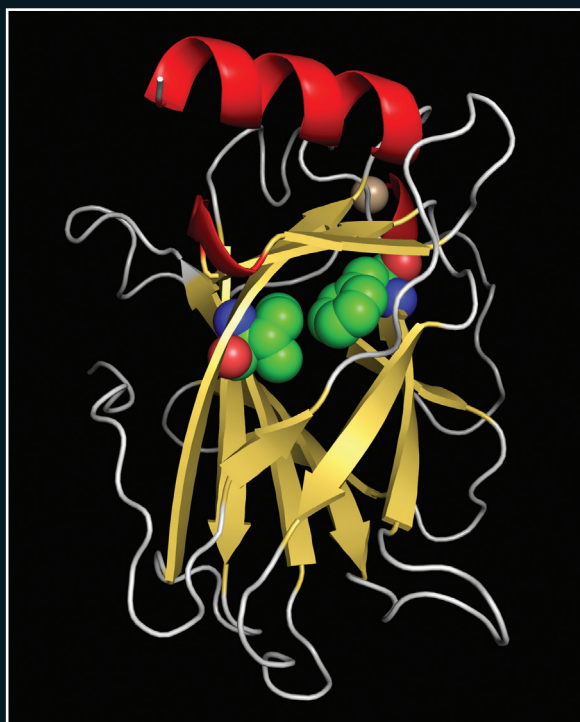


# peds

protein engineering design & selection

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The DNA-binding domain of the tumor suppressor p53 is of low intrinsic stability, making it prone to aggregation and also susceptible to inactivation by oncogenic mutations. The domain was stabilized by rational design of its hydrophobic core. Residues that form sub-optimal buried hydrogen bonds (Tyr236 and Thr253) were replaced by hydrophobic residues (Phe and Ile), as found in the more stable paralogs p63 and p73, and the effects of mutation were characterized using a range of biophysical and structural techniques. The cover shows the crystal structure of this p53 mutant. The stabilizing substitutions in the hydrophobic core of the beta-sandwich are highlighted in green. For further details please see Khoo *et al.* pp. 421–430.

### production editor

Joy Davies, Oxford University Press

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