

Reference		Match		All equivalent residues		Best Matching Residues after pruning			
Protein	Res	Protein	# Res	RMSD (Å)	# Res	Cutoff (Å)	RMSD (Å)	# Res	%
MTPU	1-193	MTPL	1-193	1.50	147	2	0.71	128	87.1%
MTPL	1-193	lambda gpV	1-246	15.52	124	10	4.23	70	56.5%
MTPL	1-193	SPP1 gp17.1	1-264	13.20	148	10	5.59	91	61.5%
Dit	1-314	SPP1 Dit NTD	1-137	6.74	123	6	2.37	109	88.6%
Dit	1-314	SPP1 Dit CTD	138-253	8.53	93	6	3.45	68	73.1%
Dit	1-314	TP901-1 Dit NTD	12-147	16.33	109	6	1.90	69	63.3%
Dit	1-314	TP901-1 Dit CTD	148-253	7.04	91	6	3.99	71	78.0%
Dit	1-167	p2 Dit NTD	1-133	16.60	82	6	3.34	48	58.5%
Dit	170-314	p2 Dit CTD	134-144, 189-298	10.44	82	6	3.25	40	48.8%
Tal	2-388	<i>L. monocytogenes</i> phage A118 gp18	3-339	6.09	310	6	2.63	232	74.8%
Tal	2-388	phage Mu gp44 (1WRU)	3-346	6.55	288	6	3.24	193	67.0%
Tal	2-388	<i>E. coli</i> T6SS c3393	15-468	11.67	269	6	3.28	135	50.2%
RBP trimer	1-636	phi11 RBP trimer	1-636	5.20	1892	6	1.96	1604	84.8%
RBP trimer CTD	143-636	phi11 RBP trimer CTD	143-636	1.88	1471	6	1.75	1460	99.3%
RBP trimer CTD	143-636	P68 Tail fiber CTD trimer	151-645	18.49	1390	6	2.48	755	54.3%
RBP tower 1	445-541	RBP tower 2	542-636	2.64	270	6	2.14	257	95.2%
FibL NTD	5-169	FibU NTD	1-121	5.95	227	6	1.89	203	89.4%
FibL NTD	5-169	TP901-1 BppU NTD	1-299	12.92	328	6	2.56	204	62.2%