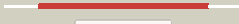



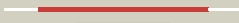






















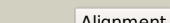







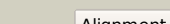






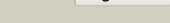

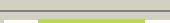

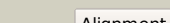
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2234_(ptpA)_2507154_2507645
Date	Mon Aug 5 13:25:36 BST 2019
Unique Job ID	8933f758b15a83e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u2pA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
2	c3jviA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase; PDBTitle: product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
3	d1dg9a_	 Alignment		100.0	36	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
4	d1d1qa_	 Alignment		100.0	32	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
5	d5pnta_	 Alignment		100.0	33	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
6	c2cwaA_	 Alignment		100.0	45	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine protein phosphatase; PDBTitle: crystal structure of tt1001 protein from thermus thermophilus hb8
7	c2qi4A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: possible phosphotyrosine protein phosphatase; PDBTitle: solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
8	c5z3mB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of low molecular weight phosphotyrosine phosphatase2 (vc1mwptp-2) from vibrio choleraeo395
9	c4etmB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: low molecular weight protein-tyrosine-phosphatase yfkj; PDBTitle: crystal structure of yfkj from bacillus subtilis
10	c4lrqC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of a low molecular weight phosphotyrosine2 phosphatase from vibrio choleraeo395
11	c3rofA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ptpa; PDBTitle: crystal structure of the s. aureus protein tyrosine phosphatase ptpa

12	c4etiA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ywle; PDBTitle: crystal structure of ywle from bacillus subtilis
13	c4picA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: arginine phosphatase ywle; PDBTitle: ywle arginine phosphatase from geobacillus stearothermophilus
14	c1zggA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
15	d1p8aa_	Alignment		100.0	29	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
16	c2fekA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
17	c4d74A_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase amsi; PDBTitle: 1.57 a crystal structure of erwinia amylovora tyrosine phosphatase2 amsi
18	c2wmyH_	Alignment		100.0	28	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
19	c4egsB_	Alignment		100.0	31	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase rpib; PDBTitle: crystal structure analysis of low molecular weight protein tyrosine2 phosphatase from t. tengcongensis
20	c5gotA_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine phosphatase family PDBTitle: crystal structure of sp-ptp, low molecular weight protein tyrosine2 phosphatase from streptococcus pyogenes
21	d1jf8a_	Alignment	not modelled	100.0	26	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
22	c2l18A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: an arsenate reductase in the phosphate binding state
23	c3rh0A_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
24	d1jl3a_	Alignment	not modelled	100.0	29	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
25	d1y11a_	Alignment	not modelled	100.0	25	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
26	c5o7bA_	Alignment	not modelled	100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine-phosphatase PDBTitle: crystal structure of the slr0328 tyrosine phosphatase wzb from2 synechocystis sp. pcc 6803
27	c3t38B_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
28	c3fdfA_	Alignment	not modelled	97.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fr253; PDBTitle: crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3

						melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
29	c3o2sB_	 Alignment	not modelled	96.6	24	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72 complex
30	c3o2qB_	 Alignment	not modelled	95.9	25	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
31	d1fmta2	 Alignment	not modelled	93.7	22	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
32	c5abrB_	 Alignment	not modelled	90.8	34	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin, 2fe-2s; PDBTitle: structure of fesi protein from azotobacter vinelandii
33	c1tvmA_	 Alignment	not modelled	90.7	12	PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
34	c1vkrA_	 Alignment	not modelled	88.8	19	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iibc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii
35	d1vkra_	 Alignment	not modelled	88.8	19	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
36	c3czcA_	 Alignment	not modelled	87.9	21	PDB header: transferase Chain: A: PDB Molecule: rmmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from streptococcus2 mutans
37	c1fmtA_	 Alignment	not modelled	86.6	22	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
38	c4mgeB_	 Alignment	not modelled	85.0	18	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
39	c3wfiD_	 Alignment	not modelled	84.6	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
40	c3nbmA_	 Alignment	not modelled	84.2	15	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
41	c5gqsA_	 Alignment	not modelled	80.0	10	PDB header: transport protein Chain: A: PDB Molecule: pts galactitol transporter subunit iib; PDBTitle: nmr based solution structure of pts system, galactitol-specific iib2 component from methicillin resistant staphylococcus aureus
42	c2l2qA_	 Alignment	not modelled	76.4	7	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
43	c2iyaB_	 Alignment	not modelled	74.3	18	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
44	c4leiB_	 Alignment	not modelled	71.3	15	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp
45	c3eagA_	 Alignment	not modelled	71.2	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
46	d1f37b_	 Alignment	not modelled	69.0	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
47	c6norB_	 Alignment	not modelled	67.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
48	c6cauA_	 Alignment	not modelled	64.9	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with ampnp
49	d1ydga_	 Alignment	not modelled	64.1	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
50	d2fug21	 Alignment	not modelled	63.7	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
51	c5zbyA_	 Alignment	not modelled	62.2	18	PDB header: hydrolase Chain: A: PDB Molecule: hydrogenase maturation protease hyci; PDBTitle: crystal structure of a [nife] hydrogenase maturation protease hyci2 from thermococcus kodakarensis kod1

52	c2f00A_	Alignment	not modelled	62.1	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
53	c3beoA_	Alignment	not modelled	61.6	17	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnac 2-epimerases
54	c3rbvA_	Alignment	not modelled	61.6	22	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
55	d1cfza_	Alignment	not modelled	57.2	20	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
56	c3kcgA_	Alignment	not modelled	57.2	19	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
57	d1u6ka1	Alignment	not modelled	54.9	16	Fold: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Superfamily: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Family: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
58	c1vj8C_	Alignment	not modelled	54.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
59	c2bibA_	Alignment	not modelled	53.9	11	PDB header: hydrolase Chain: A: PDB Molecule: teichoic acid phosphorylcholine esterase/ choline binding PDBTitle: crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus pneumoniae
60	c5lc5E_	Alignment	not modelled	53.8	15	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: structure of mammalian respiratory complex i, class2
61	c1j6uA_	Alignment	not modelled	53.5	27	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
62	c5xt2C_	Alignment	not modelled	52.5	8	PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
63	d1iiba_	Alignment	not modelled	52.4	8	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
64	d1vlva2	Alignment	not modelled	51.4	18	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
65	d1zh8a1	Alignment	not modelled	48.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c3tqrA_	Alignment	not modelled	48.2	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
67	c1i36A_	Alignment	not modelled	48.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases
68	c3ceaA_	Alignment	not modelled	45.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
69	c6gcsH_	Alignment	not modelled	45.2	10	PDB header: oxidoreductase Chain: H: PDB Molecule: 24-kda subunit (nuhm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
70	c3f4aA_	Alignment	not modelled	43.2	25	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
71	c5b3uB_	Alignment	not modelled	42.3	13	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
72	c2p6pB_	Alignment	not modelled	38.9	14	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
73	c3rfoA_	Alignment	not modelled	38.9	18	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
74	c4f67A_	Alignment	not modelled	37.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nsg) target lgr82
						PDB header: oxidoreductase

75	c4hadD_	Alignment	not modelled	36.8	18	Chain: D; PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
76	c2auvA_	Alignment	not modelled	36.7	21	PDB header: oxidoreductase Chain: A; PDB Molecule: potential nad-reducing hydrogenase subunit; PDBTitle: solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
77	d1duvg2	Alignment	not modelled	36.4	10	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
78	c6hl2C_	Alignment	not modelled	36.3	16	PDB header: electron transport Chain: C; PDB Molecule: nadh-quinone oxidoreductase subunit e; PDBTitle: wild-type nuof from aquifex aeolicus - oxidized form
79	d1m2da_	Alignment	not modelled	35.4	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
80	d1zaka1	Alignment	not modelled	35.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
81	c3db2C_	Alignment	not modelled	34.8	13	PDB header: oxidoreductase Chain: C; PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
82	c4ambB_	Alignment	not modelled	34.2	15	PDB header: transferase Chain: B; PDB Molecule: snogd; PDBTitle: crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater
83	d1j6ua1	Alignment	not modelled	33.8	27	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
84	c3aufA_	Alignment	not modelled	33.6	16	PDB header: transferase Chain: A; PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
85	c3tsaA_	Alignment	not modelled	33.5	11	PDB header: transferase Chain: A; PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase png
86	c2eq8C_	Alignment	not modelled	33.2	14	PDB header: oxidoreductase Chain: C; PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
87	c4ehxA_	Alignment	not modelled	32.8	18	PDB header: transferase Chain: A; PDB Molecule: tetraacyldisaccharide 4'-kinase; PDBTitle: crystal structure of lpxk from aquifex aeolicus at 1.9 angstrom2 resolution
88	c2e85B_	Alignment	not modelled	32.5	11	PDB header: hydrolase Chain: B; PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
89	c3kkIA_	Alignment	not modelled	32.0	18	PDB header: hydrolase Chain: A; PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
90	c3uuwB_	Alignment	not modelled	31.4	12	PDB header: oxidoreductase Chain: B; PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
91	c5ijaB_	Alignment	not modelled	30.2	21	PDB header: hydrolase Chain: B; PDB Molecule: hydrogenase-specific maturation endopeptidase; PDBTitle: [nife] hydrogenase maturation protease hybd from thermococcus2 kodakarensis
92	c4qxzA_	Alignment	not modelled	29.9	18	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from staphylococcus aureus
93	c3i2vA_	Alignment	not modelled	29.4	15	PDB header: transferase Chain: A; PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
94	c4atyA_	Alignment	not modelled	29.4	19	PDB header: oxidoreductase Chain: A; PDB Molecule: terephthalate 1,2-cis-dihydrodiol dehydrogenase; PDBTitle: crystal structure of a terephthalate 1,2-cis-2 dihydrodioldehydrogenase from burkholderia xenovorans3 lb400
95	c1zakB_	Alignment	not modelled	29.1	19	PDB header: transferase Chain: B; PDB Molecule: adenylate kinase; PDBTitle: adenylate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5'-)pentaphosphate (ap5a)
96	c5vytD_	Alignment	not modelled	29.1	21	PDB header: transferase Chain: D; PDB Molecule: gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- PDBTitle: crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis
97	c1nm3B_	Alignment	not modelled	28.9	14	PDB header: electron transport Chain: B; PDB Molecule: protein hi0572; PDBTitle: crystal structure of heamophilus influenza hybrid-prx5
98	c2q62A_	Alignment	not modelled	28.7	11	PDB header: flavoprotein Chain: A; PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
						PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein;

99	c3fojA_	Alignment	not modelled	28.6	16	PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
100	c4mkzA_	Alignment	not modelled	28.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
101	c2uzqE_	Alignment	not modelled	27.4	14	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
102	c1ofgF_	Alignment	not modelled	26.3	17	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
103	c1h6dL_	Alignment	not modelled	26.3	17	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol PDB header: oxidoreductase
104	c4fgwA_	Alignment	not modelled	25.9	25	Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(+)] 1; PDBTitle: structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 sacharomyces cerevisiae
105	d1r8ka_	Alignment	not modelled	25.7	17	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
106	c2k0zA_	Alignment	not modelled	25.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
107	c6gnfC_	Alignment	not modelled	24.8	21	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
108	c3wadA_	Alignment	not modelled	24.6	14	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicenistatin
109	c2j6pF_	Alignment	not modelled	24.3	23	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
110	c3ktdC_	Alignment	not modelled	24.1	21	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
111	c3r0jA_	Alignment	not modelled	23.8	20	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
112	d1p3da1	Alignment	not modelled	23.3	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
113	d1dxha2	Alignment	not modelled	22.9	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
114	c3ilmD_	Alignment	not modelled	22.8	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anaebaena sp. northeast2 structural genomics consortium target nsr437h
115	c4e12A_	Alignment	not modelled	22.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
116	d1w85j_	Alignment	not modelled	22.3	15	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
117	c3dv0L_	Alignment	not modelled	22.3	15	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
118	d2cq2a1	Alignment	not modelled	22.2	16	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
119	c5ayvB_	Alignment	not modelled	22.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
120	c5zikC_	Alignment	not modelled	21.6	15	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa