







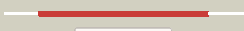


















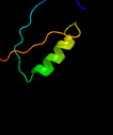

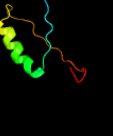
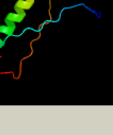


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2230c (-) _2503477_2504616
Date	Mon Aug 5 13:25:36 BST 2019
Unique Job ID	85012e824b8b3a91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2gx8B_</a>	 Alignment		100.0	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> nif3-related protein; <b>PDBTitle:</b> the crystal structure of bacillus cereus protein related to nif3
2	<a href="#">d2gx8a1</a>	 Alignment		100.0	34	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
3	<a href="#">c2nydB_</a>	 Alignment		100.0	29	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> upf0135 protein sa1388; <b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical protein sa1388
4	<a href="#">d2fywa1</a>	 Alignment		100.0	27	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
5	<a href="#">d1nmpa_</a>	 Alignment		100.0	26	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
6	<a href="#">c4iwmD_</a>	 Alignment		100.0	25	<b>PDB header:</b> unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> upf0135 protein mj0927; <b>PDBTitle:</b> crystal structure of the conserved hypothetical protein mj0927 from methanocaldococcus jannaschii (in p21 form)
7	<a href="#">c2yybA_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ttha1606; <b>PDBTitle:</b> crystal structure of ttha1606 from thermus thermophilus hb8
8	<a href="#">c3rxyA_</a>	 Alignment		99.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> nif3 protein; <b>PDBTitle:</b> crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
9	<a href="#">c3mhyC_</a>	 Alignment		95.3	19	<b>PDB header:</b> signaling protein <b>Chain:</b> C; <b>PDB Molecule:</b> pii-like protein pz; <b>PDBTitle:</b> a new pii protein structure
10	<a href="#">d1vfja_</a>	 Alignment		94.9	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
11	<a href="#">c2rd5D_</a>	 Alignment		94.7	22	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> pii protein; <b>PDBTitle:</b> structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana

12	<a href="#">c4usiC</a>	Alignment		94.4	18	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> nitrogen regulatory protein pii; <b>PDBTitle:</b> nitrogen regulatory protein pii from chlamydomonas2 reinhardtii in complex with mgatp and 2-oxoglutarate
13	<a href="#">c3ahpA</a>	Alignment		94.2	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cuta1; <b>PDBTitle:</b> crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
14	<a href="#">d2piaa</a>	Alignment		94.2	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
15	<a href="#">d2ns1b1</a>	Alignment		94.0	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
16	<a href="#">d1qy7a</a>	Alignment		94.0	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
17	<a href="#">d1nzaa</a>	Alignment		93.9	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
18	<a href="#">c4r25A</a>	Alignment		93.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory pii-like protein; <b>PDBTitle:</b> structure of b. subtilis glnK
19	<a href="#">c4e98C</a>	Alignment		93.9	18	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> cuta1 divalent ion tolerance protein; <b>PDBTitle:</b> crystal structure of possible cuta1 divalent ion tolerance protein2 from cryptosporidium parvum iowa ii
20	<a href="#">c2nuhA</a>	Alignment		93.7	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic divalent cation tolerance protein; <b>PDBTitle:</b> crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosia
21	<a href="#">c4iyqB</a>	Alignment	not modelled	93.7	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> divalent ion tolerance protein cuta1; <b>PDBTitle:</b> crystal structure of divalent ion tolerance protein cuta1 from2 ehrlichia chaffeensis
22	<a href="#">c3o8wA</a>	Alignment	not modelled	93.6	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-1); <b>PDBTitle:</b> archaeoglobus fulgidus glnK1
23	<a href="#">d1lukua</a>	Alignment	not modelled	93.5	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
24	<a href="#">d1vhfa</a>	Alignment	not modelled	93.4	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
25	<a href="#">d1naqa</a>	Alignment	not modelled	93.3	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
26	<a href="#">d1p1la</a>	Alignment	not modelled	93.3	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
27	<a href="#">c2zomC</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> protein cuta, chloroplast, putative, expressed; <b>PDBTitle:</b> crystal structure of cuta1 from oryza sativa <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic divalent cation tolerance protein; <b>PDBTitle:</b> structure of cuta from synechococcus elongatus pcc7942 complexed with2 3 molecules of bis-tris <b>PDB header:</b> structural genomics, unknown function
28	<a href="#">c6gdxA</a>	Alignment	not modelled	93.1	16	

29	<a href="#">c2zfha_</a>	Alignment	not modelled	93.0	16	<b>Chain:</b> A; <b>PDB Molecule:</b> cuta; <b>PDBTitle:</b> crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
30	<a href="#">d1kr4a_</a>	Alignment	not modelled	92.7	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
31	<a href="#">c1xk8A_</a>	Alignment	not modelled	92.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> divalent cation tolerant protein cuta; <b>PDBTitle:</b> divalent cation tolerant protein cuta from homo sapiens o60888
32	<a href="#">d2zfha1</a>	Alignment	not modelled	92.3	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
33	<a href="#">c4ozfA_</a>	Alignment	not modelled	91.4	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> glnk2 from haloferax mediterranei complexed with amp
34	<a href="#">d1hwua_</a>	Alignment	not modelled	90.9	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
35	<a href="#">c3ncpD_</a>	Alignment	not modelled	90.8	32	<b>PDB header:</b> signaling protein <b>Chain:</b> D; <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-2); <b>PDBTitle:</b> glnk2 from archaeoglobus fulgidus
36	<a href="#">c3bzqA_</a>	Alignment	not modelled	90.4	23	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A; <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
37	<a href="#">c2j9dG_</a>	Alignment	not modelled	90.3	31	<b>PDB header:</b> membrane transport <b>Chain:</b> G; <b>PDB Molecule:</b> hypothetical nitrogen regulatory pii-like <b>PDBTitle:</b> structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
38	<a href="#">d1ul3a_</a>	Alignment	not modelled	89.1	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
39	<a href="#">c4s1nA_</a>	Alignment	not modelled	88.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4
40	<a href="#">c3l7pA_</a>	Alignment	not modelled	87.4	35	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> putative nitrogen regulatory protein pii; <b>PDBTitle:</b> crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
41	<a href="#">d2cz4a1</a>	Alignment	not modelled	86.2	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
42	<a href="#">c3ce8A_</a>	Alignment	not modelled	82.6	13	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative pii-like nitrogen regulatory protein; <b>PDBTitle:</b> crystal structure of a duf3240 family protein (sba1_0098) from2 shewanella baltica os155 at 2.40 a resolution
43	<a href="#">d1osce_</a>	Alignment	not modelled	81.7	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
44	<a href="#">c5ghrA_</a>	Alignment	not modelled	79.6	14	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> A; <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein
45	<a href="#">c3av3A_</a>	Alignment	not modelled	78.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus
46	<a href="#">c2yx6C_</a>	Alignment	not modelled	76.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein ph0822; <b>PDBTitle:</b> crystal structure of ph0822
47	<a href="#">c5d4pA_</a>	Alignment	not modelled	72.7	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative nitrogen regulatory protein p-ii glnb; <b>PDBTitle:</b> structure of cpil bound to adp and bicarbonate, from thiomonas2 intermedia k12
48	<a href="#">c6cauA_</a>	Alignment	not modelled	71.4	15	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
49	<a href="#">c5f56A_</a>	Alignment	not modelled	70.7	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> single-stranded-dna-specific exonuclease; <b>PDBTitle:</b> structure of recj complexed with dna and ssb-ct
50	<a href="#">c3zu3A_</a>	Alignment	not modelled	69.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative reductase ypo4104/y4119/yp_4011; <b>PDBTitle:</b> structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
51	<a href="#">d1p3da1</a>	Alignment	not modelled	69.3	16	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
52	<a href="#">c5ebbA_</a>	Alignment	not modelled	68.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acid sphingomyelinase-like phosphodiesterase 3a; <b>PDBTitle:</b> structure of human sphingomyelinase phosphodiesterase like 3a2 (smpdl3a) with zn2+
53	<a href="#">c2ph5A_</a>	Alignment	not modelled	68.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54 <b>PDB header:</b> hydrolase

54	<a href="#">c5karA_</a>	Alignment	not modelled	67.8	15	<b>Chain:</b> A: <b>PDB Molecule:</b> acid sphingomyelinase-like phosphodiesterase 3b; <b>PDBTitle:</b> murine acid sphingomyelinase-like phosphodiesterase 3b (smpdl3b)
55	<a href="#">d2c1ha1</a>	Alignment	not modelled	66.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinic acid dehydratase, ALAD (porphobilinogen synthase)
56	<a href="#">c3k6jA_</a>	Alignment	not modelled	66.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein f01g10.3, confirmed by transcript evidence; <b>PDBTitle:</b> crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
57	<a href="#">c4bubA_</a>	Alignment	not modelled	63.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine <b>PDBTitle:</b> crystal structure of mure ligase from thermotoga maritima2 in complex with adp
58	<a href="#">c4euhA_</a>	Alignment	not modelled	62.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ca_c0462; <b>PDBTitle:</b> crystal structure of clostridium acetobutulum trans-2-enoyl-coa2 reductase apo form
59	<a href="#">c5yh1A_</a>	Alignment	not modelled	60.3	17	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins; <b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
60	<a href="#">c2pv7B_</a>	Alignment	not modelled	60.1	15	<b>PDB header:</b> isomerase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) <b>PDBTitle:</b> crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
61	<a href="#">c3p19A_</a>	Alignment	not modelled	59.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative blue fluorescent protein; <b>PDBTitle:</b> improved nadph-dependent blue fluorescent protein
62	<a href="#">c3obkH_</a>	Alignment	not modelled	57.9	18	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
63	<a href="#">c3u49B_</a>	Alignment	not modelled	57.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bacilysin biosynthesis oxidoreductase ywfh; <b>PDBTitle:</b> crystal structure of ywfh, nadph dependent reductase involved in2 bacilysin biosynthesis
64	<a href="#">d2p10a1</a>	Alignment	not modelled	55.5	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> MII9387-like
65	<a href="#">c5lzhH_</a>	Alignment	not modelled	54.3	17	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> pyrobaculum caldifontis 5-aminolaevulinic acid dehydratase
66	<a href="#">c5ldgA_</a>	Alignment	not modelled	54.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (-)-isopiperitenone reductase; <b>PDBTitle:</b> isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadp
67	<a href="#">c2f00A_</a>	Alignment	not modelled	53.4	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
68	<a href="#">c5nmwA_</a>	Alignment	not modelled	53.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
69	<a href="#">c3nywD_</a>	Alignment	not modelled	52.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a betaketoacyl-[acp] reductase (fabg) from2 bacteroides thetaiotaomicron
70	<a href="#">c3v2hB_</a>	Alignment	not modelled	51.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-beta-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
71	<a href="#">c5l53A_</a>	Alignment	not modelled	50.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (-)-menthone:(+)-neomenthol reductase; <b>PDBTitle:</b> menthone neomenthol reductase from mentha piperita in complex with2 nadp
72	<a href="#">d1j6ua1</a>	Alignment	not modelled	50.3	15	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
73	<a href="#">d1vqta1</a>	Alignment	not modelled	50.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
74	<a href="#">c3o26A_</a>	Alignment	not modelled	49.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> salutaridine reductase; <b>PDBTitle:</b> the structure of salutaridine reductase from papaver somniferum.
75	<a href="#">c5o3zK_</a>	Alignment	not modelled	49.3	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> sorbitol-6-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of sorbitol-6-phosphate 2-dehydrogenase srlid from2 erwinia amylovora
76	<a href="#">c4y96B_</a>	Alignment	not modelled	49.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from gemmata2 obscuriglobus
77	<a href="#">c2dp3A_</a>	Alignment	not modelled	48.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
						<b>Fold:</b> TIM beta/alpha-barrel

78	<a href="#">d1n55a_</a>	Alignment	not modelled	48.7	17	<b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
79	<a href="#">c2nq8B_</a>	Alignment	not modelled	48.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> malarial enoyl acyl acp reductase bound with inh-nad adduct
80	<a href="#">c2foiB_</a>	Alignment	not modelled	48.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> synthesis, biological activity, and x-ray crystal structural analysis2 of diaryl ether inhibitors of malarial enoyl acp reductase.
81	<a href="#">c6bveA_</a>	Alignment	not modelled	48.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> triosephosphate isomerase of synechocystis in complex with 2-2 phosphoglycolic acid
82	<a href="#">d1p33a_</a>	Alignment	not modelled	48.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">c5ujwD_</a>	Alignment	not modelled	47.6	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4
84	<a href="#">c2qhxB_</a>	Alignment	not modelled	46.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pteridine reductase 1; <b>PDBTitle:</b> structure of pteridine reductase from leishmania major2 complexed with a ligand
85	<a href="#">c2p10D_</a>	Alignment	not modelled	45.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mlI9387 protein; <b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
86	<a href="#">c5b1yB_</a>	Alignment	not modelled	45.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of nadph bound carbonyl reductase from aeropyrum2 pernix
87	<a href="#">d1t3va_</a>	Alignment	not modelled	45.6	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
88	<a href="#">c4x54A_</a>	Alignment	not modelled	45.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of an oxidoreductase (short chain2 dehydrogenase/reductase) from brucella ovis
89	<a href="#">c3t4xA_</a>	Alignment	not modelled	45.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
90	<a href="#">c3s6dA_</a>	Alignment	not modelled	44.8	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
91	<a href="#">d1ru8a_</a>	Alignment	not modelled	44.8	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
92	<a href="#">c2wfbA_</a>	Alignment	not modelled	44.8	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein orp; <b>PDBTitle:</b> high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
93	<a href="#">d1m6ja_</a>	Alignment	not modelled	44.8	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
94	<a href="#">c2dknA_</a>	Alignment	not modelled	44.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-alpha-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of the 3-alpha-hydroxysteroid dehydrogenase from2 pseudomonas sp. b-0831 complexed with nadh
95	<a href="#">d1uh5a_</a>	Alignment	not modelled	44.5	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
96	<a href="#">c4nbwA_</a>	Alignment	not modelled	44.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of fabg from plesiocystis pacifica
97	<a href="#">c6oz7A_</a>	Alignment	not modelled	44.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized oxidoreductase yohf; <b>PDBTitle:</b> putative oxidoreductase from escherichia coli str. k-12
98	<a href="#">d1eo1a_</a>	Alignment	not modelled	44.0	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
99	<a href="#">d1o5xa_</a>	Alignment	not modelled	43.6	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
100	<a href="#">c6m9uA_</a>	Alignment	not modelled	43.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family <b>PDBTitle:</b> structure of the apo-form of 20beta-hydroxysteroid dehydrogenase from2 bifidobacterium adolescentis strain I2-32
101	<a href="#">c6nrcC_</a>	Alignment	not modelled	43.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-acp reductase fabg; <b>PDBTitle:</b> putative short-chain dehydrogenase/reductase (sdr) from acinetobacter2 baumannii
102	<a href="#">c4nbrA_</a>	Alignment	not modelled	43.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein] reductase from2 brucella melitensis atcc 23457
						<b>PDB header:</b> hydrolase



103	<a href="#">c6j4nD_</a>	Alignment	not modelled	42.8	11	<b>Chain:</b> D: <b>PDB Molecule:</b> metallo-beta-lactamases pngm-1; <b>PDBTitle:</b> structure of papua new guinea mbl-1(pngm-1) native
104	<a href="#">c4obtA_</a>	Alignment	not modelled	42.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, cytosolic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana cytosolic triose phosphate 2 isomerase
105	<a href="#">c1j6uA_</a>	Alignment	not modelled	42.7	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
106	<a href="#">d1kv5a_</a>	Alignment	not modelled	42.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
107	<a href="#">c5idxB_</a>	Alignment	not modelled	41.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of an oxidoreductase from burkholderia vietnamiensis
108	<a href="#">c6ixjK_</a>	Alignment	not modelled	41.5	21	<b>PDB header:</b> cytosolic protein <b>Chain:</b> K: <b>PDB Molecule:</b> sulfoacetaldehyde reductase; <b>PDBTitle:</b> the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca
109	<a href="#">c4mknA_</a>	Alignment	not modelled	41.3	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of chloroplastic triosephosphate isomerase from2 chlamydomonas reinhardtii at 1.1 a of resolution
110	<a href="#">d1suxa_</a>	Alignment	not modelled	41.2	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
111	<a href="#">d1neya_</a>	Alignment	not modelled	41.2	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
112	<a href="#">c3s55F_</a>	Alignment	not modelled	40.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad
113	<a href="#">c2ntnB_</a>	Alignment	not modelled	39.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of maba-c60v/g139a/s144l
114	<a href="#">c3qstA_</a>	Alignment	not modelled	39.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, putative; <b>PDBTitle:</b> crystal structure of trichomonas vaginalis triosephosphate isomerase2 tvag_096350 gene (val-45 variant)
115	<a href="#">d1b9ba_</a>	Alignment	not modelled	39.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
116	<a href="#">c1vjtA_</a>	Alignment	not modelled	39.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
117	<a href="#">d1sbya1</a>	Alignment	not modelled	39.1	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
118	<a href="#">c4yxfB_</a>	Alignment	not modelled	38.9	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> mups; <b>PDBTitle:</b> mups, a 3-oxoacyl (acp) reductase involved in mupirocin biosynthesis
119	<a href="#">c2wtzC_</a>	Alignment	not modelled	38.9	18	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate- <b>PDBTitle:</b> mure ligase of mycobacterium tuberculosis
120	<a href="#">c2p91A_</a>	Alignment	not modelled	38.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nahh]; <b>PDBTitle:</b> crystal structure of enoyl-[acyl-carrier-protein] reductase (nahh)2 from aquifex aeolicus vf5