

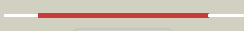
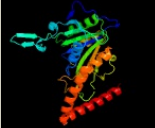


















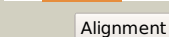




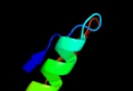
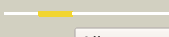
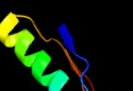

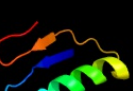



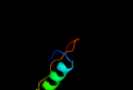





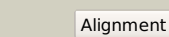








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2714 (-)_3027075_3028049
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	791095a965a5d199

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wamB_	 Alignment		100.0	99	PDB header: unknown function Chain: B; PDB Molecule: conserved hypothetical alanine and leucine rich PDBTitle: crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
2	c2p90B_	 Alignment		100.0	47	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein cgl1923; PDBTitle: the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
3	d2p90a1	 Alignment		100.0	45	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
4	c3e35A_	 Alignment		100.0	40	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein sco1997; PDBTitle: actinobacteria-specific protein of unknown function, sco1997
5	c5un02_	 Alignment		100.0	26	PDB header: apoptosis Chain: 2; PDB Molecule: proteasome assembly chaperone 2 (pac2) homologue rv2125; PDB Fragment: unp residues 17-260; PDBTitle: crystal structure of mycobacterium tuberculosis proteasome-assembly2 chaperone homologue rv2125
6	c3mnfA_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pac2 family protein; PDBTitle: crystal structure of pac2 family protein from streptomyces avermitilis2 ma
7	c3vr0D_	 Alignment		100.0	18	PDB header: protein binding Chain: D; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbab, an archaeal proteasome2 activator
8	c3gaaB_	 Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein ta1441; PDBTitle: the crystal structure of the protein with unknown function from2 thermoplasma acidophilum
9	c3wz2C_	 Alignment		100.0	13	PDB header: chaperone Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
10	c4g4sP_	 Alignment		96.9	14	PDB header: hydrolase/chaperone Chain: P; PDB Molecule: proteasome assembly chaperone 2; PDBTitle: structure of proteasome-pba1-pba2 complex
11	c2p6pB_	 Alignment		88.9	11	PDB header: transferase Chain: B; PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2

12	c3khsB	 Alignment		83.9	17	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
13	d1b26a1	 Alignment		77.9	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
14	c1bvuf	 Alignment		77.9	20	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
15	d1gtma1	 Alignment		77.2	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
16	c2tmgD	 Alignment		74.4	26	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
17	d1bvua1	 Alignment		72.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
18	d1leua1	 Alignment		71.6	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
19	d1b5ta	 Alignment		70.1	15	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Methylenetetrahydrofolate reductase
20	d2dsta1	 Alignment		65.5	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: TTHA1544-like
21	c2fmoA	 Alignment	not modelled	65.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate reductase; PDBTitle: ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
22	d1hwxa1	 Alignment	not modelled	61.8	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
23	c2h04A	 Alignment	not modelled	58.9	28	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase, receptor type, b,; PDBTitle: structural studies of protein tyrosine phosphatase beta catalytic2 domain in complex with inhibitors
24	c5jvsA	 Alignment	not modelled	58.1	23	PDB header: motor protein Chain: A: PDB Molecule: chimera protein of kinesin heavy chain and microtubule- PDBTitle: the neck-linker + dal and alpha 7 helix of drosophila melanogaster2 kinesin-1 fused to eb1
25	d1l8ka	 Alignment	not modelled	56.9	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
26	c1l8ka	 Alignment	not modelled	56.9	17	PDB header: hydrolase Chain: A: PDB Molecule: t-cell protein-tyrosine phosphatase; PDBTitle: t cell protein-tyrosine phosphatase structure
27	c4lxgA	 Alignment	not modelled	56.4	19	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
28	c5n6vE	 Alignment	not modelled	54.8	16	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrogenase vanadium-iron protein beta

28	c1bryL	Alignment	not modelled	54.8	10	chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
29	c2dt5A	Alignment	not modelled	54.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
30	d1bgva1	Alignment	not modelled	52.7	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
31	c3fkkA	Alignment	not modelled	52.3	11	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
32	c1cr6A	Alignment	not modelled	52.1	24	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
33	c3aogA	Alignment	not modelled	51.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
34	c3r3jC	Alignment	not modelled	50.5	12	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2
35	c3s3fA	Alignment	not modelled	49.6	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: tyrosine-protein phosphatase 10d; PDBTitle: crystal structure of the catalytic domain of ptp10d from drosophila2 melanogaster with a small molecule inhibitor vanadate
36	c5sxyA	Alignment	not modelled	49.5	27	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
37	c1v9lA	Alignment	not modelled	49.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
38	c3i28A	Alignment	not modelled	49.4	24	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
39	d1f74a	Alignment	not modelled	49.3	7	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	c5du2B	Alignment	not modelled	48.8	12	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
41	c2p4sA	Alignment	not modelled	48.2	15	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
42	c5xviA	Alignment	not modelled	47.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of aspergillus niger apo- glutamate dehydrogenase
43	c3lerA	Alignment	not modelled	47.1	10	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
44	c3iaaB	Alignment	not modelled	47.1	11	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
45	c3sboA	Alignment	not modelled	46.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: structure of e.coli gdh from native source
46	d1o5ka	Alignment	not modelled	45.9	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
47	c1hrdA	Alignment	not modelled	45.9	32	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase
48	c5ijzH	Alignment	not modelled	45.5	15	PDB header: oxidoreductase Chain: H: PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase(gdh) from corynebacterium2 glutamicum
49	c4n4qD	Alignment	not modelled	45.2	10	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
50	c1yn9B	Alignment	not modelled	44.6	19	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
51	c1u2eA	Alignment	not modelled	44.3	21	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketonona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
52	c4kyrA	Alignment	not modelled	44.2	33	PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase lsf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
53	c1nr1A	Alignment	not modelled	44.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate dehydrogenase PDB header: hydrolase

54	c3r3xA_	Alignment	not modelled	43.5	22	Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
55	c2bz1A_	Alignment	not modelled	43.2	20	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase, non-receptor type 14; PDBTitle: crystal structure of the human protein tyrosine phosphatase n14 at 1.2 65 a resolution
56	c4icnB_	Alignment	not modelled	42.9	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
57	c4axvA_	Alignment	not modelled	42.9	14	PDB header: hydrolase Chain: A: PDB Molecule: mpaa; PDBTitle: biochemical and structural characterization of the mpaa2 amidase as part of a conserved scavenging pathway for3 peptidoglycan derived peptides in gamma-proteobacteria
58	d1v91a1	Alignment	not modelled	42.5	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
59	c4xgiA_	Alignment	not modelled	42.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
60	c2c7sA_	Alignment	not modelled	42.4	23	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase kappa; PDBTitle: crystal structure of human protein tyrosine phosphatase kappa at 1.95a2 resolution
61	c4d9j1_	Alignment	not modelled	42.2	32	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
62	c4i19A_	Alignment	not modelled	41.6	34	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
63	c3tqkA_	Alignment	not modelled	41.5	13	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
64	c5kojD_	Alignment	not modelled	41.4	15	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase femo beta subunit protein nifk; PDBTitle: nitrogenase mofep protein in the ids oxidized state
65	c3u7vA_	Alignment	not modelled	41.2	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
66	c3k7dA_	Alignment	not modelled	40.0	14	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenyllyltransferase; PDBTitle: c-terminal (adenylylation) domain of e.coli glutamine synthetase2 adenyllyltransferase
67	d1larb1	Alignment	not modelled	39.9	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
68	d1ohea2	Alignment	not modelled	39.9	23	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
69	c2bmaA_	Alignment	not modelled	39.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
70	c3aoeC_	Alignment	not modelled	39.2	21	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
71	c3d0cB_	Alignment	not modelled	39.2	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
72	c5bovD_	Alignment	not modelled	38.8	18	PDB header: hydrolase Chain: D: PDB Molecule: putative epoxide hydrolase protein; PDBTitle: crystal structure of a putative epoxide hydrolase (kpn_01808) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.60 a3 resolution
73	d1rpma_	Alignment	not modelled	38.7	26	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
74	c2khzB_	Alignment	not modelled	38.4	8	PDB header: nuclear protein Chain: B: PDB Molecule: c-myc-responsive protein rcl; PDBTitle: solution structure of rcl
75	c2jjdA_	Alignment	not modelled	37.9	23	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase epsilon; PDBTitle: protein tyrosine phosphatase, receptor type, e isoform
76	c5xw4A_	Alignment	not modelled	37.4	29	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
77	c1tcb_	Alignment	not modelled	37.3	9	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate

78	c1oheA	Alignment	not modelled	37.2	23	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
79	c4az1B	Alignment	not modelled	36.8	25	PDB header: hydrolase Chain: B: PDB Molecule: tyrosine specific protein phosphatase; PDBTitle: crystal structure of the trypanosoma cruzi protein tyrosine2 phosphatase tcptp1, a potential therapeutic target for chagas'3 disease
80	d1n8fa	Alignment	not modelled	36.6	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
81	d1i9sa	Alignment	not modelled	36.6	27	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
82	d1lara1	Alignment	not modelled	36.6	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
83	c3n2xB	Alignment	not modelled	36.5	16	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
84	d1a3xa3	Alignment	not modelled	36.5	13	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
85	d1h72c1	Alignment	not modelled	35.9	12	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
86	c3fobA	Alignment	not modelled	35.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
87	c5hxdB	Alignment	not modelled	35.7	16	PDB header: hydrolase Chain: B: PDB Molecule: protein mpaa; PDBTitle: crystal structure of murein-tripeptide amidase mpaa from escherichia2 coli o157
88	c3u9iA	Alignment	not modelled	35.6	8	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme, c-terminal PDBTitle: the crystal structure of mandelate racemase/muconate lactonizing2 enzyme from roseiflexus sp.
89	c2g59B	Alignment	not modelled	35.2	20	PDB header: hydrolase Chain: B: PDB Molecule: receptor-type tyrosine-protein phosphatase o; PDBTitle: crystal structure of the catalytic domain of protein2 tyrosine phosphatase from homo sapiens
90	d1s4ea1	Alignment	not modelled	35.1	15	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
91	c5f4zB	Alignment	not modelled	35.1	32	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
92	c5egnB	Alignment	not modelled	34.8	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
93	c5ud6B	Alignment	not modelled	34.7	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound
94	c3sr9A	Alignment	not modelled	34.5	23	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase s; PDBTitle: crystal structure of mouse ptpsigma
95	c5jp6A	Alignment	not modelled	34.3	12	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
96	c1jpmB	Alignment	not modelled	34.0	17	PDB header: isomerase Chain: B: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
97	c4ah7C	Alignment	not modelled	34.0	7	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: structure of wild type stapylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
98	c3wg9D	Alignment	not modelled	33.6	18	PDB header: transcription Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of rsp, a rex-family repressor
99	c2c46B	Alignment	not modelled	33.1	27	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
100	c2nz6A	Alignment	not modelled	33.0	31	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase eta; PDBTitle: crystal structure of the ptprr inactivating mutant c1239s
101	d1wota	Alignment	not modelled	32.9	23	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
102	d1yfoa	Alignment	not modelled	32.4	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
103	c3dz1A	Alignment	not modelled	32.2	12	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase;

103	c9uz1A_	Alignment	not modelled	32.2	12	PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Rhodospirillum rubrum</i> at 1.87 Å resolution PDB header: lyase
104	c3e96B_	Alignment	not modelled	32.0	9	Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Bacillus subtilis</i>
105	c5b3fB_	Alignment	not modelled	31.6	22	PDB header: transferase Chain: B; PDB Molecule: phosphoribulokinase/uridine kinase; PDBTitle: crystal structure of phosphoribulokinase from <i>Methanospirillum hungatei</i>
106	c3k8zD_	Alignment	not modelled	31.1	21	PDB header: oxidoreductase Chain: D; PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudB1 a deacylated secondary glutamate dehydrogenase from <i>B. subtilis</i>
107	c4nyhB_	Alignment	not modelled	30.4	17	PDB header: hydrolase Chain: B; PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
108	c2rfgB_	Alignment	not modelled	30.3	9	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Hahella chejuensis</i> at 1.5 Å resolution
109	d1p15a_	Alignment	not modelled	30.2	27	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
110	d1xxxa1	Alignment	not modelled	30.2	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
111	c3tj1A_	Alignment	not modelled	30.1	14	PDB header: lyase Chain: A; PDB Molecule: mandelate racemase/muconate lactonizing enzyme, n-terminal PDBTitle: crystal structure of an enolase from <i>Enterobacter</i> sp. 638 (efi target2 efi-501662) with bound mg
112	c4ur7B_	Alignment	not modelled	30.1	5	PDB header: lyase Chain: B; PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
113	c6c6gA_	Alignment	not modelled	29.8	13	PDB header: transferase Chain: A; PDB Molecule: d-glycerate 3-kinase; PDBTitle: d-glycerate 3-kinase from <i>Cryptococcus neoformans</i> var. <i>grubii</i> serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
114	d1hkha_	Alignment	not modelled	29.7	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
115	c2m3vA_	Alignment	not modelled	29.5	25	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from <i>Pseudomonas aeruginosa</i>
116	c30thB_	Alignment	not modelled	29.4	12	PDB header: transferase/antibiotic Chain: B; PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
117	c5cxsA_	Alignment	not modelled	29.2	13	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
118	c4xkyC_	Alignment	not modelled	29.2	17	PDB header: lyase Chain: C; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium <i>Bacteroides thetaiotaomicron</i> at 2.1 Å resolution
119	c3wibB_	Alignment	not modelled	29.2	15	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from <i>Agrobacterium tumefaciens</i> c58
120	d1mkpa_	Alignment	not modelled	29.2	29	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like