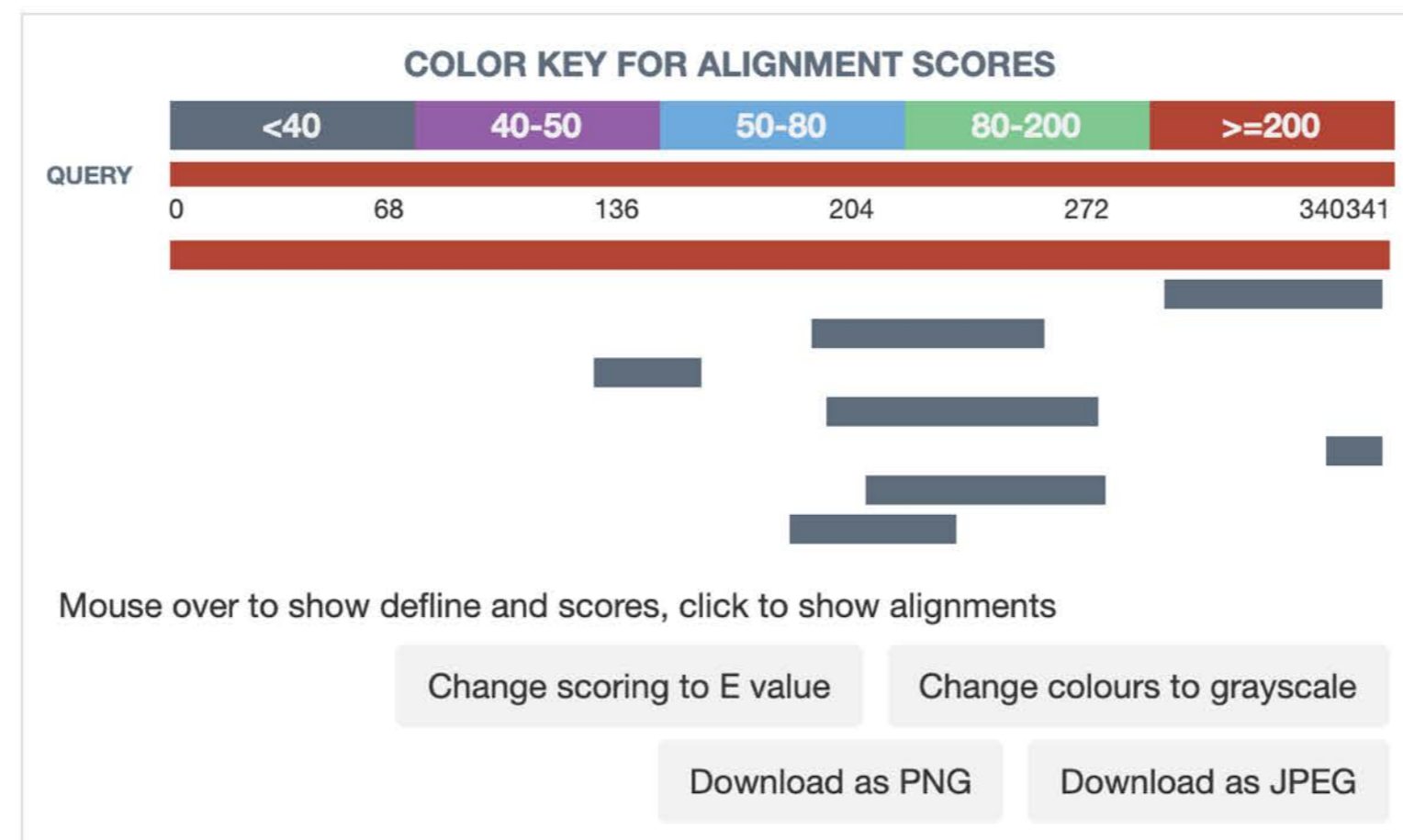


**a**

Description	Max score	Total score	Query cover	E value	Identities
P68650 Major capsid protein OS=Enterobacteria phage P21 OX=10711 GN=E PE=3 SV=1	431	431.0	99%	3e-154	62%
Q01076 Internal virion protein gp20 OS=Salmonella phage P22 OX=10754 GN=20 PE=1 SV=2	26.2	26.2	18%	0.39	27%
P10928 Baseplate wedge protein gp10 OS=Enterobacteria phage T4 OX=10665 GN=10 PE=1 SV=1	25.4	25.4	19%	0.77	30%
P16009 Baseplate central spike complex protein gp5 OS=Enterobacteria phage T4 OX=10665 GN=5 PE=1 SV=2	22.7	22.7	9%	4.8	29%
Q4Z9F2 Tail sheath protein OS=Staphylococcus phage Twort (strain DSM 17442) OX=1283338 PE=3 SV=1	22.7	22.7	22%	5.3	30%
P13390 L-shaped tail fiber protein pb1 OS=Escherichia phage T5 OX=10726 GN=ltf PE=1 SV=3	22.3	22.3	4%	7.0	53%
P25129 Attachment protein G3P OS=Pseudomonas phage Pf1 OX=2011081 GN=III PE=3 SV=1	21.9	21.9	19%	7.8	28%
Q6QGF0 Probable central straight fiber OS=Escherichia phage T5 OX=10726 GN=D17 PE=2 SV=1	21.9	21.9	13%	10.0	36%

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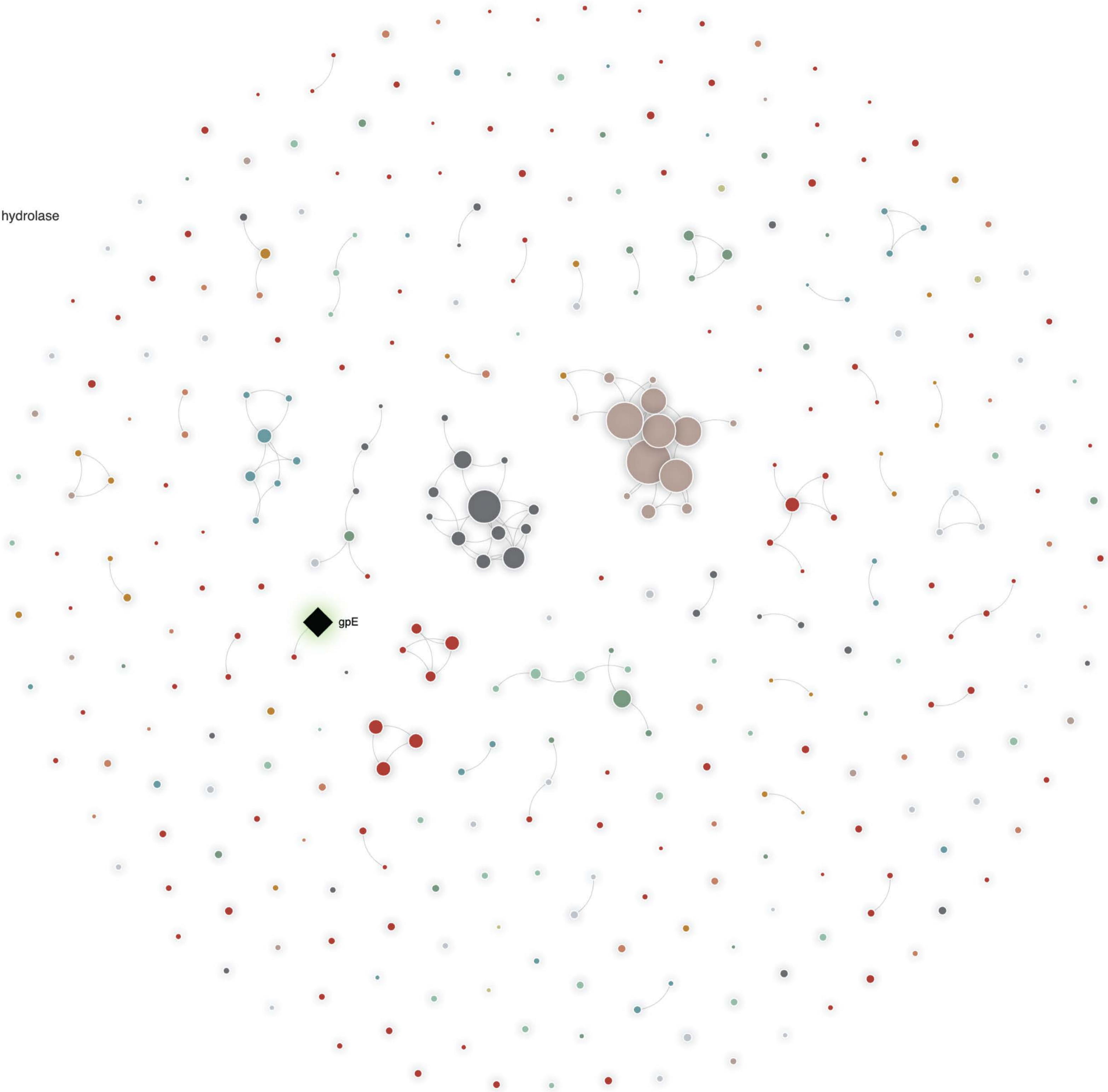
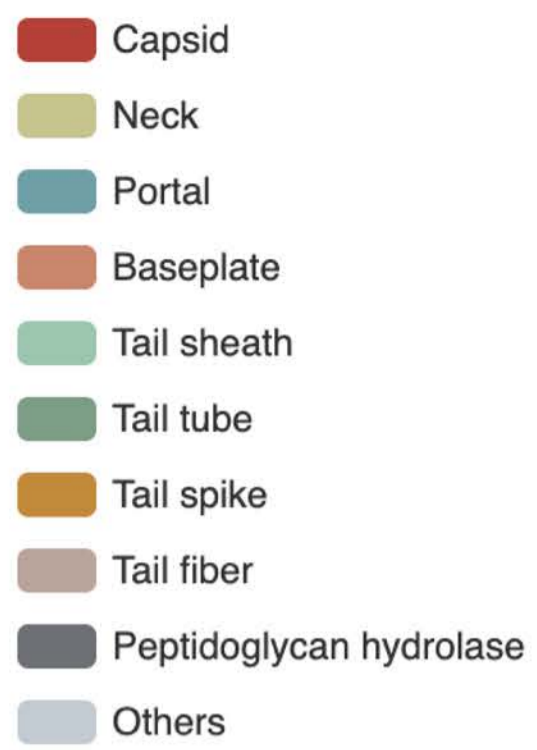
**P68650 Major capsid protein OS=Enterobacteria phage P21 OX=10711 GN=E PE=3 SV=1**

**Score:** 431     
 **Expect:** 3e-154     
 **Identities:** 62%     
 **Positives:** 73%     
 **Gaps:** 0%

Query	1	M S M Y T T A Q L L A A N E Q K F K F D P L F L R L F F R E S Y P F T T E K V Y L S Q I P G L V N M A L Y V S P I V S G E V I R S R G G S T S E F T P G Y V
Subject	1	M + + T T Q L L E Q K K F L F L L F F R + F T E + V L + I G + A Y V S P + V G + V + R R G G T P G Y V

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**C**

**d**

- Capsid
- Neck
- Portal
- Baseplate
- Tail sheath
- Tail tube
- Tail spike
- Tail fiber
- Peptidoglycan hydrolase
- Others

