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4 # Viral interference of the bacterial RNA metabolism machinery
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27 **Abstract**

28 In a recent publication, we reported a unique interaction between a protein encoded by the giant
29 myovirus phiKZ and the *Pseudomonas aeruginosa* RNA degradosome. Crystallography, site-directed
30 mutagenesis and interactomics approaches revealed this 'degradosome interacting protein' or Dip,
31 to adopt an 'open-claw' dimeric structure that presents acidic patches on its outer surface which
32 hijack two conserved RNA binding sites on the scaffold domain of the RNase E component of the
33 RNA degradosome. This interaction prevents substrate RNAs from being bound and degraded by the
34 RNA degradosome during the virus infection cycle. In this commentary, we provide a perspective
35 into the biological role of Dip, its structural analysis and its mysterious evolutionary origin, and we
36 suggest some therapeutic and biotechnological applications of this distinctive viral protein.

Introduction

The relationship between bacteria and the viruses that prey upon them is complex and ever evolving. Although studied intensively, discoveries continue to be made of different strategies employed by both virus and host to aid or evade infection, respectively. Bacteriophages have evolved multiple and varied mechanisms to efficiently infect their bacterial hosts. An ubiquitous strategy utilized by phages during infection is the production of proteins that modulate or redirect the functionality of specific host proteins.[1][2] From a bacteriophage perspective, these interactions are often crucial to evade the multitude of bacterial defense mechanisms or to alter the host metabolism in order to ensure an efficient infection cycle. The discovery of phage effector proteins that target regulatory hubs of the host bacterium could open new doors towards drug discovery and design.[3] The best studied example of such a hub is the RNA polymerase which is targeted by several phages at different interaction sites, influencing transcription by a wide range of mechanisms.[4] Another key regulatory hub is the RNA degradosome, a multiprotein complex responsible for RNA turnover and posttranscriptional gene regulation in bacteria. A general model for the *Escherichia coli* RNA degradosome has been described, with a core complex comprising the hydrolytic endonuclease RNase E, a phosphorolytic exoribonuclease, PNPase, the ATP dependent helicase RhlB, and a glycolytic enzyme, enolase.[5] However, the exact makeup and variability of the complex in important bacterial pathogens like *Pseudomonas aeruginosa* was not previously characterized.

Intracellular levels of any RNA are balanced by both synthesis and degradation, and must be well synchronized with cellular processes. As such, the degradation rate of individual RNAs is an important aspect of the control of gene expression. In bacteria, mRNA has a half-life of only 2 to 3 minutes, which allows the cell to quickly adapt to alterations in the environment and govern stress responses.[6][7] Therefore, we reasoned that an important regulatory hub such as the RNA degradosome would be a potential candidate for targeting by phage effector proteins, thereby disrupting this level of cellular control. The identification of such phage proteins had previously been limited to two examples, a phosphorylation-based inhibitor (Protein kinase 0.7, phage T7) that

63 selectively stabilizes phage transcripts and an RNA degradosome activator from coliphage T4 (Srd),
64 which has been found to destabilize host mRNAs.[8][9] In our recent publication[10], a phage effector
65 protein was identified, encoded by the giant *Pseudomonas* phage phiKZ, able to specifically target
66 the RNA degradosome of *P. aeruginosa*. This 'degradosome interacting protein' (Dip) was shown to
67 act by inhibiting the activity of the host ribonuclease RNase E. Additionally, the methods used to
68 identify Dip also shed further light on the protein composition of the *P. aeruginosa* RNA
69 degradosome. In this point-of-view commentary, we expand on this interaction and reflect on the
70 impact of identifying this inhibitor of RNase E and understanding the mechanism of Dip.

71 **The composition of the *P. aeruginosa* RNA degradosome**

72 The strategy to identify phage-encoded proteins that interact with bacterial host proteins was based
73 on the pull down of bacterial proteins (and/or complexes) during the early phase of a phage
74 infection cycle.[11] By performing affinity purifications on *P. aeruginosa* cells containing a
75 *Strep*II-tagged RNase E, Dip was identified in interaction with the RNA degradosome during
76 phiKZ-infection.[10] Moreover, this and pull-downs using six other, unrelated *Pseudomonas* phages
77 provided information on the composition of the *P. aeruginosa* degradosome itself for the first time
78 (Figure-1A and Supplementary Table 1). The exoribonuclease PNPase co-purified with RNase E
79 following infection with all used phages and was present in the pull-down experiment using
80 heterologously expressed Dip and wild type *Pseudomonas* cell lysate. In this Dip-based pull down the
81 RNA helicase DeaD was detected as well. Remarkably, during infection with the different phages,
82 one to three different DEAD-box RNA helicases (RhlB, RhlE and DeaD) were co-purified with RNase E.
83 Moreover, protein chaperone DnaK, which has previously been identified in complex with the RNA
84 degradosome in *E. coli* [12][13], was co-purified during some phage infections. These findings indicate
85 that the composition of the RNA degradosome may vary in response to different phage infections
86 and might suggest that some phages possess more indirect mechanisms to affect the RNA
87 degradosome as well.

88 Enolase could not be identified in any of the pull-down experiments, suggesting that this canonical
89 component of the *E. coli* RNA degradosome does not form part of the *P. aeruginosa* complex, even
90 though enolase is predicted to be present in the *P. aeruginosa* cytoplasm.[14] Finally, given the
91 presence of ATP synthase and NADH quinone oxidoreductase (NuoD) and in these experiments, it is
92 tempting to speculate that the list of metabolic enzymes capable of binding to the RNA
93 degradosome in different bacterial organisms can be expanded. However, whether these proteins
94 are genuine components of the degradosome assembly in *P. aeruginosa* remains to be established.

95 **The functional role of Dip during phage infection**

96 Having identified the RNA degradosome as a target of Dip, the question arose as to the functional
97 consequences of this interaction. The role of Dip could be inferred from its *in vitro* inhibition of
98 RNase E mediated cleavage of RNA substrates. This inhibitory effect was found on substrates of both
99 bacterial and viral origin, indicating a lack of any specificity towards RNA substrates. Additionally, we
100 found that the Dip protein reaches detectable levels in *P. aeruginosa* 9 minutes post infection, which
101 was in agreement with a previously published RNA-seq analysis of phage phiKZ-infected
102 *Pseudomonas* cells.[10][15] Since the protein remains present in the cells during the remaining
103 infection cycle, a time-regulated mechanism by which the phage subverts the role of the RNA
104 degradosome in transcript degradation and processing is suggested. It can be speculated that a
105 delay between initial infection and Dip production allows for RNase E mediated degradation of host
106 RNAs prior to the inhibition of this enzyme. In addition, the stabilization of the viral RNA during the
107 middle and later stages of the phage infection cycle is consistent with the fivefold increase in cellular
108 RNA levels during late infection stages.[15] In contrast, coliphage T4 uses a different strategy, since it
109 over-activates the host RNase E with Srd, increasing degradation of host RNA during early infection
110 stages.[9] The importance of Dip for efficient infection of *P. aeruginosa* by phiKZ remains to be
111 established, but it is apparent from comparative genomics analyses that this protein does not share
112 sequence homology to proteins of other (closely) related phage. In addition, the unique fold of this

113 protein raises the question of its evolutionary origin and could support the observations that phiKZ
114 forms a distinct branch of the *Myoviridae* family.[16]

115 **Towards a structure-based interaction model for Dip and the RNA degradosome**

116 Dip forms a dimer that prevents RNA from being bound and degraded by the RNA degradosome
117 (Figure 1B). Crystallography, site-directed mutagenesis and interactomics approaches revealed the
118 novel structure of Dip (PDB ID 5FT0 and 5FT1) and identified the RNase E interaction site as the
119 outer surface of the Dip dimer. Dip is able to hijack the RNA binding sites of the RNase E scaffold
120 domain via extensive, acidic patches on its outer surface. A double mutation within the acidic
121 surface patch was shown to abolish the interaction with RNase E *in vitro* (by electrophoretic mobility
122 assays) and retained the wild type phenotype of *P. aeruginosa* when overexpressed *in vivo*. This
123 suggests that multiple amino acids in the acidic surface patch contribute to the global interaction
124 between Dip and the RNase E scaffold domain. Two bacterial regulatory factors, RraA and RraB have
125 been found to control RNase E activity in a similar way in *E. coli*. Both of these regulators bind the C-
126 terminal domain of RNase E, but only RraA does so by occluding the RNA binding sites.[17] However,
127 there is no structural similarity between RraA and Dip.

128 With the current crystallographic data, it is tempting to speculate that Dip is capable of assembling
129 into a higher order structure when bound to RNase E. Such an oligomer of Dip may mimic an RNA
130 duplex strand to misguide the *P. aeruginosa* RNA degradosome. This ‘nucleic acid-mimicking’
131 strategy would not be surprising as it has already been detected in other phages. For example, the
132 Ocr protein of coliphage T7 mimics B-form DNA to hijack bacterial restriction enzymes and thereby
133 protects T7 genomic DNA.[18] Current efforts are concentrating on structural approaches to elucidate
134 the interaction model.

135

136 **Potential therapeutic applications to treat bacterial infections inspired by Dip**

137 The overuse of antibiotics has led to an ever increasing number of multidrug resistant bacteria since
138 2000.[19] Due to its remarkable capacity to withstand antibiotics, *P. aeruginosa* has joined the ranks
139 of these 'superbugs'.[20][21] Since phiKZ uses Dip to inhibit the RNA degradosome in a direct and
140 efficient way, it is tempting to apply the targeting of the degradosome in a similar manner as part of
141 a new antibacterial strategy. Even though Dip decreases the growth rate of *P. aeruginosa* and *E. coli*,
142 it does not kill these bacteria. Therefore, it should be evaluated whether the RNA binding segments
143 of the RNA degradosome would be a good antibacterial target and if the action of Dip on these
144 specific RNA binding sites can be mimicked by small molecules. However, given that previous
145 successful efforts have been made to identify compounds to target the catalytic domain of RNase E
146 in *E. coli* and *Mycobacterium tuberculosis* [22], it may be worthwhile to develop Dip-based small
147 molecule inhibitors against the scaffold domain of RNase E to complement the catalytic domain
148 inhibitors.

149 Although it remains to be seen whether Dip-based molecules can be effective inhibitors, the real
150 strength of Dip may lay in its broad interaction range rather than in its toxicity.[10] It has been shown
151 that in addition to being able to inhibit *P. aeruginosa* RNase E, Dip can inhibit the *E. coli*
152 degradosome as well. Moreover, interactions with the RNA degradosome of the distantly related
153 *Caulobacter crescentus* were detected *in vivo*. Therefore, Dip based inhibitors could be tested
154 against a series of pathogens, in isolation and in conjunction with the small molecule inhibitors
155 against the catalytic domain.

156 In addition, it is conceivable that heterologous expression of Dip might even improve the infection of
157 a series of designer phages for species like *P. aeruginosa*, *E. coli* and *C. crescentus*, by protecting
158 phage mRNA and increasing expression efficiency during the infection cycle. The ability to generate
159 designer phage with boosted virulence may be particularly appealing to the field of phage therapy,

160 which currently uses natural phage to treat, amongst others, *P. aeruginosa* infections in severe burn
161 wounds.[23][24]

162 **Biotechnological applications of Dip**

163 Since Dip can interact with the RNase E of several bacterial species and can inhibit RNA degradation
164 without killing the bacterial cell, several possible biotechnological applications can be envisaged. Dip
165 may have potential applications in improving recombinant protein expression in bacteria by
166 stabilizing the mRNA of the recombinant protein *in vivo*, by co-expression of Dip (or addition of a
167 small-molecule inhibitor). Also, Dip could be used as a protein additive in total RNA extraction kits to
168 help stabilize RNA. In both examples, the dose and timing of Dip or small molecule application would
169 need to be optimized to obtain a maximal yield, since RNase E plays important roles in RNA
170 processing as well as degradation.[26]

171 In addition, there is great research interest in identifying specific enzymes responsible for the
172 degradation or processing of RNA targets, e.g. when testing stress responses of bacteria. A specific
173 example is that of the degradation of stable RNAs, rRNA and tRNA, upon starvation. Although RNase
174 E is involved in the maturation of rRNA and tRNA, the contribution of the degradosome in the
175 degradation of these stable RNAs remains underexplored.[27][28][29] Heterologously expressed Dip or
176 Dip-based small molecule inhibitors could be employed to specifically lower the activity of the RNA
177 degradosome, and thus facilitate such experiments. Presently, such experiments are typically
178 performed using a strain of bacteria with a temperature sensitive RNase E gene product, since knock
179 outs are non-viable. Raising the bacterial culture to a non-permissive growth temperature for the
180 RNase E mutant strain will effectively result in inhibition of RNase E activity, however the change in
181 temperature could also result in multiple undesired and unrelated heat shock responses in the
182 bacterial cell. Although RraA inhibits the degradosome activity via the same mechanism as Dip, It
183 was shown that RNase E has a higher affinity for RNA than for RraA. [30] Dip on the other hand, is able

184 to displace bound RNA from RNase E and is therefore believed to have a higher affinity towards its
185 target than RraA.

186 Finally, Dip or Dip-based small molecule inhibitors could potentially be used in conjunction with
187 CRISPR-Cas editing or RNA interference applications. Both the RNA interference and CRISPR-Cas
188 mechanisms use short RNA fragments in association with a ribonuclease (complex) to target RNA or
189 DNA substrates in the cell. In the case of CRISPR-Cas for example, one may want to use a CRISPR
190 array to knock out several genes at once. The corresponding pre-crRNA will be long and could be
191 subject to degradation by the bacterial RNase E. In antisense RNA experiments, on the other hand,
192 the specificity of the antisense transcript increases with its length. However, long antisense RNAs are
193 unstable and might be subject to degradation by ribonucleases. Therefore Dip or Dip-based small
194 molecule inhibitors might improve the performance of CRISPR-Cas and long antisense RNAs *in vivo*
195 to knock down targeted gene expression.

196 In conclusion, these data indicate that molecular phage-bacteria interactions continue to reveal
197 novel mechanisms of metabolism regulation as well as unique protein structures which can inspire
198 application-driven biotechnological developments.

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A

RhlB

PNPase

3′

RNA binding site

RNA binding site

5′

RNase E

ϕKZ infection

B

Dip

RhlB

PNPase

X

RNase E

Dip

Supplementary Table 1

Table 1. MS results of the affinity purifications on *Rne::StrepII*, infected with one of seven *Pseudomonas* phages.

The numbers indicate the 'Total spectral Count' identified for a specific protein. Proteins with an asterisk were also purified during affinity purifications using other bacterial complexes and are considered as false positives.[Error! Reference source not found.]

Protein	gene	PA-number	gi-number	Accession number	Mass (Da)	Control[+] (10 min)	14/1[+] (5 min)	ϕKZ[+] (15 min)	LUZ19[+] (5 min)	LKA1[+] (10 min)	LUZ24[+] (15 min)	PEV2[+] (10 min)	YuA+ (25 min)
ϕKZ _gp37	ORF37		gi|29134973	NP_803603	30,944.20			38					
14-1_gp70*	ORF69		gi|218148610	YP_002364378	29,231.50		5						
PEV2_gp43 (conserved homologue LIT1_gp43)*	ORF43		gi|282598890	YP_003358440	63,543.70								3
YuA_ gp66*	ORF66		gi|162135148	YP_001595889	54,013.40							1	
ribonuclease E	*rne*	PA2976	gi|15598172	NP_251666	117,464.80	129	360	182	154	245	364	83	55
polynucleotide phosphorylase/polyadenylase	*pnp*	PA4740	gi|15599934	NP_253428	75,454.20	44	388	45	301	285	365	166	60
ATP-dependent RNA helicase	*rhlE*	PA2840	gi|15598036	NP_251530	62,109.20		23	35	1	1	15		
ATP-dependent RNA helicase	*deaD*	PA0428	gi|15595625	NP_249119	70,112.70	10	22			3	7		2
ATP-dependent RNA helicase RhlB	*rhl*	PA3861	gi|161486761	NP_252550	44,288.60		9			1	12		
RNA-binding protein Hfq	*hfq*	PA4944	gi|15600137	NP_253631	9,103.50					3			
(3R)-hydroxymyristoyl-ACP dehydratase	*fabZ*	PA3645	gi|15598841	NP_252335	16,774.30					1			
ABC transporter ATP-binding protein		PA4595	gi|15599791	NP_253285	61,304.10			2					
acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	*accB*	PA4847	gi|15600040	NP_253534	16,454.70	7	18	27	57	26	28	2	
alginate regulatory protein AlgP	*algP*	PA5253	gi|15600446	NP_253940	34,492.00		5			7			
Anaerobically-induced outer membrane porin OprE precursor	*oprE*	PA0291	gi|15595488	NP_248982	49,668.90				1		2		
branched-chain alpha-keto acid dehydrogenase subunit E2	*bkdB*	PA2249	gi|15597445	NP_250939	45,755.10			1					
DNA-binding protein HU	*hupB*	PA1804	gi|15597001	NP_250495	9,086.90	7		7	8	15		2	1
DNA-directed RNA polymerase subunit alpha	*rpoA*	PA4238	gi|15599434	NP_252928	36,650.50			6		1	1		
DNA-directed RNA polymerase subunit beta	*rpoB*	PA4270	gi|15599466	NP_252960	150,841.60				1				

DNA-directed RNA polymerase subunit beta'	*rpoC*	PA4269	gi|15599465	NP_252959	154,368.60		3	1		2			
elongation factor Tu	*tufA*	PA4265	gi|15599461	NP_252955	43,369.40	6	3	5		2	1	3	
F0F1 ATP synthase subunit alpha	*atpA*	PA5556	gi|15600749	NP_254243	55,394.20	4							
F0F1 ATP synthase subunit B	*atpF*	PA5558	gi|15600751	NP_254245	16,956.60		2						
F0F1 ATP synthase subunit beta	*atpD*	PA5554	gi|15600747	NP_254241	49,500.40	3	4	5		2	4	6	
GTP-binding protein EngA		PA3799	gi|15598994	NP_252488	55,007.10						3		
hypothetical protein PA3179		PA3179	gi|15598375	NP_251869	43,724.60		1						
hypothetical protein PA4460		PA4460	gi|15599656	NP_253150	19,107.60			1					
hypothetical protein PA4753		PA4753	gi|15599947	NP_253441	11,640.10			2					
lysozyme inhibitor	*mliC*	PA0867	gi|15596064	NP_249558	13,695.50		3			1			
Major porin and structural outer membrane porin OprF precursor	*oprF*	PA1777	gi|15596974	NP_250468	37,639.00	1	15	5	6	4	8	6	6
molecular chaperone DnaK	*dnaK*	PA4761	gi|15599955	NP_253449	68,403.60							3	
motility regulator	*morA*	PA4601	gi|15599797	NP_253291	159,669.70		2						
Outer membrane lipoprotein OprI precursor	*oprI*	PA2853	gi|15598049	NP_251543	8,835.10				3	4			
Outer membrane protein OprG precursor	*oprG*	PA4067	gi|15599262	NP_252756	25,194.60						3		
Peptidoglycan associated lipoprotein OprL precursor	*oprL*	PA0973	gi|15596170	NP_249664	17,925.10		4			3	2		
peptidyl-prolyl cis-trans isomerase, FkbP-type		PA3262	gi|15598458	NP_251952	26,846.20						1		
PhoP/Q and low Mg2+ inducible outer membrane protein H1 precursor	*oprH*	PA1178	gi|15596375	NP_249869	21,575.30		2	3	1		3		
poly(A) polymerase	*pcnB*	PA4727	gi|15599921	NP_253415	53,302.70		1				1		
polyhydroxyalkanoate synthesis protein PhaF	*phaF*	PA5060	gi|15600253	NP_253747	30,578.90		1	1	4	12			2
preprotein translocase subunit SecD	*secD*	PA3821	gi|15599016	NP_252510	67,677.00		5						
preprotein translocase subunit YajC		PA3822	gi|15599017	NP_252511	11,862.10					1			
recombinase A	*recA*	PA3617	gi|15598813	NP_252307	36,879.80						2		
signal recognition particle protein Ffh	*ffh*	PA3746	gi|15598941	NP_252435	49,361.00			2	5	5	2	1	
transcription termination factor Rho	*rho*	PA5239	gi|15600432	NP_253926	47,071.70		2						
transcriptional regulator MvaT, P16 subunit	*mvaT*	PA4315	gi|15599511	NP_253005	14,181.10					2			
translation initiation factor IF-2	*infB*	PA4744	gi|15599938	NP_253432	90,911.00				3	5			3
translation initiation factor IF-3	*infC*	PA2743	gi|15597939	NP_251433	20,882.70			2	10	15	8	2	1
type 4 fimbrial precursor PilA	*pilA*	PA4525	gi|15599721	NP_253215	15,512.20		2				2		

30S ribosomal protein S1	*rpsA*	PA3162	gi|15598358	NP_251852	61,869.90	16	5	27			24		3
30S ribosomal protein S2	*rpsB*	PA3656	gi|15598852	NP_252346	27,337.30			3	2		13		
30S ribosomal protein S3	*rpsC*	PA4257	gi|15599453	NP_252947	25,838.40	11	9	18	12	11	2		
30S ribosomal protein S4	*rpsD*	PA4239	gi|15599435	NP_252929	23,277.90		3				1		
30S ribosomal protein S5	*rpsE*	PA4246	gi|15599442	NP_252936	17,625.00		13	8	1	3	6	2	1
30S ribosomal protein S6	*rpsF*	PA4935	gi|15600128	NP_253622	16,164.50		1			2	3		
30S ribosomal protein S7	*rpsG*	PA4267	gi|15599463	NP_252957	17,504.70		7			1	2		3
30S ribosomal protein S9	*rpsI*	PA4432	gi|15599628	NP_253122	14,597.00		6	2		1	2		
30S ribosomal protein S10	*rpsJ*	PA4264	gi|15599460	NP_252954	11,766.70					2			
30S ribosomal protein S11	*rpsK*	PA4240	gi|15599436	NP_252930	13,629.70	4	3	3	1	5	12		1
30S ribosomal protein S12	*rpsL*	PA4268	gi|15599464	NP_252958	13,798.80		4						
30S ribosomal protein S13	*rpsM*	PA4241	gi|15599437	NP_252931	13,266.00					1			
30S ribosomal protein S15	*rpsO*	PA4741	gi|15599935	NP_253429	10,098.00			4		5.00			
30S ribosomal protein S16	*rpsP*	PA3745	gi|15598940	NP_252434	9,204.50	1		5	8	8	1	2	
30S ribosomal protein S18	*rpsR*	PA4934	gi|15600127	NP_253621	8,873.90					2			
30S ribosomal protein S19	*rpsS*	PA4259	gi|15599455	NP_252949	10,357.30					2			
30S ribosomal protein S20	*rpsT*	PA4563	gi|15599759	NP_253253	9,918.00					4	2		
30S ribosomal protein S21	*rpsU*	PA0579	gi|15595776	NP_249270	8,484.90					3			
50S ribosomal protein L1	*rplA*	PA4273	gi|15599469	NP_252963	24,234.00	7	19	8	17	10	2	3	
50S ribosomal protein L2	*rplB*	PA4260	gi|15599456	NP_252950	29,579.30		19	1	1	1	1		
50S ribosomal protein L3	*rplC*	PA4263	gi|15599459	NP_252953	22,590.60			7	1	13			
50S ribosomal protein L4	*rplD*	PA4262	gi|15599458	NP_252952	21,639.90	3	5	1	8	16	5		
50S ribosomal protein L5	*rplE*	PA4251	gi|15599447	NP_252941	20,393.20		12			4	10		
50S ribosomal protein L6	*rplF*	PA4248	gi|15599444	NP_252938	19,099.00					3			
50S ribosomal protein L10	*rplJ*	PA4272	gi|15599468	NP_252962	17,634.50		12		2	7	6		
50S ribosomal protein L11	*rplK*	PA4274	gi|15599470	NP_252964	14,907.30		5		1	2	2		
50S ribosomal protein L13	*rplM*	PA4433	gi|15599629	NP_253123	16,028.70		3	1		3	2		
50S ribosomal protein L14	*rplN*	PA4253	gi|15599449	NP_252943	13,411.90					2			
50S ribosomal protein L15	*rplO*	PA4244	gi|15599440	NP_252934	15,174.60		12	1	2	16	4		
50S ribosomal protein L16	*rplP*	PA4256	gi|15599452	NP_252946	15,401.50		8	1	3	3	3		

50S ribosomal protein L17	*rplQ*	PA4237	gi|15599433	NP_252927	14,504.30		2						
50S ribosomal protein L19	*rplS*	PA3742	gi|15598937	NP_252431	13,032.40		3	3	3	14	5		
50S ribosomal protein L20	*rplT*	PA2741	gi|15597937	NP_251431	13,365.70		6		1	1			
50S ribosomal protein L21	*rplU*	PA4568	gi|15599764	NP_253258	11,635.20	3	12	4		7	5		2
50S ribosomal protein L22	*rplV*	PA4258	gi|15599454	NP_252948	11,911.10					2			
50S ribosomal protein L23	*rplW*	PA4261	gi|15599457	NP_252951	10,949.90					4	1		
50S ribosomal protein L27	*rpmA*	PA4567	gi|15599763	NP_253257	8,990.40					2			
50S ribosomal protein L28	*rpmB*	PA5316	gi|15600509	NP_254003	9,065.60					2			
50S ribosomal protein L29	*rpmC*	PA4255	gi|15599451	NP_252945	7,201.50					8			
50S ribosomal protein L30	*rpmD*	PA4245	gi|15599441	NP_252935	6,477.60					2			
50S ribosomal protein L36	*rpmJ*	PA4242	gi|15599438	NP_252932	4,434.30					2			