

Alignment Report of alignment report.MEG, using Clustal method with PAM250 residue weight table. Page 2
Wednesday, April 12, 2000 9:08 PM

	PRDKLIAEAAKIVTKGL-----		Majority
	310	320	330
265	PNDKLISETAKSVMKEF.		b-lactamase protein.seq.PRO
265	PNDKLISETAKSVMKE-F		b-lactamase mutant.pro
278	GRKDILAAAAKIVTEGL		b-lactamase precursor.pro
277	HSDKTIAEASRIAIQAID		carbapenem.pro
296	PSERLIAEDRGAIVAGLVRHPPTHASGAGAPSRHPGP		classA b-lactamase.pro
274	NRKEVLAAAAKIVTEGL		oxy 2-precursor.pro
248	YRKDIIVKATEIVTKEFSNTSQKK		penicillinase.pro

Decoration 'Differences': Shade (with bright yellow at 10% fill) residues that match the Consensus exactly.