

Table 22-1. Genes of phage ø29 and their function

Gene	Function	No of aa	Mol. mass (kDa)	Similarity, % ^a		
				ø29/B103	ø29/GA-1	B103/GA-1
1	DNA replication	89	10.3	-	-	-
2	DNA polymerase	572	65.2	88.5	67.3	68.0
3	Terminal protein	266	31.1	74.1	51.7	53.6
4	Transcriptional regulator	125	15.1	83.2	57.6	58.4
5	ssDNA binding protein	124	13.4	73.8	37.9	45.1
6	dsDNA binding protein	104	12.0	65.0	52.7	54.8
7	Scaffolding protein	98	11.2	75.5	48.0	38.6
8	Major head protein	448	49.7	90.4	68.5	69.3
8.5	Head fiber protein	280	29.6	63.6	-	-
9	Tail protein	599	67.7	75.3	58.3	58.5
10	Connector (upper collar protein)	309	35.9	84.4	63.7	63.7
11	Lower collar protein	293	33.6	77.8	51.6	50.9
12	Preneck appendage protein	854	92.4	79.9	37.8	37.5
13	Morphogenesis (tail assembly)	365	41.0	82.7	67.0	67.3
14	Holin	131	14.9	87.1	51.9	52.3
15	Peptidoglycan hydrolase	258	26.9	74.8	37.2	40.6
16	ATPase, DNA encapsidation	332	38.9	86.3	67.5	68.8
16.7	DNA replication, membrane protein	130	15.2	68.5	48.5	47.7
17	DNA replication	167	19.4	48.1	44.8	37.9

^aFor the calculation of the percent similarity, the following amino acids were considered to be conservative: L, I, V, A, and M; F, Y, and W; K and R; D and E, Q and N; S and T. Data taken from Salas ([121](#)), and Meijer *et al.* ([90](#)).