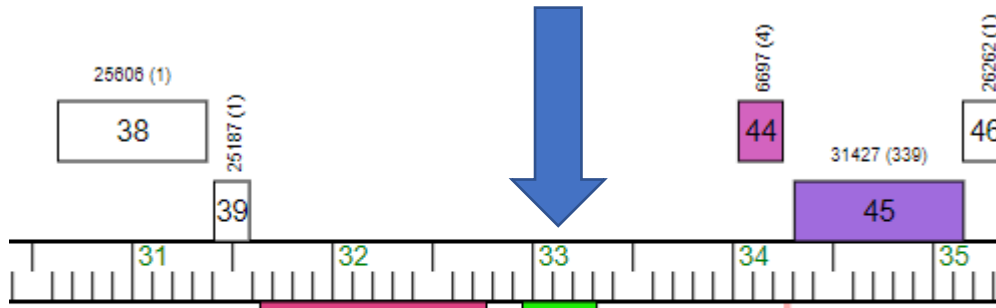


Finkle gp42



Integrase

Imm Rep

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

2. **3DTE_A** IrrE protein; *Deinococcus*, Radiotolerance, Gene regulation, Metallopeptidase, IrrE; HET: MSE; 2.6A {*Deinococcus deserti*}
 Probability: 99.75%, E-value: 1.8e-16, Score: 113.57, Aligned cols: 118, Identities: 15%, Similarity: 0.148, Template Neff: 8.8

Q ss_pred	CCCCHHHHHHhhCC-CcEEEEeCCCCcEEeC--CEEECCCCCHHHHHHHHHHHHHHHHHHHHHcCCCCC-----	
Q Widow_42	2 SIHNPWRYLAEHHP-DVRVWVTRLDGVHRGFDTG--RTIWMNRLSQAQRRTTCHETFHIRGIIIPA-----	66 (139)
Q Consensus	2 ~~~~~g~V~~~~~g~~~~~n~I~n~~~~~hEl~H~~~~~	66 (139)
T Consensus	50 ~p~i~i~i~n~n~n~g~I~n~V~~~~~n~n~g~n~n~n~n~n~I~n~n~n~n~n~P~P~F~t~a~H~E~I~g~H~n~l~n~n~n~n~n~n~n~	126 (301)
T 3DTE_A	50 PGRDTHSLMHG--LDGITLTFMPMG-QRDGAYDPEHHVILINSQVRPERQRTTAAHEISHALLGGDDLLSDLHDEYEGD	126 (301)
T ss_dssp	SSSCHHHHHHTT--CSSCEEEEECCCT-TCCEEEETTTTEEEEETTSCHHHHHHHHHHHHHHHHHHHHHHHHCHHHHHHHHHHHHCCHH	
T ss_pred	CCCCHHHHHHhh--CccEEEEeEC-CCCeEEeCCCCEEEEeCCCCHHHHHHHHHHHHHHHHHHHHHcCCcchhhhcchhcCCC	

HEXXH

Q ss_pred	--cHHHHHHHHHHHHHHhCCHHHHHHHHHHH--cCCCCCHHHHHHHHHCCCHHHHHHHHHhCCH	
Q Widow_42	67 --DAIEEARVERLTAERLITTDQLIDALRW--HRHRPSLQGLAETLWVDVPTVQCRLKTMNV	124 (139)
Q Consensus	67 ~~~~~E~n~a~n~a~n~a~n~l~l~p~n~n~n~n~n~n~n~n~n~n~n~l~a~n~n~n~n~n~n~n~n~n~n~n~l~n~n~n~	124 (139)
T Consensus	127 ~~~~~E~n~e~A~n~FA~n~l~m~P~n~	187 (301)
T 3DTE_A	127 RLEQVIETLCNVGAAALLMPAELIDDLTRFPTGR--ALAEALARADVSAATSAALYALAEATA	187 (301)
T ss_dssp	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHSSHH--HHHHHHHHHTCCHHHHHHHHHHHHTCC	
T ss_pred	cHHHHHHHHHHHHHHHHHHHHhCCHHHHHHHHHHHcCCHH--HHHHHHHHcCCCCHHHHHHHHHHHcCC	

HTH

Has both a HTH DNA binding domain and metallopeptidase domain