

Gp42 ShaboiShabazz HHpred

Template alignment | Template 3D Structure | PDBe

1. **3H4R_A Exodeoxyribonuclease 8; Exonuclease, Recombination, Hydrolase, Nuclease; 2.8A {Escherichia coli}**

Probability: 99.92%, E-value: 2.5e-21, Score: 172.12, Aligned cols: 251, Identities: 25%, Similarity: 0.415, Template Neff: 12

[illegible]

Gp42 ShaboiShabazz **RecE** domains

MTAVGLPLPLKCENCGYAERYSRQQVGERPAFCTVHERWLCA
GCRAFMNCVDGGHRVVNQAPRADVTNAVPKNDGIYANIDED
VYHGDHLSLSSSGARDLLSGTPEEFDFNRRVPRDPNKNYDF
GHAHKMVLGKGAKLKMLDPKVHGLKADGKPKSSSPTSTAMW
RKAADARKQGLIPIAKADMEKAQTMAGR VFQHQVAARLFS
K**GAAEHSIY**WHDDATGVRL**RCRPD**FLPDLSRP**ICVDYK**TAT
SANPKQFQKAVADYG**YHQQAIFY**EDGLAEIGLTGVGF LFVV
QSKTPPFSVSVCQIDPEIVELGRRQNRVAIEIFARCMEQDR
WPGYEGIQAVGMAGWAVKQIEDQLEEFELQPTA

PDB3H4R pub 2009: Structure 17, 690-702

