

Cas4 exonuclease match

Template alignment | Template 3D Structure | PDBe

27. 4R5Q_A CRISPR-associated exonuclease, Cas4 family; MCSG, STRUCTURAL GENOMICS, PSI-BIOLOGY, EXONUCLEASE, HYDROLASE, Midwest Center for Structural Genomics; 2.65A {Pyrobaculum calidifontis JCM 11548}

Probability: 99.04%, E-value: 2.3e-8, Score: 83.83, Aligned cols: 146, Identities: 15%, Similarity: 0.024, Template Neff: 10.7

```
Q ss_pred CCCCCHHHHHHCcCCcCHHHHHHHH--HcCCC---CCHHHHHHHHHHHHCcCCcEEEEcHhhcCcccCCCCCCCCCHH
Q Langerak_46 25 GSLVSGAKLLLPSPCAKFRWEQ--DNGRK---PKKAWDFGHVAHKLVLGKGAEFVLDPSVHGLKANGEPSEKPTATA 99 (309)
Q Consensus 25 ~LS-S~L~CP~G~H~L~
..+|+.+.+. .|++|+++. ..+. .+... .+.+.+.+.+.
T Consensus 54 ~LS-S~L~Cpr~G~H~L~
T 4R5Q_A 54 RRVSPSTIINDFE--YCPRLLVWQHKLGLKLLSEKSVVSIIRGRILHERYER----- 102 (216)
T ss_dssp TBCCHHHHHHHH--HCHHHHHHHHHTEEEEEETTHHHHHHHHHHHHHHHHH----- 102 (216)
T ss_pred ceecHHHHhhhh--hCcHHHHHHHHHCcCCcCcccCHHHHHHHHHHHHHHH-----
```

```
Q ss_pred HHHHHHHHHHCcCCcCHHHHHHHHHHHHHHCcchHHHHHCcCCcceeEEEEECcCCcEEEEECcCC--C---c
Q Langerak_46 100 MWRAEAEARKQGVPIHIAIDFRAYDMAERVRQHPITAGPIFADAEGQAEVALYHTDPETGVRLRGRIDWLTN--D---I 174 (309)
Q Consensus 100 ~~~~~~E~~~~~L~G~iD~i~g~i
.....+. ....+.+.+. .+.|++|+.+. | |
T Consensus 103 ~~~~~~G~D~i~g~i 137 (216)
T 4R5Q_A 103 -----LLSQYE--NVAEYKVEIG-----DLVGVVDLVIKRGGGEYIP 137 (216)
T ss_dssp -----HHTTST--TEEEEEEEET-----TEEEEEEEEEETEEEE
T ss_pred -----HHHHhc--cceeEEEEECc-----eeEEEEEEEEECCEEE
```

```
Q ss_pred eeeecCCCCCHHHHHHHHHHCcHHHHHHHHHHHHHCcCCcCCcEEEEEEcCCcEeEEEEECcHHHHHHHHHHHHHHHH
Q Langerak_46 175 DDYKTSTTANPAELKVKFYKLGDFYMQAAWYIDLVALGFAENPRFRFIVQEKEPPYVVTPIEYDDDAIAEGRRRNRQAIR 254 (309)
Q Consensus 175 ~~~~~~Ql~Ya~
+|||+.... +..|+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus 138 vd~Kt~Y~g~l~ 187 (216)
T 4R5Q_A 138 VEIKTGFSEK---HKTQLQIYISMLKARF6---YLVYRNHV--EVVHRN-----DAAALDVLK 187 (216)
T ss_dssp EEECCSSCHHH-----HHHHHHHHHHHTCSEE-----EECCSCE-----EEEECC-----GGGGHHHH
T ss_pred EEEeCCcCHH-----HHHHHHHHHHHHHHHCc-----EEEEcCce-----EeeC-----HHHHHHHH
```

```
Q ss_pred HHHHHHHHCcCCcCCcCceEcCCcHH
Q Langerak_46 255 LYAEcMETGRWPGYSDDVVTLSPAW 280 (309)
Q Consensus 255 ~~~~~~p~
.+..+..+..+..+.. .|.|.|.+.
T Consensus 188 ~~~~~~p~C~C~ 209 (216)
T 4R5Q_A 188 KIREILSAREAPP---AKCNSCIFK 209 (216)
T ss_dssp HHHHHHHHCSSCC-----CCSSSCTTT
T ss_pred HHHHHHHHCcCCcC-----cCCCCcCh
```

Exonuclease/helicase match

Template alignment | Template 3D Structure | PDBe

16. 6PPU_B UvrD/REP helicase; DNA, DNA BINDING PROTEIN, DNA BINDING PROTEIN-DNA complex; 3.5A {Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)}

Probability: 99.38%, E-value: 2e-11, Score: 125.61, Aligned cols: 195, Identities: 18%, Similarity: 0.037, Template Neff: 10.8

```
Q ss_pred CCCCCHHHHHHCcCCcCHHHHHHHH--HcCCCCCHHHHHHHHHHHHCcCCcEEEEcHhhcCcccCCCCCCCCCHHHHH
Q Langerak_46 26 SLVSGAKLLLPSPCAKFRWEQ--DNGRKPKKAWDFGHVAHKLVLGKGAEFVLDPSVHGLKANGEPSEKPTATAMWRN 103 (309)
Q Consensus 26 ~LS-S~L~CP~G~H~L~
.+|+.+.+. .|++|+++. ..+.+.+.+.|+++|.+++|.+.+.+.+.+.
T Consensus 889 ~s-s-l~CP~G~H~L~
T 6PPU_B 889 QLSVSTLVLEL--RDPKAALTRRLRRLPQRDPHALLGTTTFHEWVQRYFHAERLFDLDDLP----- 947 (1095)
T ss_pred cccHHHHHHHH--hCHHHHHHHHCcCCcCCCHHHHHHHHHHHHHHHHCcCCcCHHHCC-----
```

```
Q ss_pred HHHHHHHHCcCCcCHHHHHHHHHHHHHHCcchHHHHHCcCCcceeEEEEEEcCCcEEEEECcCC--C---ceee
Q Langerak_46 104 AEAEARQKGVPIHIAIDFRAYDMAERVRQHPITAGPIFADAEGQAEVALYHTDPETGVRLRGRIDWLTN---D---IDDY 177 (309)
Q Consensus 104 ~~~~~~E~~~~~L~G~iD~i~g~i
.....+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus 948 ~~~~~~E~~~~~G~iD~i~g~i 1015 (1095)
T 6PPU_B 948 -----GAVDSDSGRAVEESLAELQDAFVKSPWAARTPVLEVVPDMV--LGETVVRGRIDAVFAEPDGTMLVDW 1015 (1095)
T ss_pred -----CCCCcchHHHHHHHHHHHHHCcchHCcCCcEEEEeEEE--eCEEEEEEEeEEEECCCEEEEC
```

```
Q ss_pred ecCCCCCHHHHHHHHHHCcHHHHHHHHHHHHHCcCCcCCc--cEEEEEEcCCcEeEEEEECcHHHHHHHHHHHHHHHH
Q Langerak_46 178 KTSTTANPAELKVKFYKLGDFYMQAAWYIDLVALGFAENP--RFRFIVQEKEPPYVVTPIEYDDDAIAEGRRRNRQAIRL 255 (309)
Q Consensus 178 ~~~~~~Ql~Ya~
|||.....+.|.|.|.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus 1016 Ktg~Y~ 1086 (1095)
T 6PPU_B 1016 KTGDPPETPEAKEH-----AAVQLAVYRLAWAAMRGCPPEESVRAAFHYVRSQ---QTVIPETLP--GAEEVLKLLAAAPTE 1086 (1095)
T ss_pred CCCCCCHHHHHH-----HHHHHHHHHHHHHHHCcCHhheEEEEECcCC--cEEcCCcC--CHHHHHHHHHCcHh
```

```
Q ss_pred HHHHHH
Q Langerak_46 256 YAEcMET 262 (309)
Q Consensus 256 ~~~~~~
+.+.+.
T Consensus 1087 ~~~~~~ 1093 (1095)
T 6PPU_B 1087 TAEeADR 1093 (1095)
T ss_pred HHHHHhh
```