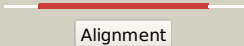

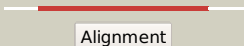

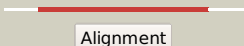







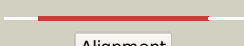


























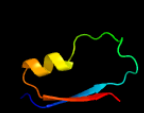
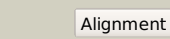
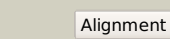


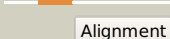

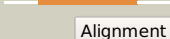



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1082_(mca)_1206525_1207391
Date	Wed Jul 31 22:05:16 BST 2019
Unique Job ID	6bd55910cda072d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1q7tA_</a>	 Alignment		100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv1170; <b>PDBTitle:</b> rv1170 (mshb) from mycobacterium tuberculosis
2	<a href="#">d1q74a_</a>	 Alignment		100.0	36	<b>Fold:</b> LmbE-like <b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like
3	<a href="#">c5cgzA_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-oxalmesaconate hydratase; <b>PDBTitle:</b> crystal structure of galb, the 4-carboxy-2-hydroxymuconate hydratase,2 from pseudomonas putida kt2440
4	<a href="#">c3we7A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0499; <b>PDBTitle:</b> crystal structure of diacetylchitobiose deacetylase from pyrococcus2 horikoshii
5	<a href="#">c3dfiA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pseudoaglycone deacetylase dbv21; <b>PDBTitle:</b> the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
6	<a href="#">c3dfmA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> teicoplanin pseudoaglycone deacetylase orf2; <b>PDBTitle:</b> the crystal structure of the zinc inhibited form of 2 teicoplanin deacetylase orf2
7	<a href="#">c2ixdB_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmbe-related protein; <b>PDBTitle:</b> crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
8	<a href="#">d1uana_</a>	 Alignment		100.0	30	<b>Fold:</b> LmbE-like <b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like
9	<a href="#">c5bmoB_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein lnmX; <b>PDBTitle:</b> lnmX protein, a putative glcnaC-pi de-n-acetylase from streptomyces2 atroolivaceus
10	<a href="#">c3ot5D_</a>	 Alignment		96.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
11	<a href="#">d1efva1</a>	 Alignment		94.2	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits

12	<a href="#">c3beoA</a>	 Alignment		94.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnac 2-epimerases
13	<a href="#">c1t9gR</a>	 Alignment		94.0	12	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit, <b>PDBTitle:</b> structure of the human mcad:etf complex
14	<a href="#">c4hwgA</a>	 Alignment		94.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
15	<a href="#">d1f0ka</a>	 Alignment		93.2	20	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
16	<a href="#">c1efvA</a>	 Alignment		92.9	12	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein; <b>PDBTitle:</b> three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
17	<a href="#">c3ih5A</a>	 Alignment		92.9	20	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
18	<a href="#">c3clrD</a>	 Alignment		92.2	22	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein subunit alpha; <b>PDBTitle:</b> crystal structure of the r236a etf mutant from m. methylotrophus
19	<a href="#">c4l2iA</a>	 Alignment		92.0	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
20	<a href="#">d1dxqa</a>	 Alignment		91.4	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
21	<a href="#">c1o94D</a>	 Alignment	not modelled	89.9	20	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
22	<a href="#">c4gj5B</a>	 Alignment	not modelled	89.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> quinone reductase; <b>PDBTitle:</b> crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
23	<a href="#">d3clsd1</a>	 Alignment	not modelled	88.6	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
24	<a href="#">d1qrdA</a>	 Alignment	not modelled	88.4	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
25	<a href="#">c5lvaA</a>	 Alignment	not modelled	88.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(p)h-fmn oxidoreductase; <b>PDBTitle:</b> crystal structure of thermophilic tryptophan halogenase (th-hal)2 enzyme from streptomycin violaceusniger.
26	<a href="#">c5ol2D</a>	 Alignment	not modelled	87.7	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein large subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
27	<a href="#">d3clsc1</a>	 Alignment	not modelled	87.6	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
28	<a href="#">d1d4aa</a>	 Alignment	not modelled	86.5	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase

29	<a href="#">c5w8sA</a>	Alignment	not modelled	85.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipid-a-disaccharide synthase; <b>PDBTitle:</b> lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
30	<a href="#">c6fahE</a>	Alignment	not modelled	84.8	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit care; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
31	<a href="#">c2jmh</a>	Alignment	not modelled	84.5	13	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
32	<a href="#">d2qwx1</a>	Alignment	not modelled	84.2	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
33	<a href="#">c5ol2E</a>	Alignment	not modelled	83.5	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
34	<a href="#">c4nesA</a>	Alignment	not modelled	83.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii udp-glcna2 epimerase in complex with udp-glcna2 and udp
35	<a href="#">d1a2oa1</a>	Alignment	not modelled	83.1	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
36	<a href="#">c3ha2B</a>	Alignment	not modelled	82.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh-quinone reductase; <b>PDBTitle:</b> crystal structure of protein (nadh-quinone reductase) from2 p.pentoseaceus, northeast structural genomics consortium target ptr24a
37	<a href="#">d1o94c</a>	Alignment	not modelled	80.5	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
38	<a href="#">c4leiB</a>	Alignment	not modelled	80.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ndp-forosamyltransferase; <b>PDBTitle:</b> spinosyn forosaminyltransferase spnp
39	<a href="#">c3dqqB</a>	Alignment	not modelled	79.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative trna synthase; <b>PDBTitle:</b> the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
40	<a href="#">c4r81C</a>	Alignment	not modelled	78.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
41	<a href="#">d1efpb</a>	Alignment	not modelled	76.2	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
42	<a href="#">c3s2uA</a>	Alignment	not modelled	75.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) <b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
43	<a href="#">d1rrva</a>	Alignment	not modelled	75.0	19	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
44	<a href="#">c3qi7A</a>	Alignment	not modelled	73.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
45	<a href="#">c3eywA</a>	Alignment	not modelled	71.4	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
46	<a href="#">c2gejA</a>	Alignment	not modelled	70.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima); <b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
47	<a href="#">c3f2vA</a>	Alignment	not modelled	68.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 14; <b>PDBTitle:</b> crystal structure of the general stress protein 14 (tde0354) in2 complex with fnm from treponema denticola, northeast structural3 genomics consortium target tdr58.
48	<a href="#">c6fahB</a>	Alignment	not modelled	67.2	22	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit card; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
49	<a href="#">c6gneB</a>	Alignment	not modelled	65.5	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable starch synthase 4, chloroplastic/amyloplastic; <b>PDBTitle:</b> catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose
50	<a href="#">c3iaaB</a>	Alignment	not modelled	65.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
51	<a href="#">c4xgjA</a>	Alignment	not modelled	65.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a domain of unknown function (duf1537) from2 pectobacterium atrosepticum (eca3761), target efi-511609, apo3 structure, domain swapped dimer <b>PDB header:</b> hydrolase

52	<a href="#">c3iuuA_</a>	Alignment	not modelled	63.1	13	<b>Chain:</b> A: <b>PDB Molecule:</b> putative metallopeptidase; <b>PDBTitle:</b> crystal structure of putative metallopeptidase (yp_676511.1) from2 mesorhizobium sp. bnc1 at 2.13 a resolution
53	<a href="#">c3tsaA_</a>	Alignment	not modelled	62.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ndp-rhamnosyltransferase; <b>PDBTitle:</b> spinosyn rhamnosyltransferase spng
54	<a href="#">d1o6ca_</a>	Alignment	not modelled	62.8	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
55	<a href="#">c5du2B_</a>	Alignment	not modelled	61.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> espg2 glycosyltransferase; <b>PDBTitle:</b> structural analysis of espg2 glycosyltransferase
56	<a href="#">c4ambB_</a>	Alignment	not modelled	60.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> snogd; <b>PDBTitle:</b> crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater
57	<a href="#">c4rieB_</a>	Alignment	not modelled	60.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase homolog; <b>PDBTitle:</b> landomycin glycosyltransferase langt2
58	<a href="#">c4kpuB_</a>	Alignment	not modelled	58.7	19	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
59	<a href="#">c5gl5B_</a>	Alignment	not modelled	55.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sterol 3-beta-glucosyltransferase; <b>PDBTitle:</b> sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex
60	<a href="#">d2ji7a3</a>	Alignment	not modelled	55.3	14	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
61	<a href="#">c3dzcA_</a>	Alignment	not modelled	54.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
62	<a href="#">c2r60A_</a>	Alignment	not modelled	53.3	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1; <b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
63	<a href="#">d1t9ba3</a>	Alignment	not modelled	52.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
64	<a href="#">c3c4vB_</a>	Alignment	not modelled	51.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
65	<a href="#">c4xcwF_</a>	Alignment	not modelled	51.8	16	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> molybdopterin adenylyltransferase; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
66	<a href="#">c3wadA_</a>	Alignment	not modelled	51.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicanistatin
67	<a href="#">c3wrbB_</a>	Alignment	not modelled	51.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gallate dioxygenase; <b>PDBTitle:</b> crystal structure of the anaerobic h124f desb-gallate complex
68	<a href="#">d1mkza_</a>	Alignment	not modelled	50.9	13	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
69	<a href="#">c6gngB_</a>	Alignment	not modelled	49.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> granule-bound starch synthase; <b>PDBTitle:</b> granule bound starch synthase i from cyanophora paradoxa bound to2 acarbose and adp
70	<a href="#">c1t9dB_</a>	Alignment	not modelled	49.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonyleurea herbicide, metsulfuron methyl
71	<a href="#">c2p6pB_</a>	Alignment	not modelled	48.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
72	<a href="#">c3fh0A_</a>	Alignment	not modelled	48.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative universal stress protein kpn_01444; <b>PDBTitle:</b> crystal structure of putative universal stress protein kpn_01444 -2 atpase
73	<a href="#">c3ia7A_</a>	Alignment	not modelled	47.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
74	<a href="#">c2q27B_</a>	Alignment	not modelled	46.1	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> crystal structure of oxalyl-coa decarboxylase from escherichia coli
75	<a href="#">c1a2oB_</a>	Alignment	not modelled	45.7	17	<b>PDB header:</b> bacterial chemotaxis <b>Chain:</b> B: <b>PDB Molecule:</b> cheb methylesterase; <b>PDBTitle:</b> structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
76	<a href="#">d1k68a_</a>	Alignment	not modelled	45.6	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>PDB header:</b> hydrolase

77	<a href="#">c5zmpA_</a>	Alignment	not modelled	44.7	17	<b>Chain:</b> A: <b>PDB Molecule:</b> lysine deacylase; <b>PDBTitle:</b> the structure of a lysine deacylase
78	<a href="#">d1efvb_</a>	Alignment	not modelled	44.2	9	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
79	<a href="#">c6oecD_</a>	Alignment	not modelled	44.1	12	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> response regulator/sensory box protein/ggdef domain <b>PDBTitle:</b> yeast spc42 trimeric coiled-coil amino acids 181-211 fused to pdb:2 3h5i
80	<a href="#">c3l7nA_</a>	Alignment	not modelled	43.4	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1228c
81	<a href="#">d1y5ea1</a>	Alignment	not modelled	43.3	23	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
82	<a href="#">c3hebB_</a>	Alignment	not modelled	42.9	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver domain protein (chey); <b>PDBTitle:</b> crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
83	<a href="#">c3lcmB_</a>	Alignment	not modelled	41.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159
84	<a href="#">c5ahkB_</a>	Alignment	not modelled	41.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase ii, large subunit; <b>PDBTitle:</b> crystal structure of acetoxyhydroxy acid synthase pf5 from2 pseudomonas protegens
85	<a href="#">c2iyaB_</a>	Alignment	not modelled	39.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
86	<a href="#">d1zpdA3</a>	Alignment	not modelled	38.8	11	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
87	<a href="#">c2xmpB_</a>	Alignment	not modelled	38.4	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
88	<a href="#">d1efpa1</a>	Alignment	not modelled	38.1	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
89	<a href="#">c3maxB_</a>	Alignment	not modelled	37.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histone deacetylase 2; <b>PDBTitle:</b> crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
90	<a href="#">c2qvgA_</a>	Alignment	not modelled	37.3	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> the crystal structure of a two-component response regulator2 from legionella pneumophila
91	<a href="#">c3okaA_</a>	Alignment	not modelled	36.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
92	<a href="#">c5enzA_</a>	Alignment	not modelled	36.5	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glcnaC 2-epimerase; <b>PDBTitle:</b> s. aureus mnaa-udp co-structure
93	<a href="#">c2q9uB_</a>	Alignment	not modelled	35.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> a-type flavoprotein; <b>PDBTitle:</b> crystal structure of the flavodiiron protein from giardia2 intestinalis
94	<a href="#">c4a69A_</a>	Alignment	not modelled	35.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 3,; <b>PDBTitle:</b> structure of hdac3 bound to corepressor and inositol tetraphosphate
95	<a href="#">c3f6cB_</a>	Alignment	not modelled	35.7	19	<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
96	<a href="#">d1c3pa_</a>	Alignment	not modelled	35.7	24	<b>Fold:</b> Arginase/deacetylase <b>Superfamily:</b> Arginase/deacetylase <b>Family:</b> Histone deacetylase, HDAC
97	<a href="#">c5li3A_</a>	Alignment	not modelled	34.1	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> acetoin utilization protein; <b>PDBTitle:</b> crystal structure of hdac-like protein from p. aeruginosa in complex2 with a photo-switchable inhibitor.
98	<a href="#">c5ji5A_</a>	Alignment	not modelled	34.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bupha.10154.a.b1; <b>PDBTitle:</b> crystal structure of a histone deacetylase superfamily protein from2 burkholderia phymatumphymatum
99	<a href="#">c3rfqC_</a>	Alignment	not modelled	33.5	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
100	<a href="#">c5dmhA_</a>	Alignment	not modelled	33.3	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein conserved in bacteria; <b>PDBTitle:</b> crystal structure of a domain of unknown function (duf1537) from2 ralstonia eutropha h16 (h16_a1561), target efi-511666, complex with3 adp.
101	<a href="#">d1f6da_</a>	Alignment	not modelled	32.8	20	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
						<b>Fold:</b> PreATP-grasp domain

102	<a href="#">d1a9xa3</a>	Alignment	not modelled	32.4	14	<b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
103	<a href="#">d1u9ca</a>	Alignment	not modelled	31.4	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
104	<a href="#">c5okiA</a>	Alignment	not modelled	31.2	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> crystal structure of the ctf18-1-8 module from ctf18-rfc in complex2 with a 63 kda fragment of dna polymerase epsilon
105	<a href="#">c6gnfC</a>	Alignment	not modelled	30.8	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
106	<a href="#">c3vufA</a>	Alignment	not modelled	30.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> granule-bound starch synthase 1, <b>PDBTitle:</b> crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
107	<a href="#">d1t64a</a>	Alignment	not modelled	30.4	15	<b>Fold:</b> Arginase/deacetylase <b>Superfamily:</b> Arginase/deacetylase <b>Family:</b> Histone deacetylase, HDAC
108	<a href="#">c1zz0C</a>	Alignment	not modelled	30.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> histone deacetylase-like amidohydrolase; <b>PDBTitle:</b> crystal structure of a hdac-like protein with acetate bound
109	<a href="#">c4k9qB</a>	Alignment	not modelled	30.1	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoylformate decarboxylase; <b>PDBTitle:</b> the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
110	<a href="#">c4bz7A</a>	Alignment	not modelled	29.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 8; <b>PDBTitle:</b> crystal structure of schistosoma mansoni hdac8 complexed with m344
111	<a href="#">c2qq1A</a>	Alignment	not modelled	29.4	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis mog; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
112	<a href="#">d1noya</a>	Alignment	not modelled	29.3	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
113	<a href="#">d1jja</a>	Alignment	not modelled	29.3	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
114	<a href="#">c4r3uD</a>	Alignment	not modelled	29.3	15	<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
115	<a href="#">c6hunA</a>	Alignment	not modelled	29.1	27	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase; <b>PDBTitle:</b> dimeric archeal rubisco from hyperthermus butylicus
116	<a href="#">c1rldB</a>	Alignment	not modelled	29.0	17	<b>PDB header:</b> lyase(carbon-carbon) <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose 1,5 bisphosphate carboxylase/oxygenase (large) <b>PDBTitle:</b> solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
117	<a href="#">d1o1ya</a>	Alignment	not modelled	28.8	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
118	<a href="#">d2ez9a3</a>	Alignment	not modelled	28.6	16	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase PP module
119	<a href="#">d1wn7a1</a>	Alignment	not modelled	28.5	29	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
120	<a href="#">c3ew8A</a>	Alignment	not modelled	28.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 8; <b>PDBTitle:</b> crystal structure analysis of human hdac8 d101l variant