

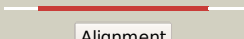

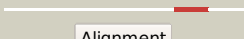



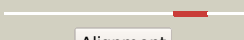


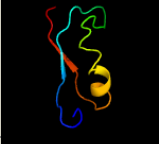













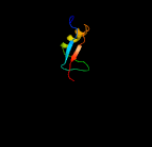
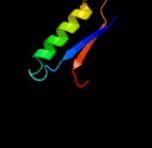



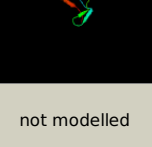


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2205c_(-)_2469395_2470471
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	d8d66b62195bd76b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cwcB_	 Alignment		100.0	38	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
2	d1to6a_	 Alignment		100.0	31	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
3	c6i3mF_	 Alignment		91.2	18	PDB header: translation Chain: F: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
4	c6i7tB_	 Alignment		90.8	14	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
5	d1vb5a_	 Alignment		90.3	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
6	c5b04C_	 Alignment		90.0	24	PDB header: translation Chain: C: PDB Molecule: probable translation initiation factor eif-2b subunit beta; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
7	c3ecsd_	 Alignment		88.9	22	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
8	c1w2wJ_	 Alignment		88.9	15	PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-phosphate 2 isomerase related to regulatory eif2b subunits
9	c5dboA_	 Alignment		88.5	22	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
10	c6qg0G_	 Alignment		88.4	19	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
11	c5b04B_	 Alignment		88.2	18	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe

12	d1a3xa2	Alignment		88.0	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
13	d1e0ta2	Alignment		87.8	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
14	d1pkla2	Alignment		87.3	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
15	c5b04G_	Alignment		87.2	16	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
16	c5widB_	Alignment		87.0	21	PDB header: flavoprotein Chain: B: PDB Molecule: flavodoxin; PDBTitle: structure of a flavodoxin from the domain archaea
17	d1pswa_	Alignment		86.6	22	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
18	c4zemB_	Alignment		86.2	22	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum
19	c4zeoH_	Alignment		86.0	21	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
20	c3a11D_	Alignment		85.1	16	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
21	d1ydga_	Alignment	not modelled	84.7	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
22	d1t5oa_	Alignment	not modelled	84.6	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
23	c2yvka_	Alignment	not modelled	83.6	21	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
24	c4ldrA_	Alignment	not modelled	83.3	26	PDB header: isomerase, cell invasion Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: structure of the s283y mutant of mrdi
25	c3trjC_	Alignment	not modelled	83.2	15	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
26	d1liua2	Alignment	not modelled	83.1	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
27	d1t9ka_	Alignment	not modelled	82.9	23	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
28	c6a34B_	Alignment	not modelled	82.5	23	PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i PDB header: translation

29	c6i3mD	Alignment	not modelled	82.4	18	Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
30	c1w5fA	Alignment	not modelled	80.9	15	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
31	d1xi3a	Alignment	not modelled	80.9	15	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
32	d2a0ua1	Alignment	not modelled	79.8	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: lF2B-like
33	c6ezoD	Alignment	not modelled	78.8	20	PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
34	c1a3wB	Alignment	not modelled	78.0	13	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
35	c4e6eA	Alignment	not modelled	77.7	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of a putative cell division protein ftsz (tfu_1113)2 from thermobifida fusca yx-er1 at 2.22 a resolution (psi community3 target, van wezel g.p.)
36	c1w59B	Alignment	not modelled	76.2	12	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
37	d2vapa1	Alignment	not modelled	75.8	12	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
38	c4c0xA	Alignment	not modelled	75.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of ppazor in complex with anthraquinone-2-2 sulfonate
39	c3khdA	Alignment	not modelled	75.2	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
40	c2h1fB	Alignment	not modelled	75.1	21	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
41	d1rq2a1	Alignment	not modelled	73.0	20	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
42	d1tk9a	Alignment	not modelled	72.6	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
43	c1aqfB	Alignment	not modelled	72.5	18	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
44	c3qtgA	Alignment	not modelled	71.9	8	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
45	c3eoeC	Alignment	not modelled	71.2	22	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
46	c2vgbB	Alignment	not modelled	71.1	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
47	c6du6D	Alignment	not modelled	71.1	17	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of the pyruvate kinase (pk1) from the mosquito aedes2 aegypti
48	c5f4bB	Alignment	not modelled	70.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
49	c1t5aB	Alignment	not modelled	70.3	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
50	c3e0vB	Alignment	not modelled	68.8	13	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
51	c5xvmB	Alignment	not modelled	68.8	12	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
52	c4fxjB	Alignment	not modelled	66.6	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
53	c2q1yB	Alignment	not modelled	66.5	16	PDB header: cell cycle, signaling protein Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
54	c5vegC	Alignment	not modelled	66.4	13	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment PDB header: lyase

55	c1izcA_	Alignment	not modelled	66.2	17	Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
56	d1izca_	Alignment	not modelled	66.2	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
57	c5ws9C_	Alignment	not modelled	65.8	15	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase (pyk) from mycobacterium tuberculosis in complex with2 oxalate, atp and allosteric activator amp
58	c4imaD_	Alignment	not modelled	64.2	17	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: the structure of c436m-hlpyk in complex with citrate/mn/atp/fru-1,6-bp
59	c1pkIB_	Alignment	not modelled	64.1	13	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
60	c1e0tD_	Alignment	not modelled	63.5	13	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
61	c3s3tD_	Alignment	not modelled	63.4	20	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
62	c3t07D_	Alignment	not modelled	62.7	13	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
63	c2ppvA_	Alignment	not modelled	62.7	25	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
64	c3d54D_	Alignment	not modelled	62.2	20	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
65	c2f9iD_	Alignment	not modelled	62.2	20	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
66	c3o63B_	Alignment	not modelled	61.5	20	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
67	c2v82A_	Alignment	not modelled	61.4	22	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
68	c4rapD_	Alignment	not modelled	61.1	21	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase tbc; PDBTitle: crystal structure of bacterial iron-containing dodecameric2 glycosyltransferase tbc from enterotoxigenic e.coli h10407
69	c2p0yA_	Alignment	not modelled	61.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
70	d2g50a2	Alignment	not modelled	60.7	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
71	c2rhoB_	Alignment	not modelled	60.3	18	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: synthetic gene encoded bacillus subtilis ftsz ncs dimer with bound gdp2 and gtp-gamma-s
72	c2yxbA_	Alignment	not modelled	59.5	18	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
73	c4fzrA_	Alignment	not modelled	59.4	15	PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase
74	c4ei8A_	Alignment	not modelled	58.9	11	PDB header: replication Chain: A: PDB Molecule: plasmid replication protein repx; PDBTitle: crystal structure of bacillus cereus tubz, apo-form
75	d1q7ra_	Alignment	not modelled	58.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
76	c5i01B_	Alignment	not modelled	58.5	13	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
77	d2f9yb1	Alignment	not modelled	57.9	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
78	c2f9yB_	Alignment	not modelled	57.9	20	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
79	c2ze3A_	Alignment	not modelled	56.4	25	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus

80	c1vcnA	Alignment	not modelled	56.3	32	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
81	c5b7pB	Alignment	not modelled	55.9	15	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: structures and functional analysis of periplasmic 5-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase from 3 aeromonas hydrophila
82	c1ofuB	Alignment	not modelled	55.6	16	PDB header: bacterial cell division inhibitor Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of sula.fts from pseudomonas aeruginosa
83	c5ugjC	Alignment	not modelled	55.2	12	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
84	c6fqbE	Alignment	not modelled	54.8	16	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
85	c2hjqA	Alignment	not modelled	54.4	15	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein enga; PDBTitle: the crystal structure of the b. subtilis yphc gtpase in complex with2 gdp
86	c3qz6A	Alignment	not modelled	54.1	10	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
87	d2hzba1	Alignment	not modelled	53.7	20	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
88	c4lzdD	Alignment	not modelled	53.6	19	PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: crystal structure of murq from h.influenzae with bound inhibitor
89	c2e28A	Alignment	not modelled	53.5	13	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
90	c3hbmA	Alignment	not modelled	53.5	12	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
91	c2yybA	Alignment	not modelled	52.6	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ttha1606; PDBTitle: crystal structure of ttha1606 from thermus thermophilus hb8
92	c2bf9A	Alignment	not modelled	52.5	11	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
93	c3tovB	Alignment	not modelled	52.2	21	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 9; PDBTitle: the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
94	c3ma8A	Alignment	not modelled	51.8	12	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
95	c2vxyA	Alignment	not modelled	51.8	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: the structure of ftsz from bacillus subtilis at 1.7a2 resolution
96	c2zwmA	Alignment	not modelled	51.6	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
97	d1ka9h	Alignment	not modelled	51.1	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
98	c4dxdA	Alignment	not modelled	51.1	17	PDB header: cell cycle/inhibitor Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: staphylococcal aureus ftsz in complex with 723
99	d1f8ya	Alignment	not modelled	50.8	5	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
100	c5b3kA	Alignment	not modelled	49.9	18	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
101	c5uqiA	Alignment	not modelled	49.8	8	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
102	c4r2lB	Alignment	not modelled	49.8	19	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
103	d1pjqa1	Alignment	not modelled	49.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
104	c3h4lB	Alignment	not modelled	49.5	28	PDB header: dna binding protein, protein binding Chain: B: PDB Molecule: dna mismatch repair protein pms1; PDBTitle: crystal structure of n terminal domain of a dna repair protein
105	d1pixa2	Alignment	not modelled	49.3	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase

						Family: Biotin dependent carboxylase carboxyltransferase domain
106	c1tz5A_	Alignment	not modelled	49.1	19	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
107	c1bknA_	Alignment	not modelled	49.0	34	PDB header: dna repair Chain: A: PDB Molecule: mutl; PDBTitle: crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
108	c1ronA_	Alignment	not modelled	48.5	15	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
109	c4f3yA_	Alignment	not modelled	48.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
110	d1dihA1	Alignment	not modelled	48.3	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	d1wv2a_	Alignment	not modelled	48.2	15	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
112	c3khdC_	Alignment	not modelled	47.9	15	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
113	c2rirA_	Alignment	not modelled	47.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
114	c1pixB_	Alignment	not modelled	46.6	15	PDB header: lyase Chain: B: PDB Molecule: glutaconyl-coa decarboxylase a subunit; PDBTitle: crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
115	c1zosE_	Alignment	not modelled	46.6	24	PDB header: hydrolase Chain: E: PDB Molecule: 5'-methylthioadenosine / s-adenosylhomocysteine PDBTitle: structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state inhibitor mt-3 imma
116	c4r3uD_	Alignment	not modelled	46.5	13	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
117	c2mswA_	Alignment	not modelled	46.2	19	PDB header: transferase Chain: A: PDB Molecule: response regulator/sensor histidine kinase; PDBTitle: ligand-induced folding of a receiver domain
118	d1w41a1	Alignment	not modelled	45.9	26	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
119	c2xhzC_	Alignment	not modelled	45.7	13	PDB header: isomerase Chain: C: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
120	c3ct7E_	Alignment	not modelled	45.6	16	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12