

**Table S2: Comparison of the codon usage of bacteriophages PAK\_P1 and PAK\_P3 with that of their host (PAK)**

		% of each codon per AA	% of each codon per AA	% codon usage [Phage] / % codon usage [PAK]
		<b>PAK</b>	<b>PAK_P1</b>	
Phe	ttc	0.95	0.75	0.79
Phe	ttt	0.05	0.25	5.21
Leu	cta	0.01	0.19	16.50
Leu	tta	0.00	0.02	9.95
Leu	ttg	0.07	0.13	1.86
Leu	ctt	0.03	0.19	7.29
Leu	ctc	0.22	0.16	0.73
Leu	ctg	0.67	0.30	0.45
Ile	atc	0.91	0.55	0.61
Ile	att	0.07	0.38	5.54
Ile	ata	0.02	0.06	2.92
Pro	cca	0.05	0.18	3.92
Pro	cct	0.05	0.38	7.92
Pro	ccc	0.30	0.14	0.48
Pro	ccg	0.76	0.29	0.39
Tyr	tac	0.80	0.61	0.77
Tyr	tat	0.20	0.39	1.89
Gln	caa	0.15	0.49	3.30
Gln	cag	0.85	0.51	0.60
Asn	aac	0.86	0.65	0.76
Asn	aat	0.14	0.35	2.43
Lys	aaa	0.13	0.42	3.34
Lys	aag	0.87	0.58	0.66
Asp	gac	0.80	0.57	0.71
Asp	gat	0.20	0.43	2.19
Glu	gaa	0.39	0.46	1.20
Glu	gag	0.61	0.54	0.88
Cys	tgc	0.90	0.63	0.70
Cys	tgt	0.10	0.37	3.75
Trp	tgg	1.00	1.00	1.00
Arg	aga	0.01	0.16	29.76
Arg	cgt	0.10	0.24	2.29
Arg	cgc	0.65	0.17	0.26
Arg	cga	0.03	0.16	4.96
Arg	cgg	0.18	0.16	0.88
Arg	agg	0.03	0.11	4.31
Gly	gga	0.05	0.25	5.18
Gly	ggt	0.10	0.28	2.85
Gly	ggc	0.73	0.30	0.41
Gly	ggg	0.12	0.17	1.41
			<b>PAK_P3</b>	
Tyr	tac	0.80	0.72	0.91
Tyr	tat	0.20	0.28	1.35
Gln	caa	0.15	0.37	2.49
Gln	cag	0.85	0.63	0.74
Asn	aac	0.86	0.78	0.91
Asn	aat	0.14	0.22	1.51

green, codons for which a tRNA is present in PAK\_P1 (light green, pseudo-tRNA).

purple, codons for which a tRNA is present in PAK\_P3.

yellow, the most frequently used codons.

pink, highest values per amino acid.

beige, lowest values per amino acid.