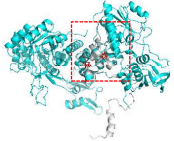
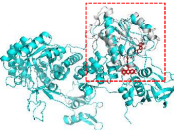
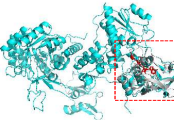
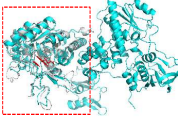
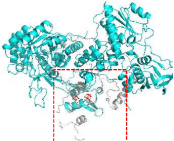


Structure-based amino acid sequence alignment between predicted *A. hadrus* PreT-PreA heterodimer and five pig DPD domains

Alignment	Schematic Diagram	Result	Sequence
Domain I (nFeS1,nFeS2)		RMSD = 0.786 (85 to 85 atoms)	21 TAMEEASRCLLCHDAPCSKSCPAKTPAKFIRSLRFRNIKGAEAETIRENNPLAGCCAEVCPYGGQLCEQACSRGTGIDK--PIEI GKLQKFLVEMEK 113 71 GALREAMRCLKADAPCQKSCPTHLDIKSFITISLNKNYGAAKMIFSDNPLGLTLCGVCPPTSDLCVGGCNLYAIEEGSINI GGLQQFASEVFK 164
Domain II (FAD)		RMSD = 0.596 (116 to 116 atoms)	128 GKIACVGAGPASLACARELALFGY--DVTIYEANEKAGVLYTYIVPSRLPQEVVDFDIATIEKLGVTFFKFNETIDAARL--E ELKAE--YDAVFVGTGL 221 369 VFTGGDMVNGGKTVVQVAEAGKDAAMAIAAYLN 401 188 AKIALIAGPASTSCASFLARLGYSDITHEKQEYVGLSTSEIPQFRLPYDVVNFIEIEMKDLGVKICGKSLSENEITLN TLKEEGYKAAFVIGL 285 476 VFAGGDIVGMANTVTSVNDGKQASWYIHKYI 508
Domain III (NADPH)		RMSD = 2.284 (85 to 85 atoms)	242 DFLK--DARLNKENM-----TLGDTLVLVGGGDVAMDCVTTAKQLGAKAT--IVYRR--TIEEAPADIDEVMAVQSMGIP IIQEFAPGELIGSKGHVTAMKFNGRD-----NESE--LTMKADQVVFVIG 353 308 DFLPLVAKSSKAGMCACHSPLPSIRGAVTVLAGDTPFCATSLRCCGARRVFLVFRKGFVNI RAVPEEVELAKEEKCEFLP FL--SPRKYIVKGGRIYAVQFVRTEQDETGWNEIDEDQIVHLKADVYISAFG 439
Domain IV (5-FU,FMN)		RMSD = 0.619 (255 to 255 atoms)	6 DLSIDFLGVKCEPNFFLSSEPVGSNYEMCAKALEAGWGGIYYKTIGIFI--PDECSPRFDITTKEGTPWVG--FKNMEQI SDKPLEVNLVEMRRLKQDYPNKNIVASIMGSN--DEEWTLAKAVTEAGVDMIECNFSCPQMTSHAMGS--DVGQNPFLVKHYCEVVT AATHLPVIAKMTPNIGNMEIPAIASMEGGAAGIAAINTVKAITNIDIENITAMPVVG--KSSISGYSAAVKPIALRFITQMKQH PDLVDVPIITVGGIETWRDALEFVLVGASNLQVTTAVMQGYRIVEDMISGLSHYMEDN 308 532 DISVEMAGLKFINPPGLASAAPTTSSMIRRAFEAGWGFALIKTFSLDKDIYVTVNSPRIVRGTTSGPMYGPQGSSFLNIELI SEKTAAYWCQSVTELKADFPDNIIVIASIMCSYKNDIMELSRKAEASGADALELN SAPHGMGERGMGLACGQDPFLVRNICRWRV QAVQIPFFAKLTPNVTDIVSITARAAGEGADVTA TNTVSLMGLKADGTPW--PAVGAGKRTTYGGVGSATAIRPIALRAVTTIARA --LFGPFLATGCSIDSAESGLQFLHSGASVLQVCSAVQNQDFTVIQDYCTGLKALLYLK 841
Domain V (cFeS1,cFeS2)		RMSD = 1.023 (79 to 79 atoms)	313 LSDLVGLALPNIVPAEDLDRSFKLLPKFDEDA CAGCGRCYVSCFDGGHQAIWDDEEARRPLNTDKCVGCHLCLNVCPVMDC I 395 921 IKDVIKALQYLGTGFELSNIEQVAVVIDEEMCINCGKCYMTCDNSGYQAIQFDPETHLPTVTD--TCTGCTLCLSVCPIDC I 1002