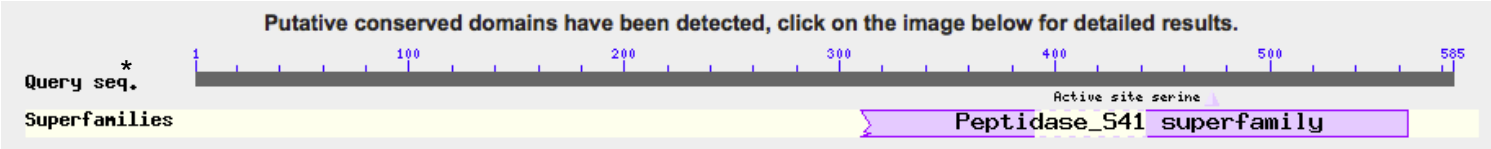
Supplementary figure 4

A



*Query: *Parachlamydia acanthamoebae* Bn9 peg.785

B

E-value: **1.45e-92**, bit-score: **299**, aligned-length: **538**, Identity to query: **35%**

```
                 10        20        30        40        50        60        70        80
          *  ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329  26 SLLRQEMVEDLHFIRKNFQIKYVPADWKLLQFGWNLNQQFDNAEAEITSLSSPTLKDYHKILNKLFTSAADYHVNVSFYS 105
3DOR_A  **  1 SLVCKNALQDLSFLEHLLQVKYAPKTWKEQYLGWDLVQSSVSAQQKLRTQENPSTSFCQQVLADFIGGLNDFHAGVTFFA 80

                 90       100       110       120       130       140       150       160
          ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329 106 TEMASLPFHLQ-GAEGRYFitWINEEKLPEECldwSIGDEVIAFDGQDIHEFVQNLRRSEHdrHNEKTDQRFAERSLTLR 184
3DOR_A  81 IESAYLPYTVQkSSDGRFY--FVDIMTFSSEI---RVGDELLEVDGAPVQDVLATLYGSNH--KGTAAEESAALRTLFSR 153

                170       180       190       200       210       220       230       240
          ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329 185 AGMFAEDVPQGNVEVDlIHKKTGEQKSYVLTWTYHPEQVKEIPL--PSLVARGISEK-QPFFQR---PYYKKMML--TPL 256
3DOR_A 154 MASLGHKVPSGRTTLK-IRRPFGTTREVRVKWRYVPEGVGDLATiaPSIRAPQLQKSmRSFFPKkddAFHRSSSLfySPM 232

                250       260       270       280       290       300       310       320
          ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329 257 YAKF-----NQPESRVVEDVHNLGARKSFVPPLGSIVWQSppDSPFHAYICETP----SRQRIGYIRIATYDGTDDEVV- 326
3DOR_A 233 VPHFwaelrNHYATSGLKSGYNIGSTDGFLPVIGPVIWES--EGLFRAYISSVTdgdgKSHKVGFLRIPTYSWQDMEDFd 310

                330       340       350       360       370       380       390       400
          ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329 327 --------EFAKLIDYFNPRTQALVVDQVNNPGGSVFYSYGLLSLLTDQPLELPKYKMAITQEEVMEALETLDTLKEITN 398
3DOR_A 311 psgpppweEFAKIIQVFSSNTEALIIDQTNNPGGSVLYLYALLSMLTDRPLELPKHRMILTQDEVVDALDWLTLLENVDT 390

                410       420       430       440       450       460       470       480
          ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329 399 DEEAIDVCGPSLHGYAVSFELVQSVIQYFQFVLSEWEEGKY-VTSPVHLL-VNTIAPSPFVTYDKPMVVLVNEFDISCGD 476
3DOR_A 391 NVESRLALGDNMEGYTVDLQVAEYLKSFGRQVLNCWSKGDIeLSTPIPLFgFEKIHPHPRVQYSKPICVLINEQDFSCAD 470

                490       500       510       520       530       540       550       560
          ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
273329 477 SFPCILQDNQRALIFGTRTAGAGGTVLGGGHPNRLGIAGYSYTASLLERHtDGTPIENLGVTPDVSYSLTPEDFQngYKG 556
3DOR_A 471 FFPVVLKDNDRALIVGTRTAGAGGFVFNVQFPNRTGIKTCSLTGSLAVRE-HGAFIENIGVEPHIDLPFTANDIR--YKG 547

          ....*..
273329 557 YKAALQE 563
3DOR_A 548 YSEYLDK 554
```

*273329 (Query): *Parachlamydia acanthamoebae* Bn9 peg.785
**3DOR_A: *Chlamydia trachomatis* Chain A, Crystal Structure Of Mature Cpaf