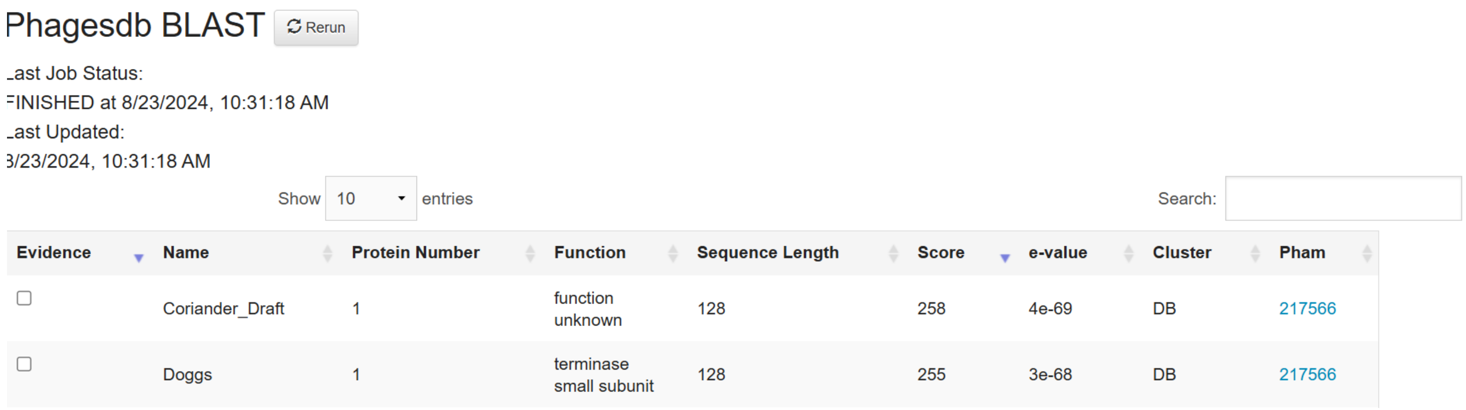
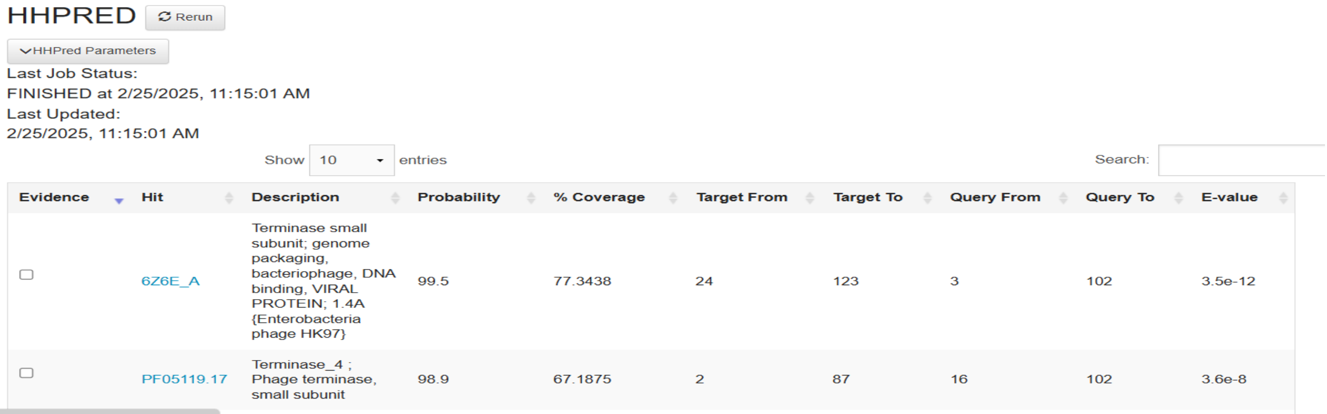
Basic Phage Information	
Phage Name	**Coriander_1**
Gene #	**Gene 1(PECAAN)** **Gene 1 (phamerator)**
Stop Coordinate	**Stop 614**
Direction (For/Rev)	**forward**
Gap (Overlap) with Previous Gene	**Overlap with Coriander_2 at 586**
Selected Start Coordinate	**228 (PECAAN)** **228 (Phamerator)**
Selected Function	**Terminase small subunit**



Phagesdb BLAST

ast Job Status:
INISHED at 8/23/2024, 10:31:18 AM
ast Updated:
/23/2024, 10:31:18 AM

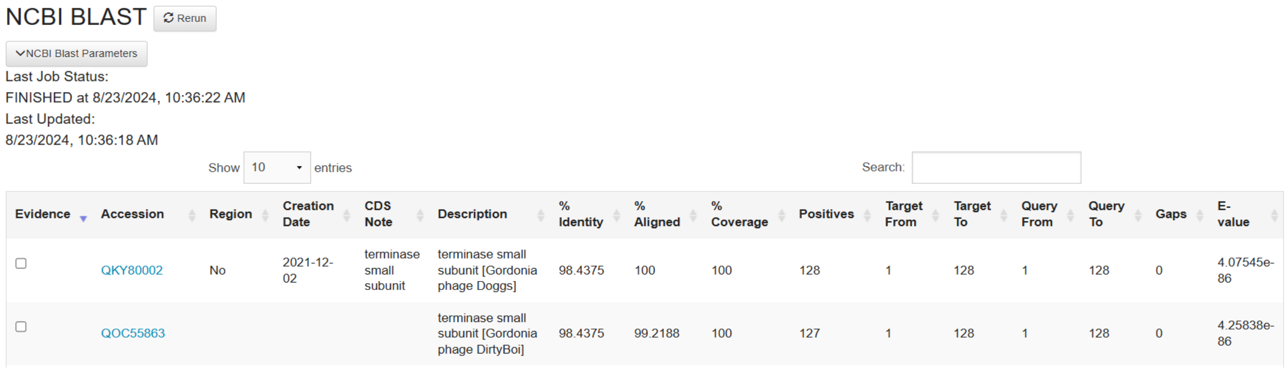
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	1	function unknown	128	258	4e-69	DB	217566
☐	Doggs	1	terminase small subunit	128	255	3e-68	DB	217566



HHPRED

Last Job Status:
FINISHED at 2/25/2025, 11:15:01 AM
Last Updated:
2/25/2025, 11:15:01 AM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	6Z6E_A	Terminase small subunit; genome packaging, bacteriophage, DNA binding, VIRAL PROTEIN; 1.4A {Enterobacteria phage HK97}	99.5	77.3438	24	123	3	102	3.5e-12
☐	PF05119.17	Terminase_4 ; Phage terminase, small subunit	98.9	67.1875	2	87	16	102	3.6e-8



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:22 AM
Last Updated:
8/23/2024, 10:36:18 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80002	No	2021-12-02	terminase small subunit	terminase small subunit [Gordonia phage Doggs]	98.4375	100	100	128	1	128	1	128	0	4.07545e-86
☐	QOC55863				terminase small subunit [Gordonia phage DirtyBoi]	98.4375	99.2188	100	127	1	128	1	128	0	4.25838e-86

Coriander_1

Gene 1:

Start 228

Pham # 212300

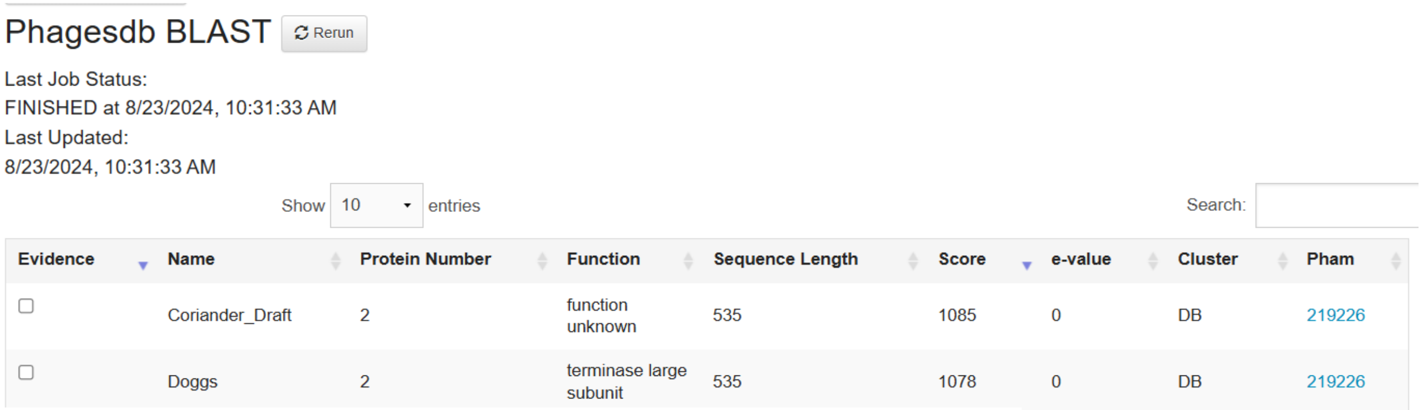
Coriander_1

Track 40

Start 31: • Found in 7 of 207 (3.4%) of genes in pham • Manual Annotations of this start: 5 of 185 • Called 100.0% of time when present • Phage (with cluster) where this start called: Coriander_1 (DB), DirtyBoi_1 (DB), Dmitri_1 (DB), Doggs_1 (DB), Hedwig_1 (DB), Moonflower_1 (DB), RayTheFireFly_1 (DB),

Candidate Starts for Coriander_1: (Start: 31 @228 has 5 MA's) (Start: 40 @240 has 4 MA's), (55, 315), (62, 339), (96, 492)

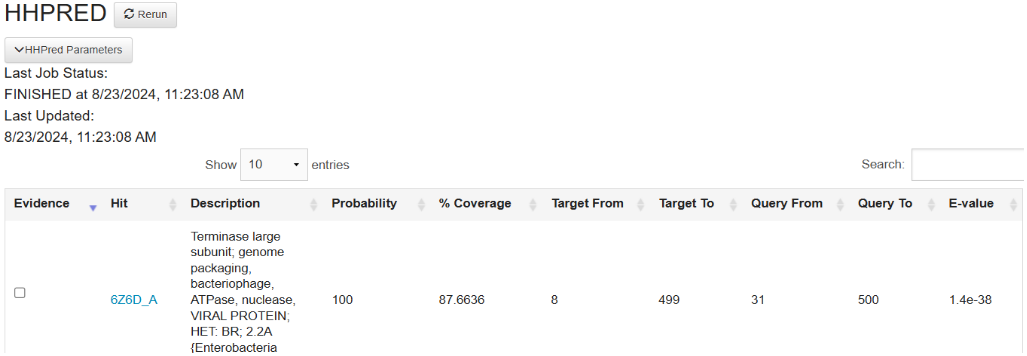
Basic Phage Information	
Phage Name	**Coriander_2**
Gene #	**Gene 2 (PECAAN) Gene 2 (Phamerator)**
Stop Coordinate	**Stop 2,193**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**Overlap with Coriander_1 at 586**
Selected Start Coordinate	**586 (PECAAN) 586 (Phamerator)**
Selected Function	**Terminase large subunit**



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:31:33 AM
Last Updated:
8/23/2024, 10:31:33 AM

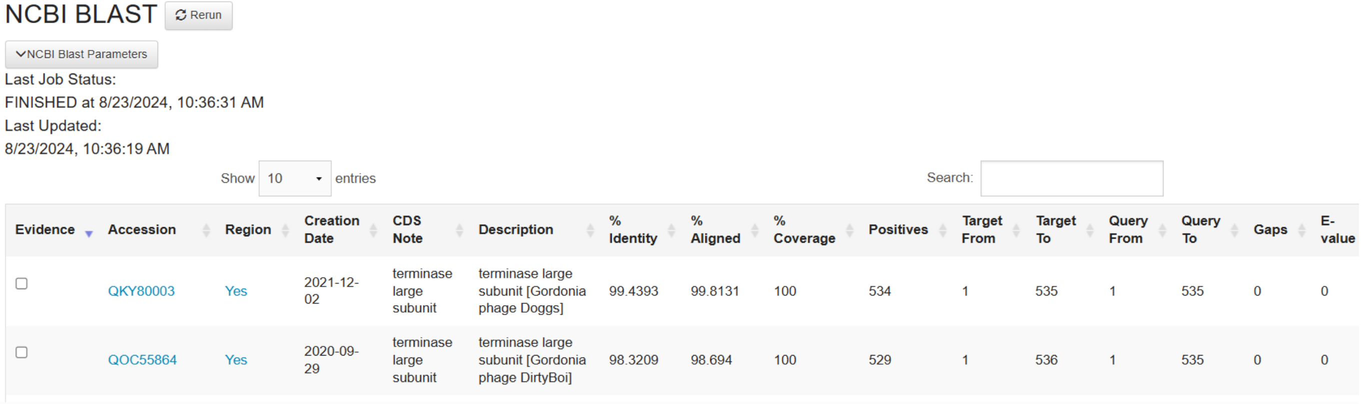
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	2	function unknown	535	1085	0	DB	219226
☐	Doggs	2	terminase large subunit	535	1078	0	DB	219226



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 11:23:08 AM
Last Updated:
8/23/2024, 11:23:08 AM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	6Z6D_A	Terminase large subunit; genome packaging, bacteriophage, ATPase, nuclease, VIRAL PROTEIN; HET: BR; 2.2A {Enterobacteria	100	87.6636	8	499	31	500	1.4e-38



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:31 AM
Last Updated:
8/23/2024, 10:36:19 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80003	Yes	2021-12-02	terminase large subunit	terminase large subunit [Gordonia phage Doggs]	99.4393	99.8131	100	534	1	535	1	535	0	0
☐	QOC55864	Yes	2020-09-29	terminase large subunit	terminase large subunit [Gordonia phage DirtyBoi]	98.3209	98.694	100	529	1	536	1	535	0	0

Coriander_2

Gene 2:

Start 586

Pham #212152

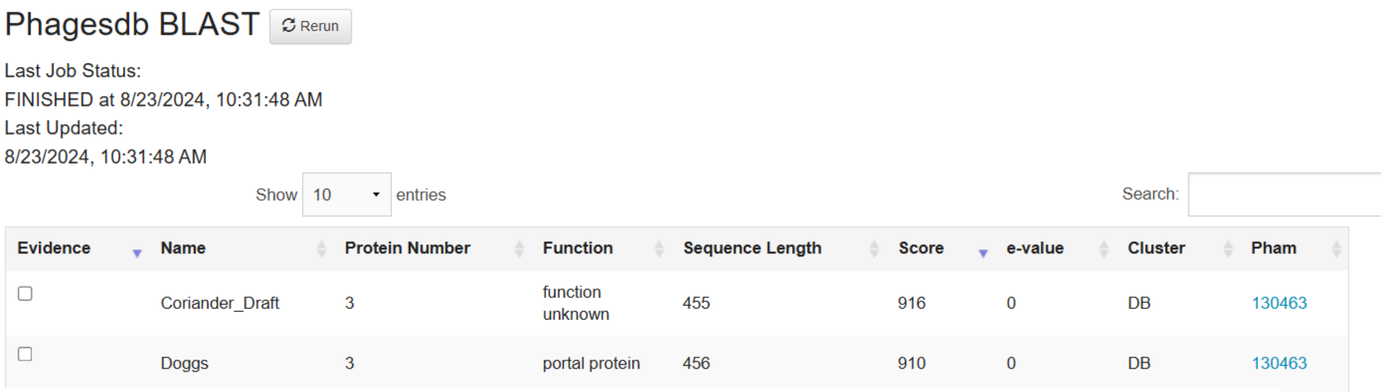
Coriander_2

Track #272

Start 121: • Found in 21 of 1438 (1.5%) of genes in pham • Manual Annotations of this start: 12 of 1235 • Called 66.7% of time when present • Phage (with cluster) where this start called: BBQValindra_2 (DB), Bowser_2 (DB), Bunker_2 (DB), Coriander_2 (DB), DirtyBoi_2 (DB), Dmitri_2 (DB), Doggs_2 (DB), Eyes_2 (DB), GEazy_2 (DB), HannahD_2 (DB), Hedwig_2 (DB), Kiko_2 (DB), Moonflower_2 (DB), RayTheFireFly_2 (DB),

Candidate Starts for Coriander_2: (Start: 121 @586 has 12 MA's) _2: (Start: 121 @586 has 12 MA's), (240, 769), (287, 886), (299, 904), (314, 952), (375, 1024), (448, 1177), (466, 1219), (517, 1312), (540, 1354), (546, 1363), (578, 1414), (596, 1444), (597, 1447), (628, 1510), (648, 1543), (671, 1570), (716, 1648), (764, 1735), (789, 1759), (846, 1852), (848, 1855), (857, 1873), (915, 1957),

Basic Phage Information	
Phage Name	**Coriander_3**
Gene #	**Gene 3(PECAAN) Gene 3 (Phamerator)**
Stop Coordinate	**3575**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**Overlap with Coriander_4 at 3569**
Selected Start Coordinate	**2208**
Selected Function	**Portal protein**

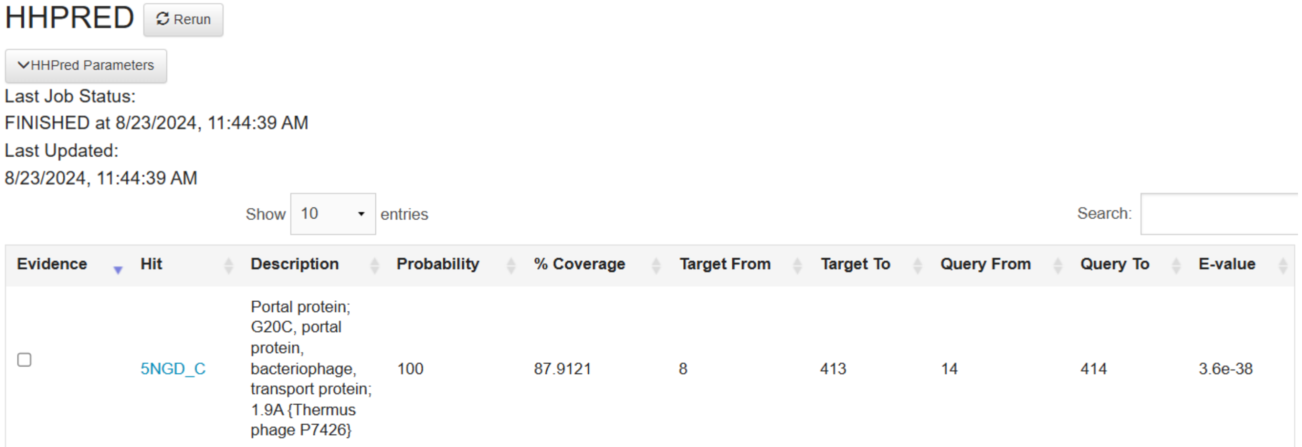


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:31:48 AM
Last Updated:
8/23/2024, 10:31:48 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	3	function unknown	455	916	0	DB	130463
☐	Doggs	3	portal protein	456	910	0	DB	130463

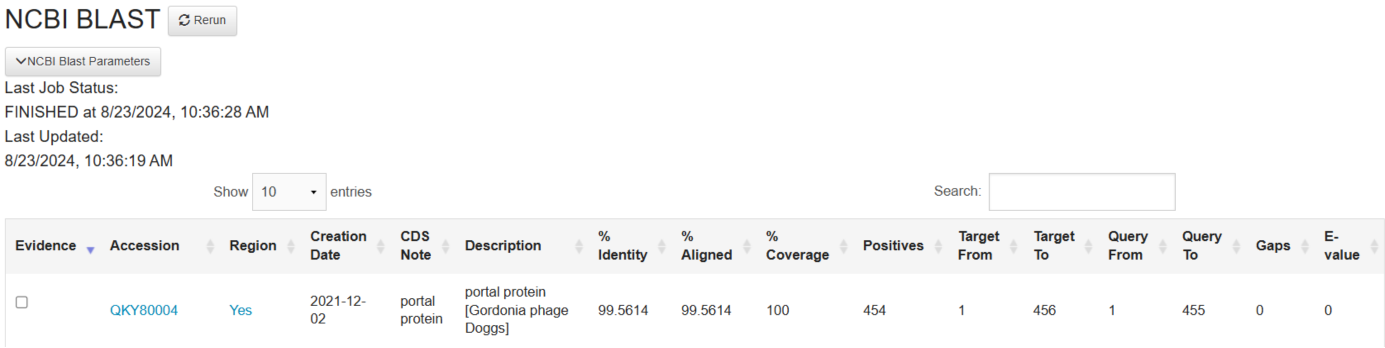


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 11:44:39 AM
Last Updated:
8/23/2024, 11:44:39 AM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	5NGD_C	Portal protein; G20C, portal protein, bacteriophage, transport protein; 1.9A {Thermus phage P7426}	100	87.9121	8	413	14	414	3.6e-38



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:28 AM
Last Updated:
8/23/2024, 10:36:19 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80004	Yes	2021-12-02	portal protein	portal protein [Gordonia phage Doggs]	99.5614	99.5614	100	454	1	456	1	455	0	0

Coriander_3

Gene 3:

Start 2208

Pham #130463

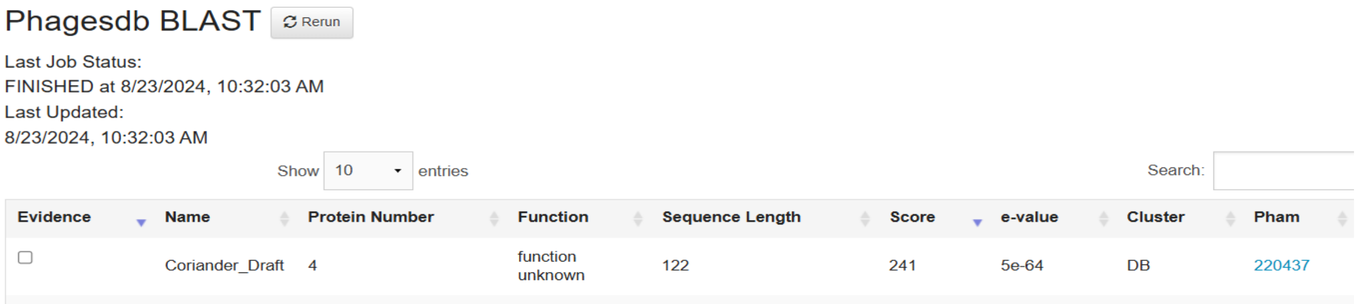
Coriander_3

Track #89

Start 31: • Found in 7 of 319 (2.2%) of genes in pham • Manual Annotations of this start: 5 of 277 • Called 100.0% of time when present • Phage (with cluster) where this start called: Coriander_3 (DB), DirtyBoi_3 (DB), Dmitri_3 (DB), Doggs_3 (DB), Hedwig_3 (DB), Moonflower_3 (DB), RayTheFireFly_3 (DB),

Candidate Starts for Coriander_3: (Start: 31 @2208 has 5 MA's) (62, 2277), (73, 2334), (74, 2346), (75, 2367), (94, 2478), (126, 2568), (176, 2781), (189, 2874), (194, 2910), (195, 2916), (221, 3042), (223, 3048), (227, 3069), (235, 3111), (258, 3264), (266, 3306), (272, 3351), (323, 3498),

Basic Phage Information	
Phage Name	Coriander_4
Gene #	Gene 4 (PECAAN) Gene 4 (Phamerator)
Stop Coordinate	3937
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlap with Coriander_ 3 at 3569
Selected Start Coordinate	3569
Selected Function	

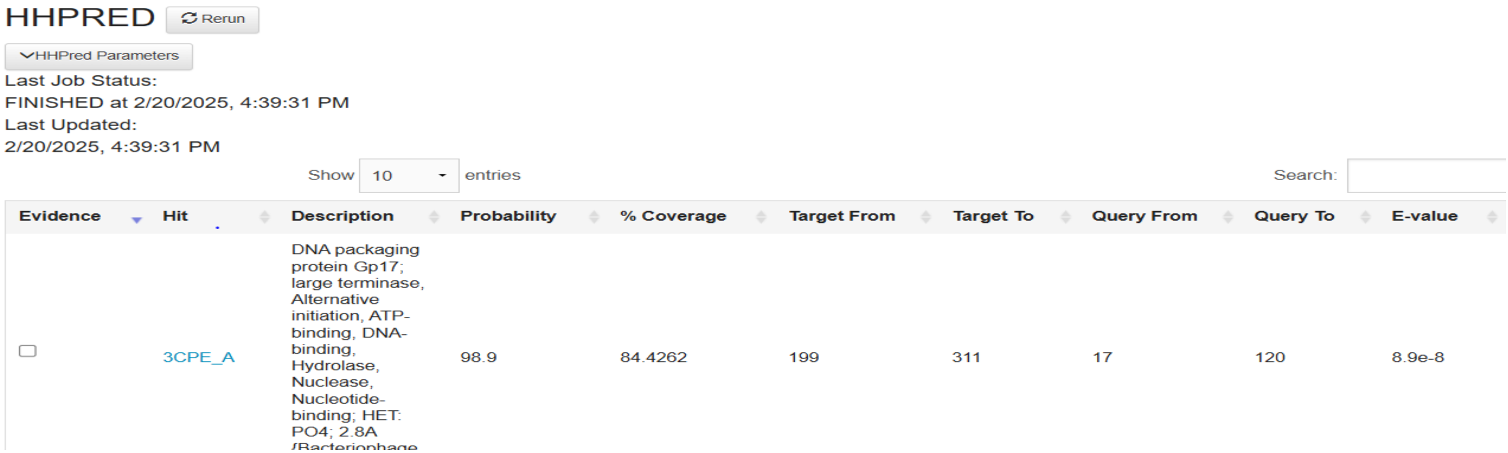


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:32:03 AM
Last Updated:
8/23/2024, 10:32:03 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	4	function unknown	122	241	5e-64	DB	220437

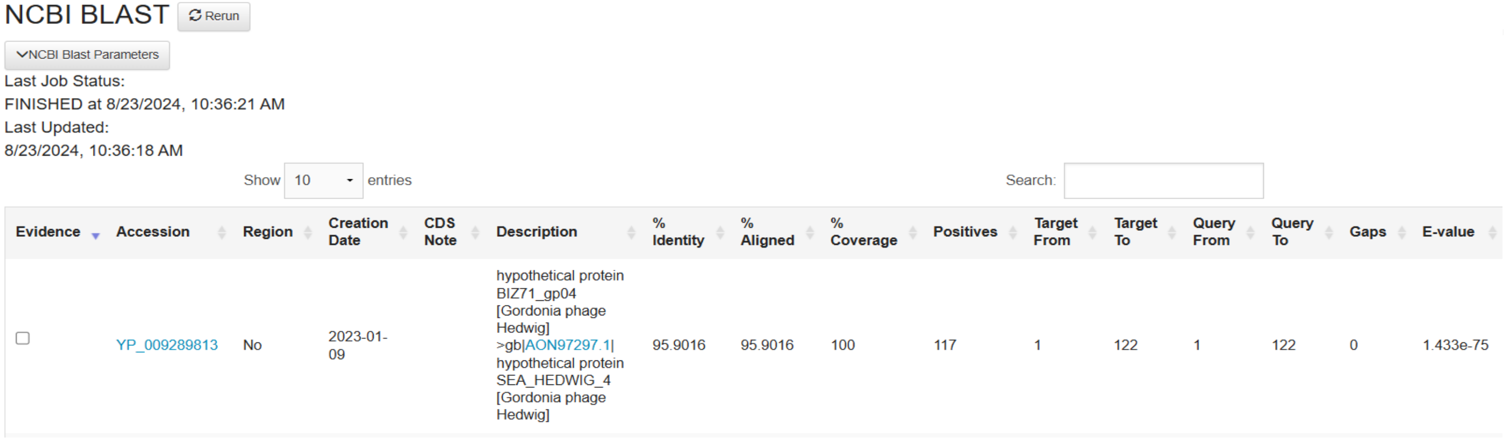


HHPRED

Last Job Status:
FINISHED at 2/20/2025, 4:39:31 PM
Last Updated:
2/20/2025, 4:39:31 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	3CPE_A	DNA packaging protein Gp17; large terminase, Alternative initiation, ATP-binding, DNA-binding, Hydrolase, Nuclease, Nucleotide-binding; HET: PO4; 2.8A {Bacteriophage	98.9	84.4262	199	311	17	120	8.9e-8



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:21 AM
Last Updated:
8/23/2024, 10:36:18 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_009289813	No	2023-01-09		hypothetical protein BIZ71_gp04 [Gordonia phage Hedwig] >gb|AON97297.1| hypothetical protein SEA_HEDWIG_4 [Gordonia phage Hedwig]	95.9016	95.9016	100	117	1	122	1	122	0	1.433e-75

Coriander_4

Gene 4:

Start 3569

Pham #213314

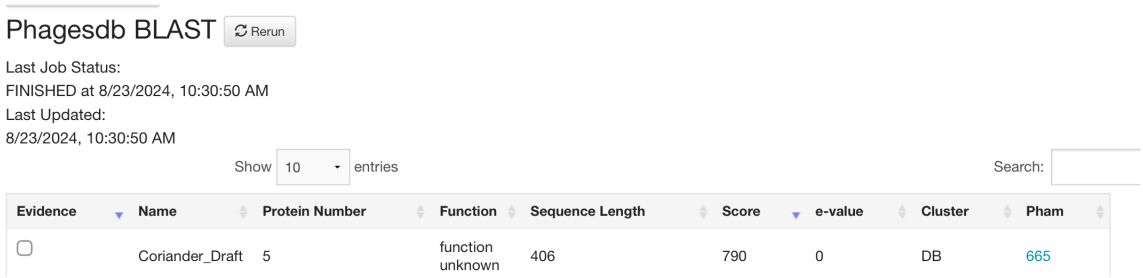
Coriander_4

Track 4

Start 3: • Found in 7 of 7 (100.0%) of genes in pham • Manual Annotations of this start: 3 of 5 • Called 71.4% of time when present • Phage (with cluster) where this start called: Coriander_4 (DB), Hedwig_4 (DB), Kiko_4 (DB), Moonflower_4 (DB), RayTheFireFly_4 (DB),

Candidate Starts for Coriander_4: (1, 2813), (2, 2852), (Start: 3 @3569 has 3 MA's) , (Start: 4 @3572 has 2 MA's), (5, 3647), (7, 3701), (9, 3773), (11, 3887), (12, 3914),

Basic Phage Information	
Phage Name	Coriander_5
Gene #	Gene 5 (PECAAN) Gene 5 (Phamerator)
Stop Coordinate	Stop 5,181
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	No overlap
Selected Start Coordinate	3961 (PECAAN) 3961 (PECAAN)



Phagesdb BLAST

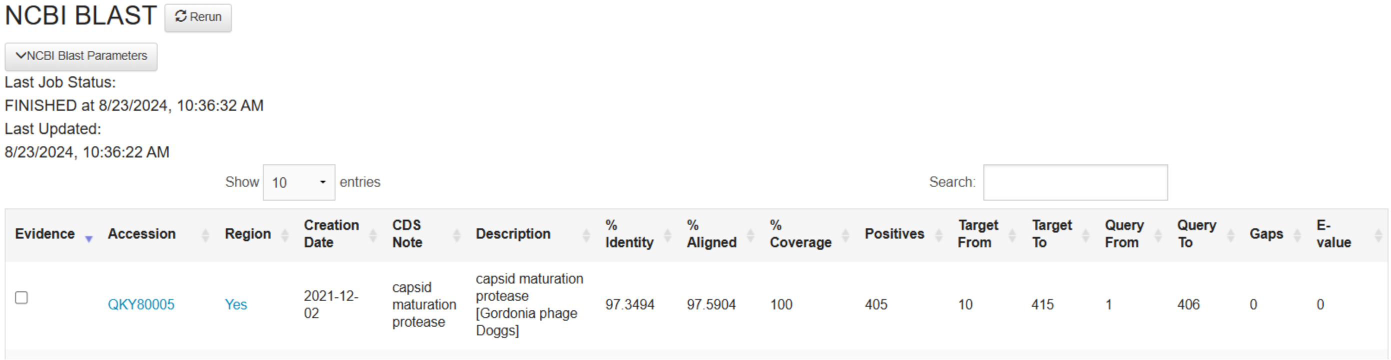
Last Job Status:
FINISHED at 8/23/2024, 10:30:50 AM
Last Updated:
8/23/2024, 10:30:50 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	5	function unknown	406	790	0	DB	665

HHPRED

Last Job Status:
FINISHED at 2/20/2025, 4:41:25 PM
Last Updated:
2/20/2025, 4:41:25 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	1TG6_G	Putative ATP-dependent Clp protease proteolytic subunit; mitochondrial ClpP, Clp/Hsp 100, ATP-dependent protease, HYDROLASE; HET: DIO, FME,	99.9	40.3941	82	248	25	189	7.3e-21



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:32 AM
Last Updated:
8/23/2024, 10:36:22 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80005	Yes	2021-12-02	capsid maturation protease	capsid maturation protease [Gordonia phage Doggs]	97.3494	97.5904	100	405	10	415	1	406	0	0

Coriander_5

Gene 5:

Start 3951

Pham #665

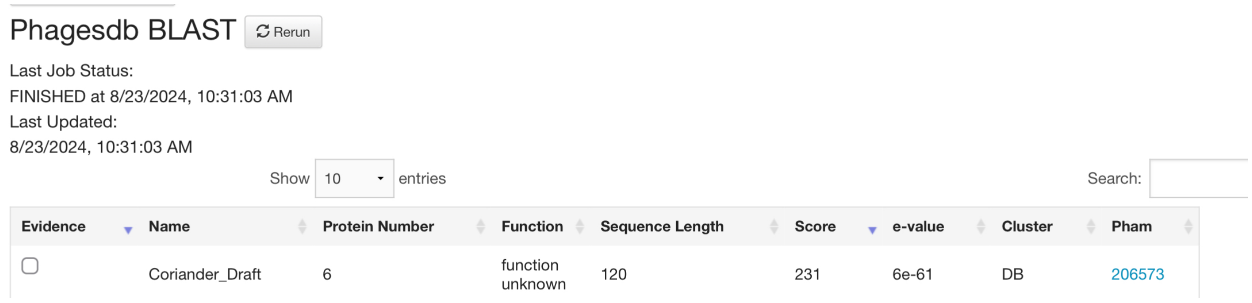
Coriander_5

Track 41

Start 35: • Found in 8 of 177 (4.5%) of genes in pham • No Manual Annotations of this start. • Called 12.5% of time when present • Phage (with cluster) where this start called: Coriander_5 (DB),

Candidate Starts for Coriander_5: (Start: 28 @3934 has 9 MA's) (35, 3961), (66, 4138), (81, 4267), (85, 4288), (86, 4291), (87, 4306), (88, 4309), (90, 4327), (94, 4354), (104, 4453), (124, 4693), (133, 4762),

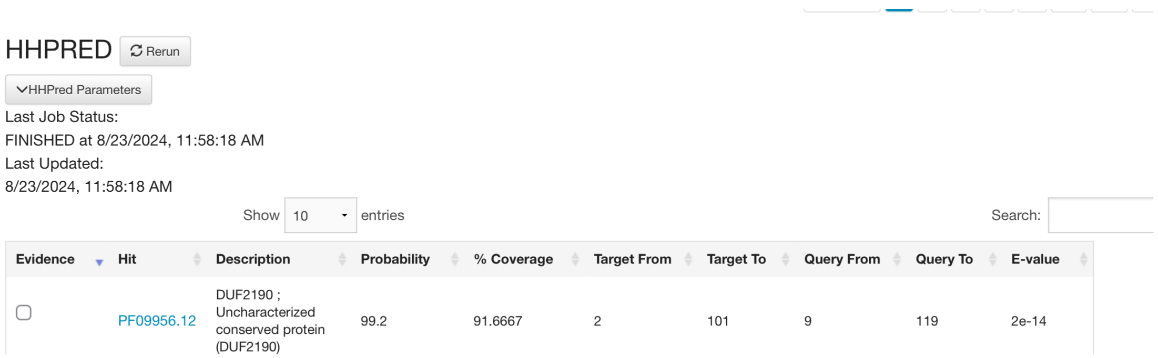
Basic Phage Information	
Phage Name	Coriander_6
Gene #	Gene 6 (PECAAN) Gene 6 (Phamerator)
Stop Coordinate	Stop 5,547
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	No Overlap
Selected Start Coordinate	5185 (PECAAN) 5185 (Phamerator)
Selected Function	Function Unknown



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:31:03 AM
Last Updated:
8/23/2024, 10:31:03 AM

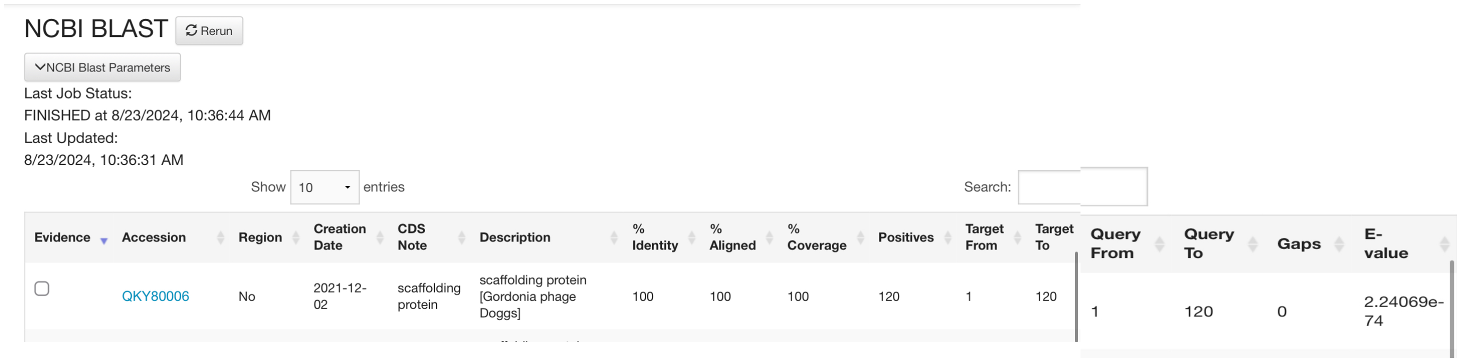
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	6	function unknown	120	231	6e-61	DB	206573



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 11:58:18 AM
Last Updated:
8/23/2024, 11:58:18 AM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF09956.12	DUF2190 ; Uncharacterized conserved protein (DUF2190)	99.2	91.6667	2	101	9	119	2e-14



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:44 AM
Last Updated:
8/23/2024, 10:36:31 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80006	No	2021-12-02	scaffolding protein	scaffolding protein [Gordonia phage Doggs]	100	100	100	120	1	120	1	120	0	2.24069e-74

Coriander_6

Gene 6:

Start 5185

Pham # 222887

Coriander_6

Track 27

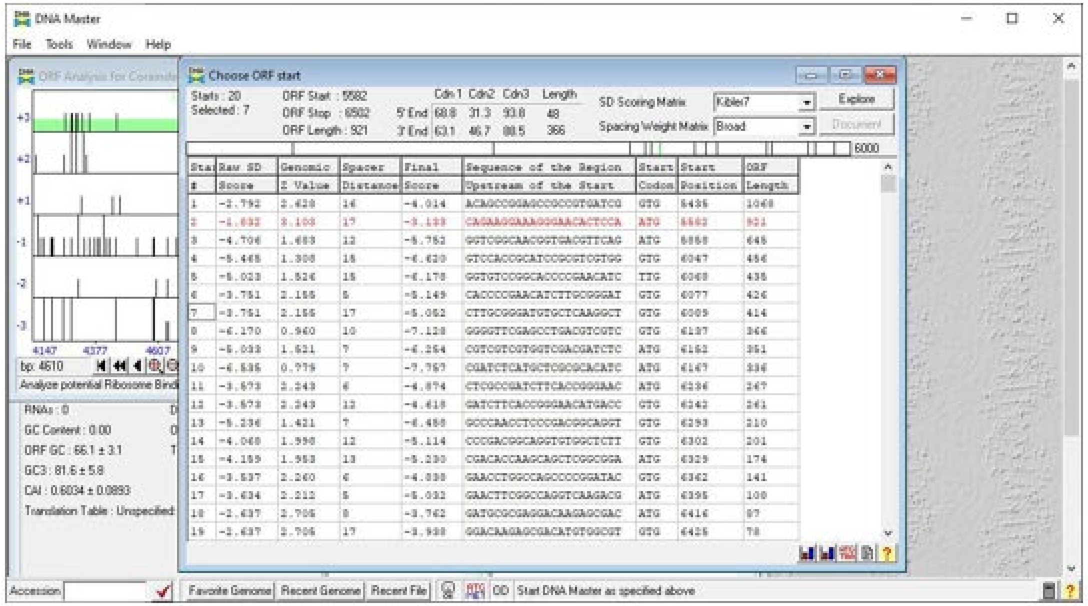
Start 12: • Found in 134 of 209 (64.1%) of genes in pham • Manual Annotations of this start: 111 of 172 • Called 100.0% of time when present • Phage (with cluster) where this start called: Coriander_56(DB),

Candidate Starts for Coriander_6: (Start: 12 @5185 has 111 MA's), (27, 5272), (50, 5428),

7 - 12

Coriander_7

DNA Master



bp: 4610

RNAs : 0
GC Content : 0.00
ORF GC : 66.1 ± 3.1
GC3 : 81.6 ± 5.8
CAI : 0.6034 ± 0.0893
Translation Table : Unspecified

Choose ORF start

Starts : 20
Selected : 7

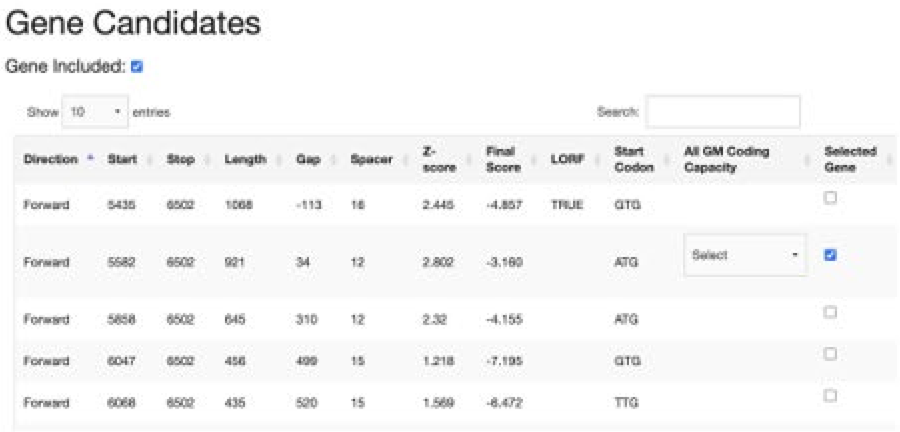
ORF Start : 5582
ORF Stop : 6502
ORF Length : 921

	Cdn1	Cdn2	Cdn3	Length
5' End	68.8	31.3	93.8	48
3' End	63.1	46.7	88.5	366

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-2.792	2.420	16	-4.014	ACAGCCGGAGCCGCCGTGATCG	GTG	5435	1068
2	-1.632	3.100	17	-3.133	CAGAAGGAAAGGGAACACTCCA	ATG	5582	921
3	-4.706	1.483	12	-5.752	GGTCGGCAACGGTGACGTTCAG	ATG	5858	645
4	-5.465	1.308	15	-6.620	GTCCACCGCATCCGCGTCGTGG	GTG	6047	456
5	-5.023	1.526	15	-6.178	GGTGTCCGGCACCCCGAACATC	TTG	6068	435
6	-3.751	2.155	5	-5.149	CACCCCGAACATCTTGCGGGAT	GTG	6077	426
7	-3.751	2.155	17	-5.082	CTTGCGGGATGTGCTCAAGGCT	GTG	6089	414
8	-6.170	0.960	10	-7.128	GGGGTTCGAGCCTGACGTCGTC	GTG	6137	366
9	-5.033	1.621	7	-6.264	CGTCGTCGTGGTCGACGATCTC	ATG	6152	351
10	-6.535	0.779	7	-7.767	CGATCTCATGCTCGCGCACATC	ATG	6167	336
11	-3.673	2.243	6	-4.874	CTCGCCGATCTTCACCGGGAAC	ATG	6236	267
12	-3.673	2.243	12	-4.618	GATCTTCACCGGGAACATGACC	GTG	6242	261
13	-5.236	1.421	7	-6.468	GCCCAACCTCCCGACGGCAGGT	GTG	6293	210
14	-4.068	1.990	12	-5.114	CCCGACGGCAGGTGTGGCTCTT	GTG	6302	201
15	-4.159	1.953	13	-5.230	CGACACCAAGCAGCTCGGCGGA	ATG	6329	174
16	-3.537	2.260	6	-4.838	GAACCTGGCCAGCCCCGGATAC	GTG	6362	141
17	-3.634	2.212	5	-5.032	GAACTTCGGCCAGGTCAAGACG	ATG	6395	108
18	-2.637	2.706	8	-3.762	GATGCGCGAGGACAAGAGCGAC	ATG	6416	87
19	-2.637	2.706	17	-3.938	GGACAAGAGCGACATGTGGCGT	GTG	6425	78

Start DNA Master as specified above

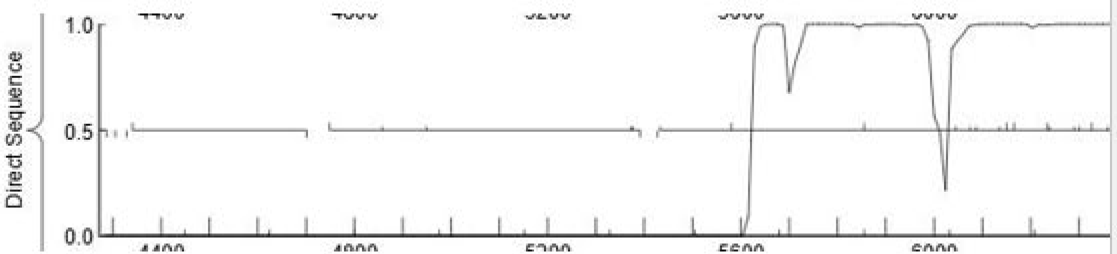


Gene Candidates

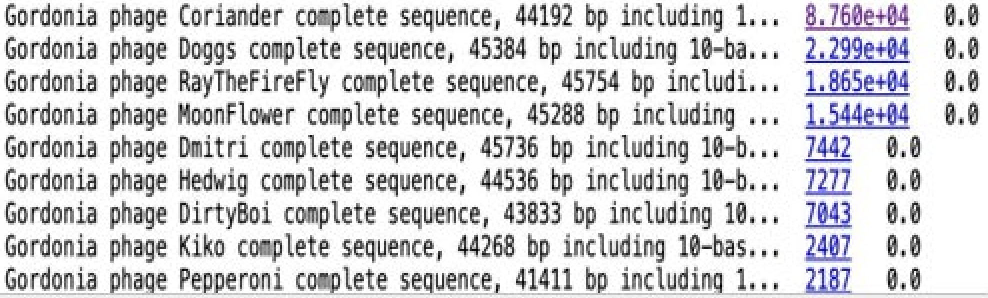
Gene Included: ☑

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	5435	6502	1068	-113	16	2.446	-4.857	TRUE	GTG		☐
Forward	5582	6502	921	34	12	2.802	-3.160		ATG	Select	☑
Forward	5858	6502	645	310	12	2.32	-4.155		ATG		☐
Forward	6047	6502	456	499	15	1.218	-7.195		GTG		☐
Forward	6068	6502	435	520	15	1.569	-6.472		TTG		☐

GeneMarks



Phagesdb - BLAST



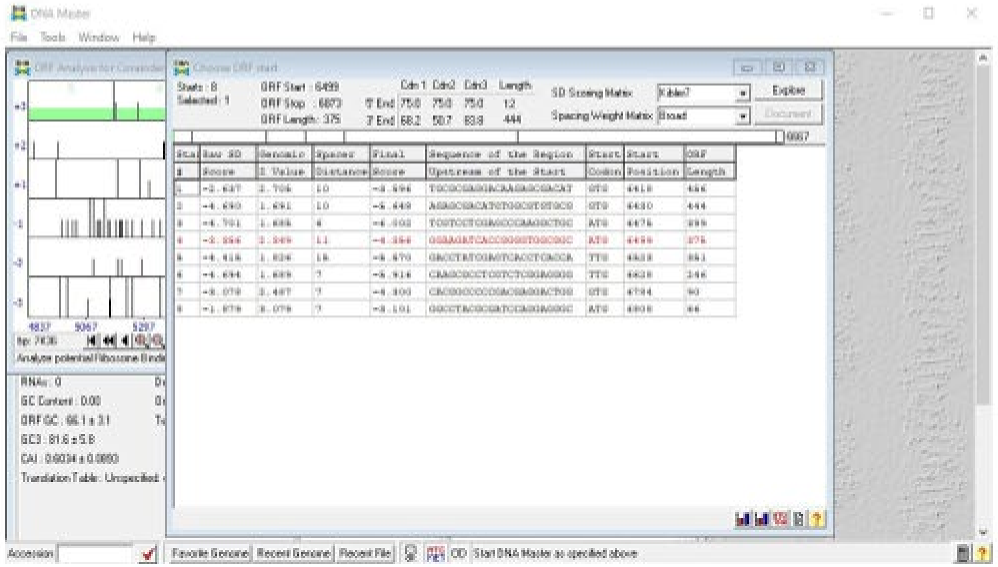
```
Gordonia phage Coriander complete sequence, 44192 bp including 1...  8.760e+04  0.0
Gordonia phage Doggs complete sequence, 45384 bp including 10-ba...  2.299e+04  0.0
Gordonia phage RayTheFireFly complete sequence, 45754 bp includi...  1.865e+04  0.0
Gordonia phage MoonFlower complete sequence, 45288 bp including ...  1.544e+04  0.0
Gordonia phage Dmitri complete sequence, 45736 bp including 10-b...  7442  0.0
Gordonia phage Hedwig complete sequence, 44536 bp including 10-b...  7277  0.0
Gordonia phage DirtyBoi complete sequence, 43833 bp including 10...  7043  0.0
Gordonia phage Kiko complete sequence, 44268 bp including 10-bas...  2407  0.0
Gordonia phage Pepperoni complete sequence, 41411 bp including 1...  2187  0.0
```

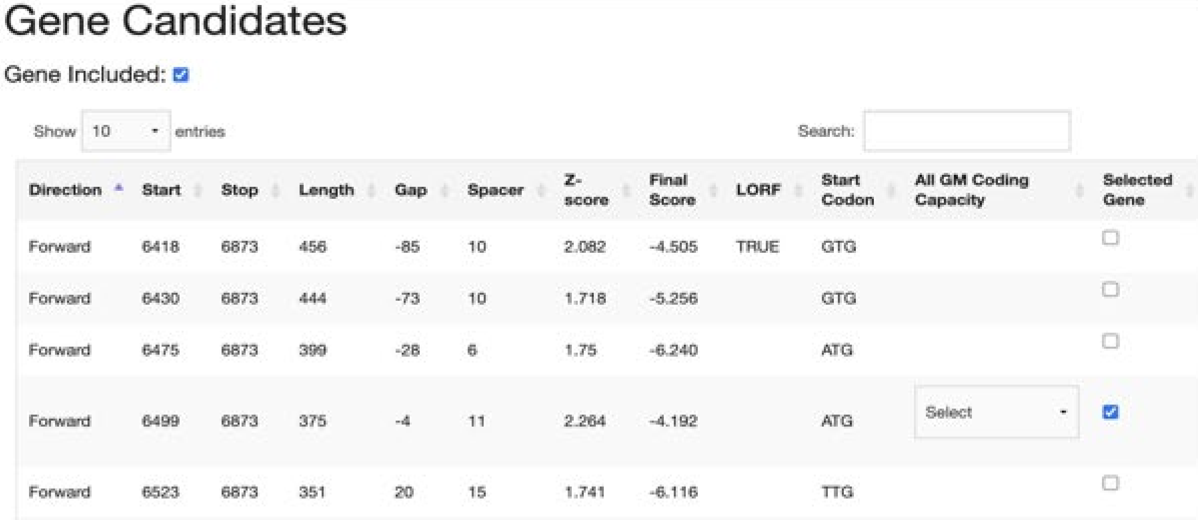
Starterator

Gene: Coriander_7 Start: 5582, Stop: 6502, Start Num: 36
Candidate Starts for Coriander_7:
(12, 5435), (Start: 36 @5582 has 139 MA's), (86, 5858), (124, 6047), (130, 6068), (131, 6077), (135, 6089), (143, 6137), (146, 6152), (150, 6167), (168, 6236), (169, 6242), (185, 6293), (188, 6302), (194, 6329), (202, 6362), (207, 6395), (212, 6416), (213, 6425), (228, 6491),

Coriander_8

DNA Master



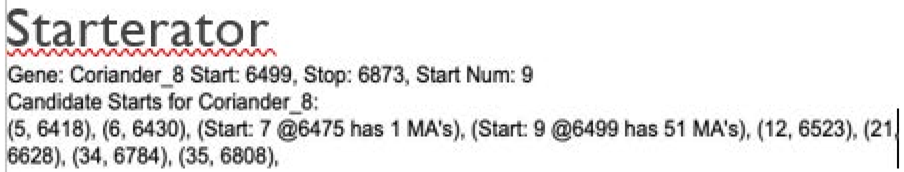


Gene Candidates

Gene Included: ☑

Show 10 entries Search:

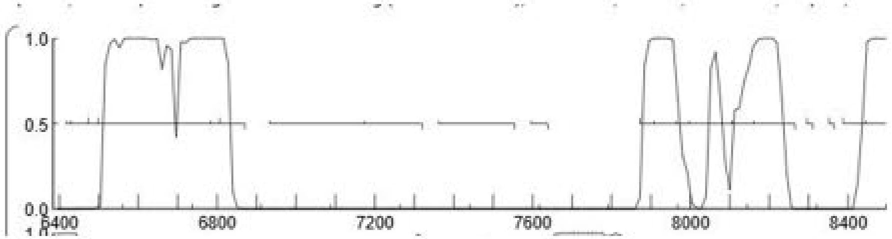
Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	6418	6873	456	-85	10	2.082	-4.505	TRUE	GTG		☐
Forward	6430	6873	444	-73	10	1.718	-5.256		GTG		☐
Forward	6475	6873	399	-28	6	1.75	-6.240		ATG		☐
Forward	6499	6873	375	-4	11	2.264	-4.192		ATG	Select	☑
Forward	6523	6873	351	20	15	1.741	-6.116		TTG		☐



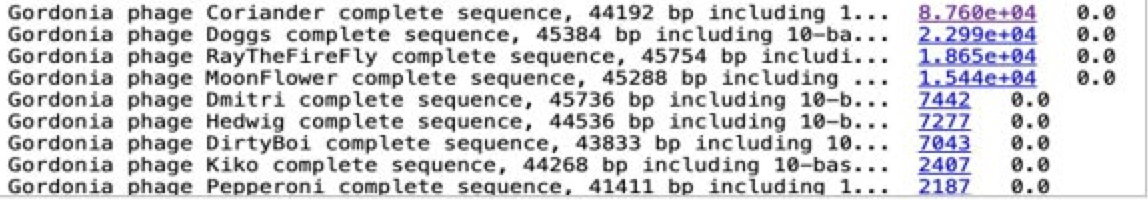
Starterator

Gene: Coriander_8 Start: 6499, Stop: 6873, Start Num: 9
Candidate Starts for Coriander_8:
(5, 6418), (6, 6430), (Start: 7 @6475 has 1 MA's), (Start: 9 @6499 has 51 MA's), (12, 6523), (21, 6628), (34, 6784), (35, 6808),

GeneMarks



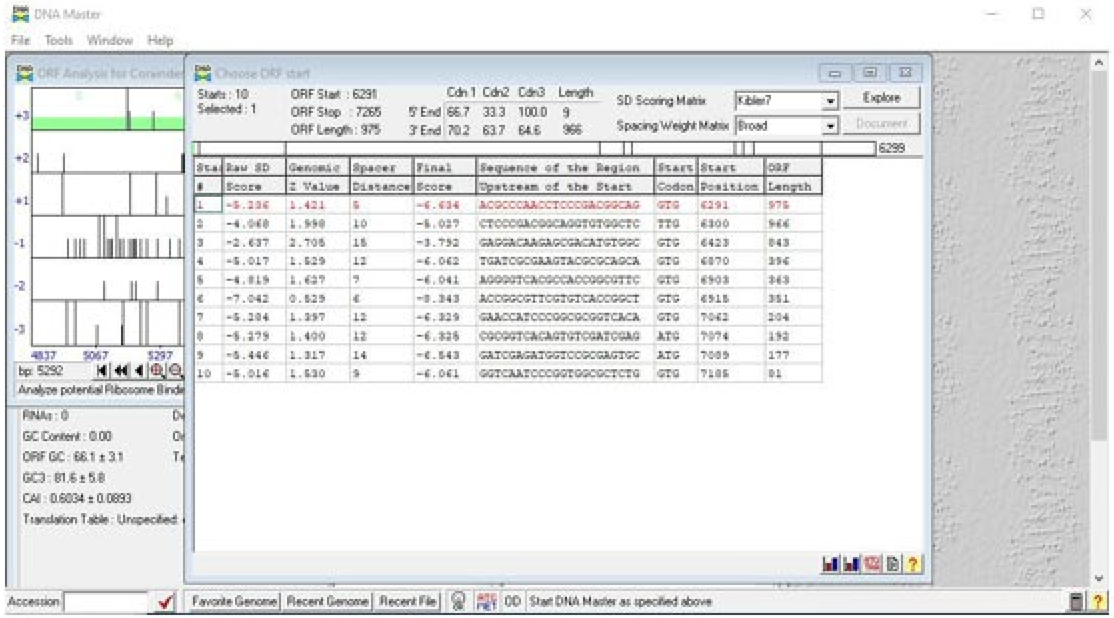
Phagesdb - BLAST



```
Gordonia phage Coriander complete sequence, 44192 bp including 1...  8.760e+04   0.0
Gordonia phage Doggs complete sequence, 45384 bp including 10-ba...  2.299e+04   0.0
Gordonia phage RayTheFireFly complete sequence, 45754 bp includi...  1.865e+04   0.0
Gordonia phage MoonFlower complete sequence, 45288 bp including ...  1.544e+04   0.0
Gordonia phage Dmitri complete sequence, 45736 bp including 10-b...  7442    0.0
Gordonia phage Hedwig complete sequence, 44536 bp including 10-b...  7277    0.0
Gordonia phage DirtyBoi complete sequence, 43833 bp including 10...  7043    0.0
Gordonia phage Kiko complete sequence, 44268 bp including 10-bas...  2407    0.0
Gordonia phage Pepperoni complete sequence, 41411 bp including 1...  2187    0.0
```

Coriander_9

DNA Master



RNAs : 0
GC Content : 0.00
ORF GC : 66.1 ± 3.1
GC3 : 81.6 ± 5.8
CAI : 0.6034 ± 0.0893
Translation Table : Unspecified

Starts : 10
Selected : 1
ORF Start : 6291
ORF Stop : 7265
ORF Length : 975

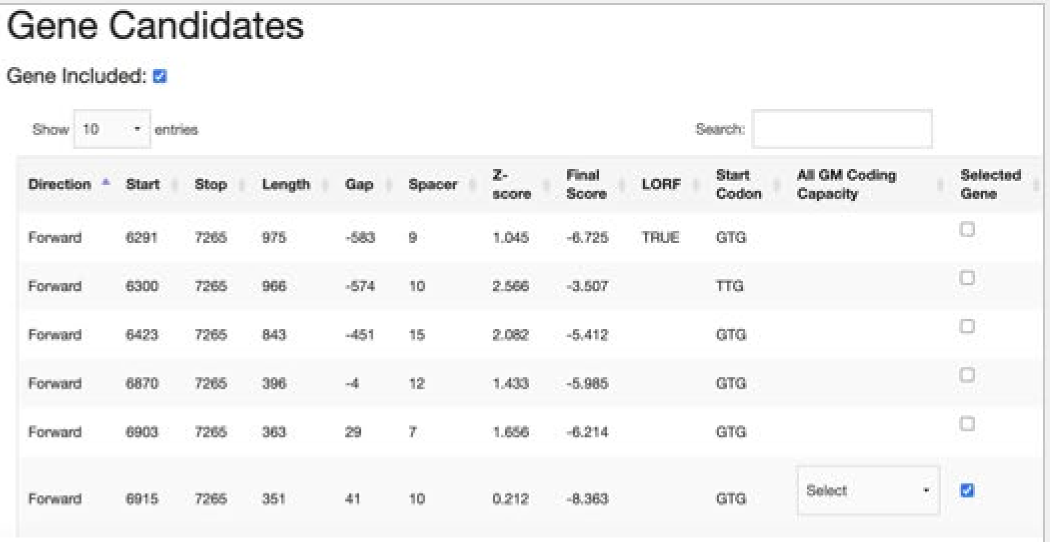
	Cdn 1	Cdn2	Cdn3	Length
5' End	66.7	33.3	100.0	9
3' End	70.2	63.7	64.6	966

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

6299

Start #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.336	1.421	5	-6.634	ACGCCCAACCTCCCGACGGCAG	GTG	6291	975
2	-4.068	1.998	10	-5.027	CTCCCGACGGCAGGTGTGGCTC	TTG	6300	966
3	-2.637	2.708	15	-3.792	GAGGACAAGAGCGACATGTGGC	GTG	6423	843
4	-5.017	1.529	12	-6.062	TGATCGCGAAGTACGCGCAGCA	GTG	6870	396
5	-4.819	1.627	7	-6.041	AGGGGTCACGCCACCGGCGTTC	GTG	6903	363
6	-7.042	0.829	6	-8.343	ACCGGCGTTCGTGTCACCGGCT	GTG	6915	351
7	-5.204	1.397	12	-6.329	GAACCATCCCGGCGCGGTCACA	GTG	7062	204
8	-5.279	1.400	12	-6.325	CGCGGTCACAGTGTCGATCGAG	ATG	7074	192
9	-5.446	1.317	14	-6.543	GATCGAGATGGTCCGCGAGTGC	ATG	7089	177
10	-5.016	1.530	9	-6.061	GGTCAATCCCGGTGGCGCTCTG	GTG	7185	81

Gene Candidates



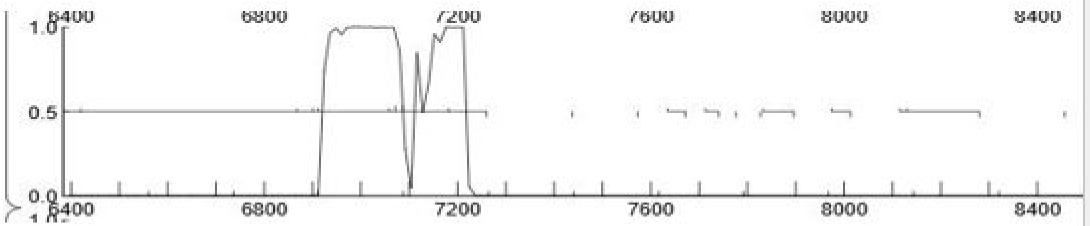
Gene Included: ☑

Show 10 entries

Search:

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	6291	7265	975	-583	9	1.045	-6.725	TRUE	GTG		☐
Forward	6300	7265	966	-574	10	2.566	-3.507		TTG		☐
Forward	6423	7265	843	-451	15	2.082	-5.412		GTG		☐
Forward	6870	7265	396	-4	12	1.433	-5.985		GTG		☐
Forward	6903	7265	363	29	7	1.656	-6.214		GTG		☐
Forward	6915	7265	351	41	10	0.212	-8.363		GTG	Select	☑

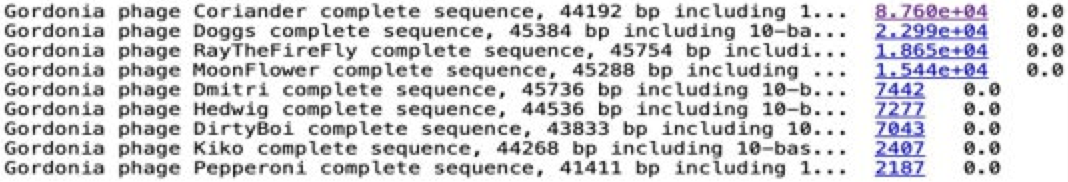
GeneMarks



Starterator

Gene: Coriander_9 Start: 6915, Stop: 7265, Start Num: 36
Candidate Starts for Coriander_9:
(2, 6291), (3, 6300), (4, 6423), (Start: 22 @6870 has 4 MA's), (Start: 33 @6903 has 1 MA's), (Start: 36 @6915 has 1 MA's), (72, 7062), (75, 7074), (80, 7089), (112, 7185),

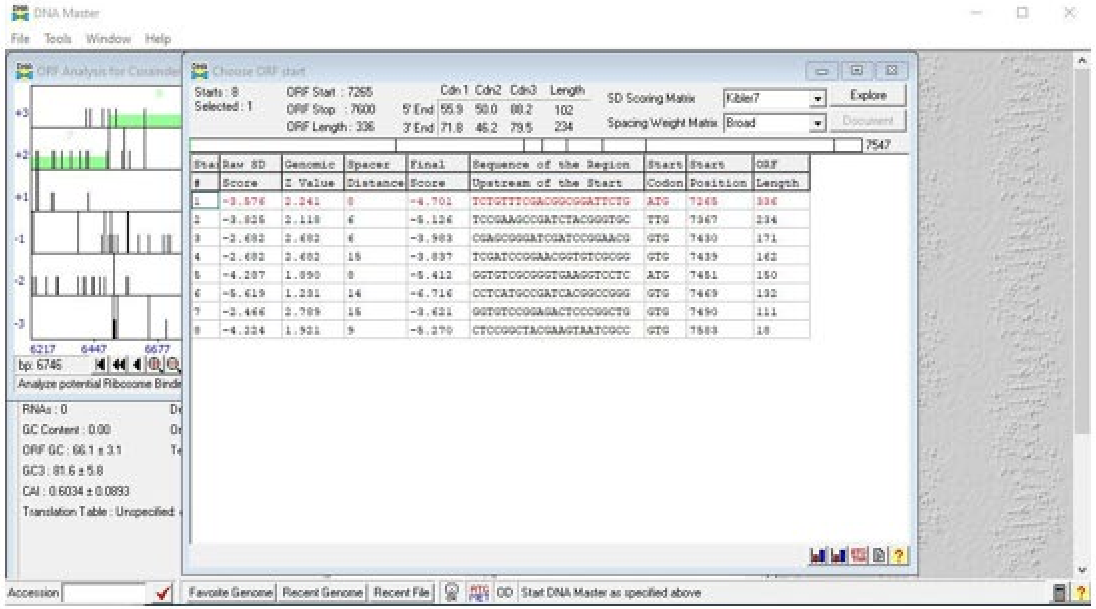
Phagesdb - BLAST



```
Gordonia phage Coriander complete sequence, 44192 bp including 1...  8.760e+04   0.0
Gordonia phage Doggs complete sequence, 45384 bp including 10-ba...  2.299e+04   0.0
Gordonia phage RayTheFireFly complete sequence, 45754 bp includi...  1.865e+04   0.0
Gordonia phage MoonFlower complete sequence, 45288 bp including ...  1.544e+04   0.0
Gordonia phage Dmitri complete sequence, 45736 bp including 10-b...  7442    0.0
Gordonia phage Hedwig complete sequence, 44536 bp including 10-b...  7277    0.0
Gordonia phage DirtyBoi complete sequence, 43833 bp including 10...  7043    0.0
Gordonia phage Kiko complete sequence, 44268 bp including 10-bas...  2407    0.0
Gordonia phage Pepperoni complete sequence, 41411 bp including 1...  2187    0.0
```

Coriander_10

DNA Master



Starts : 8
Selected : 1

ORF Start : 7265
ORF Stop : 7600
ORF Length : 336

	Cdn1	Cdn2	Cdn3	Length
5' End	55.9	50.0	88.2	102
3' End	71.8	46.2	79.5	234

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

7547

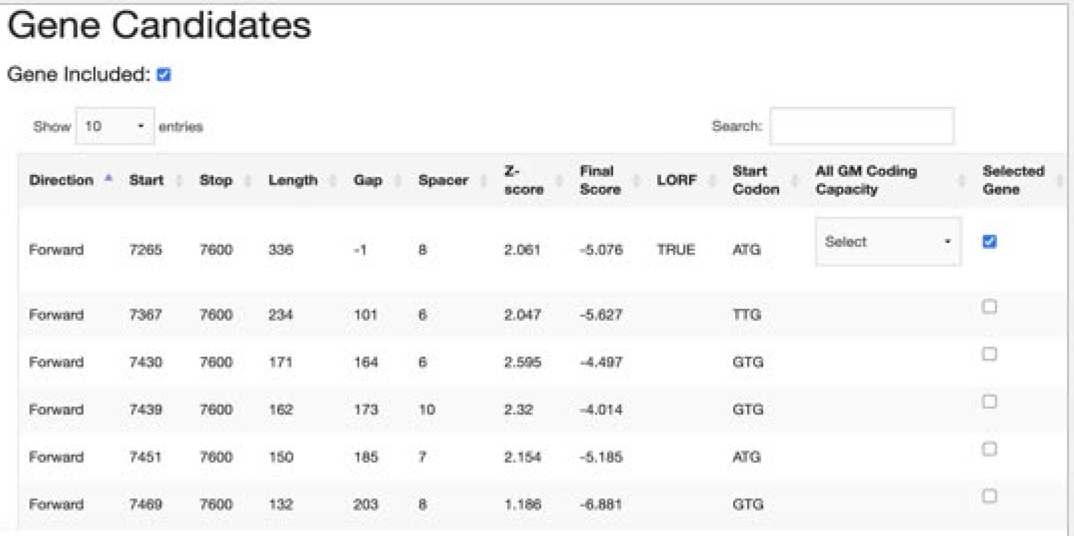
Start #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-3.576	2.241	8	-4.701	TCTGTTTCGACGGCGGATTCTG	ATG	7265	336
2	-3.826	2.118	6	-5.126	TCCGAAGCCGATCTACGGGTGC	TTG	7367	234
3	-2.682	2.682	6	-3.903	CGAGCGGGATCGATCCGGAACG	GTG	7430	171
4	-2.682	2.682	15	-3.837	TCGATCCGGAACGGTGTCGCGG	GTG	7439	162
5	-4.287	1.890	8	-5.412	GGTGTCGCGGGTGAAGGTCCTC	ATG	7451	150
6	-5.619	1.231	14	-6.716	CCTCATGCCGATCACGGCCGGG	GTG	7469	132
7	-2.466	2.789	15	-3.621	GGTGTCCGGAGACTCCCGGCTG	GTG	7490	111
8	-4.224	1.921	9	-5.270	CTCCGGCTACGAAGTAATCGCC	GTG	7583	18

bp: 6746
Analyze potential Ribosome Binding

RNAs : 0
GC Content : 0.00
ORF GC : 66.1 ± 3.1
GC3 : 81.6 ± 5.8
CAI : 0.6034 ± 0.0893
Translation Table : Unspecified

Accession

Gene Candidates



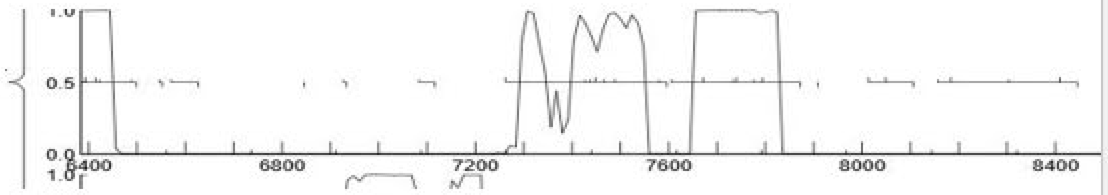
Gene Included: ☑

Show 10 entries

Search:

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	7265	7600	336	-1	8	2.061	-5.076	TRUE	ATG	Select	☑
Forward	7367	7600	234	101	6	2.047	-5.627		TTG		☐
Forward	7430	7600	171	164	6	2.595	-4.497		GTG		☐
Forward	7439	7600	162	173	10	2.32	-4.014		GTG		☐
Forward	7451	7600	150	185	7	2.154	-5.185		ATG		☐
Forward	7469	7600	132	203	8	1.186	-6.881		GTG		☐

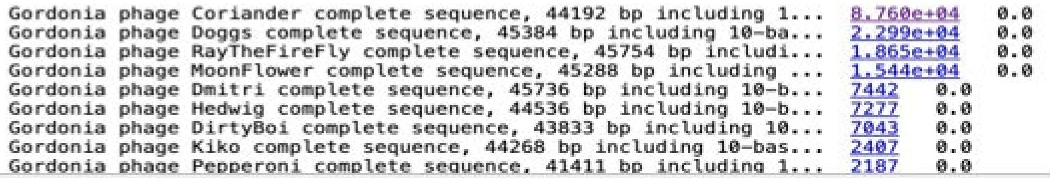
GeneMarks



Starterator

Gene: Coriander_10 Start: 7265, Stop: 7600, Start Num: 12
Candidate Starts for Coriander_10:
(Start: 12 @7265 has 32 MA's), (18, 7367), (23, 7430), (24, 7439), (26, 7451), (28, 7469), (32, 7490), (36, 7583),

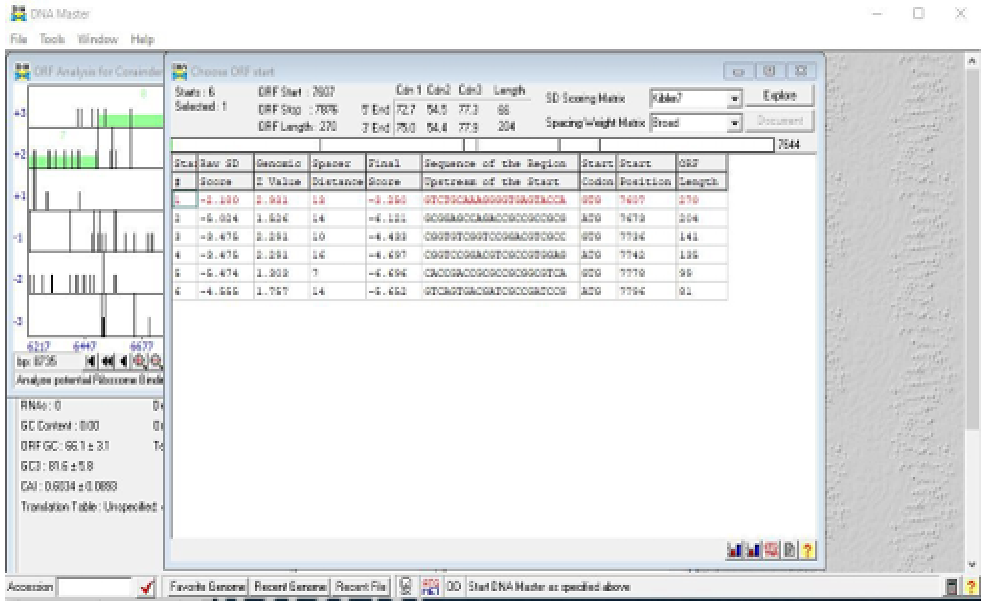
Phagesdb - BLAST

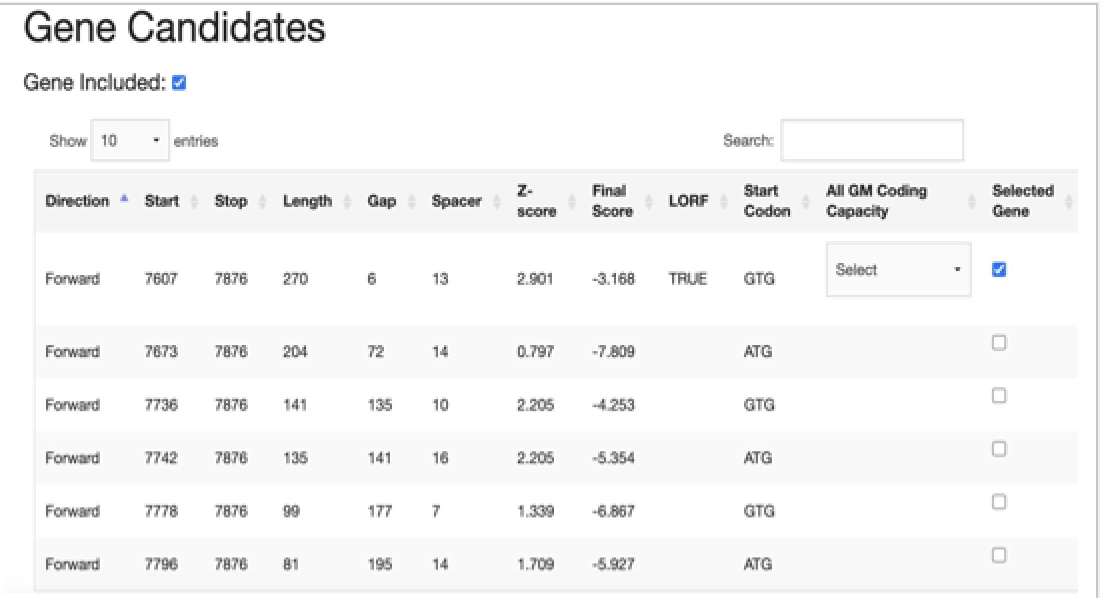


```
Gordonia phage Coriander complete sequence, 44192 bp including 1...  8.760e+04    0.0
Gordonia phage Doggs complete sequence, 45384 bp including 10-ba...  2.299e+04    0.0
Gordonia phage RayTheFireFly complete sequence, 45754 bp includi...  1.865e+04    0.0
Gordonia phage MoonFlower complete sequence, 45288 bp including ...  1.544e+04    0.0
Gordonia phage Dmitri complete sequence, 45736 bp including 10-b...  7442    0.0
Gordonia phage Hedwig complete sequence, 44536 bp including 10-b...  7277    0.0
Gordonia phage DirtyBoi complete sequence, 43833 bp including 10...  7043    0.0
Gordonia phage Kiko complete sequence, 44268 bp including 10-bas...  2407    0.0
Gordonia phage Pepperoni complete sequence, 41411 bp including 1...  2187    0.0
```

Coriander_11

DNA Master





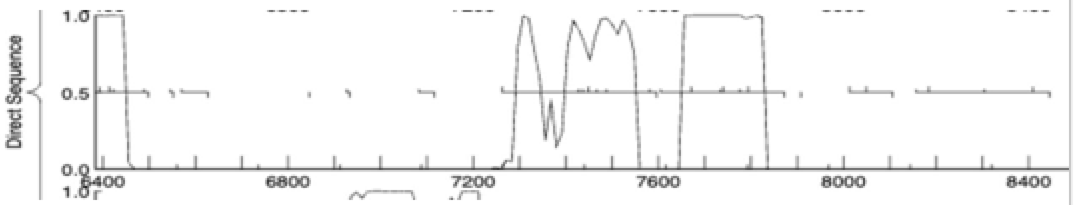
Gene Candidates

Gene Included: ☑

Show 10 entries Search:

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	7607	7876	270	6	13	2.901	-3.168	TRUE	GTG	Select	☑
Forward	7673	7876	204	72	14	0.797	-7.809		ATG		☐
Forward	7736	7876	141	135	10	2.205	-4.253		GTG		☐
Forward	7742	7876	135	141	16	2.205	-5.354		ATG		☐
Forward	7778	7876	99	177	7	1.339	-6.867		GTG		☐
Forward	7796	7876	81	195	14	1.709	-5.927		ATG		☐

GeneMarks



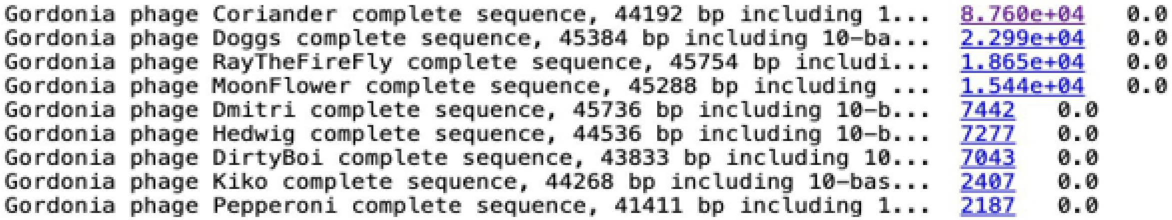
Starterator

Gene: Coriander_11 Start: 7607, Stop: 7876, Start Num: 27

Candidate Starts for Coriander_11:

(Start: 27 @7607 has 7 MA's), (41, 7673), (52, 7736), (53, 7742), (57, 7778), (60, 7796),

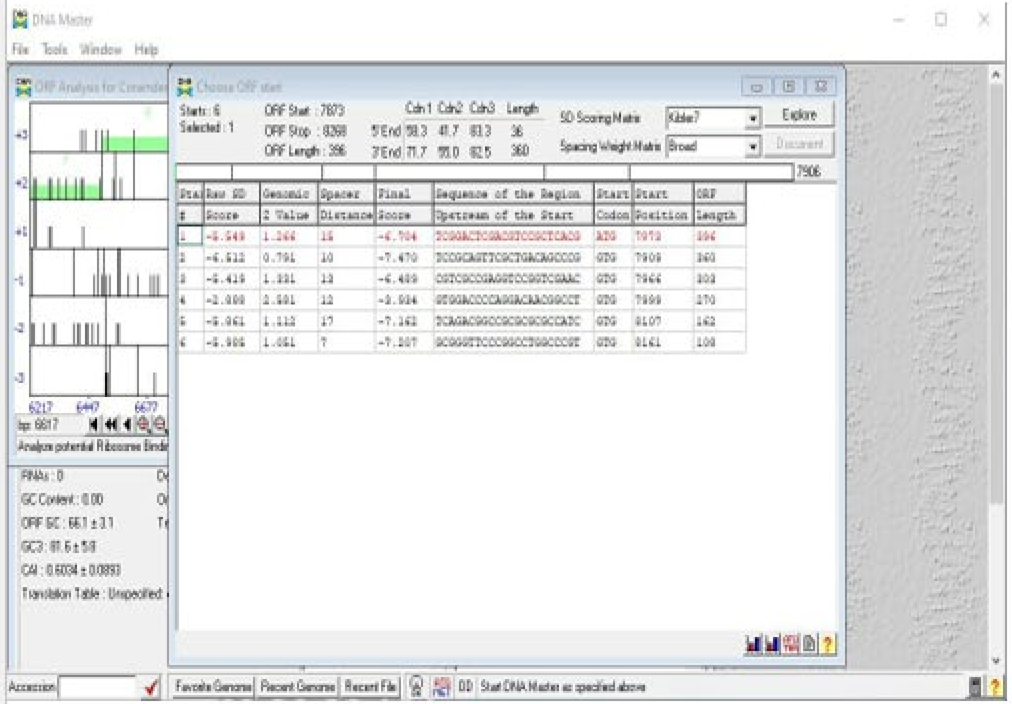
Phagesdb - BLAST



```
Gordonia phage Coriander complete sequence, 44192 bp including 1...  8.760e+04   0.0
Gordonia phage Doggs complete sequence, 45384 bp including 10-ba...  2.299e+04   0.0
Gordonia phage RayTheFireFly complete sequence, 45754 bp includi...  1.865e+04   0.0
Gordonia phage MoonFlower complete sequence, 45288 bp including ...  1.544e+04   0.0
Gordonia phage Dmitri complete sequence, 45736 bp including 10-b...  7442   0.0
Gordonia phage Hedwig complete sequence, 44536 bp including 10-b...  7277   0.0
Gordonia phage DirtyBoi complete sequence, 43833 bp including 10...  7043   0.0
Gordonia phage Kiko complete sequence, 44268 bp including 10-bas...  2407   0.0
Gordonia phage Pepperoni complete sequence, 41411 bp including 1...  2187   0.0
```

Coriander_12

DNA Master



Starts : 6
Selected : 1

ORF Start : 7873
ORF Stop : 8268
ORF Length : 396

	Cdn1	Cdn2	Cdn3	Length
5'End	58.3	41.7	83.3	36
3'End	71.7	55.0	82.5	360

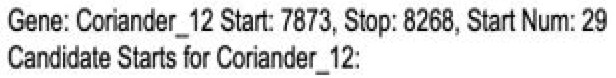
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Start #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.549	1.266	15	-6.704	TCGGACTCGACGTCCGCTCACG	ATG	7873	396
2	-6.512	0.791	10	-7.470	TCCGCAGTTCGCTGACAGCCCG	GTG	7909	360
3	-5.419	1.331	13	-6.409	CGTCGCCGAGGTCCGGTCGAAC	GTG	7966	303
4	-2.888	2.581	12	-3.934	GTGGACCCCAGGACAACGGCCT	GTG	7999	270
5	-5.961	1.112	17	-7.162	TCAGACGGCCGCGCGCGCCATC	GTG	8107	162
6	-5.906	1.061	7	-7.207	GCGGGTTCCCGGCCTGGCCCGT	GTG	8161	108

RNAs : 0
GC Content : 0.00
ORF GC : 66.1 ± 3.1
GC3 : 81.6 ± 5.9
CAI : 0.6034 ± 0.0893
Translation Table : Unspecified

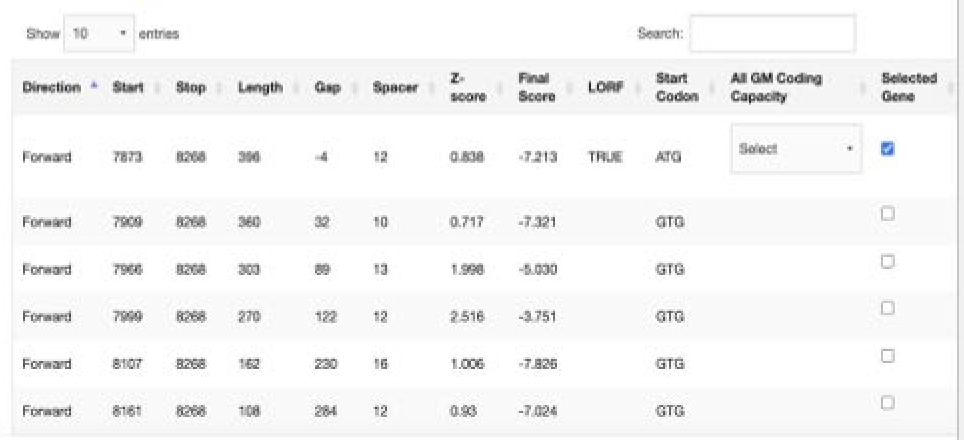
Starterator

Starterator



Gene: Coriander_12 Start: 7873, Stop: 8268, Start Num: 29
Candidate Starts for Coriander_12:

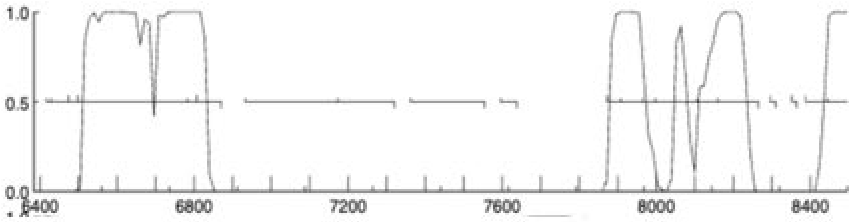
Gene Candidates



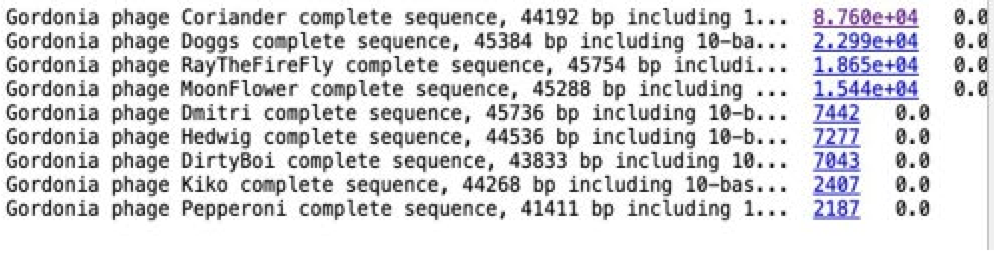
Gene Included: ☑

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	7873	8268	396	-4	12	0.838	-7.213	TRUE	ATG	Select	☑
Forward	7909	8268	360	32	10	0.717	-7.321		GTG		☐
Forward	7966	8268	303	89	13	1.998	-5.030		GTG		☐
Forward	7999	8268	270	122	12	2.516	-3.751		GTG		☐
Forward	8107	8268	162	230	16	1.006	-7.826		GTG		☐
Forward	8161	8268	108	284	12	0.93	-7.024		GTG		☐

GeneMarks



Phagesdb - BLAST



```
Gordonia phage Coriander complete sequence, 44192 bp including 1...  8.760e+04   0.0
Gordonia phage Doggs complete sequence, 45384 bp including 10-ba...  2.299e+04   0.0
Gordonia phage RayTheFireFly complete sequence, 45754 bp includi...  1.865e+04   0.0
Gordonia phage MoonFlower complete sequence, 45288 bp including ...  1.544e+04   0.0
Gordonia phage Dmitri complete sequence, 45736 bp including 10-b...  7442   0.0
Gordonia phage Hedwig complete sequence, 44536 bp including 10-b...  7277   0.0
Gordonia phage DirtyBoi complete sequence, 43833 bp including 10...  7043   0.0
Gordonia phage Kiko complete sequence, 44268 bp including 10-bas...  2407   0.0
Gordonia phage Pepperoni complete sequence, 41411 bp including 1...  2187   0.0
```

13 - 18

Phage Name	Coriander
Gene #	13
Stop Coordinate	9228
Direction (For/Rev)	forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	8389
Selected Function	none

Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, both Glimmer and GeneMark
Is there evidence for coding potential?	Yes there is coding potential via GeneMarkS however function is not listed
Is this gene present in other annotated genomes?	The gene is present in other annotated genomes; however, it is similar to phage Doggs, gene 12, with an evalue of e-161
Does the gene violate any major guiding principles?	No, this gene doesn't violate any principles. The gene is long enough with 839 bp; there's no overlap, and it has 121 bp between gene 12 and gene 13
DECISION:	Yes, this is a gene.

What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: 8389 GeneMark Start Coordinate (type NA if not supported):: 8389
Does the start site have an associated Ribosome Binding Site with a high score?	Z-score: 1.479 RBS: -5.092 This gene does not have the best RBS or Z-score due to being smaller than 2
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	ORF: 378 Start: 17131 There is no violation of the principles, no overlap with the start site of 17131, and this ORF is not the longest length
Is this start site conserved in other phage genomes as indicated by Starterator?	The Starterator doesn't match with any of the start sites. The starterator start site is not found in the ORF. There is a better consensus at site #8, position 8389.
Is this start site conserved in other phage genomes as indicated by BlastP?	NCBI: phage Doggs Q1 & S1, evalue: 0.0 PhagesDB: Phage Doggs Q1 & S1 evalue: e-161
DECISION:	The start site should be at 8389; each start site has the gene positioned at 8389

Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	PhagesDB: Doggs_12 Q1 & S1, evalue: -161 NCBI: Doggs Q1 & S1 evalue: 0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	Major tail protein; Bacteriophage, tail tube, VIRUS, VIRAL PROTEIN;{Mycobacterium phage Bxb1} Probability: 100%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, major tail protein
Is this gene a possible transmembrane protein?	no
Is the proposed function found on the SEA-PHAGES approved function list?	Yes, the function is found on the Sea-Phages approved function list
DECISION:	Yes, the function should be assigned as major tail protein

Phage Name	Coriander
Gene #	14
Stop Coordinate	9636
Direction (For/Rev)	forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	9316
Selected Function	none

Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, both Glimmer and GeneMark
Is there evidence for coding potential?	Yes, there is coding potential, but no function is listed
Is this gene present in other annotated genomes?	Similar to Phage Kiko, the gene #14 evalue of 9.3e-4
Does the gene violate any major guiding principles?	No, no major violations. It is long enough, no overlaps, and both genes before and after are in the same direction
DECISION:	Yes, this is a gene

What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: 9316 GeneMark Start Coordinate (type NA if not supported):: 9316
Does the start site have an associated Ribosome Binding Site with a high score?	Z-score: 1.625 RBS: -4.793 This isn't the best score due to being not larger than 2
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	ORF: 342 Start: 17167 The ORF is not the most extended length, it doesn't violate any principles and there's not any overlap
Is this start site conserved in other phage genomes as indicated by Starterator?	No, the ORF doesn't match the starterator at position 9316.
Is this start site conserved in other phage genomes as indicated by BlastP?	PhagesDB: Doggs_13 Q1 & S!, evalue: 2e-53 NCBI: Doggs Q1 & S1 evalue: 1e-68
DECISION:	The gene should start at 9316 due to all bioinformatics stating start site 9316.

Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	PhagesDB: Doggs_13, Q1 & S1, evalue: 2e-53 NCBI: Doggs Q1 & S1, evalue: 1e-68
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	NO quality match a.140.1.1 (A:111-153) Thymopoietin, LAP2 {Human (Homo sapiens) [TaxId: 9606] Probability: 54.1%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, tail assembly chaperone
Is this gene a possible transmembrane protein?	no
Is the proposed function found on the SEA-PHAGES approved function list?	Yes, the proposed function is found on the approved sea-phages list
DECISION:	NKF

Phage Name	Coriander
Gene #	15
Stop Coordinate	10490
Direction (For/Rev)	forward
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	9633
Selected Function	none

Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, both glimmer and genemarks
Is there evidence for coding potential?	Yes there is coding potential but no function listed
Is this gene present in other annotated genomes?	Similar to phage Doggs, gene 14, evalue of e-152
Does the gene violate any major guiding principles?	No major violations, gene is long enough at 857 bp and has no overlaps. All genes before and after are in the same direction
DECISION:	Yes, this is a gene

What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: 9633 GeneMark Start Coordinate (type NA if not supported):: 9633
Does the start site have an associated Ribosome Binding Site with a high score?	Z-score: 1.507 RBS: -5.728 No, it is not the best score due to both scores being below 2
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	ORF: 273 Start: 17236 No violation to the principles and no overlap
Is this start site conserved in other phage genomes as indicated by Starterator?	No, the start site doesn't match the starterator. The Starterator has a start site at 89505, and ORF states 17236.
Is this start site conserved in other phage genomes as indicated by BlastP?	PhagesDB: Doggs_14, Q1 & S1, evalue of e-152 NCBI: Doggs, Q1 &S1, evalue of 0
DECISION:	Start site should be at 9633, all other bioinformatics states start site at this position.

Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	NCBI: Doggs, Q1 & S1, evalue of o PhagesDB: Doggs_14, Q1 & S1, evalue of e-152
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	No quality match PhageMin_Tail ; Phage-related minor tail protein Probability : 29.3%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, the most closely related phage is the tail assembly chaperone
Is this gene a possible transmembrane protein?	No
Is the proposed function found on the SEA-PHAGES approved function list?	Yes, this function is found on the sea-phages approved function list
DECISION:	Tail assembly chaperone, due to several adjacent genes listed as tail assembly chaperone function

Phage Name	Coriander
Gene #	16
Stop Coordinate	10876
Direction (For/Rev)	forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	9633
Selected Function	none

QC SMART team

GGGAAA (10484)
The second one has to be the same start as the first.

Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, both glimmer and genemarks
Is there evidence for coding potential?	Yes, there is coding potential however, no function listed
Is this gene present in other annotated genomes?	Similar to Doggs, gene 15, evalue of 3e-57
Does the gene violate any major guiding principles?	There are no major violations. The gene is long enough with 332 bp and no overlaps. The genes before and after are in the same direction
DECISION:	Yes, this is a gene

What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: 10544 GeneMark Start Coordinate (type NA if not supported):: 10544
Does the start site have an associated Ribosome Binding Site with a high score?	Z-score: 2.129 RBS: -4.541 Yes, this is the best score due to the z-score being greater than 2
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	ORF: 231 Start: 17278 There is no overlap and there is no violation to any principles
Is this start site conserved in other phage genomes as indicated by Starterator?	The starterator's start site doesn't match. The best option would be start site 17278
Is this start site conserved in other phage genomes as indicated by BlastP?	NCBI: Doggs, Q1 & S306, evalue of 6e-68 PhagesDB: Doggs, Q1 & S306, evalue of 3e-57
DECISION:	The gene should start at position 10544 due to all bioinformatics listing the start site at 10544

Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	PhagesDB: Doggs_15, Q1 & S306, evalue of 3e-57 NCBI: Doggs, Q1 & S306, evalue of 6e-68
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	No quality match Acetone carboxylase gamma subunit; carboxylation, ligase; HET: AMP, AE4, MG, ACT; 1.87A {Xanthobacter autotrophicus Py2} Probability: 27.19%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, adjacent genes have the function of tail assembly chaperone
Is this gene a possible transmembrane protein?	no
Is the proposed function found on the SEA-PHAGES approved function list?	yes
DECISION:	NKF, however, based on the adjacent genes and the percentage of how similar each is to this gene, it's possible to list it as a tail assembly chaperone.

Phage Name	Coriander
Gene #	17
Stop Coordinate	16564
Direction (For/Rev)	forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	10886
Selected Function	none

Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, both glimmer and genemarks
Is there evidence for coding potential?	Yes, there is coding potential, but the function is unknown
Is this gene present in other annotated genomes?	Phage Doggs, gene 16, evalue of 0
Does the gene violate any major guiding principles?	There is no significant overlap, only 3 bp with gene 18. The gene is long enough at 5678 bp, both genes before and after are in the same direction
DECISION:	yes

What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: 10886 GeneMark Start Coordinate (type NA if not supported):: 10886
Does the start site have an associated Ribosome Binding Site with a high score?	Z-score: 1.265 RBS: -5.529 Not the best score due to both scores being below 2
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	ORF: 204 Start: 17305 The proposed start site does not overlap with the nearest gene, which doesn't violate the guiding principles
Is this start site conserved in other phage genomes as indicated by Starterator?	The starterator start site is 227586, and the ORF start site is 17305, meaning there is no match.
Is this start site conserved in other phage genomes as indicated by BlastP?	PhagesDB: Doggs_16, Q1 & S1, evalue is 0 NCBI: Doggs, Q1 & S1, evalue is 0
DECISION:	Start site should be at 10886, all bioinformatics list start site at 10886

Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	PhagesDB: Doggs_16, Q1 & S1, evalue of 0 NCBI: Doggs, Q1 & S1, evalue of 0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	Tape measure; Flagellotropic bacteriophage, Siphophage, Tail-tip, VIRUS;{Chivirus chi} Probability: 99.67%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, tape measure protein
Is this gene a possible transmembrane protein?	no
Is the proposed function found on the SEA-PHAGES approved function list?	yes
DECISION:	Tape measure protein

Phage Name	Coriander
Gene #	18
Stop Coordinate	17508
Direction (For/Rev)	forward
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	16561
Selected Function	none

Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, both glimmer and genemarks
Is there evidence for coding potential?	There is coding potential, no function is listed
Is this gene present in other annotated genomes?	Similar to Doggs phage, gene 17, evalue is -180
Does the gene violate any major guiding principles?	No major overlaps (overlap of 3 bp), the gene is long enough at 947. Genes before and after are in the same direction
DECISION:	Yes, this is a gene

What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: 16561 GeneMark Start Coordinate (type NA if not supported):: 16561
Does the start site have an associated Ribosome Binding Site with a high score?	Z-score: 0.727 RBS: -6.627 Not the best score, due to each score being less than 2
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	ORF: 162 Start: 17347 No overlaps and no violation to the principles
Is this start site conserved in other phage genomes as indicated by Starterator?	Starterator has the start site at 227101 and ORF start site is 17347, there is no match.
Is this start site conserved in other phage genomes as indicated by BlastP?	PhagesDB: Doggs_17, Q1 & S1, evalue of -180 NCBI: Doggs, Q1 & S1, evalue of 0
DECISION:	The gene should start at 16561 because there are 95 bp that indicate the start site at 16561

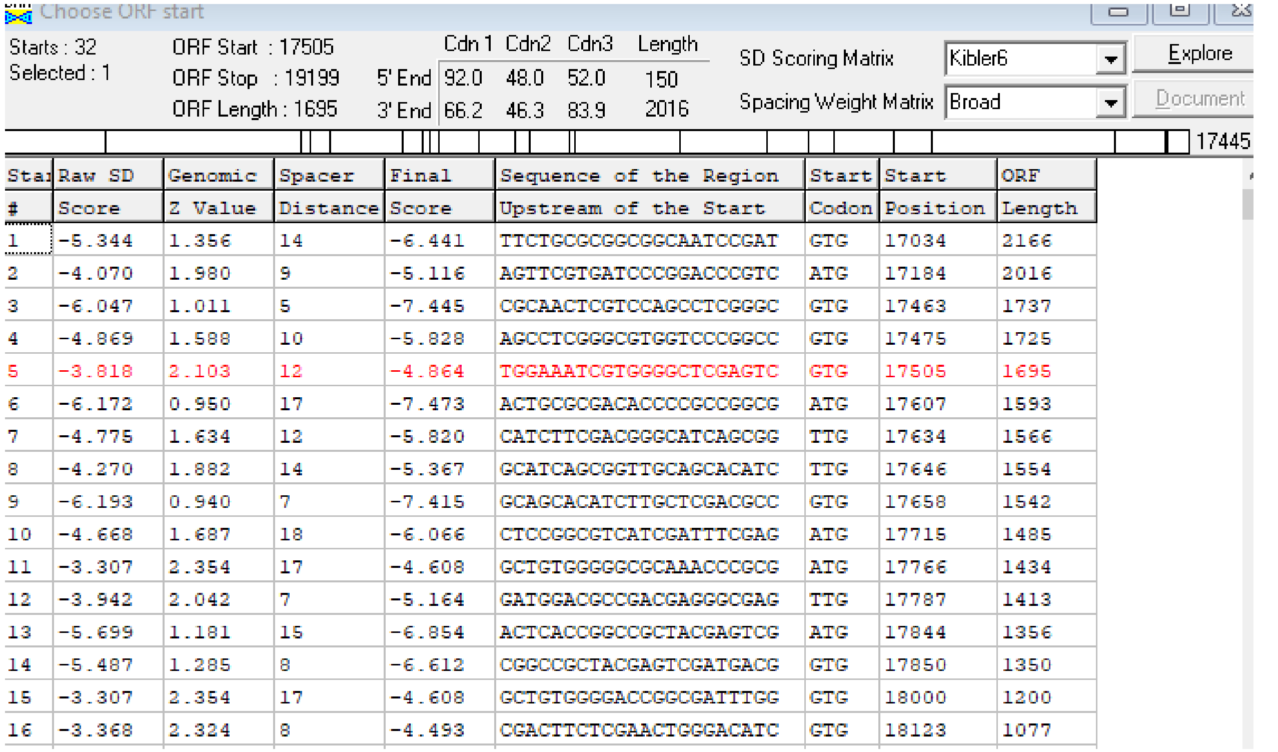
Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	PhagesDB: Doggs_17, Q1 & S1, evalue of -180 NCBI: Doggs, Q1 & S1, evalue of 0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	HYPOTHETICAL PROTEIN 19.1; VIRAL PROTEIN, DISTAL TAIL PROTEIN; 2.95A {BACILLUS PHAGE SPP1} Probability: 99.91%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, adjacent genes are listed as minor tail protein
Is this gene a possible transmembrane protein?	No
Is the proposed function found on the SEA-PHAGES approved function list?	yes
DECISION:	Tail protein

19 - 24

Coriander_Draft

Phamerator- Gene 19_ Start site 17505

PECAAN- Gene 19_Start site 17505



Starts : 32
Selected : 1

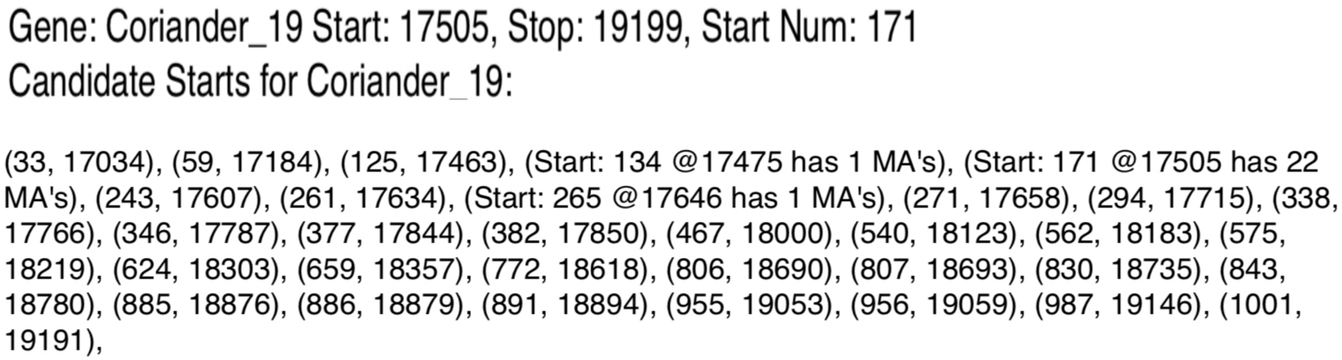
ORF Start : 17505
ORF Stop : 19199
ORF Length : 1695

	Cdn 1	Cdn2	Cdn3	Length
5' End	92.0	48.0	52.0	150
3' End	66.2	46.3	83.9	2016

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Broad

Star #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.344	1.356	14	-6.441	TTCTGCGCGGCGGCAATCCGAT	GTG	17034	2166
2	-4.070	1.980	9	-5.116	AGTTCGTGATCCCGGACCCGTC	ATG	17184	2016
3	-6.047	1.011	5	-7.445	CGCAACTCGTCCAGCCTCGGGC	GTG	17463	1737
4	-4.869	1.588	10	-5.828	AGCCTCGGGCGTGGTCCCGGCC	GTG	17475	1725
5	-3.818	2.103	12	-4.864	TGGAAATCGTGGGGCTCGAGTC	GTG	17505	1695
6	-6.172	0.950	17	-7.473	ACTGCGCGACACCCCGCCGGCG	ATG	17607	1593
7	-4.775	1.634	12	-5.820	CATCTTCGACGGGCATCAGCGG	TTG	17634	1566
8	-4.270	1.882	14	-5.367	GCATCAGCGGTTGCAGCACATC	TTG	17646	1554
9	-6.193	0.940	7	-7.415	GCAGCACATCTTGCTCGACGCC	GTG	17658	1542
10	-4.668	1.687	18	-6.066	CTCCGGCGTCATCGATTTCGAG	ATG	17715	1485
11	-3.307	2.354	17	-4.608	GCTGTGGGGGCGCAAACCCGCG	ATG	17766	1434
12	-3.942	2.042	7	-5.164	GATGGACGCCGACGAGGGCGAG	TTG	17787	1413
13	-5.699	1.181	15	-6.854	ACTCACCGGCCGCTACGAGTCG	ATG	17844	1356
14	-5.487	1.285	8	-6.612	CGGCCGCTACGAGTCGATGACG	GTG	17850	1350
15	-3.307	2.354	17	-4.608	GCTGTGGGGACCGGCGATTTGG	GTG	18000	1200
16	-3.368	2.324	8	-4.493	CGACTTCTCGAACTGGGACATC	GTG	18123	1077

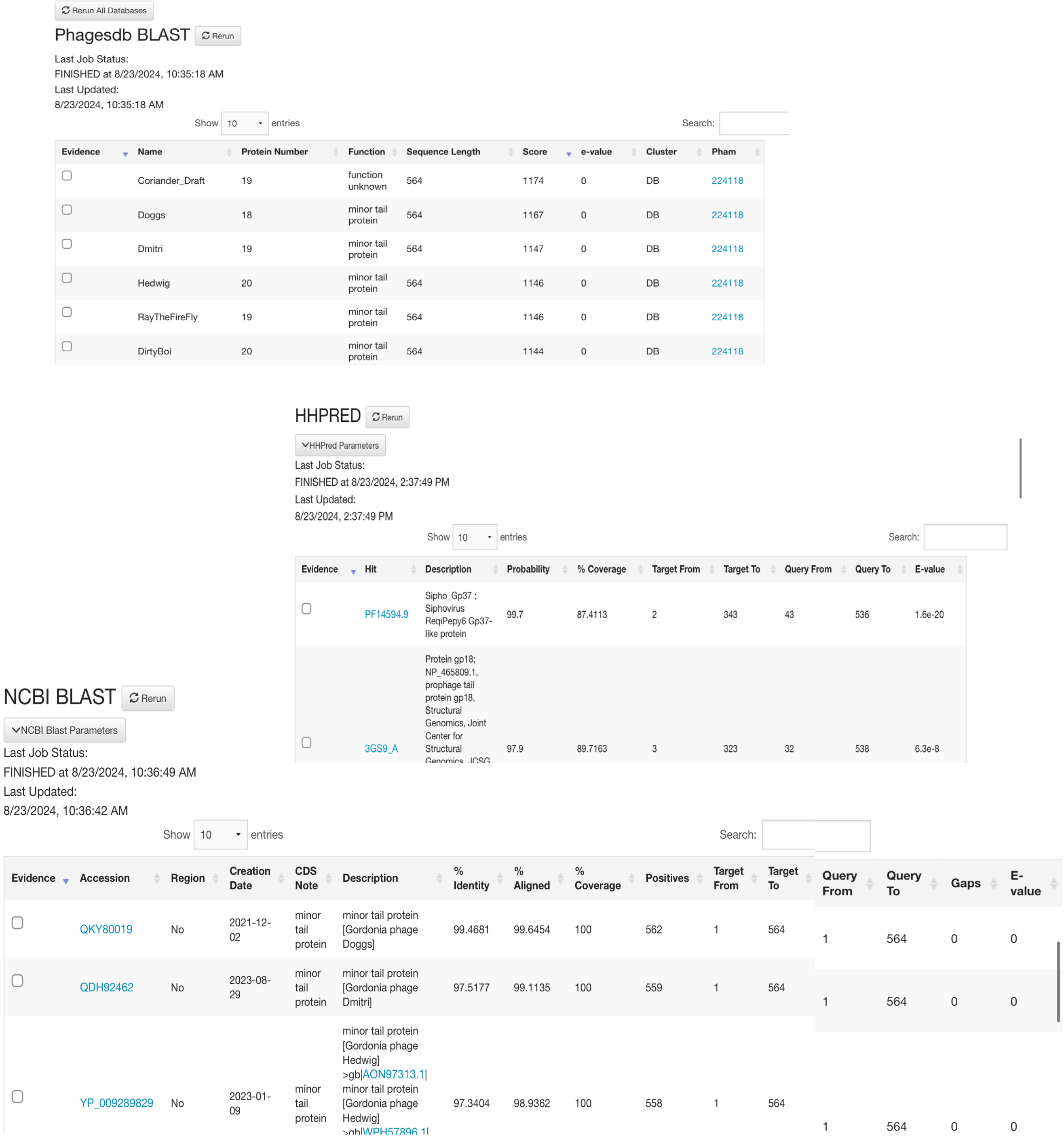
GeneMark:



Gene: Coriander_19 Start: 17505, Stop: 19199, Start Num: 171
Candidate Starts for Coriander_19:

(33, 17034), (59, 17184), (125, 17463), (Start: 134 @17475 has 1 MA's), (Start: 171 @17505 has 22 MA's), (243, 17607), (261, 17634), (Start: 265 @17646 has 1 MA's), (271, 17658), (294, 17715), (338, 17766), (346, 17787), (377, 17844), (382, 17850), (467, 18000), (540, 18123), (562, 18183), (575, 18219), (624, 18303), (659, 18357), (772, 18618), (806, 18690), (807, 18693), (830, 18735), (843, 18780), (885, 18876), (886, 18879), (891, 18894), (955, 19053), (956, 19059), (987, 19146), (1001, 19191),

Basic Phage Information	
Phage Name	**Coriander_19**
Gene #	**Gene 19 (PECAAN)** **Gene 19 (phamerator)**
Stop Coordinate	**Stop 19,199**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**Overlap with Coriander_18 at**
Selected Start Coordinate	**17505 (PECAAN)** **17505 (Phamerator)**
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:35:18 AM
Last Updated:
8/23/2024, 10:35:18 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	19	function unknown	564	1174	0	DB	224118
☐	Doggs	18	minor tail protein	564	1167	0	DB	224118
☐	Dmitri	19	minor tail protein	564	1147	0	DB	224118
☐	Hedwig	20	minor tail protein	564	1146	0	DB	224118
☐	RayTheFireFly	19	minor tail protein	564	1146	0	DB	224118
☐	DirtyBoi	20	minor tail protein	564	1144	0	DB	224118

HHPRED

Last Job Status:
FINISHED at 8/23/2024, 2:37:49 PM
Last Updated:
8/23/2024, 2:37:49 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF14594.9	Sipho_Gp37 ; Siphovirus ReqiPepy6 Gp37-like protein	99.7	87.4113	2	343	43	536	1.6e-20
☐	3GS9_A	Protein gp18; NP_465809.1, prophage tail protein gp18, Structural Genomics, Joint Center for Structural Genomics, JCSG	97.9	89.7163	3	323	32	538	6.3e-8

NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:49 AM
Last Updated:
8/23/2024, 10:36:42 AM

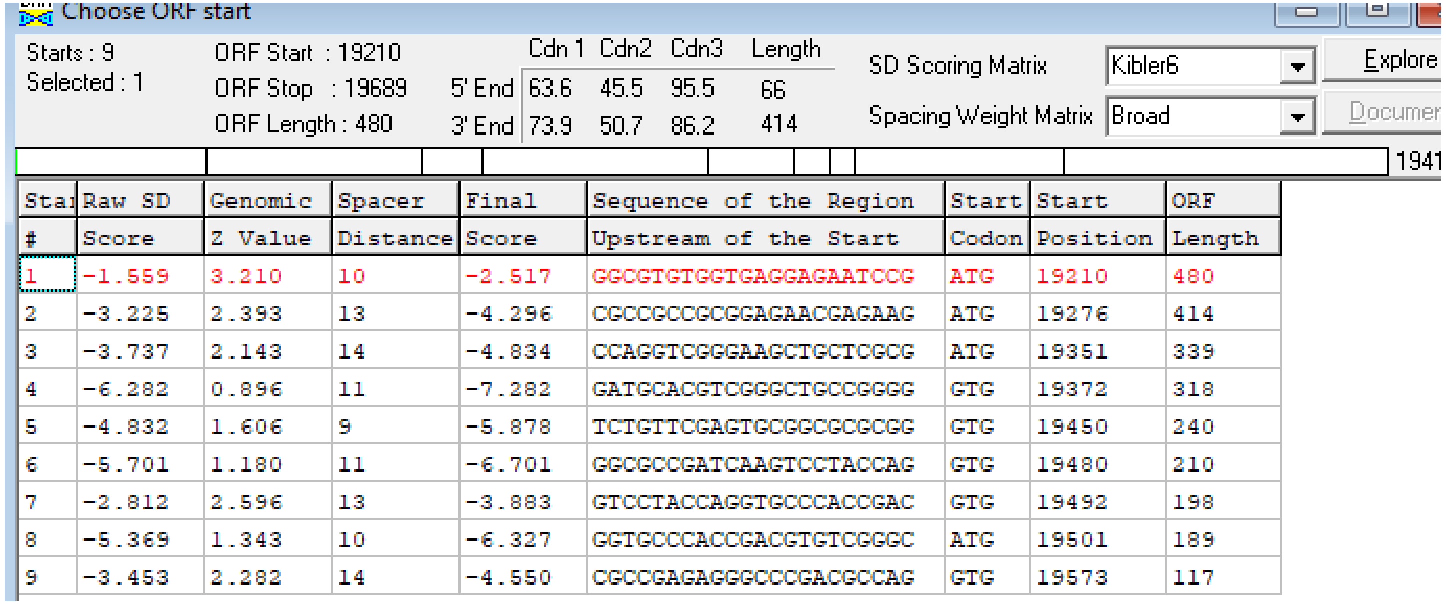
Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80019	No	2021-12-02	minor tail protein	minor tail protein [Gordonia phage Doggs]	99.4681	99.6454	100	562	1	564	1	564	0	0
☐	QDH92462	No	2023-08-29	minor tail protein	minor tail protein [Gordonia phage Dmitri]	97.5177	99.1135	100	559	1	564	1	564	0	0
☐	YP_009289829	No	2023-01-09	minor tail protein	minor tail protein [Gordonia phage Hedwig] >gb|AON97313.1| minor tail protein [Gordonia phage Hedwig] >gb|WPH57896.1|	97.3404	98.9362	100	558	1	564	1	564	0	0

Coriander_Draft

Phamerator- Gene 20_Start site 19210

PECAAN- Gene 20_Start site 19210



Starts : 9
Selected : 1

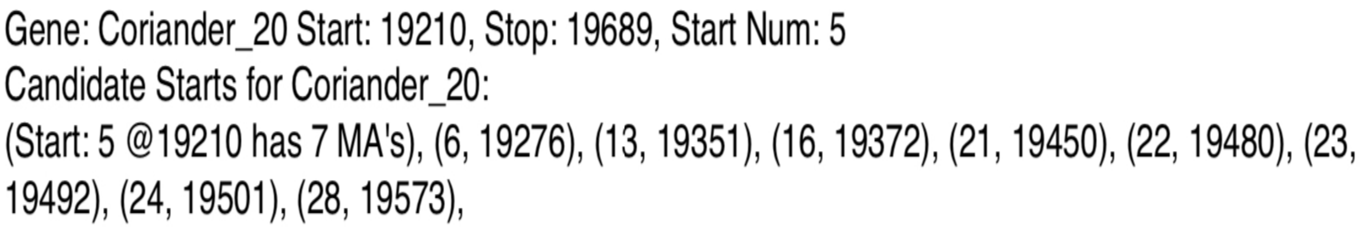
ORF Start : 19210
ORF Stop : 19689
ORF Length : 480

	Cdn 1	Cdn2	Cdn3	Length
5' End	63.6	45.5	95.5	66
3' End	73.9	50.7	86.2	414

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Broad

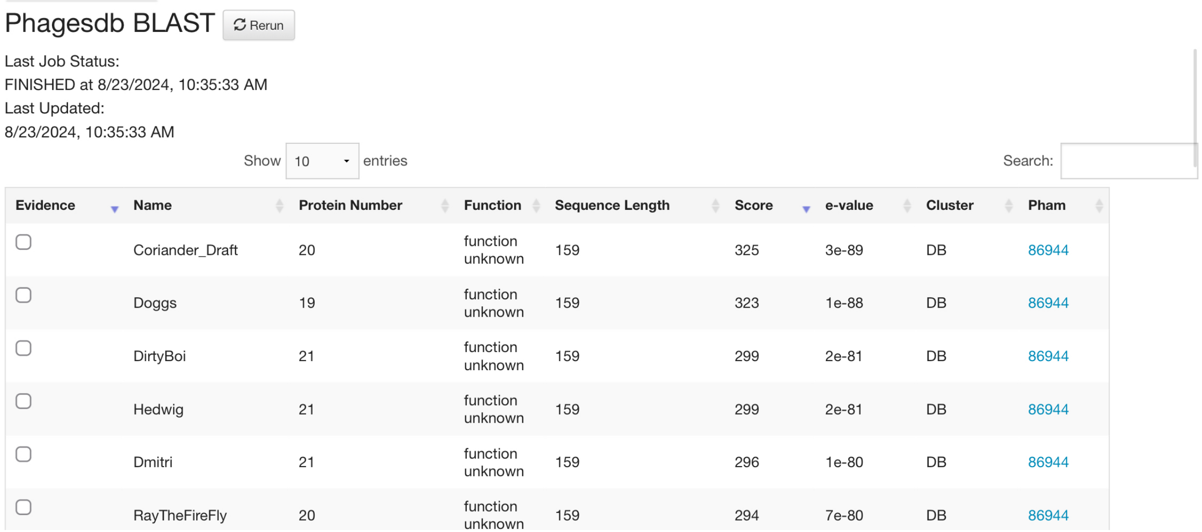
Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-1.559	3.210	10	-2.517	GGCGTGTGGTGAGGAGAATCCG	ATG	19210	480
2	-3.225	2.393	13	-4.296	CGCCGCCGCGGAGAACGAGAAG	ATG	19276	414
3	-3.737	2.143	14	-4.834	CCAGGTCGGGAAGCTGCTCGCG	ATG	19351	339
4	-6.282	0.896	11	-7.282	GATGCACGTCGGGCTGCCGGGG	GTG	19372	318
5	-4.832	1.606	9	-5.878	TCTGTTCGAGTGCGGCGCGCGG	GTG	19450	240
6	-5.701	1.180	11	-6.701	GGCGCCGATCAAGTCCTACCAG	GTG	19480	210
7	-2.812	2.596	13	-3.883	GTCCTACCAGGTGCCCACCGAC	GTG	19492	198
8	-5.369	1.343	10	-6.327	GGTGCCCACCGACGTGTCGGGC	ATG	19501	189
9	-3.453	2.282	14	-4.550	CGCCGAGAGGGCCCGACGCCAG	GTG	19573	117

GeneMark:



Gene: Coriander_20 Start: 19210, Stop: 19689, Start Num: 5
Candidate Starts for Coriander_20:
(Start: 5 @19210 has 7 MA's), (6, 19276), (13, 19351), (16, 19372), (21, 19450), (22, 19480), (23, 19492), (24, 19501), (28, 19573),

Basic Phage Information	
Phage Name	Coriander_20
Gene #	Gene 20(PECAAN) Gene 20 (Phamerator)
Stop Coordinate	Stop 19,199
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	No Overlap
Selected Start Coordinate	19210 (PECAAN) 19210 (Phamerator)
Selected Function	Function Unknown

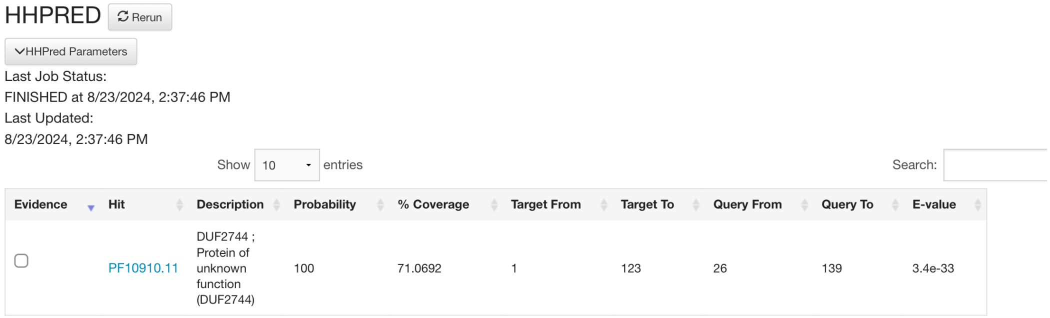


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:35:33 AM
Last Updated:
8/23/2024, 10:35:33 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	20	function unknown	159	325	3e-89	DB	86944
☐	Doggs	19	function unknown	159	323	1e-88	DB	86944
☐	DirtyBoi	21	function unknown	159	299	2e-81	DB	86944
☐	Hedwig	21	function unknown	159	299	2e-81	DB	86944
☐	Dmitri	21	function unknown	159	296	1e-80	DB	86944
☐	RayTheFireFly	20	function unknown	159	294	7e-80	DB	86944

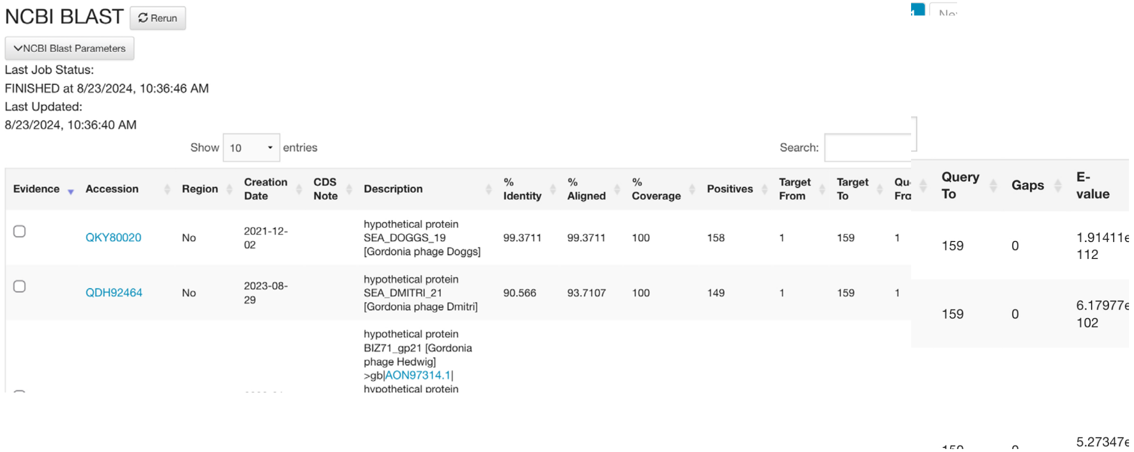


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 2:37:46 PM
Last Updated:
8/23/2024, 2:37:46 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF10910.11	DUF2744 ; Protein of unknown function (DUF2744)	100	71.0692	1	123	26	139	3.4e-33



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:46 AM
Last Updated:
8/23/2024, 10:36:40 AM

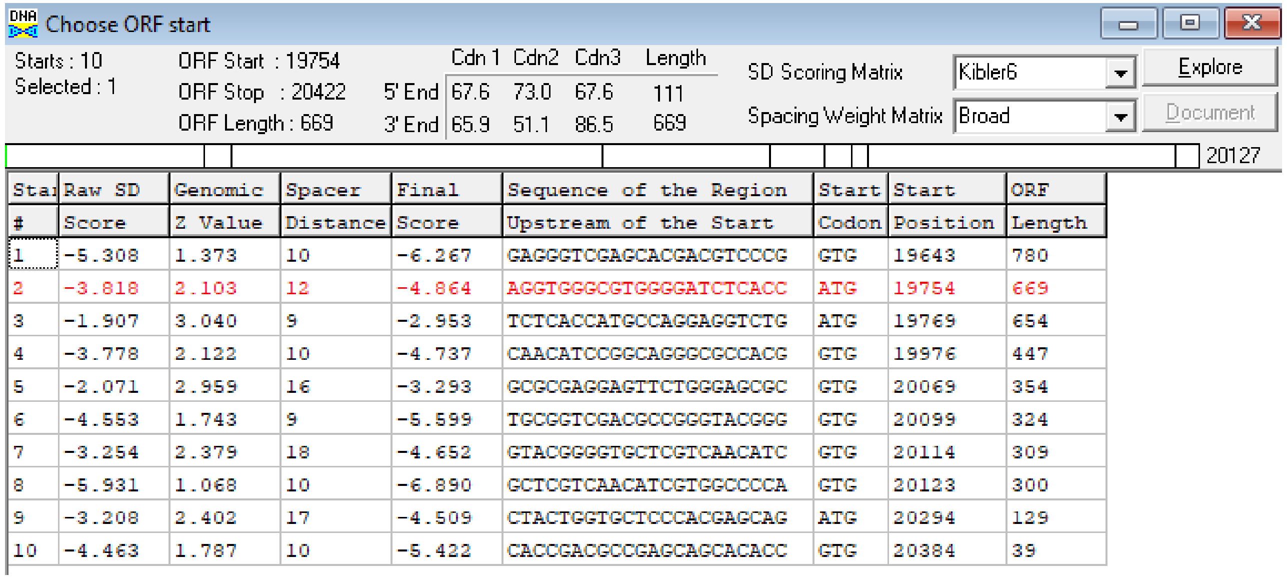
Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Qu Fro	Query To	Gaps	E-value
☐	QKY80020	No	2021-12-02		hypothetical protein SEA_DOGGS_19 [Gordonia phage Doggs]	99.3711	99.3711	100	158	1	159	1	159	0	1.91411e 112
☐	QDH92464	No	2023-08-29		hypothetical protein SEA_DMITRI_21 [Gordonia phage Dmitri]	90.566	93.7107	100	149	1	159	1	159	0	6.17977e 102
					hypothetical protein BIZ71_gp21 [Gordonia phage Hedwig] >gb|AON97314.1| hypothetical protein										5.27347e

Coriander_Draft

Phamerator- Gene 21_Start site 19769

PECAAN- Gene 21_Start site 19769



Starts : 10
Selected : 1

ORF Start : 19754
ORF Stop : 20422
ORF Length : 669

	Cdn 1	Cdn2	Cdn3	Length
5' End	67.6	73.0	67.6	111
3' End	65.9	51.1	86.5	669

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Broad

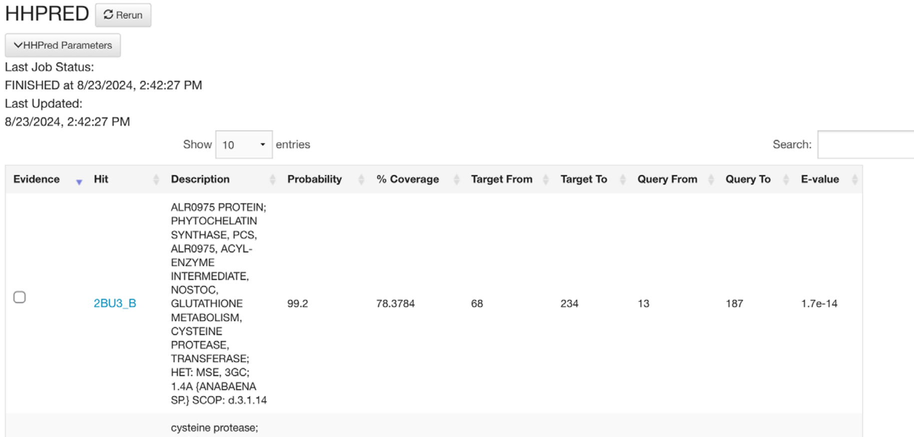
Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.308	1.373	10	-6.267	GAGGGTCGAGCACGACGTCCCG	GTG	19643	780
2	-3.818	2.103	12	-4.864	AGGTGGGCGTGGGGATCTCACC	ATG	19754	669
3	-1.907	3.040	9	-2.953	TCTCACCATGCCAGGAGGTCTG	ATG	19769	654
4	-3.778	2.122	10	-4.737	CAACATCCGGCAGGGCGCCACG	GTG	19976	447
5	-2.071	2.959	16	-3.293	GCGCGAGGAGTTCTGGGAGCGC	GTG	20069	354
6	-4.553	1.743	9	-5.599	TGCGGTCGACGCCGGGTACGGG	GTG	20099	324
7	-3.254	2.379	18	-4.652	GTACGGGGTGCTCGTCAACATC	GTG	20114	309
8	-5.931	1.068	10	-6.890	GCTCGTCAACATCGTGGCCCCA	GTG	20123	300
9	-3.208	2.402	17	-4.509	CTACTGGTGCTCCCACGAGCAG	ATG	20294	129
10	-4.463	1.787	10	-5.422	CACCGACGCCGAGCAGCACACC	GTG	20384	39

GeneMark:

Gene: Coriander_21 Start: 19754, Stop: 20422, Start Num: 42
Candidate Starts for Coriander_21:

(27, 19643), (Start: 42 @19754 has 1 MA's), (Start: 54 @19769 has 33 MA's), (82, 19976), (95, 20069), (99, 20099), (102, 20114), (104, 20123), (131, 20294), (153, 20384),

Basic Phage Information	
Phage Name	**Coriander_21**
Gene #	**Gene 21 (PECAAN) Gene 21 (Phamerator)**
Stop Coordinate	**20422**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**No Overlap**
Selected Start Coordinate	**19754**
Selected Function	lysin A protease C39 domain

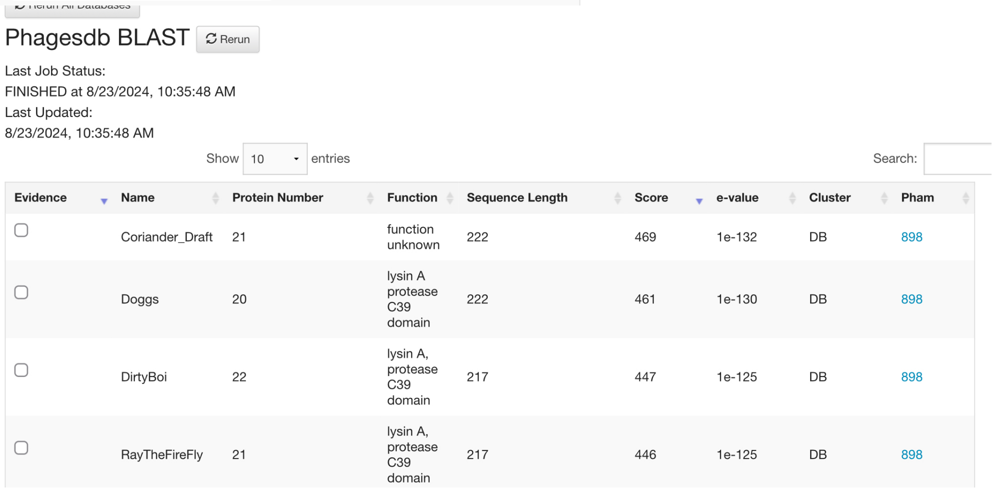


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 2:42:27 PM
Last Updated:
8/23/2024, 2:42:27 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	2BU3_B	ALR0975 PROTEIN; PHYTOCHELATIN SYNTHASE, PCS, ALR0975, ACYL-ENZYME INTERMEDIATE, NOSTOC, GLUTATHIONE METABOLISM, CYSTEINE PROTEASE, TRANSFERASE; HET: MSE, 3GC; 1.4A {ANABAENA SP.} SCOP: d.3.1.14	99.2	78.3784	68	234	13	187	1.7e-14
		cysteine protease; cysteine protease							

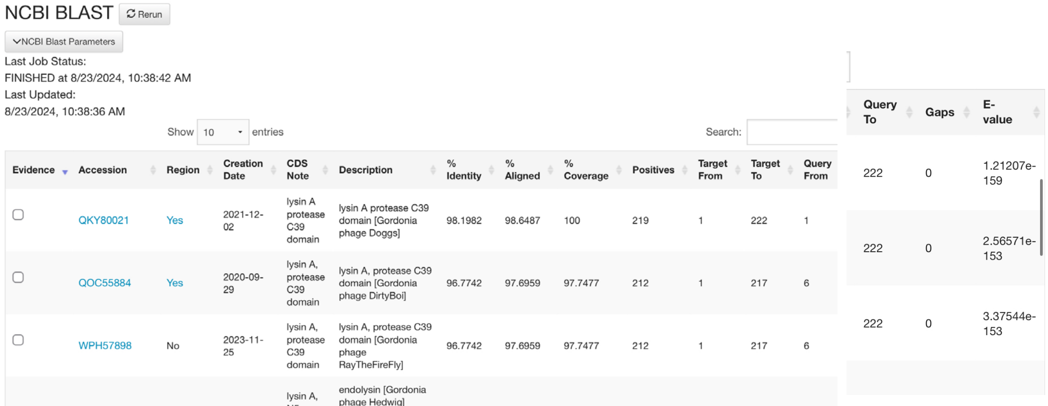


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:35:48 AM
Last Updated:
8/23/2024, 10:35:48 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	21	function unknown	222	469	1e-132	DB	898
☐	Doggs	20	lysin A protease C39 domain	222	461	1e-130	DB	898
☐	DirtyBoi	22	lysin A, protease C39 domain	217	447	1e-125	DB	898
☐	RayTheFireFly	21	lysin A, protease C39 domain	217	446	1e-125	DB	898



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:42 AM
Last Updated:
8/23/2024, 10:38:36 AM

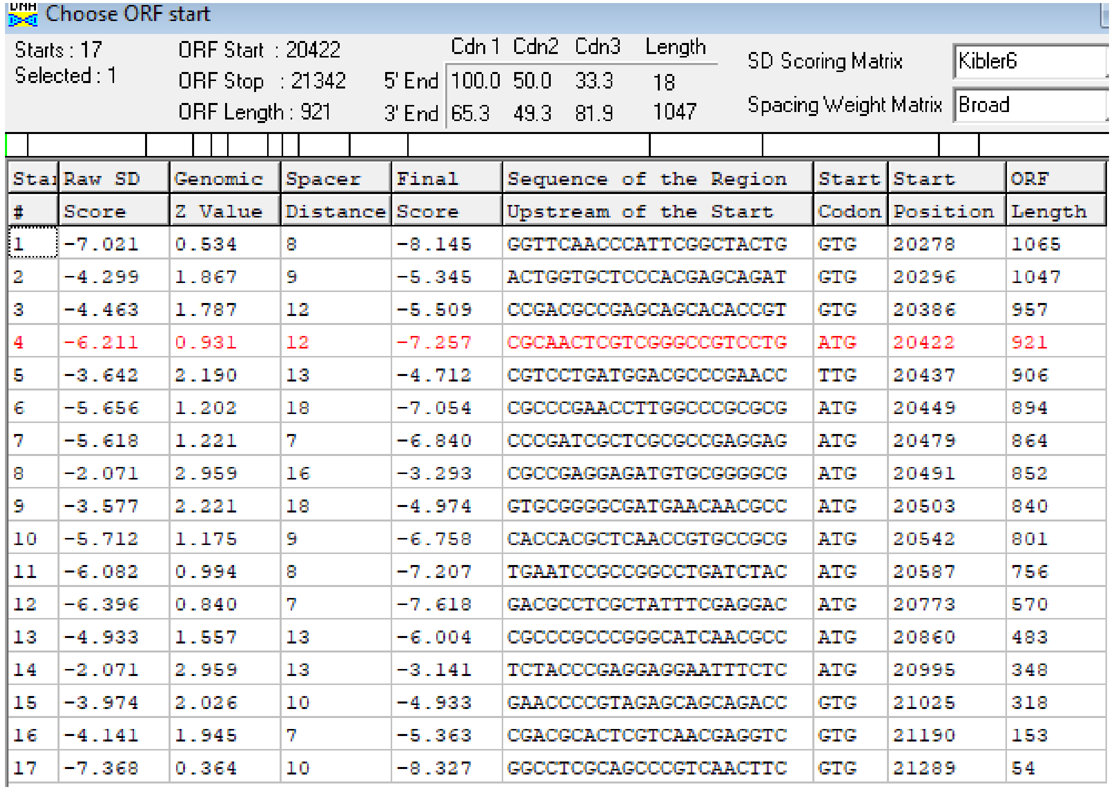
Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80021	Yes	2021-12-02	lysin A protease C39 domain	lysin A protease C39 domain [Gordonia phage Doggs]	98.1982	98.6487	100	219	1	222	1	222	0	1.21207e-159
☐	QOC55884	Yes	2020-09-29	lysin A, protease C39 domain	lysin A, protease C39 domain [Gordonia phage DirtyBoi]	96.7742	97.6959	97.7477	212	1	217	6	222	0	2.56571e-153
☐	WPH57898	No	2023-11-25	lysin A, protease C39 domain	lysin A, protease C39 domain [Gordonia phage RayTheFireFly]	96.7742	97.6959	97.7477	212	1	217	6	222	0	3.37544e-153
				lysin A,	endolysin [Gordonia phage Hedwig]										

Coriander_Draft

Phamerator- Gene 22_Start site 20422

PECAAN- Gene 22_Start site 20422



Starts : 17
Selected : 1

ORF Start : 20422
ORF Stop : 21342
ORF Length : 921

	Cdn 1	Cdn2	Cdn3	Length
5' End	100.0	50.0	33.3	18
3' End	65.3	49.3	81.9	1047

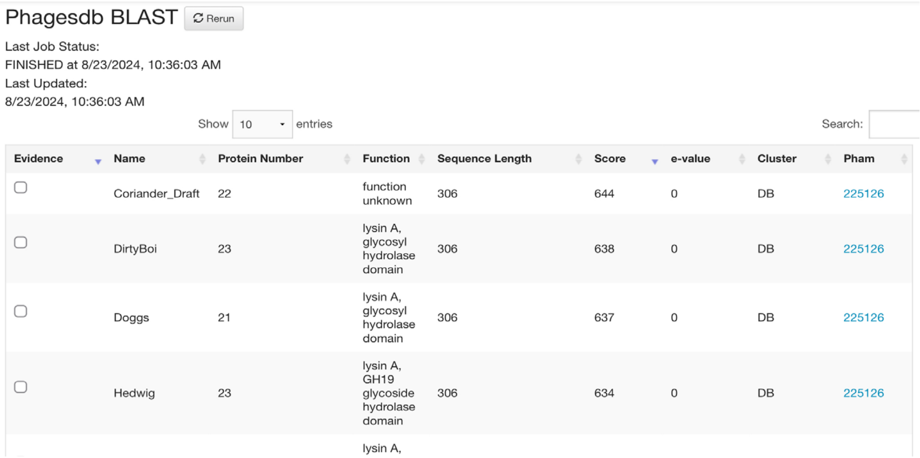
SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-7.021	0.534	8	-8.145	GGTTCAACCCATTCGGCTACTG	GTG	20278	1065
2	-4.299	1.867	9	-5.345	ACTGGTGCTCCCACGAGCAGAT	GTG	20296	1047
3	-4.463	1.787	12	-5.509	CCGACGCCGAGCAGCACACCGT	GTG	20386	957
4	-6.211	0.931	12	-7.257	CGCAACTCGTCGGGCCGTCCTG	ATG	20422	921
5	-3.642	2.190	13	-4.712	CGTCCTGATGGACGCCCGAACC	TTG	20437	906
6	-5.656	1.202	18	-7.054	CGCCCGAACCTTGGCCCGCGCG	ATG	20449	894
7	-5.618	1.221	7	-6.840	CCCGATCGCTCGCGCCGAGGAG	ATG	20479	864
8	-2.071	2.959	16	-3.293	CGCCGAGGAGATGTGCGGGGCG	ATG	20491	852
9	-3.577	2.221	18	-4.974	GTGCGGGGCGATGAACAACGCC	ATG	20503	840
10	-5.712	1.175	9	-6.758	CACCACGCTCAACCGTGCCGCG	ATG	20542	801
11	-6.082	0.994	8	-7.207	TGAATCCGCCGGCCTGATCTAC	ATG	20587	756
12	-6.396	0.840	7	-7.618	GACGCCTCGCTATTTCGAGGAC	ATG	20773	570
13	-4.933	1.557	13	-6.004	CGCCCGCCCGGGCATCAACGCC	ATG	20860	483
14	-2.071	2.959	13	-3.141	TCTACCCGAGGAGGAATTTCTC	ATG	20995	348
15	-3.974	2.026	10	-4.933	GAACCCCGTAGAGCAGCAGACC	GTG	21025	318
16	-4.141	1.945	7	-5.363	CGACGCACTCGTCAACGAGGTC	GTG	21190	153
17	-7.368	0.364	10	-8.327	GGCCTCGCAGCCCGTCAACTTC	GTG	21289	54

GeneMark:

Gene: Coriander_22 Start: 20422, Stop: 21342, Start Num: 4
Candidate Starts for Coriander_22:
(1, 20278), (2, 20296), (3, 20386), (Start: 4 @20422 has 6 MA's), (5, 20437), (6, 20449), (8, 20479), (9, 20491), (10, 20503), (12, 20542), (14, 20587), (16, 20773), (19, 20860), (21, 20995), (23, 21025), (27, 21190), (30, 21289),

Basic Phage Information	
Phage Name	Coriander_22
Gene #	**Gene 22(PECAAN) Gene 22 (Phamerator)**
Stop Coordinate	**21342**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	No Overlap
Selected Start Coordinate	**20422**
Selected Function	lysin A, glycosyl hydrolase domain

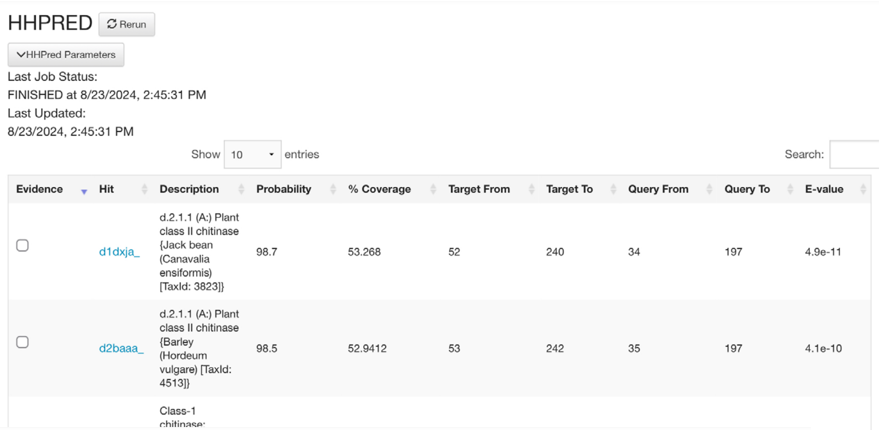


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:03 AM
Last Updated:
8/23/2024, 10:36:03 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	22	function unknown	306	644	0	DB	225126
☐	DirtyBoi	23	lysin A, glycosyl hydrolase domain	306	638	0	DB	225126
☐	Doggs	21	lysin A, glycosyl hydrolase domain	306	637	0	DB	225126
☐	Hedwig	23	lysin A, GH19 glycoside hydrolase domain	306	634	0	DB	225126
			lysin A,					

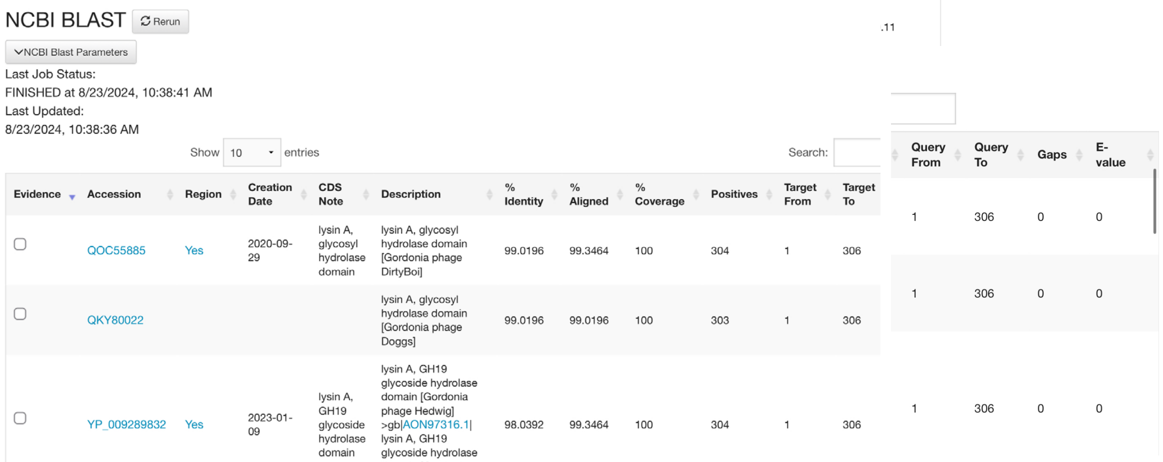


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 2:45:31 PM
Last Updated:
8/23/2024, 2:45:31 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1dxja_	d.2.1.1 (A:) Plant class II chitinase {Jack bean (Canavalia ensiformis) [TaxId: 3823]}	98.7	53.268	52	240	34	197	4.9e-11
☐	d2baaa_	d.2.1.1 (A:) Plant class II chitinase {Barley (Hordeum vulgare) [TaxId: 4513]}	98.5	52.9412	53	242	35	197	4.1e-10
		Class-1 chitinase:							.11



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:41 AM
Last Updated:
8/23/2024, 10:38:36 AM

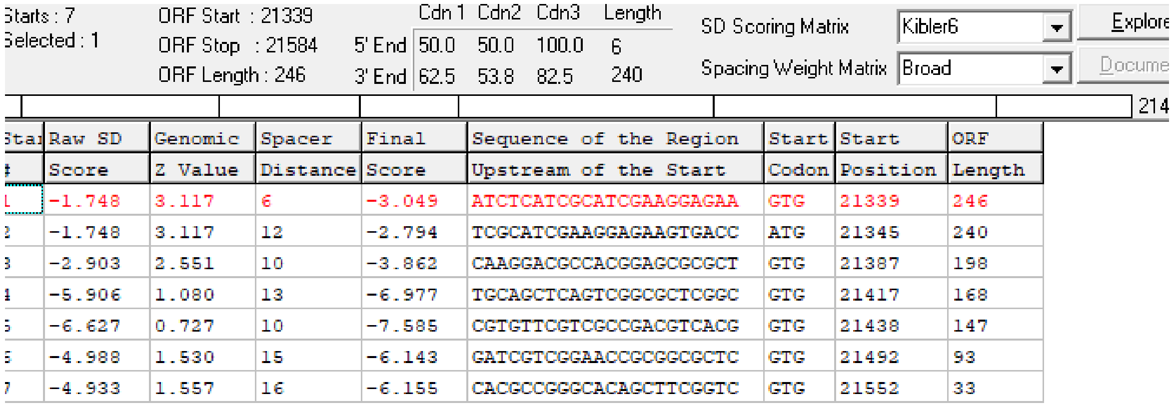
Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QOC55885	Yes	2020-09-29	lysin A, glycosyl hydrolase domain	lysin A, glycosyl hydrolase domain [Gordonia phage DirtyBoi]	99.0196	99.3464	100	304	1	306	1	306	0	0
☐	QKY80022				lysin A, glycosyl hydrolase domain [Gordonia phage Doggs]	99.0196	99.0196	100	303	1	306	1	306	0	0
☐	YP_009289832	Yes	2023-01-09	lysin A, GH19 glycoside hydrolase domain	lysin A, GH19 glycoside hydrolase domain [Gordonia phage Hedwig] >gb|AON97316.1| lysin A, GH19 glycoside hydrolase	98.0392	99.3464	100	304	1	306	1	306	0	0

Coriander_Draft

Phamerator: Gene 23_Start site 21345

PECAAN: Gene 23_Start site 21345



Starts : 7
Selected : 1

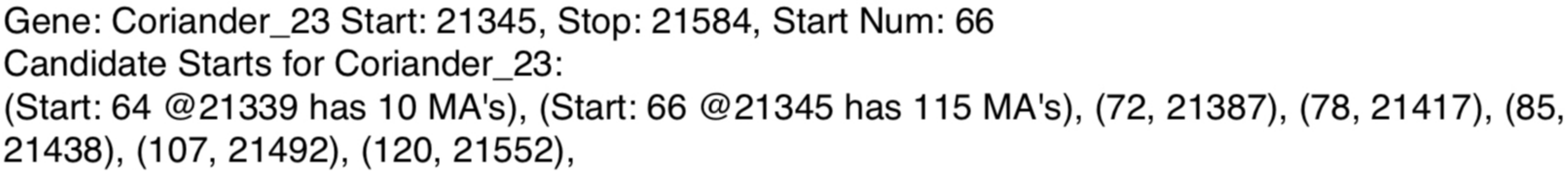
ORF Start : 21339
ORF Stop : 21584
ORF Length : 246

	Cdn 1	Cdn2	Cdn3	Length
5' End	50.0	50.0	100.0	6
3' End	62.5	53.8	82.5	240

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Broad

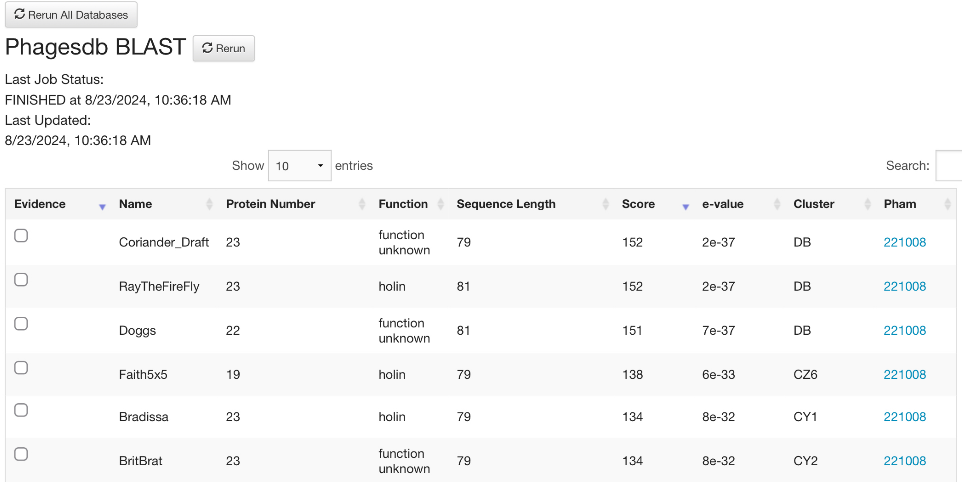
Star #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-1.748	3.117	6	-3.049	ATCTCATCGCATCGAAGGAGAA	GTG	21339	246
2	-1.748	3.117	12	-2.794	TCGCATCGAAGGAGAAGTGACC	ATG	21345	240
3	-2.903	2.551	10	-3.862	CAAGGACGCCACGGAGCGCGCT	GTG	21387	198
4	-5.906	1.080	13	-6.977	TGCAGCTCAGTCGGCGCTCGGC	GTG	21417	168
5	-6.627	0.727	10	-7.585	CGTGTTCGTCGCCGACGTCACG	GTG	21438	147
6	-4.988	1.530	15	-6.143	GATCGTCGGAACCGCGGCGCTC	GTG	21492	93
7	-4.933	1.557	16	-6.155	CACGCCGGGCACAGCTTCGGTC	GTG	21552	33

Gene Mark:



Gene: Coriander_23 Start: 21345, Stop: 21584, Start Num: 66
Candidate Starts for Coriander_23:
(Start: 64 @21339 has 10 MA's), (Start: 66 @21345 has 115 MA's), (72, 21387), (78, 21417), (85, 21438), (107, 21492), (120, 21552),

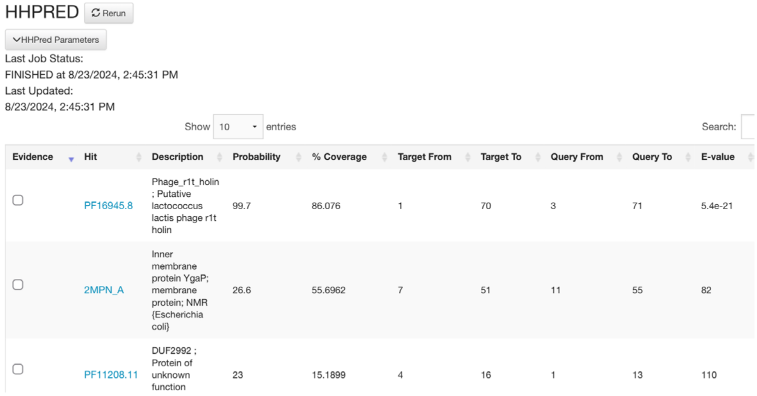
Basic Phage Information	
Phage Name	**Coriander_23**
Gene #	**Gene 23 (PECAAN) Gene 23 (Phamerator)**
Stop Coordinate	**21584**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**No Overlap**
Selected Start Coordinate	**21345**
Selected Function	Holin



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:18 AM
Last Updated:
8/23/2024, 10:36:18 AM

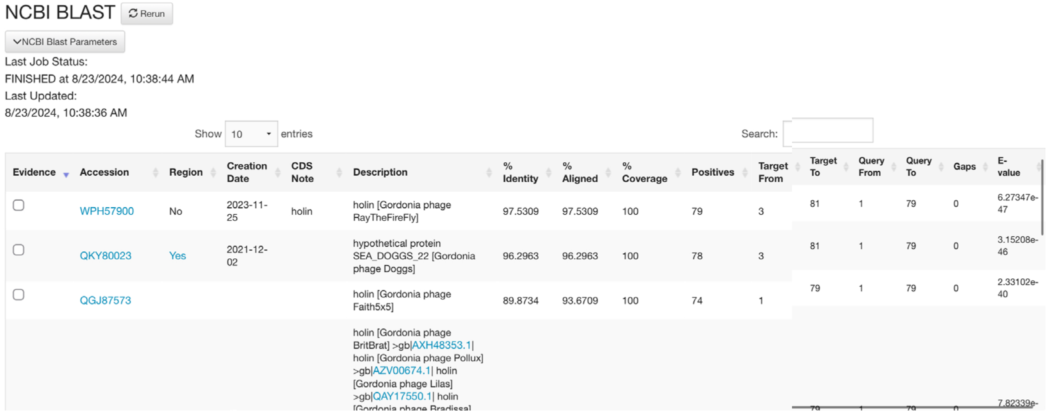
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	23	function unknown	79	152	2e-37	DB	221008
☐	RayTheFireFly	23	holin	81	152	2e-37	DB	221008
☐	Doggs	22	function unknown	81	151	7e-37	DB	221008
☐	Faith5x5	19	holin	79	138	6e-33	CZ6	221008
☐	Bradissa	23	holin	79	134	8e-32	CY1	221008
☐	BritBrat	23	function unknown	79	134	8e-32	CY2	221008



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 2:45:31 PM
Last Updated:
8/23/2024, 2:45:31 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF16945.8	Phage_r1t_holin ; Putative lactococcus lactis phage r1t holin	99.7	86.076	1	70	3	71	5.4e-21
☐	2MPN_A	Inner membrane protein YgaP; membrane protein; NMR {Escherichia coli}	26.6	55.6962	7	51	11	55	82
☐	PF11208.11	DUF2992 ; Protein of unknown function	23	15.1899	4	16	1	13	110



NCBI BLAST

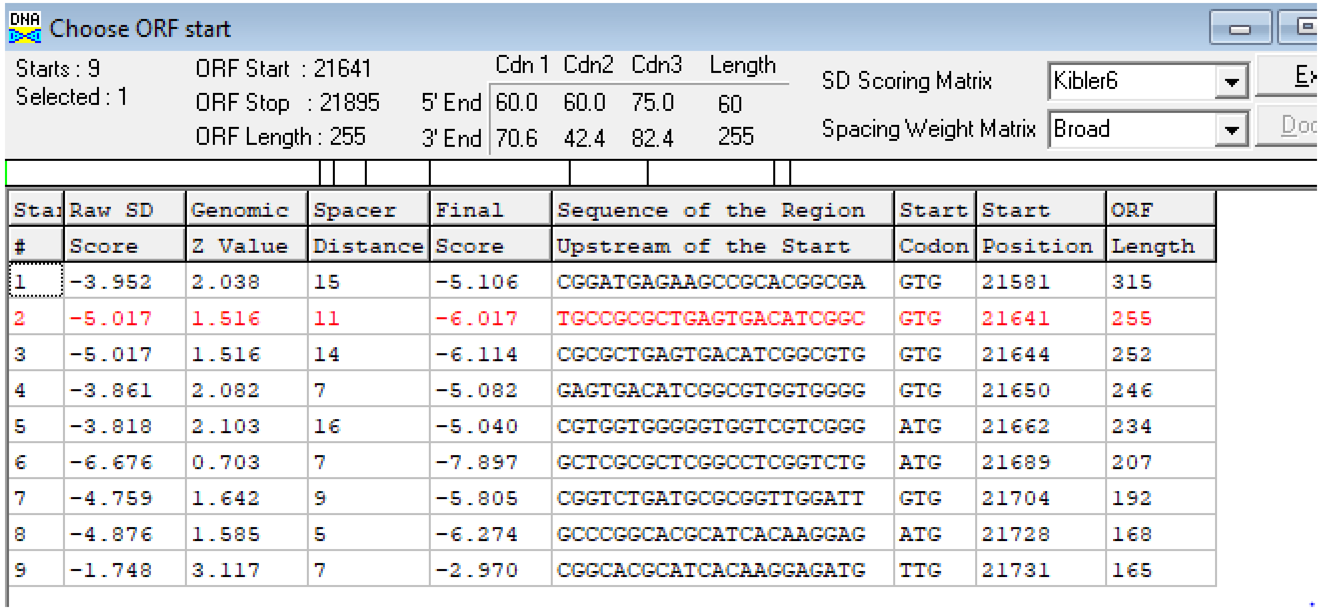
Last Job Status:
FINISHED at 8/23/2024, 10:38:44 AM
Last Updated:
8/23/2024, 10:38:36 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	WPH57900	No	2023-11-25	holin	holin [Gordonia phage RayTheFireFly]	97.5309	97.5309	100	79	3	81	1	79	0	6.27347e-47
☐	QKY80023	Yes	2021-12-02		hypothetical protein SEA_DOGGS_22 [Gordonia phage Doggs]	96.2963	96.2963	100	78	3	81	1	79	0	3.15208e-46
☐	QGJ87573				holin [Gordonia phage Faith5x5]	89.8734	93.6709	100	74	1	79	1	79	0	2.33102e-40
					holin [Gordonia phage BritBrat] >gb|AXH48353.1| holin [Gordonia phage Pollux] >gb|AZV00674.1| holin [Gordonia phage Lilas] >gb|QAY17550.1| holin [Gordonia phage Bradissa]						79	1	79	0	7.82339e-

Coriander_Draft

Phamerator: Gene 24_Start site 21581

PECAAN: Gene 24_Start site 21581



Starts : 9
Selected : 1

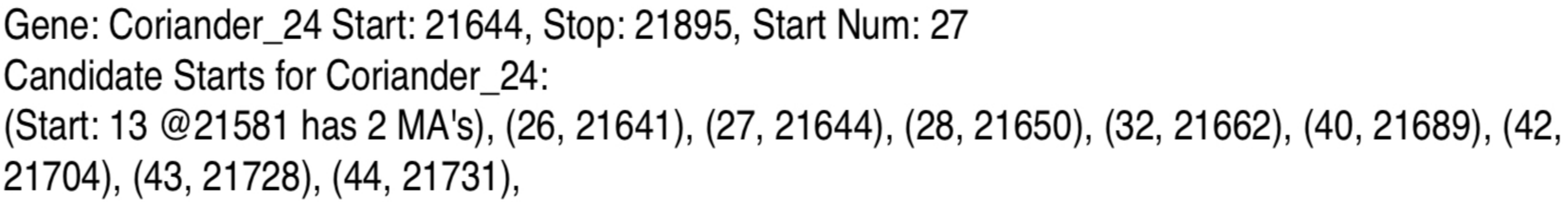
ORF Start : 21641
ORF Stop : 21895
ORF Length : 255

	Cdn 1	Cdn2	Cdn3	Length
5' End	60.0	60.0	75.0	60
3' End	70.6	42.4	82.4	255

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Broad

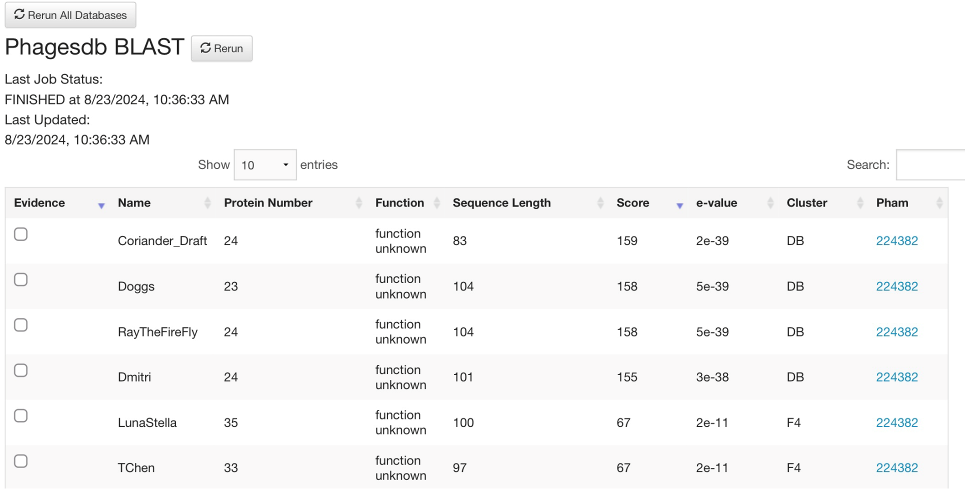
Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-3.952	2.038	15	-5.106	CGGATGAGAAGCCGCACGGCGA	GTG	21581	315
2	-5.017	1.516	11	-6.017	TGCCGCGCTGAGTGACATCGGC	GTG	21641	255
3	-5.017	1.516	14	-6.114	CGCGCTGAGTGACATCGGCGTG	GTG	21644	252
4	-3.861	2.082	7	-5.082	GAGTGACATCGGCGTGGTGGGG	GTG	21650	246
5	-3.818	2.103	16	-5.040	CGTGGTGGGGGTGGTCGTCGGG	ATG	21662	234
6	-6.676	0.703	7	-7.897	GCTCGCGCTCGGCCTCGGTCTG	ATG	21689	207
7	-4.759	1.642	9	-5.805	CGGTCTGATGCGCGGTTGGATT	GTG	21704	192
8	-4.876	1.585	5	-6.274	GCCCGGCACGCATCACAAGGAG	ATG	21728	168
9	-1.748	3.117	7	-2.970	CGGCACGCATCACAAGGAGATG	TTG	21731	165

Gene Mark:



Gene: Coriander_24 Start: 21644, Stop: 21895, Start Num: 27
Candidate Starts for Coriander_24:
(Start: 13 @21581 has 2 MA's), (26, 21641), (27, 21644), (28, 21650), (32, 21662), (40, 21689), (42, 21704), (43, 21728), (44, 21731),

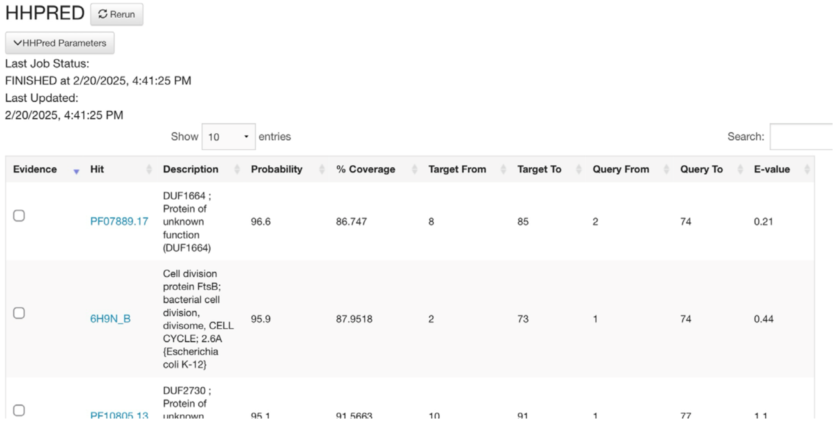
Basic Phage Information	
Phage Name	Coriander_24
Gene #	Gene 24 (PECAAN) Gene 24 (Phamerator)
Stop Coordinate	21895
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	No Overlap
Selected Start Coordinate	21581
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:33 AM
Last Updated:
8/23/2024, 10:36:33 AM

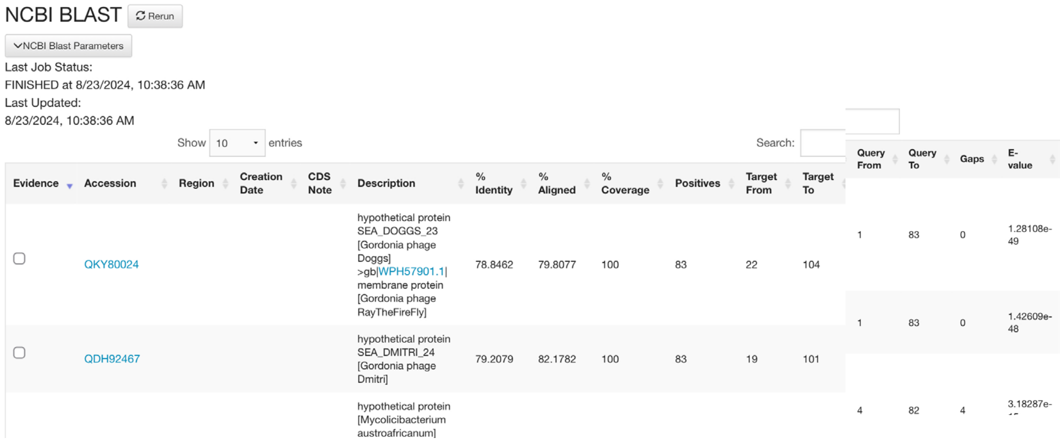
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	24	function unknown	83	159	2e-39	DB	224382
☐	Doggs	23	function unknown	104	158	5e-39	DB	224382
☐	RayTheFireFly	24	function unknown	104	158	5e-39	DB	224382
☐	Dmitri	24	function unknown	101	155	3e-38	DB	224382
☐	LunaStella	35	function unknown	100	67	2e-11	F4	224382
☐	TChen	33	function unknown	97	67	2e-11	F4	224382



HHPRED

Last Job Status:
FINISHED at 2/20/2025, 4:41:25 PM
Last Updated:
2/20/2025, 4:41:25 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF07889.17	DUF1664 ; Protein of unknown function (DUF1664)	96.6	86.747	8	85	2	74	0.21
☐	6H9N_B	Cell division protein FtsB; bacterial cell division, divisome, CELL CYCLE; 2.6A {Escherichia coli K-12}	95.9	87.9518	2	73	1	74	0.44
☐	PF10805.13	DUF2730 ; Protein of unknown	95.1	91.5663	10	91	1	77	1.1



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:36 AM
Last Updated:
8/23/2024, 10:38:36 AM

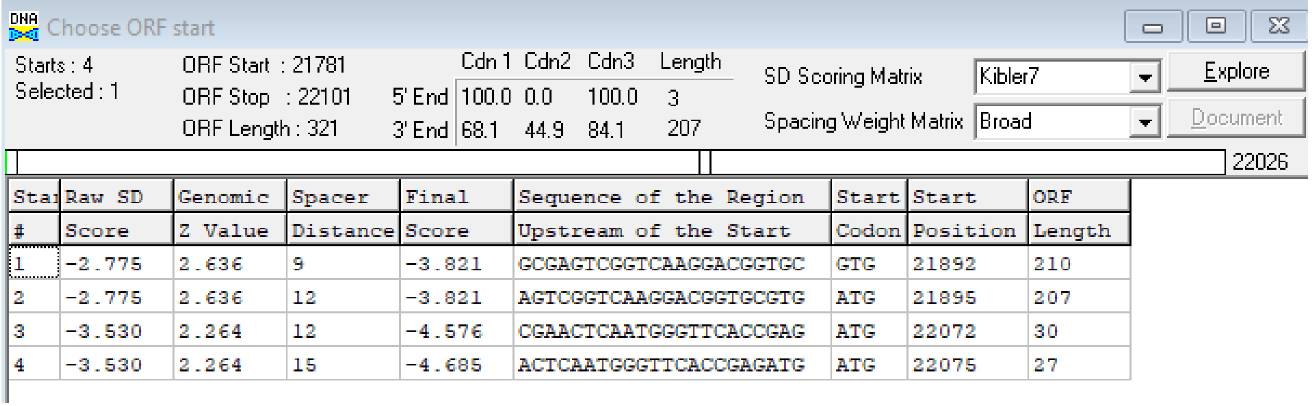
Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80024				hypothetical protein SEA_DOGGS_23 [Gordonia phage Doggs] >gb|WPH57901.1| membrane protein [Gordonia phage RayTheFireFly]	78.8462	79.8077	100	83	22	104	1	83	0	1.28108e-49
☐	QDH92467				hypothetical protein SEA_DMITRI_24 [Gordonia phage Dmitri]	79.2079	82.1782	100	83	19	101	1	83	0	1.42609e-48
					hypothetical protein [Mycolicibacterium austroafricanum]							4	82	4	3.18287e-

25 - 30

Coriander_Draft

Phamerator- Gene 25_Start site 21895

PECAAN- Gene 25_Start site 21895



Starts : 4
Selected : 1

ORF Start : 21781
ORF Stop : 22101
ORF Length : 321

	Cdn 1	Cdn2	Cdn3	Length
5' End	100.0	0.0	100.0	3
3' End	68.1	44.9	84.1	207

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

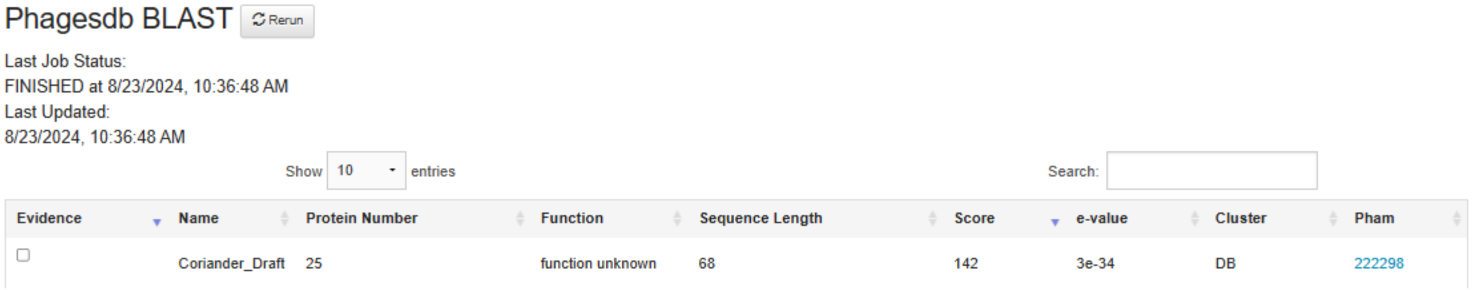
22026

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-2.775	2.636	9	-3.821	GCGAGTCGGTCAAGGACGGTGC	GTG	21892	210
2	-2.775	2.636	12	-3.821	AGTCGGTCAAGGACGGTGCGTG	ATG	21895	207
3	-3.530	2.264	12	-4.576	CGAACTCAATGGGTTCACCGAG	ATG	22072	30
4	-3.530	2.264	15	-4.685	ACTCAATGGGTTCACCGAGATG	ATG	22075	27

GeneMark

Gene: Coriander_25 Start: 21895, Stop: 22101, Start Num: 2 Candidate Starts for Coriander_25: (1, 21892), (Start: 2 @21895 has 3 MA's), (3, 22072), (4, 22075),

Basic Phage Information	
Phage Name	**Coriander_25**
Gene #	**Gene 25(PECAAN) Gene 25 (Phamerator)**
Stop Coordinate	**22101**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**Overlap with Coriander_ 26 at 22086**
Selected Start Coordinate	**21895**
Selected Function	

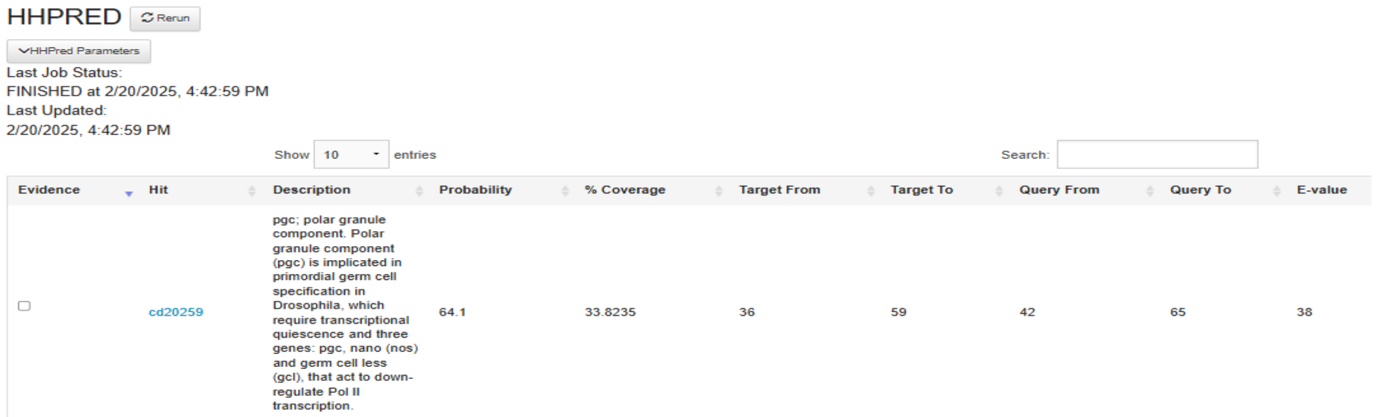


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:36:48 AM
Last Updated:
8/23/2024, 10:36:48 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	25	function unknown	68	142	3e-34	DB	222298

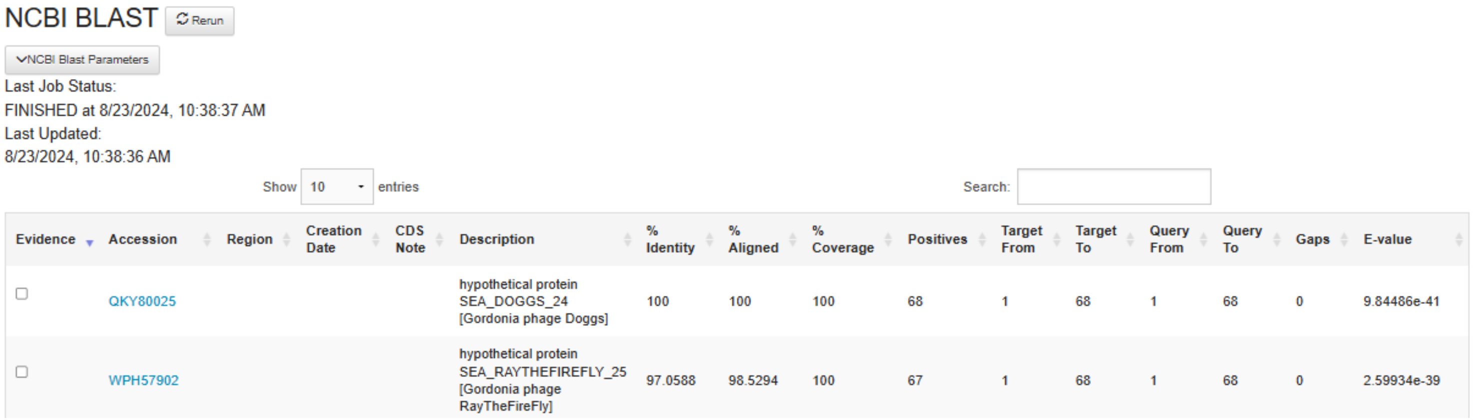


HHPRED

Last Job Status:
FINISHED at 2/20/2025, 4:42:59 PM
Last Updated:
2/20/2025, 4:42:59 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	cd20259	pgc; polar granule component. Polar granule component (pgc) is implicated in primordial germ cell specification in Drosophila, which require transcriptional quiescence and three genes: pgc, nano (nos) and germ cell less (gcl), that act to down-regulate Pol II transcription.	64.1	33.8235	36	59	42	65	38



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:37 AM
Last Updated:
8/23/2024, 10:38:36 AM

Show 10 entries Search:

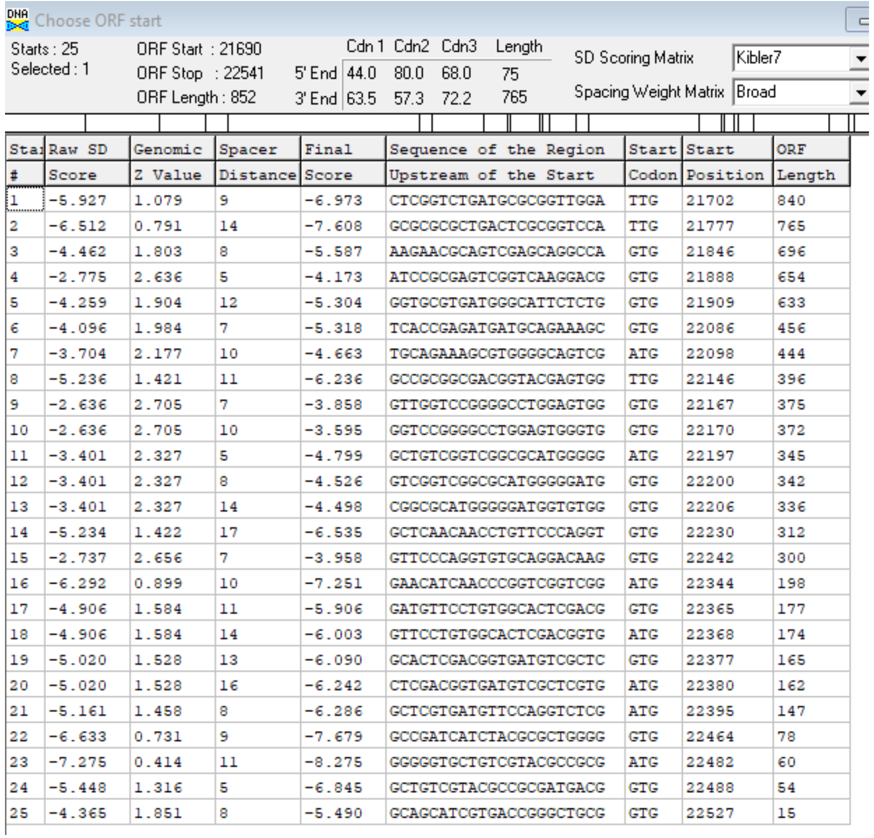
Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80025				hypothetical protein SEA_DOGGS_24 [Gordonia phage Doggs]	100	100	100	68	1	68	1	68	0	9.84486e-41
☐	WPH57902				hypothetical protein SEA_RAYTHEFIREFLY_25 [Gordonia phage RayTheFireFly]	97.0588	98.5294	100	67	1	68	1	68	0	2.59934e-39

Coriander_Draft

Phamerator- Gene 26_Start site 22086

PECAAN- Gene 26_Start site 22086

GeneMark



Starts : 25
Selected : 1

ORF Start : 21690
ORF Stop : 22541
ORF Length : 852

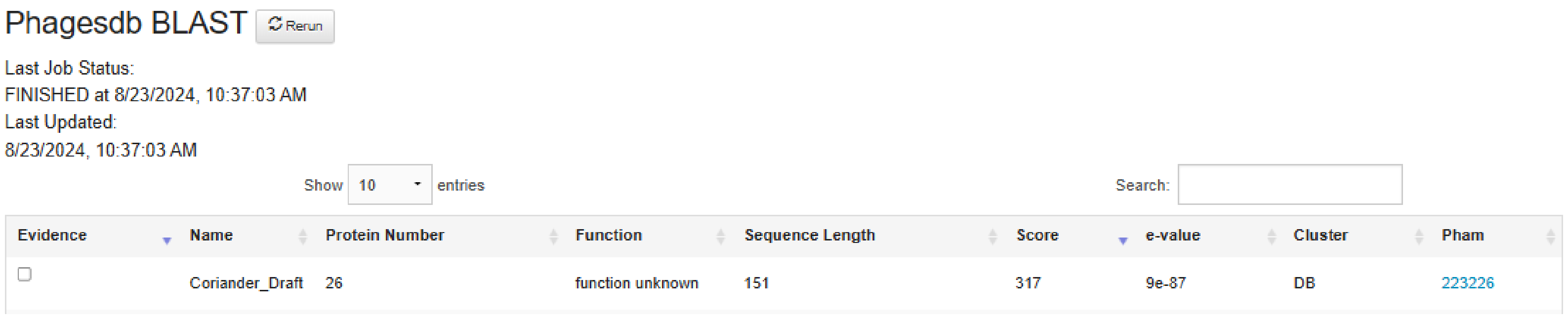
	Cdn 1	Cdn2	Cdn3	Length
5' End	44.0	80.0	68.0	75
3' End	63.5	57.3	72.2	765

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta#	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.927	1.079	9	-6.973	CTCGGTCTGATGCGCGGTTGGA	TTG	21702	840
2	-6.512	0.791	14	-7.608	GCGCGCGCTGACTCGCGGTCCA	TTG	21777	765
3	-4.462	1.803	8	-5.587	AAGAACGCAGTCGAGCAGGCCA	GTG	21846	696
4	-2.775	2.636	5	-4.173	ATCCGCGAGTCGGTCAAGGACG	GTG	21888	654
5	-4.259	1.904	12	-5.304	GGTGCGTGATGGGCATTCTCTG	GTG	21909	633
6	-4.096	1.984	7	-5.318	TCACCGAGATGATGCAGAAAGC	GTG	22086	456
7	-3.704	2.177	10	-4.663	TGCAGAAAGCGTGGGGCAGTCG	ATG	22098	444
8	-5.236	1.421	11	-6.236	GCCGCGGCGACGGTACGAGTGG	TTG	22146	396
9	-2.636	2.705	7	-3.858	GTTGGTCCGGGGCCTGGAGTGG	GTG	22167	375
10	-2.636	2.705	10	-3.595	GGTCCGGGGCCTGGAGTGGGTG	GTG	22170	372
11	-3.401	2.327	5	-4.799	GCTGTCGGTCGGCGCATGGGGG	ATG	22197	345
12	-3.401	2.327	8	-4.526	GTCGGTCGGCGCATGGGGGATG	GTG	22200	342
13	-3.401	2.327	14	-4.498	CGGCGCATGGGGGATGGTGTGG	GTG	22206	336
14	-5.234	1.422	17	-6.535	GCTCAACAACCTGTTCCCAGGT	GTG	22230	312
15	-2.737	2.656	7	-3.958	GTTCCCAGGTGTGCAGGACAAG	GTG	22242	300
16	-6.292	0.899	10	-7.251	GAACATCAACCCGGTCGGTCGG	ATG	22344	198
17	-4.906	1.584	11	-5.906	GATGTTCCTGTGGCACTCGACG	GTG	22365	177
18	-4.906	1.584	14	-6.003	GTTCCTGTGGCACTCGACGGTG	ATG	22368	174
19	-5.020	1.528	13	-6.090	GCACTCGACGGTGATGTCGCTC	GTG	22377	165
20	-5.020	1.528	16	-6.242	CTCGACGGTGATGTCGCTCGTG	ATG	22380	162
21	-5.161	1.458	8	-6.286	GCTCGTGATGTTCCAGGTCTCG	ATG	22395	147
22	-6.633	0.731	9	-7.679	GCCGATCATCTACGCGCTGGGG	GTG	22464	78
23	-7.275	0.414	11	-8.275	GGGGGTGCTGTCGTACGCCGCG	ATG	22482	60
24	-5.448	1.316	5	-6.845	GCTGTCGTACGCCGCGATGACG	GTG	22488	54
25	-4.365	1.851	8	-5.490	GCAGCATCGTGACCGGGCTGCG	GTG	22527	15

Gene: Coriander_26 Start: 22086, Stop: 22541, Start Num: 8 Candidate Starts for Coriander_26: (1, 21702), (3, 21777), (4, 21846), (5, 21888), (6, 21909), (8, 22086), (Start: 9 @22098 has 24 MA's), (13, 22146), (15, 22167), (16, 22170), (20, 22197), (21, 22200), (22, 22206), (25, 22230), (27, 22242), (38, 22344), (41, 22365), (42, 22368), (43, 22377), (44, 22380), (46, 22395), (53, 22464), (57, 22482), (59, 22488), (62, 22527),

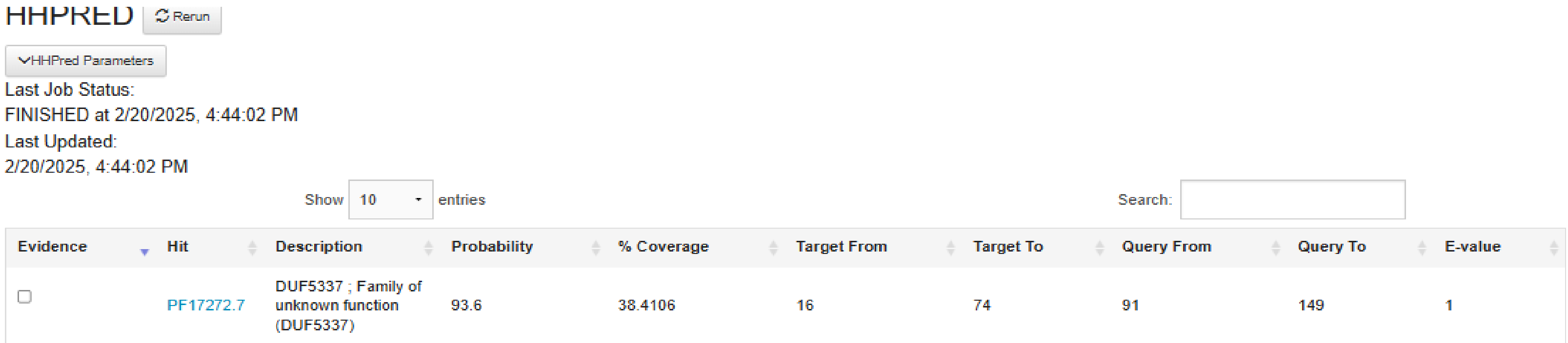
Basic Phage Information	
Phage Name	Coriander_26
Gene #	Gene 26(PECAAN) Gene 26 (Phamerator)
Stop Coordinate	22541
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	None
Selected Start Coordinate	22098
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:37:03 AM
Last Updated:
8/23/2024, 10:37:03 AM

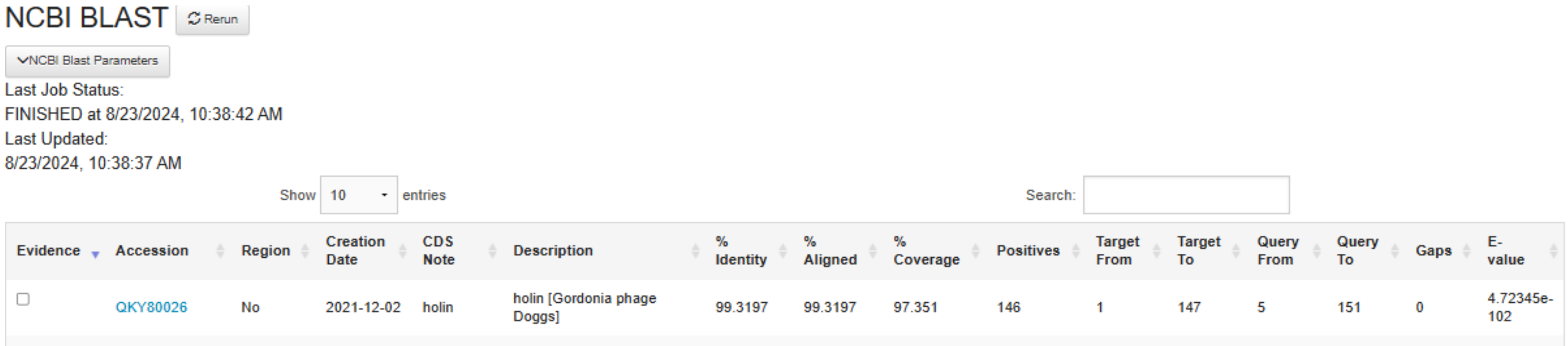
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	26	function unknown	151	317	9e-87	DB	223226



HHPRED

Last Job Status:
FINISHED at 2/20/2025, 4:44:02 PM
Last Updated:
2/20/2025, 4:44:02 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF17272.7	DUF5337 ; Family of unknown function (DUF5337)	93.6	38.4106	16	74	91	149	1



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:42 AM
Last Updated:
8/23/2024, 10:38:37 AM

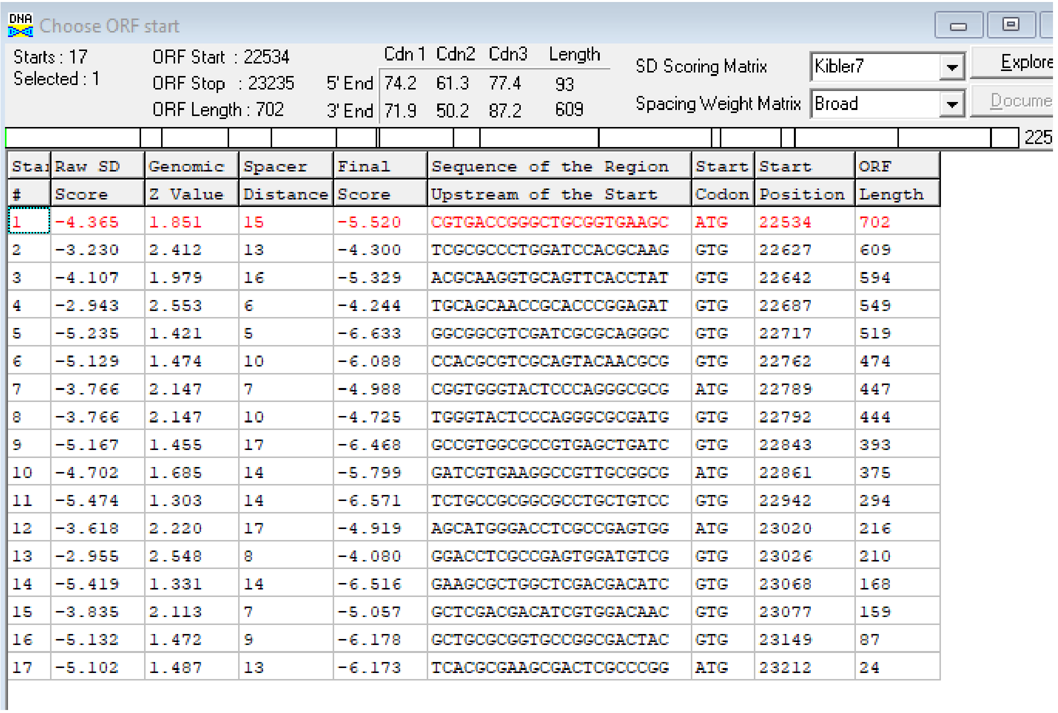
Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80026	No	2021-12-02	holin	holin [Gordonia phage Doggs]	99.3197	99.3197	97.351	146	1	147	5	151	0	4.72345e-102

Coriander_Draft

Phamerator- Gene 27_Start site 22642

Glimmer Start: Gene 27_Start site 22642

GeneMark Start: Gene 27_Start site 22534



Starts : 17
Selected : 1

ORF Start : 22534
ORF Stop : 23235
ORF Length : 702

	Cdn 1	Cdn2	Cdn3	Length
5' End	74.2	61.3	77.4	93
3' End	71.9	50.2	87.2	609

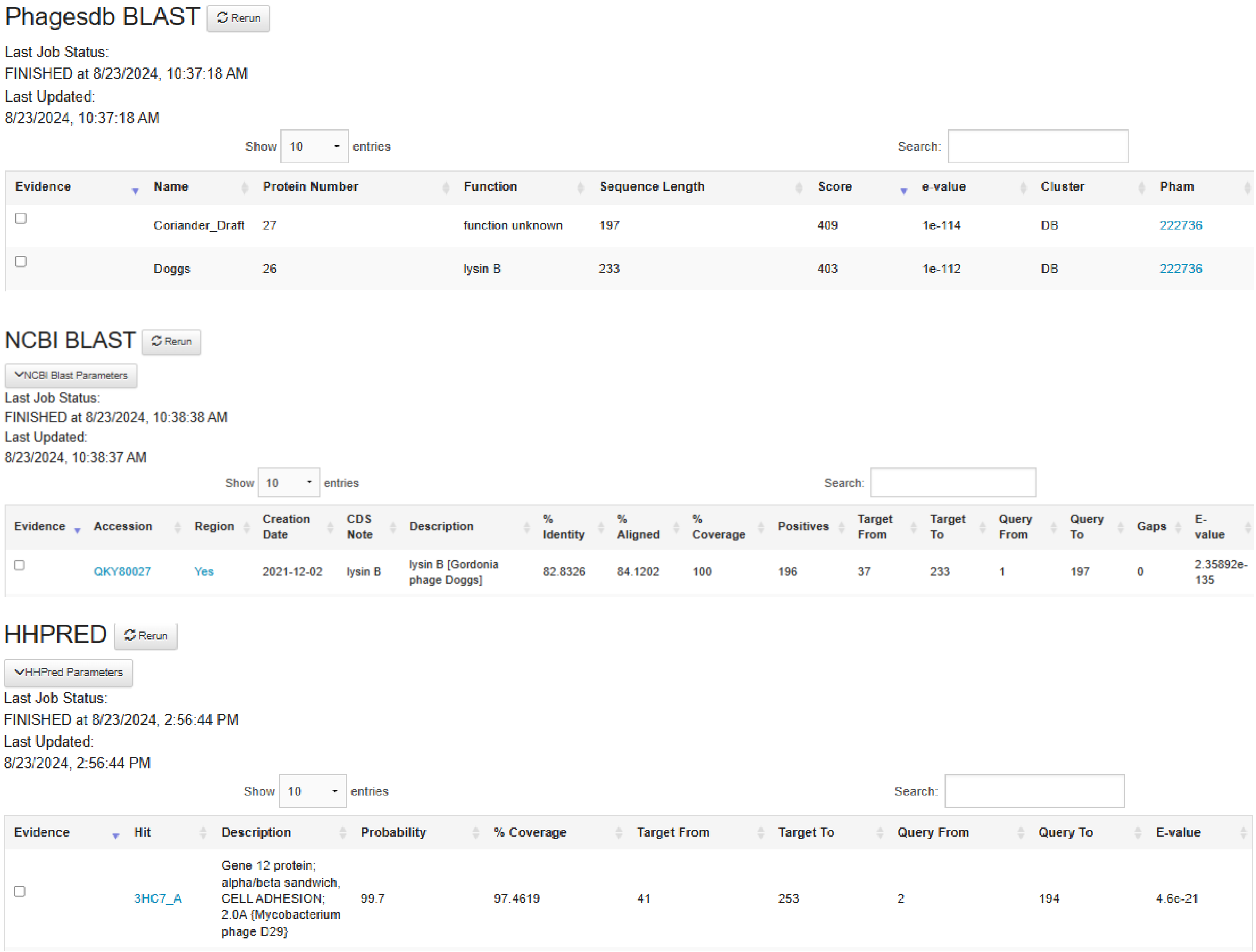
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta	Raw SD	Genomic	Spacer	Final	Sequence of the Region	Start	Start	ORF
#	Score	Z Value	Distance	Score	Upstream of the Start	Codon	Position	Length
1	-4.365	1.851	15	-5.520	CGTGACCGGGCTGCGGTGAAGC	ATG	22534	702
2	-3.230	2.412	13	-4.300	TCGCGCCCTGGATCCACGCAAG	GTG	22627	609
3	-4.107	1.979	16	-5.329	ACGCAAGGTGCAGTTCACCTAT	GTG	22642	594
4	-2.943	2.553	6	-4.244	TGCAGCAACCGCACCCGGAGAT	GTG	22687	549
5	-5.235	1.421	5	-6.633	GGCGGCGTCGATCGCGCAGGGC	GTG	22717	519
6	-5.129	1.474	10	-6.088	CCACGCGTCGCAGTACAACGCG	GTG	22762	474
7	-3.766	2.147	7	-4.988	CGGTGGGTACTCCCAGGGCGCG	ATG	22789	447
8	-3.766	2.147	10	-4.725	TGGGTACTCCCAGGGCGCGATG	GTG	22792	444
9	-5.167	1.455	17	-6.468	GCCGTGGCGCCGTGAGCTGATC	GTG	22843	393
10	-4.702	1.685	14	-5.799	GATCGTGAAGGCCGTTGCGGCG	ATG	22861	375
11	-5.474	1.303	14	-6.571	TCTGCCGCGGCGCCTGCTGTCC	GTG	22942	294
12	-3.618	2.220	17	-4.919	AGCATGGGACCTCGCCGAGTGG	ATG	23020	216
13	-2.955	2.548	8	-4.080	GGACCTCGCCGAGTGGATGTCG	GTG	23026	210
14	-5.419	1.331	14	-6.516	GAAGCGCTGGCTCGACGACATC	GTG	23068	168
15	-3.835	2.113	7	-5.057	GCTCGACGACATCGTGGACAAC	GTG	23077	159
16	-5.132	1.472	9	-6.178	GCTGCGCGGTGCCGGCGACTAC	GTG	23149	87
17	-5.102	1.487	13	-6.173	TCACGCGAAGCGACTCGCCCGG	ATG	23212	24

GeneMark

Gene: Coriander_27 Start: 22642, Stop: 23235, Start Num: 286 Candidate Starts for Coriander_27: (Start: 209 @22534 has 48 MA's), (275, 22627), (286, 22642), (312, 22687), (325, 22717), (353, 22762), (358, 22789), (359, 22792), (385, 22843), (394, 22861), (448, 22942), (476, 23020), (478, 23026), (502, 23068), (508, 23077), (569, 23149), (612, 23212),

Basic Phage Information	
Phage Name	**Coriander_27**
Gene #	**Gene 27(PECAAN) Gene 27 (Phamerator)**
Stop Coordinate	**23235**
Direction (For/Rev)	**Forward**
Gap (Overlap) with Previous Gene	**Overlap with Coriander_ 28 at 23232**
Selected Start Coordinate	Phamerator- Gene 27_Start site 22642 Glimmer Start: Gene 27_Start site 22642 GeneMark Start: Gene 27_Start site 22534 **22534**
Selected Function	**Lysin B protein**



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:37:18 AM
Last Updated:
8/23/2024, 10:37:18 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	27	function unknown	197	409	1e-114	DB	222736
☐	Doggs	26	lysin B	233	403	1e-112	DB	222736

NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:38 AM
Last Updated:
8/23/2024, 10:38:37 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80027	Yes	2021-12-02	lysin B	lysin B [Gordonia phage Doggs]	82.8326	84.1202	100	196	37	233	1	197	0	2.35892e-135

HHPRED

Last Job Status:
FINISHED at 8/23/2024, 2:56:44 PM
Last Updated:
8/23/2024, 2:56:44 PM

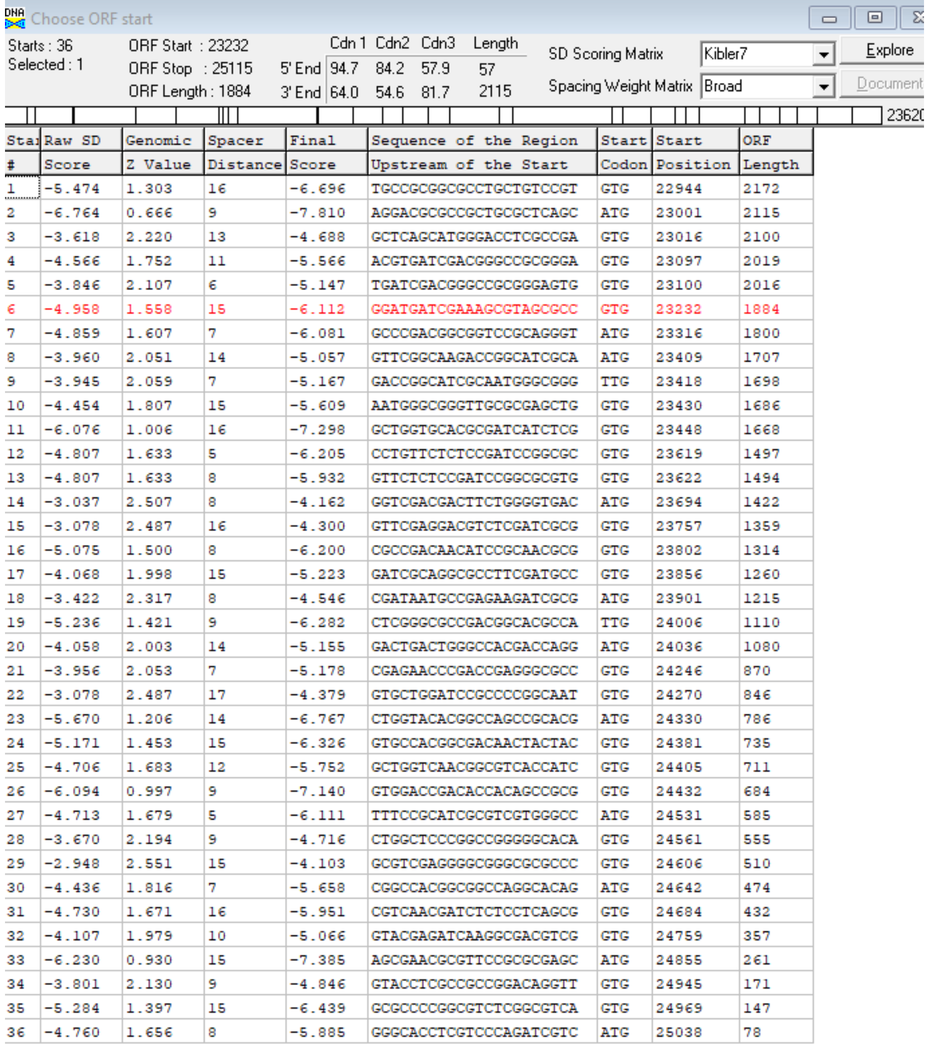
Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	3HC7_A	Gene 12 protein; alpha/beta sandwich, CELL ADHESION; 2.0A {Mycobacterium phage D29}	99.7	97.4619	41	253	2	194	4.6e-21

Coriander_Draft

Phamerator- Gene 28_Start site 23232

Glimmer Start: Gene 28_Start site 23232

GeneMark Start: Gene 28_Start site 23316



Starts : 36
Selected : 1

ORF Start : 23232
ORF Stop : 25115
ORF Length : 1884

	Cdn 1	Cdn2	Cdn3	Length
5' End	94.7	84.2	57.9	57
3' End	64.0	54.6	81.7	2115

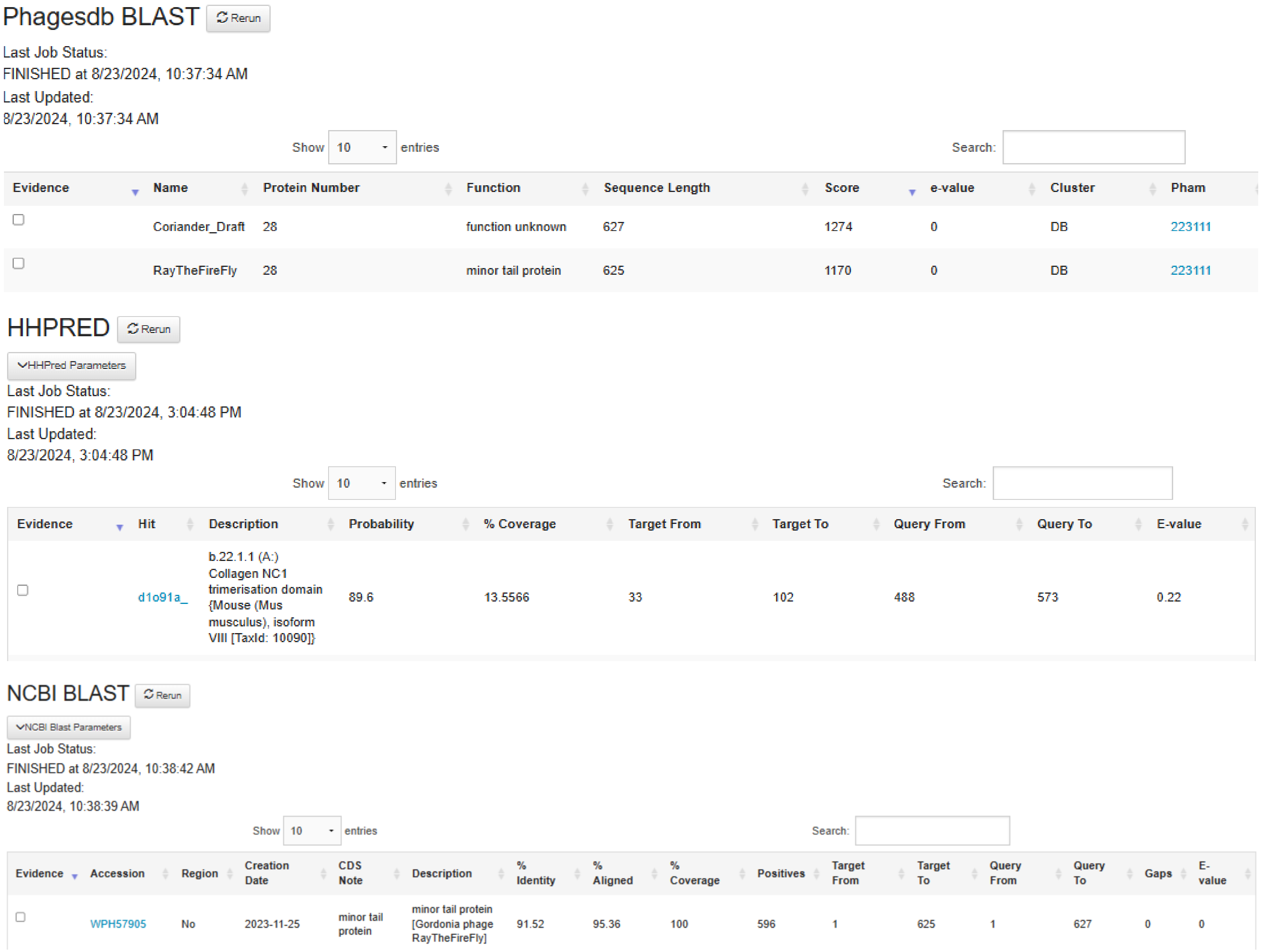
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.474	1.303	16	-6.696	TGCCGCGGCGCCTGCTGTCCGT	GTG	22944	2172
2	-6.764	0.666	9	-7.810	AGGACGCGCCGCTGCGCTCAGC	ATG	23001	2115
3	-3.618	2.220	13	-4.688	GCTCAGCATGGACCTCGCCGA	GTG	23016	2100
4	-4.566	1.752	11	-5.566	ACGTGATCGACGGGCCGCGGGA	GTG	23097	2019
5	-3.846	2.107	6	-5.147	TGATCGACGGGCCGCGGGAGTG	GTG	23100	2016
6	-4.958	1.558	15	-6.112	GGATGATCGAAAGCGTAGCGCC	GTG	23232	1884
7	-4.859	1.607	7	-6.081	GCCCGACGGCGGTCCGCAGGGT	ATG	23316	1800
8	-3.960	2.051	14	-5.057	GTTCGGCAAGACCGGCATCGCA	ATG	23409	1707
9	-3.945	2.059	7	-5.167	GACCGGCATCGCAATGGGCGGG	TTG	23418	1698
10	-4.454	1.807	15	-5.609	AATGGGCGGGTTGCGCGAGCTG	GTG	23430	1686
11	-6.076	1.006	16	-7.298	GCTGGTGCACGCGATCATCTCG	GTG	23448	1668
12	-4.807	1.633	5	-6.205	CCTGTTCTCTCCGATCCGGCGC	GTG	23619	1497
13	-4.807	1.633	8	-5.932	GTTCTCTCCGATCCGGCGCGTG	GTG	23622	1494
14	-3.037	2.507	8	-4.162	GGTCGACGACTTCTGGGGTGAC	ATG	23694	1422
15	-3.078	2.487	16	-4.300	GTTCGAGGACGTCTCGATCGCG	GTG	23757	1359
16	-5.075	1.500	8	-6.200	CGCCGACAACATCCGCAACGCG	GTG	23802	1314
17	-4.068	1.998	15	-5.223	GATCGCAGGCGCCTTCGATGCC	GTG	23856	1260
18	-3.422	2.317	8	-4.546	CGATAATGCCGAGAAGATCGCG	ATG	23901	1215
19	-5.236	1.421	9	-6.282	CTCGGGCGCCGACGGCACGCCA	TTG	24006	1110
20	-4.058	2.003	14	-5.155	GACTGACTGGGCCACGACCAGG	ATG	24036	1080
21	-3.956	2.053	7	-5.178	CGAGAACCCGACCGAGGGCGCC	GTG	24246	870
22	-3.078	2.487	17	-4.379	GTGCTGGATCCGCCCCGGCAAT	GTG	24270	846
23	-5.670	1.206	14	-6.767	CTGGTACACGGCCAGCCGCACG	ATG	24330	786
24	-5.171	1.453	15	-6.326	GTGCCACGGCGACAACTACTAC	GTG	24381	735
25	-4.706	1.683	12	-5.752	GCTGGTCAACGGCGTCACCATC	GTG	24405	711
26	-6.094	0.997	9	-7.140	GTGGACCGACACCACAGCCGCG	GTG	24432	684
27	-4.713	1.679	5	-6.111	TTTCCGCATCGCGTCGTGGGCC	ATG	24531	585
28	-3.670	2.194	9	-4.716	CTGGCTCCCGGCCGGGGGCACA	GTG	24561	555
29	-2.948	2.551	15	-4.103	GCGTCGAGGGGCGGGCGCGCCC	GTG	24606	510
30	-4.436	1.816	7	-5.658	CGGCCACGGCGGCCAGGCACAG	ATG	24642	474
31	-4.730	1.671	16	-5.951	CGTCAACGATCTCTCCTCAGCG	GTG	24684	432
32	-4.107	1.979	10	-5.066	GTACGAGATCAAGGCGACGTCG	GTG	24759	357
33	-6.230	0.930	15	-7.385	AGCGAACGCGTTCCGCGCGAGC	ATG	24855	261
34	-3.801	2.130	9	-4.846	GTACCTCGCCGCCGGACAGGTT	GTG	24945	171
35	-5.284	1.397	15	-6.439	GCGCCCCGGCGTCTCGGCGTCA	GTG	24969	147
36	-4.760	1.656	8	-5.885	GGGCACCTCGTCCCAGATCGTC	ATG	25038	78

GeneMark

Gene: Coriander_28 Start: 23232, Stop: 25115, Start Num: 19 Candidate Starts for Coriander_28: (2, 22944), (3, 23001), (5, 23016), (13, 23097), (14, 23100), (Start: 19 @23232 has 12 MA's), (23, 23316), (30, 23409), (32, 23418), (34, 23430), (37, 23448), (61, 23619), (62, 23622), (75, 23694), (82, 23757), (88, 23802), (96, 23856), (100, 23901), (108, 24006), (109, 24036), (127, 24246), (129, 24270), (137, 24330), (138, 24381), (143, 24405), (144, 24432), (152, 24531), (154, 24561), (157, 24606), (162, 24642), (163, 24684), (169, 24759), (182, 24855), (196, 24945), (200, 24969), (210, 25038)

Basic Phage Information	
Phage Name	Coriander_28
Gene #	Gene 28(PECAAN) Gene 28 (Phamerator)
Stop Coordinate	25115
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlap with Coriander_ 27 at 23232
Selected Start Coordinate	Phamerator- Gene 28_Start site 23232 Glimmer Start: Gene 28_Start site 23232 GeneMark Start: Gene 28_Start site 23316 23232
Selected Function	Minor tail protein



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:37:34 AM
Last Updated:
8/23/2024, 10:37:34 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	28	function unknown	627	1274	0	DB	223111
☐	RayTheFireFly	28	minor tail protein	625	1170	0	DB	223111

HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:04:48 PM
Last Updated:
8/23/2024, 3:04:48 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1o91a_	b.22.1.1 (A:) Collagen NC1 trimerisation domain {Mouse (Mus musculus), isoform VIII [TaxId: 10090]}	89.6	13.5566	33	102	488	573	0.22

NCBI BLAST

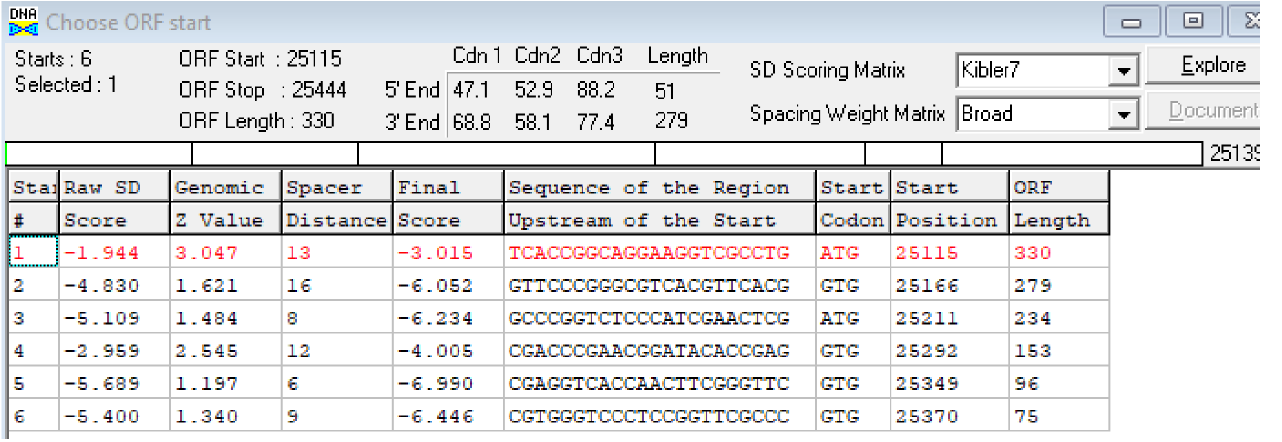
Last Job Status:
FINISHED at 8/23/2024, 10:38:42 AM
Last Updated:
8/23/2024, 10:38:39 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	WPH57905	No	2023-11-25	minor tail protein	minor tail protein [Gordonia phage RayTheFireFly]	91.52	95.36	100	596	1	625	1	627	0	0

Coriander_Draft

Phamerator- Gene 29_Start site 25115

PECAAN- Gene 29_Start site 25115



Starts : 6
Selected : 1

ORF Start : 25115
ORF Stop : 25444
ORF Length : 330

	Cdn 1	Cdn2	Cdn3	Length
5' End	47.1	52.9	88.2	51
3' End	68.8	58.1	77.4	279

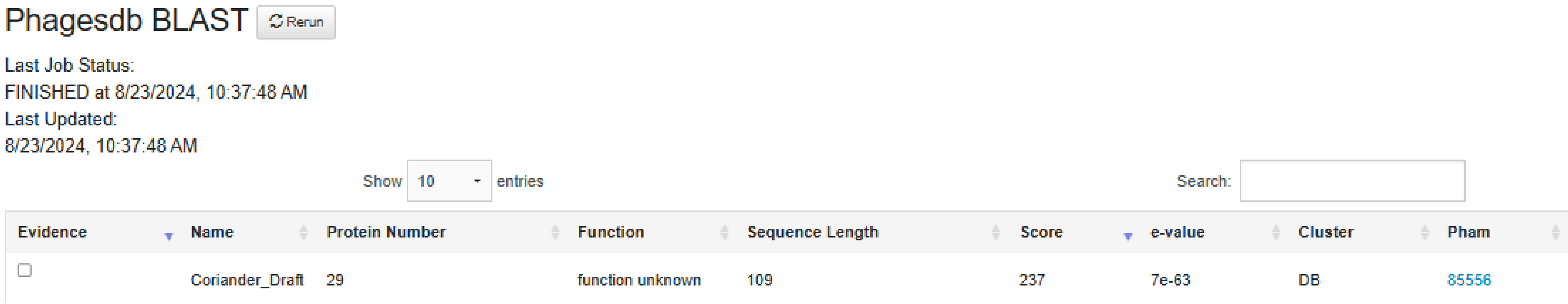
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-1.944	3.047	13	-3.015	TCACCGGCAGGAAGGTCGCCTG	ATG	25115	330
2	-4.830	1.621	16	-6.052	GTTCCCGGGCGTCACGTTCACG	GTG	25166	279
3	-5.109	1.484	8	-6.234	GCCCGGTCTCCCATCGAACTCG	ATG	25211	234
4	-2.959	2.545	12	-4.005	CGACCCGAACGGATACACCGAG	GTG	25292	153
5	-5.689	1.197	6	-6.990	CGAGGTCACCAACTTCGGGTTC	GTG	25349	96
6	-5.400	1.340	9	-6.446	CGTGGGTCCCTCCGGTTCGCCC	GTG	25370	75

GeneMark

Gene: Coriander_29 Start: 25115, Stop: 25444, Start Num: 25 Candidate Starts for Coriander_29: (Start: 25 @25115 has 49 MA's), (31, 25166), (34, 25211), (36, 25292), (41, 25349), (45, 25370),

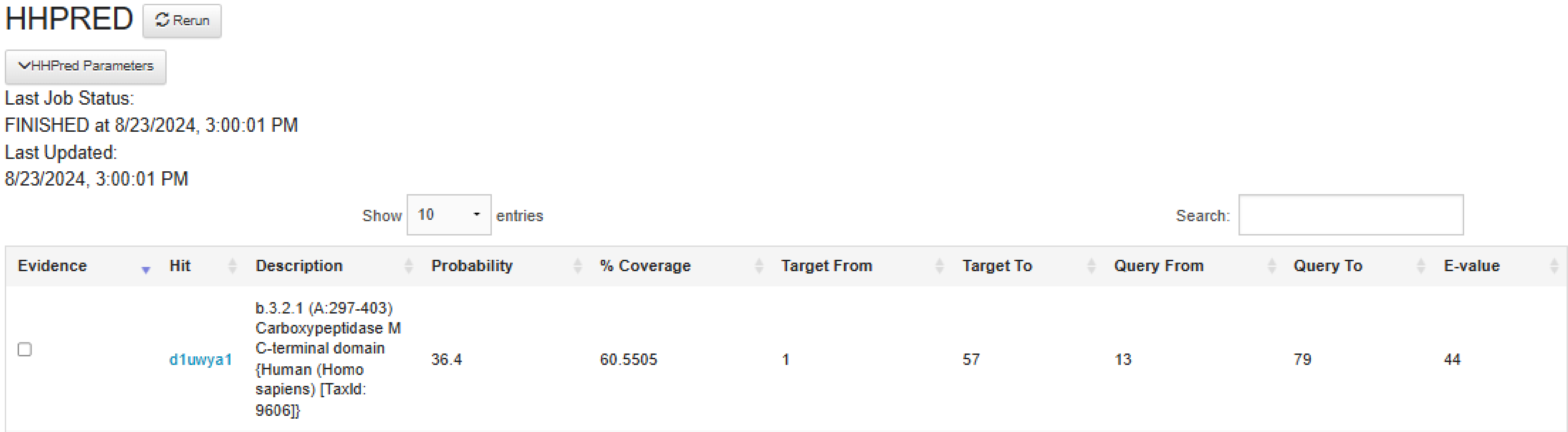
Basic Phage Information	
Phage Name	Coriander_29
Gene #	Gene 29(PECAAN) Gene 29 (Phamerator)
Stop Coordinate	25444
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	None
Selected Start Coordinate	25115
Selected Function	Function Unknown



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:37:48 AM
Last Updated:
8/23/2024, 10:37:48 AM

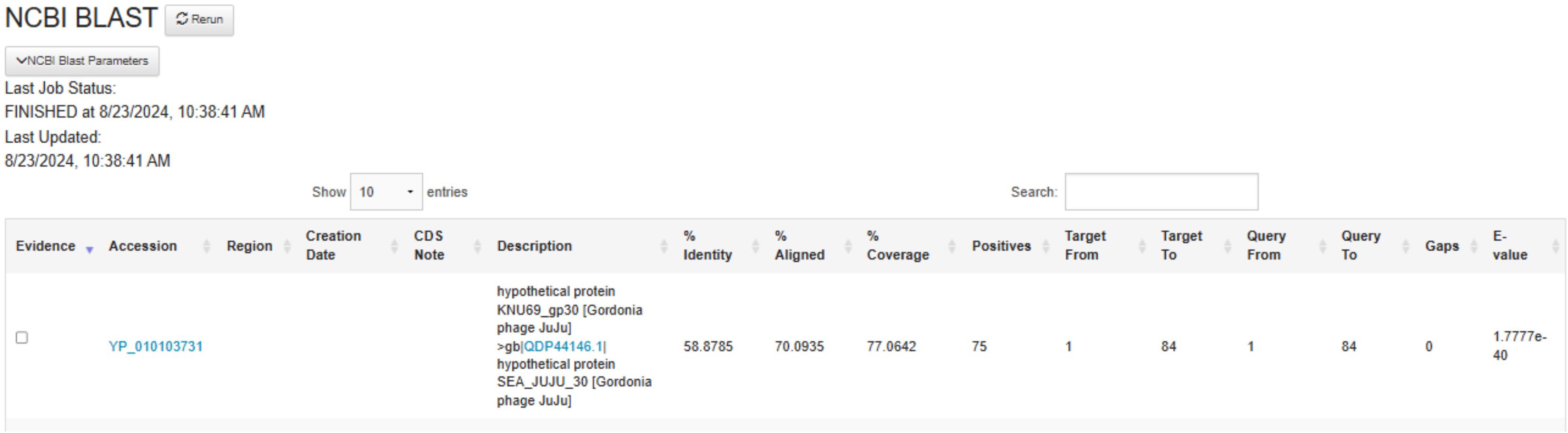
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	29	function unknown	109	237	7e-63	DB	85556



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:00:01 PM
Last Updated:
8/23/2024, 3:00:01 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1uwya1	b.3.2.1 (A:297-403) Carboxypeptidase M C-terminal domain {Human (Homo sapiens) [TaxId: 9606]}	36.4	60.5505	1	57	13	79	44



NCBI BLAST

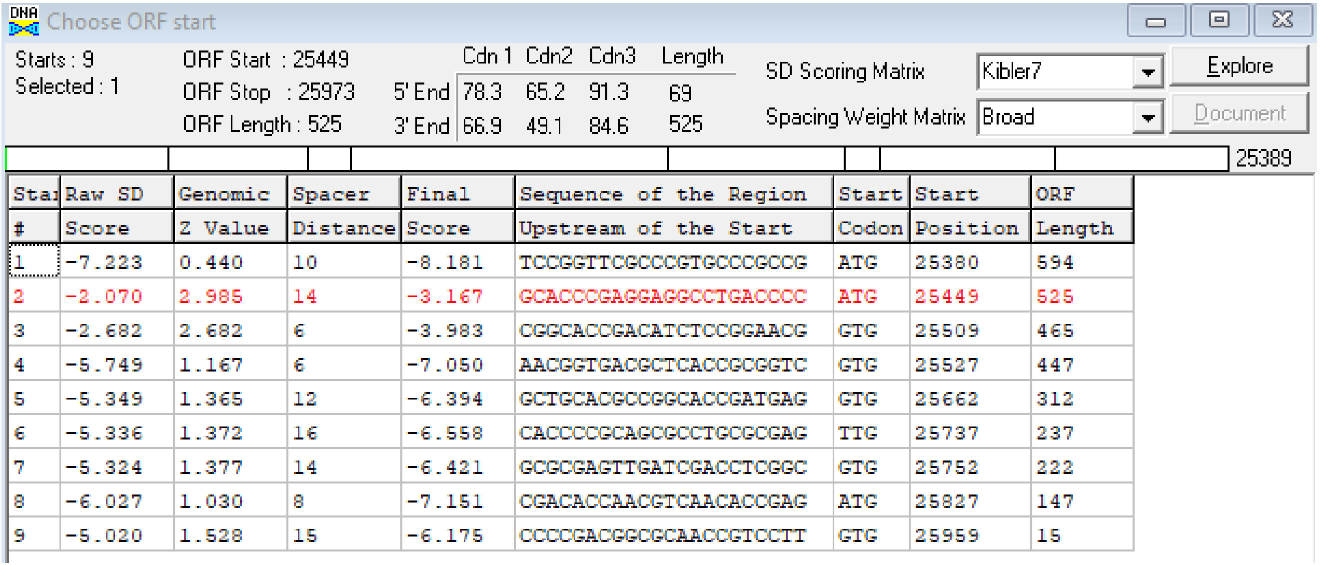
Last Job Status:
FINISHED at 8/23/2024, 10:38:41 AM
Last Updated:
8/23/2024, 10:38:41 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_010103731				hypothetical protein KNU69_gp30 [Gordonia phage JuJu] >gb|QDP44146.1| hypothetical protein SEA_JUJU_30 [Gordonia phage JuJu]	58.8785	70.0935	77.0642	75	1	84	1	84	0	1.7777e-40

Coriander_Draft

Phamerator- Gene 30_Start site 25449

PECAAN- Gene 30_Start site 25449



Starts : 9
Selected : 1

ORF Start : 25449
ORF Stop : 25973
ORF Length : 525

	Cdn 1	Cdn2	Cdn3	Length
5' End	78.3	65.2	91.3	69
3' End	66.9	49.1	84.6	525

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

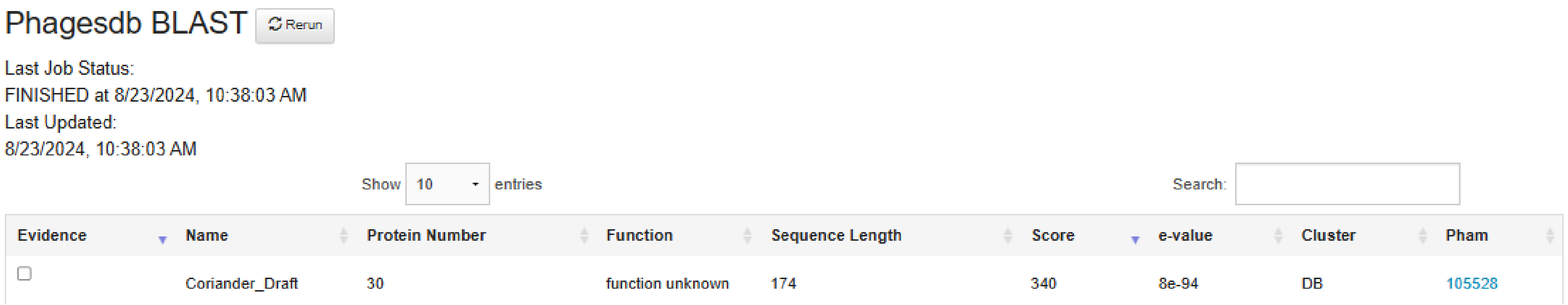
25389

Star #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-7.223	0.440	10	-8.181	TCCGGTTCGCCCGTGCCCGCCG	ATG	25380	594
2	-2.070	2.985	14	-3.167	GCACCCGAGGAGGCCTGACCCC	ATG	25449	525
3	-2.682	2.682	6	-3.983	CGGCACCGACATCTCCGGAACG	GTG	25509	465
4	-5.749	1.167	6	-7.050	AACGGTGACGCTCACCGCGGTC	GTG	25527	447
5	-5.349	1.365	12	-6.394	GCTGCACGCCGGCACCGATGAG	GTG	25662	312
6	-5.336	1.372	16	-6.558	CACCCCGCAGCGCCTGCGCGAG	TTG	25737	237
7	-5.324	1.377	14	-6.421	GCGCGAGTTGATCGACCTCGGC	GTG	25752	222
8	-6.027	1.030	8	-7.151	CGACACCAACGTCAACACCGAG	ATG	25827	147
9	-5.020	1.528	15	-6.175	CCCCGACGGCGCAACCGTCCTT	GTG	25959	15

GeneMark

Gene: Coriander_30 Start: 25449, Stop: 25973, Start Num: 6 Candidate Starts for Coriander_30: (4, 25380), (Start: 6 @25449 has 5 MA's), (9, 25509), (11, 25527), (18, 25662), (19, 25737), (20, 25752), (23, 25827), (27, 25959),

Basic Phage Information	
Phage Name	Coriander_30
Gene #	Gene 30(PECAAN) Gene 30 (Phamerator)
Stop Coordinate	25973
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	None
Selected Start Coordinate	25449
Selected Function	

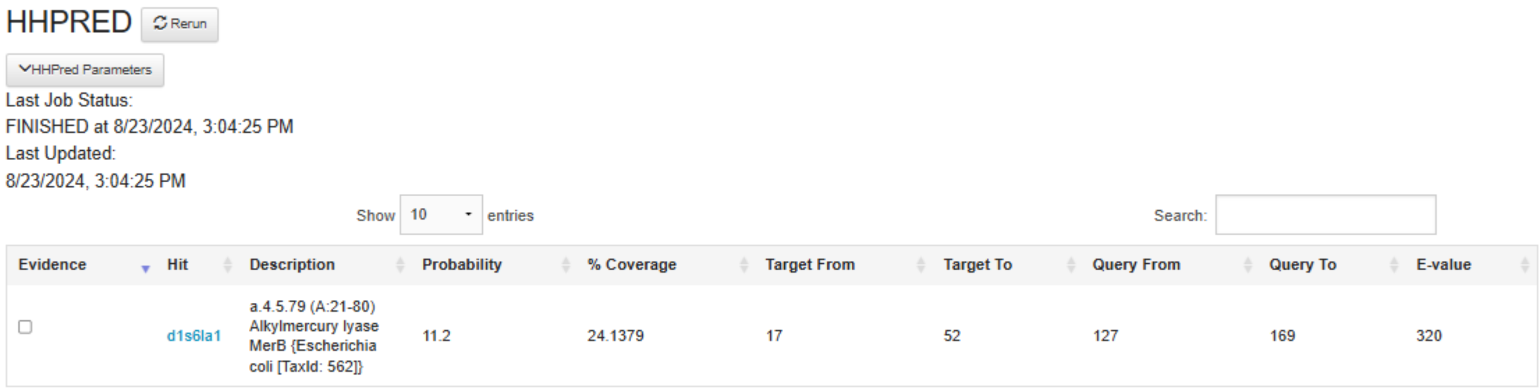


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:03 AM
Last Updated:
8/23/2024, 10:38:03 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	30	function unknown	174	340	8e-94	DB	105528



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:04:25 PM
Last Updated:
8/23/2024, 3:04:25 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1s6la1	a.4.5.79 (A:21-80) Alkylmercury lyase MerB {Escherichia coli [TaxId: 562]}	11.2	24.1379	17	52	127	169	320

NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:41 AM
Last Updated:
8/23/2024, 10:38:41 AM

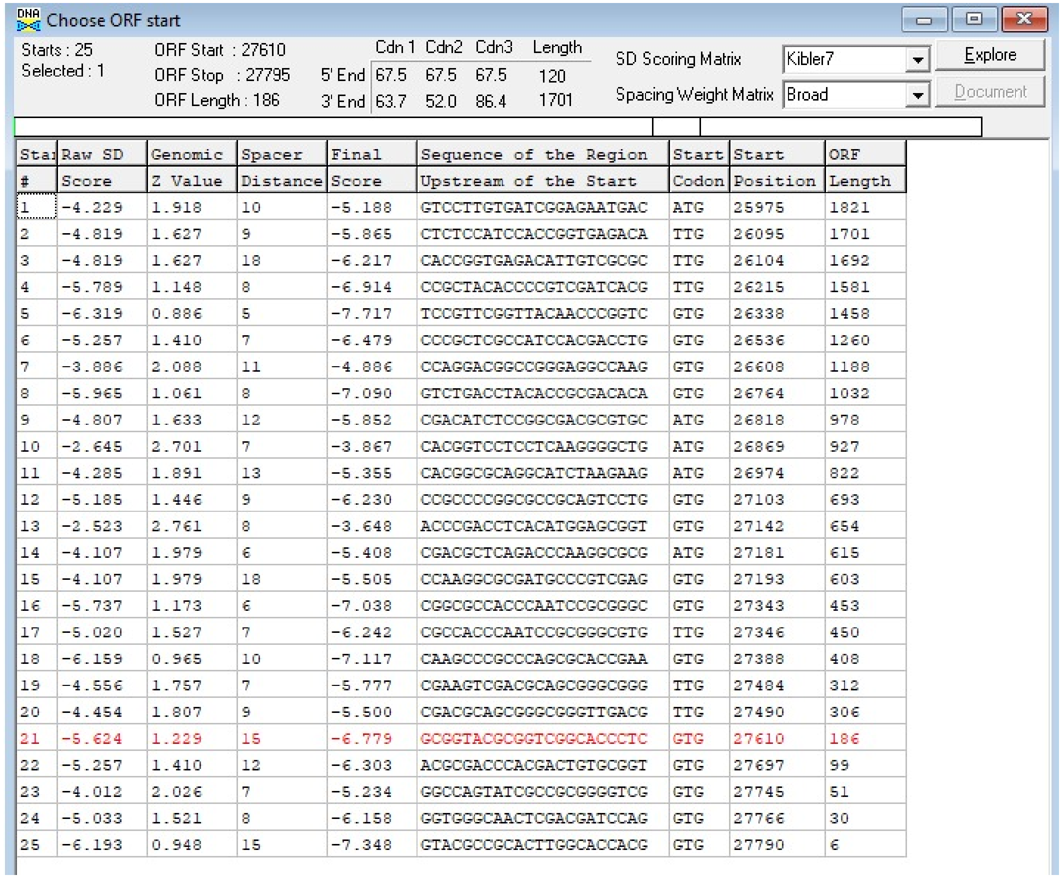
Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80030				tailspike protein [Gordonia phage Doggs]	19.9181	20.3274	87.931	149	1	153	1	153	0	6.12785e-92

31 - 36

Coriander_31

Phamerator Start: Gene 31_Start site (25975)
Glimmer Start: Gene 31_Start site (25975)
GeneMark Start: Gene 31_Start site (25975)



Starts : 25
Selected : 1

ORF Start : 27610
ORF Stop : 27795
ORF Length : 186

	Cdn 1	Cdn2	Cdn3	Length
5' End	67.5	67.5	67.5	120
3' End	63.7	52.0	86.4	1701

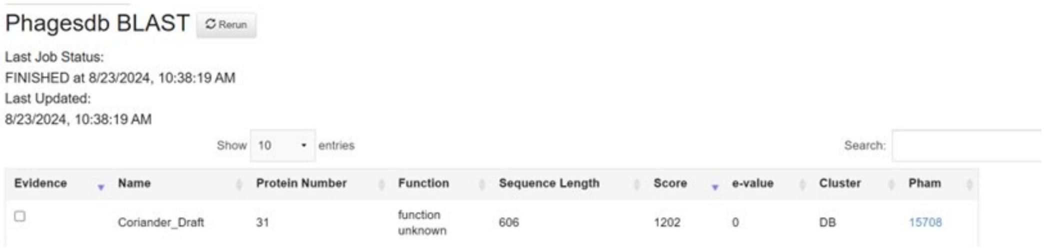
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-4.229	1.918	10	-5.188	GTCCTTGTGATCGGAGAATGAC	ATG	25975	1821
2	-4.819	1.627	9	-5.865	CTCTCCATCCACCGGTGAGACA	TTG	26095	1701
3	-4.819	1.627	18	-6.217	CACCGGTGAGACATTGTCGCGC	TTG	26104	1692
4	-5.789	1.148	8	-6.914	CCGCTACACCCCGTCGATCACG	TTG	26215	1581
5	-6.319	0.886	5	-7.717	TCCGTTCGGTTACAACCCGGTC	GTG	26338	1458
6	-5.257	1.410	7	-6.479	CCCGCTCGCCATCCACGACCTG	GTG	26536	1260
7	-3.886	2.088	11	-4.886	CCAGGACGGCCGGGAGGCCAAG	GTG	26608	1188
8	-5.965	1.061	8	-7.090	GTCTGACCTACACCGCGACACA	GTG	26764	1032
9	-4.807	1.633	12	-5.852	CGACATCTCCGGCGACGCGTGC	ATG	26818	978
10	-2.645	2.701	7	-3.867	CACGGTCCTCCTCAAGGGGCTG	ATG	26869	927
11	-4.285	1.891	13	-5.355	CACGGCGCAGGCATCTAAGAAG	ATG	26974	822
12	-5.185	1.446	9	-6.230	CCGCCCCGGCGCCGCAGTCCTG	GTG	27103	693
13	-2.523	2.761	8	-3.648	ACCCGACCTCACATGGAGCGGT	GTG	27142	654
14	-4.107	1.979	6	-5.408	CGACGCTCAGACCCAAGGCGCG	ATG	27181	615
15	-4.107	1.979	18	-5.505	CCAAGGCGCGATGCCCGTCGAG	GTG	27193	603
16	-5.737	1.173	6	-7.038	CGGCGCCACCCAATCCGCGGGC	GTG	27343	453
17	-5.020	1.527	7	-6.242	CGCCACCCAATCCGCGGGCGTG	TTG	27346	450
18	-6.159	0.965	10	-7.117	CAAGCCCGCCCAGCGCACCGAA	GTG	27388	408
19	-4.556	1.757	7	-5.777	CGAAGTCGACGCAGCGGGCGGG	TTG	27484	312
20	-4.454	1.807	9	-5.500	CGACGCAGCGGGCGGGTTGACG	TTG	27490	306
21	-5.624	1.229	15	-6.779	GCGGTACGCGGTCGGCACCCTC	GTG	27610	186
22	-5.257	1.410	12	-6.303	ACGCGACCCACGACTGTGCGGT	GTG	27697	99
23	-4.012	2.026	7	-5.234	GGCCAGTATCGCCGCGGGGTCG	GTG	27745	51
24	-5.033	1.521	8	-6.158	GGTGGGCAACTCGACGATCCAG	GTG	27766	30
25	-6.193	0.948	15	-7.348	GTACGCCGCACTTGGCACCACG	GTG	27790	6

GeneMark

Gene: Coriander_31 Start: 25975, Stop: 27795, Start Num: 16 Candidate Starts for Coriander_31: (16, 25975), (18, 26095), (19, 26104), (22, 26215), (27, 26338), (35, 26536), (37, 26608), (39, 26764), (41, 26818), (44, 26869), (46, 26974), (56, 27103), (58, 27142), (63, 27181), (64, 27193), (67, 27343), (68, 27346), (69, 27388), (72, 27484), (73, 27490), (77, 27610), (81, 27697), (84, 27745), (86, 27766), (88, 27790)

Basic Phage Information	
Phage Name	Coriander_31
Gene #	Gene 31 (PECAAN) GENE 31 (Phamerator)
Stop Coordinate	Stop 27795
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	1
Selected Start Coordinate	Phamerator Start (25975) Glimmer Start (25975) GeneMark Start (25975)
Selected Function	Tailspike protein

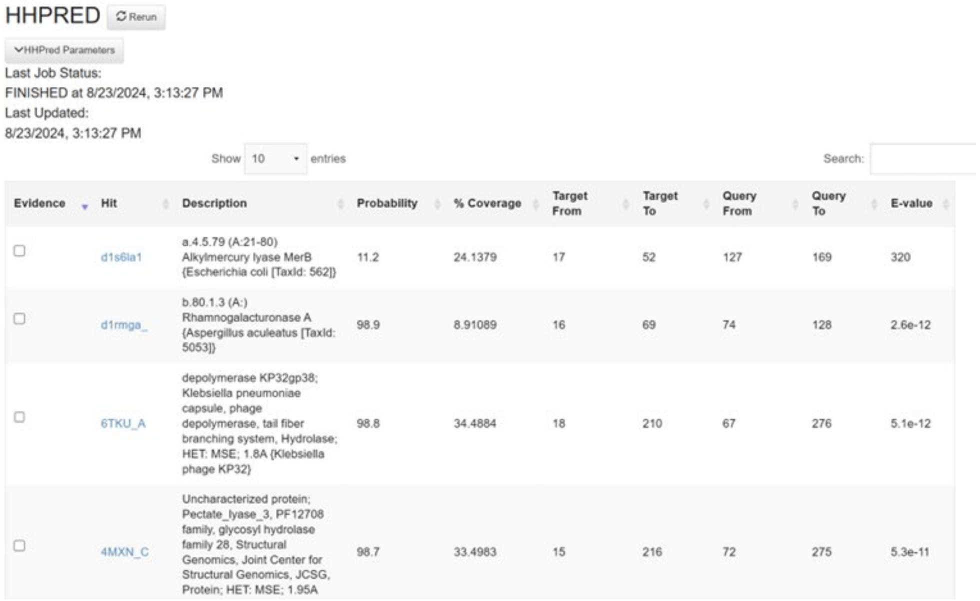


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:19 AM
Last Updated:
8/23/2024, 10:38:19 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	31	function unknown	606	1202	0	DB	15708

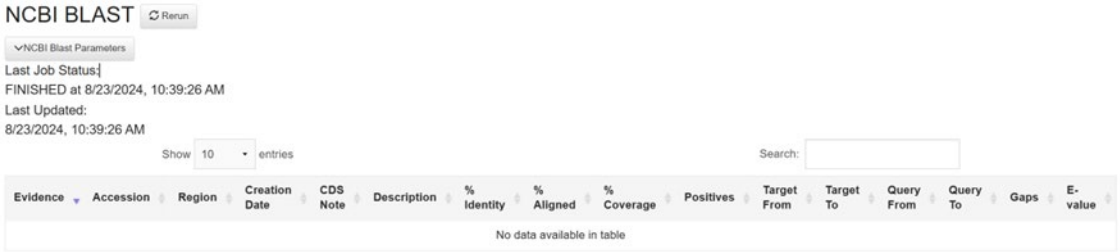


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:13:27 PM
Last Updated:
8/23/2024, 3:13:27 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1s6la1	a.4.5.79 (A:21-80) Alkylmercury lyase MerB {Escherichia coli [TaxId: 562]}	11.2	24.1379	17	52	127	169	320
☐	d1rmga_	b.80.1.3 (A:) Rhamnogalacturonase A {Aspergillus aculeatus [TaxId: 5053]}	98.9	8.91089	16	69	74	128	2.6e-12
☐	6TKU_A	depolymerase KP32gp38; Klebsiella pneumoniae capsule, phage depolymerase, tail fiber branching system, Hydrolase; HET: MSE; 1.8A {Klebsiella phage KP32}	98.8	34.4884	18	210	67	276	5.1e-12
☐	4MXN_C	Uncharacterized protein; Pectate_lyase_3, PF12708 family, glycosyl hydrolase family 28, Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein; HET: MSE; 1.95A	98.7	33.4983	15	216	72	275	5.3e-11



NCBI BLAST

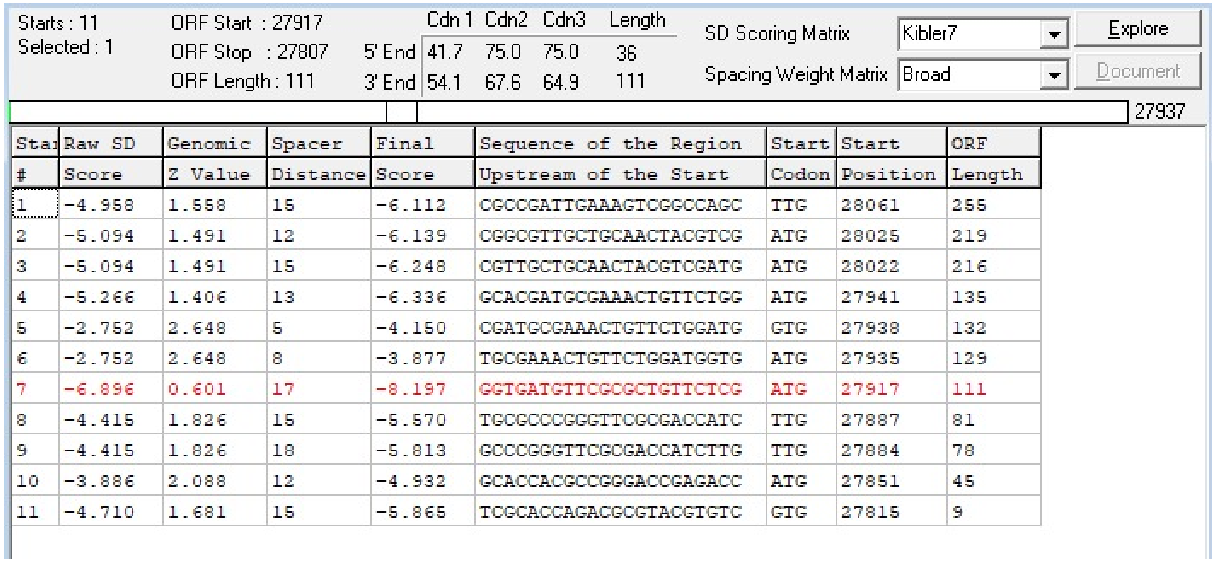
Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
No data available in table															

Coriander_32

Phamerator Start: Gene 32_Start site (28022)
Glimmer Start: Gene 32_Start site (28022)
GeneMark Start: Gene 32_Start site (28025)



Starts : 11
Selected : 1
ORF Start : 27917
ORF Stop : 27807
ORF Length : 111

	Cdn 1	Cdn2	Cdn3	Length
5' End	41.7	75.0	75.0	36
3' End	54.1	67.6	64.9	111

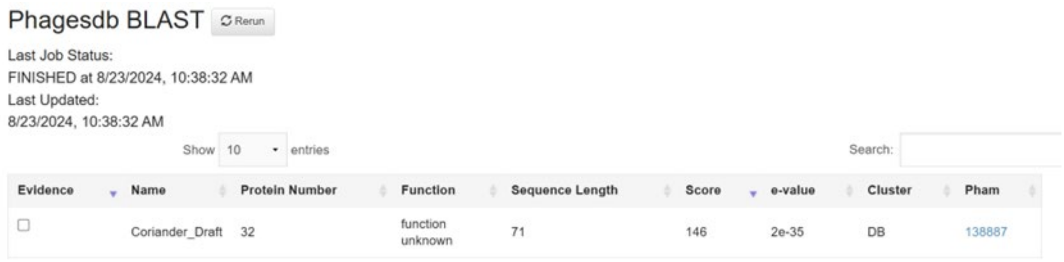
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-4.958	1.558	15	-6.112	CGCCGATTGAAAGTCGGCCAGC	TTG	28061	255
2	-5.094	1.491	12	-6.139	CGGCGTTGCTGCAACTACGTCG	ATG	28025	219
3	-5.094	1.491	15	-6.248	CGTTGCTGCAACTACGTCGATG	ATG	28022	216
4	-5.266	1.406	13	-6.336	GCACGATGCGAAACTGTTCTGG	ATG	27941	135
5	-2.752	2.648	5	-4.150	CGATGCGAAACTGTTCTGGATG	GTG	27938	132
6	-2.752	2.648	8	-3.877	TGCGAAACTGTTCTGGATGGTG	ATG	27935	129
7	-6.896	0.601	17	-8.197	GGTGATGTTCGCGCTGTTCTCG	ATG	27917	111
8	-4.415	1.826	15	-5.570	TGCGCCCGGGTTCGCGACCATC	TTG	27887	81
9	-4.415	1.826	18	-5.813	GCCCGGGTTCGCGACCATCTTG	TTG	27884	78
10	-3.886	2.088	12	-4.932	GCACCACGCCGGGACCGAGACC	ATG	27851	45
11	-4.710	1.681	15	-5.865	TCGCACCAGACGCGTACGTGTC	GTG	27815	9

GeneMark

Gene: Coriander_32 Start: 28022,28025, Stop: 27807, Hypothetical Protein

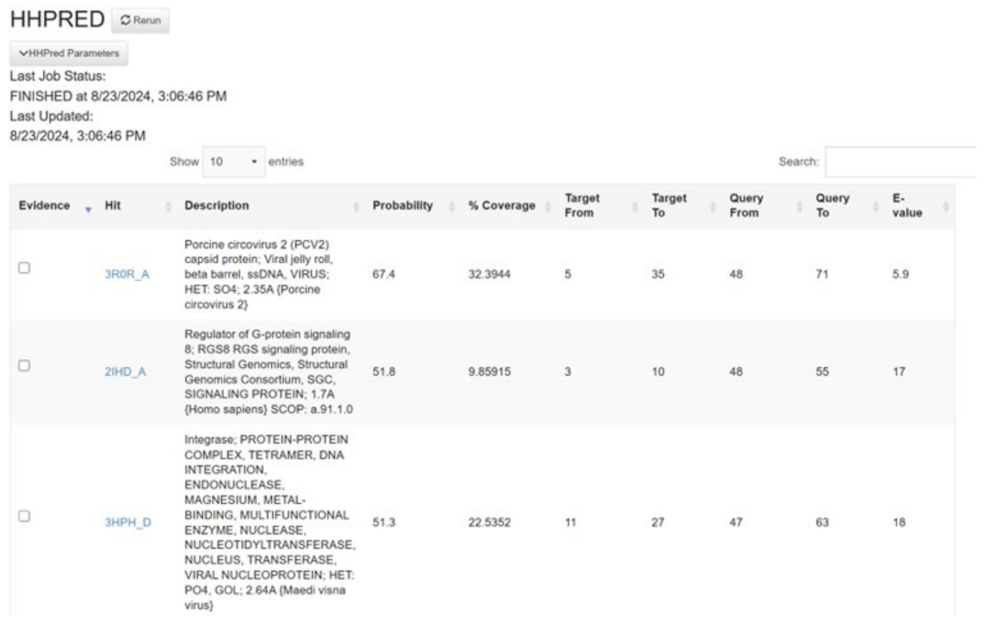
Basic Phage Information	
Phage Name	Coriander_32
Gene #	Gene 32(PECAAN) GENE 32(Phamerator)
Stop Coordinate	Stop 27807
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	290
Selected Start Coordinate	Phamerator Start (28022) Glimmer Start (28022) GeneMark Start (28025)
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:32 AM
Last Updated:
8/23/2024, 10:38:32 AM

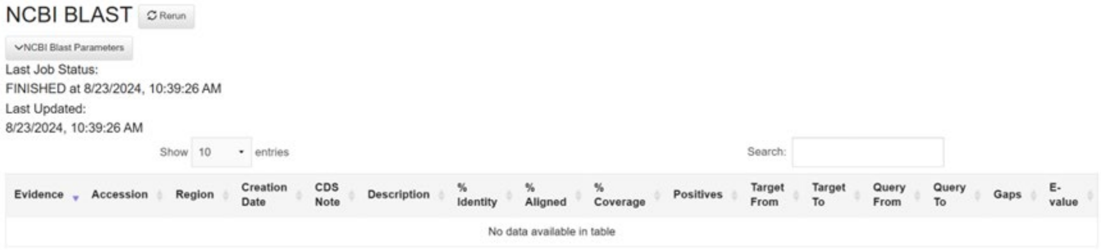
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	32	function unknown	71	146	2e-35	DB	138887



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:06:46 PM
Last Updated:
8/23/2024, 3:06:46 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	3R0R_A	Porcine circovirus 2 (PCV2) capsid protein; Viral jelly roll, beta barrel, ssDNA, VIRUS; HET: SO4; 2.35A {Porcine circovirus 2}	67.4	32.3944	5	35	48	71	5.9
☐	2IHD_A	Regulator of G-protein signaling 8; RGS8 RGS signaling protein, Structural Genomics, Structural Genomics Consortium, SGC, SIGNALING PROTEIN; 1.7A {Homo sapiens} SCOP: a.91.1.0	51.8	9.85915	3	10	48	55	17
☐	3HPH_D	Integrase; PROTEIN-PROTEIN COMPLEX, TETRAMER, DNA INTEGRATION, ENDONUCLEASE, MAGNESIUM, METAL-BINDING, MULTIFUNCTIONAL ENZYME, NUCLEASE, NUCLEOTIDYLTRANSFERASE, NUCLEUS, TRANSFERASE, VIRAL NUCLEOPROTEIN; HET: PO4, GOL; 2.64A {Maedi visna virus}	51.3	22.5352	11	27	47	63	18



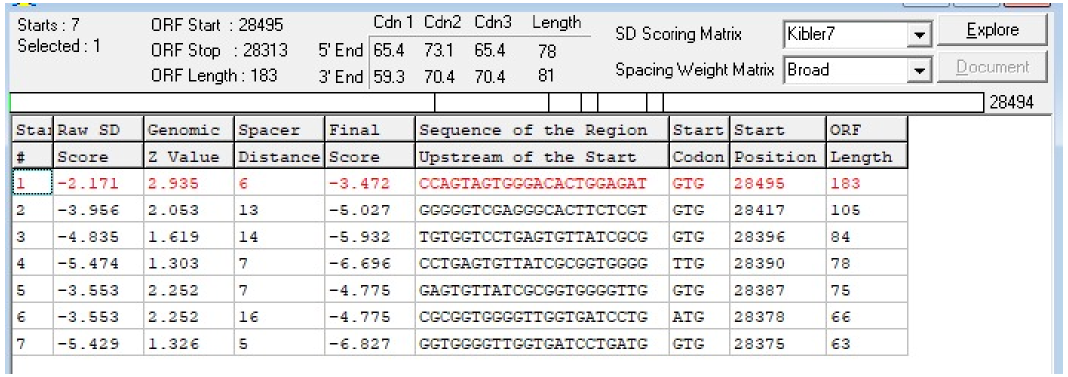
NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
No data available in table															

Coriander_33

Phamerator Start: Gene 33_Start site (28495)
Glimmer Start: Gene 33_Start site (28495)
GeneMark Start: Gene 33_Start site ()



Starts : 7
Selected : 1

ORF Start : 28495
ORF Stop : 28313
ORF Length : 183

	Cdn 1	Cdn2	Cdn3	Length
5' End	65.4	73.1	65.4	78
3' End	59.3	70.4	70.4	81

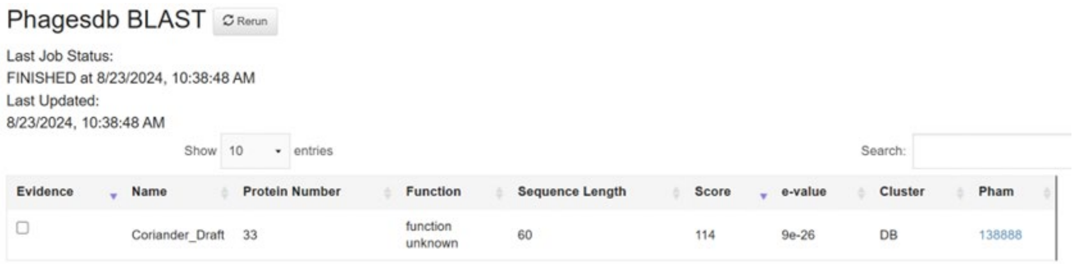
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-2.171	2.935	6	-3.472	CCAGTAGTGGGACACTGGAGAT	GTG	28495	183
2	-3.956	2.053	13	-5.027	GGGGGTCGAGGGCACTTCTCGT	GTG	28417	105
3	-4.835	1.619	14	-5.932	TGTGGTCCTGAGTGTTATCGCG	GTG	28396	84
4	-5.474	1.303	7	-6.696	CCTGAGTGTTATCGCGGTGGGG	TTG	28390	78
5	-3.553	2.252	7	-4.775	GAGTGTTATCGCGGTGGGGTTG	GTG	28387	75
6	-3.553	2.252	16	-4.775	CGCGGTGGGGTTGGTGATCCTG	ATG	28378	66
7	-5.429	1.326	5	-6.827	GGTGGGGTTGGTGATCCTGATG	GTG	28375	63

GeneMark

Gene: Coriander_33 Start: 28495, Stop: 28313

Basic Phage Information	
Phage Name	Coriander_33
Gene #	Gene 33 (PECAAN) GENE 33 (Phamerator)
Stop Coordinate	Stop 28313
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	182
Selected Start Coordinate	Phamerator Start (28495) Glimmer Start (28495) GeneMark Start ()
Selected Function	

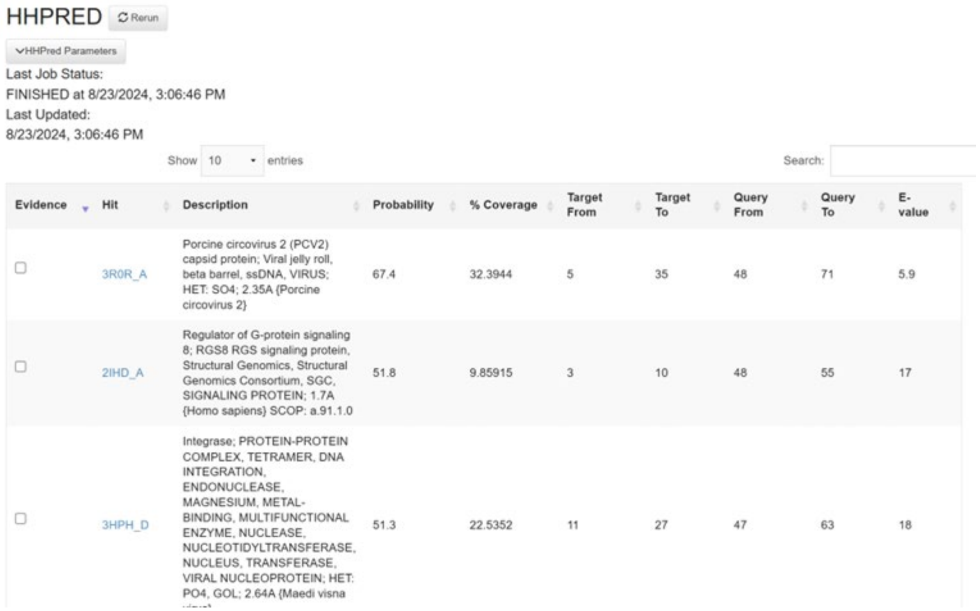


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:38:48 AM
Last Updated:
8/23/2024, 10:38:48 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	33	function unknown	60	114	9e-26	DB	138888

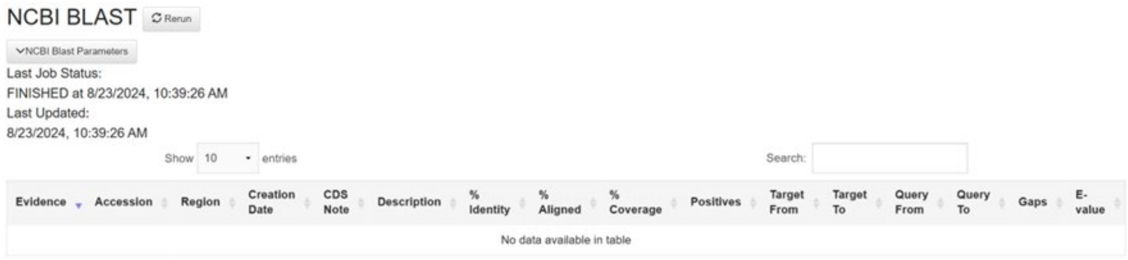


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:06:46 PM
Last Updated:
8/23/2024, 3:06:46 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	3R0R_A	Porcine circovirus 2 (PCV2) capsid protein; Viral jelly roll, beta barrel, ssDNA, VIRUS; HET: SO4; 2.35A {Porcine circovirus 2}	67.4	32.3944	5	35	48	71	5.9
☐	2IHD_A	Regulator of G-protein signaling 8; RGS8 RGS signaling protein, Structural Genomics, Structural Genomics Consortium, SGC, SIGNALING PROTEIN; 1.7A {Homo sapiens} SCOP: a.91.1.0	51.8	9.85915	3	10	48	55	17
☐	3HPH_D	Integrase; PROTEIN-PROTEIN COMPLEX, TETRAMER, DNA INTEGRATION, ENDONUCLEASE, MAGNESIUM, METAL-BINDING, MULTIFUNCTIONAL ENZYME, NUCLEASE, NUCLEOTIDYLTRANSFERASE, NUCLEUS, TRANSFERASE, VIRAL NUCLEOPROTEIN; HET: PO4, GOL; 2.64A {Maedi visna	51.3	22.5352	11	27	47	63	18



NCBI BLAST

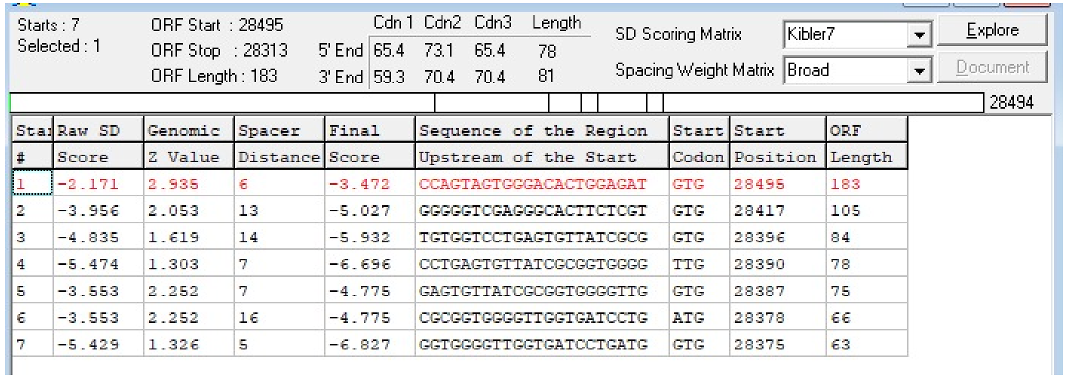
Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
No data available in table															

Coriander_34

Phamerator Start: Gene 34_Start site (29037)
Glimmer Start: Gene 34_Start site (29037)
GeneMark Start: Gene 34_Start site (29037)



Starts : 7
Selected : 1

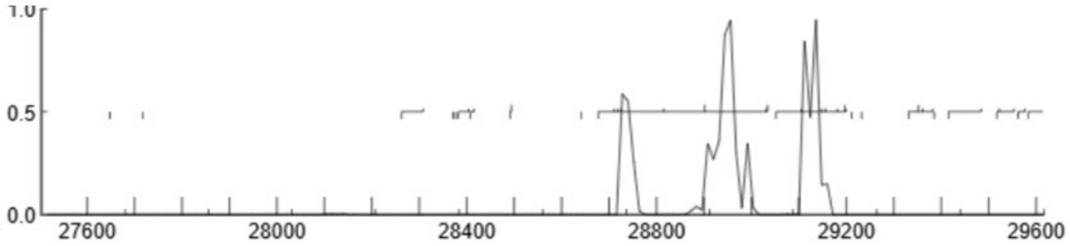
ORF Start : 28495
ORF Stop : 28313
ORF Length : 183

	Cdn 1	Cdn2	Cdn3	Length
5' End	65.4	73.1	65.4	78
3' End	59.3	70.4	70.4	81

SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

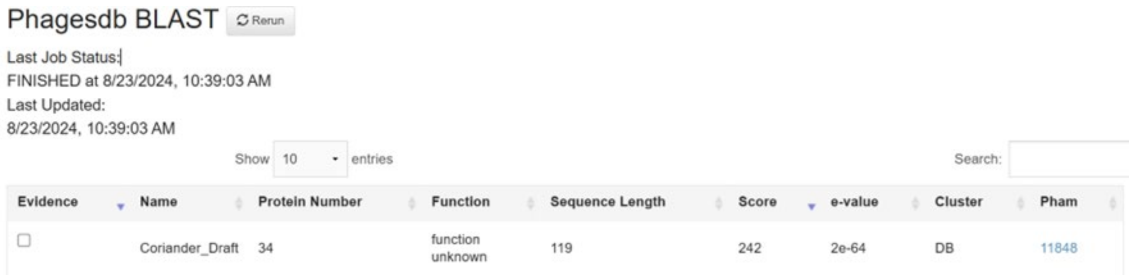
Star #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-2.171	2.935	6	-3.472	CCAGTAGTGGGACACTGGAGAT	GTG	28495	183
2	-3.956	2.053	13	-5.027	GGGGGTCGAGGGCACTTCTCGT	GTG	28417	105
3	-4.835	1.619	14	-5.932	TGTGGTCCTGAGTGTTATCGCG	GTG	28396	84
4	-5.474	1.303	7	-6.696	CCTGAGTGTTATCGCGGTGGGG	TTG	28390	78
5	-3.553	2.252	7	-4.775	GAGTGTTATCGCGGTGGGGTTG	GTG	28387	75
6	-3.553	2.252	16	-4.775	CGCGGTGGGGTTGGTGATCCTG	ATG	28378	66
7	-5.429	1.326	5	-6.827	GGTGGGGTTGGTGATCCTGATG	GTG	28375	63

GeneMark



Gene: Coriander_34 Start: 29037, Stop: 28678, Start Num: 1 Candidate Starts for Coriander_34: (Start: 1 @29037 has 3 MA's), (2, 29034), (5, 28908), (6, 28905), (7, 28830), (8, 28818), (11, 28728),(12, 28722), (13, 28713),

Basic Phage Information	
Phage Name	Coriander_34
Gene #	Gene 34 (PECAAN) GENE 34 (Phamerator)
Stop Coordinate	Stop 28678
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	15
Selected Start Coordinate	Phamerator Start (29037) Glimmer Start (29037) GeneMark Start (29037)
Selected Function	

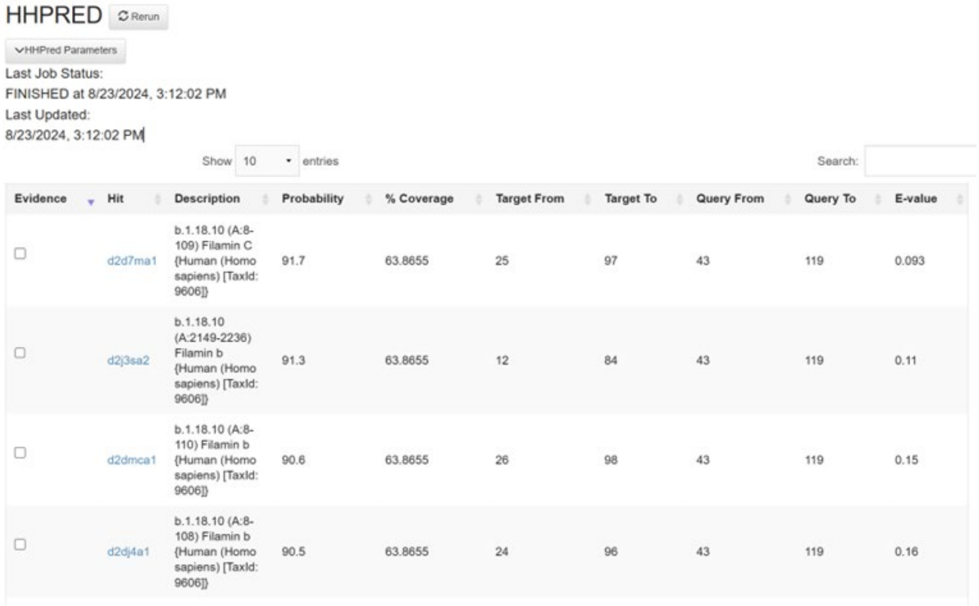


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:03 AM
Last Updated:
8/23/2024, 10:39:03 AM

Show 10 entries

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	34	function unknown	119	242	2e-64	DB	11848

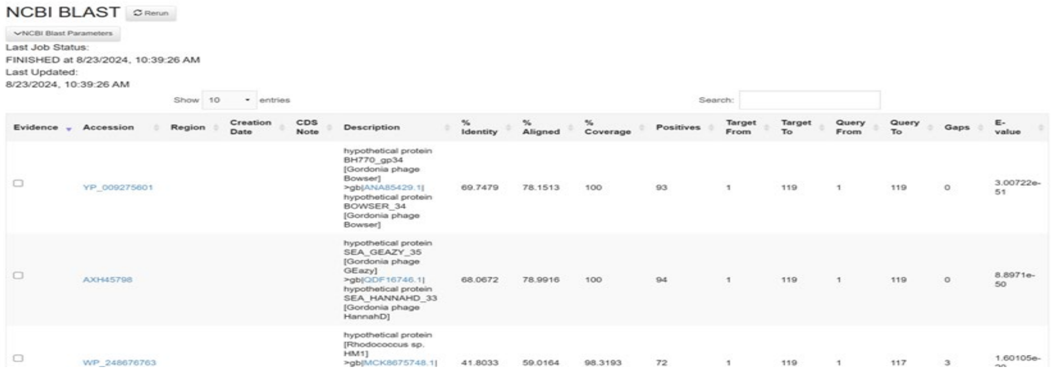


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:12:02 PM
Last Updated:
8/23/2024, 3:12:02 PM

Show 10 entries

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d2d7ma1	b.1.18.10 (A:8-109) Filamin C {Human (Homo sapiens) [TaxId: 9606]}	91.7	63.8655	25	97	43	119	0.093
☐	d2j3sa2	b.1.18.10 (A:2149-2236) Filamin b {Human (Homo sapiens) [TaxId: 9606]}	91.3	63.8655	12	84	43	119	0.11
☐	d2dmca1	b.1.18.10 (A:8-110) Filamin b {Human (Homo sapiens) [TaxId: 9606]}	90.6	63.8655	26	98	43	119	0.15
☐	d2dj4a1	b.1.18.10 (A:8-108) Filamin b {Human (Homo sapiens) [TaxId: 9606]}	90.5	63.8655	24	96	43	119	0.16



NCBI BLAST

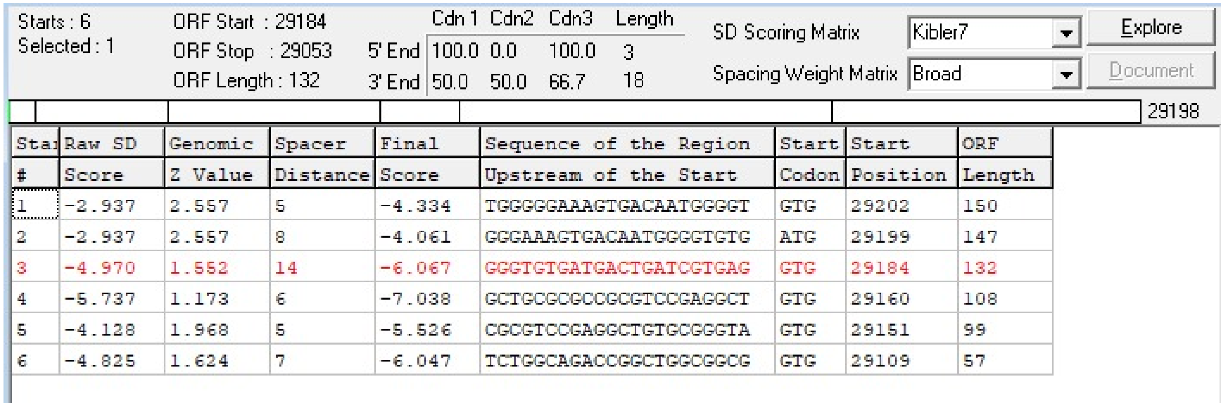
Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Show 10 entries

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_009275601				hypothetical protein BH770_gp34 [Gordonia phage Bowser] >gb|ANA85429.1| hypothetical protein BOWSER_34 [Gordonia phage Bowser]	69.7479	78.1513	100	93	1	119	1	119	0	3.00722e-51
☐	AXH45798				hypothetical protein SEA_GEAZY_35 [Gordonia phage GEazy] >gb|QDF16746.1| hypothetical protein SEA_HANNAHD_33 [Gordonia phage HannahD]	68.0672	78.9916	100	94	1	119	1	119	0	8.8971e-50
☐	WP_248676763				hypothetical protein [Rhodococcus sp. HM1] >gb|MCK8675748.1|	41.8033	59.0164	98.3193	72	1	119	1	117	3	1.60105e-

Coriander_35

Phamerator Start: Gene 35_Start site (29184)
Glimmer Start: Gene 35_Start site (28495)
GeneMark Start: Gene 35_Start site ()



Starts : 6
Selected : 1

ORF Start : 29184
ORF Stop : 29053
ORF Length : 132

	Cdn 1	Cdn2	Cdn3	Length
5' End	100.0	0.0	100.0	3
3' End	50.0	50.0	66.7	18

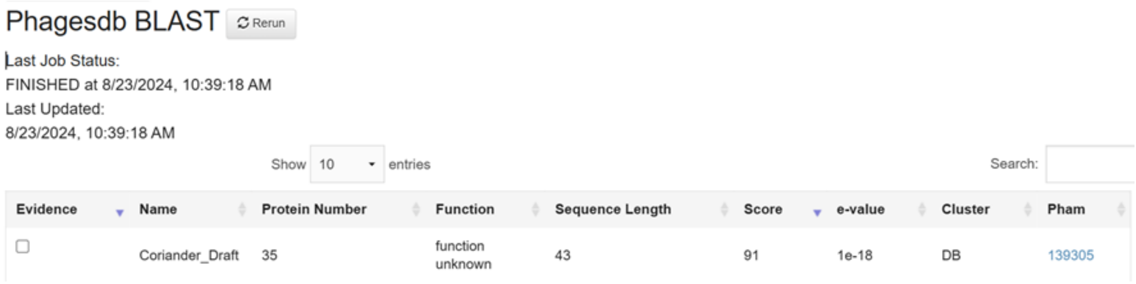
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta: #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-2.937	2.557	5	-4.334	TGGGGGAAAGTGACAATGGGGT	GTG	29202	150
2	-2.937	2.557	8	-4.061	GGGAAAGTGACAATGGGGTGTG	ATG	29199	147
3	-4.970	1.552	14	-6.067	GGGTGTGATGACTGATCGTGAG	GTG	29184	132
4	-5.737	1.173	6	-7.038	GCTGCGCGCCGCGTCCGAGGCT	GTG	29160	108
5	-4.128	1.968	5	-5.526	CGCGTCCGAGGCTGTGCGGGTA	GTG	29151	99
6	-4.825	1.624	7	-6.047	TCTGGCAGACCGGCTGGCGGCG	GTG	29109	57

GeneMark

Gene: Coriander_35 Start: 29184,28495 Stop: 29053, Hypothetical Protein

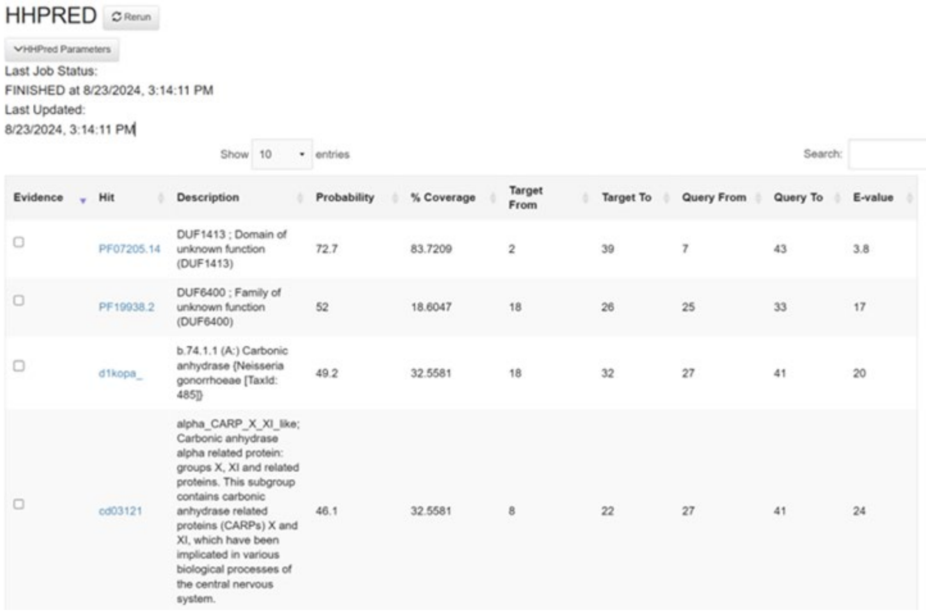
Basic Phage Information	
Phage Name	Coriander_35
Gene #	Gene 35 (PECAAN) GENE 35 (Phamerator)
Stop Coordinate	Stop 29053
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	208
Selected Start Coordinate	Phamerator Start (29184) Glimmer Start (28495) GeneMark Start ()
Selected Function	Hypothetical Protein



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:18 AM
Last Updated:
8/23/2024, 10:39:18 AM

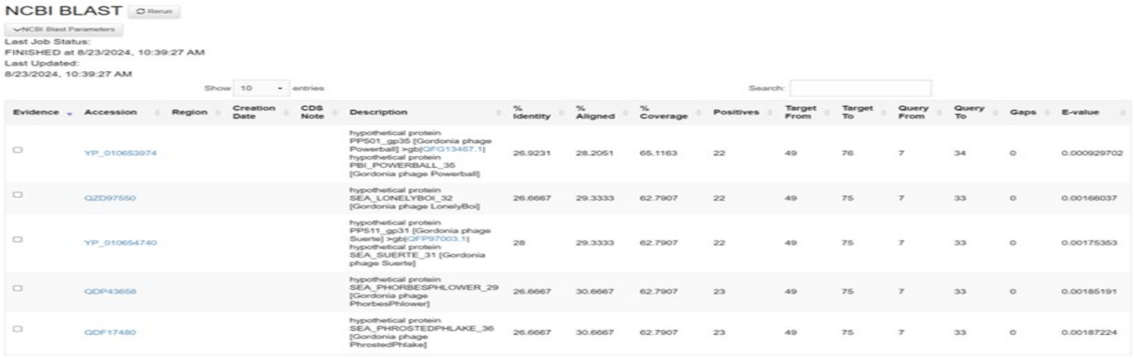
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	35	function unknown	43	91	1e-18	DB	139305



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:14:11 PM
Last Updated:
8/23/2024, 3:14:11 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF07205.14	DUF1413 ; Domain of unknown function (DUF1413)	72.7	83.7209	2	39	7	43	3.8
☐	PF19938.2	DUF6400 ; Family of unknown function (DUF6400)	52	18.6047	18	26	25	33	17
☐	d1kopa_	b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae [TaxId: 485]}	49.2	32.5581	18	32	27	41	20
☐	cd03121	alpha_CARP_X_XI_like; Carbonic anhydrase alpha related protein: groups X, XI and related proteins. This subgroup contains carbonic anhydrase related proteins (CARPs) X and XI, which have been implicated in various biological processes of the central nervous system.	46.1	32.5581	8	22	27	41	24



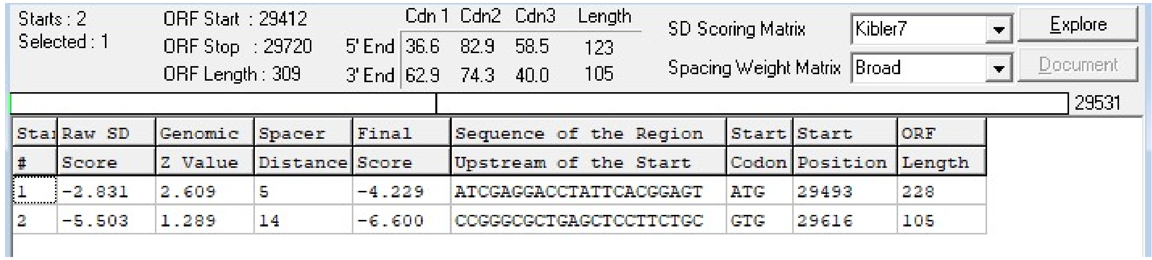
NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:27 AM
Last Updated:
8/23/2024, 10:39:27 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_010653974				hypothetical protein PP501_gp35 [Gordonia phage Powerball] >gb|QFG13467.1| hypothetical protein PBI_POWERBALL_35 [Gordonia phage Powerball]	26.9231	28.2051	65.1163	22	49	76	7	34	0	0.000929702
☐	QZD97550				hypothetical protein SEA_LONELYBOI_32 [Gordonia phage LonelyBoi]	26.6667	29.3333	62.7907	22	49	75	7	33	0	0.00166037
☐	YP_010654740				hypothetical protein PP511_gp31 [Gordonia phage Suerte] >gb|QFP97003.1| hypothetical protein SEA_SUERTE_31 [Gordonia phage Suerte]	28	29.3333	62.7907	22	49	75	7	33	0	0.00175353
☐	QDP43658				hypothetical protein SEA_PHORBESPHLOWER_29 [Gordonia phage PhorbesPhlower]	26.6667	30.6667	62.7907	23	49	75	7	33	0	0.00185191
☐	QDF17480				hypothetical protein SEA_PHROSTEDPHLAKE_36 [Gordonia phage PhrostedPhlake]	26.6667	30.6667	62.7907	23	49	75	7	33	0	0.00187224

Coriander_36

Phamerator Start: Gene 36_Start site (29293)
Glimmer Start: Gene 36_Start site (29393)
GeneMark Start: Gene 36_Start site (29393)



Starts : 2
Selected : 1

ORF Start : 29412
ORF Stop : 29720
ORF Length : 309

	Cdn 1	Cdn2	Cdn3	Length
5' End	36.6	82.9	58.5	123
3' End	62.9	74.3	40.0	105

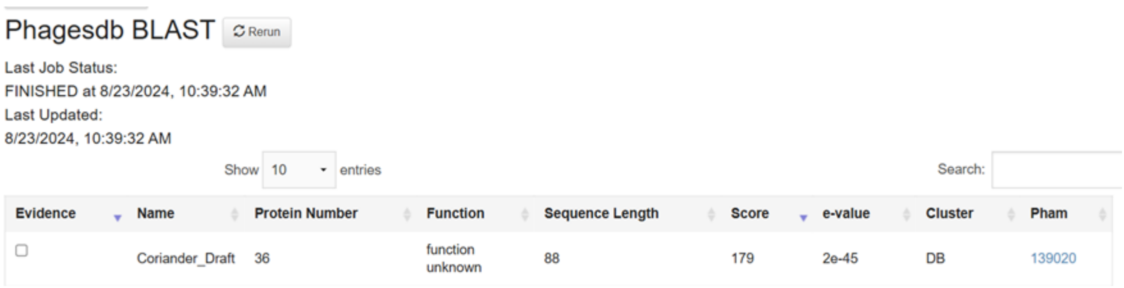
SD Scoring Matrix: Kibler7
Spacing Weight Matrix: Broad

Sta#	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-2.831	2.609	5	-4.229	ATCGAGGACCTATTCACGGAGT	ATG	29493	228
2	-5.503	1.289	14	-6.600	CCGGGCGCTGAGCTCCTTCTGC	GTG	29616	105

GeneMark

Gene: Coriander_36 Start: 29293, Stop: 29659, Hypothetical Protein

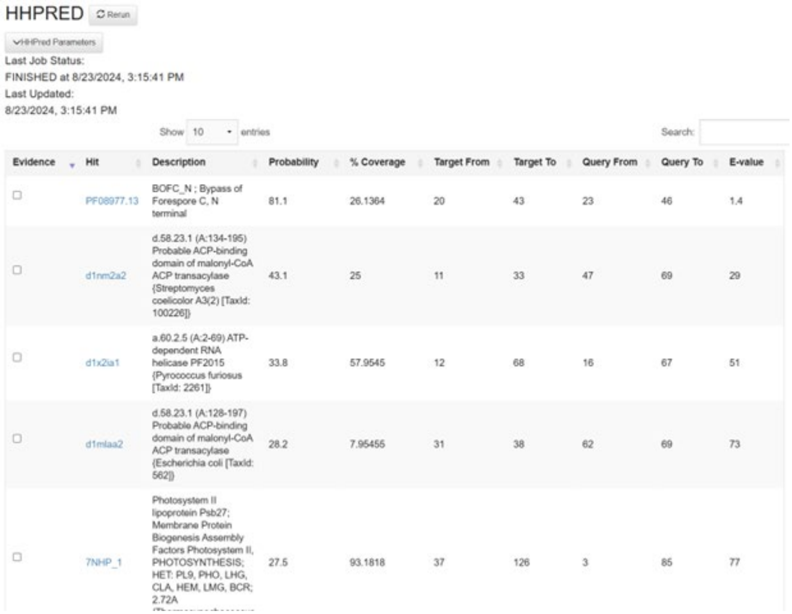
Basic Phage Information	
Phage Name	Coriander_36
Gene #	Gene 36 (PECAAN) GENE 36 (Phamerator)
Stop Coordinate	Stop 29659
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	208
Selected Start Coordinate	Phamerator Start (29393) Glimmer Start (29393) GeneMark Start (29393)
Selected Function	Hypothetical Protein



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:32 AM
Last Updated:
8/23/2024, 10:39:32 AM

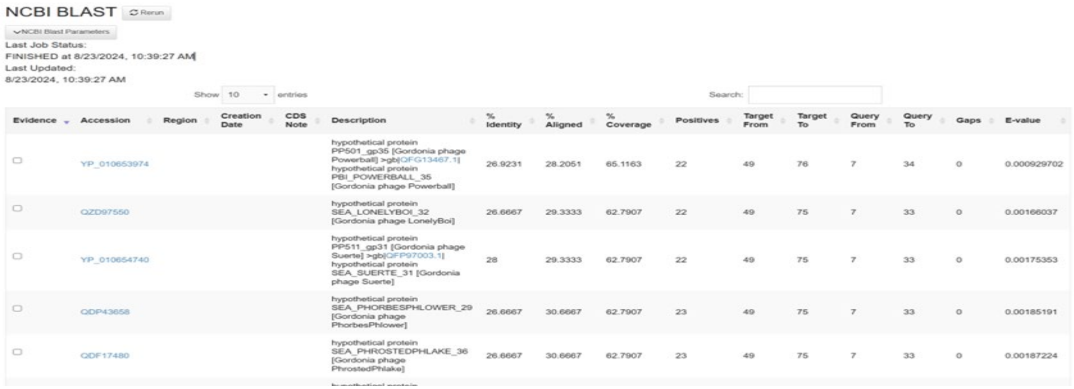
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	36	function unknown	88	179	2e-45	DB	139020



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:15:41 PM
Last Updated:
8/23/2024, 3:15:41 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF08977.13	BOFC_N ; Bypass of Forespore C, N terminal	81.1	26.1364	20	43	23	46	1.4
☐	d1nm2a2	d.58.23.1 (A:134-195) Probable ACP-binding domain of malonyl-CoA ACP transacylase {Streptomyces coelicolor A3(2) [TaxId: 100226]}	43.1	25	11	33	47	69	29
☐	d1x2ia1	a.60.2.5 (A:2-69) ATP-dependent RNA helicase PF2015 {Pyrococcus furiosus [TaxId: 2261]}	33.8	57.9545	12	68	16	67	51
☐	d1mlaa2	d.58.23.1 (A:128-197) Probable ACP-binding domain of malonyl-CoA ACP transacylase {Escherichia coli [TaxId: 562]}	28.2	7.95455	31	38	62	69	73
☐	7NHP_1	Photosystem II lipoprotein Psb27; Membrane Protein Biogenesis Assembly Factors Photosystem II, PHOTOSYNTHESIS; HET: PL9, PHO, LHG, CLA, HEM, LMG, BCR; 2.72A	27.5	93.1818	37	126	3	85	77



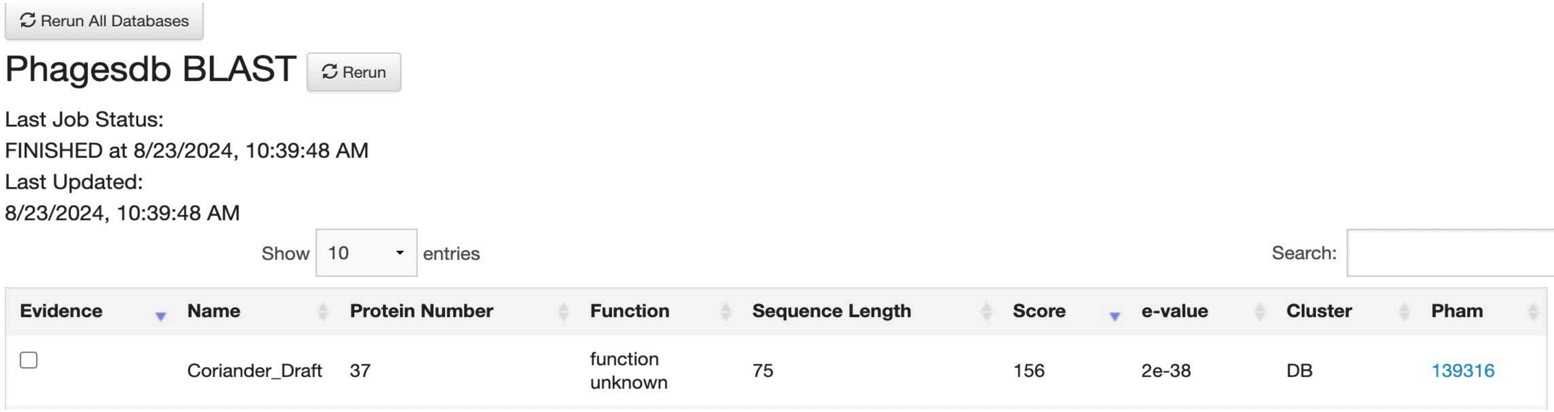
NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:27 AM
Last Updated:
8/23/2024, 10:39:27 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_010653974				hypothetical protein PP501_gp35 [Gordonia phage Powerball] >gb|QFG13467.1| hypothetical protein PBI_POWERBALL_35 [Gordonia phage Powerball]	26.9231	28.2051	65.1163	22	49	76	7	34	0	0.000929702
☐	QZD97550				hypothetical protein SEA_LONELYBOI_32 [Gordonia phage LonelyBoi]	26.6667	29.3333	62.7907	22	49	75	7	33	0	0.00166037
☐	YP_010654740				hypothetical protein PP511_gp31 [Gordonia phage Suerte] >gb|QFP97003.1| hypothetical protein SEA_SUERTE_31 [Gordonia phage Suerte]	28	29.3333	62.7907	22	49	75	7	33	0	0.00175353
☐	QDP43658				hypothetical protein SEA_PHORBESPHLOWER_29 [Gordonia phage PhorbesPhlower]	26.6667	30.6667	62.7907	23	49	75	7	33	0	0.00185191
☐	QDF17480				hypothetical protein SEA_PHROSTEDPHLAKE_36 [Gordonia phage PhrostedPhlake]	26.6667	30.6667	62.7907	23	49	75	7	33	0	0.00187224

37 - 42

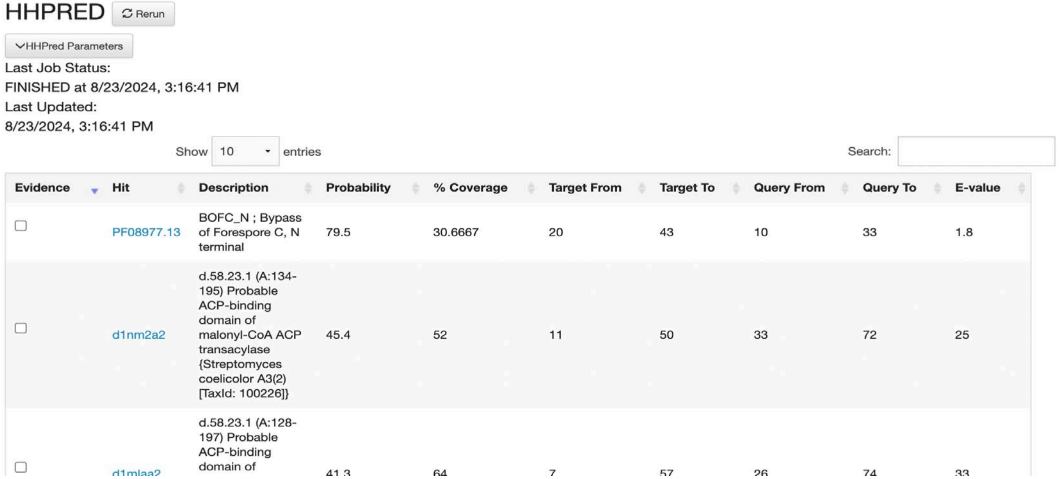
Coriander_37



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:48 AM
Last Updated:
8/23/2024, 10:39:48 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	37	function unknown	75	156	2e-38	DB	139316



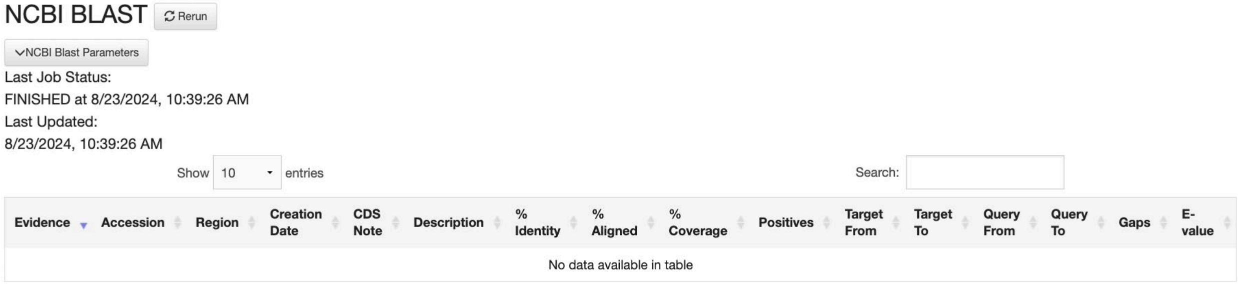
HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:16:41 PM
Last Updated:
8/23/2024, 3:16:41 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF08977.13	BOFC_N ; Bypass of Forespore C, N terminal	79.5	30.6667	20	43	10	33	1.8
☐	d1nm2a2	d.58.23.1 (A:134-195) Probable ACP-binding domain of malonyl-CoA ACP transacylase {Streptomyces coelicolor A3(2) [TaxId: 100226]}	45.4	52	11	50	33	72	25
☐	d1mlaa2	d.58.23.1 (A:128-197) Probable ACP-binding domain of	41.3	64	7	57	26	74	33

Basic Phage Information

Phage Name	Coriander
Gene #	**37**
Stop Coordinate	29,883
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes
Selected Start Coordinate	29,656
Selected Function	

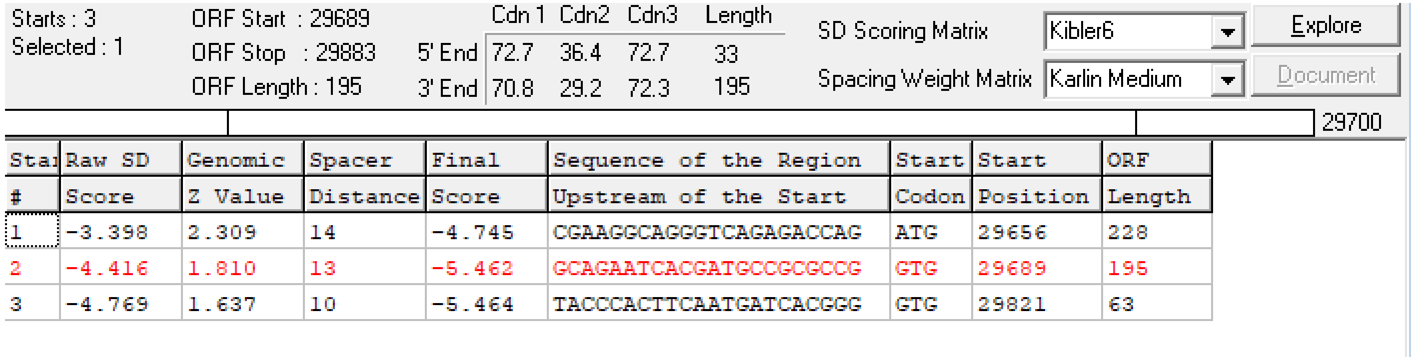


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
No data available in table															

Coriander_37



Starts : 3
Selected : 1

ORF Start : 29689
ORF Stop : 29883
ORF Length : 195

	Cdn 1	Cdn2	Cdn3	Length
5' End	72.7	36.4	72.7	33
3' End	70.8	29.2	72.3	195

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-3.398	2.309	14	-4.745	CGAAGGCAGGGTCAGAGACCAG	ATG	29656	228
2	-4.416	1.810	13	-5.462	GCAGAATCACGATGCCGCGCCG	GTG	29689	195
3	-4.769	1.637	10	-5.464	TACCCACTTCAATGATCACGGG	GTG	29821	63

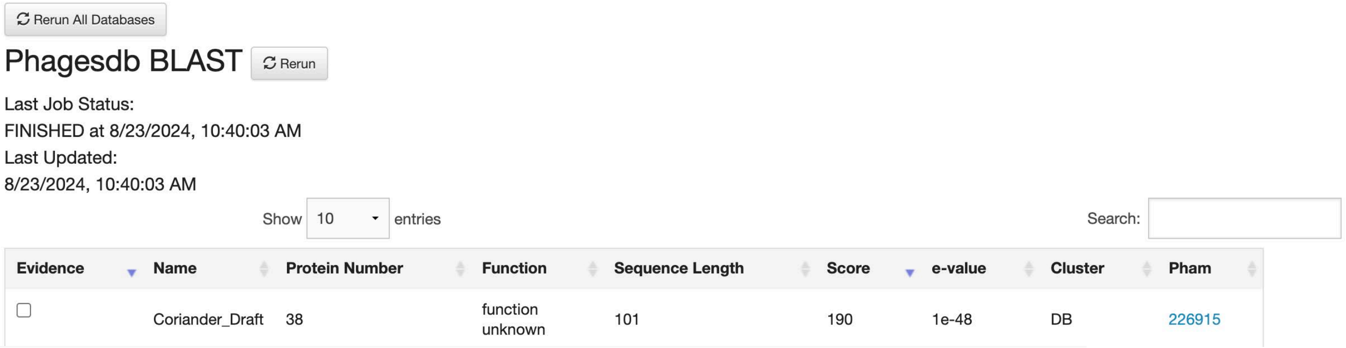
Phamerator Start: Gene 37_Start site (29656)
Glimmer Start: Gene 37_Start site (29656)
GeneMark Start: Gene37_Start site (29656)

GeneMark

Gene: Coriander_37 Start: 29,656, Stop: 29,883

Coriander_38

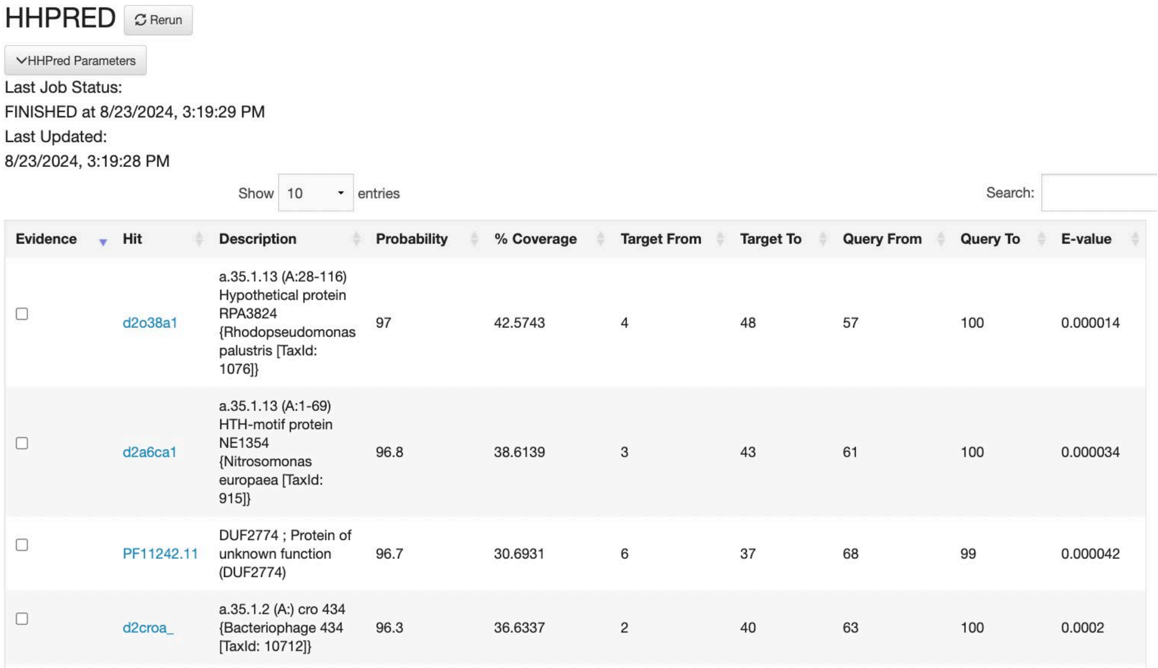
Basic Phage Information	
Phage Name	**Coriander**
Gene #	**38**
Stop Coordinate	29,997
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	Yes
Selected Start Coordinate	30,302
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:40:03 AM
Last Updated:
8/23/2024, 10:40:03 AM

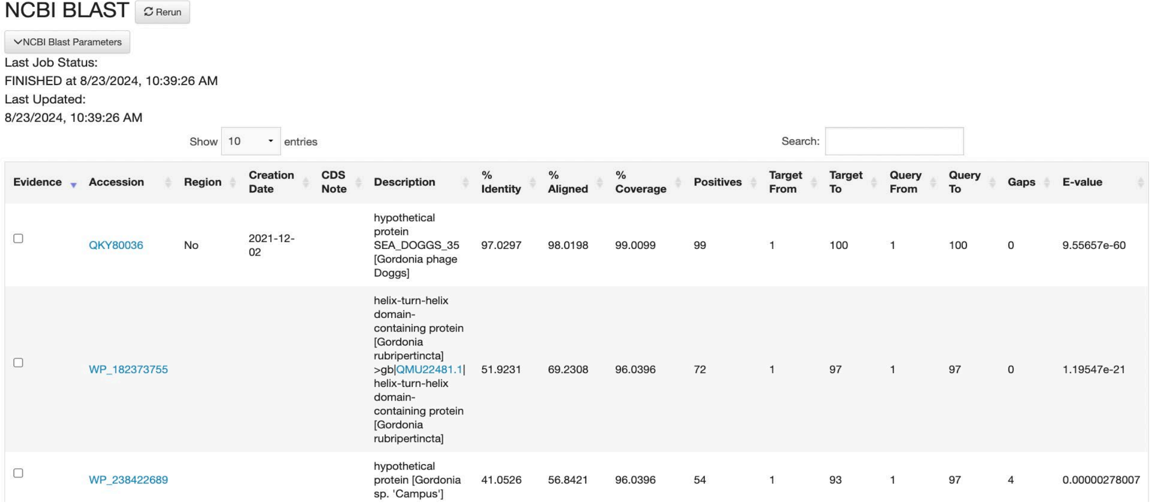
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	38	function unknown	101	190	1e-48	DB	226915



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:19:29 PM
Last Updated:
8/23/2024, 3:19:28 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d2o38a1	a.35.1.13 (A:28-116) Hypothetical protein RPA3824 {Rhodopseudomonas palustris [TaxId: 1076]}	97	42.5743	4	48	57	100	0.000014
☐	d2a6ca1	a.35.1.13 (A:1-69) HTH-motif protein NE1354 {Nitrosomonas europaea [TaxId: 915]}	96.8	38.6139	3	43	61	100	0.000034
☐	PF11242.11	DUF2774 ; Protein of unknown function (DUF2774)	96.7	30.6931	6	37	68	99	0.000042
☐	d2croa_	a.35.1.2 (A:) cro 434 {Bacteriophage 434 [TaxId: 10712]}	96.3	36.6337	2	40	63	100	0.0002

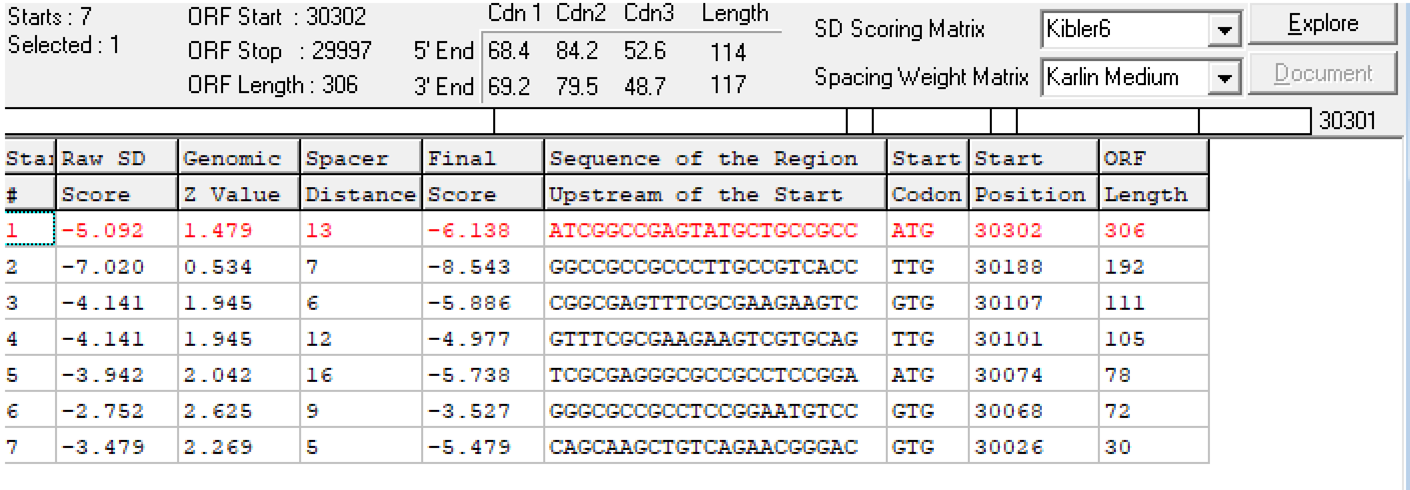


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80036	No	2021-12-02		hypothetical protein SEA_DOGGS_35 [Gordonia phage Doggs]	97.0297	98.0198	99.0099	99	1	100	1	100	0	9.55657e-60
☐	WP_182373755				helix-turn-helix domain-containing protein [Gordonia rubripertincta] >gb|QMU22481.1| helix-turn-helix domain-containing protein [Gordonia rubripertincta]	51.9231	69.2308	96.0396	72	1	97	1	97	0	1.19547e-21
☐	WP_238422689				hypothetical protein [Gordonia sp. 'Campus']	41.0526	56.8421	96.0396	54	1	93	1	97	4	0.00000278007

Coriander_38



Starts : 7
Selected : 1

ORF Start : 30302
ORF Stop : 29997
ORF Length : 306

	Cdn 1	Cdn2	Cdn3	Length
5' End	68.4	84.2	52.6	114
3' End	69.2	79.5	48.7	117

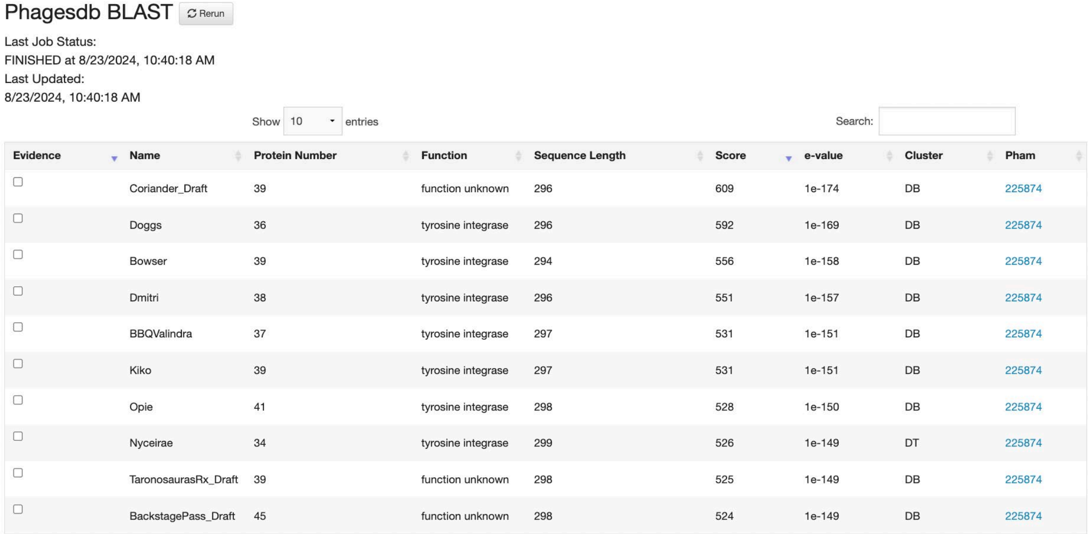
SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

Star #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.092	1.479	13	-6.138	ATCGGCCGAGTATGCTGCCGCC	ATG	30302	306
2	-7.020	0.534	7	-8.543	GGCCGCCGCCCTTGCCGTCACC	TTG	30188	192
3	-4.141	1.945	6	-5.886	CGGCGAGTTTCGCGAAGAAGTC	GTG	30107	111
4	-4.141	1.945	12	-4.977	GTTTCGCGAAGAAGTCGTGCAG	TTG	30101	105
5	-3.942	2.042	16	-5.738	TCGCGAGGGCGCCGCCTCCGGA	ATG	30074	78
6	-2.752	2.625	9	-3.527	GGGCGCCGCCTCCGGAATGTCC	GTG	30068	72
7	-3.479	2.269	5	-5.479	CAGCAAGCTGTCAGAACGGGAC	GTG	30026	30

Phamerator Start: Gene 38_Start site (30302)
Glimmer Start: Gene 38_Start site (30302)
GeneMark Start: Gene 38_Start site (30302)

Gene: Coriander_38 Start: 30302, Stop: 29997, Start Num: 1 Candidate Starts for Coriander_38: (Start: 1 @30302 has 1 MA's), (2, 30188), (3, 30107), (4, 30101), (5, 30074), (6, 30068), (7, 30026)

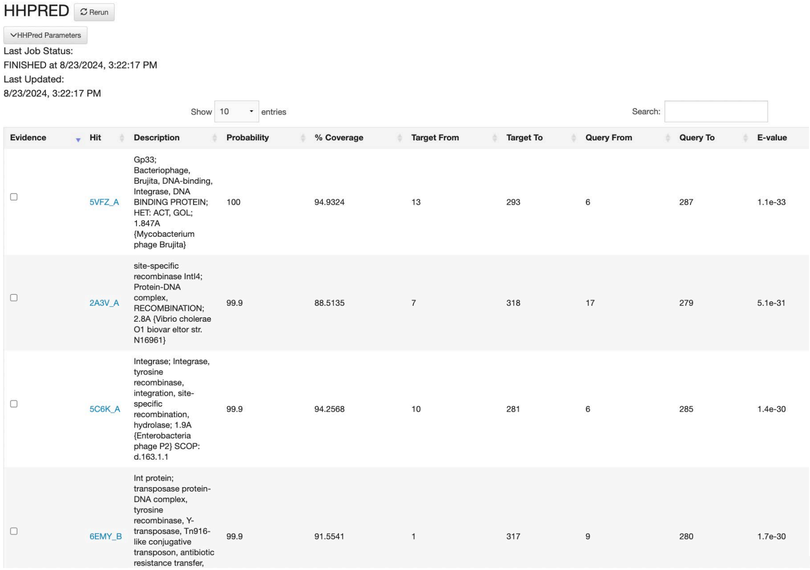
Coriander_39



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:40:18 AM
Last Updated:
8/23/2024, 10:40:18 AM

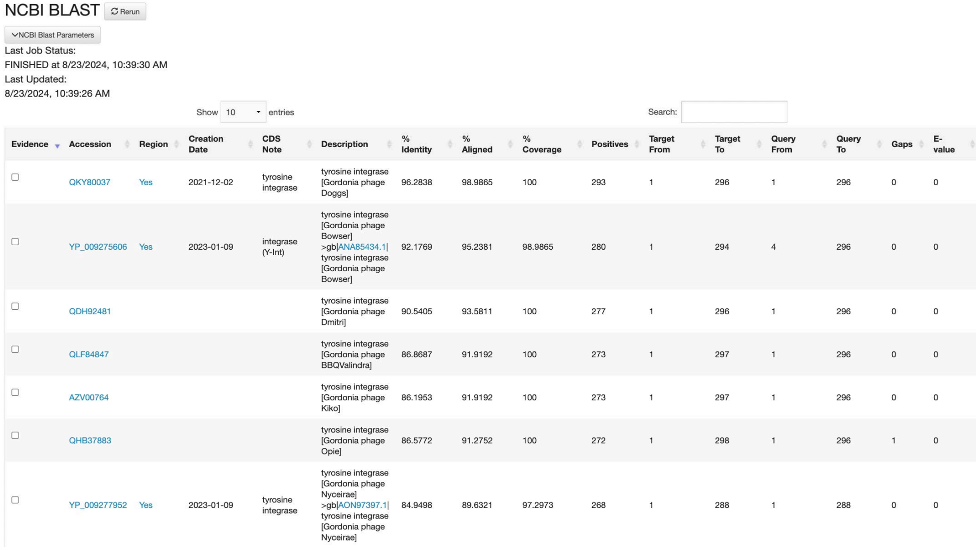
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	39	function unknown	296	609	1e-174	DB	225874
☐	Doggs	36	tyrosine integrase	296	592	1e-169	DB	225874
☐	Bowser	39	tyrosine integrase	294	556	1e-158	DB	225874
☐	Dmitri	38	tyrosine integrase	296	551	1e-157	DB	225874
☐	BBQValindra	37	tyrosine integrase	297	531	1e-151	DB	225874
☐	Kiko	39	tyrosine integrase	297	531	1e-151	DB	225874
☐	Opie	41	tyrosine integrase	298	528	1e-150	DB	225874
☐	Nyceirae	34	tyrosine integrase	299	526	1e-149	DT	225874
☐	TaronosaurasRx_Draft	39	function unknown	298	525	1e-149	DB	225874
☐	BackstagePass_Draft	45	function unknown	298	524	1e-149	DB	225874



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:22:17 PM
Last Updated:
8/23/2024, 3:22:17 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	5VFZ_A	Gp33; Bacteriophage, Brujita, DNA-binding, Integrase, DNA BINDING PROTEIN; HET: ACT, GOL; 1.847A {Mycobacterium phage Brujita}	100	94.9324	13	293	6	287	1.1e-33
☐	2A3V_A	site-specific recombinase IntI4; Protein-DNA complex, RECOMBINATION; 2.8A {Vibrio cholerae O1 biovar eltor str. N16961}	99.9	88.5135	7	318	17	279	5.1e-31
☐	5C6K_A	Integrase; Integrase, tyrosine recombinase, integration, site-specific recombination, hydrolase; 1.9A {Enterobacteria phage P2} SCOP: d.163.1.1	99.9	94.2568	10	281	6	285	1.4e-30
☐	6EMY_B	Int protein; transposase protein-DNA complex, tyrosine recombinase, Y-transposase, Tn916-like conjugative transposon, antibiotic resistance transfer,	99.9	91.5541	1	317	9	280	1.7e-30



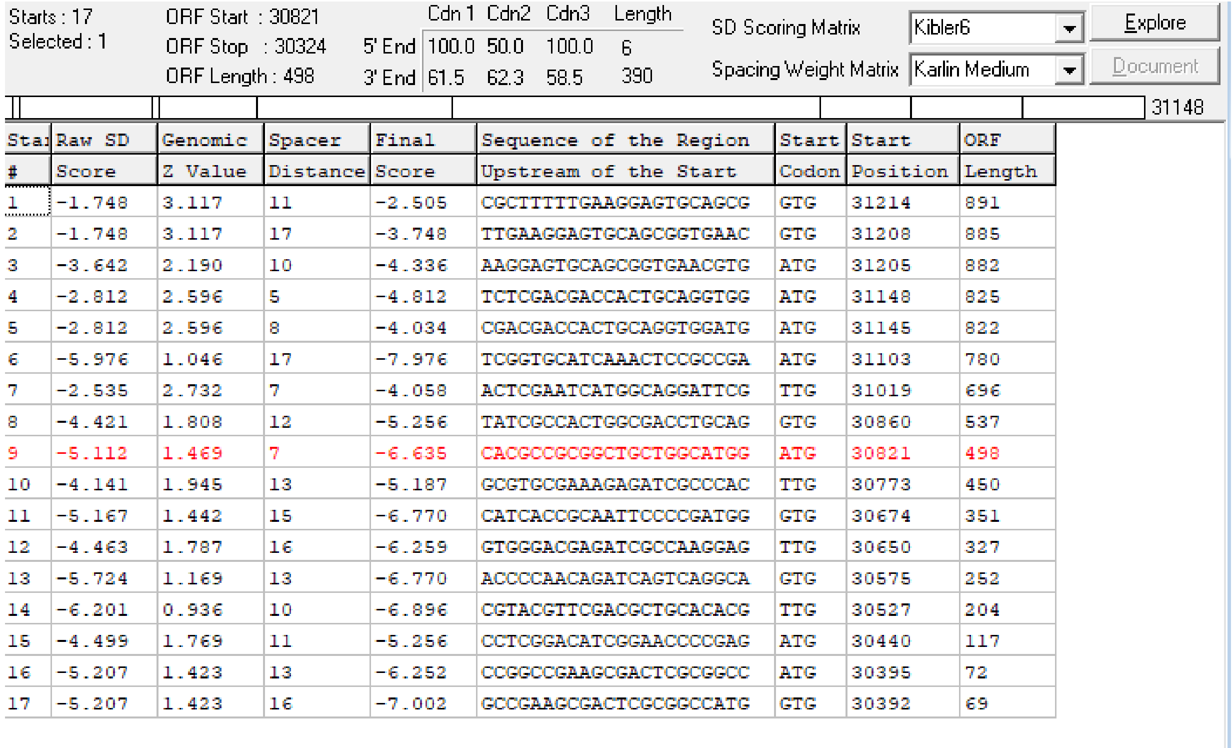
NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:30 AM
Last Updated:
8/23/2024, 10:39:26 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80037	Yes	2021-12-02	tyrosine integrase	tyrosine integrase [Gordonia phage Doggs]	96.2838	98.9865	100	293	1	296	1	296	0	0
☐	YP_009275606	Yes	2023-01-09	integrase (Y-Int)	tyrosine integrase [Gordonia phage Bowser] >gb|ANA85434.1| tyrosine integrase [Gordonia phage Bowser]	92.1769	95.2381	98.9865	280	1	294	4	296	0	0
☐	QDH92481				tyrosine integrase [Gordonia phage Dmitri]	90.5405	93.5811	100	277	1	296	1	296	0	0
☐	QLF84847				tyrosine integrase [Gordonia phage BBQValindra]	86.8687	91.9192	100	273	1	297	1	296	0	0
☐	AZV00764				tyrosine integrase [Gordonia phage Kiko]	86.1953	91.9192	100	273	1	297	1	296	0	0
☐	QHB37883				tyrosine integrase [Gordonia phage Opie]	86.5772	91.2752	100	272	1	298	1	296	1	0
☐	YP_009277952	Yes	2023-01-09	tyrosine integrase	tyrosine integrase [Gordonia phage Nyceirae] >gb|AON97397.1| tyrosine integrase [Gordonia phage Nyceirae]	84.9498	89.6321	97.2973	268	1	288	1	288	0	0

Basic Phage Information	
Phage Name	Coriander
Gene #	**39**
Stop Coordinate	30,324
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	No
Selected Start Coordinate	**31,214**
Selected Function	

Coriander_39



Starts : 17
Selected : 1

ORF Start : 30821
ORF Stop : 30324
ORF Length : 498

	Cdn 1	Cdn2	Cdn3	Length
5' End	100.0	50.0	100.0	6
3' End	61.5	62.3	58.5	390

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

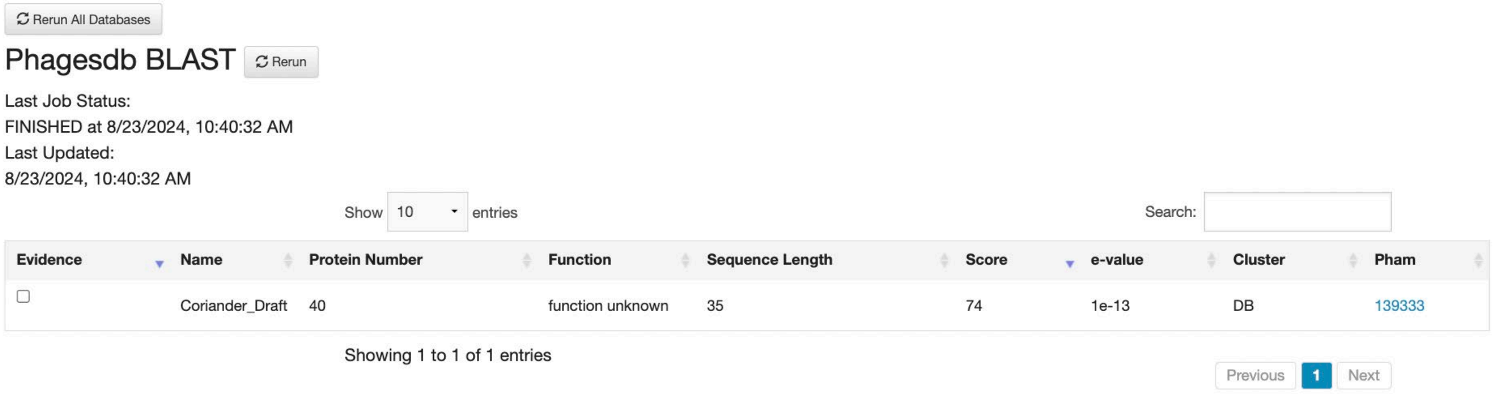
31148

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-1.748	3.117	11	-2.505	CGCTTTTTGAAGGAGTGCAGCG	GTG	31214	891
2	-1.748	3.117	17	-3.748	TTGAAGGAGTGCAGCGGTGAAC	GTG	31208	885
3	-3.642	2.190	10	-4.336	AAGGAGTGCAGCGGTGAACGTG	ATG	31205	882
4	-2.812	2.596	5	-4.812	TCTCGACGACCACTGCAGGTGG	ATG	31148	825
5	-2.812	2.596	8	-4.034	CGACGACCACTGCAGGTGGATG	ATG	31145	822
6	-5.976	1.046	17	-7.976	TCGGTGCATCAAACTCCGCCGA	ATG	31103	780
7	-2.535	2.732	7	-4.058	ACTCGAATCATGGCAGGATTCG	TTG	31019	696
8	-4.421	1.808	12	-5.256	TATCGCCACTGGCGACCTGCAG	GTG	30860	537
9	-5.112	1.469	7	-6.635	CACGCCGCGGCTGCTGGCATGG	ATG	30821	498
10	-4.141	1.945	13	-5.187	GCGTGCGAAAGAGATCGCCCAC	TTG	30773	450
11	-5.167	1.442	15	-6.770	CATCACCGCAATTCCCCGATGG	GTG	30674	351
12	-4.463	1.787	16	-6.259	GTGGGACGAGATCGCCAAGGAG	TTG	30650	327
13	-5.724	1.169	13	-6.770	ACCCCAACAGATCAGTCAGGCA	GTG	30575	252
14	-6.201	0.936	10	-6.896	CGTACGTTCGACGCTGCACACG	TTG	30527	204
15	-4.499	1.769	11	-5.256	CCTCGGACATCGGAACCCCGAG	ATG	30440	117
16	-5.207	1.423	13	-6.252	CCGGCCGAAGCGACTCGCGGCC	ATG	30395	72
17	-5.207	1.423	16	-7.002	GCCGAAGCGACTCGCGGCCATG	GTG	30392	69

Phamerator Start: Gene 39_Start site (31214)
Glimmer Start: Gene 39_Start site (31214)
GeneMark Start: Gene 39_Start site (31214)

GeneMark
Gene: Coriander_39 Start: 31214, Stop: 30324, Start Num: 56 Candidate Starts for Coriander_39: (Start: 56 @31214 has 11 MA's), (Start: 60 @31208 has 5 MA's), (Start: 63 @31205 has 9 MA's), (94, 31148), (96, 31145), (105, 31103), (129, 31019), (174, 30860), (187, 30821), (197, 30773), (217, 30674), (221, 30650), (236, 30575), (248, 30527), (263, 30440), (268, 30395), (269, 30392),

Coriander_40

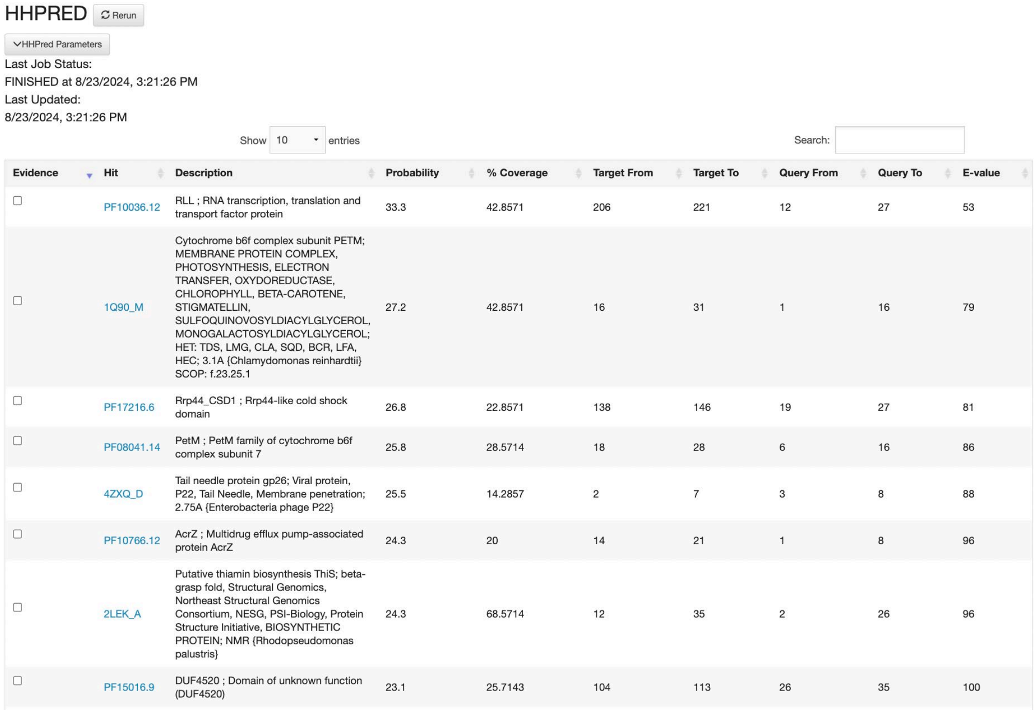


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:40:32 AM
Last Updated:
8/23/2024, 10:40:32 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	40	function unknown	35	74	1e-13	DB	139333

Showing 1 to 1 of 1 entries

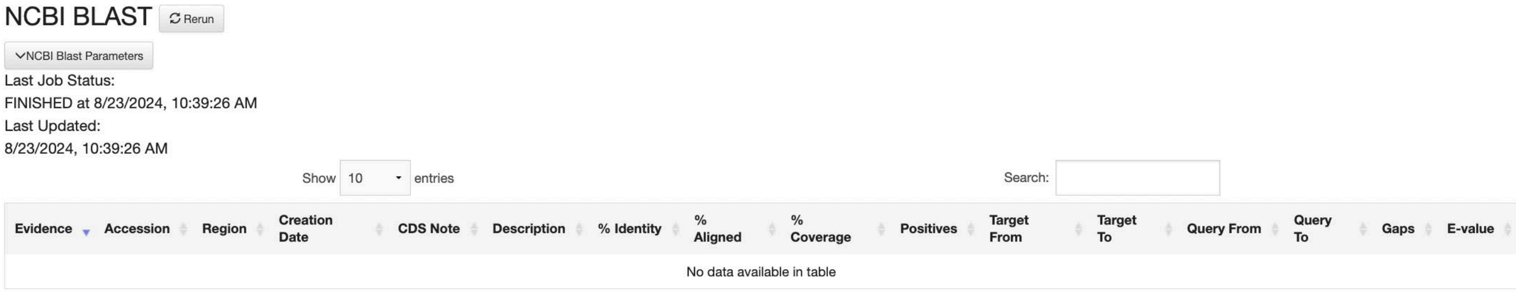


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:21:26 PM
Last Updated:
8/23/2024, 3:21:26 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF10036.12	RLL ; RNA transcription, translation and transport factor protein	33.3	42.8571	206	221	12	27	53
☐	1Q90_M	Cytochrome b6f complex subunit PETM; MEMBRANE PROTEIN COMPLEX, PHOTOSYNTHESIS, ELECTRON TRANSFER, OXYDOREDUCTASE, CHLOROPHYLL, BETA-CAROTENE, STIGMATELLIN, SULFOQUINOVOSYLDIACYLGLYCEROL, MONOGALACTOSYLDIACYLGLYCEROL; HET: TDS, LMG, CLA, SQD, BCR, LFA, HEC; 3.1A {Chlamydomonas reinhardtii} SCOP: f.23.25.1	27.2	42.8571	16	31	1	16	79
☐	PF17216.6	Rrp44_CSD1 ; Rrp44-like cold shock domain	26.8	22.8571	138	146	19	27	81
☐	PF08041.14	PetM ; PetM family of cytochrome b6f complex subunit 7	25.8	28.5714	18	28	6	16	86
☐	4ZXQ_D	Tail needle protein gp26; Viral protein, P22, Tail Needle, Membrane penetration; 2.75A {Enterobacteria phage P22}	25.5	14.2857	2	7	3	8	88
☐	PF10766.12	AcrZ ; Multidrug efflux pump-associated protein AcrZ	24.3	20	14	21	1	8	96
☐	2LEK_A	Putative thiamin biosynthesis ThiS; beta-grasp fold, Structural Genomics, Northeast Structural Genomics Consortium, NESG, PSI-Biology, Protein Structure Initiative, BIOSYNTHETIC PROTEIN; NMR {Rhodopseudomonas palustris}	24.3	68.5714	12	35	2	26	96
☐	PF15016.9	DUF4520 ; Domain of unknown function (DUF4520)	23.1	25.7143	104	113	26	35	100

Basic Phage Information	
Phage Name	Coriander
Gene #	40
Stop Coordinate	31,470
Direction (For/Rev)	Reverse
Gap (Overlap) with Previous Gene	No
Selected Start Coordinate	31,577
Selected Function	

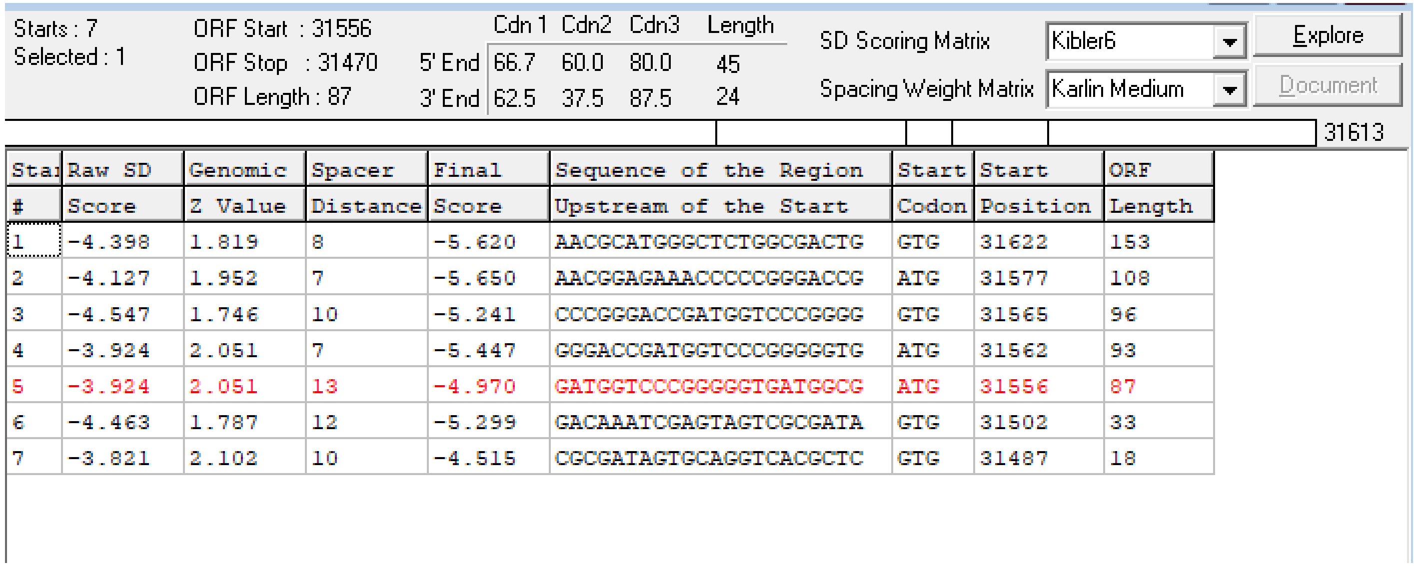


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:39:26 AM
Last Updated:
8/23/2024, 10:39:26 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
No data available in table															

Coriander_40



Starts : 7
Selected : 1

ORF Start : 31556
ORF Stop : 31470
ORF Length : 87

	Cdn 1	Cdn2	Cdn3	Length
5' End	66.7	60.0	80.0	45
3' End	62.5	37.5	87.5	24

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

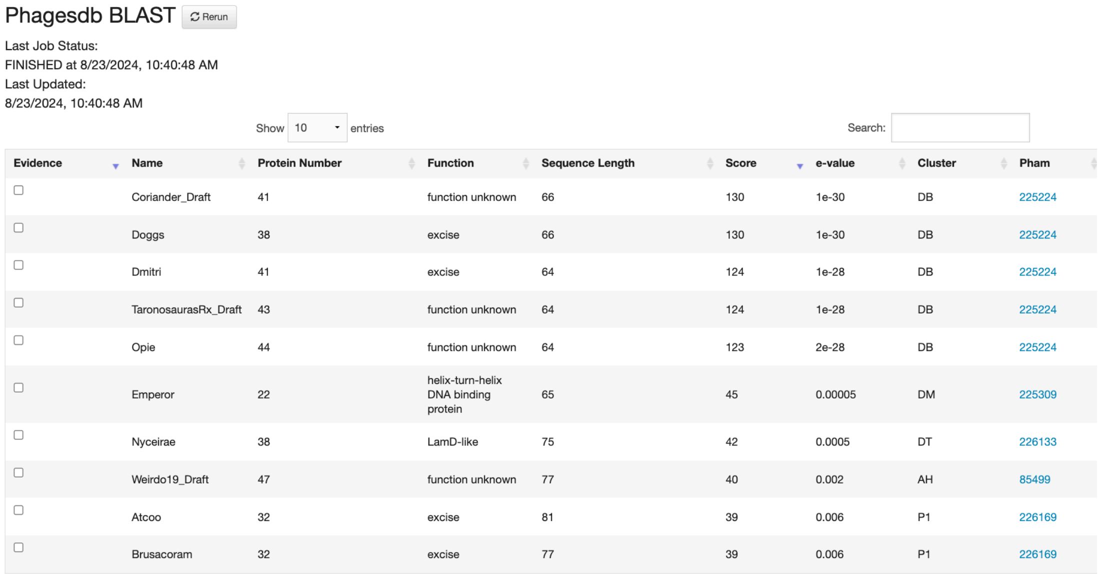
Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-4.398	1.819	8	-5.620	AACGCATGGGCTCTGGCGACTG	GTG	31622	153
2	-4.127	1.952	7	-5.650	AACGGAGAAACCCCCGGGACCG	ATG	31577	108
3	-4.547	1.746	10	-5.241	CCCGGGACCGATGGTCCCGGGG	GTG	31565	96
4	-3.924	2.051	7	-5.447	GGGACCGATGGTCCCGGGGGTG	ATG	31562	93
5	-3.924	2.051	13	-4.970	GATGGTCCCGGGGGTGATGGCG	ATG	31556	87
6	-4.463	1.787	12	-5.299	GACAAATCGAGTAGTCGCGATA	GTG	31502	33
7	-3.821	2.102	10	-4.515	CGCGATAGTGCAGGTCACGCTC	GTG	31487	18

Phamerator Start: Gene 40_Start site (31577)
Glimmer Start: Gene 40_Start site (31577)
GeneMark Start: Gene 40_Start site (31577)

GeneMark
Gene: Coriander_40 Start: 31,577, Stop: 31,470,
Hypothetical Protein

Coriander_41

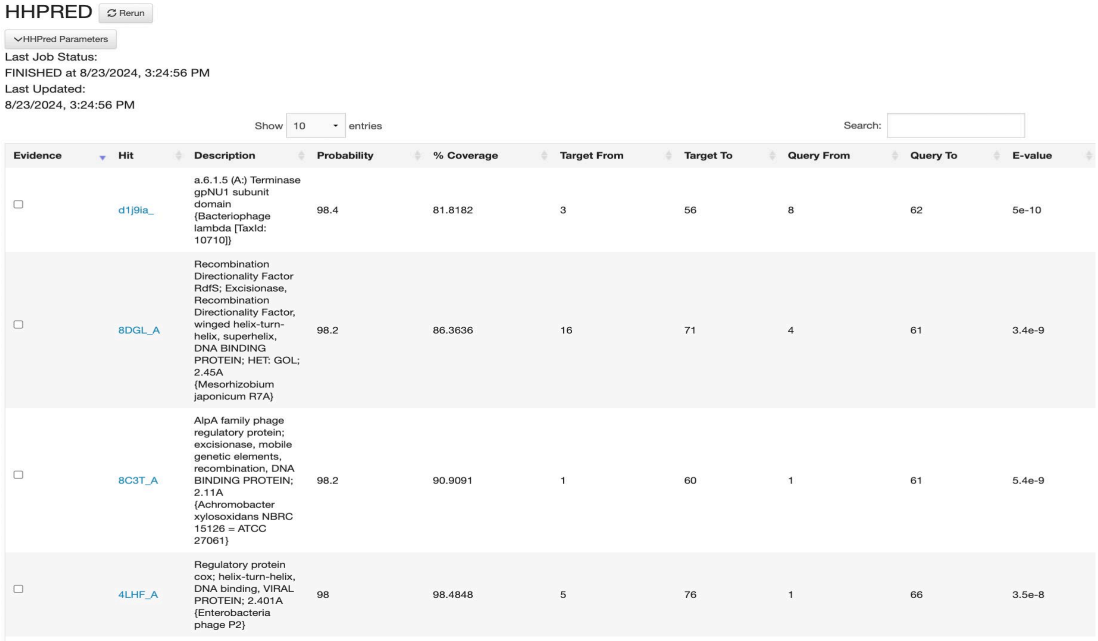
Basic Phage Information	
Phage Name	Coriander
Gene #	41
Stop Coordinate	32,126
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes
Selected Start Coordinate	31,926
Selected Function	Function unknown/Hypothetical protein



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:40:48 AM
Last Updated:
8/23/2024, 10:40:48 AM

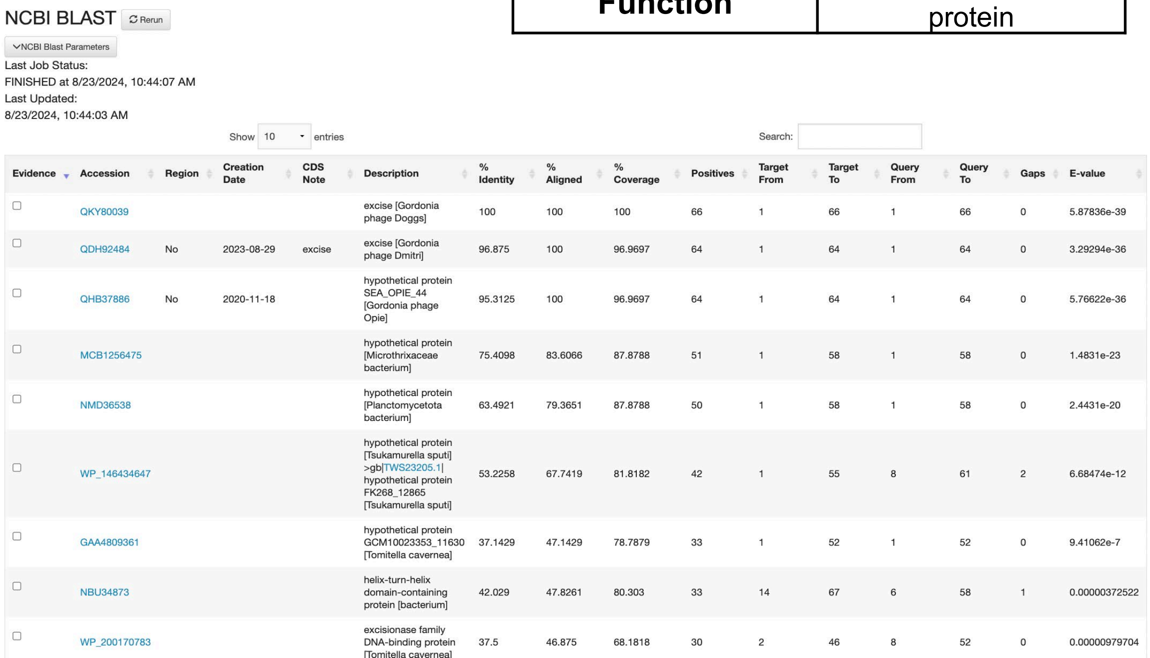
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	41	function unknown	66	130	1e-30	DB	225224
☐	Doggs	38	excise	66	130	1e-30	DB	225224
☐	Dmitri	41	excise	64	124	1e-28	DB	225224
☐	TaronosaurasRx_Draft	43	function unknown	64	124	1e-28	DB	225224
☐	Opie	44	function unknown	64	123	2e-28	DB	225224
☐	Emperor	22	helix-turn-helix DNA binding protein	65	45	0.00005	DM	225309
☐	Nyceirae	38	LamD-like	75	42	0.0005	DT	226133
☐	Weirdo19_Draft	47	function unknown	77	40	0.002	AH	85499
☐	Atcoo	32	excise	81	39	0.006	P1	226169
☐	Brusacoram	32	excise	77	39	0.006	P1	226169



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:24:56 PM
Last Updated:
8/23/2024, 3:24:56 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1j9ia_	a.6.1.5 (A:) Terminase gpNU1 subunit domain {Bacteriophage lambda [TaxId: 10710]}	98.4	81.8182	3	56	8	62	5e-10
☐	8DGL_A	Recombination Directionality Factor RdfS; Excisionase, Recombination Directionality Factor, winged helix-turn-helix, superhelix, DNA BINDING PROTEIN; HET: GOL; 2.45A {Mesorhizobium japonicum R7A}	98.2	86.3636	16	71	4	61	3.4e-9
☐	8C3T_A	AlpA family phage regulatory protein; excisionase, mobile genetic elements, recombination, DNA BINDING PROTEIN; 2.11A {Achromobacter xylosoxidans NBRC 15126 = ATCC 27061}	98.2	90.9091	1	60	1	61	5.4e-9
☐	4LHF_A	Regulatory protein cox; helix-turn-helix, DNA binding, VIRAL PROTEIN; 2.401A {Enterobacteria phage P2}	98	98.4848	5	76	1	66	3.5e-8

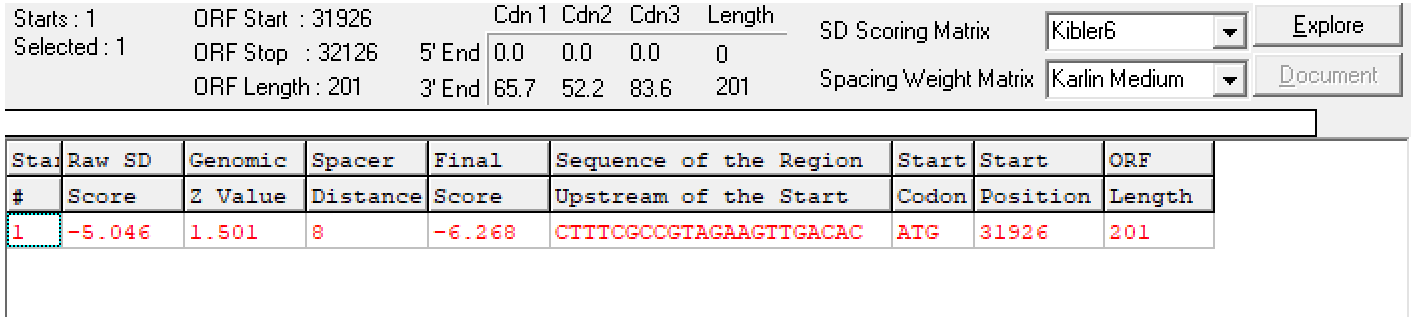


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:07 AM
Last Updated:
8/23/2024, 10:44:03 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80039				excise [Gordonia phage Doggs]	100	100	100	66	1	66	1	66	0	5.87836e-39
☐	QDH92484	No	2023-08-29	excise	excise [Gordonia phage Dmitri]	96.875	100	96.9697	64	1	64	1	64	0	3.29294e-36
☐	QHB37886	No	2020-11-18		hypothetical protein SEA_OPIE_44 [Gordonia phage Opie]	95.3125	100	96.9697	64	1	64	1	64	0	5.76622e-36
☐	MCB1256475				hypothetical protein [Microthrixaceae bacterium]	75.4098	83.6066	87.8788	51	1	58	1	58	0	1.4831e-23
☐	NMD36538				hypothetical protein [Planctomycetota bacterium]	63.4921	79.3651	87.8788	50	1	58	1	58	0	2.4431e-20
☐	WP_146434647				hypothetical protein [Tsukamurella sputi] >gb|TWS23205.1| hypothetical protein FK268_12865 [Tsukamurella sputi]	53.2258	67.7419	81.8182	42	1	55	8	61	2	6.68474e-12
☐	GAA4809361				hypothetical protein GCM10023353_11630 [Tomitella cavernea]	37.1429	47.1429	78.7879	33	1	52	1	52	0	9.41062e-7
☐	NBU34873				helix-turn-helix domain-containing protein [bacterium]	42.029	47.8261	80.303	33	14	67	6	58	1	0.00000372522
☐	WP_200170783				excisionase family DNA-binding protein [Tomitella cavernea]	37.5	46.875	68.1818	30	2	46	8	52	0	0.00000979704

Coriander_41



Starts : 1
Selected : 1

ORF Start : 31926
ORF Stop : 32126
ORF Length : 201

	Cdn 1	Cdn2	Cdn3	Length
5' End	0.0	0.0	0.0	0
3' End	65.7	52.2	83.6	201

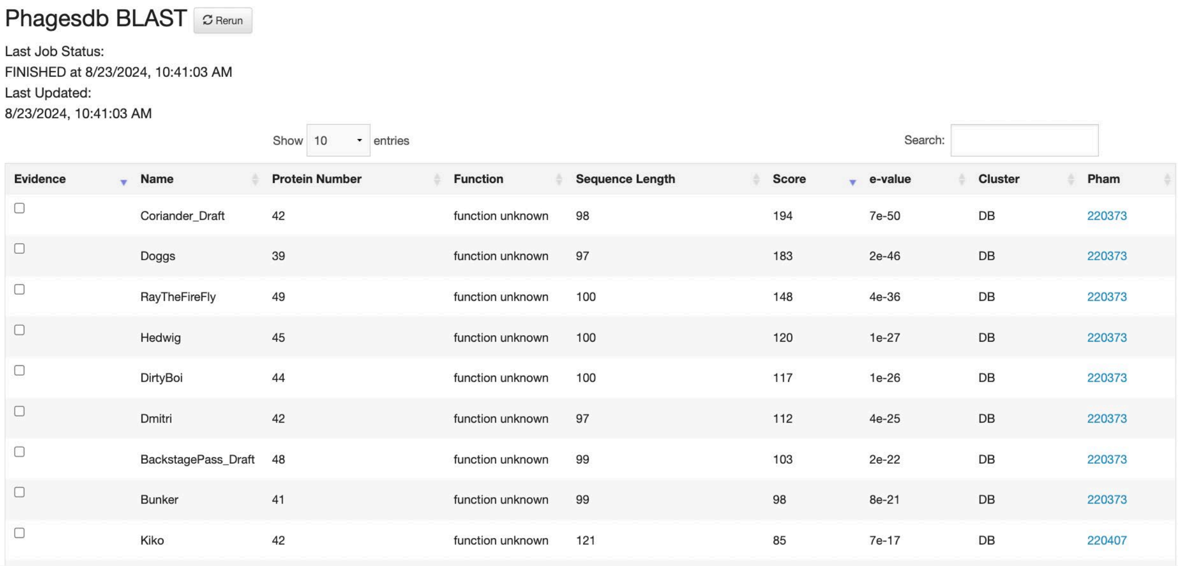
SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.046	1.501	8	-6.268	CTTTCGCCGTAGAAGTTGACAC	ATG	31926	201

Phamerator Start: Gene 40_Start site (31926)
Glimmer Start: Gene 40_Start site (31926)
GeneMark Start: Gene 40_Start site (31926)

GeneMark
Gene: Coriander_41 Start: 31926, Stop: 32126, Start Num: 1
Candidate Starts for Coriander_41: (Start: 1 @31926 has 3 MA's),

Coriander_42



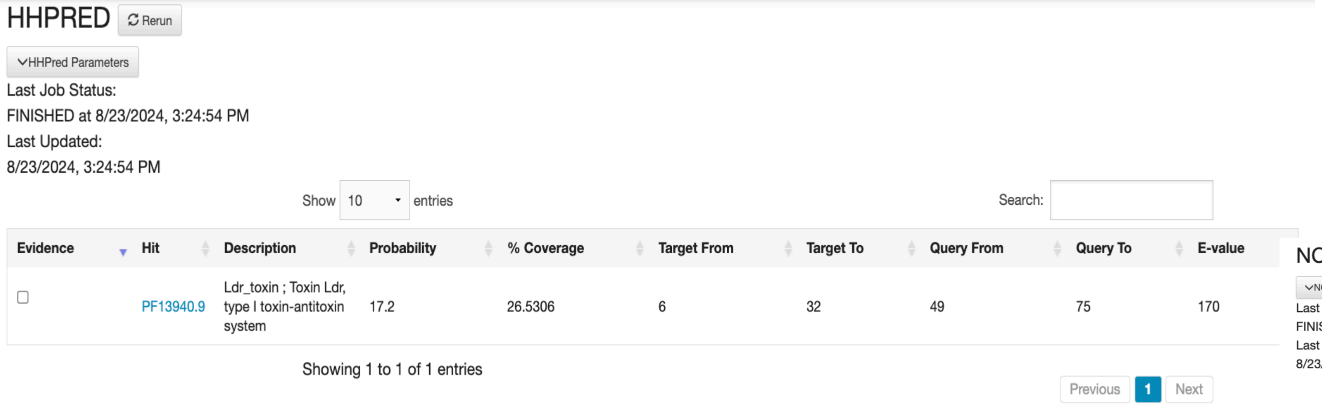
Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:41:03 AM
Last Updated:
8/23/2024, 10:41:03 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	42	function unknown	98	194	7e-50	DB	220373
☐	Doggs	39	function unknown	97	183	2e-46	DB	220373
☐	RayTheFireFly	49	function unknown	100	148	4e-36	DB	220373
☐	Hedwig	45	function unknown	100	120	1e-27	DB	220373
☐	DirtyBoi	44	function unknown	100	117	1e-26	DB	220373
☐	Dmitri	42	function unknown	97	112	4e-25	DB	220373
☐	BackstagePass_Draft	48	function unknown	99	103	2e-22	DB	220373
☐	Bunker	41	function unknown	99	98	8e-21	DB	220373
☐	Kiko	42	function unknown	121	85	7e-17	DB	220407

Basic Phage Information	
Phage Name	Coriander
Gene #	42
Stop Coordinate	32,419
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes
Selected Start Coordinate	32,123
Selected Function	



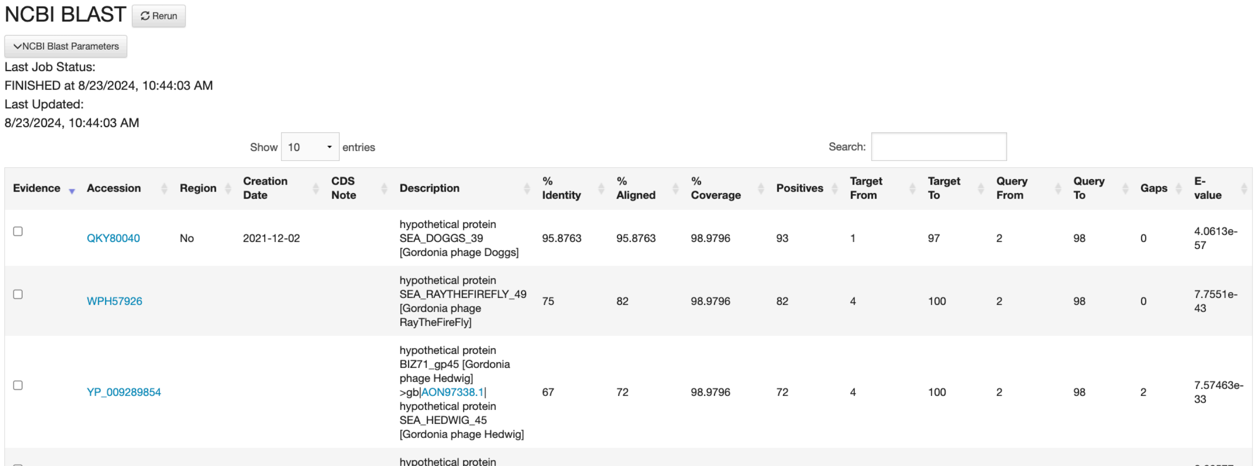
HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:24:54 PM
Last Updated:
8/23/2024, 3:24:54 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF13940.9	Ldr_toxin ; Toxin Ldr, type I toxin-antitoxin system	17.2	26.5306	6	32	49	75	170

Showing 1 to 1 of 1 entries



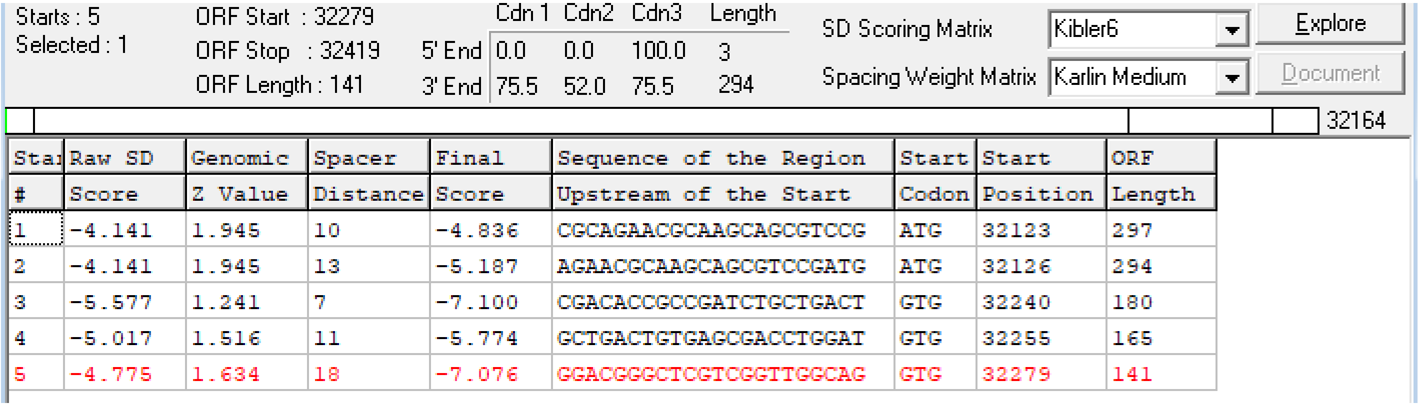
NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:03 AM
Last Updated:
8/23/2024, 10:44:03 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80040	No	2021-12-02		hypothetical protein SEA_DOGGS_39 [Gordonia phage Doggs]	95.8763	95.8763	98.9796	93	1	97	2	98	0	4.0613e-57
☐	WPH57926				hypothetical protein SEA_RAYTHEFIREFLY_49 [Gordonia phage RayTheFireFly]	75	82	98.9796	82	4	100	2	98	0	7.7551e-43
☐	YP_009289854				hypothetical protein BIZ71_gp45 [Gordonia phage Hedwig] >gb|AON97338.1| hypothetical protein SEA_HEDWIG_45 [Gordonia phage Hedwig]	67	72	98.9796	72	4	100	2	98	2	7.57463e-33
					hypothetical protein										

Coriander_42



Starts : 5
Selected : 1

ORF Start : 32279
ORF Stop : 32419
ORF Length : 141

	Cdn 1	Cdn2	Cdn3	Length
5' End	0.0	0.0	100.0	3
3' End	75.5	52.0	75.5	294

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-4.141	1.945	10	-4.836	CGCAGAACGCAAGCAGCGTCCG	ATG	32123	297
2	-4.141	1.945	13	-5.187	AGAACGCAAGCAGCGTCCGATG	ATG	32126	294
3	-5.577	1.241	7	-7.100	CGACACCGCCGATCTGCTGACT	GTG	32240	180
4	-5.017	1.516	11	-5.774	GCTGACTGTGAGCGACCTGGAT	GTG	32255	165
5	-4.775	1.634	18	-7.076	GGACGGGCTCGTCGGTTGGCAG	GTG	32279	141

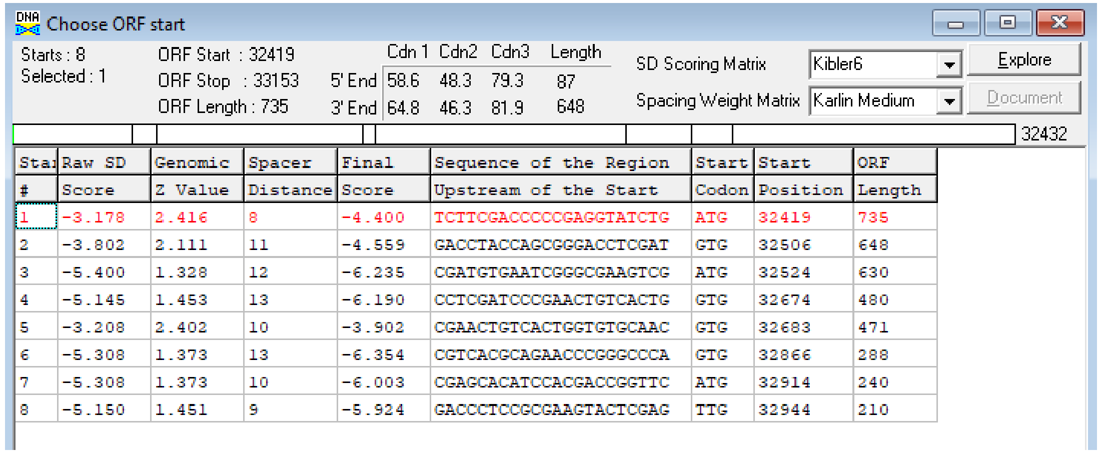
Phamerator Start: Gene 40_Start site (32123)
Glimmer Start: Gene 40_Start site (32123)
GeneMark Start: Gene 40_Start site (32123)

Gene Coriander_42 Start: 32123, Stop: 32419, Start Num: 4
Candidate Starts for Coriander_42: (4, 32123), (Start: 5 @32126 has 2 MA's), (7, 32240), (8, 32255), (9, 32279),

43 - 48

Coriander_Draft

- Phamerator- Gene 43_Start Site 32419
- 735 bp
- Gene Mark



Starts : 8
Selected : 1

ORF Start : 32419
ORF Stop : 33153
ORF Length : 735

	Cdn 1	Cdn2	Cdn3	Length
5' End	58.6	48.3	79.3	87
3' End	64.8	46.3	81.9	648

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

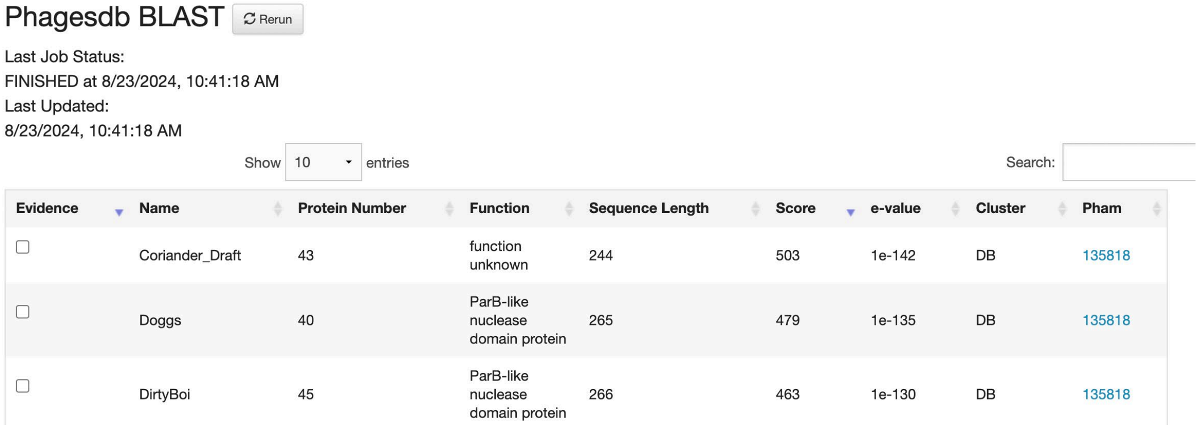
32432

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-3.178	2.416	8	-4.400	TCTTCGACCCCCGAGGTATCTG	ATG	32419	735
2	-3.802	2.111	11	-4.559	GACCTACCAGCGGGACCTCGAT	GTG	32506	648
3	-5.400	1.328	12	-6.235	CGATGTGAATCGGGCGAAGTCG	ATG	32524	630
4	-5.145	1.453	13	-6.190	CCTCGATCCCGAACTGTCACTG	GTG	32674	480
5	-3.208	2.402	10	-3.902	CGAACTGTCACTGGTGTGCAAC	GTG	32683	471
6	-5.308	1.373	13	-6.354	CGTCACGCAGAACCCGGGCCCA	GTG	32866	288
7	-5.308	1.373	10	-6.003	CGAGCACATCCACGACCGGTTC	ATG	32914	240
8	-5.150	1.451	9	-5.924	GACCCTCCGCGAAGTACTCGAG	TTG	32944	210

- Gene: Coriander_43 Start: 32419, Stop: 33153, Start Num: 6 Candidate Starts for Coriander_43: (Start: 6 @32419 has 6 MA's), (13, 32506), (14, 32524), (23, 32674), (24, 32683), (36, 32866), (40, 32914), (44, 32944),

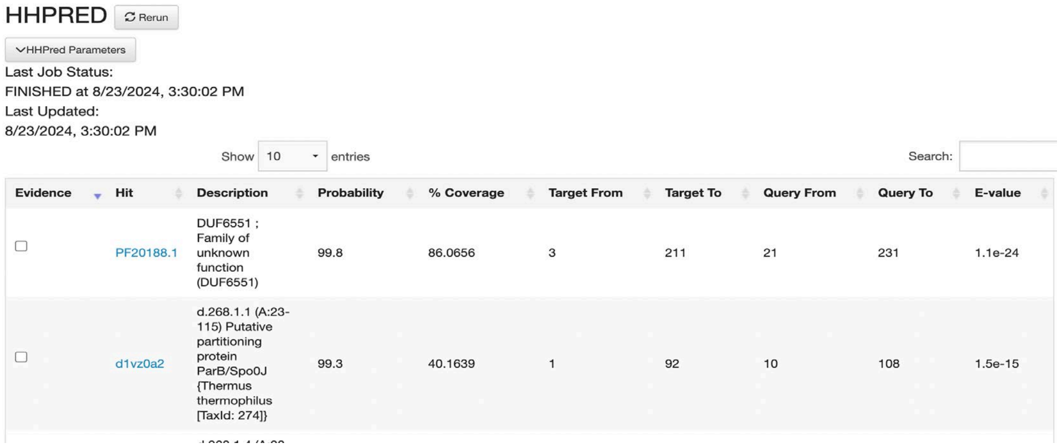
VK

Basic Phage Information	
Phage Name	Coriander
Gene #	43
Stop Coordinate	33153
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	N/A
Gene present in other annotated genomes?	
Is this start site conserved in other phage genomes as indicated by Starterator?	DGQHR_domain
Selected Start Coordinate	32419
Selected Function	ParB-like nuclease domain protein


Phagesdb BLAST

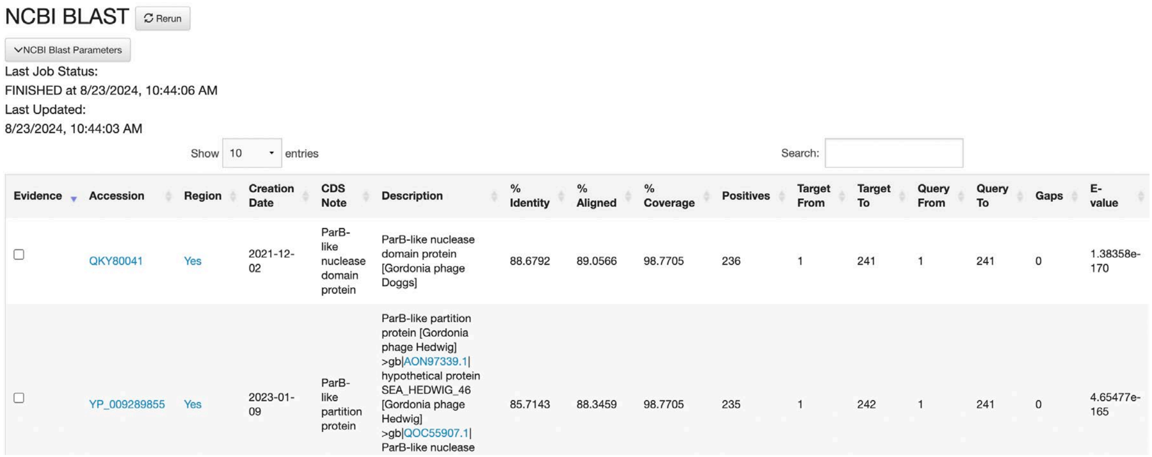
Last Job Status:
FINISHED at 8/23/2024, 10:41:18 AM
Last Updated:
8/23/2024, 10:41:18 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	43	function unknown	244	503	1e-142	DB	135818
☐	Doggs	40	ParB-like nuclease domain protein	265	479	1e-135	DB	135818
☐	DirtyBoi	45	ParB-like nuclease domain protein	266	463	1e-130	DB	135818


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:30:02 PM
Last Updated:
8/23/2024, 3:30:02 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF20188.1	DUF6551 ; Family of unknown function (DUF6551)	99.8	86.0656	3	211	21	231	1.1e-24
☐	d1vz0a2	d.268.1.1 (A:23-115) Putative partitioning protein ParB/Spo0J {Thermus thermophilus [TaxId: 274]}	99.3	40.1639	1	92	10	108	1.5e-15


NCBI BLAST

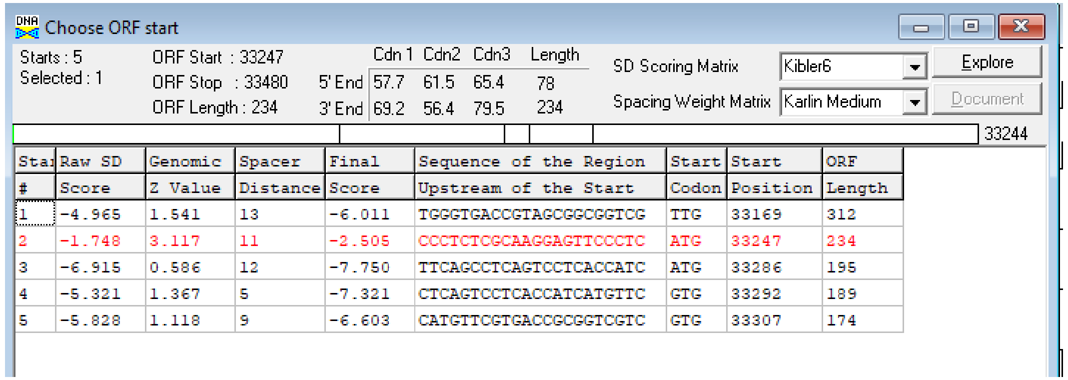
Last Job Status:
FINISHED at 8/23/2024, 10:44:06 AM
Last Updated:
8/23/2024, 10:44:03 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80041	Yes	2021-12-02	ParB-like nuclease domain protein	ParB-like nuclease domain protein [Gordonia phage Doggs]	88.6792	89.0566	98.7705	236	1	241	1	241	0	1.38358e-170
☐	YP_009289855	Yes	2023-01-09	ParB-like partition protein	ParB-like partition protein [Gordonia phage Hedwig] >gb|AON97339.1| hypothetical protein SEA_HEDWIG_46 [Gordonia phage Hedwig] >gb|QOC55907.1| ParB-like nuclease	85.7143	88.3459	98.7705	235	1	242	1	241	0	4.65477e-165

VK

Coriander_Draft

- Phamerator- Gene 44_Start Site 33247
- 234 bp



Choose ORF start

Starts : 5
Selected : 1

ORF Start : 33247
ORF Stop : 33480
ORF Length : 234

	Cdn 1	Cdn2	Cdn3	Length
5' End	57.7	61.5	65.4	78
3' End	69.2	56.4	79.5	234

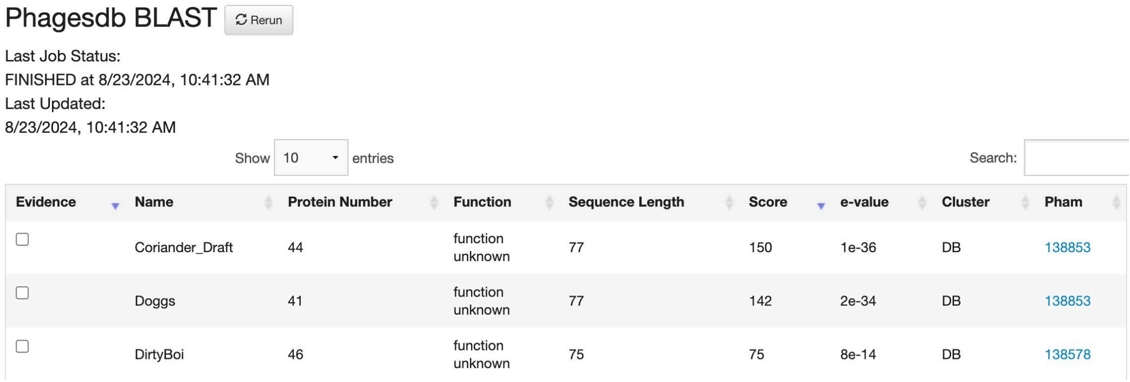
SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-4.965	1.541	13	-6.011	TGGGTGACCGTAGCGGCGGTCG	TTG	33169	312
2	-1.748	3.117	11	-2.505	CCCTCTCGCAAGGAGTTCCCTC	ATG	33247	234
3	-6.915	0.586	12	-7.750	TTCAGCCTCAGTCCTCACCATC	ATG	33286	195
4	-5.321	1.367	5	-7.321	CTCAGTCCTCACCATCATGTTC	GTG	33292	189
5	-5.828	1.118	9	-6.603	CATGTTCGTGACCGCGGTCGTC	GTG	33307	174

- Gene Mark
- Gene: Coriander_44 Start: 33247, Stop: 33480, Start Num: 2 Candidate Starts for Coriander_44: (1, 33169), (Start: 2 @33247 has 1 MA's), (3, 33286), (4, 33292), (5, 33307),

VK

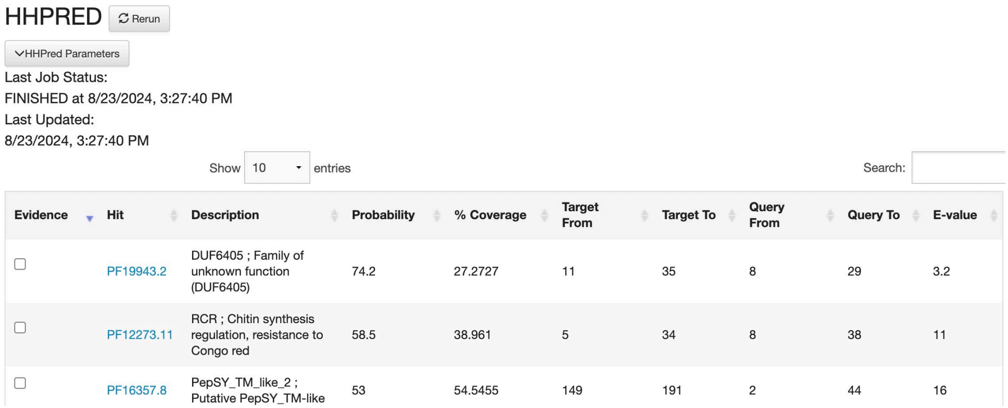
Basic Phage Information	
Phage Name	Coriander
Gene #	44
Stop Coordinate	33480
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	N/A
Gene present in other annotated genomes?	
Is this start site conserved in other phage genomes as indicated by Starterator?	
Selected Start Coordinate	33247
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:41:32 AM
Last Updated:
8/23/2024, 10:41:32 AM

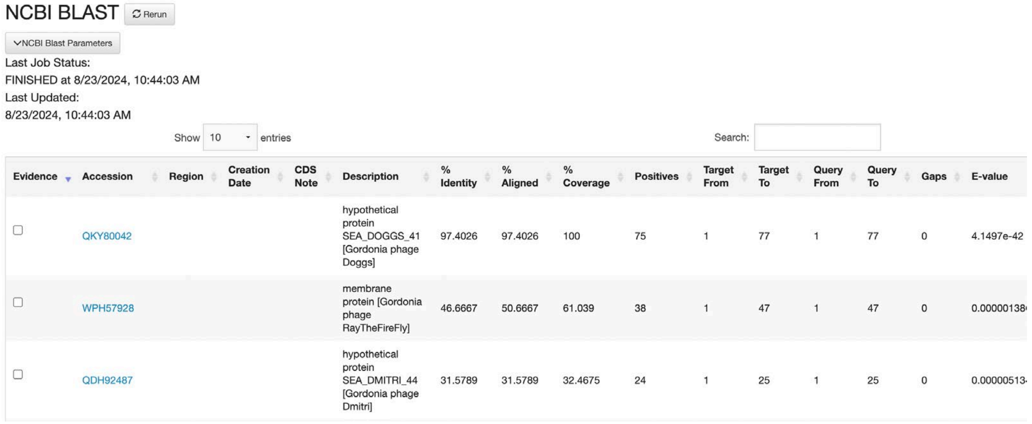
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	44	function unknown	77	150	1e-36	DB	138853
☐	Doggs	41	function unknown	77	142	2e-34	DB	138853
☐	DirtyBoi	46	function unknown	75	75	8e-14	DB	138578



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:27:40 PM
Last Updated:
8/23/2024, 3:27:40 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF19943.2	DUF6405 ; Family of unknown function (DUF6405)	74.2	27.2727	11	35	8	29	3.2
☐	PF12273.11	RCR ; Chitin synthesis regulation, resistance to Congo red	58.5	38.961	5	34	8	38	11
☐	PF16357.8	PepSY_TM_like_2 ; Putative PepSY_TM-like	53	54.5455	149	191	2	44	16



NCBI BLAST

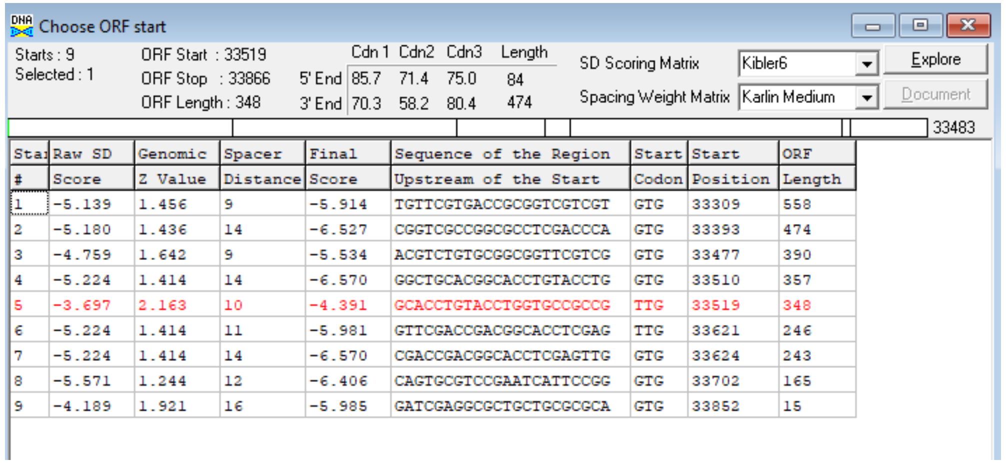
Last Job Status:
FINISHED at 8/23/2024, 10:44:03 AM
Last Updated:
8/23/2024, 10:44:03 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80042				hypothetical protein SEA_DOGGS_41 [Gordonia phage Doggs]	97.4026	97.4026	100	75	1	77	1	77	0	4.1497e-42
☐	WPH57928				membrane protein [Gordonia phage RayTheFireFly]	46.6667	50.6667	61.039	38	1	47	1	47	0	0.00000138
☐	QDH92487				hypothetical protein SEA_DMITRI_44 [Gordonia phage Dmitri]	31.5789	31.5789	32.4675	24	1	25	1	25	0	0.00000513

VK

Coriander_Draft

- Phamerator- Gene 45_Start Site 33477
- 390 bp
- Gene Mark



Starts : 9
Selected : 1

ORF Start : 33519
ORF Stop : 33866
ORF Length : 348

	Cdn 1	Cdn2	Cdn3	Length
5' End	85.7	71.4	75.0	84
3' End	70.3	58.2	80.4	474

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.139	1.456	9	-5.914	TGTTCGTGACCGCGGTCGTCGT	GTG	33309	558
2	-5.180	1.436	14	-6.527	CGGTCGCCGGCGCCTCGACCCA	GTG	33393	474
3	-4.759	1.642	9	-5.534	ACGTCTGTGCGGCGGTTCGTCG	GTG	33477	390
4	-5.224	1.414	14	-6.570	GGCTGCACGGCACCTGTACCTG	GTG	33510	357
5	-3.697	2.163	10	-4.391	GCACCTGTACCTGGTGCCGCCG	TTG	33519	348
6	-5.224	1.414	11	-5.981	GTTCGACCGACGGCACCTCGAG	TTG	33621	246
7	-5.224	1.414	14	-6.570	CGACCGACGGCACCTCGAGTTG	GTG	33624	243
8	-5.571	1.244	12	-6.406	CAGTGCGTCCGAATCATTCCGG	GTG	33702	165
9	-4.189	1.921	16	-5.985	GATCGAGGCGCTGCTGCGCGCA	GTG	33852	15

- Gene: Coriander_45 Start: 33477, Stop: 33866, Start Num: 14 Candidate Starts for Coriander_45: (3, 33309), (6, 33393), (Start: 14 @33477 has 6 MA's), (18, 33510), (19, 33519), (29, 33621), (30, 33624), (39, 33702), (52, 33852),

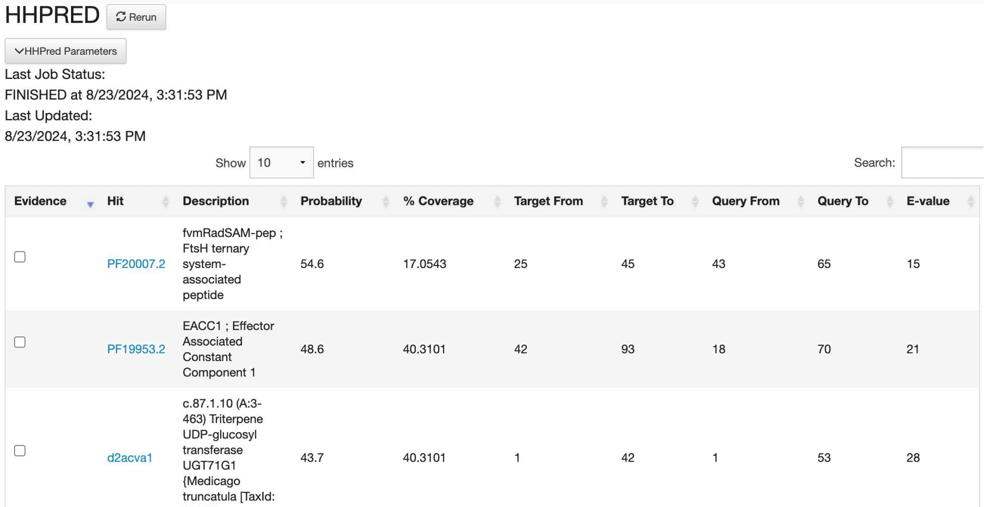
VK

Basic Phage Information	
Phage Name	Coriander
Gene #	45
Stop Coordinate	33866
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	3 bp (33477-33480)
Gene present in other annotated genomes?	
Is this start site conserved in other phage genomes as indicated by Starterator?	
Selected Start Coordinate	33477
Selected Function	

Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:41:48 AM
Last Updated:
8/23/2024, 10:41:48 AM

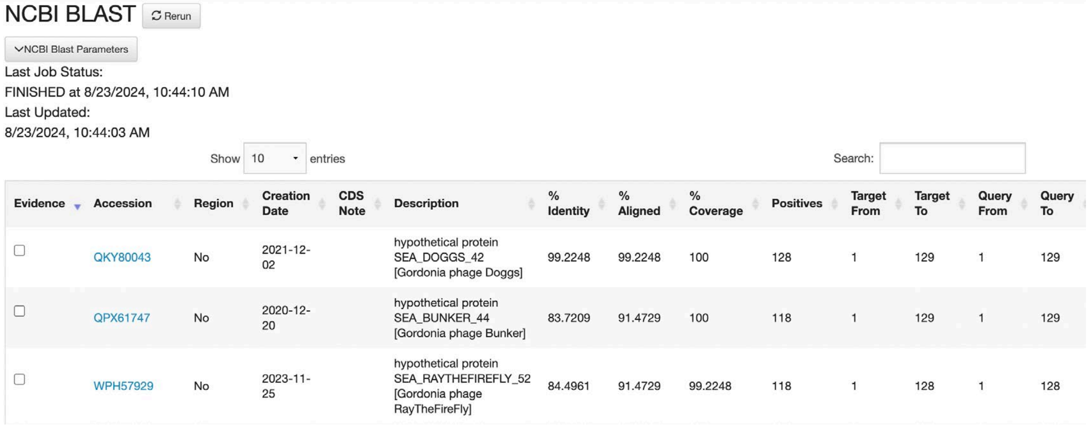
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	45	function unknown	129	254	4e-68	DB	192830
☐	Doggs	42	function unknown	129	253	2e-67	DB	192830
☐	RayTheFireFly	52	function unknown	129	218	6e-57	DB	192830



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:31:53 PM
Last Updated:
8/23/2024, 3:31:53 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF20007.2	fvmRadSAM-pep ; FtsH ternary system-associated peptide	54.6	17.0543	25	45	43	65	15
☐	PF19953.2	EACC1 ; Effector Associated Constant Component 1	48.6	40.3101	42	93	18	70	21
☐	d2acva1	c.87.1.10 (A:3-463) Triterpene UDP-glucosyl transferase UGT71G1 {Medicago truncatula [TaxId:	43.7	40.3101	1	42	1	53	28



NCBI BLAST

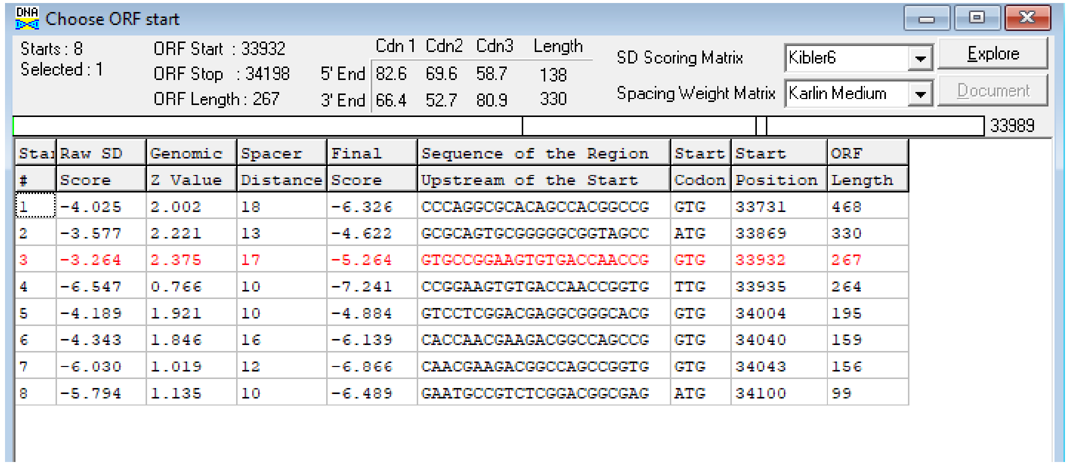
Last Job Status:
FINISHED at 8/23/2024, 10:44:10 AM
Last Updated:
8/23/2024, 10:44:03 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To
☐	QKY80043	No	2021-12-02		hypothetical protein SEA_DOGGS_42 [Gordonia phage Doggs]	99.2248	99.2248	100	128	1	129	1	129
☐	QPX61747	No	2020-12-20		hypothetical protein SEA_BUNKER_44 [Gordonia phage Bunker]	83.7209	91.4729	100	118	1	129	1	129
☐	WPH57929	No	2023-11-25		hypothetical protein SEA_RAYTHEFIREFLY_52 [Gordonia phage RayTheFireFly]	84.4961	91.4729	99.2248	118	1	128	1	128

VK

Coriander_Draft

- Phamerator- Gene 46_Start Site 33932
- 267 bp
- Gene Mark



Starts : 8
Selected : 1

ORF Start : 33932
ORF Stop : 34198
ORF Length : 267

	Cdn 1	Cdn2	Cdn3	Length
5' End	82.6	69.6	58.7	138
3' End	66.4	52.7	80.9	330

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

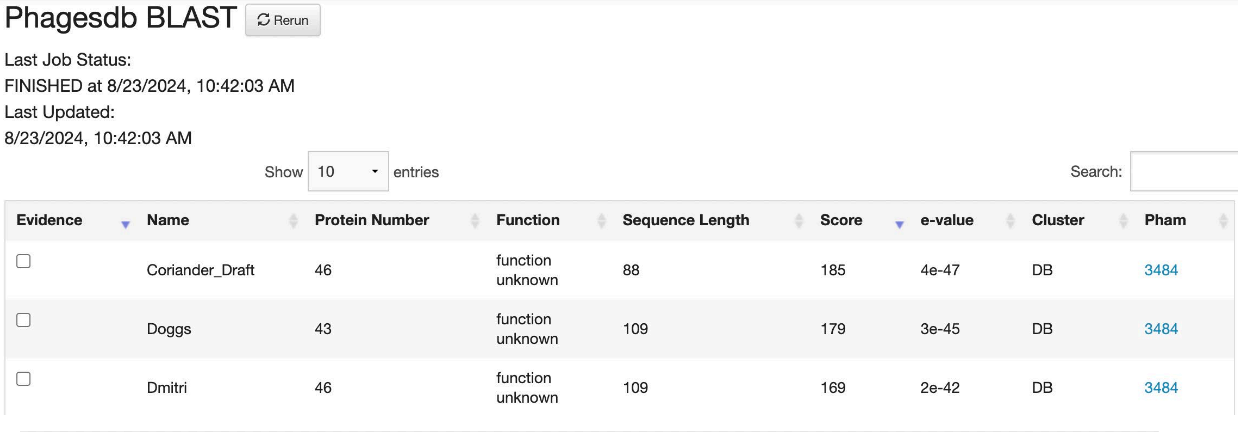
33989

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-4.025	2.002	18	-6.326	CCCAGGCGCACAGCCACGGCCG	GTG	33731	468
2	-3.577	2.221	13	-4.622	GCGCAGTGCGGGGGCGGTAGCC	ATG	33869	330
3	-3.264	2.375	17	-5.264	GTGCCGGAAGTGTGACCAACCG	GTG	33932	267
4	-6.547	0.766	10	-7.241	CCGGAAGTGTGACCAACCGGTG	TTG	33935	264
5	-4.189	1.921	10	-4.884	GTCCTCGGACGAGGCGGGCACG	GTG	34004	195
6	-4.343	1.846	16	-6.139	CACCAACGAAGACGGCCAGCCG	GTG	34040	159
7	-6.030	1.019	12	-6.866	CAACGAAGACGGCCAGCCGGTG	GTG	34043	156
8	-5.794	1.135	10	-6.489	GAATGCCGTCTCGGACGGCGAG	ATG	34100	99

- Gene: Coriander_46 Start: 33932, Stop: 34198, Start Num: 8 Candidate Starts for Coriander_46: (1, 33731), (Start: 4 @33869 has 6 MA's), (Start: 8 @33932 has 2 MA's), (9, 33935), (12, 34004), (14, 34040), (15, 34043), (20, 34100),

VK

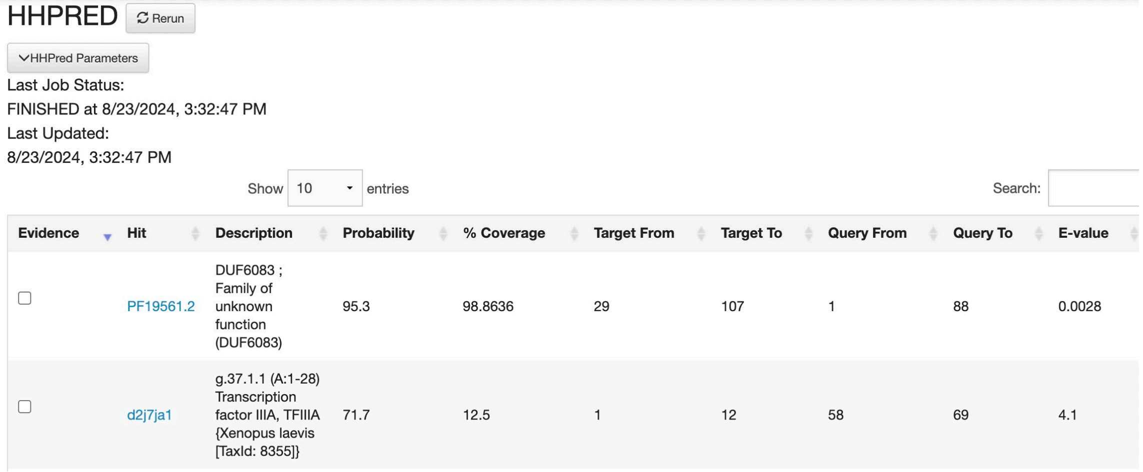
Basic Phage Information	
Phage Name	Coriander
Gene #	46
Stop Coordinate	34198
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	N/A
Gene present in other annotated genomes?	
Is this start site conserved in other phage genomes as indicated by Starterator?	
Selected Start Coordinate	33932
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:42:03 AM
Last Updated:
8/23/2024, 10:42:03 AM

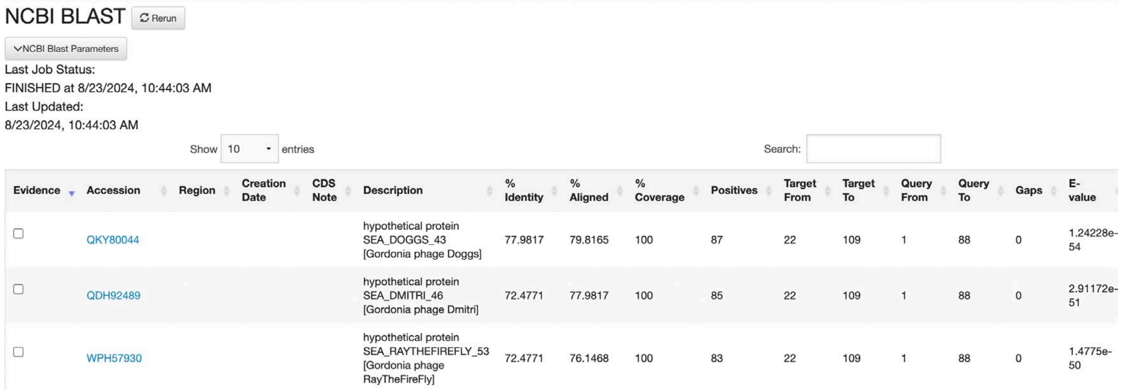
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	46	function unknown	88	185	4e-47	DB	3484
☐	Doggs	43	function unknown	109	179	3e-45	DB	3484
☐	Dmitri	46	function unknown	109	169	2e-42	DB	3484



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:32:47 PM
Last Updated:
8/23/2024, 3:32:47 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF19561.2	DUF6083 ; Family of unknown function (DUF6083)	95.3	98.8636	29	107	1	88	0.0028
☐	d2j7ja1	g.37.1.1 (A:1-28) Transcription factor IIIA, TFIIIA {Xenopus laevis [TaxId: 8355]}	71.7	12.5	1	12	58	69	4.1



NCBI BLAST

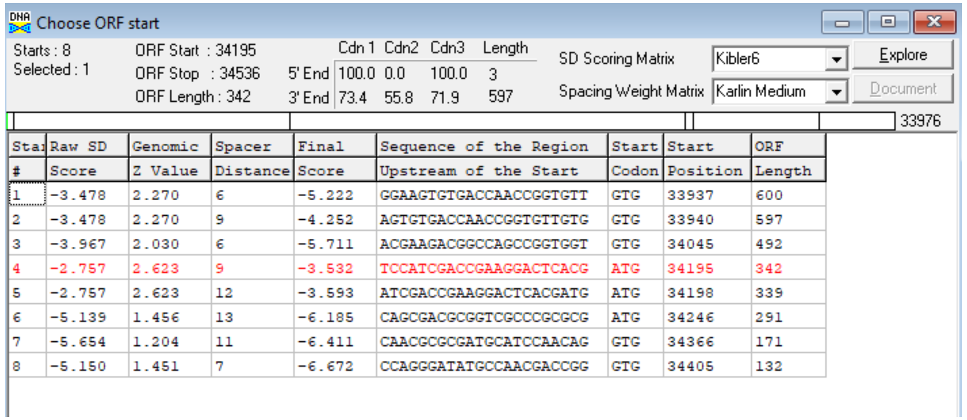
Last Job Status:
FINISHED at 8/23/2024, 10:44:03 AM
Last Updated:
8/23/2024, 10:44:03 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80044				hypothetical protein SEA_DOGGS_43 [Gordonia phage Doggs]	77.9817	79.8165	100	87	22	109	1	88	0	1.24228e-54
☐	QDH92489				hypothetical protein SEA_DMITRI_46 [Gordonia phage Dmitri]	72.4771	77.9817	100	85	22	109	1	88	0	2.91172e-51
☐	WPH57930				hypothetical protein SEA_RAYTHEFIREFLY_53 [Gordonia phage RayTheFireFly]	72.4771	76.1468	100	83	22	109	1	88	0	1.4775e-50

VK

Coriander_Draft

- Phamerator- Gene 47_Start Site 34195
- 342 bp
- Gene Mark



Starts : 8
Selected : 1

ORF Start : 34195
ORF Stop : 34536
ORF Length : 342

	Cdn 1	Cdn2	Cdn3	Length
5' End	100.0	0.0	100.0	3
3' End	73.4	55.8	71.9	597

SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

33976

Sta #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-3.478	2.270	6	-5.222	GGAAGTGTGACCAACCGGTGTT	GTG	33937	600
2	-3.478	2.270	9	-4.252	AGTGTGACCAACCGGTGTTGTG	GTG	33940	597
3	-3.967	2.030	6	-5.711	ACGAAGACGGCCAGCCGGTGGT	GTG	34045	492
4	-2.757	2.623	9	-3.532	TCCATCGACCGAAGGACTCACG	ATG	34195	342
5	-2.757	2.623	12	-3.593	ATCGACCGAAGGACTCACGATG	ATG	34198	339
6	-5.139	1.456	13	-6.185	CAGCGACGCGGTCGCCCGCGCG	ATG	34246	291
7	-5.654	1.204	11	-6.411	CAACGCGCGATGCATCCAACAG	GTG	34366	171
8	-5.150	1.451	7	-6.672	CCAGGGATATGCCAACGACCGG	GTG	34405	132

- Gene: Coriander_47 Start: 34195, Stop: 34536, Start Num: 32 Candidate Starts for Coriander_47: (14, 33937), (15, 33940), (21, 34045), (Start: 32 @34195 has 1 MA's), (Start: 33 @34198 has 3 MA's), (Start: 34 @34246 has 18 MA's), (39, 34366), (42, 34405),

VK

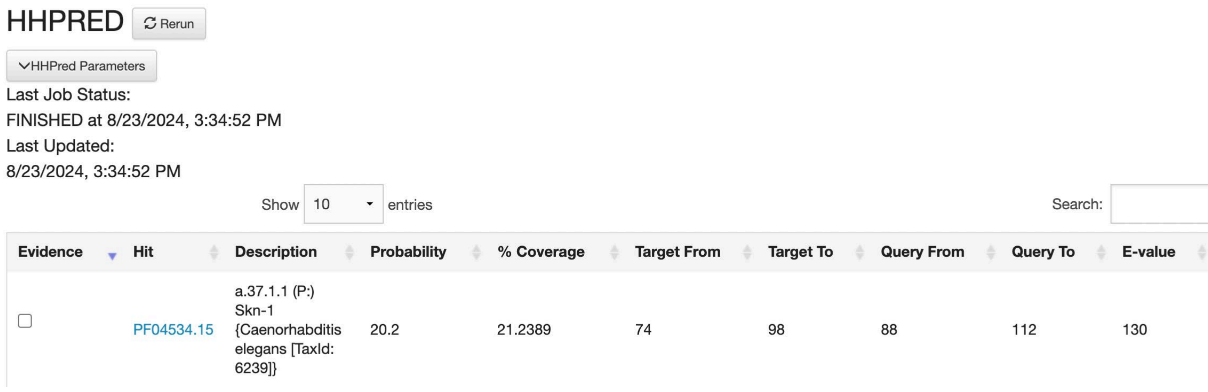
Basic Phage Information	
Phage Name	Coriander
Gene #	47
Stop Coordinate	34536
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	3bp (34195-34198)
Gene present in other annotated genomes?	
Is this start site conserved in other phage genomes as indicated by Starterator?	
Selected Start Coordinate	34915
Selected Function	

Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:42:18 AM
Last Updated:
8/23/2024, 10:42:18 AM

Show 10 entries   Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	47	function unknown	113	231	5e-61	DB	223176
☐	Doggs	44	function unknown	112	217	1e-56	DB	223176
☐	RayTheFireFly	54	function unknown	113	199	2e-51	DB	223176

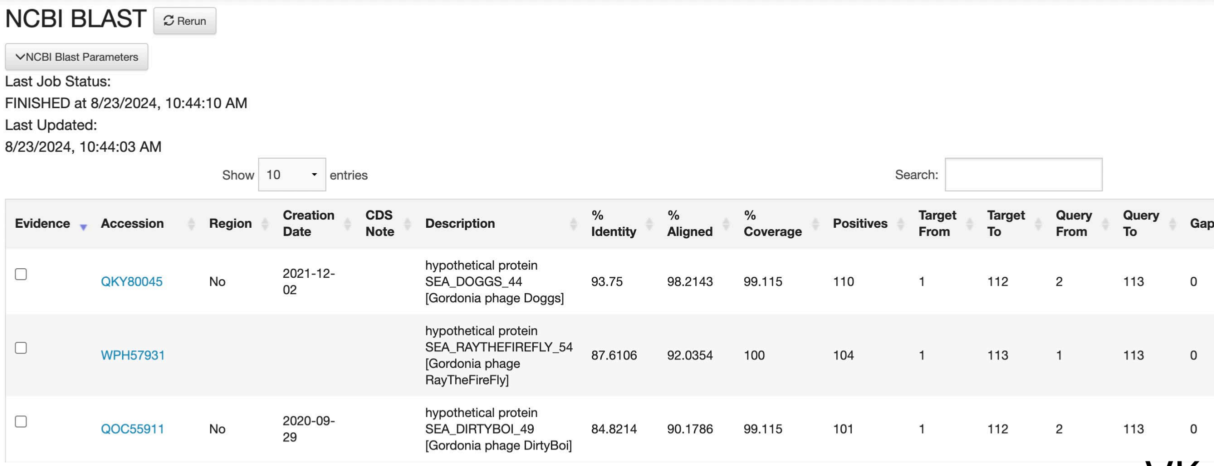


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:34:52 PM
Last Updated:
8/23/2024, 3:34:52 PM

Show 10 entries   Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF04534.15	a.37.1.1 (P:) Skn-1 {Caenorhabditis elegans [TaxId: 6239]}	20.2	21.2389	74	98	88	112	130



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:10 AM
Last Updated:
8/23/2024, 10:44:03 AM

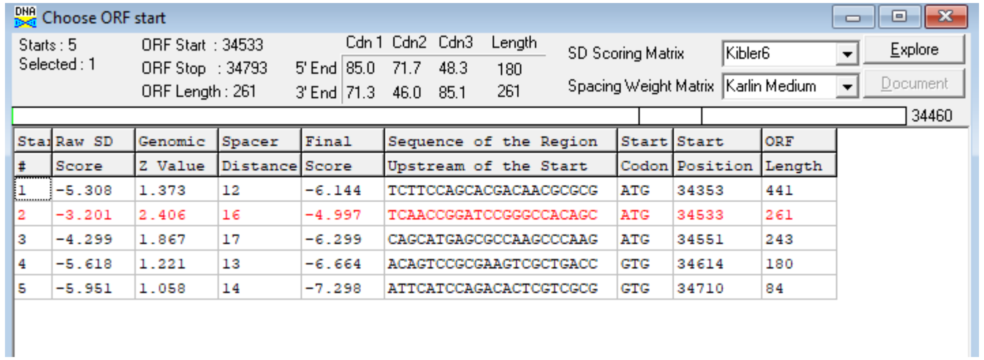
Show 10 entries   Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gap
☐	QKY80045	No	2021-12-02		hypothetical protein SEA_DOGGS_44 [Gordonia phage Doggs]	93.75	98.2143	99.115	110	1	112	2	113	0
☐	WPH57931				hypothetical protein SEA_RAYTHEFIREFLY_54 [Gordonia phage RayTheFireFly]	87.6106	92.0354	100	104	1	113	1	113	0
☐	QOC55911	No	2020-09-29		hypothetical protein SEA_DIRTYBOI_49 [Gordonia phage DirtyBoi]	84.8214	90.1786	99.115	101	1	112	2	113	0

VK

Coriander_Draft

- Phamerator- Gene 48_Start Site 34533
- 261 bp
- Gene Mark



Starts : 5
Selected : 1

ORF Start : 34533
ORF Stop : 34793
ORF Length : 261

	Cdn 1	Cdn2	Cdn3	Length
5' End	85.0	71.7	48.3	180
3' End	71.3	46.0	85.1	261

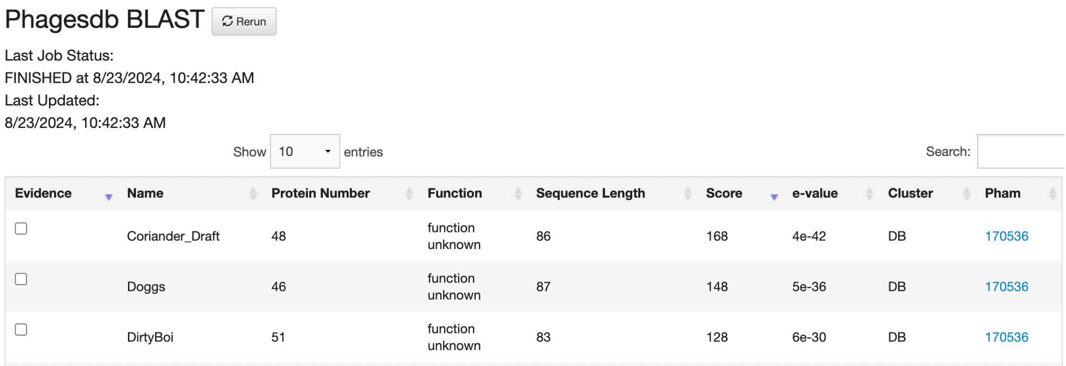
SD Scoring Matrix: Kibler6
Spacing Weight Matrix: Karlin Medium

34460

Star #	Raw SD Score	Genomic Z Value	Spacer Distance	Final Score	Sequence of the Region Upstream of the Start	Start Codon	Start Position	ORF Length
1	-5.308	1.373	12	-6.144	TCTTCCAGCACGACAACGCGCG	ATG	34353	441
2	-3.201	2.406	16	-4.997	TCAACCGGATCCGGGCCACAGC	ATG	34533	261
3	-4.299	1.867	17	-6.299	CAGCATGAGCGCCAAGCCCAAG	ATG	34551	243
4	-5.618	1.221	13	-6.664	ACAGTCCGCGAAGTCGCTGACC	GTG	34614	180
5	-5.951	1.058	14	-7.298	ATTCATCCAGACACTCGTCGCG	GTG	34710	84

- Gene: Coriander_48 Start: 34533, Stop: 34793, Start Num: 9 Candidate Starts for Coriander_48: (5, 34353), (Start: 9 @34533 has 7 MA's), (10, 34551), (13, 34614), (17, 34710),

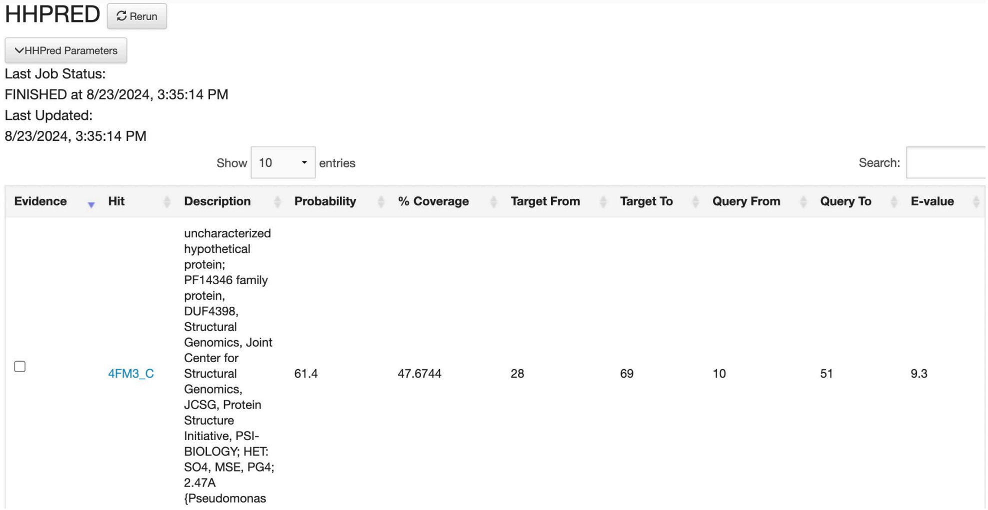
Basic Phage Information	
Phage Name	Coriander
Gene #	48
Stop Coordinate	34793
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	N/A
Gene present in other annotated genomes?	
Is this start site conserved in other phage genomes as indicated by Starterator?	
Selected Start Coordinate	34533
Selected Function	



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:42:33 AM
Last Updated:
8/23/2024, 10:42:33 AM

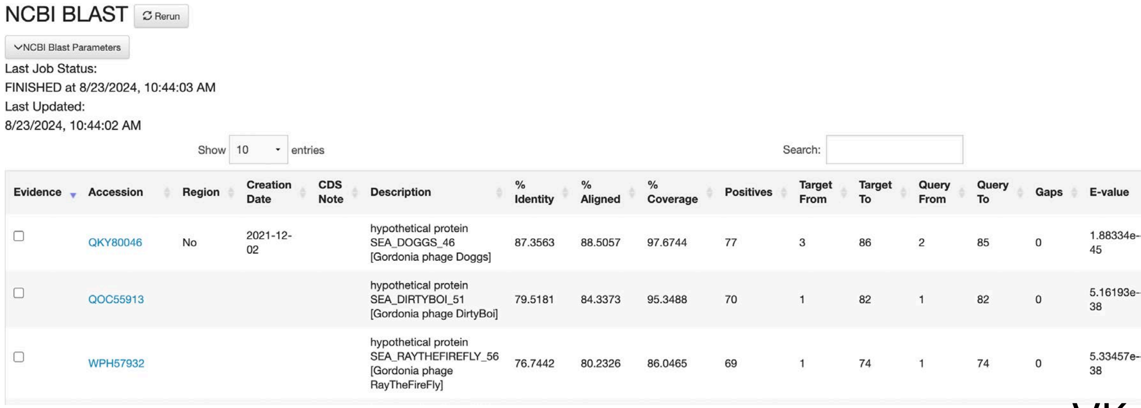
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	48	function unknown	86	168	4e-42	DB	170536
☐	Doggs	46	function unknown	87	148	5e-36	DB	170536
☐	DirtyBoi	51	function unknown	83	128	6e-30	DB	170536



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:35:14 PM
Last Updated:
8/23/2024, 3:35:14 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	4FM3_C	uncharacterized hypothetical protein; PF14346 family protein, DUF4398, Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein Structure Initiative, PSI-BIOLOGY; HET: SO4, MSE, PG4; 2.47A {Pseudomonas	61.4	47.6744	28	69	10	51	9.3



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:03 AM
Last Updated:
8/23/2024, 10:44:02 AM

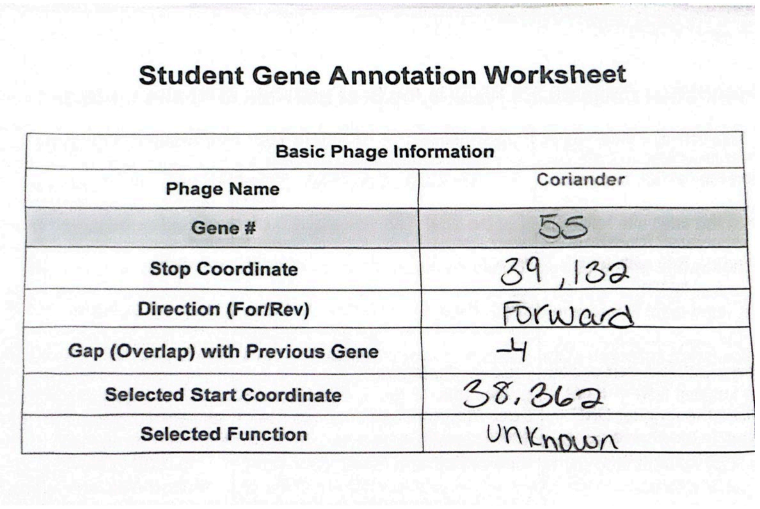
Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80046	No	2021-12-02		hypothetical protein SEA_DOGGS_46 [Gordonia phage Doggs]	87.3563	88.5057	97.6744	77	3	86	2	85	0	1.88334e-45
☐	QOC55913				hypothetical protein SEA_DIRTYBOI_51 [Gordonia phage DirtyBoi]	79.5181	84.3373	95.3488	70	1	82	1	82	0	5.16193e-38
☐	WPH57932				hypothetical protein SEA_RAYTHEFIREFLY_56 [Gordonia phage RayTheFireFly]	76.7442	80.2326	86.0465	69	1	74	1	74	0	5.33457e-38

VK

49-54

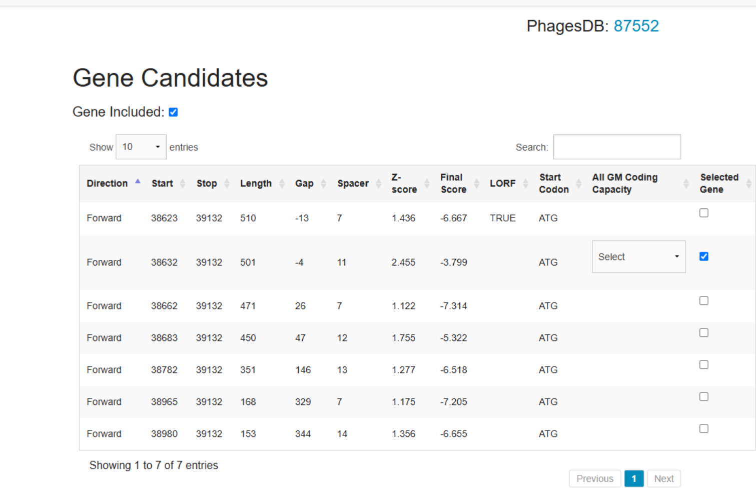
55 - 60

Gene 55



Student Gene Annotation Worksheet

Basic Phage Information	
Phage Name	Coriander
Gene #	55
Stop Coordinate	39,132
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	-4
Selected Start Coordinate	38,362
Selected Function	Unknown



PhagesDB: 87552

Gene Candidates

Gene Included: ☑

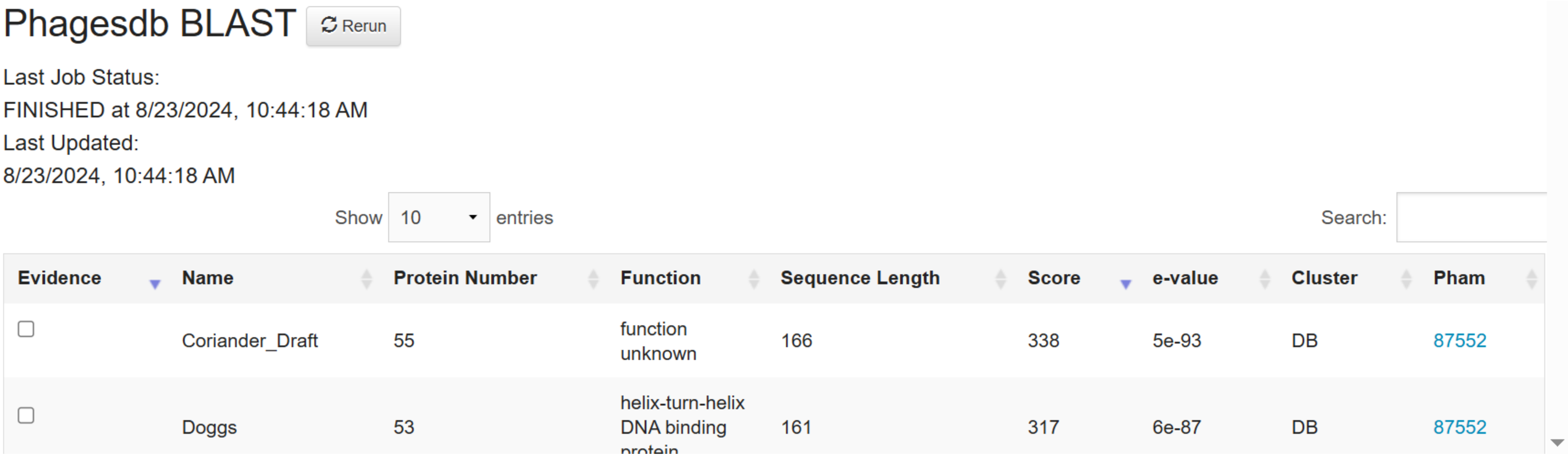
Show 10 entries

Search:

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	38623	39132	510	-13	7	1.436	-6.667	TRUE	ATG		☐
Forward	38632	39132	501	-4	11	2.455	-3.799		ATG	Select	☑
Forward	38662	39132	471	26	7	1.122	-7.314		ATG		☐
Forward	38683	39132	450	47	12	1.755	-5.322		ATG		☐
Forward	38782	39132	351	146	13	1.277	-6.518		ATG		☐
Forward	38965	39132	168	329	7	1.175	-7.205		ATG		☐
Forward	38980	39132	153	344	14	1.356	-6.655		ATG		☐

Showing 1 to 7 of 7 entries

- Gene: Coriander_55 Start: 38632, Stop: 39132, Start Num: 4 Candidate Starts for Coriander_55: (1, 38623), (Start: 4 @38632 has 8 MA's), (7, 38662), (8, 38683), (12, 38782), (15, 38965), (16, 38980),

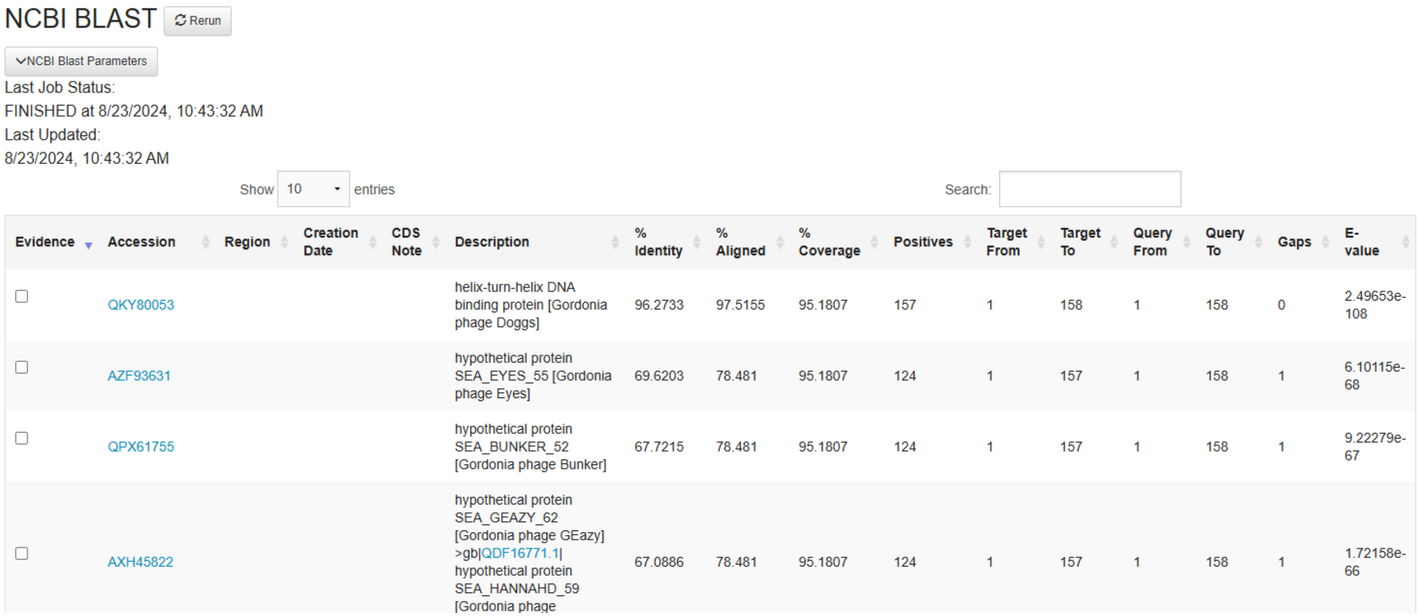


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:18 AM
Last Updated:
8/23/2024, 10:44:18 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	55	function unknown	166	338	5e-93	DB	87552
☐	Doggs	53	helix-turn-helix DNA binding protein	161	317	6e-87	DB	87552

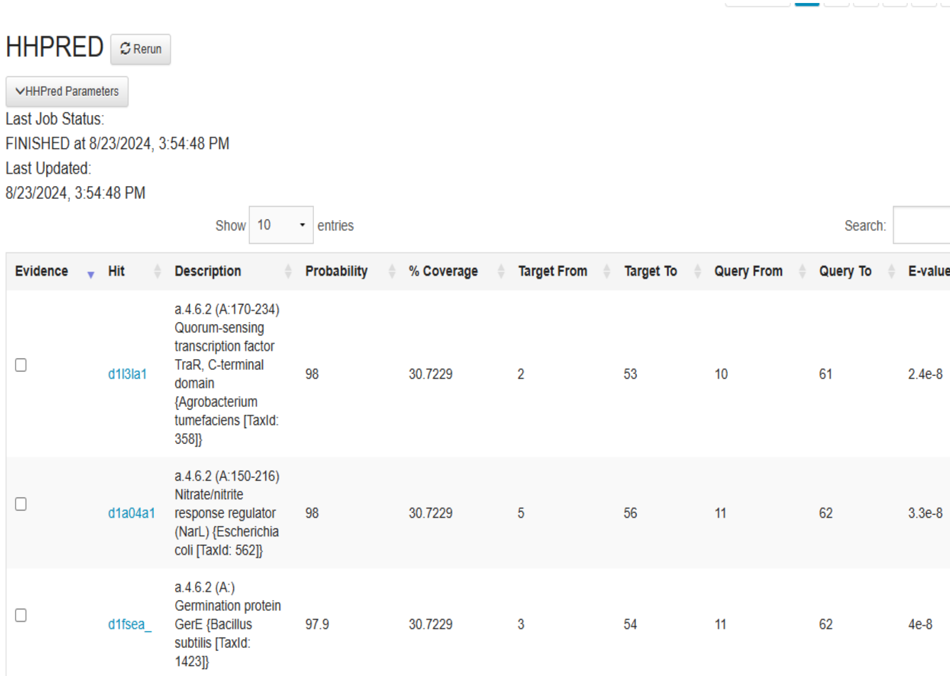


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:43:32 AM
Last Updated:
8/23/2024, 10:43:32 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80053				helix-turn-helix DNA binding protein [Gordonia phage Doggs]	96.2733	97.5155	95.1807	157	1	158	1	158	0	2.49653e-108
☐	AZF93631				hypothetical protein SEA_EYES_55 [Gordonia phage Eyes]	69.6203	78.481	95.1807	124	1	157	1	158	1	6.10115e-68
☐	QPX61755				hypothetical protein SEA_BUNKER_52 [Gordonia phage Bunker]	67.7215	78.481	95.1807	124	1	157	1	158	1	9.22279e-67
☐	AXH45822				hypothetical protein SEA_GEAZY_62 [Gordonia phage GEazy] >gb|QDF16771.1| hypothetical protein SEA_HANNAHD_59 [Gordonia phage	67.0886	78.481	95.1807	124	1	157	1	158	1	1.72158e-66



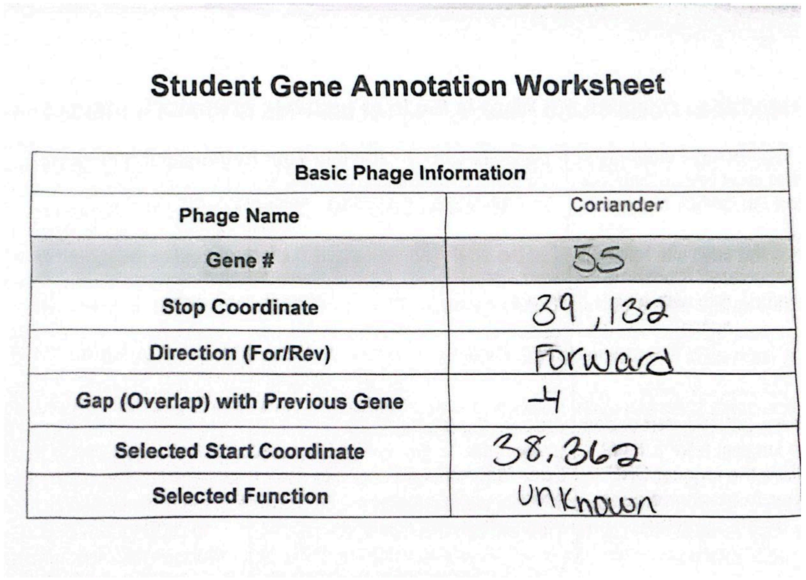
HHPRED

Last Job Status:
FINISHED at 8/23/2024, 3:54:48 PM
Last Updated:
8/23/2024, 3:54:48 PM

Show 10 entries Search:

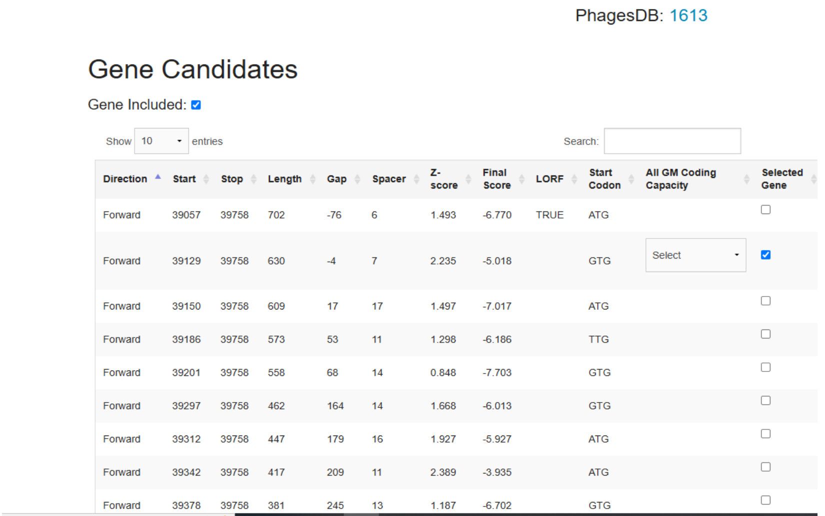
Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1l3la1	a.4.6.2 (A:170-234) Quorum-sensing transcription factor TraR, C-terminal domain {Agrobacterium tumefaciens [TaxId: 358]}	98	30.7229	2	53	10	61	2.4e-8
☐	d1a04a1	a.4.6.2 (A:150-216) Nitrate/nitrite response regulator (NarL) {Escherichia coli [TaxId: 562]}	98	30.7229	5	56	11	62	3.3e-8
☐	d1fsea_	a.4.6.2 (A:) Germination protein GerE {Bacillus subtilis [TaxId: 1423]}	97.9	30.7229	3	54	11	62	4e-8

Gene 56



Student Gene Annotation Worksheet

Basic Phage Information	
Phage Name	Coriander
Gene #	55
Stop Coordinate	39,132
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	-4
Selected Start Coordinate	38,362
Selected Function	Unknown



PhagesDB: 1613

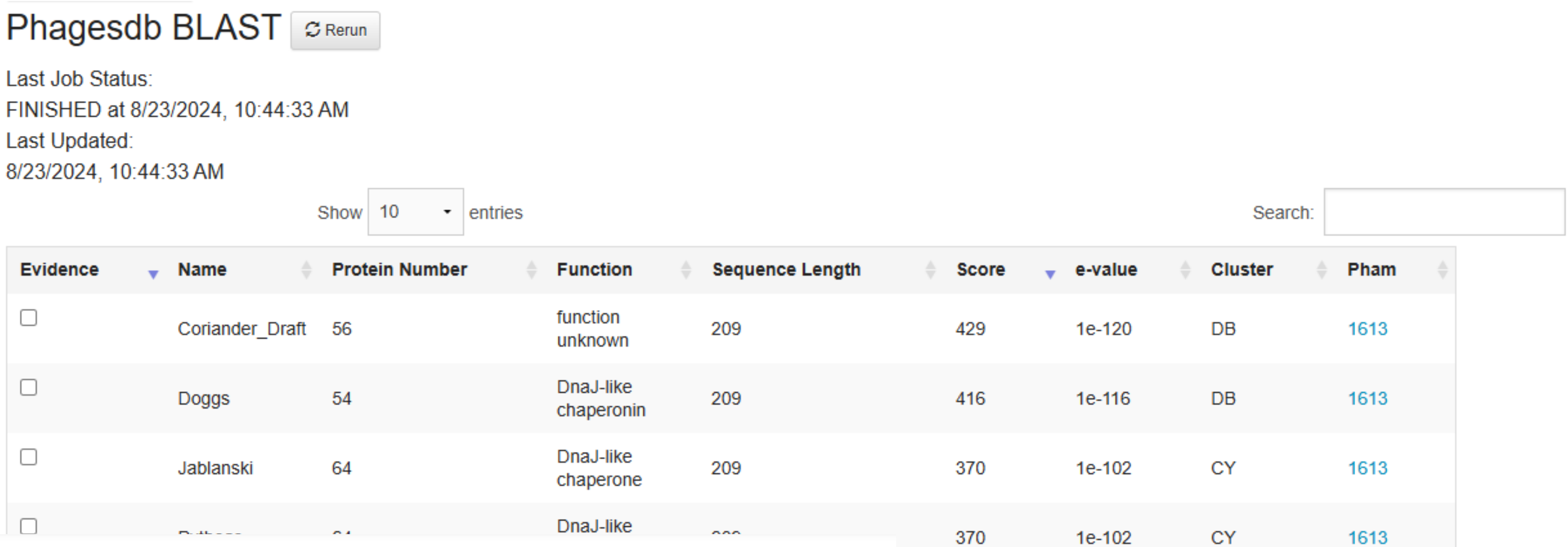
Gene Candidates

Gene Included: ☑

Show 10 entries Search:

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	39057	39758	702	-76	6	1.493	-6.770	TRUE	ATG		☐
Forward	39129	39758	630	-4	7	2.235	-5.018		GTG	Select	☑
Forward	39150	39758	609	17	17	1.497	-7.017		ATG		☐
Forward	39186	39758	573	53	11	1.298	-6.186		TTG		☐
Forward	39201	39758	558	68	14	0.848	-7.703		GTG		☐
Forward	39297	39758	462	164	14	1.668	-6.013		GTG		☐
Forward	39312	39758	447	179	16	1.927	-5.927		ATG		☐
Forward	39342	39758	417	209	11	2.389	-3.935		ATG		☐
Forward	39378	39758	381	245	13	1.187	-6.702		GTG		☐

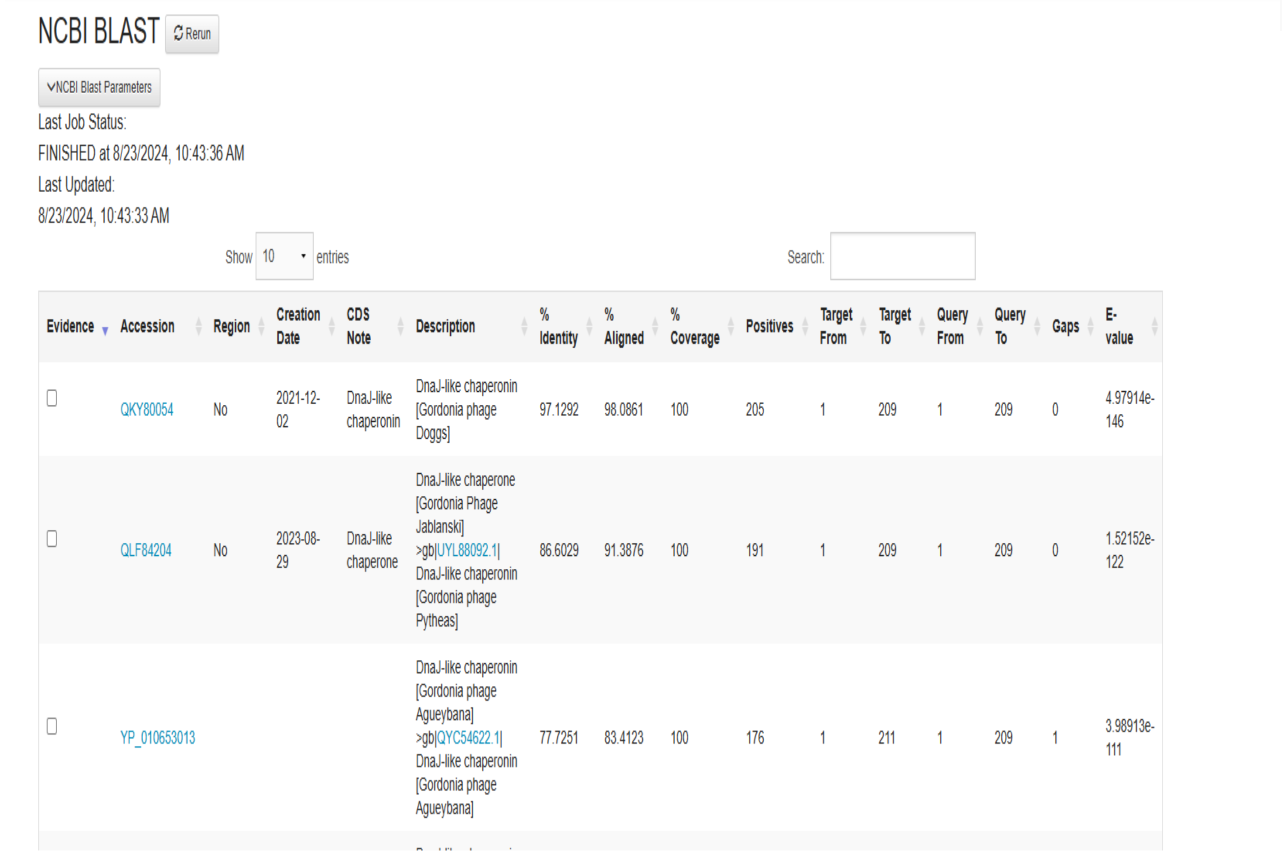
- Coriander_56 Start: 39129, Stop: 39758, Start Num: 24 Candidate Starts for Coriander_56: (13, 39057), (Start: 24 @39129 has 27 MA's), (26, 39150), (29, 39186), (31, 39201), (39, 39297), (42, 39312), (43, 39342), (44, 39378), (60, 39576), (61, 39582), (63, 39597), (64, 39600), (87, 39696), (95, 39750),



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:33 AM
Last Updated:
8/23/2024, 10:44:33 AM

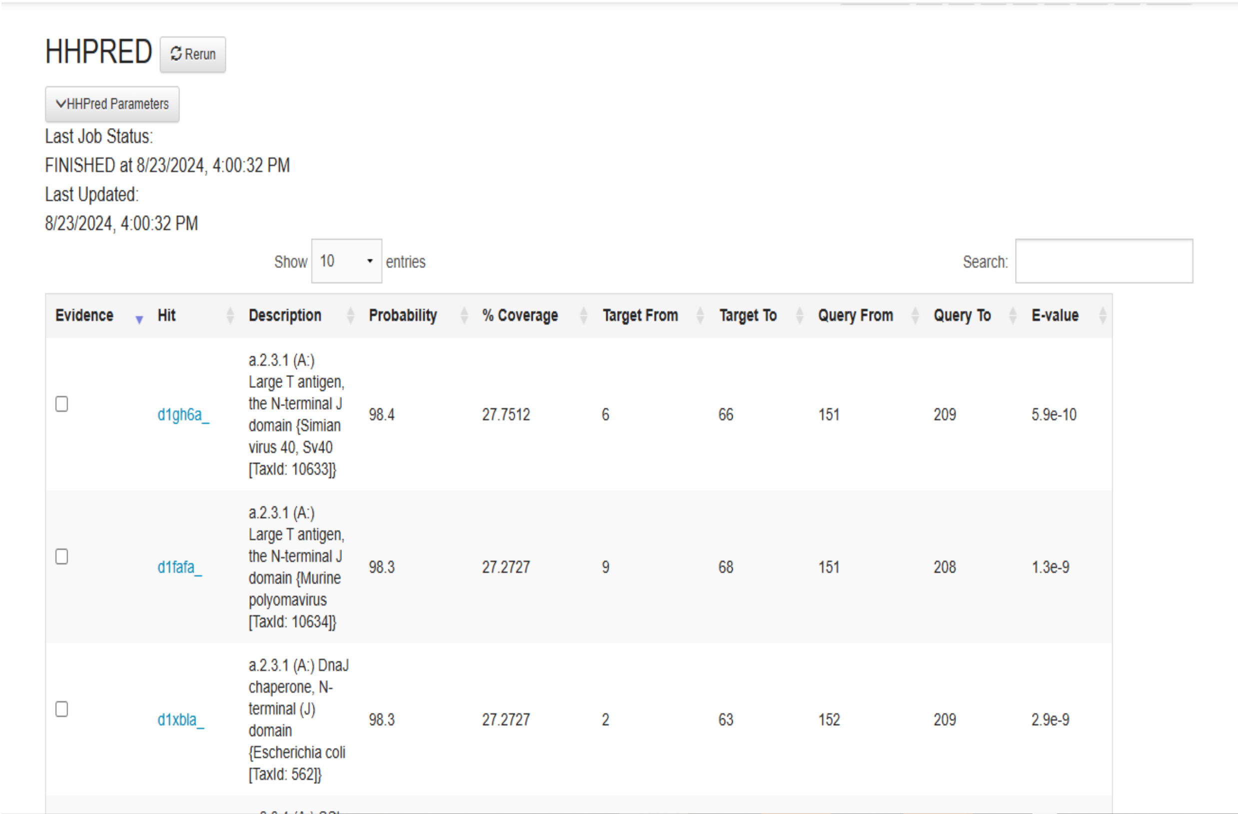
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	56	function unknown	209	429	1e-120	DB	1613
☐	Doggs	54	DnaJ-like chaperonin	209	416	1e-116	DB	1613
☐	Jablanski	64	DnaJ-like chaperone	209	370	1e-102	CY	1613
☐			DnaJ-like		370	1e-102	CY	1613



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:43:36 AM
Last Updated:
8/23/2024, 10:43:33 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80054	No	2021-12-02	DnaJ-like chaperonin	DnaJ-like chaperonin [Gordonia phage Doggs]	97.1292	98.0861	100	205	1	209	1	209	0	4.97914e-146
☐	QLF84204	No	2023-08-29	DnaJ-like chaperone	DnaJ-like chaperone [Gordonia Phage Jablanski] >gb|UYL88092.1| DnaJ-like chaperonin [Gordonia phage Pytheas]	86.6029	91.3876	100	191	1	209	1	209	0	1.52152e-122
☐	YP_010653013				DnaJ-like chaperonin [Gordonia phage Agueybana] >gb|QYC54622.1| DnaJ-like chaperonin [Gordonia phage Agueybana]	77.7251	83.4123	100	176	1	211	1	209	1	3.98913e-111

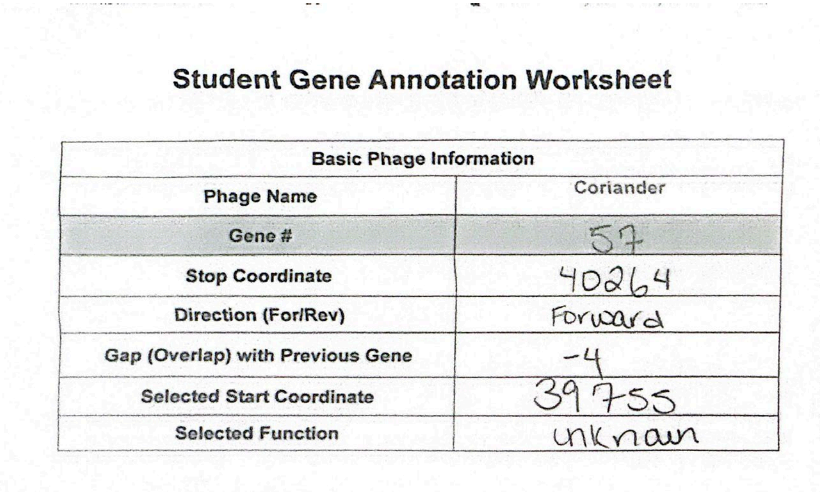


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:00:32 PM
Last Updated:
8/23/2024, 4:00:32 PM

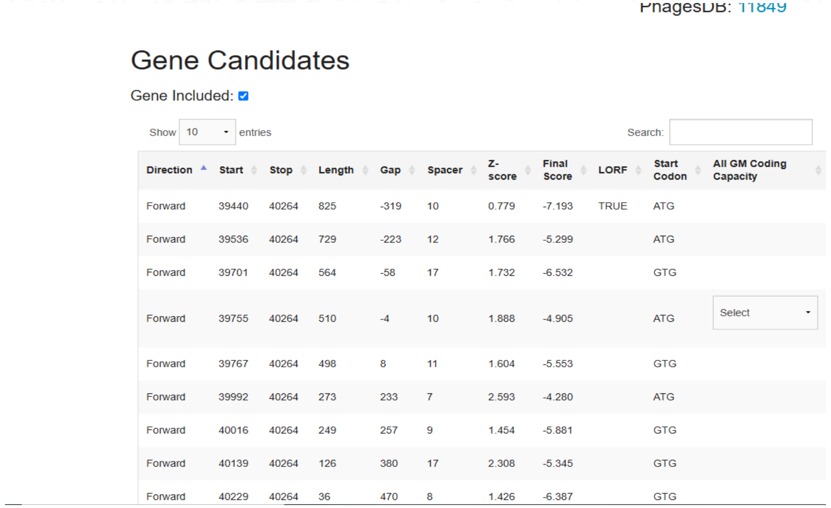
Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d1gh6a_	a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Simian virus 40, Sv40 [TaxId: 10633]}	98.4	27.7512	6	66	151	209	5.9e-10
☐	d1fafa_	a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Murine polyomavirus [TaxId: 10634]}	98.3	27.2727	9	68	151	208	1.3e-9
☐	d1xbla_	a.2.3.1 (A:) DnaJ chaperone, N-terminal (J) domain {Escherichia coli [TaxId: 562]}	98.3	27.2727	2	63	152	209	2.9e-9

Gene 57



Student Gene Annotation Worksheet

Basic Phage Information	
Phage Name	Coriander
Gene #	57
Stop Coordinate	40264
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	-4
Selected Start Coordinate	39755
Selected Function	unknown



PhagesDB: 11849

Gene Candidates

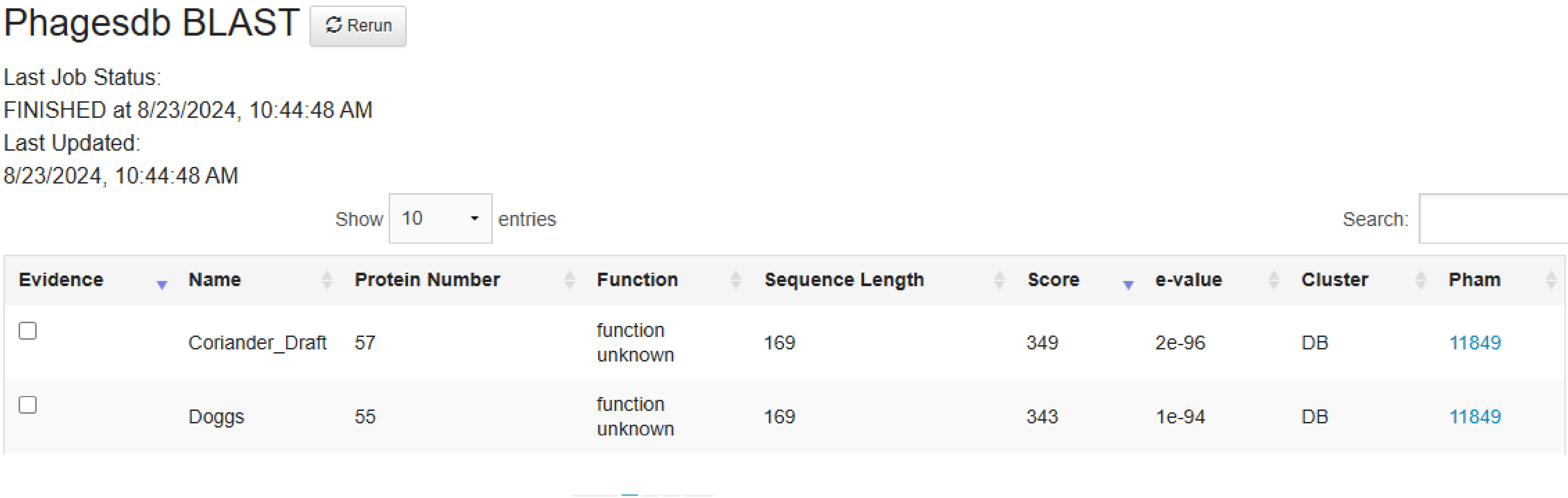
Gene Included: ☑

Show 10 entries

Search:

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity
Forward	39440	40264	825	-319	10	0.779	-7.193	TRUE	ATG	
Forward	39536	40264	729	-223	12	1.766	-5.299		ATG	
Forward	39701	40264	564	-58	17	1.732	-6.532		GTG	
Forward	39755	40264	510	-4	10	1.888	-4.905		ATG	Select
Forward	39767	40264	498	8	11	1.604	-5.553		GTG	
Forward	39992	40264	273	233	7	2.593	-4.280		ATG	
Forward	40016	40264	249	257	9	1.454	-5.881		GTG	
Forward	40139	40264	126	380	17	2.308	-5.345		GTG	
Forward	40229	40264	36	470	8	1.426	-6.387		GTG	

- Coriander_57 Start: 39755, Stop: 40264, Start Num: 4 Candidate Starts for Coriander_57: (1, 39440), (2, 39536), (3, 39701), (Start: 4 @39755 has 1 MA's), (5, 39767), (9, 39992), (10, 40016), (12, 40139), (13, 40229), (15, 40253),

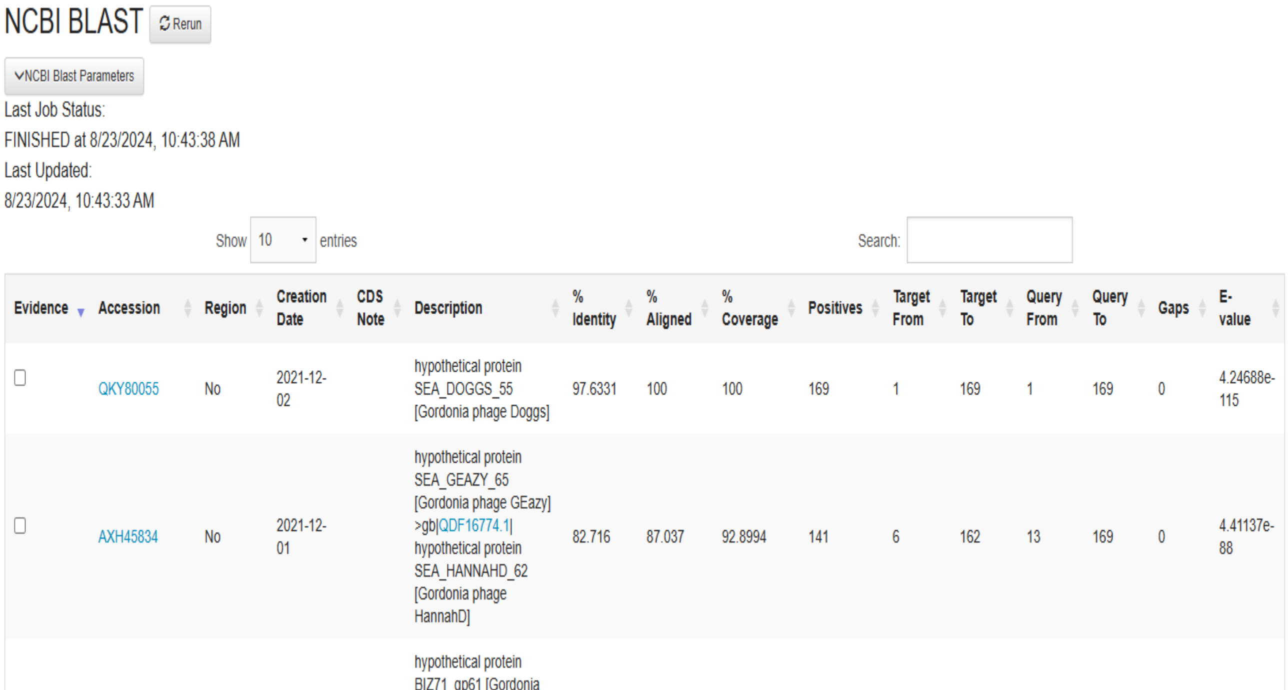


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:44:48 AM
Last Updated:
8/23/2024, 10:44:48 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	57	function unknown	169	349	2e-96	DB	11849
☐	Doggs	55	function unknown	169	343	1e-94	DB	11849

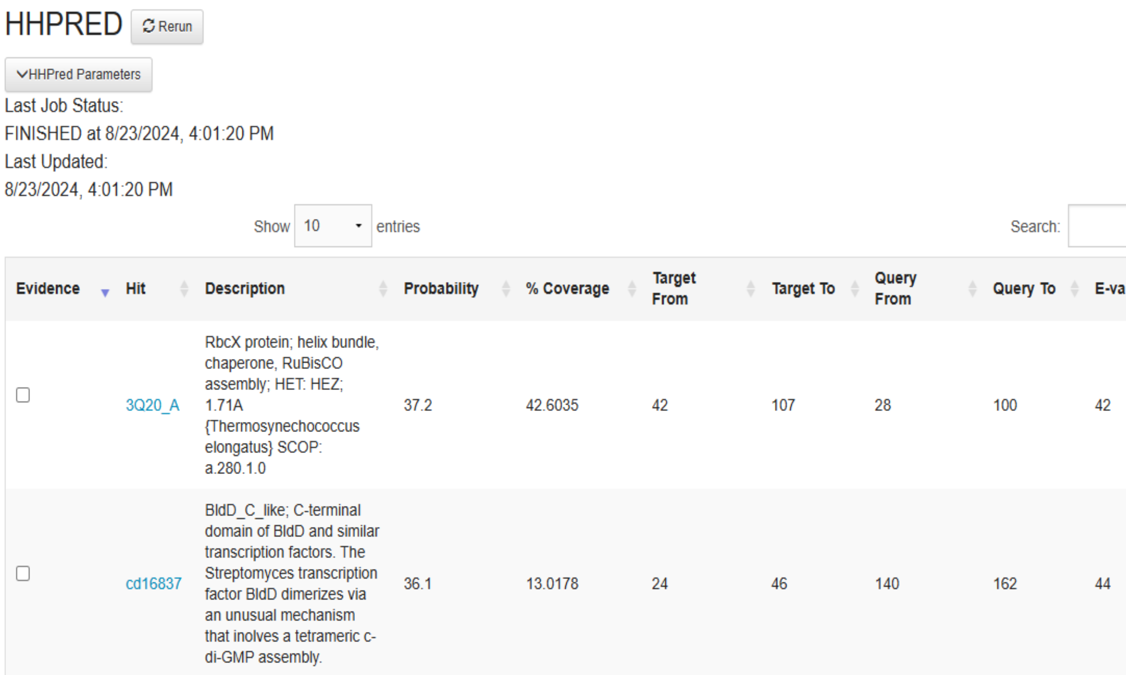


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:43:38 AM
Last Updated:
8/23/2024, 10:43:33 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80055	No	2021-12-02		hypothetical protein SEA_DOGGS_55 [Gordonia phage Doggs]	97.6331	100	100	169	1	169	1	169	0	4.24688e-115
☐	AXH45834	No	2021-12-01		hypothetical protein SEA_GEAZY_65 [Gordonia phage GEazy] >gb|QDF16774.1| hypothetical protein SEA_HANNAHD_62 [Gordonia phage HannahD]	82.716	87.037	92.8994	141	6	162	13	169	0	4.41137e-88
					hypothetical protein BIZ71_gp61 [Gordonia										



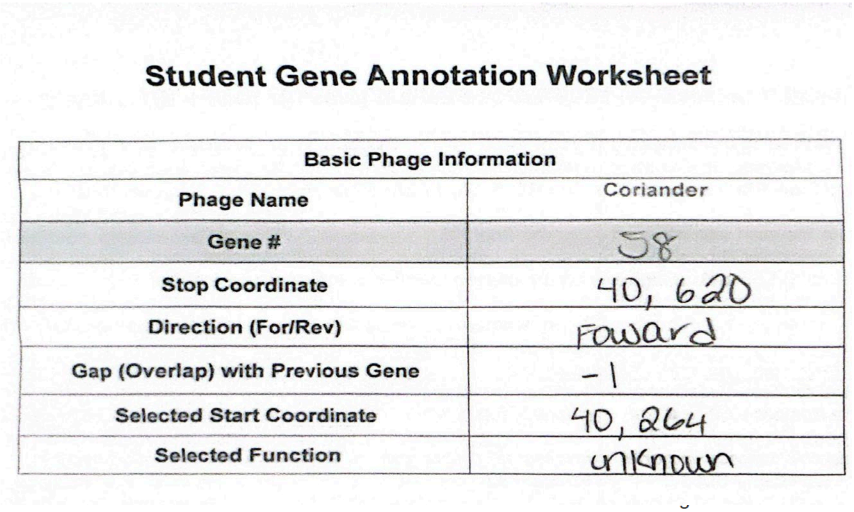
HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:01:20 PM
Last Updated:
8/23/2024, 4:01:20 PM

Show 10 entries Search:

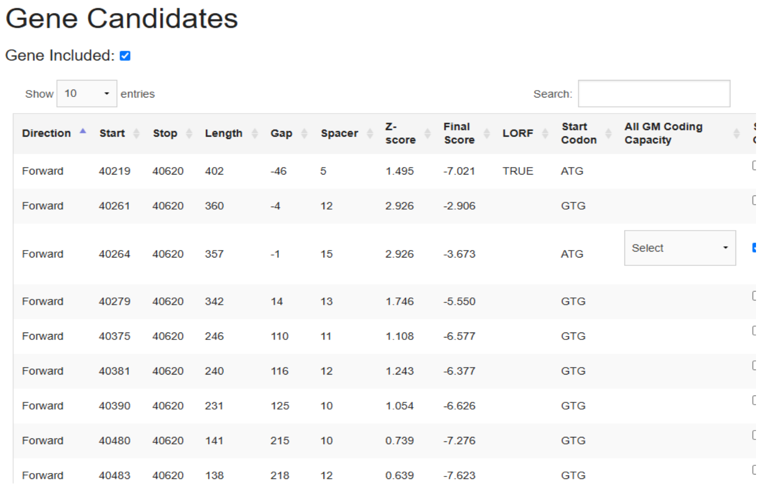
Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-va
☐	3Q20_A	RbcX protein; helix bundle, chaperone, RuBisCO assembly; HET: HEZ; 1.71A {Thermosynechococcus elongatus} SCOP: a.280.1.0	37.2	42.6035	42	107	28	100	42
☐	cd16837	BldD_C_like; C-terminal domain of BldD and similar transcription factors. The Streptomyces transcription factor BldD dimerizes via an unusual mechanism that inolves a tetrameric c-di-GMP assembly.	36.1	13.0178	24	46	140	162	44

Gene 58



Student Gene Annotation Worksheet

Basic Phage Information	
Phage Name	Coriander
Gene #	58
Stop Coordinate	40, 620
Direction (For/Rev)	Foward
Gap (Overlap) with Previous Gene	-1
Selected Start Coordinate	40, 264
Selected Function	unknown

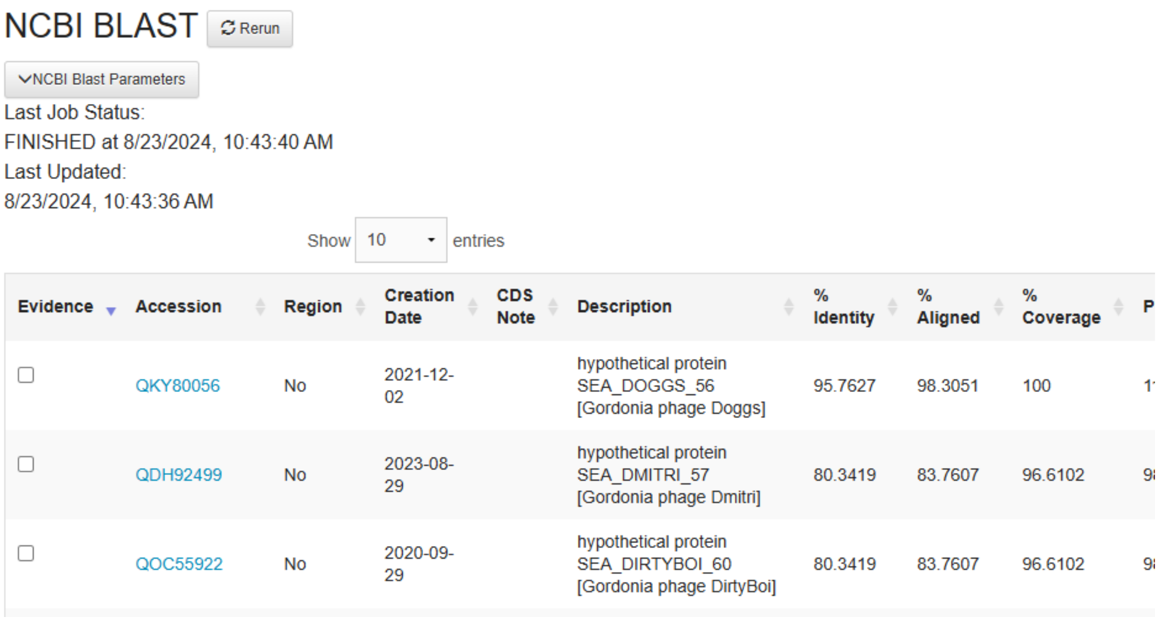


Gene Candidates

Gene Included: ☑

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	
Forward	40219	40620	402	-46	5	1.495	-7.021	TRUE	ATG		☐
Forward	40261	40620	360	-4	12	2.926	-2.906		GTG		☐
Forward	40264	40620	357	-1	15	2.926	-3.673		ATG	Select	☑
Forward	40279	40620	342	14	13	1.746	-5.550		GTG		☐
Forward	40375	40620	246	110	11	1.108	-6.577		GTG		☐
Forward	40381	40620	240	116	12	1.243	-6.377		GTG		☐
Forward	40390	40620	231	125	10	1.054	-6.626		GTG		☐
Forward	40480	40620	141	215	10	0.739	-7.276		GTG		☐
Forward	40483	40620	138	218	12	0.639	-7.623		GTG		☐

- Coriander_58 Start: 40264, Stop: 40620, Start Num: 42 Candidate Starts for Coriander_58: (29, 40219), (40, 40261), (Start: 42 @40264 has 7 MA's), (Start: 46 @40279 has 1 MA's), (56, 40375), (57, 40381), (59, 40390), (66, 40480), (67, 40483), (71, 40519), (76, 40567),

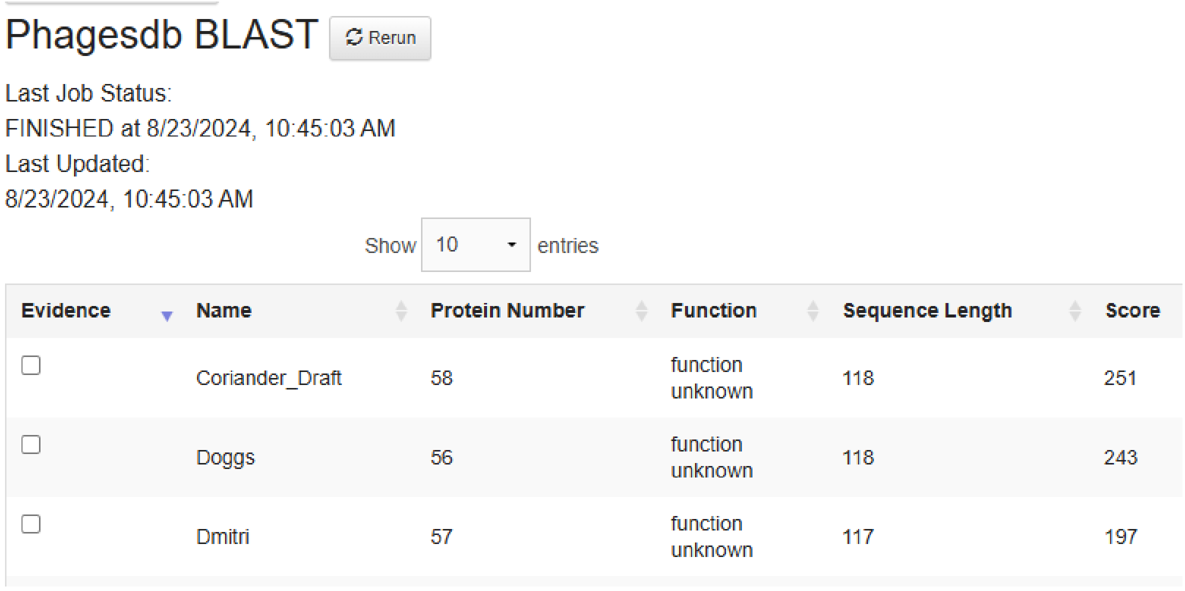


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:43:40 AM
Last Updated:
8/23/2024, 10:43:36 AM

Show 10 entries

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	P
☐	QKY80056	No	2021-12-02		hypothetical protein SEA_DOGGS_56 [Gordonia phage Doggs]	95.7627	98.3051	100	
☐	QDH92499	No	2023-08-29		hypothetical protein SEA_DMITRI_57 [Gordonia phage Dmitri]	80.3419	83.7607	96.6102	
☐	QOC55922	No	2020-09-29		hypothetical protein SEA_DIRTYBOI_60 [Gordonia phage DirtyBoi]	80.3419	83.7607	96.6102	

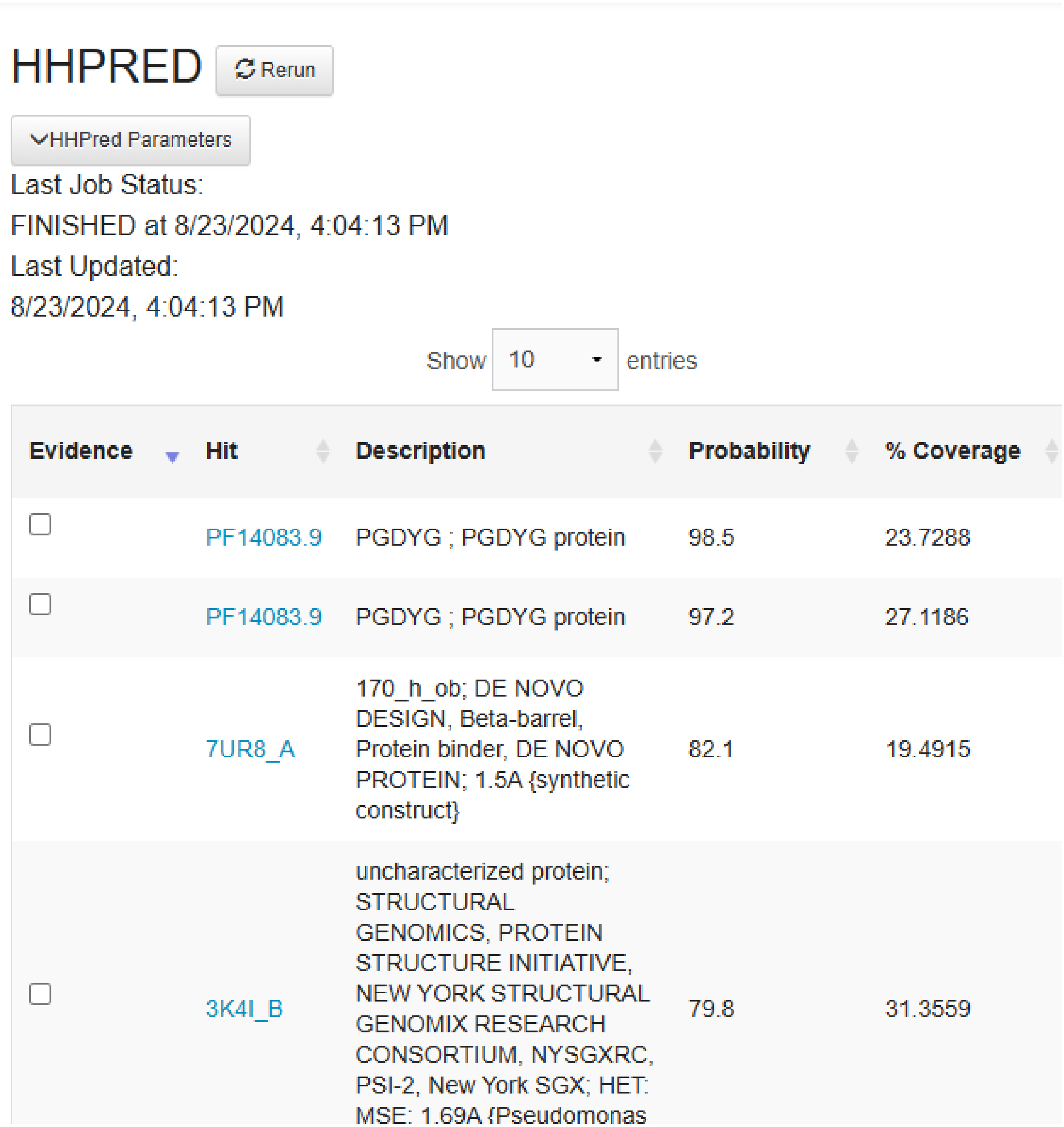


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:45:03 AM
Last Updated:
8/23/2024, 10:45:03 AM

Show 10 entries

Evidence	Name	Protein Number	Function	Sequence Length	Score
☐	Coriander_Draft	58	function unknown	118	251
☐	Doggs	56	function unknown	118	243
☐	Dmitri	57	function unknown	117	197



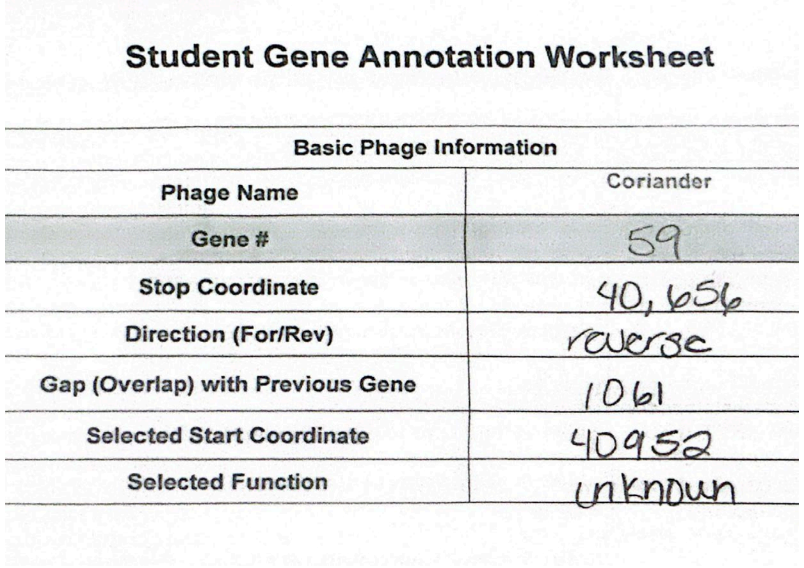
HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:04:13 PM
Last Updated:
8/23/2024, 4:04:13 PM

Show 10 entries

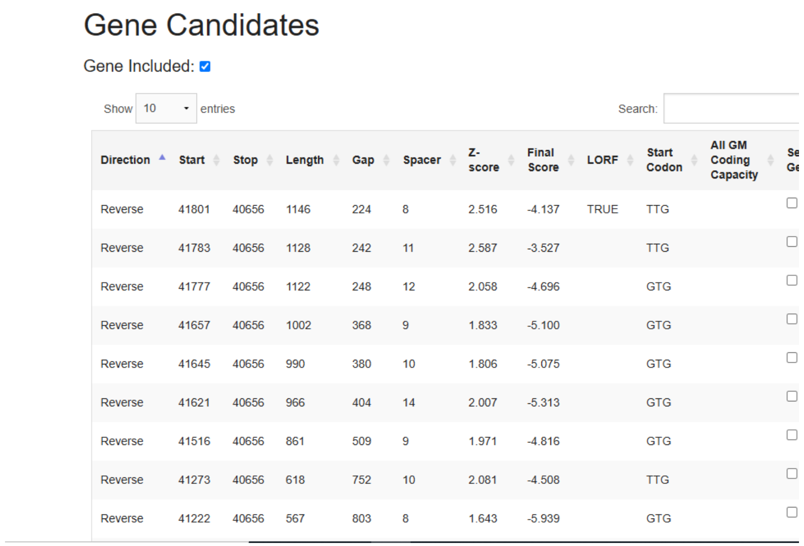
Evidence	Hit	Description	Probability	% Coverage
☐	PF14083.9	PGDYG ; PGDYG protein	98.5	23.7288
☐	PF14083.9	PGDYG ; PGDYG protein	97.2	27.1186
☐	7UR8_A	170_h_ob; DE NOVO DESIGN, Beta-barrel, Protein binder, DE NOVO PROTEIN; 1.5A {synthetic construct}	82.1	19.4915
☐	3K4I_B	uncharacterized protein; STRUCTURAL GENOMICS, PROTEIN STRUCTURE INITIATIVE, NEW YORK STRUCTURAL GENOMIX RESEARCH CONSORTIUM, NYSGXRC, PSI-2, New York SGX; HET: MSE; 1.69A {Pseudomonas	79.8	31.3559

Gene 59



Student Gene Annotation Worksheet

Basic Phage Information	
Phage Name	Coriander
Gene #	59
Stop Coordinate	40,656
Direction (For/Rev)	reverse
Gap (Overlap) with Previous Gene	1061
Selected Start Coordinate	40952
Selected Function	unknown



Gene Candidates

Gene Included: ☑

Show 10 entries

Search:

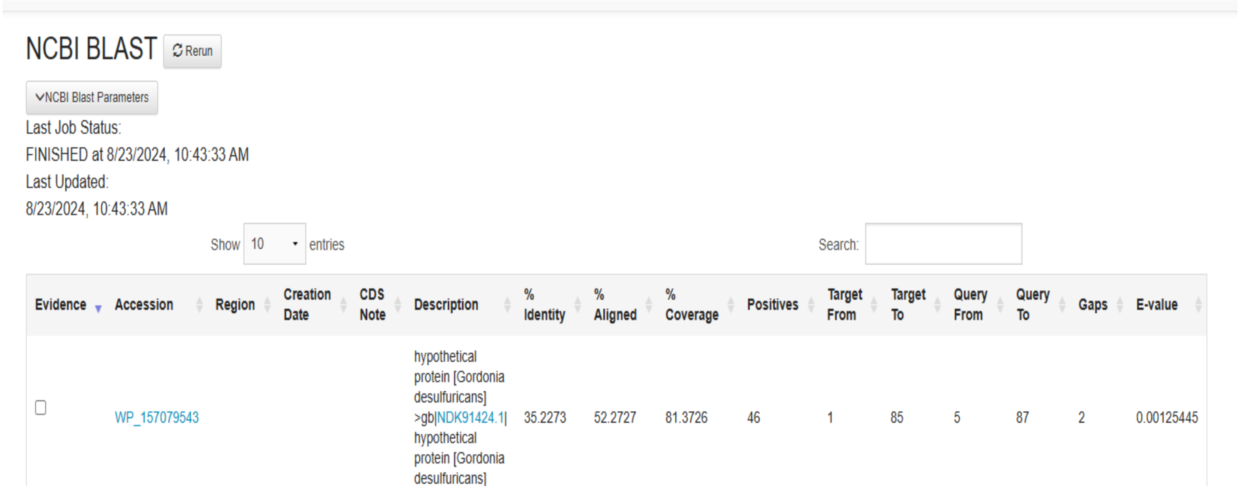
Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Se Ge
Reverse	41801	40656	1146	224	8	2.516	-4.137	TRUE	TTG		☐
Reverse	41783	40656	1128	242	11	2.587	-3.527		TTG		☐
Reverse	41777	40656	1122	248	12	2.058	-4.696		GTG		☐
Reverse	41657	40656	1002	368	9	1.833	-5.100		GTG		☐
Reverse	41645	40656	990	380	10	1.806	-5.075		GTG		☐
Reverse	41621	40656	966	404	14	2.007	-5.313		GTG		☐
Reverse	41516	40656	861	509	9	1.971	-4.816		GTG		☐
Reverse	41273	40656	618	752	10	2.081	-4.508		TTG		☐
Reverse	41222	40656	567	803	8	1.643	-5.939		GTG		☐

CORIANDER_59 START: 40952,STOP:40656.GLIMMER START:40964, GLIMMER SCORE:2.44,GENEMARK START:41012

Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:45:18 AM
Last Updated:
8/23/2024, 10:45:18 AM

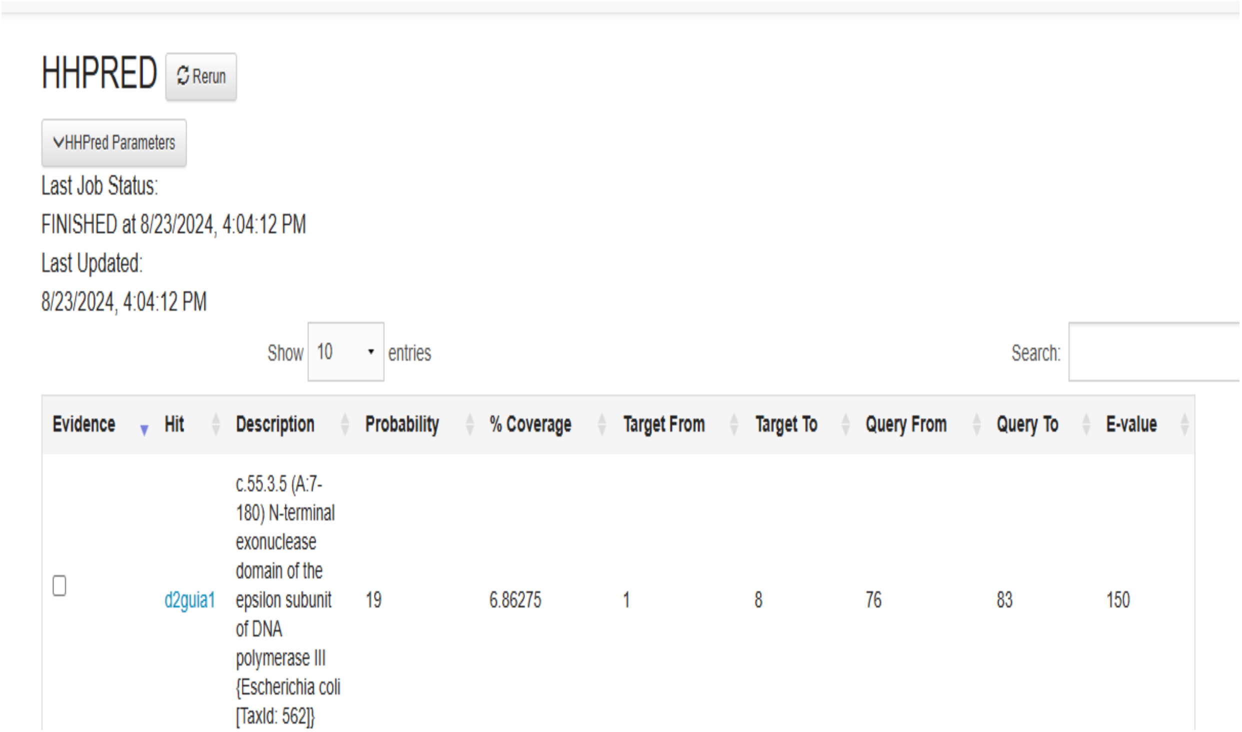
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	59	function unknown	102	207	6e-54	DB	138983
☐	BackstagePass_Draft	66	function unknown	281	137	7e-33	DB	100744
☐	Mischief19	58	DNA primase	737	28	8.1	BG	5498



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:43:33 AM
Last Updated:
8/23/2024, 10:43:33 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	WP_157079543				hypothetical protein [Gordonia desulfuricans] >gb|NDK91424.1| hypothetical protein [Gordonia desulfuricans]	35.2273	52.2727	81.3726	46	1	85	5	87	2	0.00125445



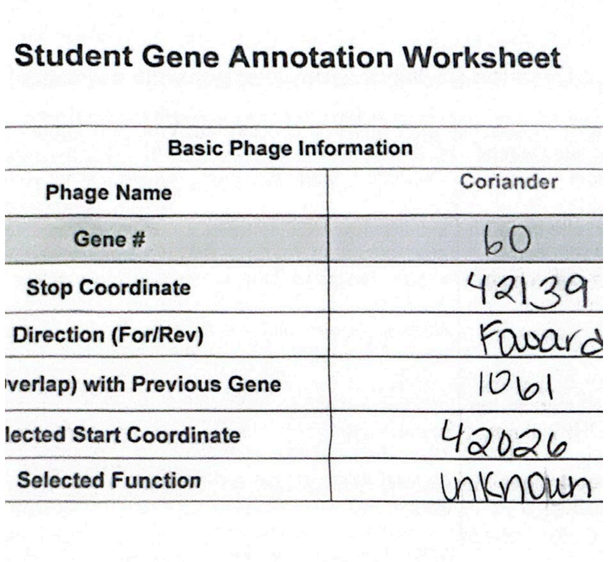
HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:04:12 PM
Last Updated:
8/23/2024, 4:04:12 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d2guia1	c.55.3.5 (A:7-180) N-terminal exonuclease domain of the epsilon subunit of DNA polymerase III {Escherichia coli [TaxId: 562]}	19	6.86275	1	8	76	83	150

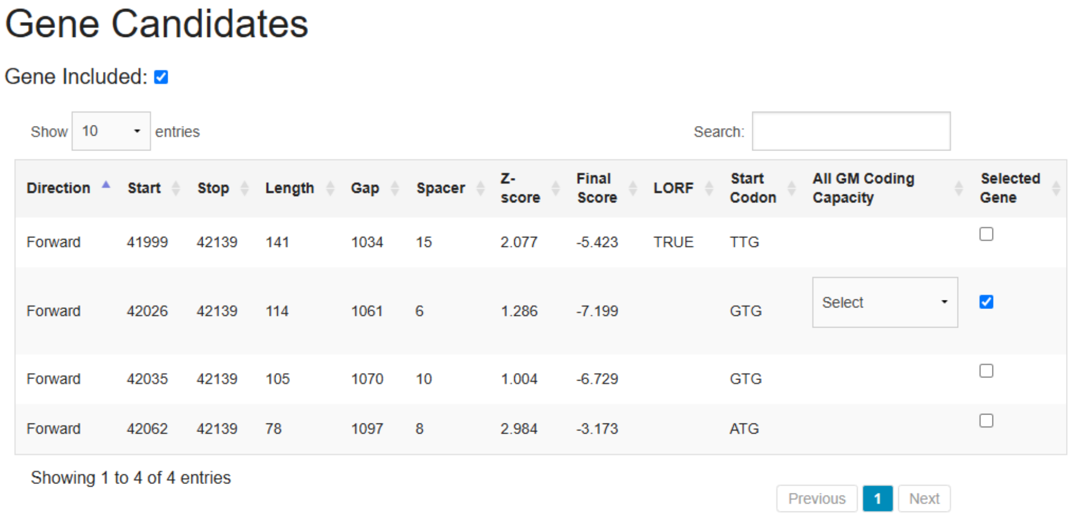
Gene 60

- Coriander_60 Start: 42026, Stop: 42139, Start Num: 2 Candidate Starts for Coriander_60: (1, 41999), (2, 42026), (3, 42035), (4, 42062),



Student Gene Annotation Worksheet

Basic Phage Information	
Phage Name	Coriander
Gene #	60
Stop Coordinate	42139
Direction (For/Rev)	Foward
verlap) with Previous Gene	1061
lected Start Coordinate	42026
Selected Function	unknown

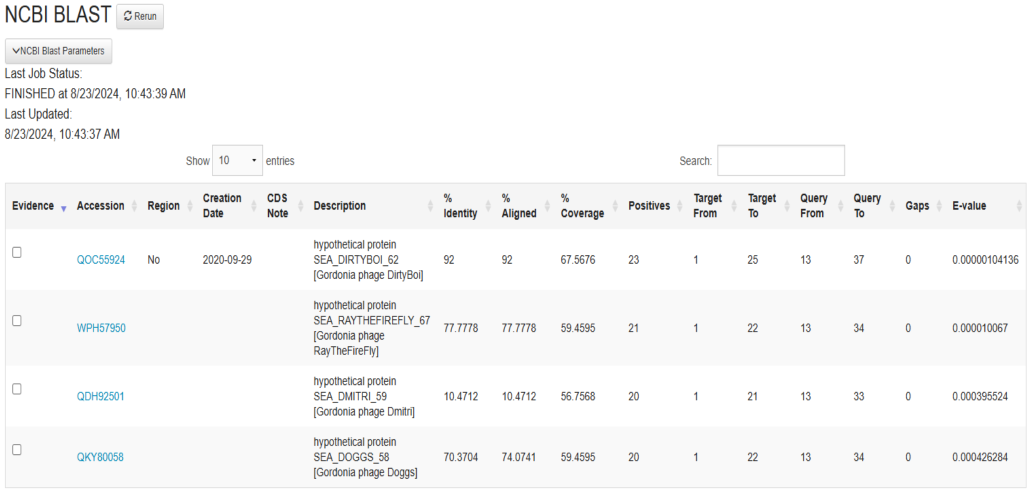


Gene Candidates

Gene Included: ☑

Direction	Start	Stop	Length	Gap	Spacer	Z-score	Final Score	LORF	Start Codon	All GM Coding Capacity	Selected Gene
Forward	41999	42139	141	1034	15	2.077	-5.423	TRUE	TTG		☐
Forward	42026	42139	114	1061	6	1.286	-7.199		GTG	Select	☑
Forward	42035	42139	105	1070	10	1.004	-6.729		GTG		☐
Forward	42062	42139	78	1097	8	2.984	-3.173		ATG		☐

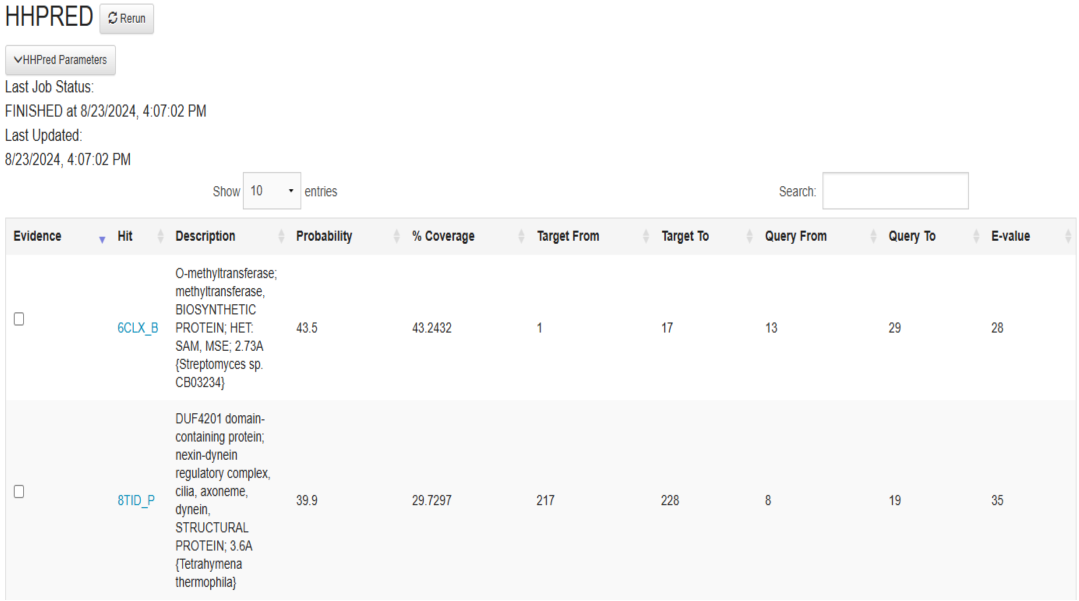
Showing 1 to 4 of 4 entries



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:43:39 AM
Last Updated:
8/23/2024, 10:43:37 AM

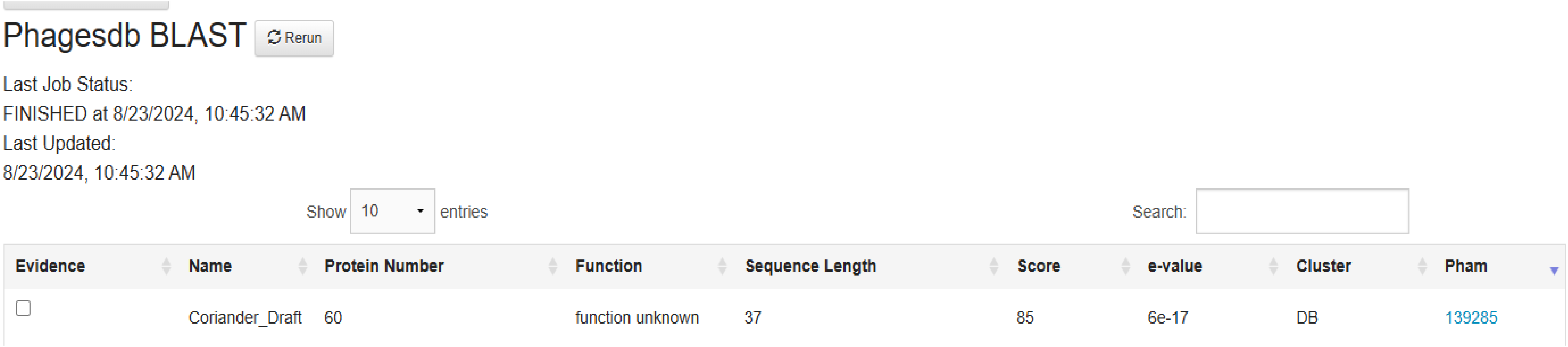
Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QOC55924	No	2020-09-29		hypothetical protein SEA_DIRTYBOI_62 [Gordonia phage DirtyBoi]	92	92	67.5676	23	1	25	13	37	0	0.00000104136
☐	WPH57950				hypothetical protein SEA_RAYTHEFIREFLY_67 [Gordonia phage RayTheFireFly]	77.7778	77.7778	59.4595	21	1	22	13	34	0	0.000010067
☐	QDH92501				hypothetical protein SEA_DMITRI_59 [Gordonia phage Dmitri]	10.4712	10.4712	56.7568	20	1	21	13	33	0	0.000395524
☐	QKY80058				hypothetical protein SEA_DOGGS_58 [Gordonia phage Doggs]	70.3704	74.0741	59.4595	20	1	22	13	34	0	0.000426284



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:07:02 PM
Last Updated:
8/23/2024, 4:07:02 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	6CLX_B	O-methyltransferase; methyltransferase, BIOSYNTHETIC PROTEIN; HET: SAM, MSE; 2.73A {Streptomyces sp. CB03234}	43.5	43.2432	1	17	13	29	28
☐	8TID_P	DUF4201 domain-containing protein; nexin-dynein regulatory complex, cilia, axoneme, dynein, STRUCTURAL PROTEIN; 3.6A {Tetrahymena thermophila}	39.9	29.7297	217	228	8	19	35



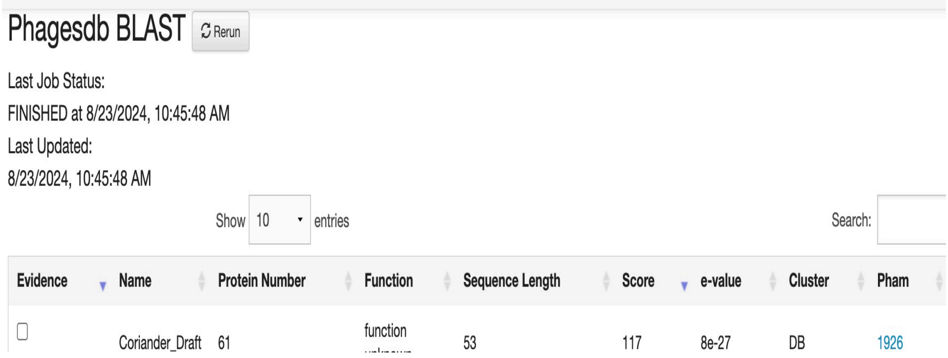
Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:45:32 AM
Last Updated:
8/23/2024, 10:45:32 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	60	function unknown	37	85	6e-17	DB	139285

61 - 66

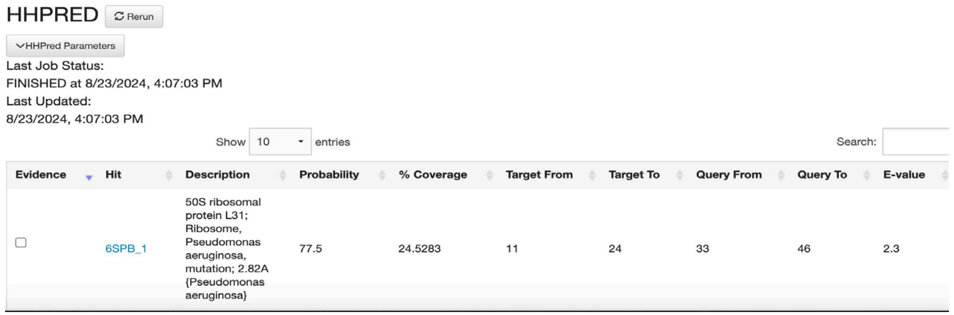
Basic Phage Information	
Phage Name	Coriander_61
Gene #	Gene 61
Stop Coordinate	42,297
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlaps with Gene 60 at 42,136 to 42139
Selected Start Coordinate	42,136
Selected Function	Function Unknown- Most likely a Hypothetical Protein



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:45:48 AM
Last Updated:
8/23/2024, 10:45:48 AM

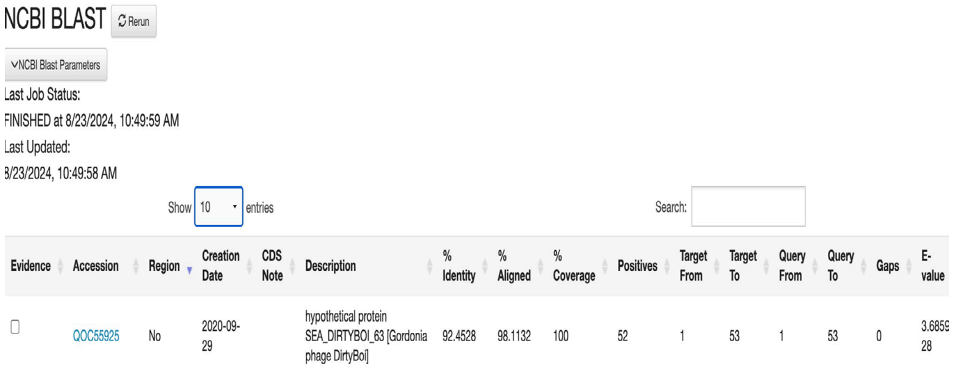
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	61	function	53	117	8e-27	DB	1926



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:07:03 PM
Last Updated:
8/23/2024, 4:07:03 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	6SPB_1	50S ribosomal protein L31; Ribosome, Pseudomonas aeruginosa, mutation; 2.82A {Pseudomonas aeruginosa}	77.5	24.5283	11	24	33	46	2.3



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:49:59 AM
Last Updated:
3/23/2024, 10:49:58 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QOC55925	No	2020-09-29		hypothetical protein SEA_DIRTYBOI_63 [Gordonia phage DirtyBoi]	92.4528	98.1132	100	52	1	53	1	53	0	3.6859 28

Coriander_61

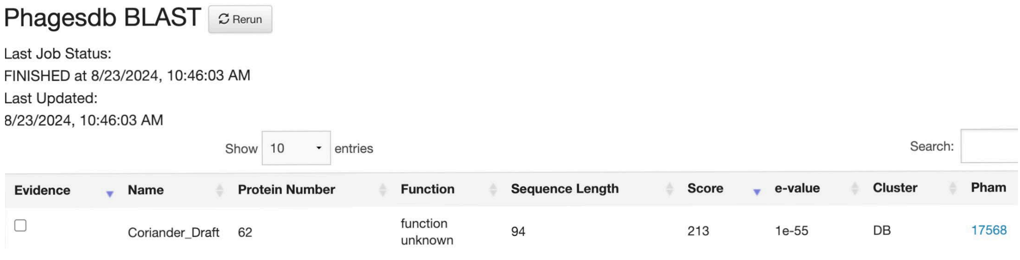
Phamerator Start: Gene 61_Start site (42136)
Glimmer Start: Gene 61_Start site (42136)
GeneMark Start: Gene 61_Start site (42136)

GeneMark

- Gene: Coriander_61 Start: 42136, Stop: 42297, Start Num: 9 Candidate Starts for Coriander_61: (7, 42118), (Start: 9 @42136 has 6 MA's), (21, 42265),

Basic Phage Information

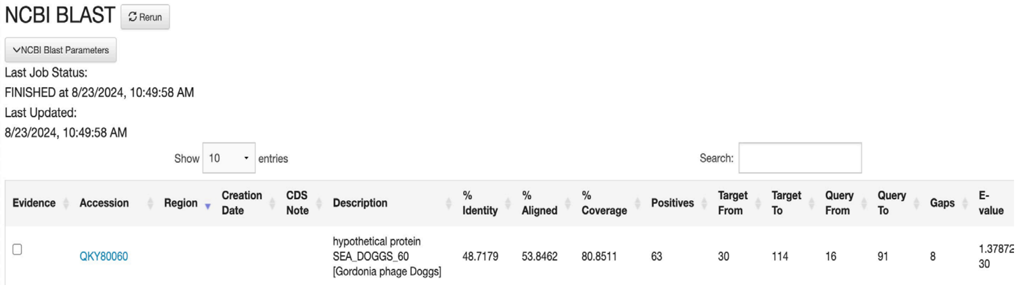
Phage Name	Coriander_62
Gene #	Gene 62
Stop Coordinate	42,578
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlaps with Gene 61 at 42,296 and 42,297
Selected Start Coordinate	42,294
Selected Function	Function Unknown- Most likely a Hypothetical Protein



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:46:03 AM
Last Updated:
8/23/2024, 10:46:03 AM

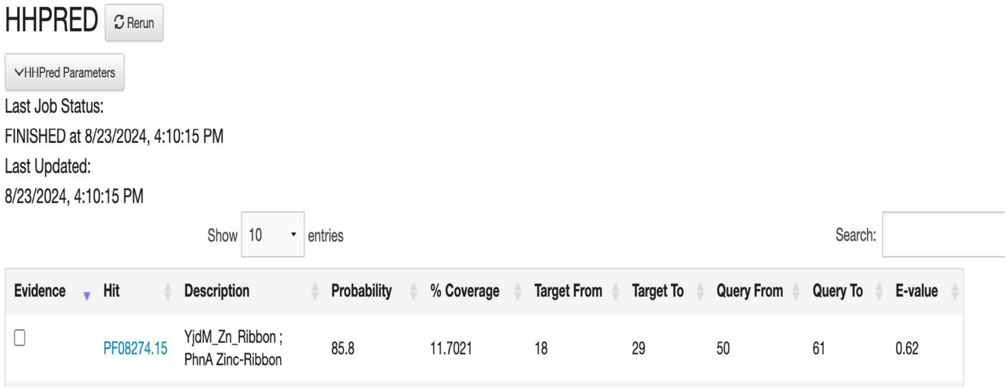
Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	62	function unknown	94	213	1e-55	DB	17568



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:49:58 AM
Last Updated:
8/23/2024, 10:49:58 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80060				hypothetical protein SEA_DOGGS_60 [Gordonia phage Doggs]	48.7179	53.8462	80.8511	63	30	114	16	91	8	1.37872 30



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:10:15 PM
Last Updated:
8/23/2024, 4:10:15 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF08274.15	YjdM_Zn_Ribbon ; PhnA Zinc-Ribbon	85.8	11.7021	18	29	50	61	0.62

Coriander_62

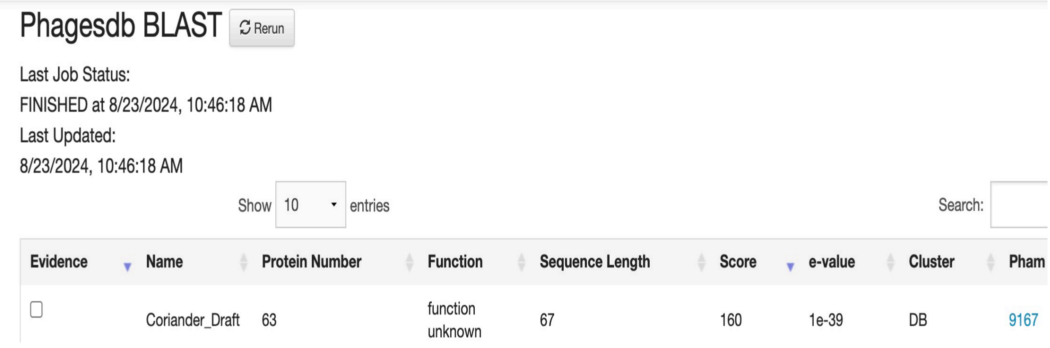
Phamerator Start: Gene 62_Start site (42294)
Glimmer Start: Gene 62_Start site (42294)
GeneMark Start: Gene 62_Start site (42294)

GeneMark

- Gene: Coriander_62 Start: 42294, Stop: 42578, Start Num: 6 Candidate Starts for Coriander_62: (1, 42243), (2, 42249), (3, 42261), (5, 42279), (6, 42294), (8, 42411), (9, 42420), (10, 42435), (13, 42543),

Basic Phage Information

Phage Name	Coriander_63
Gene #	Gene 63
Stop Coordinate	42778
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlaps with Gene 62 at 42,575 to 42,578
Selected Start Coordinate	42,575
Selected Function	Function Unknown- Most Likely a Hypothetical Protein



Phagesdb BLAST

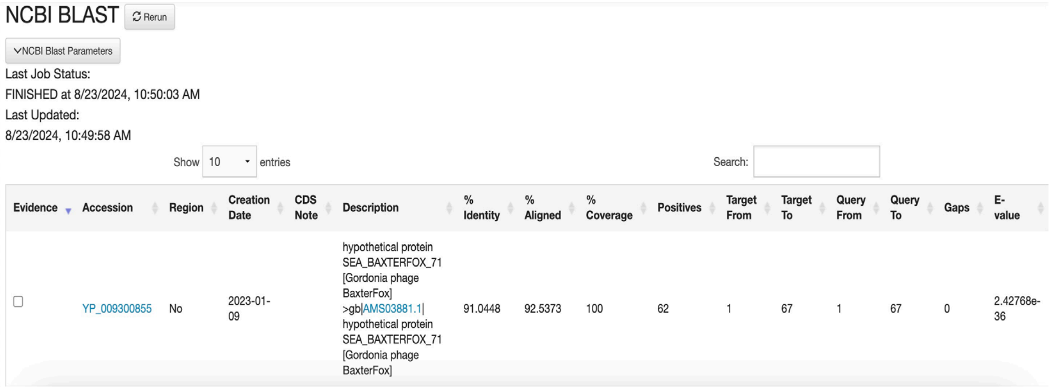
Last Job Status:
FINISHED at 8/23/2024, 10:46:18 AM
Last Updated:
8/23/2024, 10:46:18 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	63	function unknown	67	160	1e-39	DB	9167

HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:13:58 PM
Last Updated:
8/23/2024, 4:13:58 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF03966.19	Trm112p ; Trm112p-like protein	88.2	38.806	8	36	31	57	0.35



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:50:03 AM
Last Updated:
8/23/2024, 10:49:58 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_009300855	No	2023-01-09		hypothetical protein SEA_BAXTERFOX_71 [Gordonia phage BaxterFox] >gb|AMS03881.1| hypothetical protein SEA_BAXTERFOX_71 [Gordonia phage BaxterFox]	91.0448	92.5373	100	62	1	67	1	67	0	2.42768e-36

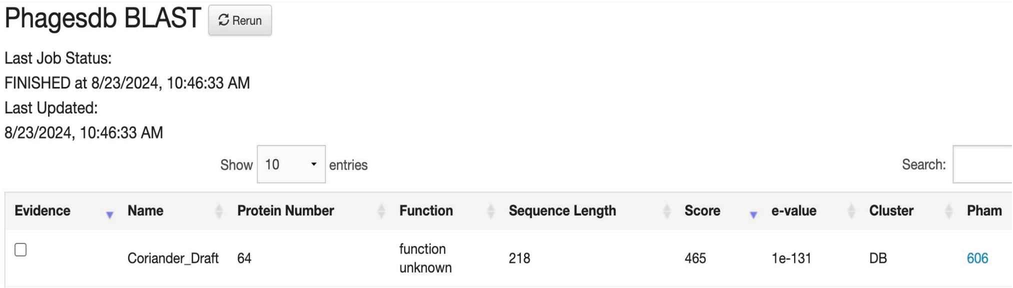
Coriander_63

Phamerator Start: Gene 63_Start site (42575)
Glimmer Start: Gene 63_Start site (42575)
GeneMark Start: Gene 63_Start site (42575)

GeneMark

- Gene: Coriander_63 Start: 42575, Stop: 42778, Start Num: 1 Candidate Starts for Coriander_63: (Start: 1 @42575 has 1 MA's), (3, 42596), (5, 42698),

Basic Phage Information	
Phage Name	Coriander 64
Gene #	Gene 64
Stop Coordinate	43,434
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlaps with Gene 63 at 42,778
Selected Start Coordinate	42,775
Selected Function	Function Unknown- Most Likely a Hypothetical Protein

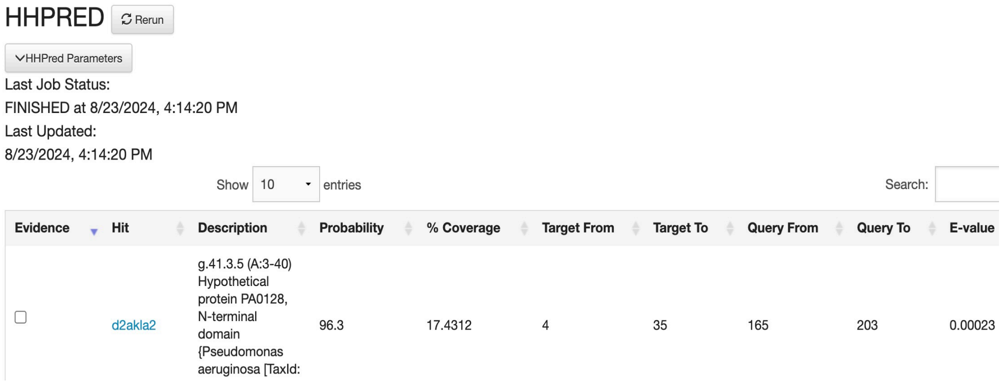


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:46:33 AM
Last Updated:
8/23/2024, 10:46:33 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	64	function unknown	218	465	1e-131	DB	606

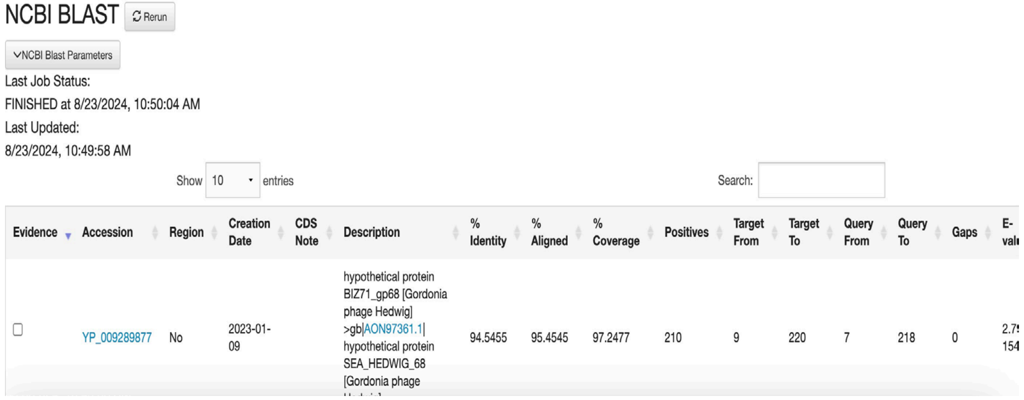


HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:14:20 PM
Last Updated:
8/23/2024, 4:14:20 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	d2akla2	g.41.3.5 (A:3-40) Hypothetical protein PA0128, N-terminal domain {Pseudomonas aeruginosa [TaxId:	96.3	17.4312	4	35	165	203	0.00023



NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:50:04 AM
Last Updated:
8/23/2024, 10:49:58 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-val
☐	YP_009289877	No	2023-01-09		hypothetical protein BIZ71_gp68 [Gordonia phage Hedwig] >gb|AON97361.1| hypothetical protein SEA_HEDWIG_68 [Gordonia phage	94.5455	95.4545	97.2477	210	9	220	7	218	0	2.7 154

Coriander_64

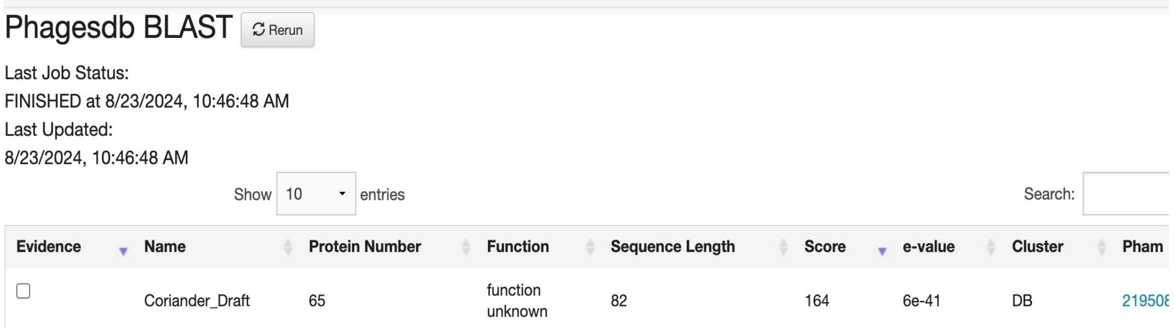
Phamerator Start: Gene 64_Start site (42775)
Glimmer Start: Gene 64_Start site (42775)
GeneMark Start: Gene 64_Start site (42775)

GeneMark

Gene: Coriander_64 Start: 42778, Stop: 43434, Start Num: 69 Candidate Starts for Coriander_64: (Start: 67 @42775 has 1 MA's), (69, 42778), (87, 43033), (88, 43057), (89, 43075), (91, 43111), (92, 43120), (94, 43135), (100, 43177), (105, 43249), (112, 43324), (114, 43345), (115, 43369), (119, 43405

Basic Phage Information

Phage Name	Coriander 65
Gene #	Gene 65
Stop Coordinate	43,793
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	None
Selected Start Coordinate	43,545
Selected Function	Function Unknown- Most likely helix-turn-helix DNA binding domain protein

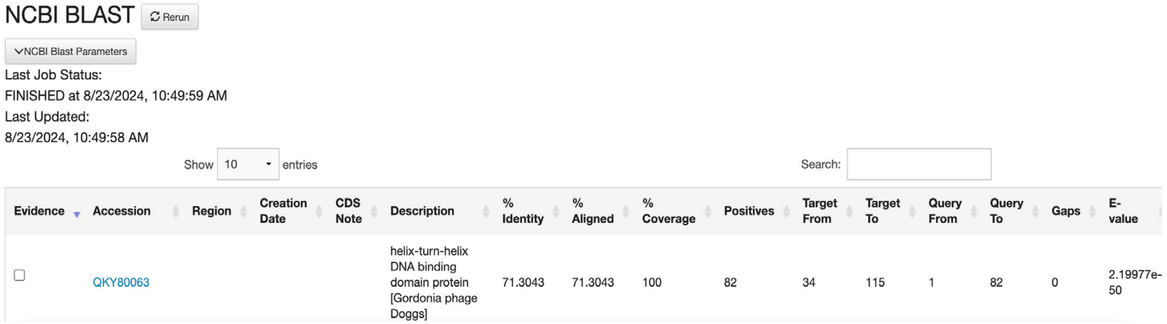


Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:46:48 AM
Last Updated:
8/23/2024, 10:46:48 AM

Show 10 entries Search:

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	65	function unknown	82	164	6e-41	DB	219508

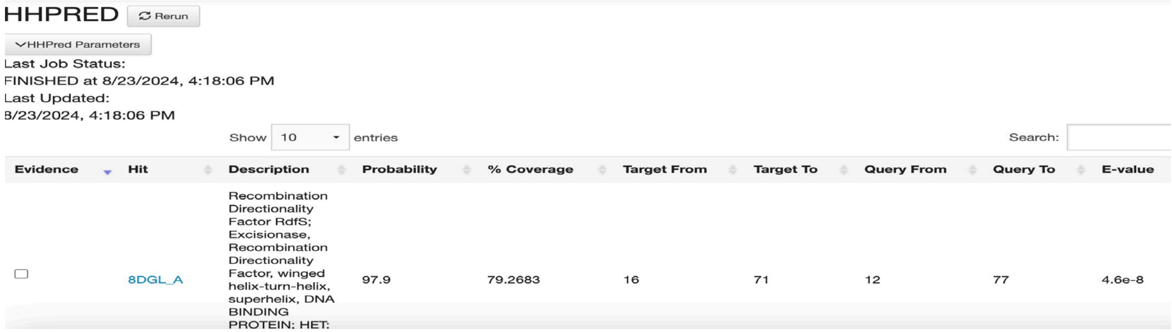


NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:49:59 AM
Last Updated:
8/23/2024, 10:49:58 AM

Show 10 entries Search:

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	QKY80063				helix-turn-helix DNA binding domain protein [Gordonia phage Doggs]	71.3043	71.3043	100	82	34	115	1	82	0	2.19977e-50



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:18:06 PM
Last Updated:
8/23/2024, 4:18:06 PM

Show 10 entries Search:

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	8DGL_A	Recombination Directionality Factor RdfS; Excisionase, Recombination Directionality Factor, winged helix-turn-helix, superhelix, DNA BINDING PROTEIN; HET:	97.9	79.2683	16	71	12	77	4.6e-8

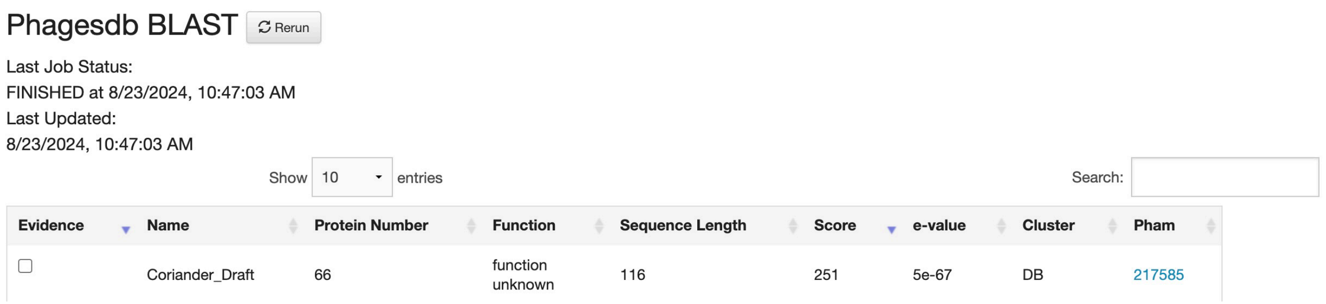
Coriander_65

Phamerator Start: Gene 65_Start site (43545)
Glimmer Start: Gene 65_Start site (43545)
GeneMark Start: Gene 65_Start site (43545)

GeneMark

- Gene: Coriander_65 Start: 43545, Stop: 43793, Start Num: 32 Candidate Starts for Coriander_65: (Start: 32 @43545 has 97 MA's), (Start: 35 @43560 has 4 MA's), (41, 43632), (50, 43737), (52, 43746)

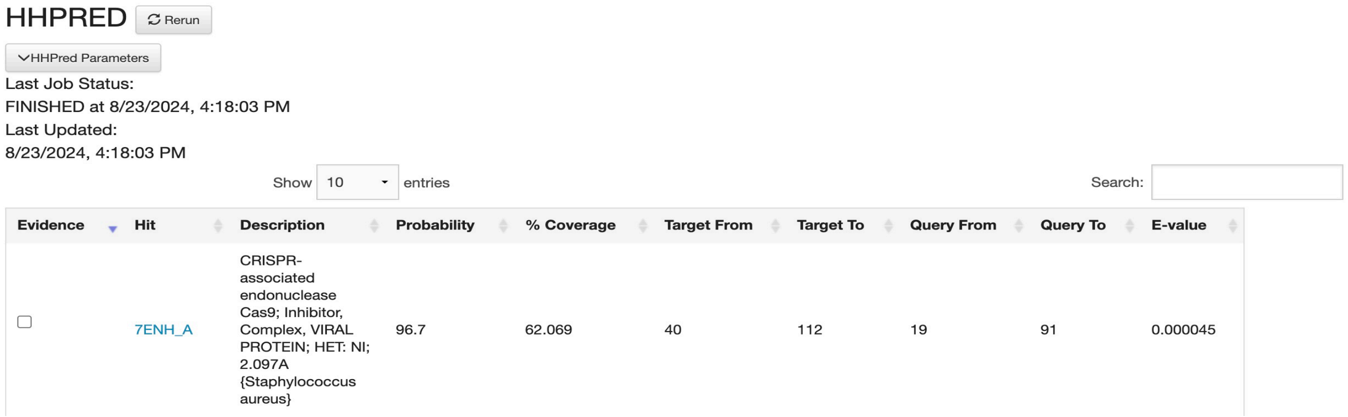
Basic Phage Information	
Phage Name	Coriander 66
Gene #	Gene 66
Stop Coordinate	44,143
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Overlaps with Gene 65 at 43,793
Selected Start Coordinate	43,793
Selected Function	Function Unknown- Most likely HNH endonuclease



Phagesdb BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:47:03 AM
Last Updated:
8/23/2024, 10:47:03 AM

Evidence	Name	Protein Number	Function	Sequence Length	Score	e-value	Cluster	Pham
☐	Coriander_Draft	66	function unknown	116	251	5e-67	DB	217585



HHPRED

Last Job Status:
FINISHED at 8/23/2024, 4:18:03 PM
Last Updated:
8/23/2024, 4:18:03 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	7ENH_A	CRISPR-associated endonuclease Cas9; Inhibitor, Complex, VIRAL PROTEIN; HET: NI; 2.097A {Staphylococcus aureus}	96.7	62.069	40	112	19	91	0.000045

NCBI BLAST

Last Job Status:
FINISHED at 8/23/2024, 10:50:04 AM
Last Updated:
8/23/2024, 10:49:59 AM

Evidence	Accession	Region	Creation Date	CDS Note	Description	% Identity	% Aligned	% Coverage	Positives	Target From	Target To	Query From	Query To	Gaps	E-value
☐	YP_009289879	No	2023-01-09	HNH endonuclease	HNH endonuclease [Gordonia phage Hedwig] >gb|AON97363.1| HNH endonuclease [Gordonia phage Hedwig]	100	100	100	116	1	116	1	116	0	4.259e-

Coriander_66

Phamerator Start: Gene 66_Start site (43793)
Glimmer Start: Gene 66_Start site (43793)
GeneMark Start: Gene 66_Start site (43793)

GeneMark

- **Gene: Coriander_66 Start: 43793, Stop: 44143, Start Num: 45 Candidate Starts for Coriander_66: (29, 43616), (31, 43646), (Start: 45 @43793 has 85 MA's), (52, 43916), (55, 43934), (71, 44126)**