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| --- | --- | --- | --- | --- |
| Coordinates | Product/Function | No. Of Combined Peptides | Overall Coverage | Start Site |
| 5039-5860 | gp6 major capsid | 5038 | 95% | Confirmed |
| 7601-8410 | gp11 major tail | 1532 | 95% | Confirmed, acetyl |
| 9483-13010 | gp14 tape measure | 1175 | 94% | Confirmed |
| 13011-14720 | gp15 minor tail protein | 931 | 95% | Confirmed |
| 2276-3598 | gp3 portal | 732 | 93% | Confirmed |
| 14807-16516 | gp16 minor tail protein | 625 | 91% | Confirmed |
| 16571-17401 | gp17 minor tail protein | 488 | 93% | Confirmed |
| 19947-21836 | gp19 minor tail protein | 401 | 81% | Confirmed |
| 17398-19950 | gp18 minor tail protein | 436 | 76% | Confirmed, acetyl |
| 23813-24451 | gp23 minor tail protein | 421 | 98% | Confirmed |
| 21836-23038 | gp20 minor tail protein | 371 | 96% | Confirmed |
| 5869-6438 | gp7 head to tail connector protein | 273 | 92% | Confirmed |
| 7087-7491 | gp10 head to tail connector protein | 255 | 97% | Confirmed, acetyl |
| 3585-4340 | gp4 capsid maturation protease | 183 | 73% | Confirmed |
| 24448-25272 | gp24 minor tail protein | 149 | 65% | Confirmed |
| 4427-5020 | gp5 scaffolding protein | 101 | 76% | Confirmed |
| 23062-23403 | gp21 minor tail protein | 86 | 94% | Confirmed |
| 32844-31507 | gp42 transposase | 29 | 27% |  |
| 53116-53529 | gp95 | 20 | 64% | Confirmed |
| 6801-7097 | gp9 head to tail connector protein | 11 | 42% |  |
| 28785-29018 | gp32 holin | 3 | 31% |  |
| 41040-41504 | gp63 | 17 | 59% | Confirmed |
| 36125-36358 | gp47 HTH DNA binding protein | 9 | 30% |  |
| 8529-9080 | gp12 tail assembly chaperone | 10 | 40% |  |
| 6435-6764 | gp8 head to tail connector protein | 10 | 29% |  |
| 26504-27775 | gp30 lysin A | 6 | 11% |  |
| 54289-55374 | gp99 glycosyltransferase | 6 | 11% |  |
| 42475-42837 | gp65 HNH endonuclease | 8 | 26% |  |
| 37690-38337 | gp54 | 3 | 13% |  |
| 27775-28776 | gp31 lysin B | 3 | 9% |  |
| 51250-51921 | gp90 | 3 | 13% | Confirmed, acetyl |
| 37033-37227 | gp51 | 3 | 22% |  |
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Please note that the start of twenty of the genes have been confirmed by proteomic analysis. These genes have homologs in other F1 related phages. The data suggests that not all of the F1 homologs have been properly annotated. As noted in the table, several of the gene products are acetylated at the amino terminus. The function of this protein modification is unknown.

When in doubt about a start site for a gene we decided to choose a start site that gave a 1:1 amino acid alignment with F1 homologs that have been annotated and approved by the Hatfull lab.

In additional to using HHpred, phamerator and blast domain homology for gene functions, if blast demonstrated an F1 homolog that was annotated with a function from a recent Hatfull approved genome annotation, we designated the Cabrinians homolog as having the same function.