Bioinformatic studies of annotated proteins from marine phage

CR1 and its evolutionary relationship with other phages

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Goa University APRIL, 2023

DECLARATION

I hereby declare that the data presented in this Dissertation report entitled, " Bioinformatic studies of annotated proteins from marine phage CR1 and its evolutionary relationship with other phages" is based on the results of investigations carried out by me in the Marine Biotechnology discipline at the School of Biological Sciences and Biotechnology, Goa University under the Supervision/Mentorship of Prof. Sanjeev C. Ghadi and the same has not been submitted elsewhere for the award of a degree or diploma by me. Further, I understand that Goa University or its authorities will be not be responsible for the correctness of observations / experimental or other findings given the dissertation. I hereby authorize the University authorities to upload this dissertation on the dissertation repository or anywhere else as the UGC regulations demand and make it available to any one as needed.

Lannet

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1.INTRODUCTION

Viruses are the most prevalent "lifeforms" in the oceans and ubiquitous companions of cellular life forms. Most of the genetic variation within the aquatic ecosystem is stored in viruses (Curtis A. Suttle, 2007). Every cellular creature under investigation seems to have its own viruses, or at the very least, selfish genetic components resembling viruses. Recent environmental investigations have revealed that the "most abundant biological entities on the planet" are viruses, particularly bacteriophages. On Earth, there are thought to be 10³¹ viruses, the majority of which are bacteriophages (Breitbart M., Rohwer F., 2005).

Bacteriophages are nano-sized biological entities that infect bacteria for their survival and replication. The term "bacteriophage" comes from the Greek bæk toriou (bacterio)- bacteria and feidʒ (phage) —to kill or devour. They have been isolated from almost everywhere on our planet: common environments like soil and surface waters as well as extreme environments like hot springs, deep seas, etc. (Romancer et al., 2006). In nature, they keep the dominant bacterial population under control, and their infection is usually self-limiting. They are considered to play a key role in bacterial adaptive evolution by means of gene transfer (Davies, 2016).

The most frequently used classification divides tail components of bacteriophages according to their biological cycle (Fauquet and Pringle, 2000). Two groups are identified, lytic, or virulent, and lysogenic, or temperate, bacteriophages. In marine ecosystems, though they are anticipated to carry out infection mechanisms by both mechanisms, temperate phages are predicted to be more common (Tuttle M. J., Buchan A., 2020). Lytic phages, upon infection, cause the lysis of the host cell, while temperate phages insert their genome into the host genome and are then termed prophages. Bacterial hosts containing such phages are called lysogens. Prophages do not express their lytic genes until the host is under stress. This stress signals the virus to induce the expression of lytic genes, causing bacterial cell lysis. This lysis is visible in the form of plaques.

In the present study, a bacterial strain, CR1, is used and studied. Bacterial strain CR1 is a marine polysaccharide-degrading bacteria belonging to the genus *Microbulbifer* (Poduval et al., 2019). The genome studies of CR1 strain indicate the presence of lysogenic prophage.

Polysaccharides are the most frequent and complex organic substances in the ocean. Gammaproteobacteria belonging to and related to the genus *Microbulbifer* are an emerging group of complex carbohydrate-degrading marine bacteria (Nathan et al., 2005). Members of this genus can degrade complex carbohydrates such as cellulose, alginate, and chitin. The cell walls of macroalgae, in particular, include a high diversity of sulfated polysaccharides (carrageenans, agarans, fucoidans, ulvans, etc.), many of which are highly sulfated in contrast to terrestrial polysaccharides. These sulfated polysaccharides are a crucial source of nutrition for heterotrophic organisms and are biosynthesized by macroalgal primary producers (Aquino et. al., 2005).

OBJECTIVES

- Induction of lysogenic phage in *Microbulbifer* CR1 strain.
- Time dependence study to achieve maximum phage titre.
- Evolutionary studies of prophage proteins identified from the genome of *Microbulbifer* CR1 strain.

LITERATURE REVIEW

Marine bacteriophages:

The most prevalent type of biological organism is a bacteriophage. They can be found in extreme habitats, such as those with very high or very low temperatures, soil and seas, oceanic and terrestrial surfaces, and harsh environments in general (Clokie et al., 2011). Bacteria are the most common type of living organism in the oceans and are infected by most marine viruses, commonly referred to as "bacteriophages." Marine viruses are found at concentrations up to $\sim 1 \times 108$ ml–1, resulting in an estimated $\sim 4 \times 1030$ viruses in the oceans (Suttle 2005). However, the majority of bacteriophages are found in the vast, uncultured dark matter of the microbial biosphere. Marine bacteriophages have a significant impact on the makeup of microbial communities and the biogeochemical cycling of crucial components (Perez et al., 2016). One kilogram of marine sand may contain a million different viral genotypes, and it is estimated that there are 5,000 viral genotypes in 200 litres of saltwater. On the other hand, certain molecular and cultural studies have found that viruses move between various biomes. These findings suggest that viral diversity can be high locally but low globally. Additionally, viruses can assist horizontal gene transfer by hopping between environments (Breitbart, Rohwer, 2005). Viruses reach their host by passive diffusion, and the contact is proportional to the host's size and abundance (Murray and Jackson, 1992).

The importance of lysogeny in marine environments:

When a phage infects an appropriate host, one of two main replication routes can take place. One is the lytic cycle, in which the freshly generated viral offspring are released as the host cell explodes and the phage genome replicates right away after infection. The second is the lysogenic cycle, in which the host cell passes on the phage genome from generation to generation in an infectious state until the lytic cycle is triggered by elements like UV radiation or rapid host growth. Temperate phages are those that can develop lysogeny with their hosts, whereas virulent phages cannot. Because of their lytic powers, bacteriophages are known to be numerous and significant parts of oceanic food webs. Marine phages use a variety of infection tactics, but despite their apparent predominance, non-lytic phage-host interactions, such as lysogeny, are still poorly understood. According to estimations from sequenced marine genomes, lysogenization occurs in around half of marine bacteria. Prophages are frequently referred to as "time bombs" because of their delay before induction (Paul, 2008; Brum et al., 2016). Lysogeny is frequently associated with ocean conditions that are unfavorable to rapid host growth. Many of the marine phages can develop a symbiotic association with their hosts, termed as "lysogeny" (Ackermann and Dubow, 1987). A long-lasting relationship with the bacterial host is maintained by temperate phages that enter lysogeny, as opposed to lytic phages. The advantages of lysogeny from the perspective of phages are obvious, most notably the capability to survive times of low host abundance and the fact that it may provide a refuge from stressors. This situation can lead to the evolution of cooperative relationships that promote effective phage and bacterial reproduction. Large DNA insertions from temperate phages, which have the potential to interfere with gene expression and burden the cell's fitness, are integrated into the bacterial chromosome. They have also been demonstrated to help their bacterial hosts by supplying additional capabilities in a bacterium-phage symbiotic relationship known as lysogenic conversion (Feiner et. al. 2015).

Role of phages in biogeochemical cycles:

Viruses are commonly thought of as pathogens that wreak harm on plants and animals. Twort (1915) and d'Herelle (1917) were the first to describe the presence of substances that may both infect and kill bacteria. d'Herelle (1926) was one of the first researchers to look at viruses in aquatic environments was (Wilhelm SW, Subtle CA, 1999) The viral shunt pathway is a mechanism that prevents marine microbial particulate organic matter (POM) from migrating up trophic levels by recycling it into dissolved organic matter (DOM), which can be readily taken up by microorganisms. It has been demonstrated that the lysis of bacteria by viruses promotes nitrogen cycling and the growth of phytoplankton. In the water, there are roughly 1023 viral infections per second. These infections affect a variety of creatures, from prawns to whales, and are a significant cause of mortality. As a result, viruses have a significant impact on the structure of marine communities and drive several biogeochemical cycles. But in recent years, it has become more and more obvious that they are

essential to the world's oceans. The effect of viruses on the cycling of nutrients and carbon in the oceans is currently of significant interest (Steven W. Wilhelm, Curtis A. Suttle, 1999). They play a key role in the biogeochemical cycling of major elements, for example, by diverting the flow of carbon into dissolved and particulate organic matter through the lysis of their bacterial hosts, thus influencing the amount of carbon that is sequestered in the deep ocean by the biological pump.

Quantifying nutrient and energy flux requires an understanding of the mechanisms for the supply and recycling of organic carbon in aquatic systems. Because all organisms store energy in the form of chemical bonds inside complexes made of carbon, carbon can be thought of as a general tracer of energy transfer through biological systems. The majority of carbon enters the biological system through photosynthesis, where it is changed into sugars by plants and algae. Dissolved organic carbon (DOC) and particulate organic carbon (POC) are the two operating pools into which organic carbon in marine environments is typically divided. One of the main components of marine dissolved organic matter (DOM) is polysaccharides, and bacteria-derived polysaccharidases are primarily responsible for their breakdown. The identification of the mechanisms by which marine dissolved organic matter (DOM) is produced and regenerated is critical to developing a robust prediction of ocean carbon cycling (Lelchat et. al., 2019).

Numerous biomedical research has shown that in order to access their primary receptors, bacteriophages depolymerize their host capsule, slime, or biofilms via polysaccharidases (Bayer *et al.* 1979; Sutherland 1999; Sutherland *et al.* 2004). These enzymes, which are often found on phage tails, exhibit a great degree of functional and molecular diversity, and have the ability to affect viral biological characteristics, including host specificities (Sutherland 1999; Scholl, Adhya, and Merril 2005; Cornelissen *et al.* 2011, 2012; Yele *et al.* 2012). To the best of our knowledge, there is no experimental proof that marine phages have polysaccharidase activity. However, polysaccharides, also known as EPS, are actively produced by marine bacteria and either attached to the cell surface of the bacteria or discharged into the surrounding environment (Leiman *et al.* 2007).

A computational study of prophages:

Experimental approaches for the detection of lysogeny have certain limitations, such as that they require exposure to stressors or dilution of lysogen (Howard-Varona et al., 2017). They are inefficient

at detecting defective phages. With the advances in sequencing technologies, computational approaches are now being adopted for the detection of lysogeny.

Bacteriophages, especially those featuring a temperate lifestyle, are also the major driving force of horizontal gene exchange and bacterial evolution (Brussow et al., 2003; Casjens SR, 2005; Hendrix et al., 2004). Many bacterial genomes contain defective remnants of prophages that are a sign of previous infections or complete, fully functional prophages. They frequently make up a sizeable amount of the genetic material of bacteria (Klummp et al., 2013). A prophage region is described as a cluster or stretch of genes, possibly encoding proteins with bacteriophage-like core functions (i.e., terminase, portal, capsid), interspersed with genes of unknown function or or activities besides host lysis, morphogenesis, packaging, immunity, or phage replication. A real prophage is ultimately inducible, as opposed to defective prophages, which are the non-inducible by products of once-functional temperate bacteriophages. Every infection can provide fresh genetic material to a host or a progeny virus, accelerating the evolution of both the host and the viral assemblages. Exciting new information is always being discovered by probing this enormous pool of genetic and biological variation.

Any type of functional genomics study requires the full genome sequence of the bacteriophage being studied. Computational identification and examination of bacteriophage genomes, followed by phylogenetic analyses, are needed to understand the relationships between phage proteins and their roles.

Materials and Methods

4.1. Host bacteria and culture conditions:

The *Microbulbifer* strain CR1 was obtained from the culture collection of the Biotechnology- School of Biological Sciences and Biotechnology Goa University. The given bacterial strain grows only in specific media, i.e., artificial seawater (ASW). Hence, it was grown and maintained on ASW agar plates at room temperature. The agarolytic activity of the bacteria was checked by flooding the ASW + 2% agar plate with lugol's iodine after incubation at RT for 48 hrs.

4.2. Induction of phages by nutrient starvation:

- **Primary inoculation** The Microbulbifer CR1 was inoculated and grown in ASW broth containing 0.2% agar under shaking conditions for 24 hours at room temperature.
- Secondary inoculation 100µl of the primary culture broth was inoculated in ASW broth containing 0.2% glucose and was allowed to grow for 24 hours under shaking conditions at room temperature.
- Induction 100µl of ASW from the secondary culture was inoculated in ASW media without any nutrient source. The flask was kept in a shaker for the induction of lysogen.

4.3. Solid propagation of phages:

The double agar overlay technique, as described by Clokie and Kropinski, 2008, was used for phage propagation. The sterile petri-plates were first poured with ASW bottom agar (ASW + 2% agar). 1 mL of lysate was mixed with 1 mL of the grown host culture. This host-phage mix was then seeded into 2 ml of sterile molten soft agar (ASW + 1%) mixed, and poured onto sterile bottom agar. The plates were incubated at 30 °C for 24 hours for the visualization of plaques.

4.4. Induction of phage at different time intervals:

The phage induction by the starvation method was carried out for various time intervals (hours, 5 hours, 7 hours, 10 hours, 24 hours, and 48 hours). After incubation, the phages were visualized using the soft agar overlay method, as described above. The phage titre was calculated in terms of phage forming units per millilitre (pfu/ml).

4.5. Phylogenetic tree analysis:

The prophage sequences predicted from the CR1 bacterial genome were used for further analysis (Poduval et al., 2018, Renuka more, 2021). Out of the three complete prophage regions that were identified, one was used for this study. The annotated proteins (excluding hypothetical and predicted sequences) were used for phylogenetic analysis. The amino acid sequences with a sequence similarity cut-off of >90% and a minimum query coverage of 45% (in some proteins >25% also taken) for each protein were retrieved from the non-redundant protein database and the UniProt/SwissProt database by blastp. The amino acid sequence was aligned using the default parameters of MUSCLE on MEGA11. The sequences were trimmed, and gaps were removed. The neighbour-joining tree and maximum-likelihood trees were then built using default parameters and a bootstrap value of 1000.

Results and Discussion

5.1. Host Bacteria:

The bacterial strain CR1 was grown on ASW agar plates at room temperature for 48 hours. The bacteria formed a clearance zone when Lugol's iodine was poured on the plate. This indicates the agar degrading activity of CR1.



Fig. 5.1a. Bacterial strain CR1 on ASW agar plate.



Fig. 5.1b. Agarolytic activity of strain CR1.

5.2. Induction of Prophage:

The bacterial strain CR1 was allowed to grow in a medium without any carbon source. After incubation, the double agar overlay technique was performed by inoculating 1 ml of the culture. The plates showed the formation of clear plaques of about 1-2 mm in diameter. The formation of the plaques indicated the induction of prophage.

Nutrient starvation is a novel approach for the induction of prophages described by (Poduval et al., 2019). Limited nutrients resulted in the creation of a stressful environment for the bacteria, leading to the release of prophages from the host genome and the subsequent activation of lytic genes. Lysis was evident in the form of visible plaques.



Fig. 5.2. Induction of Prophage. Double agar overlay shows clear plaques of phage CR1

5.3. Induction of phage at different time intervals:

1 ml of the host culture growing in the absence of a carbon source was used to perform a double agar overlay at different time intervals. Previous studies showed that complete lysis was observed after 24 hours of incubation, and thereafter, the titre gradually decreased. Hence, in order to attain a high titre of plaques, the double agar overlay was done within the 24-hour time interval. The plaques were counted for each interval, and the Plaque forming unit per ml (Pfu/ml) was calculated.

Incubation time (In hrs)	3 hours	5 hours	7 hours	10 hours	24 hours	72 hours
Pfu/mL	84	67	56	45	30	12

 Table 1. Phage titre at different time



Fig 5.3. Phage titre at different time intervals



5.4. Sequence

phylogenetic tree analysis:

Based on the previous studies (Poduval et al., 2019; More, 2021), the CR1 strain has several complete and incomplete prophages. One of the complete prophages, i.e., region 1, has been taken to study its phylogenetics. Region 1 had 33 proteins annotated, out of which 14 are hypothetical and not included in the study, while the rest 19 were studied.

Below are the annotations and position of proteins studied:

S. NO.	ANNOTATION	POSITION
HEAD PF	ROTEINS	
1.	PHAGE head completion-stabilization protein	1342713633
2.	PHAGE gpE+E	2326523381
BASEPLA	ATE PROTEIN	
3.	PHAGE putative baseplate assembly protein V	1647017186
4.	PHAGE: gp16	2114322309
5.	PHAGE baseplate assembly protein J	1752718534
6.	PHAGE gp33	1110412117
CAPSID	PROTEINS	
7.	capsid scaffolding protein	1024511066
8.	PHAGE CR1 gp36	72998324
9.	PHAGE gp15	2234722856
10.	PHAGE gp23	1551915965
TAIL PRO	DTEINS	

11.	PHAGE tail component protein	1342713633
12.	PHAGE tail protein	1718317530
13.	PHAGE tail completion protein-like protein	1509515526
14.	PHAGE tail tape measure protein	2339325897
15.	PHAGE putative phage tail protein	2590526333
16.	PHAGE phage tail protein D	2633327406
17.	PHAGE gp9	2936029674
18.	PHAGE gp13	2295723238
19.	PHAGE tail collar domain protein	1915021051

Table 2. PHAGE CR1 protein annotations and its position.

5.4.1. PHAGE CR1 Gp9 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Gp9 protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Gp9 phage protein of *Pseudomonas mirosoviensis* exhibited a 65% sequence similarity with *Phage CR1* Gp9 protein, the phylogenetically closest species with standing members in the tree. Phage protein Gp9 is a component of non-contractile tail, by hydrolyzing the glycosidic connection between rhamnose and galactose in the O-antigen polysaccharide, which is a part of the phage protein Gp9, the capsid is brought close to the cell membrane and mediates initial attachment to the lipopolysaccharides (LPS) of the host cell. *Pseudomonas mirosoviensis* are mostly environmental bacteria widely distributed in soil, water, and air. Most of the host species found in top hits are present in all habitats but their common habitat is terrestrial, except *Comamonas piscis*, which is marine.



Fig 5.5. Phylogenetic analysis of Phage CR1 Gp9. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																																
Species/Abbrv		* *	*										*			•					*											*
1. Phage CR1 Gp9	MK	K <mark>C</mark> F	Р Н <mark>С</mark>	RA	ΝA	W A	R T S	R E	LS	PLL	RE	IΥ	(QC	S D	VE	G H	I T N	/ V A	ΤL	E A S	RT	S P	S A K	A N	ΡΑΙ	ΤL	ΡS	SQ	W P [·]	TLS	ТАР	K P
2. Peduovirus P2	FH	CF	L C	QН	ΑA	ΗA	R T S	S R Y	I T I	тт	ΚE	RYH	+Q C	QΝ	VN	S A	TF	I T	YE	s v q	RY	ΙК	PGE	VН	AVR	P L	ΡS	G Q	Q	MWN		
3. Eganvirus ev186	FH	CF	РК С	нн	ΑA	ΗA	RT	S R Y	LTI	ΕΝΤ	ΚE	RYH	+ Q C	QΝ	IN	S C	: T F	ΜT	ME	ТІЕ	RF	ЧΤ	P G A	I D	PAP	РТ	V G	G Q	RP	LWL		
4. Bordetella bronchiseptica	MK	C F	Р Н С	GΤ	ΜA	ΤA	RT	5 K E	LS	RTL	RE	۷Q۱	(Q C	R D	I E	G H	I T N	/ M <mark>A</mark>	ΤL	E A V	RT	S P	S <mark>G K</mark>	P D	ΡΕΙ	V L	ΡF	SP	RS	K D A	MRP	R A
5. Achromobacter sp. SD115	MK	C F	ь н с	GΤ	ΜA	ΤA	RT	K E	LS	RTL	RE	VK	(Q C	R D	I E	G H	ITW	/ M <mark>A</mark>	TL	E A V	R T	S P	S G K	P D	PEI	AL	ΡY	ТР	RP	LΥΑ	MRP	RP
6. Achromobacter sp.	MK	C F	ь н с	G S	WA	Т٧	R T S	S E	LS	RTL	RE	VNF	Q C	ΚD	I E	G H	ITW	/ I A	LL	E A T	R T	S P	S G K	P D	PEI	AL	ΡY	ТР	K L I	РҮТ	IRP	RQ
7. Bordetella avium	MK	C F	ь н с	G F	W A	тν	R T S	S E	LS	RTL	RE	VNF	Q C	ΚD	I E	G H	ITW	/ I A	SL	E A T	R T	S P	S <mark>G K</mark>	P D	PEI	AL	ΡY	SP	R P :	S Y M	IRP	RQ
8. Alcaligenaceae	MK	C F	ь н с	G S	W A	тν	R T S	S S E	LS	RTL	RE	VNF	Q C	KD	I E	G H	ITW	/ I A	SL	E A T	R T	S P	S <mark>G K</mark>	P D	P E I	A L	ΡY	ТР	K P I	РҮТ	I R P	RQ
9. Duganella alba	IP	P C F	Р Н С	DA	RA	ΤA	RS	R Q	LS	ΚΤL	RE	IYY	(Q C	ΤD	VE	G H	I T F	V A	SL	E A T	RT	S P	S S K	P R	ТΕV	R L	ΡL	SP	AV	V H R	VMH	Q L
10. Pedomonas mirosovicensis	MQ	Q C F	Р Н С	ΤA	ΡΑ	V A	RT	R A	νт	ALY	RE	I H Y	(Q C	S D	VE	G H	I T F	A A	SL	S V N	RT	S P	S A K	P N	P G I	D L	ΡL	SV	RKI	РЕН	LAN	NE
11. Salmonella enterica subsp. enterio	IR	R C F	Р Н С	D G	ΚA	I A	RS	R E	LS	ΡTL	RQ	IS Y	(Q C	I D	PE	G H	ТҮ	'L <mark>A</mark>	ΗL	EIV	RΤ	S P	S A K	PN	ΑΑΙ	ΤL	ΡY	SP	н -		IRP	QP
12. Paraburkholderia aspalathi	LR	R C F	Р Н С	ΤS	RV	ΤA	R T S	R E	LS	RTM	RE	IVF	M C	ΕD	PE	A H	ISF	V A	ΤL	E A V	RΤ	S P	S A K	P D	ΡΑΙ	TL	ΡI	SΕ	нν	RDR	VMQ	QM
13. Paraburkholderia domus	LR	R C F	Р Н С	ΤS	RV	ΤA	R T S	R E	LS	RТΜ	RE	IVF	M C	ΕD	ΡE	A H	ISF	V A	TL	E A V	RT	S P	S A K	P D	ΡΑΙ	A L	ΡI	SΕ	ΗV	r d r	VMQ	QM
14. Caballeronia udeis	LS	C F	ь н с	RS	RV	ΙA	R T S	S R E	LS	ΑТМ	RE	I T F	· v c	FD	ΗE	G H	I T F	V A	QL	E A V	RT	S P	S A K	P N	PLV	G <mark>L</mark>	ΡN	IS P	нν	RER	VMS	Q L
15. Burkholderia phage FLC5	LA	CF	Р Н С	RS	RV	ΙA	RT	S R E	LS	ΓТΜ	RE	IVF	· v c	V D	ΥT	G H	I T F	V A	QL	E A V	RT	S P	S A K	P N	ΕAΙ	S L	ΡL	SP	нν	KER	VMK	Q L
16. Alcanivorax sp. S71-1-4(2)	MR	R C F	Р Н С	ΤS	GΑ	A A	RS	R Q	LS	RLL	ΚE	۷Y۱	(Q C	ΚN	PA	S F	AW	/ V <mark>A</mark>	Q V	E A V	R G	S P	S G M	P N	ΡΑV	N L	ΡV	SP	WΡ	ΙTS	DEN	QI
17. Pusillimonas sp. NJUB218	MR	R C F	Р Н С	G N	RA	QΙ	RT	S I E	QS	РТМ	R D	VYF	E L C	ΕN	LT	G H	I S W	/ V <mark>A</mark>	ΤL	E A V	RΤ	I A P	S G M	ΡN	РΚV	D L	ΡI	LΤ	RV	YDL	LNP	S D
18. Alcaligenaceae bacterium	MP	P C F	Р Н С	RΤ	RA	qν	RT	/ K D	LS	ΡTL	RW	VYF	L C	N N	LA	G H	I S W	/ V <mark>A</mark>	ΤL	E A D	RΤ	S P	S G M	P D	PRI	A L	ΡI	ΜA	RVI	AAH	LQQ	S P
19. Vibrio cholerae	IC	CF	Р Н С	SS	ΚA	ΤA	RS	RE	LS	ΑTL	RE	I C Y	(Q C	ΤD	WE	G H	ТҮ	M <mark>A</mark>	ΗL	EIV	RΤ	S P	S A K	ΡN	PS I	A L	ΡF	SR	H <mark>G</mark> (Q S R	AVA	S A
20. Roseateles depolymerans	IR	R C F	Р Н С	RA	K S	RA	V K	R E	ΜTI	ТМ	RE	۷T۱	A C	ΤN	V H	G H	ITW	/ V A	GL	EVN	R T	S P	S A T	ΡN	ΡΑV	ΤI	ΡI	SS	ΗL	A T Q	LDL	AP
21. Alcanivorax sp. S71-1-4	MR	C F	Р Н С	ΤS	GΑ	A A	RS	RQ	LS	RLL	ΚE	VYY	(Q C	ΚN	PA	S F	AW	/	Q V	E A V	R G	S P	S G M	P N	P A V	N L	ΡV	SP	WΡ	ΙTS	DEN	QI
22. Comamonas piscis	ME	CF	Р Н С	ΚA	ТС	ΕI	R T S	K P	VS	ΑТМ	RE	τIN	(Q C	ΤN	VE	G H	I T F	V A	ТТ	EIV	RΤ	S P	S A T	P D	РΤ۷	N L	ΡL	SΤ	ΗМΙ	RVV	LDN	A G
23. Escherichia coli K-12	FH	CF	L C	QН	A A	H A	RT	RY	ГТІ	тт	KE	RYH	l Q C	QN	VN	S A	TF	ΙT	YE	s v q	RY	VK	PGE	VΗ	VVR	P L	ΡS	GQ	QII	MWN		

Fig. 5.6. Multiple sequence alignment of Phage CR1 Gp9 protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* Gp9 protein from bacteriophages of various hosts it was observed that cysteine, proline, histidine, cytosine, and others are highly conserved at amino acid positions 3, 4, 5, 6 and 14 other positions, respectively

5.4.2. PHAGE CR1 Gp13 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Gp13 protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage Gp13 protein of *Saudiphocaensis* and *Stutzerimonas kunmingensis* exhibited 89% sequence similarity with *Phage CR1* Gp13 protein, the phylogenetically closest species with standing members in the tree. To break down the peptidoglycan layer and make it easier for the viral genome to enter the host bacteria, phage protein Gp13, which is connected to tail proteins, makes contact with the host cell wall first. Essential for the tail assembly.*Marinobacter sp., Candidatus Oceanisphaera merdipullorum,* and *Halomonas gudaonesis* are marine species. *Halomonas gudaonesis* is isolated from a saline soil contaminated by crude oil and involved in its degradation (Wang et al., 2007).



Fig. 5.7. Phylogenetic analysis of Phage CR1 Gp13. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																																																									
Species/Abbrv						*	1											*		*	*	* *	*							*					* *	*		•	*														*				
1. Phage CR1 Gp 13	MA	TP	TE	Q	D	LE	SI	1	τı	GI	K	EH	I T	TL	T	LR	R	PN		GE	L	RC	S L	S	LS	N		NP	D	V E	T				PR	I.		T	L T	RC	H		EN	D		DL		ΓV	A	GT			FF	Q	PA	SQ	K
2. Marinobacter nauticus	M S	KP	Τ/	Т	VΕ	LD	SI	1	KR	N I	QΕ	E V	/ S	K L	т	LR	ιĸ	Ρ/	\S	G E	L	RC	S L	S	LA	D		N N	D	VD) S	I T	K	V L	PR	1 5	N	Т	LΤ	EQ	E	V R	EN	D	ΡA	DL	A	AC	G	ΤE		A G	FL	L	ΡК	RL	ĸ
3. Marinobacter sp. bablab jr008	M S	KP	TS	Т	νE	LD	T	1	KR	N	2 E	EV	A	K L	Ť	LR	K	P /	S	G E	L	RC	5 L	S	LA	D	. 1	NN	D	VD	S	I T	K	V L	PR	1 9	N	РТ	LΤ	EQ	E	V R	EN	D	PA	DL	A	AC	G	ΤE	1.	AG	FL	L	PK	RL	ĸ
4. Marinobacter oulmenensis	M S	KQ	T /	E	V E	LD	SI	21	KR	D	G	DV	/ T	TE	т	LR	K	PN	15	G E	L	RC	S L	5	LA	D	LL	NL	E	VD	A	T	R	V.L	PR	1 5	Т	PV	LΤ	EQ	E	AR	NN	D	PA	DL	V	AC	G	G E	1	s s	FL	L	PK	RL	ĸ
5. Marinobacter bohaiensis	M S	K P	Τ /	T	VΕ	LD	T	1	KR	N	2 E	EN	A	K L	т	LR	K	P /	S S	G E	L	RC	sι	S	LA	D		NN	D	VD	S	M T	K	V L	PR	1 5	N	PS	ĽТ	EQ	E	V R	EN	D	P. A	DL	A./	AC	G	ΤE	10	AG	FL	L	PK	RL	ĸ
6. Stutzerimonas kunmingensis	- M	S K	SE	Ρ	I V	LE	QF	1	KR	G	EN	SI	Т	E I	т	LR	ĸ	P /	A	GE	L	RC	6 L.	к	L A	D		NO	D	V N	A	T I	R	V V	PR	1 2	v	РΤ	LΤ	EQ	E	V A	AL	D	V A	DL	L	5 C	AI	DA		AG	FL	Q	кт	GS	Т
7. Pseudoalteromonas sp. MMG013	M S	KP	TH	P	νт	L E	1	1	TR	G	ΕТ	TI	K	E I	к	LR	K	PF	K A	G E	L	RC	6 L	S	LA	D	LL	NL	D	VN	A	MT	T		PR	1 5	D	PI	LT	KQ	D	N	DL	E	D	NL	V		A	G E	A	A N	FF	۷	PK	NN	ĸ
8. Pseudomonas sp. SCT	- M	SK	TS	E	I V	LE	QI	1	QR	G	ΕТ	TI	Т	E I	Т	LR	K	P /	A	G E	L	RC	5 1.	к	LT	D	L	NG	D	VN	A	TI	R	V	PR	1 5	Q	Τ	LΤ	EQ	E	AA	AL	D	A	DL	LI	I C	AI	DT	V	A G	FL	Q	кт	GS	Т
9. Pseudomonas saudiphocaensis	MT	KP	YS	D	LV	LE	QI	1	PR	G	EN	TI	Т	E I	т	LR	ĸ	P/	A	G E	L	RC	S L	к	LA	D	. 1	NO	D	V N	A	T I	RI	V	PR	1 9	Q	РТ	LT	EQ	E	V A	AL	D	V A	DL	LC	5 C	A	DA	1.1	AG	FL	Q	кт	GS	Т
10. Kosakonia quasisacchari	M S	H E	DN	V	Τ	LQ	T	1	KR	G	EQ	1.1	D	S L	т	LN	ĸ	PN	A	G 1	L	RC	s L	S	LA	A	V A	N/	E	VD	A	LI	K	V L	PR	1 1	S	P S	LΤ	EQ	E	V G	AL	D	LA	ÐN	V.	AL	A	GK	V	V G	FL	S	PA	SO	Q
11. Kosakonia oryzendophytica	M S	NE	DN	V	Т	L E	N	1	TR	G	EQ	SI	Т	V I	т	LN	K	PN	A	G 1	L	RC	s v	S	LA	A	V A	N/	E	VD	A		K	V L	PR	1 1	s	P S	LΤ	EQ	E	V S	AL	D	L V	DN	V	A L	A	GK	V	VG	FL	S	PA	S/	R
12. Lysobacter capsici	M S	NT	TT	E	Τ	LE	TF	2	VR	G	E Q	RI	E	RI	т	LR	K	P/	A	GE	L	RC	s I	A	LA	EI	LL	KL	D	V A	A	LH	V	V L	PR	1 1	N	ΡT	LΤ	AH	D	VG	QL	D	P	DL	M	T I	G	S E	V	۷G	F E	L	PK	AD	R
13. Vulcaniibacterium tengchongense	M S	K P	T	T	νт	L E	TF	P L	VR	GI	Q	K I	E	RI	т	LR	l K	P 1	ΓA	G E	L	RC	s v	A	I A	D		RS	D	V A	A	LH	V	V L	P R	1,1	s	РТ	LТ	SH	D	V G	QL	D	P	DL	A	AL	A	S E	V	V G	FF	M	T R	AD	R
14. Candidatus Oceanisphaera merdipullorur	ΜT	QP	TC	L	E	LD	T	• V	TR	K	S G	DV	/ Т	EV	т	LR	K	PH	< A	G E	L	RC	s L	N	L T	D	1.1	QI	D	VN	A	G	K		PR	1 5	Q	ΡV	LΤ	ΕA	E	VQ	NN	D	PA	DL	V	2L	G	G E	V	AG	FL	V	ΡK	KN	ĸ
15. Shewanella dokdonensis		- M	TE	т	VΤ	LD	N	1	S R	GI	T	QI	T	DI	Т	LR	K	PP	(A	GE	L	RC	5 L	N	LN	D	L	NN	D	VN	IS	LT	11		PR	1 5	S	P M	LΤ	KD	E	AR	QL	E	ΡE	DL	LI	LL	G	GA	V	AN	FL	L	PK	QL	R
16. Halomonas gudaonensis	M T	DP	TE	Т	VΕ	LD	V F	1	QR	G	S Q	T.V	/ T	EL	T	R	K	PH	(S	G /	L	RC	s v	A	LT	D	V L	QN	D	VT	A	LT	T	11	PR	1 1	Q	P S	LS	K /	E	G	DN	D	P A	DL	V.	Q C	G	GV	V	AG	FL	L	PR	K /	R
17. Comamonas testosteroni	MN	EP	VE	۷	νт	LD	Y	1	KR	GI	Т	EV	/ Т	A I	Т	LR	t K	PI	. A	G	L	RC	5	к	G	E	LL	NL	D	VG	i S	V Q	MI		PR	1 1	т	Т	LL	QH	E	V A	QL	D	ΡA	DL	A	EL	S	MK	V	A S	F F	A	R K	SI	R

Fig. 5.8. Multiple sequence alignment of Gp13 protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* Gp15 protein from bacteriophages of various hosts it was observed that methionine, leucine, proline, and others are highly conserved at amino acid positions 1, 10, 13, and 24 other positions, respectively.

5.4.3. PHAGE CR1 Gp15 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Gp15 protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. During the development of the capsid, the phage Gp15 protein assembles and becomes connected with the gp16. The gp15-gp16 complex attaches to the host inner membrane as well as the viral DNA, likely guiding the genome's leading end through the periplasm and regulating the amount of DNA that is translocated into the host cell. Phage Gp15 protein of *Burkholderia phage BcepMu USA/Summer/2002*, exhibited 60% sequence similarity, and *Pseudomonas psychrotolerans* exhibited 100% sequence similarity with *Phage CR1* Gp15 protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.9. Phylogenetic analysis of Phage CR1 Gp15. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																											
Species/Abbrv																											*
1. phage cr1 Gp15	VGL	FAGA	YQE	DATC	KVS	AVEN	IVR	GRH	KTI	NPGA	AKP	GDD	TEW	EMT	SSL	AYFQ	MVI	DGD	VVV	EID	PLN	FVE	TVN	SVD	RLE	EQR	AALG
2. Peduovirus P2	VAV	VI. <mark>A</mark> S G	YIS	AWGC	KTI	SSN	GVN	GIS	ASV	FWDL	QES	GTD	ADL	LNE	SGV	TFEN	YTR	TAQ	VVA	DIT	ATL	IRD	T V D	S I N	AKF	REL	KTNG
3. Burkholderia phage BcepMu USA/Summer/	2002 <mark>V</mark> S V f	LEAA	YIR	SPAG	TIN	FSNO	QLV	G V E	RPL	SAMI	DDP	QSD	VNM	LNE	QGI	TFEN	VRR	TGD	VIN	EID	QGL	DS	L <mark>V</mark> E	SVN	GFG	RKL	GDG
4. Serratia phage KSP20	AQL	VIAS	YSY	DGC	ETI	ASN	AVS	NIT	KDV	FWAL	QAE	DSD	ANE	LNA	NEV	TFEV	YTR	TAQ	ILA	DLT	PAN	VKD	V V S	5 1 N	AKL	QGL	VTAG
5. Pandoraea sp.	VQL	R F A G A	YQR	DTG	EVD	AVEN	/	GRH	KEII	DAGS	5 A K A	GDD	TEF	KVT	SSL	SYYK	LTL	NGA	VLV	EID	LVN	LIE	NVQ	ED	RLA	AQR	KAIG
6. Pseudomonas psychrotolerans	VPL	F A G A	YQQ	DDTG	DVT	AVEN	/	GRH	ETI	EMGC	GKP	GDD	TEH	KIT	TTC	SYYK	LTV	DGT	TVI	EID	LLA	FIE	NVG	S E D	RLA	KQR	AALG
7. Pseudomonas jilinensis	VQL	RFAGA	FQR	DDTG	EVS	AVEN	/	GRH	EEI	SFGC	YEP	GED	TEH	SIT	TTC	TYYN	LTI	DNE	VLV	EID	ILN	MVE	I VD	S V D	RLA	EQR	AAIG
8. Pseudomonas aeruginosa UCBPP-PA14	VAT	MDGA	ILD	G P N S	TDE	ASNE	(E K	GTS	RPV	EFLD	GDE	TCR	ANL	LNN	AN I	AFVT	RVR	TMD	LVM	DIT	KTY	VKD	VTE	G L R	AFM	RDL	KNQG
9. Xanthomonas bromi	VQL	R F A G A	YQR	DDSG	EVD	AVEN	/	GRH	K E I I	PGT	r a k s	GDD	TEF	SVK	TSA	SYYK	LTI	NGA	TVI	EID	LVN	MTE	I VN	S V D	LLA	AQR	RAIG
10. Xanthomonas oryzae	VQL	R F A G A	YQR	DTA	QVD	AVEN	/	GRH	REII	PGT	I G K S	GDD	TEF	SVK	TSA	SYYK	LTI	NGA	TVI	EID	MVN	MIE	I V N	SVD	LLA	AQR	RAIG
11. Xanthomonas phaseoli	VQL	R F A G A	YQR	DDSG	GVD	AVEN	/	GRH	KEII	DPGT	r a k s	GDD	TEF	SVK	TSA	SYYK	LTI	NGA	TVI	EID	LMN	MTE	I VN	S V D	LLA	AQR	HAIG
12. Xanthomonas arboricola	VQL	R F A G A	YQR	DDSG	DVD	A V E N	/ V <mark>V</mark> R	GRH	SEII	PGT	ГАКБ	GDD	TEF	SVK	TSA	SYYN	LTI	NGA	TVI	EID	LVN	MTE	I VN	S V D	LLA	AQR	RAIG
13. Xanthomonas campestris	VQL	R F A G A	YQR	DDSG	DVD	A V E N	/	GRH	KEII	PGT	K A K S	GDD	TEF	SVK	TSA	SYYK	LSI	NGA	SVI	EID	LIN	MIE	I <mark>V</mark> N	S V D	LLA	PHR	RAIG
14. Xanthomonas perforans	VQL	F <mark>A G</mark> S	YQR	DDAT	EVD	AVEN	/	GRH	KEII	PGT	G K S	GDD	TEF	AVK	TSA	SYYK	LMI	NGS	TVI	EID	LMN	MIE	I V N	S V D	LLA	PHR	RAIG
15. Xanthomonas cannabis	VQL	R F A G A	YQR	DDSG	EVD	A V E N	/ V <mark>V</mark> R	GRH	KEII	DPGT	r a k s	GDD	TEF	SVK	TSA	SYYK	LSI	NGA	PV I	EID	LIN	MIE	I VN	S V D	LLA	PHR	RAIG
16. Xanthomonas dyei	VQL	R F A G A	YQR	DDSG	DVD	AVEN	V V R	GRH	SEII	PGT	r a k s	GDD	TEF	SVK	TSA	SYYK	LTI	NGA	TVI	EID	LVN	MTE	I VN	S V D	LLA	AQR	RAIG
17. Xanthomonas melonis	VQL	FAGA	YQR	DDSG	DVD	AVEN	V V R	GRH	KEII	PGN	AKP	GDD	NEF	SVK	TSA	SYYK	LSI	NGA	PV I	EID	LMN	MIE	I V N	SVD	LLA	PHR	RAIG
18. Thermomonas hydrothermalis	VML	FAGA	YQR	DTG	AVD	AVEI	VVR	GRH	EEI	EPGH	KAKA	GDD	TEF	KFK	TTA	SYYN	LSV	NGE	VLV	EID	PN	FIE	VG	VD	RML	EQR	MAIG



Based on the multiple sequence alignment of *Phage CR1* Gp15 protein from bacteriophages of various hosts it was observed that methionine, asparagine, glycine, and others are highly conserved at amino acid positions 1, 11, 13, 15 and 37 other positions, respectively.

5.4.4. PHAGE CR1 Gp16 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Gp16 protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. At the baseplate's bottom, phage Gp16 creates a dome that closes the central channel. Gp16 protein opens a channel at the baseplate's bottom for DNA ejection when calcium activates it. Phage Gp16 protein of *Alcanivorax sp. S71-1-4*, exhibited 99% sequence similarity with *Phage CR1* Gp16 protein, the phylogenetically closest species with standing members in the tree.

The genus *Alcanivorax* is one of the most abundant and well-studied organisms for oil degradation. Due to its affinity for metabolising hydrocarbons and derivatives of crude oil, the ubiquitous marine bacterial genus *Alcanivorax* is categorised as an obligatory hydrocarbon clastic bacterium (OHCB).



Fig. 5.11. Phylogenetic analysis of Phage CR1 Gp16. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																																															Т
Species/Abbrv			*	*											*																							*									
1. Phage CR1 Gp16	MP	AD	(HH	Gν	RV	Е	I N	E G 1	R	PI	RT	1.7	Т	5 1	G	LV	AT	A S	D.	A D	A E		ΡL	DT	AV	LV	TN	II F		A L	S A	AG	ΤS	GΤ	LA	K A	L D	A I	AD	H	G N	PV	MV	VV	/ R	V A	EG
2. Peduovirus P2	- M \$	5 D Y	(нн	G V	Q V I	Е	I N	E <mark>G</mark> 1	R	v I	s T	V S	т	A L I	V <mark>G</mark>	м <mark>v</mark>	СТ	A S	D	A D	<mark>a</mark> e	ΤF	ΡL	NK	ΡV	L I	ΤN		γs,	A I	sк	A G	кκ	GΤ	L A	ΑS	LQ	A I	AC	Q :	sκ	ΡV	тν	V N	1 R 1	V E I	DG
3. Serratia phage KSP20	MTC	ON F	FH	G A	RV	K E I	ΝTΙ		Ţ	A I	ND	VC	S 1	r v	I G	l V	ΑV	AD	D.	A D	A T	ΤF	ΡL	DТ	ΡV	LI	ΤF	V I	S	V L I	GК	A G	КΤ	G S	LY	κs	L K	AI	S D	Q	V S	ΤR	VI	٧V	/ R 1	V A J	A A
4. Burkholderia phage BcepMu USA/Summer/2002	2 <mark>M</mark> A A	A N Y	LH	G V	ΕТ	Е	ΚE	T G S	R	PV	κv	V	s /	N V	I G	LΤ	GΤ	A P	1	G •		• •	ΡV	ΝT	ΡV	QL	S C	VD	A A	A Q	FG	ΡQ	LΑ	G T	ΙP	QΑ	L D	A۷	YC) Y (G S	GΤ	V I	V I	R	I K	т <mark>с</mark>
5. Alcanivorax sp. S71-1-4	M P (ע א כ	нн	GΥ	RV	Е	I N	E G /	A R	ΡI	RT	V A	т	A I	I G	L V	ΑT	A S	D	A D	A T	L F	ΡL	NK	AV	'L V	S N	L L F	۲A <mark>ا</mark>	A L :	S G	A G	ΤE	GΤ	L R	ΚA	LΤ	ΑI	SE	Q	ΤN	ΡI	м <mark>v</mark>	VV	/ R	V P J	E G
6. Pseudomonas aeruginosa UCBPP-PA14	M S -	F	FH	G V	T V 1	ΓN	V D	1 G /	A R	тт	ΑL	P /	S 5	s v	I G	LC	D٧	FT	P	G A	Q A	S A	ΚP	ΝV	ΡV	LL	ΤS	K	(D <mark>)</mark>	A A .	A A	F G	I G	SS	ΙY	LA	CE	A I	ΥN	R	A Q	ΑV	I V	A	/ G	V E 🤇	A A
7. Pseudomonas helleri	MAA	A D Y	(нн	G V	RVI	Е	I N	E <mark>G</mark> S	5 R	тт	QT	V S	т	N V	I G	LΤ	CI	ΑE	D	A D	<mark>a</mark> a	F F	ΡE	DR	ΡV	LI	ΤN	I I N	IQ,	A L I	GΚ	A G	ТΤ	GΤ	LA	A S	L D	A I	AC	Q.	ΤN	ΡV	v <mark>v</mark>	VV	/ R	A K I	κG
8. Pseudomonas aeruginosa	M A 1	T D Y	нн	GΥ	R V I	E	I N	e g 1	r R	ΡI	RT	V S	т	۷ V	V G	м <mark>v</mark>	СТ	s s	D	A D	A V	ΚF	ΡL	ΝK	ΡV	'L L	ΤC	νı	. т ,	A S I	GΚ	A G	ΕQ	GΤ	LA	RS	L D	A I	AC	Q	A S	ΡV	тν	V V	/ R	V E J	E G
9. Thalassospira marina	M P 1	T D Y	(нн	G V	R V	Е	V S I	D G 1	R	ΡI	R T	ΙE	т	A L	I G	l V	ΑT	G D	D.	A D	<mark>a</mark> a	F F	ΡL	NR	ΡV	'L V	ΤС	L F	D	5 I	S N	A G	ТΤ	GΤ	L P	ΥA	L D	A I	KC	н	ΞN	ΡI	v <mark>v</mark>	V V	/ R 1	V A C	QG
10. Stutzerimonas stutzeri	M S 1	T D Y	(нн	G V	R V I	E	I N	E G 1	r R	ΡI	R T	V S	т/	A V I	V <mark>G</mark>	м <mark>v</mark>	СТ	A S	D	A D	A V	ΚF	ΡL	ΝK	ΡV	'L L	тс	νı	. т ,	A S I	G S	A G	ΕQ	GΤ	L A	RS	L D	A I	AC	Q	A S	ΡV	тν	V V	/ R 1	V E J	E G
11. Pandoraea apista	M P 1	r d y	нн	Gν	R V I	Е	LNI	D G 1	R	ΡI	RT	I E	т	A V	G	м <mark>v</mark>	VΤ	S Q	2 D .	A D	<mark>a</mark> a	ΕY	ΡL	ΝT	ΡV	' L K	ΤN		λ A	AL.	ΑK	A G	т к	GΤ	L A	ΡA	L D	A I	AC	Q (ΤN	C A	тν	11	/ R	V A J	EG
12. Pandoraea anapnoica	M P S	5 D Y	(нн	G V	R V I	Е	LNI	5 G 1	r R	ΡI	R T	ΙE	т	A V	I G	м <mark>v</mark>	νт	s q	D .	A D	A T	ΕY	ΡL	ΝT	ΡV	' L K	ΤN		λ A	AL.	ΑK	A G	т к	GΤ	L A	ΡA	L D	A I	A D	Q.	ΤN	C A	тν	1 I N	/ R 1	V A J	E G
13. Thalassospira profundimaris	MAT	r d y	нн	Gν	R V	Е	V S I	D <mark>G</mark> 1	R	PI	R T	I E	т	٩V	I G	v <mark>v</mark>	СТ	G E	т	A D	<mark>a</mark> d	ΤF	ΡL	NR	PA	LI	T C	I N	I N C	31	SΑ	A G	ТΤ	GΤ	L P	ΥA	LD	A I	KC	н	GΝ	ΡL	тν	V V	/ R 1	V P I	E G
14. Stutzerimonas kunmingensis	MAT	T D Y	нн	Gν	R V I	Е	I N	E G 1	R	ΡI	R T	V S	т	A V I	V G	м <mark>v</mark>	СТ	A S	D	A D	A V	ΚF	ΡL	ΝK	ΡV	LL	ТΟ	νı	. т ,	A S I	G S	A G	ΕL	GΤ	L A	RS	L D	A I	AC	Q.	A S	ΡV	тν	V V	/ R	V E J	E G
15. Morganella morganii	MAC	ς D γ	(нн	G V	R V	Е	I N I	D G 1	r R	ΡI	R T	V S	т/	A L I	V <mark>G</mark>	м <mark>v</mark>	СТ	A D	D.	A D	<mark>A</mark> K	QF	ΡL	ΝK	ΡV	'L V	ΤС	L F	۲s	A L I	GΚ	A G	DТ	GΤ	L A	НS	LQ	A I	S C	Q.	ТΚ	ΡV	тν	V V	/ R 1	V E 🤇	Q <mark>G</mark>
16. Oceanospirillaceae bacterium	M P /	A D F	нн	Gν	R V	Е	I N	E G 1	R	ΡI	RT	V S	т	٩V	I G	F V	ΑT	G D	D.	A D	<mark>a</mark> d	F F	ΡL	ΝT	PK	LI	ΤN	VF	۲E <mark>/</mark>	A Q I	GΚ	A G	V N	GΤ	LA	КΤ	L D	ΑI	AC	Q (ΤN	ΑI	c <mark>v</mark>	V V	/ R	V E 1	ΤG
17. Dechloromonas denitrificans	M P 1	r d <mark>y</mark>	нн	G V	<mark>r v</mark> i	E	LΤ	G	R	P	RT	I E	s /	A L	G	l <mark>v</mark>	A T	G S	D	A D	<mark>a</mark> v	A F	ΡL	D T	ΑT	LI	т	V	۲ ۲	<mark>a</mark> s	G K	A G	ΤL	GΤ	L A	кт	L D	A I	A C	H (G S	P A	сī	٧V	R	V P [DG

Protein Sequences	
Species/Abbrv	
2 Peduovirus P2	V TVY MRVED TO DAD TV NILLETTD NOVTEL KAVI AAES V TVY KORILEV VEDI DTKEVAVA LASVCOKI BAEGVI SAWCKI SEVKAVI
3. Serratia phage KSP20	RVIVVRVAAAGTEAKTOSOIIGGSODGSVTGMFALLTAEOKVGVRPRILGVPMVDTOEVTAOLRVIAKOLRAFSYSVCDGETIAEAKTYF
4. Burkholderia phage BcepMu USA/Summer/2	2002 T V I <mark>V I R I K T G</mark> A D P T K V T A A I I G A V N A <mark>G</mark> M R T <mark>G M K A L K D T </mark> Y N L Y <mark>G</mark> Y F S K I L I A P A Y C T Q N <mark>V</mark> S V E L E A M <mark>A</mark> V Q L G A I A <mark>Y</mark> I D A P I T T L A Q A L A G F
5. Alcanivorax sp. S71-1-4	I M V V V V V P EQEDDA ATTS N V I C D V T D Q V T C M K ALL S AQ AQ L Q V K P R I L Q A P C L D N Q A V T A M V E I AQ S L R G V Y V S A I G A G V S E V L T Y I
6. Pseudomonas aeruginosa UCBPP-PA14	VIVAVGVEAAETPEAQASAVIGGVSAGERTGLQALLDGKSRFNAQPRLLVAPGHSAQQVATAMDGLAEKLRAIAILDGPNSTDEAAVAYA
7. Pseudomonas helleri	V V V V V RAKKGATDAETT SNI I GTTTAGKLTGMKALLTAQNTI KVKPRI LGVPGLDSI PVASELASI AQKLRGFAY V SAHGMTKEEAVTYF
8. Pseudomonas aeruginosa	VIVVVRVEEGADEAETISNIIGGVTGQVTGMKALLAAEAQUGVKPRILGVPGLDSLPVTTELVAIAEQLRAFAYANAHNETVSDAIAYF
9. Thalassospira marina	TVVVVRAGGEDEAELISKYTOTVVNQKTGLQALTAAKALOVIPALOAPGLDNQNVTTELVAAAQUTRSFAMASCWDETEDATAYA
11 Pandoraea anista	a tvy v keen a to a fill a tradition of a diger to walk at the saken k very open in to v potential a very saken basen a tradition of a diger v basen a tradition of a diger v basen a tradition of a diger v basen a diger v b
12. Pandoraea anaproica	A T V I V B V A EG A T D A FT T S A I I G T S D G K Y T G M KALL S A KN K V G V D P I I G V P G E D S I A V S S E L T G I A O KL B A F O V S A W F A T K F F V V T Y
13. Thalassospira profundimaris	LT V V V V PEGADEAETT SNLIG G V VNGKKTGMQALTAAK PLLG VOPRILG V PGLDNEN V TAELVSIAQLTRSFA VASCYGET LEEAIAY F
14. Stutzerimonas kunmingensis	VTVVVRVEEGADEAATTSNIIGGVSTGEVLGMKALLAAEAQLGVKPRILGVPGLDSLPVTTELVAIAEKLRGFAYASAYGETVSDAIAYF
15. Morganella morganii	V T V V V R V E Q G E S E A E T T S N I T G G A T D G R K T G MQ A L L V A K A H T G V K P R I I G V P G H D T Q A V T S K L V T I A Q T L R A F A Y A S A Y G Q T I P D V L D Y F
16. Oceanospirillaceae bacterium	I C V V V R V E T G A D E A E T T S N V I G G V D N G K M L G MQ A L L A AQ G Q F A V K P R I I G A P G L D T Q A V S A E L V G I AQ K L R G F A V V S A Y G A T K E D A V A Y F
17. Dechloromonas denitrificans	A C I V V R V P D G A A P A E L T S N L I G S V T A G Q M K G M K A L L S S Q A K F G I K P R I L G I P G L D S L P V A T E L I A I A K Q L R G F A Y L S A N G E T K E E A V T Y F
Protein Sequences	
Species/Abbrv	
1. Phage CR1 Gp16	ESTADAITYRDSFGAREIMLIWRDFLSWDTTQNAEASDWAVARAMGLRAKIDNDIGWHKTLSNMPVNGVGISKDVYWDLQDPNTDAGLL
2. Peduovirus P2	KTISEVKAYRQNFSQRELMVIWPDFLAWDTVTSTTATAYATARALGLRAKIDQEQGWHKTLSNVGVNGVTGISASVFWDLQESGTDADLL
3. Serratia phage KSP20	ETIAEAKTYREQEAEREGMLIWPNFIAYNSYSGENEEFPAVAYALGLRAKIDNEQGWHKSLSNVAVSNVLGITKDVFWALQAEDSDANEL
4. Burkholderia phage BcepMu USA/Summer/2	2002 TTLAQALAGRGPAGSDRVRLCYPHVKVYDTATNAERLEPLSSRAAGLRARVDLDKGYWWSSSNQQLVGVTGVERPLSAMIDDPQSDVNML
5. Alcanivorax sp. 571-1-4	A G V SE V L TYR AN F A A REI MILIWPD F M SWD TQ A N A D A Q A WA V A R A L G L R A K I D Q D T G WH KT L SN V P V N G V TG L SK D V F WD L Q D PN TD A G L I
6. Pseudomonas aeruginosa UCBPP-PA14	STDEAAVY AYAKNEGSKRIFMVD GVQVWDSATNAARKAPSATAADLFAWTDAEYGFWSSPSNKETKOTTOTSKPVEFLDGDETCRANLI
8. Pseudomonas aerusinosa	
9. Thalassospira marina	ET I ED ALAY RD G EGAR FUNLING PENNOT TVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN KUVUD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG VSGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT LSNVAVOG V SGIN V VDD DVANA FRTAVATA RALGURA OLDA DTGWHKT RALGURA OLDA DTGWHKT V VDA
10. Stutzerimonas stutzeri	ETYSDATAY BAGEGARELMLIWPDFYSWDTYANANA PASALARALGURAKI DEOVOWHKTUSN VPVNGVSGUSKDI YFDLON PATDAGUL
11. Pandoraea apista	ATKEEVVTYRENFGARETMLIWPDFVSWDTTKNAEASAYAVARALGMRAKIDNETGWHKTLSNVPVNGVTGLSKDVFWDLQDPSTDAGFL
12. Pandoraea anapnoica	ATKEEVVTYRENFGARETMLIWPOFVSWDTTKNAEASAYAVARALGURAKIDNETGWHKTLSNVPVNGVTGLSKDVFWDLODPSTDSGFL
13. Thalassospira profundimaris	ET I E E A I A YR D G F G A R E I M L I WR D F V N WD T Q A N A E R N A Y A T A R A L G L R A Q I D E D I G WH K T L S N V P YN G Y S G I N K D Y YWD L G S P A T D A G Y L
14. Stutzerimonas kunmingensis	ET V SDA I A YRAG FGA RELMLIWPDF V SWDT V AN AN A PASAIAR ALGLRAK LDEQ V GWH KTLSN V PVNG V SGL SKD I Y FD LQN PATD AG LL
15. Morganella morganii	Q TIPD V LD Y R KN F SOR ELM LI Y POFLS WD S V KN A E AN A Y A V A R A LG LR A K I D E E I GWH KT LSN I G V NG Y TG I S AD I S WELQ D P A TD AG LL
16. Oceanospirillaceae bacterium	ATKEDAVAYRNNEGQREIMIIWPEFSGWDTVTDSTITESAVARALGLRAKIDNDIGWHKTLSNVAVNGVTGLDKDVFWDLQDPATDAGYL
17. Dechloromonas denitrificans	
Protein Sequences	
Species/Abbry	
1. Phage CR1 Gp16	Y W DEOD PINTOLAGY EN A A DYTTEVNYN GYRFWGSIRECSD DPLEAFENYTRTAOY EADTWAEAH I WAVD KRYTYSEV KOTLAGTNAK FREEK
2. Peduovirus P2	FWD LQ ESG TO AD LLN ESG VTT LIR DG FR FWGN RT CSD DPLFL FEN YT RT AQ V VAD TMAEAHMWAVD KPITAT LIRD I VDG I NAK FR ELK
3. Serratia phage KSP20	FWALQAEDSDANELNANEVTTLIKRDGFRFWONRTTDKDE-YIFEVYTRTAQILADTIAEAQFTTYDSPLTPANVKDVVSGINAKLQGLV
4. Burkholderia phage BcepMu USA/Summer/2	2002 S A M I D D P Q S D V N M L N E Q G I T T V F S S S G L R L WG N R T A A WP T V T H F E N V R R T G D V I N E S L R Y F S Q Q F <mark>V D</mark> A P I D Q G L I D S L V E S V N G F G R K L I
5. Alcanivorax sp. S71-1-4	FWD LQ D PN TD A G L LN A G D V T T L I R H N G F R FWG S R T C S D D P L F A F E S Y T R T A Q V L A D T M A D A H MWA YD K D L H P S L V KD I L E G V N R K M S S L T
6. Pseudomonas aeruginosa UCBPP-PA14	EFLDGDETCRANLLNNANIATIIRDDGYRLWGNRTLSSDSKWAFVTRVRTMDLVMDAILAGHKWAYDRGITKTYVKDVTEGLRAFMRDLK
7. Pseudomonas helleri	FWDLQDPNTDAGVLNQNEVTTLVQSSGVRFWGSRTCSDDPLFQFENYTRTAQVLADTMAEAHMWAVDKPLHPSLVKDMLEGLNAKFRELT
8. Pseudomonas aeruginosa	YWDLQNPATDAGLLNAAEVTTLIRREGERFWGSRTCSADPLFAFENYTRTAQVLADTMAEAHFWAYDKPMHASLVRDIVEGINAKFRELI
9. Thalassospira marina	WOLDNPALDAGELMAADVILLINNKGYRFWGSRICSADPIAFAFENYYRTADVLADIMAEAH-WAVDKMAAPILVKDILDGINAKMADLV
10. Stutzenimonas stutzeni 11. Pandoraea apista	TY DEDNIP ALD A GENNA DE VIT LEIKK DOF K FWGSKI CSADY FAFEN Y TO YKI A QYLADIMA E AHYWA YWA MANFYSL YKU I VEGI NA KAKELY
12. Pandoraea anaphoica	EWD LODPSTD ACTINATION OF FRANK RESIDENT AND LADTWAFAH WAVD CPUNPST AND LADTWAFAH WAVD CPUNPST AND LESINAK RSW
13. Thalassospira profundimaris	Y W D LO S P A T D A G Y LN A K D Y T T L I N N K G Y R F W G S R T C S A D P L F A F EN Y T R T A D Y L A D T M A E A H E WAYD K PMN P T L Y RD I I D G Y N A K E R D L Y
14. Stutzerimonas kunmingensis	Y F D L Q N P A T D A G L L N A D E VT T L I R R D G F R F WG S R T C S A D P L F A F E N Y T R T A Q V L A D T M A E G H F WAYD K P M H A S L V R D I V E G I N A K F R E L I
15. Morganella morganii	SWELQ DPATDAGLLNENDITTLIREDGFRFWGSRTCSDDPLFAFENYTRTAQVLADTMAEAHMWAYDKPMTPTLVKDMIDGINAKMRSLT
16. Oceanospirillaceae bacterium	FWD LQ D P A T D A G Y L N K N E V T A L I N K N G F R FWG N R T C A S D P L F A F E N Y T R T A Q Y L M D T I A E A H L W A Y D K P M H A S L I K D I I E G I N A K F S E L K
17. Dechloromonas denitrificans	FWD L Q D P STD AG F LN A A D VIT L I R R D G Y R FWG S RT CT A D P L F A F E S Y V RT AQ I L A D T I A E A H FWA VD K P L N Q T L I K D I I E G V N A K F R E L K
Protein Sequences	
Species/Abbrv	* * * * * *
1. Phage CR1 Gp16	NAVDKELTPSLYKDILAGINAKERELKGQGYILGGEAWEDENANSKETLKDGKLNIDYDYEVPEAENITFQQRITDRYLIDEAAQIAA
2. Peduovirus P2	NAVDKPITATLIRDIVDGINAKFRELKTNGYIVDATCWFSEESNDAETLKAGKLYIDYDYTPVPPLENLTLRORITDKYLANLYTSVNS
3. Serratia phage KSP20	TTVDSPLTPANVKDVVSGINAKLQGLVTAGRLIGAACWFDIVDNPKTSIPQGKAVVRYNYSPVPPLEDLTMIQTFTDQYYEAAFASLGG
4. Burkholderia phage BcepMu USA/Summer/2	2002) FVD APID Q GLID SLVESVNGFGRALIGD GALLGFKAWFD PARN PREELAAGHLLIN YRYTV PPPLERLTVETEITSEYLLTLKGGN
5. Alcanivorax sp. 571-1-4 6. Pseudomonas aeruginosa LICRPP. PA14	
7 Pseudomonas helleri	NAVNKIDI HPSTVKIMI FOLINA KOFTANAVI I GOFAWYN FOLINTKOTI KSGKI EL DYNYT DYDDI SERDI SERDI TODYL YN FATDING
8. Pseudomonas aeruginosa	NAVOKPMHASUVRDIVEGINAKFRELIRGGYLIGGECWEDEAANDKDTLKAGKLFLDYDYTPVPPLEDLMLRORITDRYLVDFAAGIKA
9. Thalassospira marina	NAVDKPMAPTLVRDILDGINAKMRDLVAOGYLLGGSAWFDPTKNSKENLKAGKLMISYDYTPYPPLENLLFEQKITDDYLVDFAAAVAA
10. Stutzerimonas stutzeri	NAVD K PMH PSL V R DI VEGI NAK FREL V RNGYLLGGECWYD EAAND KDTL KAG KL YLDYD YT PY PPLENLLLRORITD RYL VDFAAGMTA
11. Pandoraea apista	NAVD G P LN P S L A R D I I E G V N A K L R S M V T A G Y L I G G A A W Y D E T A N T K E T L K S G Q L F I D Y D Y T P V P P L E N L Q F R Q R I T D R Y L V D F A A K V A Q
	NAME OF A DECISION OF A DECISIONO OF A D
12. Pandoraea anapnoica	A YOGPEN PSEARDTTESTNAKERSMYN AGYEL GGAAWYDETANTKETENSGOCFTDYDY PYPPEENEOFRORTORTEVDFAARVAQ
12. Pandoraea anapnoica 13. Thalassospira profundimaris	A V D K PM N PT L V RD I I D G V N A K F R D L V A R G V L I G G E A W F D PA K N S K E N L K A G K L M I S V D Y T V PP L E N L M F E G K I T D D Y L V D F A T M V A A
12. Pandoraea anapnoica 13. Thalassospira profundimaris 14. Stutzerimonas kunmingensis	A V D K PM P T U V D I D G V M A K R D U V R GY L I GG A MY D P A M S K EN L KA GK L MI S YD VT P V P L EN L M F EQ K I T D D Y L V D F A T M V A KA V D K PM P T U V P I I D G V M A K R D U V R GY L I GG E C WI D E A A N D KD T L KA G K L I L D YD YT P V P P L EN L L R O R I T D R Y L V D F A A G I T A
12. Pandoraea anapnoica 13. Thalassospira profundimaris 14. Stutzerimonas kunmingensis 15. Morganella morganii 16. Organella morganii	A VU GEL NA LE SIN A A KERDE VA REST NA A KERDE VA REGULA REGULA REGULA SUGLE IN THE LA SUGLE IN THE VERTICE A KERDE VA A VA G A VU KENN PTL VRDI I DE VA KERDE VA REGULA REGULA REGULA REGULA SUGLE SUGLE VERTICE A SUGLE VA DE VA A SUGLE VA A VU KENN A SLVRDI VEGINA KERDEL I REGULA EGE WEDE A AND KD TEKA SKENLKA GKLE LU VU VERTICE A SUGLE VA DE VA A A VU KENT PTL VKDMI DE INA KERELI REGULA GE VED PONNSKEELK DE GULA I DVD VT PV PEAENIKI RORITORYL MD FA SKI KE
12. Pandoraea anapnoica 13. Thalassospira profundimaris 14. Stutzerimonas kummingensis 15. Morganella morganii 16. Oceanospirillaceae bacterium 17. Derbiorompas desiriufie an	A A YU GELN PSU KRUTTESTNA ALKSMYN AGYLIGGA MYT DE TANTKELKSGUL TO TAYTY PYPLEN LUKRKIT KURTU DE A A YAQ A YU GELN PSU KRUTTESTNA KREDI YA KREDI YA KRUTTEGA ANY DE TANTKESKEN KA GKUM SYDYT PYPLEN LUKRKIT DDYL VOFA TMYA A A YD KPMTASU YRDI YEGINA KRERELI RGGYLIGGECWED PA KNOKOTU KA GKUFLDYD YT PYPLEN LULRORIT DRYL VOFA TMYA A A YD KPMTASU YRDI YEGINA KRERELI RGGYLIGGECWED PA NSKEELKDGQLA I DYD YT PYPLEN LULRORIT DRYL WDFA A GITA A A YD KPMTPTL Y KDMI DGINA KMRSU TTQGYLLGGECWED PA NSKEELKDGQLA I DYD YT PYPLEN LULRORIT DRYL MDFA SKI KG A A YD KPMTASU YRDI YEGINA KRESELKSNGYI I DGTAWED PA NNTKDTU KSGKU YI DYD YT PYPLEN LULRORIT DRYL WDFA A A YAA
12. Pandoraea anapnoica 13. Thalassospira profundimaris 14. Stutzerimonas kunmingensis 15. Morganella morganii 16. Oceanospirillaceae bacterium 17. Dechloromonas denitrificans	MAYD KENN PTEURU HER IN AK KERDEVA AGYEL IGGA MYED PANN SKENEK KAGKEVI DYD YTPYPEEN LWIFKOK ITD DYL VD FATM VAA MAYD KPM PTEURU HER IN AK KERDEVA GGYEL IGGEC MYED PANN SKENEK KAGKEFED YD YTPYPEEN LWIFKOK ITD DYL VD FATM VAA MAYD KPM PTEURU HER IN AK KERDEVA GGYEL IGGEC MYED PANN SKENEK KAGKEFED YD YTPYPPEEN LWIFKOR ITD RYL VD FATM VAA MAYD KPM PTEU YED II DG'IN AK KERDEVA GGYEL IGGEC MYED PANN SKENEK KAGKEFID YD YTPYPPEEN LWIFKOR ITD RYL MD FASKI KG MAYD KPM HASEL KED II EGIN AK SELKSNG YI ID GT MYED PANN TKD TEKSGKEVI DYD YTPYPPEEN LWIFKOR ITD RYL WEFAAAVAA MAYD KPLNQTEI KD II EGIN AK SELKSNG YI ID GT MYED PANN TKD TEKSGKEVI DYD YTPYPPEEN LWIFKOR ITD RYL VEFAAAVAA
12. Pandoraea anapnoica 13. Thalasospira profundimaris 14. Stutzerimonas kummingensis 15. Morganella morganii 16. Oceanospirillaceae bacterium 17. Dechloromonas denitrificans	NAVD KENN PTEURU DI I DEVINAKER DU VAKER U I GGAMED DE INTKELKSKUK MISYOYT PVPLENLMEREK I TD DYU VD FATMAA NAVD KENN PTEURU DI I DEVINAKER DU VD FATMAA NAVD KENN PTU VKD I I DE UNAKER DU VD FATMAA NAVD KENN PTU VKD I I DE UNAKER U I BGEVI I GGE (MED BAAN DKD TEKAGKUMI SYOYT PVPLENLME EQKIT D DYU VD FATMAA NAVD KENN PTU VKD I I DE UNAKER U I BGEVI I GGE (MED DAN SKEELKKGKUMI SYOYT PVPLENLME EQKIT D RYU VD FATMAA NAVD KENN PTU VKD I I DE UNAKERSUT TO GYU I GGE (MED DAN SKEELKKGKUMI SYOYT PVPLENLME EQKIT D RYU VD FATMAA NAVD KENN ASU KENN PTU VKD I I EG VNAKEREL I BGEVI I GGE (MED DAN SKEELK KG KUMI DYD YT PVPLENLME EQKIT D RYU MD FASKI KG NAVD KENN ASU KENN SU I KO I I EG VNAKEREL KALGYI I D G KAMYD PAVN D EVTLKAG KUMI DYD YT PVPLENLME FQ RIT D RYU AD FAAQUAA
12. Pandoraea anapnoica 13. Thalaasospira profundimaris 14. Stutzerimonas kunmingensis 15. Morganella morganii 16. Oceanospirillaceae bacterium 17. Dechloromonas denitrificans	A YU GEN NE U KU I E ESIN AL KSWA NA GYLIGGE ANF DE IANT KELK SUGET DID U TYPY PELEN LAFEG K. KI U KY U DE ATAV AQ A YU GEN NE TU YE DI I DG YA AK F RDL YA RG YLIGGE ANF DE AAND KD TLK AG KLWI SYOYT PY PELEN LAFEG KI TD RYL VD FA TAV AQ A YU KPMHA SLUYRDI YE GIN AK I RELI RG GYLIGGE CWFD EA AND KD TLK AG KLWI SYOYT PY PPLEN LI RORITD RYL VD FA TAV AA YA YU KPMHA SLUYRDI YE GIN AK I RELI RG GYLIGGE CWFD EA AND KD TLK AG KLWI SYOYT PY PPLEN LI RORITD RYL VD FA TAV AA YA YU KPMHA SLUYRDI YE GIN AK I RELI RG GYLIGGE CWFD EA AND KD TLK AG KLWI SYOYT PY PPLEN LI RORITD RYL VD FA TAV AA YA YU KPMHA SLUYRDI YE GIN AK I RELI RG GYLIGGE CWFD PA NN SKEELK DG QLA I DY DYT PY PPLEN LI RORITD RYL AD FA SA YA YU KPMHA SLUYRDI YE GIN AK KE SE KAS GYII DG KA WYD PA YN DE YTLK AG KLYI DYD YT PY PPLEN LWFR RITD RYL AD FA AQLAA NA YU KPIN QTLI KDII E GIN AK F RELKALG YII DG KA WYD PA YN DE YTLK AG KLYI DYD YT PY PPLEN LWFR RITD RYL AD FA AQLAA
12. Pandoraea anapnoica 13. Thalassospira profundimaris 14. Stutzerimonas kummingensis 15. Morganella morganii 16. Oceanospirillaceae bacterium 17. Dechloromonas denitrificans	AAVD KENNPTLYKDIIDGINAAK RELINGGYLIGGE WEDPANSKEHLKAGKLMISYDYTPYPPLENLMEENKE UDDYLVDFATWAA MAVD KENNPTLYKDIIDGINAKE RELINGGYLIGGE WEDPAANDKOTLKAGKLMISYDYTPYPPLENLMEENKITDRYLVDFATWAA MAVD KENTPTLYKDMIDGINAKE RELINGGYLIGGE WEDPAANDKOTLKAGKLFIDVDYTPYPPLENLMEENKITDRYLVDFATWAA MAVD KENTPTLYKDMIDGINAKE SELKSDYIIDGINAKE SELKOGYLIGGE WEDPAANSKEELKOGQLAIDVOYTPYPPLENLMERGRITDRYLVDFATWAA MAVD KENTPTLYKDIIDGINAKE SELKSDYIIDGKAWYDPAANTKOTLKAGKLYIDYDYTPYPPLENLMERGRITDRYLVDFATWAA MAVD KENTAL KDIIDGINAKE SELKALGYIIDGKAWYDPAANTKOTLKAGKLYIDYDYTPYPPLENLMERGRITDRYLVDFAANAA MAVD KENTAL KDIIDGINAKE SELKALGYIIDGKAWYDPAANDEYTLKAGKLYIDYDYTPYPPLENLMERGRITDRYL ADFAAQLAA E sequence alignment of Gp16 protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* Gp16 protein from bacteriophages of various hosts it was observed that methionine, tyrosine, histidine, and others are highly conserved at amino acid positions 1, 5, 6, 7 and 144 other positions, respectively
5.4.5. PHAGE CR1 Gp23 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Gp23 protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. The majority of the capsid is generated by the hexamerization of the phage Gp23 protein. Two chaperones are necessary to aid in the folding of the main capsid protein; these are the host chaperone GroL and the phage-encoded gp23-specific chaperone, gp31. Phage Gp23 protein of *Marinobacterium sedimentorum* exhibited 97% sequence similarity with *Phage CR1* Gp23 protein, the phylogenetically closest species with standing members in the tree. *Marinobacterium sedimentorum* is present in deep sea sediments.



Fig. 5.13. Phylogenetic analysis of Phage CR1 Gp23. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																																																			
Species/Abbrv												*							*		*	*			•	*	* *							*		*		* *	•												*
1. Phage CR1 Gp23	MA	D S I	T D	L /	DV	AE	PL	L /	KL	GF	TA	RF	QI	LΑ	GΤ	L.	A R	K L	R	ΤS	Q R	ER	1 5	ΑT	λK	ΤР		K A	YR	PF	K	R	ΝK	RG	RV	KR	R A	MF	V	K L	RQ	NR	ΥL	Κ/	R	G N	S T	E		V G	F
2. Peduovirus P2	- M	NE	KF	F E	DF	LT	G <mark>L</mark>	I E	s I	S F	S 6	RF	R	LS	ΑE	L,	<mark>A</mark> K	RL	R	Q S	QQ	RR	<u>۷</u> ۱	A N	γĸ	A P	DG	ΤР	ΥA	PF	Q١	/ R	кκ	ΤG	RV	K R	к-	M F	F A	ΚL	ĒΤ	SR	F L	H I	(R)	A S	ΡE	Q	A S I	МE	F
. Marinobacterium sedimentorum	- MI	N D I	. T F	LE	Т	V T	PL	LO	K	GF	AE	RF	Q I	LA	RΤ	Ľ,	A T	EL	R	<mark>r</mark> S	QR	QR	2 I J	A E C	ξH	N P	DG	ΤА	FΑ	ΡF	S C	Ε	ΕK	A G	RI	K R	ΚA	M F	E L	км	RQ	<mark>a</mark> r	F L	K /	4 R !	S N	AN	S	V S	V G	F
. Marinobacterium stanieri	- M	s d <mark>I</mark>	N F	LE	SV	A S	ΡL	LQ	ι κ <mark>ι</mark>	ΕF	AE	R	κ	LΑ	RQ	L (GΤ	E L	R	<mark>R</mark> S	Q R	QR	2 I J	A D (R	N P	DG	S A	F A	ΡF	R/	\ E	ΑK	ΤG	RI	R R	ΚG	M F	Т	K L I	RТ	<mark>a</mark> K	F L	K٦	í R	Y N	AN	S	V S	V G	F
. Marinobacterium iners	- M	S D I	Q F	LE	т	ΑT	ΡL	LE	κι	G F	K E	R	(R I	LΑ	RΤ		S I	E L	R	<mark>R</mark> S	Q R	QR	۲ <mark>۱</mark>	A E C	R	N P	DG	SΑ	Y A	PF	RC	5 Q	ΑK	ΤG	RV	R R	ΚA	M F	Т	κL	R T	тк	ΥL	Κ/	λ K '	Y N	AN	IS I	V S	ΤG	F
Halomonas anticariensis	ΜA	D D I	Q A	LE	DV	A A	PL	LA	ι κ <mark>ι</mark>	ΕA	KE	RF	Q I	LΑ	RS	- L <mark>-</mark>	<mark>a</mark> R	E L	R	<mark>r</mark> S	Q R	ER	11	K A (R	N P	DG	ΤР	ΥT	ΡF	кv	V R	ΑK	QG	S I	K R	RA	M F	S	K L .	ΑT	тκ	W L	К /	λT Έ	тq	GC	т	ΑE	LG	F
Halomonas alkaliantarctica	MS	DE	. A A	LE	AV	ΙE	ΡL	17	κι	GF	AE	RF	R I	LA	RE	v,	A H	DL	R	I S	Q R	QR	11	K A	Q	N P	DG	S A	ΥE	ΡF	ΑI	R	G Q	ΤG	S I	R R	ΚA	M F	S	K L	RT	<mark>A</mark> K '	Y L	К /	λ K (GΗ	A G	A /	ΑT	V G	F
Halomonas cupida	- M	D D I	Q S	LE	ΕV	V A	PL	LE	κι	ΤF	KE	RF	t κ <mark>ι</mark>	LΑ	RΤ	п. <mark>,</mark>	A T	ΑL	R	R R	QR	ER	۲ <mark>۱</mark>	A D C	Q	N P	DG	SΑ	ΥE	ΡF	KI	R	S Q	A G	FΥ	R R	QP	^P M F	ΕM	КΙ	RQ	<mark>a</mark> Ki	ΥM	RT	í R /	A A	PN	IS/	A E	V S	F
Halomonas gudaonensis	ΜA	D D I	R A	LE	DV	VD	ΡL	LE	R	EF	RE	R/	R	LΑ	RQ	н <mark>,</mark>	<mark>a</mark> r	QL	R	I N	Q R	QR	11	K A (Q	N P	DG	ΤA	ΥE	ΡF	ΑI	R	G Q	s <mark>G</mark>	S I	R R	ΚA	M F	s	K L I	RΤ	<mark>a</mark> Ki	ΥL	К /	λ K (G S	A S	A /	ΑT	I S	F
). Halomonas ilicicola	LΜ	D D I	. D A	LA	DV	V A	PL	L	K N	EF	ĸq	RF	A I	LA	RK	v,	<mark>a</mark> r	DL	R	<mark>R</mark> S	Q R	ER	11	K A	Q	N P	DG	ΤА	Y A	PF	κŀ	I R	ΑK	Q <mark>G</mark>	A I	R R	ΚA	M F	s	КΙ	RТ	<mark>a</mark> Ki	Y L	κ /	λ K (G S	LE	S /	ΑE	V G	F
I. Halomonas sp. PBN3	ΜТ	D D I	S A	LE	DV	AG	AL	L I	Г К <mark>I</mark>	QF	KE	RF	Q	L N	ΤS	а <mark>,</mark>	<mark>a</mark> r	ΕL	R	<mark>R</mark> S	QQ	QR	۲ <mark>۱</mark>	A A	R	N P	DG	ΤA	Y A	PF	кι	R	QК	QG	RI	K R	KR	R M F	Т	ΚL	RQ	<mark>a</mark> r '	ΥL	K١	/Q !	S T	AN	I S	I A	۱G	F
2. Halomonas pacifica	- M	D S I	R D	LE	AV	ΑE	ΡL	LA	R	ΤF	AE	RF	R	LA	RТ	п. <mark>,</mark>	A T	EL	R	R R	Q R	ER	11	A A	R	A P	DG	ΤР	F E	ΡF	ĸ,	R	RQ	AG	FV	R R	QP	M F	т	RI	RQ	A KI	нL	R 7	r ĸ	A H	PG	Q	ΑE	V G	F
3. Halomonas desiderata	MA	DD	Q Q	L A	DV	A A	ΡL	LA	κι	ΕÆ	RE	RF	A I	LA	RТ	а <mark>,</mark>	A Q	DL	R	R S	Q R	AR	11	RA	R	N P	DG	ΤР	F A	PF	QI	R	GR	QG	A I	R R	R A	M F	E A	K L :	sт	A KI	W L	К /	λT Έ	тq	GC	т	AV	LG	F
4. Halomonas pellis	MA	DD	Q Q	LA	DV	A A	PL	LA	κι	ΕÆ	RE	RF	A	LA	RТ	۰ı,	A Q	DL	R	R N	Q R	AR	11	RA	R	N P	DG	ΤР	Y A	PF	QI	R	GR	QG	A I	R R	R A	M F	F A	K L :	sт	A KI	W L	К /	λT Ι	vq	GC	т	AV	LG	F
5. Halomonas sp. M20	MA	ו א כ	. R A	LE	DV	AG	AL	LA	κι	EF	S A	RF	Q	L N	QQ	11	G R	E L	R	R S	Q Q	QR	11	A A	R	N P	DG	S A	F A	PF	кι	R	Αĸ	кg	RI	K R	Q.	M F	E A	K L	RQ	A KI	нL	K١	/ Q !	s s	A D	A	I A	۱G	F
5. Larsenimonas suaedae	MP	DD	QF	LE	DV	A A	PL	LA	κι	D A	KE	RF	R	LA	R S	v,	A T	DL	R	R A	QR	ER	11	K A C	χĸ	N P	DG	тs	Y A	PF	ĸ	R	DQ	QG	τī	R R	R A	M F	G	κL	RТ	A K	ΥL	κı	R	тs	P⊦	G	ΑE	I G	F
7. Pseudomonas nitroreducens	MA		DT	LE	DV	AG	P	LF		EF	VA	RF	κ	LA	A D	L,	A R	RL	R	R S	QQ	KR	11	A M	ĸ	N P	DG	S G	ΥТ	AF	кι	R	GK	AG	нт	K R	R A	M	т	ĸц	RT	A R	ΥL	к /	λ K (G D	s q	A	I V	LS	F
. Pseudomonas aeruginosa	MA	D P I	. D T	LE	DV	AG	P	L F		EF	AQ	R		LA	A D	τ.	A R	RL	R	R S	Q Q	KR	11	A E C	ĸ	N P	DG	S P	ΥI	ΡF	кι	R	GК	AG	RI	K R	R A	ME	Т	κL	RТ	A R	ΥL	к /	λ K (G N	AE	А	I V	LS	F
. Pseudomonas nitrititolerans	MA	DD	R A	LE	DV	AG	AL	LN	I K L	QF	KA	RF		ΙT	Q S	а,	A R	DL	R	R S	QQ	QR	11	A A C	ĸ	N P	DG	ΤР	Y A	PF	кι	R	АΚ	AG	RI	K R	RK	(M F	E A	КL	RТ	A R	YL	RI	Q	S D	A S	s	I A	I G	F
). Salinicola aestuarinus	AS	DDI	N C	LC	DV	LA	PL	Πe	0	D /	RS	RF	0	LA	RT	v	а т	DL	R	R S	OR	ER	211		o	N P	DG	sт	E A	P F	R S	R		olo	D I	RR	D A	ME	s	ТΙ	R T	A K	YL	R T	r R	sт	PN	IS /	АТ	AG	F



Based on the multiple sequence alignment of *Phage CR1* Gp23 protein from bacteriophages of various hosts it was observed that aspartic acid, leucine, tryptophan, and others are highly conserved at amino acid positions 3, 5, 8, 11 and 57 other positions, respectively.

5.4.6. PHAGE CR1 Gp33 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Gp16 protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. The function of Gp33 protein is when the sliding clamp is present, it activates transcription at late promoters. binds to the upstream dsDNA as well as the host RNA polymerase (RNAP). Phage Gp33 protein of *Alcanivorax sp. S71-1-4*, exhibited 99% sequence similarity with *Phage CR1* Gp33 protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.15. Phylogenetic analysis of Phage CR1 Gp33. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences	
Species/Abbry	
1. PHAGE CR1 gp33	MONATERSLENAYLARIAQ LNGVDSAGQKFAATPAVOQKLEDRLLEOEDLESINVIGVDNQGGEKLGLLGTELIGSTADTASGERQTFOPTSLOAVT
2. Peduovirus P2	MRQETREKENAYLSRVAELNGIDDVSKKFTVEPSVTQTLMNTMQESSDELTRINIVPVSEMKGEKIGIGVTGSIASTTDTAGGERQPKDESKLASNI
3. Serratia phage KSP20	MENITRELFDQYISROAQLNRVSAVAAKFAVDPTVOQKLEAAAQESDSFLSKINVFGVTQQIGQKVLIGSKGPLAGVNNSTTTRRNPADNSKMEPVI
4. Haemophilus phage HP1c1	
6. Pseudomonas furukawaii	MRNETRVLYNAFTOOLGOLNGY PDYSKKFNYEPTIE OKLETRIOESS SFLSRINYYG YREOEGEKYGLDID SPTASTTOTEKOAROTHOPTGLDORI
7. Pseudomonas jilinensis	MRNDTRKLFEAVCAALAQLNGVDPGTRSFTVEPSVQDTLETRMQESSAFLGSINMIGVSQQAGEKIGLGGPIAGTTDTNTADRQTSDPTNFDKHC
8. Alcanivorax sp. 571-1-4	MRTETRTLENAYLNQLAMLNGISDACQKFAATPTYEQKLEERIQDSSDFLSRINYIGYDNQSGEKYGIDVGSTIASTTDTGSGEREPYDPSNLDAHC
9. Paraburkholderia acidipaludis	MRNETRHAFNAMMSALAQLNG LENAAAKFAVD PSVQQTLENRITESSEFLGKINVIGVAEQQGQKIGLGVGSPIASTTDTSTKORTTVDASOLDPN(
10. Paraburkholderia oxyphila	MERCINICA NATIKALAQUNU V PAGEKES V DIS VQN LESKITES SAFLGKINVIG V LEQQQQA GLQVGSVIASITDIS A KEROTI KOPSDLANU MERCINICA SAVATI ROLUGVOR V NO KAVA BAVQAKITETETA ESSAFLGKINVIG V LEQQQA KAVGI V GSAVSTIDIS A KEROTI DI PAGI AGV
12. Idiomarina sp.	MRNETRKLFNDFONRLATING VESVGAKFTVEPSVOOTLETRMOESSEFLNSINVIG VNEOOGEKLGLGISGT AGRTDTNND PTDPTDMEGS!
13. Caballeronia udeis	MQ N K T R L A F N A Y L E A L A Q L N G Y P S A A A K F A Y D P S Y Q Q K L E T R M Q E S S T F L S K I N Y M P Y S E Q Q G E K L G L G L G G P L A S T T D T K Y K D R E T T D P T D L D S H L
14. Idiomarina abyssalis	MRNETRKLENDFQSRLATLNGVDSVGAKFTVEPSLQQTLETRMQESSEFLNSINVIGVNEQSGEKLGLGVSGTIAGRTNTKNEDRQPIDPTDMEGAC
15. Thauera butanivorans	MRNOTRRLFNAVVEQLAKLNGVDSATAQFTVEPSVQQKLETKIQESSEFLGRINIVGVPEQAGDKIGLGISAPVASTINITLADRATRDLTTIDEQ(
17. Shewanella baltica	MRNUTRKLENATLAQUCSUNI DATIA TANIS VOILETKIQES CELSKINN GVA EQSIEN OLGI 1974 OTTSIQUQ TSIVSIL MRNUTRTIENGVI SVATINSI ETATAKETVA PSVOILETKIQES CELSKINV VVIKKSKEKIGI GVISGTIA GTOTTOTOS POALO PTDIDA I
18. Shewanella dokdonensis	MRNETROLFNAYTHOLCALNGYDSTNTKFTYTPSVOQTLETRMQESSEFLTRINIVPVNEKSGEKLGLGINSTIASTIDTTKODRQAIDPTDLDAAC
19. Mycetohabitans sp. B2	MRN TTRORFNAFVAQLAELNGVPNAAEKFTVEPSVQQTLENRLTESSEFLQRINVIGVAEQQQQKLGLGVGSPIASTTDTSVKDRTTVDATDLDPSC
20. Stenotrophomonas maltophili	MARNOTRLLYTAFLSQIASLNGVADAGQVFSVDPTIQQKLETRMQESSDFLSRINIIGYNELKGQKVGIGVSSTIAGRTDTGNERSPRDVSGIDSQ'
21. Pandoraea fibrosis	MRKETRSAFNGYLRQIEKLNGIESATAKFAVEPSVOOKLETKMQESAFFLGKINVVGVOEQSGEKLGIGIGGSPIASTTDTSVKERQTVDPAELDANC
23. Marinobacterium sedimentori	
24. Stenotrophomonas lactitubi	MRNETRLLYAAVLSQIASLNOVADAGQVENVDPTYQQTLETRMQESSDFLGRINIIGYNELKGQKVGIGVSSTIAGRTDTGNERSPRDVSGIDSQ
Protein Sequences	
1. PHAGE CR1 gp33	OT BETS BAVEN CONTRACTOR OF THE PART BAWENT PREPARE VERTER AND THE AND CONTRACTOR OF THE OTHER AND THE
2. Peduovirus P2	Q P K D F S K L A S N K Y E C DO I N F D F Y I R Y K T L D L W A R Y O D F D L R I R N A I I K R O S L D F I M A G F N G Y K R A E T S D R S N P M L O D Y A Y G W L O K Y R N E A P A R Y M
3. Serratia phage KSP20	N PA DN SKME PY DYM C RK VN Y DYG I SY EQ L DAWAH Q PN FO PL I SSAMAR QM SLD R I M T G FNG T SY A D PSN RAAN PL L Q D CG I G I L E K I R K E A PH R Y I
4. Haemophilus phage HP1c1	TGRNLANLDQNGFELAETDSGIIVPWALFDSFAIFKDRLVEYSEYFQNQVALDILQIGWNGQSVADNTTKADUSDVNKGWLKLLQEQRAANFM
5. Pseudomonas nitroreducens	Q T RD VT VLDN L GVI CT QTN FD SHI T YK KLD AWRK FKD FO AR I RD ALL RROALD RIMI GWNG TSRAAT SNI ATN PLLOD VNI GWLEKM RLTN AAR VM
7. Pseudomonas iilinensis	O TSO PTNEDKING V CSO TNEDTHI RY KLOWNER POPOLORINE V ROALDRIWI CENGVS KAATSO KVAN PLOD VN VROALDRIWI CENGVS KVAN PLOD VN VROALDRIWI KVAN PLOD VN VROALDRIWI KVAN PLOD VN VROALDRIWI KVAN PLOD VN VROALDRIW
8. Alcanivorax sp. 571-1-4	E P V D P S N L D A H G Y M C T Q T N F D T A L R Y A K L D A W R H F I D F Q A K I R N A I L K R Q A L D R I M I G F NG I S R A A T S D R T A N P L L Q D Y N I G W L Q K W R L H A S D Q Y M
9. Paraburkholderia acidipaludis	TTVD A SDLD PNGYFCTQTNFDTHLTY A KLD AWAKFPDFQTRIRD A IVKRQALDRICIGFNGTSRAPSSDRNANPLLQDVNKGWLQKYREQAAERVL
10. Paraburkholderia oxyphila	D T R D P S D L D A N G Y V C T Q T N F D T H I P Y A R L D A W A K F Q D F Q T R I R D A L V Q R Q A L D R I C I G F N G T S R A A T S D R N A N P L L Q D V M K G W L Q K Y R E Q A V E R V L
11. Cupriavidus sp. UGS-1	
12. Idiomarina sp. 13. Caballeronia udeis	
14. Idiomarina abyssalis	Q P I D P T D M E G A G Y F C H Q T N F D T A L R Y N K I D AW A K F K D F Q T R I R D A I L K R Q A L D R I M I G F N G T Q A A A E T O R N A N P L L Q D V N I G W L Q K M R T H A A E R V M
15. Thauera butanivorans	A TROLTTLOEQGYFCTQTNFDTHLTYAKIDMWAKFPDFQTRIRDVILRRQALDRIMIGFNGTSRAATSNPTTNPLLQDVNIGWLQKYRTHAAARVM
16. Stutzerimonas stutzeri	Q T S D V S S L D D R G Y T C T Q T N F D T H I R Y A Q L D A W A K F P D F Q A R L R D A I L R R Q A L D R I L I G W N G T S R A A T S N P A T N P L R Q D Y N Y G W L Q K M R T E N A T R Y L
17. Shewanella baltica 18. Shewanella dokdonensis	Q A DEFTIL DALGYD CTQTNEDTAL RYAK I DIWMAKEPDED AR I ROATLAGUALDRI MIGENGTSRAATSNRTANEL COVNIGWLKKI ROHAPORHMI O A DEFTIL DALGYD CTQTNEDTVI DYAK I DIWMAKEPDED TIL KONALDDINI HIGENGTSRAATSNRTANEL COVNIGWLKKI ROHAPORHMI
19. Mycetohabitans sp. B2	TT V DAT DLDPS GY FCT KTDFDTHLTY AKLDAWAK FD DFD I RV RDALVK R DALDRICIG FN GTS RAATS DROOH PLLODVN K GWLOK V REQAPER VL
20. Stenotrophomonas maltophili	a S P R D V S G L D S Q T Y E C K Q T D F D T A I R Y A L L D A W A K F P D F Q A K L R D A L V K R Q A L D R L M I G F H G T S A A A T T D R T A H P N L E D V N I G W L Q Q Y R T N A P A R V L
21. Pandoraea fibrosis	Q T Y D P A E L D A N G Y Y C S Q T N SD T H I T Y Q K L D A WA K F PD F Q T R V R D Y I L R R Q A L D R I C I C F N G Y K R A A T S N R A E N P L L Q D Y N K G W L Q K Y R E F A P A R Y M
22. Marinobacterium stanieri	Q T KD P T N L D E R G Y L C R KN N S D T H I T YA K L D WA K F P D F O T F I R D A L L R R O A L D R I T I G F N G A S Y S A D S D I A T N P L L Q D YN I G W Y O K Y R D E A A E R Y L
24. Stenotrophomonas lactitubi	
Protein Sequences	
Species/Abbrv	• •
1. PHAGE CR1 gp33	ROHANNEVII STANQOTYTYGASGOTYNLOSLY MAYSNL I ERUSYSESTOLYVLYGRGLLMDEYFNY INROTPPTEM ASDEVMSTREIGELPAL
3. Serratia phage KSP20	R KE A PH R V I S N I T V T S R D I T K + G T Y G N V S A A V Y D A K N S L M D E W H K N P D N V Y I L A G D L L T S N F PA I N O T N P N T EM L A G D L I Y A D E R Y G N M P T F I
4. Haemophilus phage HP1c1	Q E Q R A A N FM T E ST K S S K I T I O D N A D Y A N L D D L A F D L K Q G L - D F R H Q N R N D L V F L V G A D L V S K E T K L I Q H G L T P T E K A A L G S H N L M G S F G G M N A I T
5. Pseudomonas nitroreducens	R LTNAAR YMTEGDKEAGKILIGATGDEKNIDAL YYAMYNELIEPWYQEDSEL YYYCCRELLADKYFPLYNKDQAPSEQLAADYYMSOKRIGGLPAAF
6. Pseudomonas furukawali 7. Pseudomonas illipopsis	RY NA A RY MTEG K KG SG KI Y I BA DG DY KN LD A LY I DW VE FI H PY Y Q ED TR LY A I CORK LLAD KY FP I I NQ HA PS MIL ASD I Y TS DK KL GN L PA Y F
8. Alcanivorax sp. 571-1-4	
9. Paraburkholderia acidipaludis	REQ A A ERVIKE VAKGTOKVTIG AGGOVKTLDALVVD ALSSLVEPWYRDD TGLVVICG RGLLHD KYFPILN TQQAPTEQMAADMIVSO KRIGGLPAVS
10. Paraburkholderia oxyphila	R EQ A Y E R Y L K E Y Y K A S G K Y Y Y G A G G D Y K T LD A L Y Y D Y L S N L Y D P W Y R D T G L Y Y I C G R G L L H D K Y F P I L N T Q Q A P T E Q L A A D M I Y S Q K R I G G L P A Y S
11. Cupriavidus sp. UGS-1	R QH A A A R Y L K E G T K S A G K I L I G A G G D Y A N LD A L Y MD A V A G M I E P W Y R R D T K L Y A I L G D D L L H D K Y F P L V N K D Q A P T E Q L A T D L I I S O K R V G G K Q A V A
12. Idiomarina sp. 13. Caballeropia udeis	NO NA A ERVINE YVE A SOK ET VOTS GOVEN LUAL VYDM VNNU DOM NODTEL VULTGER KLUSOKVE PLVNSOL VPTEKTAADMIN SOK RIGCUQAVE
14. Idiomarina abyssalis	
15. Thauera butanivorans	R TH A A A R V H A E V V A A S G K V T V G A G K D Y K N L D A L V F D A V S N L I D P W Y R E D T A L V A V M G R R L L D D K Y F P I I N T T O P P S E T L A A D V I I S O K R V G G L P A V F
16. Stutzerimonas stutzeri	R TENATRYLAR VYSAS 6 QITIG DYKN LDALY ED LYN EMIEPY YQED POLY YICG RKLLAD KYFPIYW QTHAPTRQLAAD IYIS 6 KRYGN LPAYF
17. Shewanella baltica	R O HA POR HNA EV VESSGKIVIGT - DVANLDAL VYDM VNMH DPWHODDTEL VVICGR KLLAD KYFFIIN KONA PTEAMAADMI SOKRIGCLGAVF
18. Shewanella dokdonensis	TETA TURTIM NEVY AUSTRALITIOTA - MIANTALA UN MANNETERMINODITETA AL CORRELA DEVERTIVA KNEPTETIA AD LI SOKREGOLPAVE DE OAPENVIGE, GASSKIA TA ASA TI DA AVVIATSNIVER VAN TATUVICE GERKELA DEVERTIVA KNEPTETIA AD LI SOKREGOLPAVE
20. Stenotrophomonas maltophili	ARTNAPARYLDEVKAASGKVVVGADGDVKNLDALVFDAVSNLIDPWHRKDPGLVAVVGRGLLHDKYFPLVNADOPSTEKLATDVII BORRLEGLOVAL
21. Pandoraea fibrosis	R F A P A R V M S - G K T A G K I V I G D G D V A N L D A V V I D A I S S L I D PW H Q E D T D L V V L C G R G L A H E K Y F P M I N R V E K P T E Q L A G Q I I M S G R P A A V
22. Marinobacterium stanieri	R D E A A E R Y L S E V V D A S E K I N V Y A G G E Y E N LD A L Y E D A V N L I E P Y Y R E D T E L Y A I M C R D L L A D K Y E P I V N Q N H A P T E T I A A D L V I S E K R Y E G L P A V F
23. Marinobacterium sedimentoru	UTRADA PARVMDEVYAA SGAVN V FAGODYEN DALV V DAVN NI DVW FREDTALVAN MGROLEADIKY FPL MOAQPASEMLAT DVVL SK KRVGGLPAA
24. Stenotrophomonas lactitubi	way a way a way a surpluse way a sur



Based on the multiple sequence alignment of *Phage CR1* Gp33 protein from bacteriophages of various hosts it was observed that methionine, asparagine, threonine, and others are highly conserved at amino acid positions 1, 3, 5, and 61 other positions, respectively.

5.4.7. PHAGE CR1 Gp36 protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of PHAGE CR1 Gp36 protein has been done and sequence alignment followed by performed using hits. phylogenetic tree analysis were the top few When a procapsid is being formed, the phage Gp36 protein assembles on the inner side of the capsid and aids in the ejection of bacteriophage DNA into the host cellcatalyzes the cleavage of the host pep tidoglycans while acting as an exolysin. Phage Gp36 of Alcanivorax sp. S71-1-4, exhibited 99% sequence similarity with *Phage CR1* Gp36 protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.17. Phylogenetic analysis of Phage CR1 Gp36. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.



Based on the multiple sequence alignment of *Phage CR1* Gp36 protein from bacteriophages of various hosts it was observed that aspartic acid, leucine, tryptophan, and others are highly conserved at amino acid positions 3, 5, 8, 11 and 57 other positions, respectively.

5.4.8. PHAGE CR1 GpE+E protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 GpE+E protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. The host translocase MraY activity, which catalyses the production of lipid I, an essential step for the host cell wall biosynthesis, is inhibited by the phage GpE+E protein, resulting in host cell lysis. Phage GpE+E protein of *Halomonas spp*, exhibited 92% sequence similarity with *Phage CR1* GpE+E protein, the phylogenetically closest species with standing members in the tree. *Halomonas spp*. are Gram-negative bacteria belonging to the family of Halophiles that prefer to grow in saline environments (commonly referred to NaCl or KCl), such as salt lakes and marshes, oceans, or other saline areas on earth.



Fig. 5.19. Phylogenetic analysis of Phage CR1 GpE+E. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																																		
Species/Abbrv	*	*		*			*	*	*		*						*			*		4	*			*			*					*
1. PHAGE CR1 GpE+E	M	А	N	A	V	V	F	ΗN	N	Р	P	A A	N	1 D	Ρ	M	EL	E	E	L	L	R <mark>V</mark>	VE	R	ĸ	А	R	D	R	N.	Γī		E	
2. Peduovirus P2	М	А	D	/ A	٧	T	F	H١	N	Р	P :	SE	L	Y	Ρ	M :	s L	Т	E	L	1.1	тν	VF	RE	K	A	L	R	R	s	G N	1	N	
3. Halomonas nanhaiensis	М	А	D	A	N	V	F	H١	N	E	P :	s A	N	1 D	G	M	E L	E	Е	L	M	Q V	V F	RE	R	А	R	К	R	н	EC	5 5	K	
4. Halomonas	Μ	А	D	A	F	V	F	H١	N	Р	P :	s A	N	1 D	S	M	G L	E	Е	L	A	R V	VF	RE	K	A	R	E	R	N -	Г	P	ĸ	
5. Halomonas alkaliantarctica	Μ	А	D	A	N	V	F	H١	N	3	P	ES	5 N	1 D	Ρ	Μ	P L	E	Е	L	M	N V	VF	RE	R	A	R	Q	R	۲l	ΕI	Γŀ	I Q	
6. Pseudomonas chlororaphis	М	А	D	A	٧	V	F	H١	N	Ą	P	A D	D N	1 D	Q	L (G L	Q	Е	L	M	E V	VF	RE	R	А	R	٧	R	s !	S 1		E	
7. Pseudomonas sp. Marseille-Q511	М	А	D	A	٧		F	H١	N	Р	P	A A	N	1 D	Ρ	L :	s L	Т	Е	L	M	E V	V F	RE	R	А	R	Е	R	sl	E١	/ N	E	
8. Pseudomonas aeruginosa	М	А	D	A	L	V	F	H١	N	Ą	P	A D	D N	1 D	Ρ	L (G L	A	D	L		E V	V F	RE	R	А	R	Т	R	N	E	° [S	
9. Agitococcus lubricus	М	А	D	A	٧	V	F	H١	N	Р	P	λ	N	1 S	D	M :	s L	E	Е	L	M	ס כ	V F	RE	Q	A	R	Q	R	vI	E٦		G	
10. Moraxellaceae bacterium	М	А	D	A	٧	V	F	H١	N	Р	P	λ	N	1 E	С	M :	s L	Т	Е	L	M	Q V	V F	RE	Q	А	R	Q	R	vI	E٦		G	
11. Sphingomonas jatrophae	М	А	D	A	٧	V	F	H١	N	Р	P	A A	N	1 D	Ρ	M	P L	P	Е	L	M :	s v	V F	R A	Ē	A	А	К	R	A	G /	\ E	E	
12. Marinobacterium stanieri	М	А	D	A	N	V	F	H١	N	R	P	CD	N	1 D	G	M	E L	V	E	L	M	ס כ	VF	RE	к	А	R	к	R	N	ES	5 0	S	
13. Marinobacterium sedimentorur	M	А	D	A	N	V	F	H١	N	Г	Ρ	R D	N	1 D	G	M	E L	S	Е	L	A	GΝ	VF	RE	к	А	R	Е	R	Ν	EC	5 0	к	
										1												1			-			1						

Fig. 5.20. Multiple sequence alignment of GpE+E protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* GpE+E protein from bacteriophages of various hosts it was observed that methionine, alanine, aspartic acid, and others are highly conserved at amino acid positions 1, 2, 3, and 16 other positions, respectively.

5.4.9. PHAGE CR1 Baseplate assembly protein J:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Baseplate assembly protein J** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage baseplate assembly protein J of *Pseudomonas sp. TCU-HL1* exhibited 97% sequence similarity with *Phage CR1* Baseplate assembly protein J protein, the phylogenetically closest species with standing members in the tree. *Pseudomonas sp. TCU-HL1* degrading plant-produced monoterpenes, specially Borneol, a plant terpene that is widely used in traditional Chinese medicine (Tsang et al., 2016).



Fig. 5.21. Phylogenetic analysis of Phage CR1 baseplate assembly protein J. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Destain Comunes	
Protein Sequences	
1. PHAGE baseplate assembly protein I	A KNRIDISOLPPPTVVEEIDYEDLLETRKOELISRYPEDYLOYESDPMVKLLEENAYLETLLRORINDAAVSVMLAYASSSDLDNLSAFFGN
2. Peduovirus P2	MPIIDLNQLPAPDVVEELDFESILAERKATLISLYPERTLTLESEPLVKLLEENAYRELIWRORVNEAARAVMLACAAGNDLDVIGANYNT
3. Pseudomonas sp. PvP089	A TRM I D L S L L P P D V V EM L D F E A L L V T R KAQ Y L S S Y P A A R L A L K S D P V T K L I E E S T Y R E L V L R Q R V N D A A K A S L L A Y A T G A D L EN R A A D Y G V
4. Pseudomonas sp. S36	MNSPIDLSRLPAPNIIEPLDYETILAERKARLIALYPEELLALESEPLYKLLEENAYRELYLRORINEAARAYMLAYANDADLEHLGALFEV
5. Pseudomonas asiatica	- MATIDISQUPAPDAVEDUSYADILAERKAALIALYPAATLELESEPUVKQUEENAERELIURORINEAALAYMUPYATGODUDNIAARYV
7 gamma proteobacterium HTCC5015	I - MITULI SKI PPUNI JE SLEDI KSOMI ADVATEV DASULE I DAUPAVALLUESSTRELI SKI PAGVKAVLLATSSGSULEN LAGARGA
8. Pseudoalteromonas luteoviolacea(2)	NESATOLOK LPPPNITEPTSFEQTKNEMLNEVKARVADAETNLASEPAVKLTEVFAVRELMVRORVNEGAEAVLLAKATOVELDVLGARFGN
9. Pseudoalteromonas caenipelagi	KNP I D L S R I P A P D I V E S L D Y E T L L Q S N K T Q L L E L A P ED T L E L E S E P A V K I L Q L C A Y R E L L L R Q R V N E A A R A V M L A F A S G T T L E H L G A L M G X
10. Pseudoalteromonas sp. MMG013	GFTA IDLSKLPVPDVIEELDYESILIAMINDLVSRAPASALELE <mark>SE</mark> PVR <mark>K</mark> ILEVCALRELILR <mark>ORIN</mark> EAAKG <mark>VMLA</mark> YASGADLDNLGAFFEN
11. Alteromonadaceae bacterium 2753L.S.0a.0	JNFSATDLDKLPPPNTTEPLSFEQTKNEMLNEYKARYADAETNLASEPAVKLTEVFAYRELMVRORVNEGAEAVLLAKATDVELDYLGARFGV
12. Marinobacterium sedimentorum	JAFT AVDLS KLPFPAAVEELDFESILAALIADLQERDASYSALVESDPAVKILEVCAVREMLVRORNNEAIKAVTLACAAGSDLDQIAARVN
14. Teredinibacter turnerae	IN AN TIRST PARD TIRST DARKAN TO TELLAN TIRGELS A POTENTIAL POTENTIAL VOLCATERLE AND ANA AND AAN AND AAN AT TIRTE DARKAN TA
15. Salinisphaera halophila	AT TMIDUS LUPPPD VYEN UD FEALLY TRKAOVISSY PLARIALKSDPYTKLIEES TYRELVIRORYNDAA KASILAYATGADLEN RAADYGN
16. Halomonas alkaliantarctica	NFTGIDLSKLPPPNIIEPLSYEQIKNDMLTOYKARYPDAEITLASEPAVKLIEAFAYRELKMRQRVNEAAEAVLLAKAADTELDYLGARFGN
17. Xenorhabdus hominickii]-MPT <mark>IDL</mark> SQ <mark>LPP</mark> DVV <mark>E</mark> PLDY <mark>E</mark> QLLEERKKGLISLY <mark>P</mark> ERTLQ <mark>LE</mark> SEPLV <mark>K</mark> LLEENVYRELLLR <mark>QR</mark> V <mark>N</mark> EAARAYMVAYSTGSDLDQLGANNN
Protein Sequences	
Species/Abbrv	* * * * * * * * *
1. PHAGE baseplate assembly protein J	IDNISAFFGVERLILEPEDRSTVPPTPAVLESDTRIRERTQLALDGFSTAGPAGAYLFHALSASPLVKDVSVKAPKFEYAELSPEVEASLPAU
3 Pseudomonas sp. PvP089	
4. Pseudomonas sp. S36	EHLGALFEVSRLVTDPGNPDAIPPEPPSYETDSELRRRIQLSLDGLSTACPAQAYVFHALSANGNVKDASVSSPA
5. Pseudomonas asiatica	DNIAARYD YARLITREODLEAD PPITREYETNSAFRERILLSLDGLSTAG PEAAYIFHARSASGO YLDAAAEAPRFEVVDRDAD·····A
6. Pseudomonas sp. TCU-HL1	I EN LA <mark>A</mark> FYG <mark>V R R</mark> LLITPENTATT <mark>PP</mark> TPAVW <mark>E</mark> ADTSL <mark>R S R</mark> TQ <mark>L</mark> AME <mark>G</mark> F <mark>B</mark> TAGPAGAY RFHALSADGA V KDVA VDA PRFARASLSPELKTQLPA:
7. gamma proteobacterium HTCC5015	D Y L G A R F G V E R Q I V E A G D P Q A L P P I P A T Y E D N E R Y R E R I Q L A L E G F S T A G P I G A Y V F H AM R A S S F Y K D V A V D A P L F G P A T L T T E Q T A T L P N I
8. Pseudoalteromonas luteoviolacea(2)	ID YLG ARF G YERQLID AGD AD AN PP V PPT FETNDRY KERIQLALEG FSTAGP V GGY V FHALKAS PLVK RV AVD APQ FAV APLT E CQ TGL PT
9. Pseudoalteromonas sp. MMG013	TENEGAL MEYTIKLI I I PADINAN PETAAV MEKUDU TAALI QUDI TADEL CATI TAALI SANGUVUMAS VI TEVISMASI DAG VMAQUPPT INNI GALEFEVTDI I I DI ODI TEAVED VADI VEADINO E DO I OTAVEGVI TAO PECAVI VI ALI SANGUVINAKEVIS DI ESO ATVISOAT
11. Alteromonadaceae bacterium 2753L.S.0a.0	D Y LG AR F G V ER OL I D A GD A D A N P P I P P T F E T N E R Y A E R I OL A LEGF ST A G P Y G Y Y F H A LKA S P O Y KD Y A V D A P O F T Y A O L T E GO T O L P A L
12. Marinobacterium sedimentorum	DQIAARYN VERLTI V PAAPNAI PPT PAVMESDTEL RRRVQL SFEGF <mark>S</mark> TAG PEGAYIFHALGADAQ VLD V S VHAPTFASVEVS PEAKALL PEU
13. Desulfobulbus elongatus	EHLG <mark>A</mark> LMG <mark>VAR</mark> LTIIAANPNAN <mark>PP</mark> TPAVL <mark>E</mark> HDDDY <mark>RARIQL</mark> ALDGL <mark>S</mark> TAGPEL <mark>AY</mark> IY <mark>H</mark> ALS <mark>A</mark> SGL <mark>VLD</mark> AS <mark>VTTP</mark> TFSKATISQSLQAQLPAT
14. Teredinibacter turnerae	DNRAADYG <mark>VQR</mark> LVITPADLTAV <mark>PP</mark> VAAVM <mark>E</mark> DDEAL <mark>RYRTRL</mark> SLEAL <mark>S</mark> VA <mark>G</mark> SRG <mark>AY</mark> EF <mark>H</mark> GLS <mark>A</mark> SASIANIS <mark>V</mark> DS <mark>P</mark> TFVAAQISPALQAQLPA(
15. Salinisphaera halophila	EN RAAD Y G V Q K LI L R PAD POAV P P V PAIMES DE AL RY R T R L S LE ALSSAGS RGAYEFHGLSASAN I AS V S VD S P R F S G LA V PD EL KALL PAI
16. Halomonas aikaliantarctica	ID T GARFGVERQIVE AGD 7QALPPI PATYEDNE KYRERIQLALEGFSI AGPI GATVFHAMRVSSFVLDVA VDAPI FASAQLSNEQLALLPAT DO GANNNYGRUIVE DA DNE TV DD TAVMESNI VOUDALEGFSI AGPI GATVFHAMRVSSFVLDVA VDAPI FASAQLSNEQLALLPAT
17. Aeromabdus nominicki	
Protein Sequences	
Species/Abbrv	× · · · · · · · · · · · · · · · · · · ·
1. PHAGE baseplate assembly protein J	K F E Y A E L S P E V E A S L P A G A L Y <mark>E</mark> L A T D D <mark>A</mark> G <mark>L</mark> S T P Y P G D V A Y T L E S T D G T G T P E Q D L I D T <mark>V</mark> M T S L D D E D V R P L <mark>T D</mark> N P R Y L P V E L V D Y T L E <mark>A</mark> T I I
2. Peduovirus P2	PAC V T I S V L S R EN NG V A S ED L LA V V R NAL NG ED V R P VAD R V T V Q S A A I V E V Q I NAT L
3. Pseudomonas sp. PvP089	PRESGLAVSDELKALLPEGAIVLVCDVTAGLTDPLPGDVSLAVUPRVDSQETPENLVAKVQAGLSAESVRPVTDRPAQLGQPVNFEVLATL
4. Pseudomonas sp. 556	
6. Pseudomonas sp. TCU-HL1	PRFARASLSPELKTQLPASAIVLVAAHDAALSEPHPGDVAITVLSRDGDGTPSPELLARVDAALNAEDVRPLTDRPRVLAAEVRPYQVRATL
7. gamma proteobacterium HTCC5015	PLFG PAT L T T E Q T A T L P N G T M V L Q C T Y D A G L T A PQ PGD V A I S T L S T Q G N G S P S E G L N Q S V L A H L N A D D V R P L T D H V R L R PT E I I E Y H I D A V L
8. Pseudoalteromonas luteoviolacea(2)	PQ FA VA PLTE EQQ TG L PTG TTV LQ CTYD <mark>AG L</mark> SE PQ PGD VA I T <mark>V L</mark> STEG S <mark>G</mark> A PSTELNAA <mark>V</mark> ITALSADD V R P L <mark>TD</mark> H V R L RATD I TE VALSATL
9. Pseudoalteromonas caenipelagi	Y F SMASIDAG VMAQL PPGSIVLQVDDDAGLLEPMPGDVVITVLSRENNGVPDVATLQAVYDALNAESVRPLTDNVHTQAAQLIDFTIIANL
10. Pseudoalteromonas sp. MMG013	PT F SQ AT V SQ AT L DQ L PPN SI V LQ V DD D AG LA DP M PG DV AN SV U S RNG AG TA PQ T LL DQ V EA AL SA DE V RP LT DF V I V RS AQ I V N Y SI D AT T I
12. Marinobacterium sedimentorum	T FAS EVS FASAL I PEGANVI OVO DAGI AD PMPGDVA I AVO S DEGA GEA O PEVA TVA ATI S SETVA PITO H PRVSTVA TVA ST SA STVA PITO H PRVSTVA STVA STVA STVA STVA STVA STVA STVA
13. Desulfobulbus elongatus	PTFSKATISOSLQAQLPANAIVLQVEEGAGLPNPMPGDVVITVUSRENNGLPSAATLQAVTDALNAESVRPVTDHVHTQAAQLIDFGITASI
14. Teredinibacter turnerae	Y T F V A A Q I S P A L Q A Q L P A G A I V L V C D Y P <mark>A G L S N P L P G D V</mark> S L A V L P S L N S Q I P A A D L V Q L <mark>V</mark> Q Q A L S A E D V R P I T D R P R A L A G Q A T D Y A V T A V L
15. Salinisphaera halophila	PRF SGLAVPDELKALLPAGAI V <mark>L</mark> VCDVT <mark>AGLTDPLPGDV</mark> SLA <mark>VL</mark> PRADS <u>Q</u> EPPEDLVAK <mark>V</mark> QAGLSAES <mark>VRP</mark> V <mark>TD</mark> RPRAQLGQPVNFEVL <mark>ATL</mark>
16. Halomonas alkaliantarctica	TEASAQLSNEQLALLPAGTTILQCTYD AGLAN PQ PGDVA IS VLSTQSNGTPTTELNQS VLAHLNADDVR PLTDHVRLRPTEI I EYQ I EAVL
17. Xenornabdus nominickii	N N N I V TIM S KEN KOVASKOLLEK VEKALNDEN V KAV VADRLKVOSAN I VEVEI NAVL
Protein Sequences	
Species/Abbry	
1. PHAGE baseplate assembly protein I	UVDYTY EATIYY K POVEGO AVMSAVELSADSFIEDOKI LOSDIAI SAVYKALH SOVARVOLTSPASDIAIAAFOAPHOTSIOLHYOGYED
2. Peduovirus P2	V E Y Q I N <mark>A T L</mark> Y L Y P G P E S E P I R A A A V K K L E A Y I T A Q H R <mark>L G</mark> R D I R L S A I Y A A L H V E G Y Q R V E L A A P L A D I V L N S T Q A S F C T E Y R V V T G G S D E -
3. Pseudomonas sp. PvP089	P VN F E VL <mark>A T L</mark> E L E <mark>P G P</mark> E P S V <mark>V</mark> Q A A S R A S L D K A V A A A R D L E G Q L S L <mark>S</mark> A V <mark>Y A A L H</mark> VQ <mark>G V</mark> R <mark>R V</mark> D L K K <mark>P</mark> T T E I V C D K R H V P Q C V S I S L S T K V V A -
4. Pseudomonas sp. 536	J LD Y T LD AT L Y L Y PO PD ST V V L A E A R A Q A D A Y T SE Q H Q L O RD I T L S G L Y A A L H R P O V Q R V E L A A P T A S L T V T P Q Q A A H C SMI T L R E O G I D E
5. Pseudomonas asiatica	PYEINATLY VIADY DSELIVEEARAKAREYAD TOHRLGYDYTLGGVYAALH RPGYQRYDLHH RYCTWTINRQQAPYCTAINIDYGGIDE
7 gamma proteobacterium HTCC5015	REFUVENTIETETETETETETETETETETETETETETETETETET
8. Pseudoalteromonas luteoviolacea(2)	TEYALSATUHUY POPDAESWAQAQASAQSWVNENIKUGRDYTUSGUYAALHUPOYORVCUHSPTTDUVMHGHOAAVCKNYTVEIGGRHY
9. Pseudoalteromonas caenipelagi	I DETTIIANLYTEP CEP DTN VVLQEANDKLSTYLEENQELGESITLS GIYAALH VA CVQEVETIA BVADIICTSAQAARCTTKTINH GGIAE
10. Pseudoalteromonas sp. MMG013	Ĵ VNYSID <mark>A</mark> TIYFLN <mark>OP</mark> DSEV <mark>V</mark> LAAAQTAIEQYVESRHL <mark>LO</mark> QDYT <mark>LS</mark> GV <mark>YAALH</mark> QP <mark>OV</mark> Q <mark>RV</mark> ELAS <mark>P</mark> AADIVIDNRSASYCTGITLTH <mark>O</mark> GYDE
11. Alteromonadaceae bacterium 2753L.S.0a.0	ġ TEYALS <mark>ATL</mark> HLY <mark>PGP</mark> DAES <mark>V</mark> RIQAQESAQNWVNENHK <mark>LG</mark> RDIT <mark>LS</mark> GL <mark>YAALH</mark> LP <mark>GVQRVEL</mark> HS <mark>P</mark> TTDLVMLGHQAAYCTNIAVLV <mark>G</mark> GRNY
12. Marinobacterium sedimentorum	PAEYS YEAV LTFF POPDREV WATAL VALES FVERQHALGRDYTL GLYAALHOEG YQN VEL IA PAAGI YV PWDTVAY CTGIDL TD GTDE
13. Desulfobulbus elongatus	TO FUT AVEL TAVE OF A VELOCAN EQUATIVE EN OR LONG STILLE OF ALL OF PROVINCE A ADA OF A TO LECTS AQAAR OF EKNINH OG TAS
15. Salinisphaera halophila	TURE TO TRANSPORT TO TRANSPORT TO A REAL TO TRANSPORT TO A LEVEN VERY NET KAN AD VECO KRETER AND V
16. Halomonas alkaliantarctica	I EYQ I EAVLH EY POPDAES WRQAAETAYQAWY I DNHKLORD I SLOALYSYLH RPOYOR VELLAPANDL VVNGHQAAFCTSVN I STOOGRNY
17. Xenorhabdus hominickii) VEVEIN <mark>AVL</mark> VIF PTP ESEPIRKAAEQKLKHVVEAQHR <mark>LG</mark> RDIR <mark>LG</mark> AI <mark>YAALH</mark> VE <mark>GVORV</mark> ELKAPLKDVVLDKTQASY <mark>C</mark> TKTTLTM <mark>G</mark> GSDE –

Fig. 5.22. Multiple sequence alignment of Phage CR1 Baseplate assembly protein J highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* Baseplate assembly protein J protein from bacteriophages of various hosts it was observed that isoleucine, aspartic acid, leucine, and others are highly conserved at amino acid positions 5, 6, 7, and other positions, respectively.

5.4.10. PHAGE CR1 Capsid scaffolding protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Capsid scaffolding protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage capsid scaffolding proteim of *Alcanivorax sp. S71-1-4*, exhibited 99% sequence similarity with *Phage CR1* Capsid scaffolding protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.23. Phylogenetic analysis of Phage CR1 Capsid scaffolding protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences	
Species/Abbrv	
1. PHAGE CR1 capsid scaffolding protei	MEKDK <mark>SKKFRV</mark> ALSGKTVDGREISPLQIQEIAQTYDPKKYGARIMNEHLRGILPDSYFKALGDVLSVEAKEDGKWGLYAEISPTNOLVEINKNR
2. Peduovirus P2	MAKKSKFFRIGVEGDTCDGRVISAQDIQEMAETEDPRVYGCRINIEHLRGILPDGIFKRYGDVAELKAEKIKGKWALFAKITPTDDLIAMNKAA
3. Haemophilus phage HP1c1	WN K ST D F I C I A T S G Y T V D G R Q I T A Q E L H E M A E T Y D P E H Y T A N L W P E H R R W F · · · · · · · N M G Q Y I E L K A E E N K G E T Q L F A I I A P N K E L I E Y N R A G
4. Alcanivorax sp. S71-1-4	NSTKSKMFRVATSONTVDORELSVQQIKDLAASYDPKKYGARVWCEHLRGLLPDSVFKAFGDVRSVEAREVGGKWGLFAEIDPTPELVTINRAR
5. Pseudoalteromonas sp. MMG013	MSKKSKFFRVFTEGDTTDGRVVERGWIEDMAAT YN TAN YGARIWLEH IRSVLPDSPFKAYGDVLAVKAEE VGGKLALFAQTDPTPDLIAMNKSR
6. Pseudoalteromonas luteoviolacea	WAKKSKFFRVFTEGNTTDGRVVERSWIEDMAATYDOAKYGARIWLEHIRSVLPDSPFKAYGDVRAVKAOEVDGKLALFAOIDPTDDLVAMNKKRI
7. Marinobacterium stanieri	MAKKSKWFRYGYAGDTTDGREIDPKWLEEMAETYN PETYGAR YN CEHYRGMAPDGSFGAFGDYLALKTETYEDKYALYAOTSPNDDLYALNKKR
8 Marinobacter sp. 1-3A	
9 Shewapella sp	WARKERS VITE CHUTTE COVER OW KDIVDTVNTAKYCARIWIEHIDCITED SPEKAVCOVTAVKAFEVDCKITIEAO ID PTEELVANNIKNDI
10 Shewanella dokdonensis	WKKSKEEDVETEGOTTOGDELOONWLEELAESVNTAVYGADIWLEHIDGILDDSPEKAVGDVTAVKAEKVDGKLALSAOLSPTEDILAMNKAD
11. Chewanella baltica	
12. Chevenella platica	
12. Snewanella algidipiscicola	MARKS KPFR VF TECHT TO VET VT A KTO A KTO LEHT KOTT PUS AFKATOD VT A VKAEE VOOK LT LFAQTE PIDELT AMNOKK
13. Shewanella putrefaciens	MAKKSKFFRVFTEGHTTDGRVVERQWITDTVETYNTAKYGARTWLEHTRGTTPDSAFKAYGDVTAVKAEEVDGKLTLFAQTEPTDELTAMNQKK
14. Spongilbacter tropicus	SKFFRVAVEGOTTDGRAITREQTVDMASTYSPEKYGARIWMEHIRGUVADSSFPALGDVVELKAEEIKGKMGLVAAINPTKELLAINEKR
15. Spongilbacter sp.	SKFFRVAVEGQTTDGRAITTEQTVDMASTYSPEKYGARIWNEHIRGLYADSSFPALGDVVELKAEEIKGKMGLYAAINPTKELLAINEKR
16. Janthinobacterium sp. BJB426	RHATSQFFRVATEGATTDGRNIDRATIEQIAATYNPKTYGARIWIEHIRGIIPDSQFKAYGDVIAVKAEEVGKKLALFAQTEPTPELVAINKAK
-	
Protein Sequences	
Spacies (Abbo)	
1 PHACE CP1 caprid scaffolding motor	MINT C NYN RWUNCE, BURRATANAN CEU WERERAU OF ANNESI CONVERSION FOR FORMULA FOR ANNES
2. Pedverdere P2	
2. Peduovirus P2	DULIAMN KAAQ KVYTSMETOPNIOKCYLVOLAVIDD KASLGTEYLEFCKILSPENLISVAIPVELEFEDLPETVALTEKVKSIPGRKQASDDARL
3. Haemophilus phage HP1c1	RELIEVNRAGOVIETSIEITPNSGRAVISGIGVTDSPASVGTTELKFFEQRGSVCGEFIKVDSAREDVEEERNVFRKLFSTLNPNNNNHKEDH
4. Alcanivorax sp. S71-1-4	PELVTIN RAROKVYSSIEIDPDTGGPYLGGLSVTDSPASTGTDMLMFSRQQRPESTFTDYIEGPLEFIEIEEQEGLFSRVKTLLGASSKKSDDKF
5. Pseudoalteromonas sp. MMG013	POLIAMNKS ROKI YTS VEIDPKS CKCYLAGLAVTDS PASLGTEMLEFS A TOKPONLFTAAVAIELEFEDS TEHKGLFSKYSSLLNKNKKHNDGNF
6. Pseudoalteromonas luteoviolacea	_ D D L V A M <mark>N K K RQ K I Y T S V E I D P</mark> K S G K C <mark>Y L A G L A VT D S P A S L G T E</mark> M L E F <mark>S</mark> A S Q K P E N L F T A A I E A E L E F E D D E E Q E G L F S K V S A L L N K N K K Q T D G N F
7. Marinobacterium stanieri	_ D D L V A L N K K R K K V Y T SME I D H G K D K A Y L Y G L A V T D S P A S L G T E M L E F A A K Q K P E N Y F S A A R E V E L E F E D + + + + + S I L D K V K S L F S K S E A T H A E Q H
8. Marinobacter sp. 1-3A	ÞÖLVKMSKDR <mark>QKIYTSIE</mark> V DP GS G EAYFI G LA <mark>VTDSPASLGTE</mark> MLQF S STQR <mark>P</mark> ENLFSAAL E AELDFTAEDPTLFT <mark>KVK</mark> ALFSKHRDASAAKF
9. Shewanella sp.	E E L V A MN KN R Q K V Y T S V E I D P K T G K C G L V G L A V T D S P A S L G T E M L A F S A T Q R P E N L F T S A V E V E L E F D D I S D E P G L F A K V K A L L G K S K A D A K N D F
10. Shewanella dokdonensis	E D L L AMN K A R Q K I Y T S V E I D P K T G K C Y L T G L A V T D S P A S L G T E M L A F S A K Q K P D N L F T A A V E T T L E F E D D E P G L F N R V K A L L G K A S K V T S D E F
11. Shewanella baltica	^T BELIAMNOKK <mark>OK VYTSVEIDP</mark> KTOKCYLS <mark>OLAVTDSPASLOTE</mark> MLAFSATOR PENLFTSAVE VDFEFEEVSDELGLFA <mark>KYK</mark> ALLSKNKAEAKTDF
12. Shewanella algidipiscicola	🖥 ELIANNOKKOK VYTSVEI DPKTOKCYLSGLAVTDSPASLGTEMLAFSATOR PENLFTSAVE VDFEFEEVSDE PGLFAKYKALLGKNKAE AKTDF
13. Shewanella putrefaciens	DELLANNOKKOK VYT SVEI DPKTOK CYLSQLAVTD SPASLGTEN LAFSAT OR PENLFTSAVE VD FEFEEVSDE PGLFAKYKALLGKN KAE AKTD F
14 Spongilhacter tropicus	KELLA IN EK DAKLYTSTELD DOSCOAVY GIG VTOSDASI GTEALKESAEND DENTESSAVEVOLENEAESK DEGLESKI KELLKOD KAETGAES
15 Sponglibacter sp	KEN I A IN EK POKI Y TSI EL DEGSCOAVYYGI GYTDSDASI GTEAT KESAENDEN I ESSAMEVHI EMEAESKEGI ESKI KELL KED KAETGAEE
16 Japthipobacterium co. BIR426	
ro. janumobacterium sp. bjb420	Servin KARKET STERVE SSCHLUNG COT MARALES FRANCESCHER SCHERE SCH
Protein Sequences	
Coories (Abbru	
1. BHACE CB1 coord cooffedding protei	THE VERY PETCENT OF AN AVENUE AND A REVISED AND AND AND AND AND AND AND AND AND AN
2. Perhade entre pa	
2. Peduovirus P2	KYRSIPGRKQASDDARLNDVHEAVTAVAEHVQEKLSATEREMETAPSALKQEVIDADETSQAFIKLKNSLDHTETQQKKSKATQQGDLMMNL
3. Haemophilus phage HP1c1	REFSTENPRNNNNH KEDHAQFAQLTEAVKGEDAKI DNH SETKEPTAEQFNQLLTTVQALDKKI NELSQEQTTVPGVPTVEKENNGYNTESKGF
4. Alcanivorax sp. 571-1-4	RVRTLLGASSKKSDDKFSDVHSAVETTAQSVVAMEERFAALPEVDTELKKVRTDLDALTQKLSQTP-QSQRPAHSGGDGTELTDC
5. Pseudoalteromonas sp. MMG013	KY SSLUNKNKKHNDGNFGDINQAVETIAQSFSQFEANTQKQLETTTNHYNDLSEKHNQLQNAFDT <mark>LKEQL</mark> SNEEGGQG <mark>R</mark> APAT <mark>GG</mark> NGQVQ TD C
6. Pseudoalteromonas luteoviolacea	_ <mark>K V</mark> SALUNKNKKQTDGN <mark>F</mark> G D ISKAVEAIAHSFTQLESDTQKQLSETTNNYNALNEKHTQLQEAFNT <mark>LK</mark> EQUSNEEGGQQ <mark>R</mark> KP <mark>ATGG</mark> DGQIQ <mark>TD</mark> C
7. Marinobacterium stanieri	<u> </u>
8. Marinobacter sp. 1-3A	K V K A L F S K H R D A S A A K F G D F R A D L E K T L E L F V T D G Q Q L R A S M D E M S G E Y R Q M K T E L D S L K T N F N S <mark>L K</mark> S E I E S S P N H S Q R A P <mark>A</mark> T <u>G G</u> Q E E I L <u>T D C</u>
9. Shewanella sp.	K V K A L L G K S K A D A K N D F A D V H Q A V E E I A K T V A D T G E D F T A K L D E S V N D L N K L Q T D F N E L S S K F N A L K T Q L E K E E T G Q R R S P A T G G D N I K T D C
10. Shewanella dokdonensis	R V K A L L G K A S K V T S D E F S D V HQ A V E A L AQ T T A D V E T R Y AQ Q F T R Q Q T T L S Q V T T E L E Q L T A N F N T L K Q Q L D N E P H H S Q R Q P A S G G D N T V K T D C
11. Shewanella baltica	KYKALLSKNKAEAKTOFADVHQAVEEIAQAVAHAETQFGSNVTKGMEDLTKLQTDFNELSTQFNALKTQLEKEETGQRKSPATGGDTNMKTDC
12. Shewanella algidipiscicola	KYKALLGKNKAEAKTDFADVHQAVEELAQAVADAENQFGAKVSKGMEDLTKLQTDFNELSTQFNALKGOLEKEETGORKSPATGGDTNIKTDC
13. Shewanella putrefaciens	KYKALLGKNKAEAKTDFADYHOAVEELAOAVAHVETOFGSKVTKGMEDLTKLOTDFNELSTOFNTLKTOLEKFFOGOR SPATGODTNMKTOL
14. Sponglibacter tropicus	KIKELLKRDKAETGAEEGDONEAVTILANEVVALTKKIEDGATASAOEISDIMEKETTVNSEINALKTOLGKEHOHSOBPPATGODGEVIADC
15 Spongilhacter sp	KIKELIKED KAETGAEEGDONEAVTU ANEVVALTKKIED GATASAOEISDINEKETTVNSEINALKTOLGVEHONGODDATGOGEVIADC
16 Janthinohacterium en BIP426	A VENTIL CRESNING COLLEGATION CALL AND VALUE AND V
ro. janumobacterium sp. bjb426	S CARLES STATES STATES STATES AND STATES AND STATES AND SAVE SAVE SAVE SAVE SAVE SAVE SAVE SAVE

Fig. 5.24. Multiple sequence alignment of Capsid scaffolding protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* Capsid scaffolding protein from bacteriophages of various hosts it was observed that serine, lysine, phenylalanine, and others are highly conserved at amino acid positions 5, 6, 8, and 88 other positions, respectively.

5.4.11. PHAGE CR1 head completion-stabilization protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 head completion-stabilization protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage head completion-stabilization protein *Chitinolyticbacter meiyuanensis* and *Chromobacterium alkanivorans*, exhibited 100% sequence similarity with *Phage CR1* head completion-stabilization protein, the phylogenetically closest species with standing members in the tree. *Chitinolyticbacter meiyuanensis* capable of hydrolysing chitin and shrimp shell to *N*-acetyl glucosamine (GlcNAc). Chitin the most abundant amino-polysaccharide polymer occurring in marine environment, and *C. meiyuanensis* is capable of hydrolysing by producing chitinase enzyme (Zhang et al, 2020).



Fig. 5.25. Phylogenetic analysis of Phage Capsid scaffolding protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.



Based on the multiple sequence alignment of *Phage CR1* Capsid scaffolding protein from bacteriophages of various hosts it was observed that methionine, arginine, aspartic acid, and others are highly conserved at amino acid positions 1, 2, 4, and 56 other positions, respectively.

5.4.12. PHAGE CR1 putative baseplate assembly protein V:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 putative baseplate assembly protein V** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage putative baseplate protein V of *Alcanivorax sp. S71-1-4*, exhibited 99% sequence similarity with *Phage CR1* putative baseplate protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.27. Phylogenetic analysis of Phage CR1 putative baseplate assembly protein V. (a.) *Maximum likelihood tree* (b.) *Neighbourhood Joining tree*.



Fig. 5.28. Multiple sequence alignment putative baseplate assembly protein V highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* putative baseplate assembly protein V from bacteriophages of various hosts it was observed that glutamic acid, arginine, asparagine, and others are highly conserved at amino acid positions 6, 9, 813 and 44 other positions, respectively.

5.4.13. PHAGE CR1 tail component protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 tail component protein** has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits.Phage tail protein of *Marinobacter sp. X15-166B*, exhibited 100% sequence similarity with *Phage CR1* tail component protein, the phylogenetically closest species with standing members in the tree. The *Marinobacter sp. X15-166B* cultivated from marine sediments near the harbours.



Fig. 5.29. Phylogenetic analysis of Phage CR1 tail component protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences																																				
Species/Abbrv			*	*	* *	*		*		* *	*		*	*		* *	*	* *	* *	*	4	۲		*	*		1	* *							* *	*
1. Phage CR1 tail component protein	MR	VV	ΤA	S Q	G <mark>D</mark> T	VD	L I	CW	RE	YG	RT	A	G V	ΤE	A	VL	E A	NF	GL	A	i L C	6 A	VL	ΡL	GI	RV	/ T	LΡ	DV	LP	ΤÇ	KÇ	ТТ	V K	LW	D
2. Peduovirus P2	- M	КΤ	F <mark>A</mark>	LQ	G <mark>D</mark> T	LD	ΑI	ΟV	RY	YC	RT	E	G V	VE	т	V L	A <mark>A</mark>	NP	י G נ	A	E L C	6 A	VL	ΡH	G T	AV	E I	L P	DV	QΤ	AF	V A	ET	<mark>V</mark> N	LW	E
3. Pseudomonas lalkuanensis	MD	Q V	I A	RQ	G <mark>D</mark> T	LD	ΑI	CW	RΗ	YG	RT	A	5 V	ТЕ	А	V L	e a	NF	י <mark>G ו</mark>	AE	E L C	6 A	VL	ΡL	G T	ΤL	N	L P	ΡQ	A P	'QF	'QF	(R T	<mark>V</mark> Ç	LW	D
4. Pseudomonas sp. 09C 129	ΜA	A <mark>V</mark>	I A	AQ	G <mark>D</mark> T	V D	SΙ	C W	SΥ	YG	RT	A	3 V	ТΕ	А	VL	e a	NF	G I	A D) L (i P	1.1	ΡH	G T	RV	/ T	L P	DA	A P	<mark>۷ Q /</mark>	E C	RV	V N	LW	D
5. Pseudomonas denitrificans (nom. rej.)	M A	v <mark>v</mark>	I <mark>A</mark>	AQ	G <mark>D</mark> T	VD	SΙ	CW	н ү	YC	RT	A	G V	ТЕ	S	V L I	D <mark>A</mark>	NF	י <mark>G ו</mark>	A D) L (6 P	1.1	ΡH	G T	R V	/ T	L P	D A	<mark>a</mark> p	<mark>۷ Q /</mark>	E Ç	RV	V N	LW	D
6. Pseudomonas resinovorans	MD	Q <mark>V</mark>	I A	RQ	G <mark>D</mark> T	LD	ΑI	CW	RΗ	YG	RT	A	3 V	ТЕ	А	V L	e a	NF	י <mark>G ו</mark>	A D) L (6 A	VL	ΡL	G T	ΡI	н	L P	ΡQ	<mark>A</mark> P	'QF	'Q F	(R V	V Ç	LW	D
7. Pseudomonas aeruginosa(2)	MA	A <mark>V</mark>	I A	s q	G <mark>D T</mark>	VD	ΑI	C W	RY	YC	RT	A	G V	тЕ	L	V L	E A	NF	י <mark>ה ו</mark>	AD) L (B P	1.1	ΡH	G T	QV	/ T	L P	DA	A P	, Q ∖	E Ç	RV	LN	LW	D
8. Pseudomonas aeruginosa	MA	v <mark>v</mark>	I A	AQ	G <mark>D</mark> T	VD	SΙ	CW	н ү	YC	RT	A	G V	ТЕ	Α	V L I	D <mark>A</mark>	NF	G L	AC) L (B P	1.1	ΡH	G T	R V	/ I	L P	D A	<mark>A</mark> P	<mark>۷ Q /</mark>	E Ç	RV	V N	LW	D
9. Pseudomonas nitroreducens	MA	v <mark>v</mark>	I A	AQ	G <mark>D T</mark>	V D	SΙ	C W	н ү	YC	RT	s c	G V	ΤЕ	S	V L I	D <mark>A</mark>	NF	י G נ	A C) L (5 P	1.1	ΡH	G T	н <mark>v</mark>	/ T	L P	DA	A P	Q A	E Ç	RV	V N	LW	D
10. Azotobacter beijerinckii	MA	A <mark>V</mark>	I A	НQ	G <mark>D T</mark>	VD	ΑL	C W	RΗ	YC	RT	A	s v	V E	Α	V L	E A	NF	י <mark>ה ו</mark>	AD) L (5 P	ΕĽ	ΡH	<mark>G</mark> Q	R V	/ T	L P	ΕQ	A P	Q F	νQ Τ	Q T	<mark>V</mark> Ç	LW	D
11. Azotobacter vinelandii	MA	т <mark>v</mark>	I A	НQ	G <mark>D T</mark>	LD	ΑL	CW	RΗ	YC	RT	Α :	5 V	VE	Α	VL	e a	NF	י <mark>ה ו</mark>	AC) L (B P	ΕL	ΡH	<mark>G</mark> Q	R V	/ T	L P	ΕQ	<mark>a</mark> p	'Q F	'QF	<mark>(Q</mark> L	<mark>V</mark> N	LW	D
12. Marinobacter sp. X15-166B	M R	ΕT	R A	LQ	G <mark>D T</mark>	V D	LΙ	CY	RH	YC	Y T	D	G V	ΤЕ	V	V L	E A	NF	י G נ	A	с н <mark>с</mark>	5 P	VL	ΡM	G T	RV	/ н <mark>I</mark>	L P	ΕV	A A	Q F	і т к	ст s	V Ç	LW	D
13. Klebsiella pneumoniae	MK	K V	R A	YQ	G D T	VD	ΑL	CW	RΗ	YC	RT	Q	G V	ΤЕ	Q	V L	Q A	NF	Gl	AB	H C	5 P	ΕL	ΡH	GL	QV	E I	L P	DΙ	A T	TS	т	Q T	VQ	LW	D
14. Erwinia typographi	- M	к <mark>v</mark>	R A	LQ	Y D T	VD	A L	C W	RH	YG	R T	Q	G V	ΤE	Q	V L (Q <mark>A</mark>	N F	G L	A	i Y <mark>C</mark>	P	V L	P H	<mark>G</mark> L	ΕV	E I	L P	DV	A P	' A V	'T S	QT	<mark>V</mark> Q	LW	D

Fig. 5.30. Multiple sequence alignment of tail component protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* tail component protein from bacteriophages of various hosts it was observed that methionine, valine, alanine, and others are highly conserved at amino acid positions 1, 4, 6, and 33 other positions, respectively.

5.4.14. PHAGE CR1 tail completion protein-like protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 tail completion protein-like protein**, has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage tail protein of *Marinobacter sp. X15-166B* and *Alcanivorax sp. S71-1-4*, exhibited 100% sequence similarity with *Phage CR1* tail completion protein-like protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.31. Phylogenetic analysis of Phage CR1 tail completion protein-like protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences	
Species/Abbrv	
1. PHAGE CR1 tail completion protein	MIKIVNKLQAL RDHLVAK I PHLKQNPDKLLTFVDTGEIHAAAGLVDHSNRVTANIIVTDWSGSLEDITVPVLDWLQRFETDHPSSPRIRVEADVINHT
2. Peduovirus P2	MLKPDSLRRALTDAVTVLKTNPDMLRIFVDNGSIASTLAALSFEKRYTLNVIVTDFTGDFDLLIVPVLAWLRENOPDIGQKKGFTFYADINNDS
3. Larsenimonas suaedae	MKKLTALROYLIDAVPHLORDPOGLUTFVEDGTIEFSAGPLSHGVTFTAQLVLTDFADDVOTVMVPLLDWLAVYQPDLAPAEAVRFEAEVLSNS
4. Kushneria phyllosphaerae(2)	MKKLTALROHLIDAVPHLORDPOQLUTFVEDGALEFAPGPLSHGYTFTAQIVLTDFADDIDTVMIPLDDWLGVYQPDLVPAEAIRFEAEILNND
5. Kushneria indalinina	MKKLTALRQYLLDAIPHLQRDPDQLLTFVEDGTIEFAPGPLSHGYTFTAQIVLTDFADDLDTVMIPLLDWLAVYQPDLIPAEALKFEAEILNND
6. Kushneria phyllosphaerae	MKKLTALRQHLLDAVPHLQRNPDQLLTFVEDGTIEFAPGPLSHGYTFTAQIVLTDFADDIDTIMIPLDDWLAVYQPDLVPAEAVRFEAEILNND
7. Pseudomonas luteola	MNKPESLRAHLMAAVPELRHNPDRLLVFIDQGKVRCTAAALSFEYGYNLQIILTDFAGHPDAVMLPLLAWVRTNQSELKSAEGIQFEVDILDHS
8. Pseudomonas aeruginosa	MKKPELLRDHLLAAIPELKRNPDRLLVFVDNGSMRSTAAPLSFEYSYTLNLILTDFAGSPDAVAVPLFAWILTSQRELKGRDAIKFEADILNNK
9. Pseudomonas umsongensis	MNKPDSLRAHLLAAIPELKHNPDRLLIFIDNGKIRCTAAALSFEYAYDLQIILTDFAGHPDSVMLPLLGWLRVNQSELKSAEGIKFEADVIDHS
10. Pseudomonas marincola	MNKLNSLRTHLIANVPELKYNQERLLIFVDQGRIRATAAPLSFEYSFTLNIILTDYTGSPDAVAVPLLAWVLVNQSELKGKESIQFEVDVIDEN
11. Pseudomonas sp. C2B4	MNKPOSLRVHLLAAIPELKHNPDRLLIFIDNGKIRCTAAALSFEYAVDLQIILTDFAGHPDSVMLPLLGWLRVNQSELKSAEGIKFEADVIDHS
12. Halomonas alkaliantarctica	MIKLHALRKHLIDAVPELKRGPDKLLTFITDGGIAFARGQLSHEVRVEAQIVVTDYAGSIDTVMIPLLQWLGRYQPDLDPDEAIRLEAEILSNQ
13. Halomonas gudaonensis	MNKLHALRKHLIDAVPELKRGPEKLLTFVQDGTIAFARGQLSHEYRVDAQLVVTDYSGSLDTLMIPLLQWLSRYOOPDLEPDEAIRLEAEILSNQ
14. Halomonas elongata	MRKLSALRQYLIDAVPOLKROPORLLTFVEDGSVQFSRGPLSHGYRFTAQLILTDYAGEIDAIMLFLDWLSIYQPOLEPEQAVSFEAEILNND
15. Halomonas organivorans	MRKLSALRQYLIDAVPELKRDPDRLLTFVEDGSVAFSRGPLSHGYRFTAQLILTDVAGEIDAVMLPLLDWLSVYQPDLESEQAVAFEAEILNHN
16. Variovorax sp. S12S4	MKKPQLLRDYITRACPDLATNPERLTVFIERGQIVHTGTPLSFEWRYTLNIVITDWTGSTDVLVVPVAWLKRFQPDIRRERAFRFESEIIDHK
17. Marinobacter sp. X15-166B	MRKLEDLRRHVLANVPKLKRNPDKLLTFIEDGNIEFWQGPLSHSYAIPIQLIVTDYAGSVDDIVIPVLSWLKVREPGLDPMNTVRFEAELLNNN
18. Salinicola socius	MKKLDALRQHLIDAVPGLSRDPDRLLTFVEDGSIEFARGPLSHGYTYTAQLVLTDYAADIDAVMIPLLDWLSIYQPDLDPKQAVSFEAEILSNS
Protein Sequences	• • • • • • • • • • • • • • • • • • •
1 PHAGE CP1 tail completion protein	NINY TAN I VITOWSGSI ED I TVID VI DWI DEFETDHESSEDI DVITANVI NHTEVELSI SI ELE DAVKVADDO TVEAD PETERGETNAI DEWEKANG
2. Peduovirus P2	Y TIN VIVIDET GDEDILLIV PVI AWIRENOPDIGOK KGET EV AD INND SSEDISISIMITER TIVSVDGALHVKNSE PPPPEPELVSKWDE
3. Larsenimonas suaedae	FTAOLYLTDFADDYDTYWYPLLDWLAYYOPDU APAEAYRFEAEYLSNSAYDLALRYOLTERYIAKDTGKISYEHRMPRFDYDHLSGYAAPES
4. Kushneria phyllosphaerae(2)	FTAQIVLTDFADDIDTVMIPLUDWLGVYOPDLVPAEAIRFEAEILNNDAVDLALRVOLTERVVAKDTGRLDISHRMPRFDIERHLSDYVEPEG
5. Kushneria indalinina	FTAQIVLITD FADDLD TYMIPLLDWLAVY OPDLIPAEALKFEAEILNNDAYDLALRVOITERVVAKDTGOINISHRMPRFDIERHLSDYVEPEG
6. Kushneria phyllosphaerae	FTAQIVLTD FADDID TIMIPLLDWLAVYQ PDLVPAEAVRE EAEILNNDAVD LALRVQINER VVAKTT GOIHAHHRMPRFD TEEQVAEWQG PQG
7. Pseudomonas luteola	YN LQIIIL TD FAGH P <mark>D</mark> AVML PLLAW V RTNOSELKSAEGIQ FEVDILDHSKVDMAITLPLTERVIVKDNGTYSIEHGEPQYTEAELLAEWQTPDG
8. Pseudomonas aeruginosa	Y T L N L I L TD F A G S PD A V A V P L F A WILT S Q R E L K G R D A I K F E A D I L N N K A V D L S I T L P L T E R V I V K D D G T L Q V S H A E P V V D D E E L L A E WG - A N G
9. Pseudomonas umsongensis	Y D L Q I I L T D F A G H P <mark>D</mark> S V M L P L <mark>L G W L</mark> R V N Q S E L K S A E G I K <mark>F E A</mark> D V I D H S K V <mark>D</mark> M S L S L P L T E R V I V K D G T F T V K H A E P Q Y R P Y L L I A E WQ S P Q P
10. Pseudomonas marincola	FTLNIIL TD YTGSPDAVAVPLLAWVLVNQSELKGKESIQFEVDVIDENQVDMSLTLPLTERVIVKEDGTLQITHEEPQLEETFTLESMSIPHD
11. Pseudomonas sp. C2B4	Y D L Q I I L T D F A G H P D S V M L P L L G W L R V N Q S E L K S A E G I K <mark>F E A</mark> D V I D H S K V D M S L S L P L T E R V I V K D D G T F T V K H A E P Q Y T P Y V L L A E WQ A P Q L
12. Halomonas alkaliantarctica	V E A Q I V V TO Y A G S L D T V M I P L L Q W L G R Y Q P D L D P D E A I R L E A E I L S N Q A W D L A L T V S L T E R V A L D T G T I N A E H R M P A Y P I E R L E S E W E S P E N
13. Halomonas gudaonensis	V D A Q L V V T D Y S G S L D T L M I P L L Q W L S R Y Q P D L E P D E A I R L <mark>E A</mark> E I L S N Q S W D L A L T V R L T E R V V A L D A G T I N A E H R M P A Y P I E R L A S EWE S P T D
14. Halomonas elongata	FTAQLIL TD YAGEI D AIML <mark>P</mark> LLD <mark>WL</mark> SIY Q PDLEPEQAVS <mark>FEA</mark> EILNNDAV <mark>D</mark> LALRVRLD ERY VAKES <mark>G</mark> RITAE <mark>H</mark> RM <mark>P</mark> RFERPVKIAEWETAGV
15. Halomonas organivorans	FTAQLILI TD YAGEI D AVMLPL <mark>LDWL</mark> SYY <mark>Q</mark> PDLESEQAVA <mark>FEA</mark> EILNHNSY <mark>D</mark> LALRYRLD <mark>ERY</mark> VATET <mark>G</mark> RITAE <mark>H</mark> RM <mark>P</mark> RFERPVKIAEWETAGY
16. Variovorax sp. S12S4	YTLNIVI TD WTGSTDVLVVPVVAWLKRFQPDIRRERAFR <mark>FE</mark> SEIIDHKTADIGIEID <mark>LTETV</mark> AVKVGGVLTTR <mark>H</mark> GE <mark>P</mark> LLAVPDLAAEWRIMDD
17. Marinobacter sp. X15-166B	I PIQLI V TO YAGS V D DI VI P VL SWL KV RE PGL D PMNT V R FEA ELLNNN SY DI AIT VNI TERVI VTADG - LDI EH VL P KPPMEDL HGFYDG V ES
18. Salinicola socius	Y T A Q L Y L TO Y A A D I D A V M I P L L D W L S I Y Q P D L D P K Q A V S F E A E I L S N S A V D L A L R V Q L T E R V V A K K R G Q I H V E H R M P K F E R E E L I A E W D G E Q G
Fig. 5.32. Mu	ltiple sequence alignment of tail completion protein-like protein highlighting the

Fig. 5.32. Multiple sequence alignment of tail completion protein-like protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* tail completion protein-like protein from bacteriophages of various hosts it was observed that methionine, lysine, leucine, and others are highly conserved at amino acid positions 1, 3, 7, and 35 other positions, respectively.

5.5.15. PHAGE CR1 tail protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 tail protein**, has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage tail protein of *Marinobacter sp. X15-166B*, exhibited 100% sequence similarity with *Phage CR1* tail protein, the phylogenetically closest species with standing members in the tree.



Fig. 5.33. Phylogenetic analysis of Phage CR1 tail protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.



Fig. 5.34. Multiple sequence alignment of tail protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* tail protein from bacteriophages of various hosts it was observed that methionine, valine, alanine, and others are highly conserved at amino acid positions 1, 4, 6, and 33 other positions, respectively.

5.5.16. PHAGE CR1 tail collar domain protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 tail collar domain protein**, has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage tail protein of *Desulfoluna butyratoxydans*, exhibited 59% sequence similarity with *Phage CR1* tail collar domain protein, the phylogenetically closest species with standing members in the tree. *Desulfoluna butyratoxydans*, an anaerobe isolated from estuarine sediments.



Fig. 5.35. Phylogenetic analysis of Phage CR1 tail collar domain protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.



Fig. 5.36. Multiple sequence alignment of tail collar domain protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* tail collar domain protein from bacteriophages of various hosts it was observed that tyrosine, leucine, threonine, and others are highly conserved at amino acid positions 5, 9, 10, and 36 other positions, respectively.

5.5.17. PHAGE CR1 tail tape measure protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 tail tape measure protein**, has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage tail tape measure protein *Peduovirus P2*, exhibited 74% sequence similarity with *Phage CR1* tail tape measure protein, the phylogenetically closest species with standing members in the tree. *Peduovirus P2* is an *E. coli* phage.



Fig. 5.37. Phylogenetic analysis of Phage CR1 tail tape measure protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences	
Species/Abbrv	
1. Phage CR1 Tail tape	MAKDI KI QI V LETINKSSKPI AN I TKGTKSTSKALRETRDSLRDI QQAQKKI TAFRALKRDSEATARAFSNAQQETDRLAREI ANTAN PS
2. Peduovirus P2	MISNNYKLQYLLRAVDQASKPIKSIKTASKSLSGDIRELQKSLKELNGHASKIEGFRKISAQLAVTGHALEKARQEAEALATQFKNTERPI
Streptococcus phage Dp-1 Burkholderia phage BcenMu USA/Summer/2	
5. Bacillus phage SPP1	NI REFORMULY RTVD S RTEKFEN AMN RLAR I TO SLAST VG AL RGAL MS PAA V PAA AS L VG VG SLGPMI G VAAGA AG IG SAFAT AGA AY
6. Fromanvirus D29	MPNSAGVEVARISVKVSPNTKEFRELKTDLEKIERESADVPVNADLNAAQAKADFKRLMMQLKTEAA
7. Pseudomonas toyotomiensis	MANDL KME VILQAID RATRPIRAITQGSIGLGRALKDSRDQLKAMQAQQRDISSWRTLRTAAGQTEQSLQQARDRVKELGRQMAATGVPT
8. Pseudomonas oleovorans	MANDL KMEVILQAIDRATRPIRAITQGSIGLGRA <mark>L</mark> KDSRDQ <mark>L</mark> KAMQAQQRDISSWRTL RTAAGQTEQSLQQARDRVKE <mark>L</mark> GRQMAANGVPT
9. Pseudomonas marincola	MARDLFLK <mark>V</mark> GLQALDRASR <mark>P</mark> LRAIANGSISLGRA <mark>L</mark> KDTRAE <mark>L</mark> KGLQGQQRDVSSFRALRTETEKTGTALQANRDKVRQ <mark>L</mark> SQALASTANPT
10. Pseudomonas leptonychotis	MARDILLER YGLQTIDRAS RPIRAIANGTIGIGRALKDTRADIKGIQSQQRDVSSFRMIKGEAEKTGSALQAS RDKVRQLSQAMANTATPT
11. Pseudomonas brassicacearum	
12. Pseudomonas jilinensis	MARDIKIQ V UQALDKA I KEMIKSYMOOSI GLANSUKQI KUN LKOLQNQQKDYSSI KSI SI AIQKIGAALQASQEKYKQI SKELONI QHPI
14. Pseudomonas viridiflava	MANDL KLRVLLVA I DKASGPLKA I HHGSVGVA RSLKE A RARLKDLN VOOKDVSAWRTORAAA EOTEOALGAA RGKVRALSOOLAA TGAPT
15. Pseudomonas lalucatii	MARDLKLE VYLHALDRAS RPFKA I AGSGYGLARTLRDTRGELKGLOAQOKDI AS FRSLKGAS EQTASALOAN RDRI RELGOOLGN TAO PT
16. Pseudomonas mosselii	MAND L R L R V L L D A I D K A S A P L KQ I S K G S L E T A R E L K A A R D R L K E L N AQQ K D V S AW R T Q I T Q S R Q T G Q A L D A A R A K V R A I AQ E M A A A G A P T
17. Pseudomonas abyssi	MAQ K L K L E <mark>V</mark> V L Q A L D R A T K <mark>P</mark> I R A I T Q G S V G L G R E <mark>L</mark> K T T R D Q <mark>L</mark> K Q L Q R Q Q G D I S S W R T L N N A T K Q T T Q A I S A N R D R V R E L S R Q M A Q T S T P T
18. Halopseudomonas gallaeciensis	MARDIK VQ Y Y LQALDRAT R PMRTAMGSSI GLANS L KQTRDH L KGLQAQQRD YSSFRTISNAT RRTGADI KASQD R VAQ L S RQL RDTQT PT
19. Halopseudomonas oceani	MAQ KLKLE V VLQALDRATKPIRALTQGS VGLGREL KTTRDQL KQLQRQQGD I SSWRTLNNATKQTTQA I SANRDR V RELSRQMAQTSTPT
Protein Sequences	
Species/Abbry	
1. Phage CR1 Tail tape	R LAREIANTAN PSRQLQRDFKRAAQLSGDLKQKLGSQKIELQQLRSGLSQAGUNTRNLGSEQRKLSSGVAQANRAMENQQNRLRRLTQLQ
2. Peduovirus P2	L A T Q F K N T E R P T R A Q A K V L E S A K R A A E D <mark>L</mark> Q A K Y N R L T D S V K R Q R E <mark>L</mark> A A V <mark>G I</mark> N T R N <mark>L</mark> A H D <mark>E</mark> Q G L K N R I S E T T A Q L N R Q R D A L V K <mark>L</mark> N A V K
3. Streptococcus phage Dp-1	<mark>Y A D V F A R A A A D T N A E T S D M A E A M K Y V A P V A H S M G L S L E E T A A S I G L <mark>M</mark> A D A <mark>G L</mark> K G S Q A G T T L <mark>R</mark> G A L S R I A K P T K A M V D A N G N M I Q L K T A T</mark>
4. Burkholderia phage BcepMu USA/Summer/20	1022 LATRIARGAAQ RQ GL GADML GTYATAAATAA PYI GAYRQAAT FEAG <mark>L</mark> RD I A <mark>I</mark> TGN L TRD E E FRI GETMRRAAL AT SQ GHN SI LAAGMDA
5. Bacillus phage SPP1	ELGS AF AT AGA AY GALAAT I GGVI KA S QD LD KL QA KLDD AT DA KE RAMEQI KN LQA S LGKE R KALDT LEDF K SN WQDI A K S VQS LN T F K
6. Promanvirus D29	
8. Pseudomonas oleovorans	ELGENMANGVETTING MULA VALANTIK KEHO FOOTOLOGI RIKANAADISI KAUSIHEKELKAKI EHINKSI ADA DUQI KKMQ KLAQAK
9. Pseudomonas marincola	DUSQALASTANPT KOLNNEF KRAVREASSUKOKHSEQORELOGLIRGKUSAAGUSTISTIKNUGOHERELIRSKI SATNOALTOOFSRI KRUGRAV
10. Pseudomonas leptonychotis	L SQAMAN TAT PT KOLNN EF KRAV REATH L KOKH SEQOREL OG L RGKL SAA GI ST RN L GOHEREL RSK I SATTOAL TOO EN RL KRL GRAK
11. Pseudomonas brassicacearum	T A <mark>L</mark> SQQF A A T G K P T K A M T K D F H A A I K A A H A <mark>L</mark> K Q Q H I A Q Q S Q L Q T L R T R <mark>L</mark> N S A A <mark>I</mark> S T R N <mark>L</mark> G Q A <mark>E R</mark> E L R T K I S S T N G V I S Q Q E N R L R R <mark>L</mark> A M A K
12. Pseudomonas jilinensis	<mark>b l</mark> s r e l g n t Q h P t K A L N S E F R R A V R E A Q G <mark>L</mark> K S K H Q E Q Q R E L Q G L R S R <mark>L</mark> S E A <mark>G I</mark> S T R N <mark>L</mark> G D H <mark>E R</mark> R L R T D I A T A N Q A L G K Q E A A L R R <mark>L</mark> A R A R
13. Pseudomonas mendocina	<mark>↓ L</mark> S Q Q L A N T A T P T K A L N Q Q F Q R T V R E A T A <mark>L</mark> K A K H A E Q Q R E L Q G L R G K <mark>L</mark> S A A <mark>G I</mark> S T A Q <mark>L</mark> G Q A <mark>E R</mark> D L K A K V T A T N Q A M A T Q E A R L K R <mark>L</mark> A R A K M
14. Pseudomonas viridiflava	L S Q Q L A A T G A P T K A L T R D F Q A A Y K A A Q A L K Q Q H T S Q Q G T L Q A L R A R L N S A G I S T R S L S Q A E R E L R S R I S A T N G Y I S Q Q E Q R L R K M A M A K
15. Pseudomonas lalucatii	ELGQQLGNTAQPTQKIRDEFRSNLREGHALKAKHAEQQRELQGLRGQLNAAGISTRTLGQHERDLRGKINQTNQALALQEARI.KRLAKK
16. Pseudomonas mosselli 17. Pseudomonas abussi	A LAQEMAA AGAPI KAMASSMKI AV KEAQKLKI EHQQQAEKLQQLKI KLHGAGISI KDLGNHEKVLKEQI GAI NKAI SI QGKRMD KLAKAK
18. Halopseudomonas gallaeciensis	LIS ROM ROTOT PT RAINTEE RRANKE ANAL RAKHO FOORTI OGI RSNINS AGISTRNIG GHEROI RGFITRANDAL TO FORI BRI ARAA
19. Halopseudomonas oceani	ELS ROMAQTST PT RALSNDF RRAV REAHAL KOKHQEQQROLOGL RGKLNEAGISTRNLGEHERTL RORIDSTNNOLOEQERRIK RLARAK
·	
Protein Sequences	
Protein Sequences Species/Abbry	
Protein Sequences Species/Abbrv 1. Phage CR1 Tail tape	L R <mark>L</mark> T Q L Q K Q Y Q R T Q A T R G Q L <mark>A</mark> G G <mark>B</mark> A R A V <mark>A</mark> G G S A A L Y A <mark>G</mark> A R G L S S <mark>G</mark> V S <mark>F</mark> D S G V S Q V Q A <mark>L</mark> T R L D K D S P L L A Q L R Q Q A K D L G C S <mark>T</mark> Q F T A G Q A
Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2	L R R <mark>L T Q L Q K Q Y Q R T Q A T R G L A G G G A R A V A G G S A A L Y A G A R G L S S G Y S F D S G V S Q V Q A L T R L D K D S P L L A Q L R Q O A K D L G C S T Q E T A G Q A L Y K <mark>L</mark> N A V K Q R Y Q A G K E L A G N M <mark>A</mark> S V <mark>G</mark> A A G V G I A A A G T M A <mark>G</mark> V K L L M P G Y E <mark>F</mark> A Q K N S E L Q A <u>V</u> I G V A K D S A E MA A L <mark>R</mark> K Q <mark>A</mark> R Q L G D N <mark>T</mark> A A S <mark>A</mark> D D A</mark>
Protein Sequences Species/Abbrv 1. Phage CRI Tail tape 2. Peduovirus P.2 3. Streptococcus phage Dp-1	L R R L T Q L Q K Q Y Q R T Q A T R G Q L A G G G A R A Y A G G S A A L Y A G A R G L S S G Y S F D S G Y S Q Y Q A L T R L D K D S P L L A Q L R Q Q A K D L G G S T Q F T A G Q A L Y K L NA Y K Q R Y Q A G K E L A G M M A S Y G A A G G Y G I A A A G T M A G Y K L L M PG Y E F A Q K N S E L Q A Y I G Y A K D S A E MA A L R K Q A R Q L G D N M A A S A D D A M I Q L K T A T A G L T Q E E R N R H L Y T L Y G Q N S L S G M L A L L D A G P Q I L E P A L A F A G M Y A A L G P L L I A G M M T T I Y K L R I A T Q F L G P A F M G T M G T I
Protein Sequences Species/Abbrv 1. Phage CRI Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2 6. Burkline apen 500	L R R L T Q L Q K Q Y Q R T Q A T R G Q L A G G G A R A V A G G S A A L Y A G A R G L S S G Y S F D S G Y S Q Y Q A L T R L D K D S P L L A Q L R Q O A K D L G G S T Q F T A G Q A U Y K, M A Y K Q R Y Q A G K E L A G N M A S Y G A A G G G I A A A G T M A G Y K L L M P G Y E F A Q K N S E L Q A Y I G Y A K D S A E MA A L R K Q A R Q L G O N T A A S A D D A M I Q L K T A T A G L T Q E E R N R H L Y L Y M Q N S L S G M L A L L D A G P Q I L E P A L A F A G M Y A A L G P L L L I A G M M T I I Y K L R I A I Q F L G P A F M G T M G T M 102 L L A A G M D A K E A G Q K S N L G R Y A T A T N A D M K D L A G M Y S F S E T L - G I K G D A A L K E A F N R A A Y G G K L G R E - L K D M K A L P E M T A A F A A K G 102 L A A G M D A K E A G Q K S N L G R Y A T A T N A D M K D L A G M Y S F S E T L - G I K G D A A L K E A F N R A A Y G G K L G R E - L K D M K A L P E M T A A F A A K G 102 L A A G M D A K E A G Q K S N L G R Y A T A T N A D M K D L A G M Y S F S E T L - G I K G D A A L K E A F N R A A Y G G K L G R E - L K D M K A L P E M T A A F A A K G 102 C M T T Y K L R N D A M K D L Y K Y D Y Y G Y Y G Y Y G Y Y G A Y Y G
Protein Sequences Species/Abbry 1. Phage CRI Tal Lape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2 5. Bacillus phage SPP1 6. Eromanderis DP3	L R R L T Q L Q K Q Y Q R T Q A T R G Q L A G G G A R A V A G G S A A L Y A G A R G L S S G V S F D S G V S Q Y Q A L T R L D K D S P L L A Q L R Q Q A K D L G G S T Q F T A G Q A L V K L NA V K Q R Y Q A G K E L A G N M S Y G A A G Y G I A A G T M A G Y K L L M P G Y F F A Q K N S E L Q A Y I G V A K D S A E MA A L R K Q A R Q L G O N T A A S A D D A MI Q L K T A A G L T Q E E R N R H L V T L Y G Q N S L S G M L A L L D A G P Q I L E P L L A F A G M V A L G P L L I A G M M T I I V K L R I A I Q F L G P A F M G T M G T M 20 L L A G M D A K E A G Q K S N L L G R V A T T N A D M K D L A G M Y S F S E T L • . G I K G D A A L K R A A Y G K L G R F E . L K D M A K A L P E M T A A F A A K G 20 L B A G M D A K E A G Q K S N L L G R V A T T N A D M K D L A G M Y S F S E T L • . G I K G D A A L K E A F N R A A Y G K L G R F E . L K D M A K A L P E M T A A F A A K G 20 S L N T F K S Y L N Q L Q P M F R G L A R G G E S - L A K S M Q N A F K A P N T E A P G A F I R T Y M N L M Y A F G P L G N N E G A T A M Y K W S A S L G S S Y K F Q A Y Q 20 L R T F K S Y L N Q L Q P M F R G L A R G G E S - L L A K S M Q N A F K A P N T E A P G A F I R T Y M N L M Y A F G P L G K N E G A T A M Y K W S A S L G S S Y K F Q A Y Q 20 L R T F K S Y L N Q L Q P M F R G L A R G G E S - L L A K S M Q N A F K A P N T E A P G A F I R T Y M N L M Y A F G P L G K N E G A T A M Y K W S A S L G S S Y K F Q A Y Q O H T P T A M Y K Y G Y L G M A F K A P N T E A P G A F I M Y M I M Y A F G P L G K N E G A T A M Y K W S A S L G S S Y K F Q A Y Q O H T P T A M Y K Y A S M Y A Y G Y L G M A M Y M G Y A M Y A F G M Y A Y G Y L G M A M Y M G Y A M Y A F G M Y A M Y A G M Y A M Y M G Y A M Y M Y A F G M Y A M Y M G Y A M Y M Y A G Y M Y M Y A S S M Y A M Y M Y A F G M Y A M Y M Y A F G M Y M Y A M Y M Y A F G M Y M Y A M Y M Y A M Y M Y A M Y M Y A M Y M Y
Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomaa toxotomiensis	L RR UTOLO KO YQ RTO A T RG QLAGG G AR A V A G G SAAL Y A G A RG LS SG Y SFD SG Y SQ YQ A UTRLD KD SPLLAQ L RQ O A KDLG G ST Q FT A GQ A LY K LNA Y KQ RY Q A G KE LAG NM A SY G A A G Y G I A A A G T M G Y K LLM PG YE F A Q KN SE LQ A Y I G Y A KD S A E MA A L R KQ A RQ LG D NT A A S A D D A MI QL KT A T A G LT Q E RN RH LY T LY Q QN SL SG MLA LLD A G PQ I LE PA LA F A G M YA A LG P LL I A G MM T T Y K LR I A I Q F LG P A FM G T MG T I 2021 LA A G MD A KE A G Q K SN LL G RY A T A T A A D M KD L A G MY Y SF SE T L - G I K GD A A LK E A FN RA A Y G G K LG RF E - LK D M K A LA P FM LA FF A K G Y Q S LN T F K S Y LN Q LQ PM F RG L A RG Q E S - LA K SM QN A F K A PN T E A PG A F I RT YMN LM YA F G PLG KN E G A T A A W K WS A S LG S S Y K F Q A Y Q D LT RT A WI G YG I Y A LA A PL YG L V A G LLA G L S SG L A S S G Y Y A G A R LLA PG LD F D A SM X YO S K Y C L A L B P S LL S A F G A G A G Y YA LG M G Y A S A L G S S Y K F Q A Y Q D LT RT A WI G YG I Y A LA A PL YG L
Protein Sequences Species/Abbrv 1. Phage CRI Tail tape 2. Peduovirus P.2 3. Streptococcus phage Dp-1 4. Burkholderia phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas oleovorians	L R R L T Q L Q K Q Y Q R T Q A T R G Q L A G G G A R A Y A G G S A A L Y A G A R G L S S G Y S F D S G Y S Q Y Q A L T R L D K D S P L L A Q L R Q Q A K D L G C S T Q F T A G Q A L Y K L NA Y K Q R Y Q A G K E L A G M M A S Y G A A G Y G I A A A G T M A G Y K L L M PG Y E F A Q K N S E L Q A Y I G Y A K D S A E MA A L R K Q A R Q L G D N T A A S A D D A M I Q L K T A T A G L T Q E R N R H L Y L Y G Q N S L S G M A L D A G PQ I L E P A L A F A G M Y A L G P L L I A G M M T I Y K L R I A I Q F L G P A F M G T M G T 1002 L L A A G M D A K E A G Q K S N L L G R Y A T A T N A D M K D L A G M Y G S F E T L • G I K G D A A L K E A F N R A Y G G K L G R F E • L K D M A K A L P E M A A F A A K G Y Q S L M T F K S Y L N Q L Q P M F R CL A R G C E S - L ÄK S M Q N A F K A P N T E A P G A F I R T Y M N L M Y A F G P L G N A T A T A M M K D L A G M Q N A F K A P N T E A P G A F I R T Y M N L M Y A F G P L G N A T A T N A M M K D L A G M Y A T A T N A D M K D L A G M Y A T A T N A D M K D L A G M Y A T A T A T A T A T A T A T A T A T A
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Protein Sequences Species/Abbrv 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 9. Pseudomonas marincola 10. Pseudomonas leptorychotis	L R R L T O L O KO Y O R T O A T R G O L A G G G A R A V A G O S A A L Y A G A R G L S S G V S F D S G V S O Y O A L T R L D K D S P L L A O L R O A K D L G O S T O F T A G O A L V K L NA V K Q R Y Q A G K E L A G N M S Y G A A G Y G I A A A G T M A G Y K L L M PG Y E F A Q K N S E L Q A Y I G Y A K D S A E MA A L R K Q A R Q L G D N T A A S A D D A M I O L K T A T A G L T Q E R N R L V T L Y B O N S L S G M A L D A G P Q I L E P A L A F A G M Y A A L G P L L I A G M M T I V K L R I A I Q F L Q P A Y I G Y A K D S A E MA A L R K Q A R Q L G D N T A A S A D D A M I O L K T A T A G L T Q E R N R L V T L Y B O N S L S G M A L D A G P Q I L E P A L A F A G M Y A A L G P L L I A G M M T I V K L R I A I Q F L Q P A F M T M T D Z L A A G M A K S A G Y K N L G R V A T T N A D M K D L A G M Y S F S T T G I K G D A A L K E A F N R A A Y G K L G R F E - L K D M Å K A L P F M T A A F Å A K G Y Q S L NT F K S V L NQ L Q P M R G L A R G E S - L A K S M Q N A F K A P N T E A P G A F I R T V N L M Y A F G P L G K N E G A T A M Y K W S A S L G S S V K Q A Y Q
Protein Sequences Species/Abbry I. Phage CRI Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas devorans 9. Pseudomonas ieptonychotis 10. Pseudomonas Ieptonychotis 11. Pseudomonas Irassicacearum	L RR U TO LOK O YO OR TO A T RGOL A GG G AR A Y A G O SA AL Y A G A RG L S SG Y S FD SG Y S Y A U TR LD KD S PLLA Q L ROO A K DL G O ST Q FT A GQ A L Y K L NA Y KQ RY Q A G K E L A G NM A S Y G A A G Y G I A A A G T M A G Y K L L M PG Y E F A Q K N S E L Q A Y I G Y A KD S A E MA A L R KQ A R Q L G D NT A A S A D D A M I QL KT A T A G L T Q E R N RH L Y L Y Q Q N S L S G M L A L D A G PQ I L E P A L A F A G M Y A L O F L L I A G M T T I Y K L R I A I Q F L Q P A M T T M A D M KD L A G M Y S F S FT L - G I K GD A A L K E A FN RA A Y G G K L G R FE - L K D M K K A P P T M G T I 202 L A A G M D A K E A G Q K S N L L G P A T A T A NA D M KD L A G M Y S F S FT L - G I K GD A A L K E A FN RA A Y G G K L G R FE - L K D M K A A Q F M A T A T A A D M KD L A G M Y S F S FT L - G I K GD A A L K E A FN RA A Y G G K L G R FE - L K D M K A A Q F M A T A T A A P A L Y G L A G L A G L P S L L S A F G A G A G Y V A L G M G T I A FI A A K G 202 L A A G M D A K E A G Q K N L L G R Y A T A T A A D N K D L G L Y Y G A A L Y A G L A G L P S L L S A F G A G A G Y V A L G M G T I A A F A A K G 203 L A A C M T T Q L A G S M A G G C S - L A K S M Q N A F K A P N T E A PG A F I R T Y M N L M Y A F G P L G K N E G A T A A W Y K W S A S L G S S Y K F Q A Y Q D L T R T A W I G Y G I Y A I A A P L Y G L Y Y G L L A G L S Y F I A T N T L N N S Y O S L T R L D N N S PE L E A L R E Q A R Q L G A S T Q F T A G Q S 4 Q R L A Q A R A H Y D K T Q Q L A G S M A G S G A A G L A S G S G I L Y A G A R L L A PG L D F D A S M S K Y Q S L T R L D K N S PE L E A L R E Q A R Q L G A S T Q F T A G Q S 4 K R C R A K Q Q Y E K T Q C L A G S M A G T G A A G L A T C S G I L Y A G A R L L A PG L D F D A S M S K Y Q A L T R L Q N A PQ L Q A L R Q C A R Q L G A S T Q F T A G Q S 4 K R C R A K Q Q Y E K T Q C L A G S M A G T G A A G L A T C S G I L Y A G A R M A PG L E F D A S M S K Y Q A L T R L Q N A PQ L Q A L R Q C A R Q L G A S T Q F T A G Q A 4 K R C R A K Q Y E K K G T Y G A M A G T A A G L A T C S G I L Y A G A R M A M A S Q Y E K A K G Y E K A
Protein Sequences Species/Abbrv 1. Phage CRI Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyatomiensis 8. Pseudomonas oleovorans 9. Pseudomonas prasticacerum 10. Pseudomonas brassicacerum 12. Pseudomonas pillnensis 2. Pseudomonas pillnensis	L R R L T Q L Q K Q Y Q R T Q A T R C Q L A G G G A R A V A G G S A L Y A G A R G L S S G Y S F D S G Y S Q Y Q A L T R L D K D S P L L A Q L R Q O A K D L G G S T Q F T A G Q A L Y K N A Y K Q R Y Q A G K E L A G M A S Y G A A G Y G L A A G T M A G Y K L M P G Y F F A Q K N S E L Q A Y I G Y A K D S A EMA A L R K Q A R Q L G N T A A S A D D A M I Q L X T A T A G L T Q E F R N R H L Y L Y G O N S L G M A L I D A G P Q I L P A L A F A G M Y A L I I A G M NT I Y K R I A I Q F L G P A F M G T M G T 1002 L A A G M D A K E A G Q K S N L L G R Y A T A T N A D M K D L A G M Y Y S F S E T L • G I K G D A A L K E A F N R A A Y G G K L G R F E • L K D M A K A L P E M A A F A A K G Y Q S N T F K S Y L N Q L Q P M F R G L A R G G E S • L A K S M Q N A F K A P N T E A P G A T I R T V N L M Y A F G P L G K N E G A T A W Y W S A S L G S Y K Y Q A Y Q • • • • • • • • O L T R T A M I G Y I Y A I A A P L Y G L • • • • • • Y A G L L A L A P G L D F D S M S K Y Q S L T R L D K N S P E E A L R E Q A R Q L G A S T Q T T A G Q S M Q R L Q A R A Q Y D K T Q Q L A G S M A G S G A A G L A S G S G I L Y A G A R L L A P G L D F D A S M S K Y Q S L T R L D K N S P E L A A L R E Q A R Q L G A S T Q F T A G Q S M Q R L A Q A R A Q Y D K T Q Q L A G S M A G S G A A G L A S G S G I L Y A G A R L L A P G L D F D A S M S K Y Q S L A R L D K N S P E L A A L R E Q A R Q L G A S T Q F T A G Q S M Q R L A Q A R A H Y D K T Q Q L A G S M A G T G A A G L A T G S G I L Y A G A R L A P G L D F D A S M S K Y Q S L A R L D K N S P E L A A L R E Q A R Q L G A S T Q F T A G Q S M Q R L A Q A R A H Y D K T Q Q L A G S M A G T G A A G L A T G S G I L Y A G A Q M M A P G L D F D A S M S K Y Q A L T R L Q K D A P Q L Q A L R Q O A R Q L G A S T Q F T A G Q S L K R L G R A K Q Y E K T Q A L A G S M A G T G A A G L A T G S G I L Y A G A Q M M A P G L D F D A S M S K Y Q A L T R L Q K D A P Q L Q A L R Q O A R Q L G A S T Q F T A G Q A L K R L A R A K E Q Y Q Y K T Q L A G S M A G T G A A G L A T G S G I L Y A G A Q M M A P G L E F D A S M S K Y Q A L T R L Q K D
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Protein Sequences Species/Abbrv 1. Phage CR1 Tal tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage SepMu USA/Summer/2 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomienisis 8. Pseudomonas devorans 9. Pseudomonas internotychotis 11. Pseudomonas iplinensis 13. Pseudomonas julinensis 13. Pseudomonas mendocina 14. Pseudomonas Internatii 15. Pseudomonas Internatii	L R R L TO L O KO Y Q R TO A T R G Q L A G G G A R A V A G G S A A L Y A G A R G L S S G V S F D S G V S Q V A L T R L D K D S P L L A Q L R Q A K D L G S T Q F T A G Q A L Y K L N A V K Q R Y Q A G K E L A G N M S V G A A G Y G I A A A G T M A G V K L L M P G Y E F A Q K N S E L Q A Y I G V A K D S A E MA A L R K Q A R Q L G D N T A A S A D D A M I Q L K T A T A G L T Q L Q C S K L L I Y G Q N S L S G M A L D A G P Q I L E P A L A F A G M V A L G P L L I A G M M T I V K L R I A I Q F L Q P A F M G T M G T M G Y U I Y A T A T A A D M K D L S G M X V S F S E T · · · · G I K G D A A K A Y G K L G R F F · L K D M Å K A L P F M T A T A M A D M K D L S G M Y S F S E T · · · · · · G I K G D A A K A S Q K G K S A G Y G I A A A T M A M Y K S S S L Q S Y Y S P S T · · · · · · · · · G I K G D A A K A Y G K L G A F K · · L K D M Å K A L P F M T A A F Å A K G Y Q S L N T F K S V L N Q L Q P M R G L A R G G E S · L A K S M Q N A F K A P N T E A P G A F I A T WN M L W A F G P L G M S G T A G A G L A S C S G I L Y A G A R L L A P G L D F D A S M S Y Q S L T R L D K N S P E L A L R E O À R Q L G S T Q F T A G Q S M Q R Q L A Q A R A Y D K T Q Q L A G S M À G S G A A G L A S C S G I L Y A G A R L L A P G L D F D A S M S K Y Q S L T R L D K N S P E L A L R E O À R Q L G A S T Q F T A G Q S M Q R Q L A Q A R A Y D K T Q Q L A G S M À G S G A A G L A S C S G I L Y A G A R L L A P G L D F D A S M S K Y Q S L A R L D N S P E L A L R E O À R Q L G A S T Q F T A G Q S L K R L G A R Q Q Y E K T Q L L A G S M A G T G A A G L A T C S G I L Y A G A R L L A P G L D F D A S M S K Y Q S L A R L D N S P E L A L R E O A R Q L G A S T Q F T A G Q A L A R Q Y G Y Y A L T R Q K D Q Y E K T Q L A G S M A G T G A A G L A T C S G I L Y A G A M M A P G L E F D A S M S K Y Q A L T R L Q K D A P Q L Q A L R Q Q A R Q L G A S T Q F T A G Q A L R R U A M A K Q Y E K T Q L A G S M A G T G A A G L A T C S G I L Y A G A M M A P G L E F D A S M S K Y Q A L T R L Q K D D P Q L Q A L R D Q A R Q L G A S T Q F T A G Q A R A L R Q K Q Y E K T Q L A G S M A A G T
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Protein Sequences Species/Abbrv J. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2 5. Bacillus phage SPP1 6. Fromarvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 10. Pseudomonas internola 10. Pseudomonas internola 11. Pseudomonas internola 12. Pseudomonas internola 13. Pseudomonas viridiffava 15. Pseudomonas viridiffava 15. Pseudomonas internola 16. Pseudomonas internola 17. Pseudomonas internola 18. Halopseudomonas gallaectensis 19. Halopseudomonas oceani Protein Sequences Species/Abbrv 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage SPP1 6. Fromarvirus D29 7. Pseudomonas loyotomiensis 8. Pseudomonas internola 10. Pseudomonas internola 10. Pseudomonas internola 11. Pseudomonas internola 12. Pseudomonas internola 13. Pseudomonas internola 14. Pseudomonas internola 15. Pseudomonas internola 15. Pseudomonas internola 16. Pseudomonas internola 17. Pseudomonas internola 18. Pseudomonas internola 19. Pseudomonas internola 19. Pseudomonas internola 11. Pseudomonas internola 11. Pseudomonas internola 11. Pseudomonas internola 12. Pseudomonas internola 13. Pseudomonas internola 14. Pseudomonas internola 15. Pseudomonas internola 16. Pseudomonas internola 17. Pseudomonas internola 18. Pseudomonas internola 19. Pseudomonas internola 11. Pseudomonas internola 11. Pseudomonas internola 12. Pseudomonas internola 13. Pseudomonas internola 14. Pseudomonas internola 15. Pseudomonas internola 16. Pseudomonas internola 17. Pseudomonas internola 18. Pseudomonas internola 19. Pseudomonas internola 19. Pseudomonas internola 11. Pseudomonas internola 11. Pseudomonas internola 12. Pseudomonas internola 13. Pseudomonas internola 14. Pseudomonas internola 15. Pseudomonas internola 16. Pseudomonas internola 17. Pseudomonas internola 18. Pseudomonas internola 19. Pseudomonas internola 19. Pseudomonas internola 10. Pseudomonas internola 11. Pseudomonas internola 12. Pseudomonas internola 13. Pseudomonas internola 14.	R R L Q Q K Y Q R Q T R Q A G P R V G S A G
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Protein Sequences Species/Abbry Protein Sequences Species/Abbry Protein Sequences Species/Abbry Sequedomonas logation Special Sequences Species/Abbry Protein	NR TO OK GY QUITQ A TRUCQ A GO G A MAYA G S A L Y G A MG G S S A L Y G A MG G S S D S O S O QUITA LOND P L A G MO A COLDUSS Q I A A GO A A A COLDUSS Q I A COLDUSS Q I A COLDUSS Q I A A COLDUSS Q I A A COLDUSS Q I A A COLDUSS Q

Protein Sequences	
Species/Abbrv	
1. Phage CR1 Tail tape	N L S M L G D T M S Y V A P V A A G L N V P L E T V A A M A G K L G D A G L Q G Q R G G T A L R G L L S R L A A P P K MA A D A L R K L N V E V K D A E G N M R P L P D L L S E L S
2. Peduovirus P2	DFDGMSDALTYAAPVAKNAGVSIEETAAMVGALHDAKIITGSMAGTGSRAVISRLQAPTGKAWDALKELGVKTSDSKGNTRPIFILLKEM
3. Streptococcus phage Up-1	
 Burkholdena priage ocepinio convoluminarizzo Bacillus nhaga SPD1 	
6 Fromanvirus D29	LET GLOW IS TO AFT TISN
7. Pseudomonas tovotomiensis	N LOM LGET M KY VAR
8. Pseudomonas oleovorans	N LOMLGETMKYVAPVAAGVGQDIETMAAMAGKLGDAGIQESMGGTALRAIISRLAAPPKMAADALNELGISAKDAQGNMRDMPTVLQEIV
9. Pseudomonas marincola	N LQMLGETMKYAG PVAASVGQDIETVAA MAGKLGDAG LQGSMGGTALRAILGRLSAPPKMAADALDKLGVSAKDAQGNLRDMPTVLQEIV
10. Pseudomonas leptonychotis	N LQMLQETMKYAG PVAAS VGQDIET V <mark>AA</mark> MA <mark>K</mark> KL GD AG <mark>H</mark> QQSMGQTAL RAILGRLSAPPKAAADALDTLGISAK <mark>D</mark> ADQNLRDMPTVLQEIV
11. Pseudomonas brassicacearum	N L Q M L G ET M K Y V A P V A S S V G Q D I ET V A A M A G K L G D A G I Q G S M G T A L R A I L N R L S S P P K A A A E A L D R L G I S A I D A Q G N M R Q M P E I L T E L Y
12. Pseudomonas jilinensis	N L Q M L G ET M K Y A A P Y A A A L G Q D I ET Y A A M A G K L G D A G L Q G S M G T A L R A I M N R L S A P P K M A A N A L D A L G Y S A K D A M G N M R Q L P N I L E D L Y
13. Pseudomonas mendocina	N L Q M L G ET M K Y V A P V A A G V G Q D I ET M A A M A G K L G D A G L Q G S M G G T A L R A I I S R L A A P P K M A A D A L N E L G I S A K D S M G N M R D M P T V L Q E I Y
14. Pseudomonas viridiflava	NLQMLGETMKYVAPVASSVGQDIETVAAMAGKLGDAGIQGSMGGTALRAILNRLSSPPKAAAKALAKLGISAKDAKGNMRQMPELLTELY
15. Pseudomonas lalucatii	NLOWLGETMKY VAPVAAGVGODIETVAAMAGKIGDAGIQGSMGGTALRAIISRLAEPPKMAAKALAKLGVEAKDAQGNLRDLPSVLAELF
17. Pseudomonas abyssi	
18. Halopseudomonas gallaeciensis	
19. Halopseudomonas oceani	SLEMLGETMKYAAPNAAAYGQDIEIMAAAAGKLGDAGIQGMAGTALRAILSRLAAPPKMAADAIAELGLQVADAEGNMRPLPDLLKEIF
Protein Sequences	
Species/Abbrv	
1. Phage CR1 Tail tape	EXAMPLED LL SE I SSKTTKM <mark>G</mark> D VERSGLERA <mark>T</mark> AG TE <mark>A</mark> VSA FQ V <mark>L</mark> VDQ AG SG SL <mark>Q</mark> Q M I D I LL RAQ <mark>G</mark> EA Q Q TA E VMAD N LG <mark>G</mark> D L E A <mark>L</mark> KSA A D
2. Peduovirus P2	ENTRPIFTILKEMFEKNR-LE TAQQAEYMKT <mark>IFE</mark> EE <mark>A</mark> SSAAAY <mark>L</mark> MTAASTGKLDKLTAAFKASD <mark>E</mark> KTAELVNIMQDNLG E DFKAFQSAYL
3. Streptococcus phage Dp-1	GIASAVPQVVEVISQVIENIVMT · ISTVMPQLV · EAGIKILEALINGLVQSLPTIIQAAVQIITALFNGLVQALPTLIQAGLQILSALIN
4. Burkholderia phage BcepMu USA/Summer/20	22 G S A Q A L N T I D Q D - Y Y R R A E L A T Y A W G R G T Q I A G R A L L P S L T D L M N T Y - T P L I D R T A Q F A A A H P G L I R G V Y G F A T A Y I G M K Y A T L A A G W -
5. Bacilius phage SPP1 6. Fromanufrus D29	ADMRLET KINALMMART KETINMI TQUGLEGT KLI KLQMST MAAT LKQLVVAAAQTAFAV KMAAS YAQMKIT SETTAL KNGT ONG WIT
7 Pseudomonas tovotomiensis	ENVEDNET VIOFIVEKT KAMEDAFRAGELKEN AFFALSSELVIVOOAGNET KEIGTIREFRETEKT MUNIKALUMEN KEIGTIREFRETEKT
8. Pseudomonas oleovorans	ON M RDM PT V LOE I VEKT KAMGDAERAGELKGIAGEEAFSGLOVLVOO AGNGELON FIGILREARGEAEOTAKVMADNMRGDLDALNSAWI
9. Pseudomonas marincola	GN L R DM PT V L Q E I Y E K T K N M GD A D R A G L L K A H A G E E A V A G L Q V L V K Q A G T G G L D D F I S T L R K T E G E A S T A K T M A D N L R G D L S A L G S A W I
10. Pseudomonas leptonychotis	GN L R DM PT V L Q E I Y E K T K N L GD A D R A G L L K A <mark>1</mark> A G E E <mark>A</mark> V A G M Q V <mark>L</mark> V K Q A G T G A L Q E F I G T L R K T E G E A S T T S K V M A D N L R G D L S A <mark>L</mark> G S A W E
11. Pseudomonas brassicacearum	G N M R Q M P E I L T E L Y K K T K H M <mark>G</mark> T A D R A G L L K H <mark>I</mark> A <mark>G</mark> E E <mark>A</mark> Y S A L Q V <mark>L</mark> Y K Q A G T G E L <mark>Q</mark> T F I Q T L R Q A Q <mark>G</mark> E A G K T A S V M A D N L A <mark>G</mark> D L S A <mark>L</mark> N S A W E
12. Pseudomonas jilinensis	I GN M R Q L PN I L E D L Y R KT E H M <mark>G</mark> N A E R A G Y L K A <mark>L</mark> A <mark>G</mark> E E <mark>A</mark> Y S G L T Y <mark>L</mark> M N Q A G S G E L <mark>Q</mark> G F I A T L R Q T E <mark>G</mark> E A S N T A K Y M A D N M R <mark>G</mark> D L A A <mark>L</mark> G S A W C
13. Pseudomonas mendocina	N N N N N N N N N N N N N N N N N N N
14. Pseudomonas viridiflava	GNM RQ M PE I L TE L Y K K T KH L GN A D R AG L K N T A G E E A V SA L Q V L I KQ A G SG E L O SF I G T L RQ A Q G E A S K T A K V M A D N L A G D L SA L N SA W L
15. Pseudomonas lalucatii 16. Pseudomonas mosselii	ON L RDL PS VLAELH SKI KALONAD KAGEE KALADEE AF SGL VV VV DA AG SGKI DO FIGTI KV AQ O EA ETTA VMADNI KODI DSLG SAWI
17. Pseudomonas abyssi	ENMEDIPELIKE INDERAKTING AD FAGALIKE TADE AVAN TAD
18. Halopseudomonas gallaeciensis	GNM ROL PDIL DEL YSKT RAM GNAE RAGYFKALAGEE AVSGLTYL YN QAGSGEL DGFI GTL REARGEAGRT AG YMADN L ROD LAALGSAWI
19. Halopseudomonas oceani	GNMRPLPDLLKEIHDRTAALGSTERGAILKA <mark>I</mark> AGEE <mark>A</mark> GSALTV <mark>L</mark> TQQAGNGGL <mark>Q</mark> TLIGQLRTAQGEAARTAQVMGDNLGGDIAA <mark>L</mark> KSVWA
Protein Sequences	
Protein Sequences Species/Abbrv	
Protein Sequences Species/Abbry Phage CR1 Tail tope	G O L E A L K S A A D T V O I S L N D T L R P A L R N L A Q G A T E V Y G K I N T W Q E N PEL T A T I A K V V G G T A A I S V A L O T T A L T L A G I I G P V A L A R Y G L I
Protein Sequences Species/Abbry 1. Phage CRI Tail tope 2. Peduovirus P2 3. Streptocours phase Dp. 1	G G D - E A L K S A A D T V G I S - N D T - R P A L R N L A Q G A T E V V G K I N T W L Q E N P E L T A T I A K V V G G T A A L S V A L G T T A L T I A G I L G P V A L A R V G I G G D F K A F Q S A V E A V G T D L F D Q E G A L R K L T Q T A T K V V K L D G W Q K N K L A S T I G I I A G A L A L T Q I A L G L V A W P V I T G I N A I I A A A C G G D F K A F Q S A V E A V G T D L F D Q E G A L R K L T Q T A T K V V K L D G W Q K N K L A S T I G I I A G A L A L T Q I L G V A W P V I T G I N A I I A A A C G G D F K A F Q S A V E A V G T D L F D Q E G A L R K L T Q T A T K V V K L D G W Q K N K L A S T I G I I A G A L A L T Q A T G I V A W P V I T G I N A I A A A C G G L F A L T Q S A V E A V G T D L F D Q E G A L R K L T Q T A T K V V K L D G W Q K N K L A S T I G I I A G A L A L T Q A T G I V A W P V I T G I N A I A A A C
Protein Sequences Species/Abbrv 1.Phage CRI Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholdra phage BrendMu USA/Summer/200	GÖDLEALKSAADTYÖISLNDTERPAERNEAQGATEYYGKINTÖV QEN PELTATI AKVYGGTAALSVALÖTTALTEAGILGPVALARYGE GÖDFKAFQSAYEAVÖTDEFDQQEGAERKETQTATKYVEKEDGÖV QKNKS <mark>L</mark> ASTIGIIAGGAEAETGII ÖAIGEVAWPVITGINAIIAAAG QAGEQILSALINGEVQA PAI QAAVQIIMSEVQAEENEPMIIEAANQIVNAEENIGGIQILMALIEGELQVEPEETAAILEAGV QAGEQILAAGW
Protein Sequences Species/Abbry 1. Phage CRI Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/200 5. Bacillus phage SPP1	GÖDLEALKSAADTVÖTSINDTLRPALRNLAQGATEVVOKINTMI OENPELTATIAKVVOGTAALSVALÖTTALTLAGILGPVALARVOLT GÖDFKAFQSAYEAV ÖTDLFDQVEGALRKLTQTATKVVIKLOGMI QKNKSLASTIGI I AGGALALTGI I GÅI GLVAWPVITGI NAI I AAAT QAGI QILSALINGI VQALPAI I QAAVQI I MSLVQALIENLPMI E AANQI VNALIENI GGI QILMALI EGLI QVLPELITAAI LLEAGV Q2 GMKVATLAAGW GLNFF VKSPLNMVSTALTTVGAKWTI MAGGSKALAGKKAAN JARMAASNAANARMASWI VANGFÖRGAL VVGRAL LPFGLAQGGM KNGI LONGUVIKNAI MAAQSANAVKKISAFASMLAAGI KOMI AFGVRLAAN AANARMAANAARMASWI AAN SKUVAN VI AVI ALVAL KEVTVI
Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromanivus D29	G G D L E A L K S A A D T V G I S L N D T L R P A L R N L A Q G A T E V Y G K I N T W I Q E N P E L T A T I A K V Y G G T A L S Y A L G T T A L T L A G I L G P V A L A R Y G I I G G D F KA F Q S A Y E A V G T D I F D Q E G A L R K L T Q T A T K Y V K L D G W I Q K N S L S T I G I I A G A L A L S Y A L G T T A L T L A G I L G P V A L A R Y G I I Q A G L I L S A L I NG V Q A L P A I I Q A A Q I I M S L Y Q A L I E N L M I L E A A MO I Y N A L I E N I G G I Q L MA L I E G L Q V V P E L I T A A L L L A A C Q A G L Q I L S A L I NG V Q A L P A I Q A A Q I I M S L Y Q A L I E N L M I L E A A MO I Y N A L I E N I G M I Q L M A L E G L Q V V P E L I T A A L L L A A C Q Z G M K V A T L A A G W G L N F F Y K S P L N W S T A L T T Y G A KWT L W A G G G S R L A G K F A A Y I G R A G S L F MG F G R G A L V Y G R A L L P F G L A Q G M K N G I I Q M G L WI K N A I M A A Q S A N A Y K R I S A F A S M L A A G I A F G Y R L A A A A N A A R M A S W Y I A M G P I G W I T A Y I A L V A I K E Y T Y T G A L Q A G C P L T T Y V A E L G T A L T T A L Q A L Y D S F K Q L S E T L Y T S L G I G A F G V I Q A V I J L S L I T A L T I A S L Y A L G F L T Y T S L G I G A F G I Y Y T I S S L I A T A Q F M P T I V S S F K Q L S E T L Y T S L G I G A F G V I Q X O L T T I S S L I A F Q T I I
Protein Sequences Species/Abbry 1. Phage CRI Tail tope 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/200 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomiensis	GGD EALKSAADTYG ISINDTERPALRNEAQGATEVYGKENTMEQENPELTATEAKYVGGTAALSVALGTTALTAGELGPVALARYGE GGD EALKSAADTYG ISINDTERPALRNEAQGATEVYGKENTMEQENPELTATEAKYVGGTAALSVALGTTALTAGELGPVALARYGE GGD KAFQSAYEAYGTDEDQQEGALRKETQTATKYVEKEDGMEQKNSELSSTEGIAGGALALTGIEGALGENGALVGYUPELTAALAAC QAGEQILSALVGAUPALPALQAAVQEIMSEVQALENEMEMENEMENEMENEGUQAKALSVALGENGGENEMENEGIQUENALEENIGGIQLEMALEGUQVUPELTAALLEAGV QAGEQILSALVGAUPALARYGEN QGKVATLAAGW GGUVKATLAAGW GUVKATLAAGW GUVKATLAAGW GUVKATLAAGW GUVKATLAAGW GUVKATLAAGW GUVKATLAAGW GUVKATLAAGUVKATUAG
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Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp.1 4. Burkholderia phage BCepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromanivus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas marincola 10. Pseudomonas leptonychotis 11. Pseudomonas leptonychotis 11. Pseudomonas leptonychotis 11. Pseudomonas illancis 13. Pseudomonas mendocina 14. Pseudomonas indifava	G & D - E A L K S A A D T V & I S L N D T L R P A L R N L A Q G A T E V V G K I N T W L Q E N P L T A T L A K V V G G T A L S V A L G T T A L T L A G L G P V A L A R V G L G G D K A F Q S A V E A V G T D L D Q Q E G A L R K L Q T A T K Y V K L D G W Q K N S L S T I G L I G G A L A L S V A L G T T A L T L A G L G P V A L A R V G L Q A Q Q L I D Q E G A L R K L Q T A T K Y V K L D G W Q K N S L S T I G L I G G A L A L S V A L G T T A L T L A G L G P V A L A R V G L Q A Q Q L I D Q L D Q E G A L R K L Q T A T K Y V K L D G W Q K N S L S T I G L I G G A L A L S V A L [B L Q A V Q L P A L] A A A Q A A A A K Q A A R V I K L Q A T K Y V K L D G W Q K N S L S S L S T I G L I G G A L A L S V A L [E L I Q V L P E L I T A A L L L E A G V Q A L P A L Q A V Q A L P A L Q A V Q L I N S L Y Q A L I E N L M I L E A A Q V N A L I E N I G G I L M A L A G S L P M G F G R G A L V G R A L L P F G L A Q G M K N T L A A G W Y A T L A A G W Y V T T L T T A Q Q D G P L R S L T T Y Q A K M S L M A A G A A N A A N A A R M A A S W V I A G P I G W I T A V I A L V A I K E Y T V T G G A L G P L T W V V A T L G T A L T T A L Q Q M Q P L V H Y D S F K Q L S E T L V T S L G I G E A F G Q I Y G A V Q L P A T I I S S L I A F G V R L A A A A A A A M A A R M A A S W V I A G P I G W I T A V I A L V A I K E Y T V T G G A L G P L U Y V A E T I G A L Q Q D G P L R S I T Q I T R V I G S I K T W V E Q N P A L A S Q L V K M A A G L G L I M A T M G G L T L M L A S I L G P F A M Y R G M I R G D L D A L N S A WE D L G I Q U Q D Q O R P M R T I G G I T R V I G S I K T W V E Q N P A L A S Q L V K M A A G L G L I M A T M G G L T L M L A S I L G P F A M Y R G M R G D L D A L N S A WE D L G I Q U Q Q O R Q N R M N G Y L I G I T R V I G G V K W I A E N P L A S Q L V K M A A G L G L M A M A G A L T L M A S I L G P F A M Y R G M R G D L S A L G S A WE D L G I Q M Q D Q N C P M R V A S L I G I I G V K G W I A E N P L A S Q L V K M A A G L G L M A M G A L T L M A S I L G P F A M Y R G M A G D L S A L N S A WE D L G I Q M Q D
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Protein Sequences Species/Abbry 1. Phage CR1 Tail tope 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas topovorans 9. Pseudomonas leptonychotis 10. Pseudomonas leptonychotis 11. Pseudomonas leptonychotis 11. Pseudomonas dilensis 13. Pseudomonas indicata 14. Pseudomonas dilensis 15. Pseudomonas lailancia 16. Pseudomonas dilensis 17. Pseudomonas dallacti 18. Halopseudomonas gallacciensis 19. Halopseudomonas oceani Protein Sequences Species/Abbry 1. Phage CR1 Tail tope 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas dievorans 9. Pseudomonas marincola 10. Pseudomonas marincola 10. Pseudomonas marincola 11. Pseudomonas marincola 11. Pseudomonas marincola 11. Pseudomonas marincola 11. Pseudomonas marincola 11. Pseudomonas marincola 12. Pseudomonas marincola 13. Pseudomonas marincola 14. Pseudomonas traisdicaerum 14. Pseudomonas traisdicaerum 14. Pseudomonas marincola 15. Pseudomonas marincola 16. Pseudomonas marincola 17. Pseudomonas traisdicaerum 17. Pseudomonas traisdicaerum 18. Pseudomonas traisdicaerum 19. Pseudomonas traisdicaerum 19. Pseudomonas traisdicaerum 10. Pseudomonas traisdicaerum 10. Pseudomonas traisdicaerum 11. Pseudomonas traisdicaerum 12. Pseudomonas traisdicaerum	G D E L
Protein Sequences Species/Abbry 1. Phage CR1 Tall tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromarvirus D29 7. Pseudomonas topyotomiensis 8. Pseudomonas oleovorans 9. Pseudomonas iperonychotis 11. Pseudomonas iperonychotis 11. Pseudomonas iperonychotis 13. Pseudomonas viridiflava 13. Pseudomonas viridiflava 14. Pseudomonas viridiflava 15. Pseudomonas viridiflava 15. Pseudomonas gallacetensis 19. Halopseudomonas gallacetensis 19. Halopseudomonas gallacetensis 19. Halopseudomonas oceani Protein Sequences Species/Abbry 1. Phage CR1 Tall tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/200 5. Bacillus phage SPP1 6. Fromarvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 8. Pseudomonas galiaceterum 12. Pseudomonas galiaceterum 13. Pseudomonas marincola 10. Pseudomonas marincola 11. Pseudomonas marincola 12. Pseudomonas inflinava 13. Pseudomonas lalucatil	G D E L S ND T A N A A G A T A T A T A T A T A T A T A T A T A T A T A T A T A T A T A T A T A T A T A
Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas lopovorans 9. Pseudomonas betonychotis 11. Pseudomonas brasiscacearum 12. Pseudomonas brasiscacearum 13. Pseudomonas brasiscacearum 14. Pseudomonas viridifava 15. Pseudomonas mantocina 11. Pseudomonas mascelii 17. Pseudomonas mascelii 17. Pseudomonas mascelii 17. Pseudomonas mosselii 18. Halopseudomonas oceani Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/201 5. Bacillus phage SPP1 6. Fromanvirus D29 7. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 8. Pseudomonas oleovorans 9. Pseudomonas plainensis 10. Pseudomonas prasiscacearum 12. Pseudomonas intincola 10. Pseudomonas intincola 11. Pseudomonas intincola 11. Pseudomonas intincola 11. Pseudomonas intincola 11. Pseudomonas intincola 11. Pseudomonas intincola 12. Pseudomonas intincola 13. Pseudomonas mendocina 14. Pseudomonas intincola 15. Pseudomonas intincola 16. Pseudomonas intincola 17. Pseudomonas intincola 18. Pseudomonas intincola 19. Pseudomonas intincola 11. Pseudomonas intincola 11. Pseudomonas intincola 13. Pseudomonas intincola 14. Pseudomonas intincola 15. Pseudomonas intincola 16. Pseudomonas intincola 17. Pseudomonas intincola	G 0.1 0.1 0.1 0.1 0.1 0.1 0.0 0.1 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0
Protein Sequences Species/Abbry	G D E AL KS AND T B S IND T RP A RN AQCA TE V/OK INT B QENPS TA T A T A T A T A T A T A T A T A T A T A T A T A T A <td< th=""></td<>
Protein Sequences Species/Abbry 1. Phage CR1 Tail tape 2. Peduovirus P2 3. Streptococcus phage Dp-1 4. Burkholderia phage BcepMu USA/Summer/2015 Bacillus phage SPP1 6. Fromanvirus D29 7. Paeudomonas toyotomiensis 8. Pseudomonas intervirus 10. Pseudomonas toyotomiensis 11. Pseudomonas brasiscaeearum 12. Pseudomonas viridiflava 13. Pseudomonas injuensis 13. Pseudomonas viridiflava 15. Pseudomonas modicina 14. Pseudomonas gallaciensis 19. Pseudomonas gallaciensis 19. Pseudomonas gallaciensis 19. Halopseudomonas gallaciensis 19. Halopseudomonas gallaciensis 19. Halopseudomonas gallaciensis 19. Halopseudomonas oceani Protein Sequences Species/Abtry 11. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 8. Pseudomonas toyotomiensis 9. Pseudomonas gallaciensis 11. Pseudomonas gallaciensis 12. Pseudomonas marincola 13. Pseudomonas marincola 14. Pseudomonas gallac	G D I N D I R D T

Protein Sequences	
Species/Abbrv	
1. Phage CR1 Tail tape	D L MN FLLSFLPESLQGVLRAIVRHSPVGLIVGHWD RIIGFLQGLPERFKALGGMIMDGLVSGTKALFPVLTTISKVGQLLPDSIKEKU
2. Peduovirus P2	IGV - VEGEKAAFAPVGELFIPEN VICENEQAWWENCEAP - VKATQDIENRCKDIGVMFGQALADALMEP
Streptococcus phage Dp-1 A Burkholderia phage RcopMu LISA/Summer/2002	IS LESKIAS EVEN USAN USAN USAN USAN USAN USAN USAN USA
5. Bacillus phage SCP1	STWING I KTEET AGIVSVGKTV WIGI KSEET SWIS WINS EE IN IGS IGDNI MOG I NIGVTSWGDVTSTESDI TN AD KTI WKIN
6. Fromanyirus D29	VI AD VAEWVGSW-SSGVOVSDEGOLPGKI KSWEDDAGSW
7 Pseudomonas tovotomiensis	
8. Pseudomonas oleovorans	GLWAELKAGFSGGIGDIAKTILNFSPLGLEHRAMAGVLSYFVDIPARFTDFGGMLIDGLVNGITSSLGRVKDAITGAGGATIDWFKOKL
9. Pseudomonas marincola	GLWAELKOGFSGGLGGIAATILNFSPLGLFYRAFAG <mark>V</mark> LNYFAEMPSRFTDFGGMLIDGLVNGITNSLGRVKGALTGAGASTIGWFKETL
10. Pseudomonas leptonychotis	GUWAEIKOGFSGGLGGIAATILNFSPLGLFYRAFAG <mark>W</mark> MNYFADMPARFTEFGGMLIT <mark>GL</mark> VNGITSSLGRVNDAISGAGESTIGWFKEKL
11. Pseudomonas brassicacearum	SAWDELKSGFSGGVKGILMVLANFSPLGLVYQAFAG <mark>V</mark> LSYLVDMPSRFTEFGGMIIT <mark>GL</mark> IN <mark>G</mark> LSNGLGLLKDVMGNISDSTIGWF <mark>K</mark> EK <mark>L</mark>
12. Pseudomonas jilinensis	G L <mark>W</mark> G E I K E G F N G G L V G I A G L I V N F S P V G L F Y R A F A A <mark>V</mark> M G Y F I E L P A K F T D L G G M L M S <mark>G L</mark> V N <mark>G</mark> I R E G L G A V K N A I T G A G A A T I G W F <mark>K</mark> D T <mark>L</mark>
13. Pseudomonas mendocina	S V <mark>M</mark> S E I KT A F D G G L V G I A G L L L KWN P L N L F R N A F T G <mark>V</mark> MN Y F I D M P A R F S E F G G F L V Q <mark>G L</mark> I D <mark>G</mark> F T S M F P R V T A L I S G A A D S I I T T F <mark>K</mark> G L L
14. Pseudomonas viridiflava	NAWAEITAGFNDGLGGIVKAIVNFSPLGLVYQAFAG <mark>V</mark> LSYLVDMPNRFTEFGGMIIN <mark>GL</mark> VN <mark>G</mark> LLAKMGHIKGAISSIGDSTIGWF <mark>K</mark> EK <mark>L</mark>
15. Pseudomonas lalucatii) GL <mark>W</mark> GEI KAGF SGGLAGI AT T LLNF S PLGLLYRAFAG <mark>V</mark> MGYLVEL PGKF SEF GGMLMT <mark>GL</mark> AN <mark>G</mark> I RNALGS V KTAVLDAGD SAIGYF <mark>K</mark> EK <mark>L</mark>
16. Pseudomonas mosselii	NA WEELRSDFDRGVGGT I NILGNFN PVGLVYQAFAA <mark>V</mark> MNYLFEL PTRFTEFGNMI VN <mark>G</mark> LMSGLGQ I KDAVSALGDST I GWF <mark>K</mark> EK <mark>L</mark>
17. Pseudomonas abyssi	A A EITTAFGGGILGVN KLIANWS PLGMFY KAFAA <mark>V</mark> MSWFVELP······GNLID <mark>GL</mark> VA <mark>G</mark> LKRLAPGLVSALSKIASMLPASV KRVL
18. Halopseudomonas gallaeciensis	G LWA E I KAGENGGFAG I A E L I VN FSP VG L FYRAFSA WMRYFVDMPERFTDYGRQMLAG LVNG I TNGLGAVKSA I TNAGGQM I GWFKDKL
19. Halopseudomonas oceani	A L W A E I TT A F D G G I L G V G Q L I A N WS P L G M F Y K A F A A <mark>W</mark> MS WF V E L P G N L I D G L V A G L K R L A P G L V S A L S K I A S M L P A S V K R V <mark>L</mark>
B. 1.1. 6	
Protein Sequences	
Species/Abbrv	• • •
1. Phage CR1 Tail tape	D S I KEK LKI I NSPSRVFAR I GODT MAKILG LKI QRYQNQPVAK VSSVAARLAGAGRAANDPI QTNQPLMGGRALI VEQIN VYAAPGQDEVSI
2. Peduovirus P2	DAL ML PLNAFN KLRVLEKLG - VINKESDTIDQTAARTHTATYGTGDYIPATS - SYAGYQAYQPYTAGRSYVDQSKNEYTAPGT QL
Streptococcus phage Up-1 A Bushelderie ebage Reentilis USA (Summer (2002)	
 Burkholdena priage Bcepiviu USA/Summer/2002 Bacillus phage CPD1 	
6 Eromanyirus D29	
7. Pseudomonas tovotomiensis	
8. Pseudomonas oleovorans	DWF KOKLGTHS PS RVF A ELGGFT MOGLE KGLLSGOSGPLGAVLGLG KOLAAAGA ISA I AMDN RPPLGAPRAAO VOO AAPI PAPGMDE OOL
9. Pseudomonas marincola	GWF KET LG I R SPSR V F A E LG G F TMOG L A DG L T G G E G G P L O A L T G I G K R L T O A G A L G A L AMD N R P P L SN G SO A V A S A A P N V P S AG MD E O G L
10. Pseudomonas leptonychotis	GWF <mark>KEKLGIHSPSRVF</mark> AELGDF T MOGLAOGLTGGEAGPLO <mark>A</mark> LTGIGKKLTQAGALGAIAMDNRPPLSSGSQAVASAAPNVPSAGMDEQAL
11. Pseudomonas brassicacearum	GWF <mark>K</mark> EK <mark>LGIHSPSRVF</mark> AEL G GF T MA <mark>G</mark> LAQ <mark>G</mark> LVNGQAKPLS <mark>A</mark> MTRLSQQLTAAGPQVSLLVDNRAPISPAPAPIYDSHDHYPAP <mark>G</mark> MDAQAV
12. Pseudomonas jilinensis	GWF <mark>K</mark> DT <mark>LGIRSPSRVF</mark> AALQDD T MAQLQVQLERSQRGPLS <mark>A</mark> VLDAGKAMAQAGALQAVAVDSRPALAATQAPIVVQGDTITAP <mark>G</mark> TDLAQL
13. Pseudomonas mendocina	TTF <mark>K</mark> GL <mark>LGIHSPSRVF</mark> AEL <mark>G</mark> GY <mark>T</mark> MQ <mark>G</mark> YGQ <mark>G</mark> LLAEQSNPLS <mark>A</mark> LQRIGNNLVAAGSQGQVAFDARAPLANTGRPIVIEGDTI G <mark>G</mark> GDIASM
14. Pseudomonas viridiflava	I GW F <mark>K</mark> E K <mark>L G I H S P S R V F</mark> A A L <mark>G</mark> G F <mark>T</mark> M A <mark>G</mark> L T Q <mark>G</mark> L E D G Q N G P L N <mark>A</mark> V A R M S K Q L T A A G A A S S L T V D T R A P V R A A Q A S A Y S S N D T Y T S P <mark>G</mark> M D A Q A I
15. Pseudomonas lalucatii	IGY F <mark>K</mark> EK <mark>LQIH SPSRVF</mark> AELQGH T MAQLSQQLERGQGGPLA <mark>A</mark> I GSLGKQLAQAGALGAVALDSRAPLANGGAPVVVQGDTLAAPQTDVAGL
16. Pseudomonas mosselii	IGWEKEK <mark>LGIHSPSRVF</mark> AELGGF T TEGLAMGLDDGAKAPLE <mark>A</mark> VNRMGQQLTDAGTFTPITMDDRAPLGAASAASYDSHDTYPTPGMDALAI
17. Pseudomonas abyssi	A S V K R V L G I H S P S R V F A E L G G F T M Q G L A Q G I Q R Q Q G E P L A A V A G V S Q R M A S A A - • G G I R F D S R R P L S A R P A Y A G S T G S R Y A A D G M S P Q A I
18. Halopseudomonas gallaeciensis	GWF KD K LG I H S P S R V F A S L G D D T M A G L Q R G L Q R S Q G G P L N A V L G A G Q A M V K A G A L Q A V A T D S R P P I S G G G P S T V V Q G D T L A P A G A D L A Q T
19. Halopseudomonas oceani	A SYKRYLGTHSPSKYFAELOGFEMQOLAQO IQRQQGEPLAAYAGYSQRMASAA GGIRFDSRRPLSARPAYAGSTGSRYAADOMSPQAI
8	
Protein Sequences	
Species/Abbrv	
1. Phage CR1 Tail tape	E G I Q R Y Q N Q P V A K V S S V A A R L A G A G R A A N D P I Q T N Q P L MG G R A L I V E Q I N V Y A A P G Q D E V S I A R Q V R A E L A N L N Q S R A R A G R G A L H D Q E II
2. Peduovirus P2	DTLDQTAARTHT <mark>A</mark> TYGTGDYIPATS - SYAGYQAYQPYTAGRSYVDQSKNEYTAP <mark>G</mark> TQLDRQLQDALEKYERDKRA <mark>R</mark> ASMMHDG
3. Streptococcus phage Dp-1	NG I D I Q EN G V I E K V K S V Y E KMADQ L P EA PD F ED V R KA AG S P R VD L F N TG S D N S KN N Q G EQ T V V N V V R N D VD K L S RG L Y N R S K E T L S G F G
4. Burkholderia phage BcepMu USA/Summer/2002	I G I G R S S A V A A R A A AGMA T Q A A A A A S LQ R I N A A RG G S PAGA S V A G S G I T V T V Q G G S PDG V K D Q V K Q S L K D L E KM LA K K E K K E K K A Y K S
5. Bacilius phage SPP1	
7. Resudemonas touotomioneis	NOT MES GV DPSGT LAGTST KELKQT SAG KAALQAQDPL AAPDP AATG KQF SQDDATSKATTE FQTEALST KD REES KNALS V GKA
8 Pseudomonas oleovorans	
9. Pseudomonas marincola	
10. Pseudomonas leptonychotis	DGL T G G E A G P L O A L T G I G K K L T O A G A L G A I A MON R P P L S S G S O A V A S A A P N V P S A G M D E O A L A R L V A I F V A K I O O R S O V R A R S T I S D O D
11. Pseudomonas brassicacearum	DU LYN GOAKPLSAMT RLSOOLT AAGPOVSLLVDN RAPISPAPAPIYDSHDH YPAPGMDAOAVG RAVRAELARIASEKGA BOBSKLSDLE
12. Pseudomonas jilinensis	VIGLERS QRGPLS AVLDAGKAMAQAGALQAVAVDS RPALAATQAPIVVQGDTITAPIG TDLAQLEQMIN RVLDQREQOKAVIRI IR SALVDTN
13. Pseudomonas mendocina	N GULA EQ SN PL S <mark>A</mark> L Q R I G N N L V A A G S Q G Q V A F D A R A P L A N T G R P I V I E G D T I
14. Pseudomonas viridiflava	2 <mark>0</mark> L E D G Q N G P L N <mark>A</mark> V A R M S K Q L T A A G A A S S L T V D T R A P V R A A Q A S A Y S S N D T Y T S P <mark>G</mark> M D A Q A I G R A V R A E L A R I A R E K D A <mark>R R R</mark> S Q L S D L E
15. Pseudomonas lalucatii	Q <mark>G</mark> L E R G Q G G P L A <mark>A</mark> I G S L G K Q L A Q A G A L G A V A L D S R A P L A N G G A P V V V Q G D T L A A P <mark>G</mark> T D V A G L R Q M L N Q L L D E R E R G K A A <mark>R</mark> V <mark>R</mark> S A L Y D R D
16. Pseudomonas mosselii	M <mark>G</mark> L D D G A K A P L E <mark>A</mark> V N R M G Q Q L T D A G T F T P I T M D D R A P L G A A S A A S Y D S H D T Y P T P <mark>G</mark> M D A L À I G R A V R A E L A R I D S E K A A <mark>R</mark> Q <mark>R</mark> S R L T D Q E
17. Pseudomonas abyssi	N <mark>G</mark> I Q R Q Q G E P L A <mark>A</mark> V A G V S Q R M A S A A G G I R F D S R R P L S A R P A Y A G S T G S R Y A A D <mark>G</mark> M S P Q A I A H A V A A E L D R R E R A A G A <mark>R</mark> A R S L Y D Q E
18. Halopseudomonas gallaeciensis	R <mark>G</mark> LQRSQGGPLN <mark>A</mark> VLGAGQAMVKAGALQAVAIDSRPPISGGGPSIVVQGDTLAPA <mark>G</mark> ADLAQIEQLFNRLLDQRERHKAA <mark>R</mark> V <mark>R</mark> SALSDYD
19. Halopseudomonas oceani	2 🖸 Q R Q Q G E P L A <mark>A</mark> V A G V S Q R M A S A A 6 G I R F D S R R P L S A R P A Y A G S T G S R Y A A D 🖬 M S P Q A I A H A V A A E L D R R E R A A G A <mark>R</mark> A <mark>R</mark> S S L Y D Q E

Fig. 5.38. Multiple sequence alignment of tail tape measure protein highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* tail tape measure protein from bacteriophages of various hosts it was observed that methionine, alanine, valine, and others are highly conserved at amino acid positions 1, 2, 9, and 96 other positions, respectively.

5.5.18. PHAGE CR1 tail protein D:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 tail protein D**, has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Baseplate hub protein of *Eganvirus ev186* and *Peduovirus P2*, exhibited 91% and 95% sequence similarity with *Phage CR1* tail protein D, the phylogenetically closest species with standing members in the tree. *Eganvirus ev186* and *Peduovirus P2* are *E. coli* phage (Seed KM., Dennis JJ., 2005, Viral host database).



Fig. 5.39. Phylogenetic analysis of Phage CR1 tail protein D. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.

Protein Sequences	
Species/Abbry	
1. Phage CR1 tail protein D	VIGSTLEPDYRLALGEODITPLIROHLVSLDIADNRTGHSDOLTLVLEDTRGDIE IPPTGAKLKASIGWKGEALVDKGTEEVOEATHSGOPDITVV
2 Egapyinus ev186	AGT SLAPA EMITENSO DET SNESD REI SLEMT DN RGEFADOLD LEUD TOCKVELPLRGAVETUN GNOGSALLNKGDET VDELEHRGAPD LET LE
2. Eganni da certos	
3. Peduovirus P2	
4. Halomonas sp.(2)	MNAYPKPSYKITLDGIDTTPRINGKLISLSLREQKGLEADQLDTTLADHDGQLATPPRGAELQVAFGWQEEGLVDKGRFTVDEVQHSGIPDQLTTT
5. Halomonas sp. 15WGF	MNAYPK <mark>PSYRITL</mark> DGT <mark>DITP</mark> RING <mark>RLIS</mark> LSLREQRGLEADQLDITLADHDGQLAIPPRGAELQVAFGWQKEGLVDKGRFT VDE VQHTGTPDQLTVF
6. Halomonas meridiana	MNAYPK <mark>P</mark> SYRITLDGS <mark>DITP</mark> RING <mark>RLIS</mark> LSLREQ RG LA <mark>ADQLDITLADHDG</mark> QLAIPPRG <mark>AEL</mark> QVAF <mark>GW</mark> QEEGLVDKGRFT VDE VQHTGTPDQLTII
7. Halomonas sp.	MNAY PK P S Y R I T L D G T D I T P R I N G R L I S L S L R E Q R G L E A D Q L D I T L A D H D G Q L A I P P R G A E L Q V A F G W Q E E G L V D K G R F T V D E V Q H S G T P D Q L T I I
8. Halomonas elongata	IPV PY H R PSY R V T LAGO DIT PKLNG R LT SURIKAO R DO ESDOLDIT LT DHD GELAI PPSG AMLSVAIGWKDEGLID R GT YH VD EVEHSGSPD KLTII
9 Halomonas sp. GD1P12	. MSLOPDY RITLOGOVISPEERARIASITI HDRRGMOADOLDIVITDDDGMIDIPPTGAELLIAIGWKGOPISERGTELVDEVEHTGAPDTINIL
10 Halomonas piezetolorans	NNAV DE VOLTE DE TEDETE LE DE ODELE CADALELE I DE ODELE ANDI DE CALE OVALE MOLE CLUDICO E TUDICO E TUDICO E TUDICO E CUDICO E CUD
14. Establishe descloseres hesterius	
11. Ectothiorhodospiraceae bacteriur	UHTHRAPSTREVVUGTDTSPTTNGREVSEVTTENRGTEADTEDETEADTEDETEADTEDETVERGAETTAATGWUGE-EVERGSTVDETENSGSPDQVETT
12. Kushneria phosphatilytica	I I I I I I I I I I I I I I I I I I I
13. Salinicola socius	M G R P A R P D Y R L A I N G Q Q I T P R V R G R L Q R L T L T D R R G L E A D Q L D L V L T D D D G Q L A L P R R G V E I H V A I G W S G E P L T Q R G T F I Y D E V E H S G A P D M L S I F
Protein Sequences	
Provide Million -	
Species/Abbry	
1. Phage CR1 tail protein D	TEP DUTTVVAYSAGLAGPLTEKKNRSWHGVALGEMVATTAGEAELTERTSAVESQESTPHTDOTDESDINLLSRTAERLDAUGTVKAGELLELPAG
2. Eganvirus ev186	ĮA PILITI RA RUADERGTUNS RICES MHDTI IGEL VISTI AKRAKUTAS VADS LKKI PVPHIDOS QESDAVFLITRLADRAGATVS VKAGKLLELKAG
3. Peduovirus P2	A PO V V T I R A R S A D F R G T I N S R R E G S WHD T I I G A I V K A I A T R N R I E A S V A P S I A G I K I PH I D Q S Q E S D A K F I T R I A F R N G G E V S V K MG K I I F I K A G I
4. Halomonas sp.(2)	ITED QLTTRAR SADMRGQL PG KRTQGWHDV LGETVTTAG RNSLEPVVA AALNGTRIG HIDD TD ESDIN FLTRIGERVDA FAATKAG RMLETVAG I
5 Halomonas sp. 15WCC	TRACT VEAPSADWRODI POKETO CHEDVIL CELVIT LACENELEPVYAAALNOL PLOHIDOTDESDINGLIDELCEPVAAALAALKACENLIT VAC
6 Halomonas modelana	
6. Halomonas mendiana	
7. Halomonas sp.	I POCTITRARSADARGOLPGKRIGGWHDVILGETVITTAGRAALEPVVAAVLAGTRIGHIDDIDESDLAFLIRLGERVDATAATRAGRALFIVAGT
8. Halomonas elongata	IS POKETERARAADMGEQEPKKRTQSWHDPTEGDIEGATAGRNGESPVEGGELASEPEPHEDOTOESDENFETREGKRYDAVATEKSGRELFTPAGE
9. Halomonas sp. GD1P12	A P D T L N I R A S S AN L R A G L P G K R T Q S M D S V T V R D L L E T I A A R H D L T P S V G A T L A G V R V T H I D Q T D E S D L H F L T R L A E R F D A V A T V K T G H L I F V P A G L
10. Halomonas piezotolerans	T F D Q L T T R A R S A D M R G Q L P G K R T Q G W H D V T L G E T V T T L A G R N S L E P V V A A A L N G L R L G H T D Q T D E S D L N F L T R L G E R Y D A L A A L K A G R M L F T V A G L
11. Ectothiorhodospiraceae bacteriur	ASPOOVLIRAR SADMRGGUPGOKSRSWHDT VAELVEELAKEHGUEPKLGEHUGGURVRHIDOTSESDUHULTRUAERVDALAAVKAGRUUFUPAA.
12 Kushneria nhosphatilutica	S PROLITI RAPAA DAGS LI POKRSOS MADITI GELVOTI ACRAELS PAVODILISCI PLOHIDOTOESDI NELTRI CKRAV ALIALIK SERVI ETI VO
12. Rushineria prosphadiyota 13. Saliaisala saskus	
13. Salmicola socius	
Protein Sequences	
Species/Abbry	
1. Phage CR1 tail protein D	A LE LE A G RH I S A S G Q N LE P A L I T R S D S D T H T W R S P T R D R Y T G V L C R W R N T R K N R N E E Y T A G L Q G R R K Q L R G T Y P T E H E A K R A A E A E W R R L Q R D N F
2. Eganvirus ev186	KILFLKAG SAM TASG KPV POMTIT IN DGD RHOFA LAD R GAYTGYTAKWIHTKDPK POEYMAG FADN VLALTTYYAS KAO AMRAAO AKWDKLD RG VA
3 Peduovirus P2	TI FUKAGO GVI ANG KAUPOVITI TESDO PHHEALADE GAYTOVIA KWUHIKOPK PO FYMAG FADAVEALITI VYAT KAO AMPAADAKWOKUD ROVA
A Halomonas so (2)	THE TY ACCOUNT ACCOUNT AND A THE TRANSPORT OF A STATE OF A ST
E Halomonas sp. 1530/20	
6. Halomonas sp. 15wGP	
6. Halomonas mendiana	THEFT VADQGE ABORAMPATTETREDGDQHRYSVTDRDATSGVRAYWNDTRGAERQTVLAGTEEN ARQERPTTATEDDALAAARAEWQRTORGLA
7. Halomonas sp.	x MLFTV A GQGLTA SGRAMPATTLT R DGDQH RYSVTD RDAY SGY KAYWNDT RGAERHTVLAGTEEN A KQLRPTYATEDDALAASRAEWQRIDROLA
8. Halomonas elongata	XLLFTPAGDGKAASGASLGGLTTTRKDGDRHRYSRTSRESYTGYKAFWNDPRKAKRQEVVAGGTEKLKE <mark>LR</mark> AVFATEADAMDEARSENQRIDRREA
9. Halomonas sp. GD1P12	
	ILTEVPADQATTATOLITEPTTERRQTGDQHRYERATREAYSGVTALWNNTAHATREAYTYGEPENAQQLRHTYVSETEALEAAQALWQRLQRGTA
 Halomonas piezotolerans 	TTE YY MAQATTATATUTTY Y TEATTATATUTY Y TEATTATAN Y NATURANA A KAYAYA U YU Y
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur	A TREFTY A GO GLE A S G FALP PETER KURDON KAT KATA KATA YAN NA TA KATA YALPENA QQLKITTY STEAT TA AQA A MOKA MKATA AMLETY A GO GLE A S G FALP PITER KATA RA DO HRY SY TO ROAYSOY KAY WNO TR GA EROTYLA GWEEN A KQLR PTYA TEODALA AA RA EN KATA G XLEFI PAAAA STA S G FALP PITER RHOAD O HRY YKA A RA WNO TS GOR REKY VA G TEGN PKELR PTYA TEODALA AA RA EN FREUGRGAA
 Halomonas piezotolerans Ectothiorhodospiraceae bacteriur Kushneria phosphatilytica 	LT F Y M AQ ALT ATALTT F F TE K KU AD QH KY EKAT KEANSKYTAL WAN ATAT KEAVY VELPENAQUENTT YSTEAT LAAQAT WQK UKATA XML F Y M AQ G E TA SG RAM PG TE TR R D G D QH R Y S Y D RD A Y SG YKAY WND T RG A E RQ T VLAG MEEN A KQ LR PT YA T ED D A LAA AR A E F R R LORG A A XL F I PAAAA ST A SG LA LPAAT ET R HD D D QH R Y S X TD RD AY TG YKAY WND T SG A R KY VA ET G N P KELR PT YA T KED A LAA AR AE F R R LORG A A XL F I Y M A A A ST A SG LA LPAAT ET R HD D D QH R Y S X TD RD AY TG YKAY WND T SG A R KY KAY KAY KELR FT YA S SAD AW E A A KSEW R R D R G A A
 Halomonas piezotolerans Ectothiorhodospiraceae bacteriur Kushneria phosphatilytica Salinicola socius 	NIEFY XGGGLTASGRAWPGGITERR BOOHRYS VERDAWSSY KAURAN TRANKIAV VELPENAUQU KITY VSTEAT LAAQA MUQKU KAURAN RULFIY AGAAAS ASGEPL PPITLR RHDAD OHRYS VERDAWSG VRAVIND TRAARR TVLA GUEENAKOLK RFY AT TEDALAA ARA FUQ RUGAGA RULFI PAAAAS ASGEAL PPITLR RHDAD OHRYS KADRDAYTG VRAVIND TSGGR REKV VAGTEGN PKELR PTY AT KEDALAA ARA FUR RUGRGAA RALFI VGEALTASGLALPANT LTR RDGDOHRS STORDSYTG VRAVIND TSGGR REKV VAGTEGN PKELR PTY AT KEDALAA KAK FUR RUGRGAA
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius	ILTE VY AGQALT A TRALTTE PTELK KU BUQH KYLKALKLANSKYTALMANA TRAA PRIAVY VULPENAQQLKITTYSTEA TAAQALMQK UKKUTA SULETY KQGLT A SGANPGYT LTRRDGON RYSKADROA WY TGYKA VW NDTRGA PROTVLAGVEN KQLR PTYATODALAA RAKTWOR I RRGLA RLLFI PAAAASTASGE PL PPITLRRHDADQH RYVKADROA WTGYRA VW NDTSGGRREK VVAGTEGN PKELR PTYATODALAA RAKTWOR I RRGLA XMEFTLVGEALTASGLALPAATLTRRDGON RYSKADROA WTGYKA VW NDTKGA PREVVAGTEGN PKELR PTYATKEDALAA RAKTWOR I RRGAA ILLFI PACASTASGLALPAATLTRRDGON RYSKADROA WTGYKA VW NDTKGA PREVVAGTEGN PKELR PTYA TSEDALAA RAKTWOR I RRGAA ILLFI PACQST ATGLEI PITIRRODGON RYSKADROA WTGYKA VW NDTKGA PREVVAGTEGN PKELR PTYA SEDALAA RAKTWOR I RRGAA
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius	ILT F VY AGQALT AT GLET P FILL R RD GD QH RY SKAT RLAN SKAT WINDTRGAR REV VALG VEN AQQL R TY AY SOD ALAARA KA W Q R I PRELA RULF I Y K GQGLT AS GRAN PGIT L R RD GD QH RY SKAD RD AY T G YR AY WINDTRGAR REV VAG TEGN PKELR PT YA T KED ALAARA KA
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius	IL FY VARQAT A TRITTE PTILLER OLD BURNELKELELANSKY KALKAN WNDTRAARER VIAL WENARQUERTT VAN UNDER AAR ANDE VAN WNDTRAAREN VAN UNDER AAR EN ARQUER YN TEDAL AAARAE NOR UR BURG A 8 LEFIPAAAAS ASGEPL PPITLER HDAD OH RY VKADR DAYTG VRAYWNDT SGGRREK VVAGTEGN PKELR PTY AT KEDAL AAARAE PRELORGAA 2 MLFT LVGEAL FASGLAL PAAT LTR NDGD OH RY VKADR DAYTG VRAYWNDT SGGRREK VVAGTEGN PKELR PTY AT KEDAL AAARAE PRELORGAA 2 MLFT LVGEAL FASGLAL PAAT LTR NDGD OH RY SYSDRD SYSGYTASWYDT GGAER KEVIAGAKDKSKELR ET YASEADAME AAKSEW RRIORGAA 2 LFIPAC OST AT GLEIPPITIR RODGD OH RY SYSDRD SYSGYTASWYDT EGAER RDVIAGSDDN PKRLR PIYA SED ALAAA KSEW ORLK RG TA
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushmeria phosphatilytica 13. Salinicola socius Protein Sequences	ILTE VY AGQALT AS GANP GAIT TR RDGON RYSKAT KALKALANSKYTALONNA TRAARKI AV VOLPENAQUENIT YSTEATLAAUAT MQKEKKUKA AULETY KQGALT AS GANP GAIT TR RDGON RYSKAT ROANYSGYTA VWNDT RGAR RYTVLA UN WENAKQE RYYA TODALAA AR AK MQRI RA RLLFI PAAAAS AS GAS GEPL PPITIER HDAD QH RYVKAD RDAYTG YRAYWND TSGGR REKVVAG TEGN PKEL RPTYA TODALAA RA KA KOFREL OR GAA AMLET LVGEALT AS GLALPAAT UT R RDGOOH RYSKAD ROANYTG YKAYWND TSGGR REKVVAG TEGN PKEL RPTYA TSED ALAA AR AC FREL OR GAA ILLFI PAG QST AT GLEI PPITIER RDGOOH RYSKAD ROANYTG YKAYWND TSGGR REKVVAG TEGN PKEL RPTYA TSED ALAA AR KEW RR I OR RGAA ILLFI PAG QST AT GLEI PPITIER ROGOOH RYSKAD ROANYTG YKAYWND TSGA RREVIA GAAD NA RA KA KEW RA AK SEW RR I OR RGAA
10. Halomonas piezotolerans 11. Ectothiodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbry	INTE VY AG QALTA AG RAN PGITLER RDG QH RY SEKT KLEATSEVIAL MANA TRAA REATVIALE VEN AG QLEKITY VSTEAT AAQAL MQK UK KUKA KAKA KAKA KAKAKA KAKAKAKA KAKAKAKA
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatüytica 13. Salinicola socius Protein Sequences Species/Abbrv 1. Phage CR1 tali protein D	TI F VY AG QALT A SEANP GALT KARDA DA UN KYLKAN KAT KARA KAWND TRAA RELAVIVELEKA AQQLKITT VSTEDALAA AA KARDA KUQKI KA KUKA KUKA KUKA KUKA KUKA KUKA KUKA
10. Halomonas piezotolerans 11. Ectothichodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbry 1. Phage CRI tail protein D 2. Ezamirus ev186	TI F VY AG Q LI A S G AN P G UT TR R DG Q H R V S V N R D AN S G V A V W N D T R G A R CT V LA G V E N A Q LI K H T V S T E D A LA AR A K A K A K A K A K A K A K A K A K
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbrv 1. Phage CR1 tail protein D 2. Eganvirus ev186 3. Perluminus P2	TITE VY AGGAL A A SEAL OF PUTELER AGGAL BUGHEVST KATER LANGA WE ANALYA KULA VY ALGYLEN AGGAL TITY VST FLA AGGAL AG
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbrv 1Phage CR1 tail protein D 2. Eganvirus ev186 3. Peduovirus P2 4. Halomonas cs.(2)	TI F VYRQQ I A A RAMPG I TI TR RDG O H RY SY NR DA NYSQYTA UWND TRAA RETV VA DENA AQQL KITY YSTE DA LAAARA WQQL KA KA WQQL KA KA WQQL KA SAA A G F RL Q RG LA RL F I Y Q G I TA SG RAMPG I TI TR RDG O H RY SY NR DA NY G YRA YWND TRAA RETV I AG WE NA KQL R F Y A TE DA LAAARA WQQL R G A RL F I Y Q EAL TA SG LAL PAAT LT R RDG O Q H RY SY ND DS YT G YRA YWND TRAA REKE V A G TE GN PKEL R F Y A TE DA LAAARA E F RR L Q RG AA AL F I Y Q EAL TA SG LAL PAAT LT R RDG O Q H RY SY ND DS YT G YRA YWND TRAA REKE V I AG AKDK SK EL R F Y A TE DA LAAARA E F RR L Q RG AA A L F I P A G Q ST A TG L E I P I I I R RDG D Q H RY SY SD R D SY T G YKA YWND TRAA REKE V I AG AKDK SK EL R F Y A SEAD AME AAKS E W RR L Q RG AA A L F I P A G Q ST A TG L E I P I I I R RDG D Q H RY SY SD R D SY T G YKA YWND TRAA RE R R V I A G AKD K SK EL R F Y A SEAD AME AAKS E W RR L Q RG AA A L F I P A G Q ST A TG L E I P I I I R RD D C Q H RY S Y SD R D SY T G YKA YWND TRAA RE R R V I A G SD DN P KR L R P I Y A SSED A LAAA K SE W Q R L K RG T A YMAG E ADNY L AL TY Y A SKAQ A MR AA Q A KWD KL Q RG Y A E F SI T L A LG R AD L Y P E TP YR Y SG F K RV I D E Q A W L I SK Y TH N L N N SG F T TG L L E YL S YMAG E ADNY FAL TT Y Y A SKAQ A MR AA Q A KWD KL Q RG Y A E F SI T L A LG R AD L Y F E TP YR VSG F K RV I D E Q A W L I SK Y TH N L N N SG F T TG L L E YL S YMAG E ADNY FAL TT YY A TKAQ A WR AA Q A KWD KL Q RG YA E F SI T L A LG R AD L Y F E TP YR VSG F K RV I D E Q A W L I SK Y TH N L N N SG F T TG L L E YL S YMAG E ADNY FAL TT YY A TKAQ A WR AA Q A KWD KL Q RG YA E F SI T L A LG R AD L Y F E TP YK YSG F K RV I D E Q AWL I SK Y TH N L N N SG F T TG L L E YL S YMAG E ADNY FAL TT Y Y T T A C A A K A Y A K W D KL Q RG YA E F SI T L A LG R AD L Y F E TP YK YSG F K RV I D E Q AWL I SK Y TH N L N N SG F T TG L L E YL S YMAG E ADNY FAL TT YY A T KAQ A WR AA Q A KWD KL Q RG YA E F SI T L A LG R AD L Y F E TP YK YSG F K RV I D E Q AWL I SK Y TH N L N N SG F T TG L L E YL S YMAG Y YN Y A T K A Q A WR AA Q A K WD KL Q RG YA E F SI T L A LG R AD L Y F T P YK YSG F K RV I D E Q
10. Halomonas piezotolerans 11. Ectothichodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbrv 1. Phage CR1 tail protein D 2. Eganvirus ev186 3. Peduovirus P2 4. Halomonas sp(2)	TI F VY AG QG LE AS GRAP GG UT LE REDG QH RY SKAD ROANY SKAT KLAN SKAV WND TRAAR RUTVLE VENA QQ LKITT VST FLA TAAQAT MQK LKKBIA RULF FIX AG QG LE AS GRAP GG UT LE REDG QH RY SKAD ROANY SCYNA YWND TRAAR RUTVLE WEN AK QL RETY AT KED ALAA RA KE F RR LO RG AA RULF FILV GEALT AS GLALPAAT LT R RDG QH RY SKAD RDAYT CYKAY WND TRAAR RKV VA GTEGN PKEL R PT YA TKED ALAA RA KE F RR LO RG AA ILLF I PACAS S AS GE PL P FITL R RDG QH RY SKAD RD SY TCYKAY WND TKAA R RKV VA GTEGN PKEL R PT YA TKED ALAA RA KE F RR LO RG AA ILLF I PACQ ST AT GLE I P FITL R RDG DQ H RY SKAD RD SY TCYKAY WND TKAA R RKV VA GTEGN PKEL R PT YA TKED ALAA RA KE W RR LO RG AA ILLF I PACQ ST AT GLE I P FITL R RDG DQ H RY SKAD RD SY TCYKAY WND TKAA RRAK F V TA G SKD N PKEL R PT YA SEAD AME AA KSE W RR LO RG AA ILLF I PACQ ST AT GLE I P FITL R RQ DGD QH RY SVSD RD SY SCYI A SWYD T E GAE RRDV I AG SKD N PKRL R PT YA SEAD AME AA KSE W RR LO RG AA ILLF I V AG SCO ST AT GLE I P FITL R RQ DGD QH RY SVSD RD SY SCYI A SWYD T E GAE RRDV I AG SKD N PKRL R PT YA SSED ALAAA KSE W RR LO RG AA ILLF I V AG SCO N V AL TT YY AS KAQ AM RA AQ A KW RA LO RG N FT LELT LD KAR PALTA ET P VL CQ GWK PQ ID GAA ML VV SVAL SLSD SG LT Q RL E QL P G YMA GEAD N V AL TT YY AS KAQ AM RA AQ A KWD KL O RG VAE FS IT LALG RAD LP PET PV RVSG FK RVID E Q DWT I TK YTHFLNN SG FTT GLLE VKL S YN AG EAD N V FALTT YY AS KAQ AM RA AQ A KWD KL O RG VAE FS IS LATG RAD I YTET PV KV SG FK RVID E Q DWT I TK YTHFLNN SG FTT GLLE VKL S YL AG TE CAN V GA R PT YA TEDD ALAA S RAE WOR I O RG I A E FS IT LALG RAD LY PET PV KV SG FK RVID E Q DWT I TK YTHFLNN SG FTT SLLE VKL S YL AG TE CAN V GA R PT YA TEDD ALAA S RAE WOR I O RG I A E FS IT LALG RAD LY PET PV KV SG FK RVID E Q DWT I TK YTHFLNN SG FT SLLE VKL S YL AG TE CAN V GA R PT YA TEDD ALAA S RAE WOR I O RG I A E FE TI ALG RAD LY FT PL TL AG FK PUID AT AN LY SE YTHAL ND GG FT SLLE VKL S YL AG TE CAN V GA R PT YA TEDD ALAA S RAE WOR I O RG I A E FE TI ALG RAD LY FT PL TL AG FK PUID AT AN LY SE YTHAL ND GG FT SLLE VKL S
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbrv 1. Phage CR1 tail protein D 2. Eganvirus ev186 3. Peduovirus ev2 4. Halomonas sp.(2) 5. Halomonas sp.(2)	TI E TV ROUGALTA AR AMPG OT LIK ROUGD VAN KAN KAN KAN KAN KAN KAN KAN KAN KAN K
10. Halomonas piezotolerans 11. Ectothiodospiaceae becteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbry 1. Phage CR1 tail protein D 2. Eganvirus ev186 3. Peduovirus P2 4. Halomonas sp. 15WGF 6. Halomonas sp. 15WGF 6. Halomonas sp. 15WGF	TI F V PAGA LA ARA FAR PE LI LA RA DA UN PER LA RA DA VA UN DA VIGUENTA AL ANNA TA LA VIGUENTA AL ANA UN UN VITA AL ANA UNA LA RA VINDA TA ANA VINDA
10. Halomonas piezotolerans 11. Ectothiodospiraceae bacteriur 12. Kushneria phosphatilytica 13. Salinicola socius Protein Sequences Species/Abbry 1. Phage CR1 tail protein D 2. Eganvirus ev186 3. Peduovirus P2 4. Halomonas sp.(2) 5. Halomonas meridiana 7. Halomonas sp.	TI F V K G G L A S G A M P G UT T R R D G D Q H R Y V K A D R D A Y T G V R A Y M D T S G G R E K V V A G T E G N P K E L R P T Y A T E D A L A A R A R E F R R L Q R G A A C L F I P A A A S A S G E P L P I T L R R D G D Q H R Y V K A D R D A Y T G V R A Y M ND T S G G R E K V V A G T E G N P K E L R P T Y A T K E D A L A A R A F F R R L Q R G A A A L L F I P A A A S A S G E P L P I T L R R D G D Q H R Y V K A D R D A Y T G V R A Y M ND T S G G R E K V V A G T E G N P K E L R P T Y A T K E D A L A A R A F F R R L Q R G A A A L L F I P A G Q S T A T G L E I P I I I R R D G D Q H R Y S V S D R D S Y T G V K A V M ND T K G A E R K V I A G K KD K S K E L R E T Y A S E A D A M E A A K S E W R R L Q R G A A L L F I P A G Q S T A T G L E I P I I I R R Q D G D Q H R Y S V S D R D S Y T G V K A V M ND T K G A E R K V I A G S D D N F K L R P I Y A S E D A L A A A K S E W R R L Q R G A A L L F I P A G Q S T A T G L E I P I I I R R Q D G D Q H R Y S V S D R D S Y T G V K A V M ND T K G A E R K V I A G S D D N F K L R P I Y A S E D A L A A A K S E W R R L Q R G A A L L L F I P A G Q S T A T G L E I P I I I R R Q D G D Q H R Y S V S D R D S Y T G V K A Y M ND T K G A E R K V I A G S D D N F K L R P I Y A S E D A L A A A K S E W R R L Q R G A A L L F I P A G Q S T A T G L E I P I I I R R Q D G D Q H R Y S V S D R D S Y T G V K A Y M ND T K G A E R K V I A G S D D N F K L R P I Y A S E D A L A A A K S E W R R L Q R D A L A L A A K S E W R R L Q R D A L A L A A K S E W R R L Q R D A L A L A A L A G A L L A L A A K S E W R L Q R C Y A E F S I S L A T G R A D L Y P T Y N Y S G F K R V I D G A A W L V Y S Y A L S L S D S G L T Q R L L E Q L P G Y M A G E A D N V F A L T T Y Y A S K A Q M R A Q A K W D K L Q R G Y A E F S I S L A T G R A D L Y P T Y R Y S G F K R V I D G A A W L V S Y A L S L S D S G L T Q R L E Q L P G Y M A S C A C W Y A T Y A T K A Q A M R A Q A K W D K L Q R G Y A E F S I S L A T G R A D L Y P T P V K Y S G F K R V I D G A A W L Y S Y Y A L S L S D S G T T S L L E V R L S Y M A G E A D N Y A T Y A T T A A A Q A
10. Halomonas piezotolerans 11. Ectothiorhodospiraceae bacteriur 12. Kushneria phosphatilytca 13. Salinicola socius Protein Sequences Species/Abbry 1. Phage CR1 tail protein D 2. Eganvirus ev186 3. Peduovirus P2 4. Halomonas sp.(2) 5. Halomonas sp.(2) 5. Halomonas sp. 8. Halomonas sp. 8. Halomonas sp.	TI F V PAGQ I LA SG AN PG I TI TA RDG DQ H RY V KAD RDA NY G V KAV WND TRAA RETV VI DE VAN QQ LKITI V STITE I CAQAN WAD KUMA HAY KANYA WND TRAA RETV I AG WE EN AKQU R TV AT KED ALAAAR MQ R L MAGA HWQ KUMA HAY KAWND TSGGR REK V VAG TEGN PKEL R PT VAT KED ALAAAR MQ R L MAGA HWQ KUMA GA A RLLF I PAAAAS ASG E PL P PI TI R RDG DQ H RY V KAD RD A Y TG V KAV WND TRAA REK V VAG TEGN PKEL R PT VAT KED ALAAAR AF F R RLQ RG AA ALEF I V GEAL KASG LALPAAT LT R RDG DQ H RY S V SD RD SY TG VKAV MND TKAA REK V VAG TEGN PKEL R PT VAT KED ALAAAR KE F R RLQ RG AA I LF I PAGQ ST ATG LE I PI TI R RDG DQ H RY S V SD RD SY TG VKAV MND TKAA REK V VAG TEGN PKEL R PT VA SEADA ME AAK SE W RR I G RG AA I LF I PAGQ ST ATG LE I PI TI R RDG DQ H RY S V SD RD SY TG VKAV MND TKAA RE R RU V I AG SD DN PK RL R PI VA S SED ALAAA KS E W RR I G RG AA YN LF I PAGQ ST ATG LE I PI TI R RDG DQ H RY S V SD RD SY SG VI AS WY DT E G AE RRDV I AG SD DN PK RL R PI Y A S SED ALAAA KS E W RR I G RG AA YN AG EADN VLALTT VY AS KAQ AMRAAQ A KWD KL Q RG VAE FS I TLALG R AD L FPET PV RV SG FK RV I D G AAM LVV SVAL SLSD SG LTQ RL L E QL PG YM AG EADN VLALTT VY AS KAQ AMRAAQ A KWD KL Q RG VAE FS I TLALG R AD L FPET PV RV SG FK RV I D E QAWL I SK V THN L NN SG FT TG LL E V KLS YN AG EADN VLALTT VY AT KAQ AMRAAQ A KWD KL Q RG VAE FS I SLATG RAD L Y TET PV KV SG FK RV I D E QAWL I SK V THN L NN SG FT TG LL E V KLS YN AG EADN VFALTT VY AT KAQ AMRAAQ A KWD KL Q RG VAE FS I SLATG RAD L Y TET PV KV SG FK RV I D E QAWL I SK V THN L NN SG FT TG LL E V KLS YN AG EADN VFALTT VY AT KAQ AMRAAQ A KWD KL Q RG V AE FS I SLATG RAD L Y TET PV KV SG FK RV I D E QAWL I SK V THN L NN SG FT TG LL E V KLS YN AG TE RNAKQL R PT YA TEDD ALAAS RA WQ RI Q RG LAE FE LT LALG RAD L Y TET PV KV SG FK RV I D E QAWL I SK V THN L NN SG FT TS LL E V KLS YL AG TE EN AKQL R PT YA TEDD ALAAS RA WQ RI Q RG L AE FE LT LALG RAD L I PET PL TLAG FK PQ I D ATAWL V SE V TH SLND GG LG T V C E V KG - YL AG TE EN AKQL R PT YA TEDD ALAAS RA WQ RI Q RG L AE FE LT LALG RAD L I PET PL TLAG FK PQ I D ATAWL V SE V TH SL
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Fig. 5.40. Multiple sequence alignment of Phage CR1 tail protein D highlighting the conserved regions.

Based on the multiple sequence alignment of *Phage CR1* tail protein D from bacteriophages of various hosts it was observed that proline, tyrosine, arginine, and others are highly conserved at amino acid positions 7, 9, 10, and 130 other positions, respectively.

5.5.19. PHAGE CR1 Putative phage tail protein:

The BLASTp using non-redundant protein database and UniProt/SwissProt database of the protein sequence of **PHAGE CR1 Putative phage tail protein**, has been done and sequence alignment followed by phylogenetic tree analysis were performed using the top few hits. Phage tail protein of *Pseudomonas jilinensis*, exhibited 94% sequence similarity with *Phage CR1* Putative phage tail protein, the phylogenetically closest species with standing members in the tree. *Pseudomonas jilinensis* was isolated from oil production water.



Fig. 5.41. Phylogenetic analysis of Phage CR1 putative phage tail protein. (a.) Maximum likelihood tree (b.) Neighbourhood Joining tree.



Based on the multiple sequence alignment of *Phage CR1* putative phage tail protein from bacteriophages of various hosts it was observed that methionine, leucine, glycine, and others are highly conserved at amino acid positions 1, 3, 5, 6 and 66 other positions, respectively.

CONCLUSION

The host of the lysogenic bacteriophage CR1 is *Microbulbifer* strain *CR1*, which is a marine polysaccharide degrading bacteria. *Microbulbifer* strain CR1 is a lysogen, whose specific phage CR1 was induced by nutrient starvation. Induction at different time intervals results in different phage titres. The titre is maximum at 3 hrs of induction and then gradually decreases as time of induction and incubation in nutrient deficient environment increases

The prophage CR1 consists of 33 proteins, out of which 14 are hypothetical proteins, 2 are head proteins, 4 proteins are involved baseplate assembly, 4 proteins are in capsid formation, and the rest 9 proteins involved with tail proteins to perform their function. The present study indicates that the proteins of phage *CR1 are* closely related to the proteins of bacteriophages associated with the host bacteria from different marine environments, viz., *Alcanivorax sp. S71-1-4, Pseudomonas jilinensis, Marinobacter sp. X15-166B, Desulfoluna butyratoxydans, Chitinolyticbacter meiyuanensis, Marinobacterium sedimentorum, and Halomonas spp.*

A few terrestrial species are also obtained, showing relationships in some of the trees, like *Pseudomonas saudiphocaensis, Stutzerimonas kunmingensi, Chromobacterium alkanivorans, Pseudomonas mirosoviensis*, and *Pseudomonas sp. TCU-HL1* is one of the few bacteriophages hosts whose phage proteins show close relatedness to those of the CR1 phage. Along with this, *Eganvirus ev186, Peduovirus P2*, and *Burkholderia phage BcepMu USA/Summer/2002* were among the top few blast hits. These phages have been reported to infect *E. coli*. (Seed KM., Dennis JJ., 2005, Viral host database).

Proteins from *Alcanivorax sp. S71-1-4* phage show maximum relations with *PHAGE CR1* proteins. Though the host of the bacteriophage used in the present study is a polysaccharide degrading bacterial strain, none of the closely related bacteriophages or the host bacteria have reported the presence of complex polysaccharide degrading enzymes expect *Chitinolyticbacter meiyuanensis*. The Phage CR1 head completion-stabilization protein from *Chitinolyticbacter meiyuanensis* shows close evolutionary relation to the head completion-stabilization protein from CR1 phage (Zhang et al., 2020). The phylogenetic analysis shows a close association with crude oil degrading bacteria like *Alcanivorax sp. S71-1-4* (obligatory hydrocarbon clastic bacterium), and *Pseudomonas jilinensis*. Previous studies predicted that phage CR1 belongs to the order *Caudovirales*, and the phylogenetic tree analysis show maximum similarity with the species belong to the same order.

6. FUTURE PRSOPECTS

- Concentration and purification of phage.
- DNA isolation of the phage.
- Viral genome sequencing analysis.
- Atomic force microscopy can be explored more in order to study the lytic cycle of the phage and the morphological changes that the phage causes in host bacteria.
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A.1. Artificial seawater agar:			
1.	Tris base	6.05 g/L	
2.	MgSO ₄	12.32 g/L	
3.	KCl	0.74 g/L	
4.	(NH ₄) ₂ HPO ₄	0.13 g/L	
5.	NaCl	17.52 g/L	
6.	CaCl ₂	0.14 g/L	
Dissolve in distilled water and adjust the pH to 7 with concentrated			
HCl. Make up the volume to 1000 mL with distilled water.			

Agar: 2%

Table 3. Composition of ASW agar

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1. INTRODUCTION

Viruses are the most prevalent "lifeforms" in the oceans and ubiquitous companions of cellular life forms. Most of the genetic variation within the aquatic ecosystem is stored in viruses (Curtis A. Suttle, 2007). Every cellular creature under investigation seems to have its own viruses, or at the very least, selfish genetic components resembling viruses. Recent