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Improved methods for building protein models in electron density maps and the location of errors in these models

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2311	Refined 1.83 Å structure of trypanosomal triosephosphate isomerase crystallized in the presence of 2.4 M-ammonium sulphate. A comparison with the structure of the trypanosomal triosephosphate isomerase-glycerol-3-phosphate complex. <i>Journal of Molecular Biology</i> , <b>1991</b> , 220, 995-1015	6.5	148
2310	DNase I-induced DNA conformation. 2 Å structure of a DNase I-octamer complex. <i>Journal of Molecular Biology</i> , <b>1991</b> , 222, 645-67	6.5	168
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2308	Ser-His-Glu triad forms the catalytic site of the lipase from <i>Geotrichum candidum</i> . <b>1991</b> , 351, 761-4		499
2307	Structure of human cyclophilin and its binding site for cyclosporin A determined by X-ray crystallography and NMR spectroscopy. <b>1991</b> , 353, 276-9		246
2306	Crystal structure of insecticidal delta-endotoxin from <i>Bacillus thuringiensis</i> at 2.5 Å resolution. <b>1991</b> , 353, 815-21		646
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