



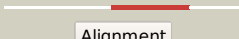



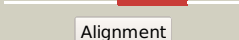



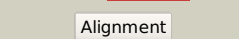

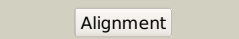

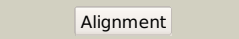









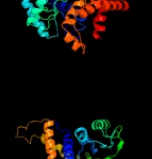
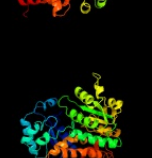
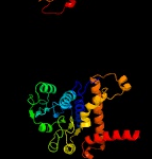

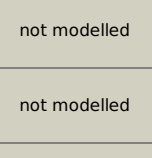


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2476c_(gdh)_2777398_2782272
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	06b9169357dad32c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1hrdA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> glutamate dehydrogenase
2	<a href="#">c3r3jC_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2
3	<a href="#">c1nr1A_</a>	 Alignment		100.0	23	<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
4	<a href="#">c2bmaA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase (nadp+); <b>PDBTitle:</b> the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
5	<a href="#">c2tmgD_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
6	<a href="#">c1bvuf_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> glutamate dehydrogenase from thermococcus litoralis
7	<a href="#">c5ijzH_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase(gdh) from corynebacterium2 glutamicum
8	<a href="#">c3aocC_</a>	 Alignment		100.0	21	<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)
9	<a href="#">c3sboA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> structure of e.colii gdh from native source
10	<a href="#">c4xgiA_</a>	 Alignment		100.0	23	<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
11	<a href="#">c2yfqA_</a>	 Alignment		100.0	23	<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

12	<a href="#">c1v9lA_</a>	Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
13	<a href="#">c3aogA_</a>	Alignment		100.0	21	<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)
14	<a href="#">c3k8zD_</a>	Alignment		100.0	23	<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 decryptified secondary glutamate2 dehydrogenase from b. subtilis
15	<a href="#">c5xviA_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of aspergillus niger apo- glutamate dehydrogenase
16	<a href="#">c1bxgA_</a>	Alignment		100.0	22	<b>PDB header:</b> amino acid dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine dehydrogenase; <b>PDBTitle:</b> phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
17	<a href="#">d1bvua1</a>	Alignment		100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
18	<a href="#">c1lehB_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> leucine dehydrogenase; <b>PDBTitle:</b> leucine dehydrogenase from bacillus sphaericus
19	<a href="#">d1b26a1</a>	Alignment		100.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
20	<a href="#">d1euza1</a>	Alignment		99.9	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
21	<a href="#">d1gtma1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
22	<a href="#">d1bgva1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
23	<a href="#">d1v9la1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
24	<a href="#">c5b37A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan dehydrogenase; <b>PDBTitle:</b> crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
25	<a href="#">d1hwxal</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
26	<a href="#">d1l1fa2</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
27	<a href="#">d1b26a2</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
28	<a href="#">d1bvua2</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate dehydrogenase 1,

29	<a href="#">c5k12F_</a>	Alignment	not modelled	99.1	21	mitochondrial; <b>PDBTitle:</b> cryo-em structure of glutamate dehydrogenase at 1.8 a resolution
30	<a href="#">d1v9la2</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
31	<a href="#">d1gtma2</a>	Alignment	not modelled	99.0	24	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
32	<a href="#">d1hwxa2</a>	Alignment	not modelled	98.7	24	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
33	<a href="#">d1euza2</a>	Alignment	not modelled	98.3	25	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
34	<a href="#">d1leha2</a>	Alignment	not modelled	98.3	24	<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="#">d1bgva2</a>	Alignment	not modelled	98.2	27	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
36	<a href="#">d1c1da2</a>	Alignment	not modelled	97.7	20	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
37	<a href="#">d1leha1</a>	Alignment	not modelled	97.2	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
38	<a href="#">d1c1da1</a>	Alignment	not modelled	96.7	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
39	<a href="#">d1vgya3</a>	Alignment	not modelled	82.2	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
40	<a href="#">d1bc9a_</a>	Alignment	not modelled	81.6	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
41	<a href="#">d1pbva_</a>	Alignment	not modelled	81.4	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
42	<a href="#">c2nyiB_</a>	Alignment	not modelled	79.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> unknown protein; <b>PDBTitle:</b> crystal structure of an unknown protein from galdieria sulphuraria
43	<a href="#">c4oivA_</a>	Alignment	not modelled	74.1	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec7; <b>PDBTitle:</b> crystal structure of sec7p catalytic domain
44	<a href="#">c5zz5D_</a>	Alignment	not modelled	73.1	22	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> redox-sensing transcriptional repressor rex
45	<a href="#">d1re0b_</a>	Alignment	not modelled	70.4	18	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
46	<a href="#">c1vgyA_</a>	Alignment	not modelled	67.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
47	<a href="#">c3wg9D_</a>	Alignment	not modelled	64.9	23	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of rsp, a rex-family repressor
48	<a href="#">c2r09A_</a>	Alignment	not modelled	64.3	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3; <b>PDBTitle:</b> crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor
49	<a href="#">c3w7bB_</a>	Alignment	not modelled	61.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
50	<a href="#">d1r8se_</a>	Alignment	not modelled	60.9	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
51	<a href="#">c3o1lB_</a>	Alignment	not modelled	60.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
52	<a href="#">c6bbqA_</a>	Alignment	not modelled	60.7	15	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3,adp-ribosylation factor 6; <b>PDBTitle:</b> model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
53	<a href="#">c3wz2C_</a>	Alignment	not modelled	58.2	13	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
54	<a href="#">d2aq0a1</a>	Alignment	not modelled	58.0	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
55	<a href="#">d1sc6a3</a>	Alignment	not modelled	52.1	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal)

						domain
56	<a href="#">d1jqoa_</a>	Alignment	not modelled	50.4	42	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate carboxylase
57	<a href="#">c1jqoA</a>	Alignment	not modelled	50.4	42	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxylase; <b>PDBTitle:</b> crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
58	<a href="#">d1xsza1</a>	Alignment	not modelled	50.2	20	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
59	<a href="#">c3n0vD</a>	Alignment	not modelled	48.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
60	<a href="#">d2bnma1</a>	Alignment	not modelled	48.2	60	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
61	<a href="#">d1m6ex_</a>	Alignment	not modelled	48.1	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Salicylic acid carboxyl methyltransferase (SAMT)
62	<a href="#">d2hsqa1</a>	Alignment	not modelled	46.9	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
63	<a href="#">d1ku1a_</a>	Alignment	not modelled	46.0	19	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
64	<a href="#">d3d37a1</a>	Alignment	not modelled	45.8	14	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
65	<a href="#">c2mdaB_</a>	Alignment	not modelled	45.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine 3-monooxygenase; <b>PDBTitle:</b> the solution structure of the regulatory domain of tyrosine2 hydroxylase
66	<a href="#">c2jpcA_</a>	Alignment	not modelled	44.0	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
67	<a href="#">d1jqna_</a>	Alignment	not modelled	43.9	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate carboxylase
68	<a href="#">c2uval_</a>	Alignment	not modelled	43.7	42	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> fatty acid synthase beta subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
69	<a href="#">d2r09a1</a>	Alignment	not modelled	42.7	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
70	<a href="#">d2g9wa1</a>	Alignment	not modelled	42.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
71	<a href="#">c2vkzH_</a>	Alignment	not modelled	42.2	33	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
72	<a href="#">c3nrbd_</a>	Alignment	not modelled	41.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
73	<a href="#">d1vqza2</a>	Alignment	not modelled	40.9	14	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> LpIA-like
74	<a href="#">c5nh1A_</a>	Alignment	not modelled	40.6	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gasdermin-d; <b>PDBTitle:</b> structure of the c-terminal domain of human gasdermin d
75	<a href="#">d1fiua_</a>	Alignment	not modelled	39.9	56	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease NgoIV
76	<a href="#">d1u8sa1</a>	Alignment	not modelled	39.6	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Glycine cleavage system transcriptional repressor
77	<a href="#">d1cjaa_</a>	Alignment	not modelled	39.3	30	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Actin-fragmin kinase, catalytic domain
78	<a href="#">c1irjA_</a>	Alignment	not modelled	38.8	27	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> exendin-4; <b>PDBTitle:</b> solution structure of exendin-4 in 30-vol% trifluoroethanol
79	<a href="#">c3qwqA_</a>	Alignment	not modelled	38.7	14	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> crystal structure of the extracellular domain of the epidermal growth2 factor receptor in complex with an adnectin
80	<a href="#">c2v9vA_</a>	Alignment	not modelled	37.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of moorella thermoacetica selb(377-511)
81	<a href="#">c2olvA_</a>	Alignment	not modelled	37.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> structural insight into the transglycosylation step of

						bacterial cell2 wall biosynthesis : donor ligand complex
82	<a href="#">d1x2ga2</a>	Alignment	not modelled	37.1	13	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> LplA-like
83	<a href="#">d1gpa3</a>	Alignment	not modelled	35.9	21	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
84	<a href="#">d1zpa1</a>	Alignment	not modelled	35.9	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> SPO238-like
85	<a href="#">c5hr4j</a>	Alignment	not modelled	35.6	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> J: <b>PDB Molecule:</b> mmei; <b>PDBTitle:</b> structure of type iii restriction-modification enzyme mmei in complex2 with dna has implications for engineering of new specificities
86	<a href="#">d2f06a1</a>	Alignment	not modelled	35.4	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> BT0572-like
87	<a href="#">c3ketA</a>	Alignment	not modelled	34.9	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
88	<a href="#">c1u8sB</a>	Alignment	not modelled	34.3	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional <b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor
89	<a href="#">d2a3ra1</a>	Alignment	not modelled	34.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
90	<a href="#">c3mn1B</a>	Alignment	not modelled	33.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable yrbi family phosphatase; <b>PDBTitle:</b> crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
91	<a href="#">c4ba6A</a>	Alignment	not modelled	33.7	20	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase cel5a; <b>PDBTitle:</b> high resolution structure of the c-terminal family 65 carbohydrate2 binding module (cbm65b) of endoglucanase cel5a from eubacterium3 cellulosolvans
92	<a href="#">c5xta</a>	Alignment	not modelled	33.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, mitochondrial; <b>PDBTitle:</b> structure of asymmetric apo/holo alas dimer from s. cerevisiae
93	<a href="#">c6ao3B</a>	Alignment	not modelled	32.9	18	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> gasdermin-d; <b>PDBTitle:</b> crystal structure of the murine gasdermin d c-terminal domain
94	<a href="#">d1qpza1</a>	Alignment	not modelled	32.3	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
95	<a href="#">c6hrhA</a>	Alignment	not modelled	32.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, erythroid-specific, <b>PDBTitle:</b> structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
96	<a href="#">d2bjca1</a>	Alignment	not modelled	32.0	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
97	<a href="#">c3obiC</a>	Alignment	not modelled	31.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
98	<a href="#">d2c8ma1</a>	Alignment	not modelled	31.2	22	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> LplA-like
99	<a href="#">d2qka1</a>	Alignment	not modelled	30.4	17	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Avirulence protein AvrPto <b>Family:</b> Avirulence protein AvrPto
100	<a href="#">c2qkwa</a>	Alignment	not modelled	30.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> structural basis for activation of plant immunity by2 bacterial effector protein avrpto
101	<a href="#">c3iacA</a>	Alignment	not modelled	30.2	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronate isomerase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
102	<a href="#">d1libx</a>	Alignment	not modelled	30.0	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> CAD domain
103	<a href="#">c1libB</a>	Alignment	not modelled	30.0	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> chimera of igg binding protein g and dna <b>PDBTitle:</b> nmr structure of df40 and df45 n-terminal domain complex
104	<a href="#">c4ifuA</a>	Alignment	not modelled	29.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
105	<a href="#">d1az5a</a>	Alignment	not modelled	29.1	17	<b>Fold:</b> Acid proteases <b>Superfamily:</b> Acid proteases <b>Family:</b> Retroviral protease (retropepsin)
						<b>PDB header:</b> hormone/growth factor receptor <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor;



106	<a href="#">c1nqlA_</a>	Alignment	not modelled	28.5	15	<b>PDBTitle:</b> structure of the extracellular domain of human epidermal growth factor2 (egf) receptor in an inactive (low ph) complex with egf.
107	<a href="#">c2qeua_</a>	Alignment	not modelled	28.4	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxymuconolactone decarboxylase; <b>PDBTitle:</b> crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
108	<a href="#">c1xsza_</a>	Alignment	not modelled	28.3	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> guanine nucleotide exchange protein; <b>PDBTitle:</b> the structure of ralf
109	<a href="#">d1f2ri_</a>	Alignment	not modelled	27.8	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> CAD domain
110	<a href="#">c3sztB_</a>	Alignment	not modelled	27.8	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
111	<a href="#">d2i53a2</a>	Alignment	not modelled	27.6	25	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
112	<a href="#">c3vr0D_</a>	Alignment	not modelled	27.5	17	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pbab, an archaeal proteasome2 activator
113	<a href="#">c1d0rA_</a>	Alignment	not modelled	27.4	33	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon-like peptide-1-(7-36)-amide; <b>PDBTitle:</b> solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
114	<a href="#">d1ytda1</a>	Alignment	not modelled	27.0	37	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
115	<a href="#">c1tkcA_</a>	Alignment	not modelled	26.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> specificity of coenzyme binding in thiamin diphosphate2 dependent enzymes: crystal structures of yeast3 transketolase in complex with analogs of thiamin4 diphosphate
116	<a href="#">d1r9ja3</a>	Alignment	not modelled	26.9	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
117	<a href="#">d1lefaa1</a>	Alignment	not modelled	26.9	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
118	<a href="#">c4hgnB_</a>	Alignment	not modelled	26.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
119	<a href="#">c3louB_</a>	Alignment	not modelled	26.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
120	<a href="#">c2jz8A_</a>	Alignment	not modelled	26.3	78	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bh09830; <b>PDBTitle:</b> solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55