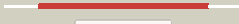
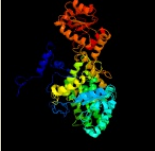

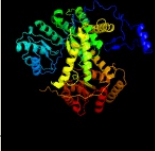
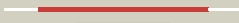
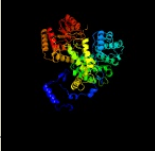

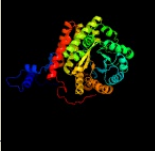

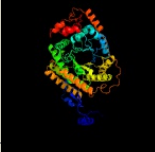

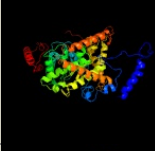
















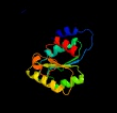




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1492_(mutA)_1682163_1684010
Date	Fri Aug 2 13:30:07 BST 2019
Unique Job ID	596e3fb852a29821

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6reqB_</a>	 Alignment		100.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> protein (methylmalonyl-coa mutase); <b>PDBTitle:</b> methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
2	<a href="#">c3bicA_</a>	 Alignment		100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> methylmalonyl-coa mutase, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa mutase
3	<a href="#">c1e1cA_</a>	 Alignment		100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
4	<a href="#">d7reqb1</a>	 Alignment		100.0	34	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
5	<a href="#">d7reqa1</a>	 Alignment		100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
6	<a href="#">c4r3uB_</a>	 Alignment		100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase large subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
7	<a href="#">c4xc8B_</a>	 Alignment		100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> isobutyryl-coa mutase fused; <b>PDBTitle:</b> isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
8	<a href="#">d7reqb2</a>	 Alignment		100.0	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
9	<a href="#">d7reqa2</a>	 Alignment		100.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
10	<a href="#">d1ccwa_</a>	 Alignment		99.2	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
11	<a href="#">d1xrsb1</a>	 Alignment		98.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain

12	<a href="#">c2yxbA</a>	Alignment		98.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
13	<a href="#">c1xrsB</a>	Alignment		98.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lysine 5,6-aminomutase beta subunit; <b>PDBTitle:</b> crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
14	<a href="#">d1fmfa</a>	Alignment		98.6	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
15	<a href="#">c1y80A</a>	Alignment		98.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
16	<a href="#">c4r3uD</a>	Alignment		98.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase small subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
17	<a href="#">c4jgiB</a>	Alignment		98.6	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
18	<a href="#">c1bmtB</a>	Alignment		98.5	13	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
19	<a href="#">d3bula2</a>	Alignment		98.5	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
20	<a href="#">c2i2xD</a>	Alignment		98.4	10	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> methyltransferase 1; <b>PDBTitle:</b> crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
21	<a href="#">c3ezxA</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monomethylamine corrinoid protein 1; <b>PDBTitle:</b> structure of methanosarcina barkeri monomethylamine2 corrinoid protein
22	<a href="#">c1k98A</a>	Alignment	not modelled	98.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> adomet complex of meth c-terminal fragment
23	<a href="#">c4hh3C</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> flavoprotein/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> structure of the appa-pps2 core complex from rb. sphaeroides
24	<a href="#">d1ccwb</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Glutamate mutase, large subunit
25	<a href="#">c3whpA</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
26	<a href="#">c5c8eC</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
27	<a href="#">c3nhzA</a>	Alignment	not modelled	94.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> two component system transcriptional regulator mtra; <b>PDBTitle:</b> structure of n-terminal domain of mtra
28	<a href="#">d1zesa1</a>	Alignment	not modelled	94.6	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related

29	<a href="#">d1ys7a2</a>	Alignment	not modelled	93.8	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
30	<a href="#">c2mswA_</a>	Alignment	not modelled	92.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/sensor histidine kinase; <b>PDBTitle:</b> ligand-induced folding of a receiver domain
31	<a href="#">c4hh0B_</a>	Alignment	not modelled	92.5	15	<b>PDB header:</b> flavoprotein,signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides
32	<a href="#">c1ys7B_</a>	Alignment	not modelled	91.2	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed2 with mg2+
33	<a href="#">c3ktoA_</a>	Alignment	not modelled	91.1	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
34	<a href="#">d1yioa2</a>	Alignment	not modelled	91.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
35	<a href="#">d1mvoa_</a>	Alignment	not modelled	90.5	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
36	<a href="#">c5iejA_</a>	Alignment	not modelled	89.5	18	<b>PDB header:</b> protein <b>Chain:</b> A: <b>PDB Molecule:</b> sdrG; <b>PDBTitle:</b> solution structure of the bef3-activated conformation of sdrG from2 pseudomonas melonis fr1
37	<a href="#">c3a0rB_</a>	Alignment	not modelled	89.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
38	<a href="#">d1krwa_</a>	Alignment	not modelled	88.4	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
39	<a href="#">c5tqjA_</a>	Alignment	not modelled	88.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 burkholderia phymatum
40	<a href="#">c2qzjC_</a>	Alignment	not modelled	86.4	12	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> crystal structure of a two-component response regulator from2 clostridium difficile
41	<a href="#">c6ifhA_</a>	Alignment	not modelled	85.8	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation initiation phosphotransferase f; <b>PDBTitle:</b> unphosphorylated spo0f from paenisporosarcina sp. tg-14
42	<a href="#">c1zn2A_</a>	Alignment	not modelled	85.3	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
43	<a href="#">d1xfha1</a>	Alignment	not modelled	84.6	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
44	<a href="#">c5e3jB_</a>	Alignment	not modelled	84.2	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator rsta; <b>PDBTitle:</b> the response regulator rsta is a potential drug target for2 acinetobacter baumannii
45	<a href="#">c2zayA_</a>	Alignment	not modelled	83.8	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator from desulfuromonas2 acetoxidans
46	<a href="#">c4qpiC_</a>	Alignment	not modelled	83.8	11	<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
47	<a href="#">c5yaaD_</a>	Alignment	not modelled	83.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> meiosis regulator and mrna stability factor 1; <b>PDBTitle:</b> crystal structure of marf1 nyn domain from mus musculus
48	<a href="#">d1wu7a1</a>	Alignment	not modelled	81.9	16	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
49	<a href="#">c5ulbA_</a>	Alignment	not modelled	81.8	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter; <b>PDBTitle:</b> crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
50	<a href="#">d2a9pa1</a>	Alignment	not modelled	81.5	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
51	<a href="#">d1zh2a1</a>	Alignment	not modelled	81.1	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
52	<a href="#">c5ajtA_</a>	Alignment	not modelled	80.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribohydrolase lonely guy; <b>PDBTitle:</b> crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea
53	<a href="#">c2h51B_</a>	Alignment	not modelled	80.0	29	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-1; <b>PDBTitle:</b> crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
54	<a href="#">c4b09F_</a>	Alignment	not modelled	79.6	9	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein baer; <b>PDBTitle:</b> structure of unphosphorylated baer dimer

55	<a href="#">c3r0jA_</a>	Alignment	not modelled	79.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> possible two component system response transcriptional <b>PDBTitle:</b> structure of phop from mycobacterium tuberculosis
56	<a href="#">c2c2zB_</a>	Alignment	not modelled	79.1	33	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-8 p10 subunit; <b>PDBTitle:</b> crystal structure of caspase-8 in complex with aza-peptide michael2 acceptor inhibitor
57	<a href="#">c5x5jA_</a>	Alignment	not modelled	79.1	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ader; <b>PDBTitle:</b> crystal structure of response regulator ader receiver domain
58	<a href="#">c3w9sB_</a>	Alignment	not modelled	78.8	11	<b>PDB header:</b> signaling protein/antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> ompr family response regulator in two-component regulatory <b>PDBTitle:</b> crystal structure analysis of the n-terminal receiver domain of2 response regulator pmra
59	<a href="#">c2c1eB_</a>	Alignment	not modelled	78.7	33	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-3 subunit p12; <b>PDBTitle:</b> crystal structures of caspase-3 in complex with aza-peptide michael2 acceptor inhibitors.
60	<a href="#">c3cfyA_</a>	Alignment	not modelled	78.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative luxo repressor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of putative luxo repressor2 protein from vibrio parahaemolyticus
61	<a href="#">c2jk1A_</a>	Alignment	not modelled	78.6	17	<b>PDB header:</b> dna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase transcriptional regulatory protein hupr1; <b>PDBTitle:</b> crystal structure of the wild-type hupr receiver domain
62	<a href="#">d1peya_</a>	Alignment	not modelled	78.4	5	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
63	<a href="#">c2zwmA_</a>	Alignment	not modelled	78.4	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein yycf; <b>PDBTitle:</b> crystal structure of yycf receiver domain from bacillus2 subtilis
64	<a href="#">c2qljB_</a>	Alignment	not modelled	76.6	38	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-7; <b>PDBTitle:</b> crystal structure of caspase-7 with inhibitor ac-wehd-cho
65	<a href="#">c3c3mA_</a>	Alignment	not modelled	76.5	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
66	<a href="#">c3hdgE_</a>	Alignment	not modelled	76.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolfinella3 succinogenes
67	<a href="#">c3jteA_</a>	Alignment	not modelled	75.6	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
68	<a href="#">c3snkA_</a>	Alignment	not modelled	75.1	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator chey-like protein; <b>PDBTitle:</b> crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
69	<a href="#">c5uicA_</a>	Alignment	not modelled	74.8	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> structure of the francisella response regulator receiver domain, qseb
70	<a href="#">c3f6cB_</a>	Alignment	not modelled	74.2	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
71	<a href="#">c2hqrA_</a>	Alignment	not modelled	73.3	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
72	<a href="#">d1ny5a1</a>	Alignment	not modelled	73.0	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
73	<a href="#">c4ldaF_</a>	Alignment	not modelled	71.9	20	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> tadz; <b>PDBTitle:</b> crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
74	<a href="#">c2qr3A_</a>	Alignment	not modelled	71.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
75	<a href="#">c5zbiA_</a>	Alignment	not modelled	71.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytokinin riboside 5'-monophosphate <b>PDBTitle:</b> crystal structure of type-i log from pseudomonas aeruginosa pao1
76	<a href="#">c3sipB_</a>	Alignment	not modelled	71.0	33	<b>PDB header:</b> hydrolase/ligase/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> caspase; <b>PDBTitle:</b> crystal structure of drice and diap1-bir1 complex
77	<a href="#">d1u0sy_</a>	Alignment	not modelled	70.6	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
78	<a href="#">c2qxyB_</a>	Alignment	not modelled	70.6	11	<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
79	<a href="#">c3p45F_</a>	Alignment	not modelled	70.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> caspase-6; <b>PDBTitle:</b> crystal structure of apo-caspase-6 at physiological ph

80	<a href="#">d3c1sc1</a>	Alignment	not modelled	69.9	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
81	<a href="#">c2q4oA</a>	Alignment	not modelled	69.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein at2g37210/t2n18.3; <b>PDBTitle:</b> ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
82	<a href="#">d2q4oa1</a>	Alignment	not modelled	69.7	22	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
83	<a href="#">c2p2cD</a>	Alignment	not modelled	69.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> caspase-2; <b>PDBTitle:</b> inhibition of caspase-2 by a designed ankyrin repeat protein (darpin)
84	<a href="#">c3hdvB</a>	Alignment	not modelled	69.2	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 pseudomonas putida
85	<a href="#">c5ow0B</a>	Alignment	not modelled	68.5	9	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein, beta subunit; <b>PDBTitle:</b> crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
86	<a href="#">c2nt3A</a>	Alignment	not modelled	67.8	14	<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)
87	<a href="#">c2lpmA</a>	Alignment	not modelled	67.1	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> chemical shift and structure assignments for sma0114
88	<a href="#">c4rweA</a>	Alignment	not modelled	67.0	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport protein; <b>PDBTitle:</b> the crystal structure of a sugar-binding transport protein from2 yersinia pestis co92
89	<a href="#">d1ydha</a>	Alignment	not modelled	66.6	20	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
90	<a href="#">d1x94a</a>	Alignment	not modelled	66.1	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
91	<a href="#">c2j48A</a>	Alignment	not modelled	65.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> two-component sensor kinase; <b>PDBTitle:</b> nmr structure of the pseudo-receiver domain of the cika protein.
92	<a href="#">d1t35a</a>	Alignment	not modelled	65.7	19	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
93	<a href="#">c4h60A</a>	Alignment	not modelled	65.6	18	<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
94	<a href="#">c3trjC</a>	Alignment	not modelled	65.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
95	<a href="#">c2qipA</a>	Alignment	not modelled	65.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function vpa0982; <b>PDBTitle:</b> crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
96	<a href="#">c3hv2B</a>	Alignment	not modelled	64.2	15	<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
97	<a href="#">d1qkka</a>	Alignment	not modelled	64.1	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
98	<a href="#">c3rqia</a>	Alignment	not modelled	64.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein; <b>PDBTitle:</b> crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
99	<a href="#">c3sbxC</a>	Alignment	not modelled	63.2	26	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
100	<a href="#">d1cmwa2</a>	Alignment	not modelled	63.2	14	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
101	<a href="#">d2d69a1</a>	Alignment	not modelled	62.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
102	<a href="#">c3grcD</a>	Alignment	not modelled	62.5	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sensor protein, kinase; <b>PDBTitle:</b> crystal structure of a sensor protein from polaromonas sp.2 js666
103	<a href="#">d1p6qa</a>	Alignment	not modelled	62.4	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
104	<a href="#">c5itsD</a>	Alignment	not modelled	62.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytokinin riboside 5'-monophosphate phosphoribohydrolase; <b>PDBTitle:</b> crystal structure of log from corynebacterium glutamicum

105	<a href="#">c4ggmX_</a>	 Alignment	not modelled	62.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine pyrophosphatase lpxi; <b>PDBTitle:</b> structure of lpxi
106	<a href="#">c2rjnA_</a>	 Alignment	not modelled	61.8	12	<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
107	<a href="#">c3gt7A_</a>	 Alignment	not modelled	61.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of signal transduction2 histidine kinase from syntrophus aciditrophicus
108	<a href="#">c3sirD_</a>	 Alignment	not modelled	60.9	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> caspase; <b>PDBTitle:</b> crystal structure of drice
109	<a href="#">d2ayxa1</a>	 Alignment	not modelled	60.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
110	<a href="#">c5e5nD_</a>	 Alignment	not modelled	60.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> polyketide synthase pks1; <b>PDBTitle:</b> ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
111	<a href="#">c2fp3A_</a>	 Alignment	not modelled	60.4	20	<b>PDB header:</b> hydrolysis/apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase nc; <b>PDBTitle:</b> crystal structure of the drosophila initiator caspase dronc
112	<a href="#">c4q7eA_</a>	 Alignment	not modelled	60.4	9	<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
113	<a href="#">c4d6yA_</a>	 Alignment	not modelled	60.2	11	<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
114	<a href="#">c5t3yA_</a>	 Alignment	not modelled	59.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> solution structure of response regulator protein from burkholderia2 multivorans
115	<a href="#">d1jx6a_</a>	 Alignment	not modelled	58.4	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
116	<a href="#">c3lteH_</a>	 Alignment	not modelled	57.8	12	<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
117	<a href="#">c3quaA_</a>	 Alignment	not modelled	57.5	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis
118	<a href="#">d1jbea_</a>	 Alignment	not modelled	56.8	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
119	<a href="#">c1ny5A_</a>	 Alignment	not modelled	56.3	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
120	<a href="#">d1qe0a1</a>	 Alignment	not modelled	55.5	15	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS