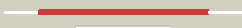



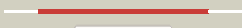








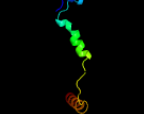

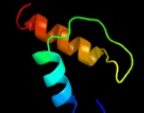

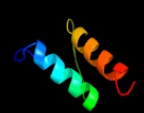










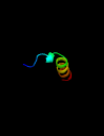




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3688c_(-)_4130071_4130535
Date	Fri Aug 9 18:20:38 BST 2019
Unique Job ID	51eab8980f7ec3cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1ng6a_</a>	 Alignment		100.0	33	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/YqeY domain
2	<a href="#">c3ip4B_</a>	 Alignment		99.0	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; <b>PDBTitle:</b> the high resolution structure of gatcab
3	<a href="#">c3al0B_</a>	 Alignment		99.0	10	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
4	<a href="#">c4ye6A_</a>	 Alignment		89.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> the crystal structure of the intact human glnrs
5	<a href="#">c3tl4X_</a>	 Alignment		78.6	14	<b>PDB header:</b> ligase <b>Chain:</b> X: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the trna binding domain of glutamyl-trna2 synthetase from saccharomyces cerevisiae
6	<a href="#">d1hwxa2</a>	 Alignment		65.8	19	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
7	<a href="#">c4yycA_</a>	 Alignment		65.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative trimethylamine methyltransferase; <b>PDBTitle:</b> crystal structure of trimethylamine methyltransferase from2 sinorhizobium meliloti in complex with unknown ligand
8	<a href="#">d1l1fa2</a>	 Alignment		62.3	19	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
9	<a href="#">c5k12F_</a>	 Alignment		54.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate dehydrogenase 1, mitochondrial; <b>PDBTitle:</b> cryo-em structure of glutamate dehydrogenase at 1.8 a resolution
10	<a href="#">c2lkyA_</a>	 Alignment		51.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
11	<a href="#">d1z1za1</a>	 Alignment		46.1	25	<b>Fold:</b> Phage tail protein-like <b>Superfamily:</b> Phage tail protein-like <b>Family:</b> Lambda phage gpU-like

12	<a href="#">d1euza2</a>	Alignment		45.2	28	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
13	<a href="#">c2m0nA_</a>	Alignment		44.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
14	<a href="#">c2kvcA_</a>	Alignment		42.9	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
15	<a href="#">c2yfqA_</a>	Alignment		39.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
16	<a href="#">c5mz2L_</a>	Alignment		38.5	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> rubisco small subunit; <b>PDBTitle:</b> rubisco from thalassiosira antarctica
17	<a href="#">c5eu0B_</a>	Alignment		38.3	22	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin 1; <b>PDBTitle:</b> fic domain of bep1 from bartonella rochalimae in complex with b1aa
18	<a href="#">d1rbli_</a>	Alignment		38.2	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
19	<a href="#">d1bgva2</a>	Alignment		38.0	14	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
20	<a href="#">d1svdm1</a>	Alignment		37.8	35	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
21	<a href="#">d1bxni_</a>	Alignment	not modelled	37.5	19	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
22	<a href="#">d1bwvs_</a>	Alignment	not modelled	37.4	30	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
23	<a href="#">d1gtma2</a>	Alignment	not modelled	36.7	18	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
24	<a href="#">c2d7dB_</a>	Alignment	not modelled	34.8	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> 40-mer from uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
25	<a href="#">c5nv3P_</a>	Alignment	not modelled	33.4	24	<b>PDB header:</b> lyase <b>Chain:</b> P: <b>PDB Molecule:</b> ribulose biphosphate carboxylase small chain 1; <b>PDBTitle:</b> structure of rubisco from rhodobacter sphaeroides in complex with cabp
26	<a href="#">c2qneA_</a>	Alignment	not modelled	31.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
27	<a href="#">c2ybvN_</a>	Alignment	not modelled	30.6	38	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> ribulose biphosphate carboxylase small subunit; <b>PDBTitle:</b> structure of rubisco from thermosynechococcus elongatus
						<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline ceramidase 3,soluble cytochrome

28	<a href="#">c6g7oA</a>	Alignment	not modelled	29.8	11	b562; <b>PDBTitle:</b> crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
29	<a href="#">d1v9la2</a>	Alignment	not modelled	27.2	18	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
30	<a href="#">d1uzhc1</a>	Alignment	not modelled	27.0	43	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
31	<a href="#">c2i7kA</a>	Alignment	not modelled	25.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
32	<a href="#">d1heya</a>	Alignment	not modelled	23.1	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
33	<a href="#">c4fetA</a>	Alignment	not modelled	23.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spore cortex-lytic enzyme prepeptide; <b>PDBTitle:</b> catalytic domain of germination-specific lytic tansglycosylase sleb2 from bacillus anthracis
34	<a href="#">d1b26a2</a>	Alignment	not modelled	22.3	16	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
35	<a href="#">c3o14B</a>	Alignment	not modelled	22.0	11	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
36	<a href="#">c3mixA</a>	Alignment	not modelled	21.9	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar biosynthesis protein flha; <b>PDBTitle:</b> crystal structure of the cytosolic domain of b. subtilis flha
37	<a href="#">c2l4bA</a>	Alignment	not modelled	21.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
38	<a href="#">c6cfxD</a>	Alignment	not modelled	20.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> upf0335 protein ase63_04290; <b>PDBTitle:</b> bosea sp gapr solved in the presence of dna
39	<a href="#">c3ilhA</a>	Alignment	not modelled	19.9	29	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> crystal structure of two component response regulator from cytophaga2 hutchinsonii
40	<a href="#">c1nr1A</a>	Alignment	not modelled	19.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of the r463a mutant of human glutamate dehydrogenase
41	<a href="#">c3a5iB</a>	Alignment	not modelled	19.2	21	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar biosynthesis protein flha; <b>PDBTitle:</b> structure of the cytoplasmic domain of flha
42	<a href="#">d1ir1s</a>	Alignment	not modelled	18.4	45	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
43	<a href="#">d1gk8i</a>	Alignment	not modelled	17.8	45	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
44	<a href="#">d1bvua2</a>	Alignment	not modelled	17.3	13	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
45	<a href="#">c4qpiC</a>	Alignment	not modelled	16.9	21	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle response regulator ctra; <b>PDBTitle:</b> 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
46	<a href="#">d1jbea</a>	Alignment	not modelled	16.5	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
47	<a href="#">d2v6ai1</a>	Alignment	not modelled	15.7	45	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
48	<a href="#">c2h1oH</a>	Alignment	not modelled	15.3	18	<b>PDB header:</b> gene regulation/dna complex <b>Chain:</b> H: <b>PDB Molecule:</b> trafficking protein a; <b>PDBTitle:</b> structure of fitab bound to ir36 dna fragment
49	<a href="#">c3gl9B</a>	Alignment	not modelled	15.1	10	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
50	<a href="#">d1wdds</a>	Alignment	not modelled	14.9	35	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
51	<a href="#">c4d6yA</a>	Alignment	not modelled	14.8	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory, fis family protein; <b>PDBTitle:</b> crystal structure of the receiver domain of ntrx from2 brucella abortus in complex with beryll fluoride and3 magnesium
52	<a href="#">c4q7eA</a>	Alignment	not modelled	14.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator of a two component regulatory system; <b>PDBTitle:</b> non-phosphorylated hemr receiver domain from leptospira biflexa
53	<a href="#">d2a6aa2</a>	Alignment	not modelled	14.3	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> YeaZ-like

54	<a href="#">d1bkja_</a>	Alignment	not modelled	14.2	14	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
55	<a href="#">c5dc1B_</a>	Alignment	not modelled	14.1	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> phob family transcriptional regulator; <b>PDBTitle:</b> structure of a lantibiotic response regulator: n terminal domain of 2 the nisin resistance regulator nsrr
56	<a href="#">c3sboA_</a>	Alignment	not modelled	14.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> structure of e.coli gdh from native source
57	<a href="#">c4dadA_</a>	Alignment	not modelled	13.5	33	<b>PDB header:</b> signaling protein, signal transduction <b>Chain:</b> A: <b>PDB Molecule:</b> putative pilus assembly-related protein; <b>PDBTitle:</b> crystal structure of a putative pilus assembly-related protein2 (bps2195) from burkholderia pseudomallei k96243 at 2.50 a resolution3 (psi community target, shapiro l.)
58	<a href="#">d2r25b1</a>	Alignment	not modelled	13.4	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
59	<a href="#">c3hv2B_</a>	Alignment	not modelled	13.4	30	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator/hd domain protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
60	<a href="#">c5n5eM_</a>	Alignment	not modelled	13.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> pfc_05175; <b>PDBTitle:</b> crystal structure of encapsulated ferritin domain from pyrococcus2 furiosus pfc_05175
61	<a href="#">c2qv0A_</a>	Alignment	not modelled	13.2	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein mrke; <b>PDBTitle:</b> crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
62	<a href="#">c4xgiA_</a>	Alignment	not modelled	13.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
63	<a href="#">c3aogA_</a>	Alignment	not modelled	13.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
64	<a href="#">d1ej7s_</a>	Alignment	not modelled	13.1	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
65	<a href="#">d1uzdc1</a>	Alignment	not modelled	13.0	43	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
66	<a href="#">c2fhoA_</a>	Alignment	not modelled	12.8	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> spliceosomal protein sf3b155; <b>PDBTitle:</b> nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
67	<a href="#">d8ruc1</a>	Alignment	not modelled	12.7	45	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
68	<a href="#">c5hdjA_</a>	Alignment	not modelled	12.7	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nfra1; <b>PDBTitle:</b> structure of b. megaterium nfra1
69	<a href="#">c3aoeC_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
70	<a href="#">c2qxyB_</a>	Alignment	not modelled	12.6	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator from thermotoga2 maritima
71	<a href="#">c2f9jP_</a>	Alignment	not modelled	12.4	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> P: <b>PDB Molecule:</b> splicing factor 3b subunit 1; <b>PDBTitle:</b> 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
72	<a href="#">c5lwkB_</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> maer response regulator bound to beryllium trifluoride
73	<a href="#">d1zesa1</a>	Alignment	not modelled	12.2	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
74	<a href="#">c6cg8A_</a>	Alignment	not modelled	12.1	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> upf0335 protein b7z12_12435; <b>PDBTitle:</b> structure of c. crescentus gapr-dna
75	<a href="#">c3u8pB_</a>	Alignment	not modelled	12.1	11	<b>PDB header:</b> fluorescent protein, electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b562 integral fusion with enhanced green <b>PDBTitle:</b> cytochrome b562 integral fusion with egfp
76	<a href="#">c3n2sD_</a>	Alignment	not modelled	11.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadph-dependent nitro/flavin reductase; <b>PDBTitle:</b> structure of nfra1 nitroreductase from b. subtilis
77	<a href="#">c5tpjA_</a>	Alignment	not modelled	11.6	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> denovo ntf2; <b>PDBTitle:</b> crystal structure of a de novo designed protein with curved beta-sheet
78	<a href="#">d1zcha1</a>	Alignment	not modelled	11.4	19	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
79	<a href="#">c2nt3A_</a>	Alignment	not modelled	11.4	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator homolog; <b>PDBTitle:</b> receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
						<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> cpae2 pilus assembly protein;

80	<a href="#">c4myrD_</a>	Alignment	not modelled	11.4	22	<b>PDBTitle:</b> crystal structure of a putative cpae2 pilus assembly protein (cpae2)2 from sinorhizobium meliloti 1021 at 2.72 a resolution (psi community3 target, shapiro)
81	<a href="#">c2rjnA_</a>	Alignment	not modelled	11.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver:metal-dependent <b>PDBTitle:</b> crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
82	<a href="#">d1f5va_</a>	Alignment	not modelled	11.1	19	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
83	<a href="#">c3k8zD_</a>	Alignment	not modelled	11.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of gudb1 a decrypted secondary glutamate2 dehydrogenase from b. subtilis
84	<a href="#">c4qicC_</a>	Alignment	not modelled	10.9	11	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> sensory transduction regulatory protein, anti-anti-sigma <b>PDBTitle:</b> co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
85	<a href="#">c3crnA_</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
86	<a href="#">d1krwa_</a>	Alignment	not modelled	10.7	35	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
87	<a href="#">c3lteH_</a>	Alignment	not modelled	10.5	26	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
88	<a href="#">c5heiE_</a>	Alignment	not modelled	10.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nfra2; <b>PDBTitle:</b> structure of b. megaterium nfra2
89	<a href="#">c1bvuf_</a>	Alignment	not modelled	10.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> glutamate dehydrogenase from thermococcus litoralis
90	<a href="#">c4h60A_</a>	Alignment	not modelled	10.4	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chey; <b>PDBTitle:</b> high resolution structure of vibrio cholerae chemotaxis protein chey42 crystallized in low ph (4.0) condition
91	<a href="#">c3of4A_</a>	Alignment	not modelled	10.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
92	<a href="#">c5ocsB_</a>	Alignment	not modelled	10.4	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-depndent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
93	<a href="#">c3gkaB_</a>	Alignment	not modelled	10.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
94	<a href="#">c4b5nA_</a>	Alignment	not modelled	10.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
95	<a href="#">c3n0rA_</a>	Alignment	not modelled	10.0	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr stress response regulator at 1.25 angstrom2 resolution
96	<a href="#">c3to5A_</a>	Alignment	not modelled	9.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chey homolog; <b>PDBTitle:</b> high resolution structure of chey3 from vibrio cholerae
97	<a href="#">c4g97A_</a>	Alignment	not modelled	9.7	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of the response regulator phyr from brucella abortus
98	<a href="#">c1hrdA_</a>	Alignment	not modelled	9.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> glutamate dehydrogenase
99	<a href="#">c6fkib_</a>	Alignment	not modelled	9.5	9	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit beta, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3