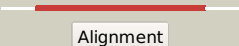



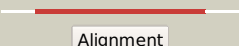





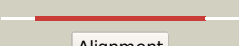





















Phyre2

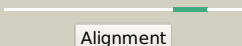

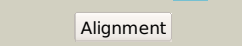
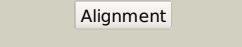
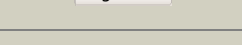

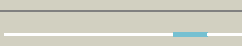
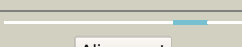
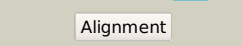

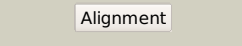
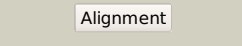

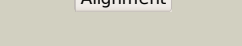

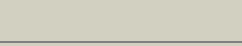
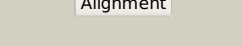
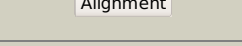
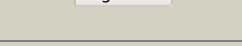
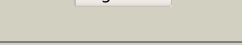
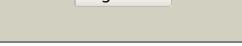

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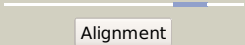
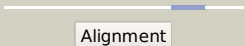
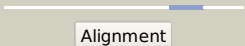
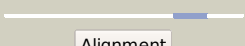

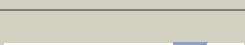
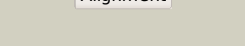
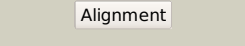

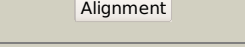
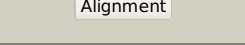
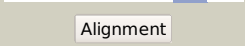

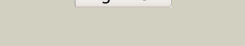





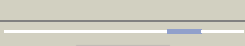

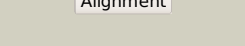

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dtfB_	 Alignment		100.0	85	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
2	d2a1ha1	 Alignment		100.0	37	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
3	c2abjG_	 Alignment		100.0	37	PDB header: transferase Chain: G: PDB Molecule: branched-chain-amino-acid aminotransferase, cytosolic; PDBTitle: crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
4	c4dqnA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: putative branched-chain amino acid aminotransferase ilve; PDBTitle: crystal structure of the branched-chain aminotransferase from2 streptococcus mutans
5	c3uzbA_	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structures of branched-chain aminotransferase from deinococcus2 radiodurans complexes with alpha-ketoisocaproate and l-glutamate3 suggest its radio-resistance for catalysis
6	c3u0gA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: putative branched-chain amino acid aminotransferase ilve; PDBTitle: crystal structure of branched-chain amino acid aminotransferase from2 burkholderia pseudomallei
7	c6h65A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of the branched-chain-amino-acid aminotransferase2 from haliangium ochraceum
8	d1iyea_	 Alignment		100.0	34	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
9	c6gkrC_	 Alignment		100.0	29	PDB header: transferase Chain: C: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of branched-chain amino acid aminotransferase from2 thermobaculum terrenum in plp-form (holo-form)
10	c6nstD_	 Alignment		100.0	30	PDB header: transferase Chain: D: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of branched chain amino acid aminotransferase from2 pseudomonas aeruginosa
11	c1wrvB_	 Alignment		100.0	33	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: crystal structure of t.th.hb8 branched-chain amino acid2 aminotransferase

12	c5ce8B_	Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: crystal structure of branched-chain aminotransferase from thermophilic2 archaea thermoproteus uzoniensis
13	c3wwjE_	Alignment		100.0	21	PDB header: transferase Chain: E: PDB Molecule: (r)-amine transaminase; PDBTitle: crystal structure of an engineered sitagliptin-producing transaminase,2 ata-117-rd11
14	c4ce5A_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: at-omegata; PDBTitle: first crystal structure of an (r)-selective omega-transaminase2 from aspergillus terreus
15	c4m0jA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: d-amino acid aminotransferase; PDBTitle: crystal structure of a d-amino acid aminotransferase from burkholderia2 thailandensis e264
16	c3cswB_	Alignment		100.0	27	PDB header: transferase Chain: B: PDB Molecule: putative branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of a putative branched-chain amino acid2 aminotransferase (tm0831) from thermotoga maritima at 2.15 a3 resolution
17	c5cm0A_	Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: branched-chain transaminase; PDBTitle: crystal structure of branched-chain aminotransferase from thermophilic2 archaea geoglobus acetivorans
18	c4tviB_	Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: aminotransferase, class iv; PDBTitle: x-ray crystal structure of an aminotransferase from brucella abortus2 bound to the co-factor plp
19	d1daaa_	Alignment		100.0	22	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
20	c2xpfB_	Alignment		100.0	29	PDB header: lyase Chain: B: PDB Molecule: 4-amino-4-deoxychorismate lyase; PDBTitle: crystal structure of putative aminodeoxychorismate lyase2 from pseudomonas aeruginosa
21	c4jxuB_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: structure of aminotransferase ilve2 from sinorhizobium meliloti2 complexed with plp
22	c5k3wA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: cputa1; PDBTitle: structural characterisation of fold iv-transaminase, cputa1, from2 curtobacterium pusillum
23	d1i2ka_	Alignment	not modelled	100.0	19	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
24	c6bb9A_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: 4-amino-4-deoxychorismate lyase; PDBTitle: the crystal structure of 4-amino-4-deoxychorismate lyase from2 salmonella typhimurium lt2
25	c3luIA_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: 4-amino-4-deoxychorismate lyase; PDBTitle: crystal structure of putative 4-amino-4-deoxychorismate lyase.2 (yp_094631.1) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 1.78 a resolution
26	c2zgiA_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A: PDB Molecule: putative 4-amino-4-deoxychorismate lyase; PDBTitle: crystal structure of putative 4-amino-4-deoxychorismate lyase
27	c3snoA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: hypothetical aminotransferase; PDBTitle: crystal structure of a putative aminotransferase (ncgl2491) from2 corynebacterium glutamicum atcc 13032 at 1.60 a resolution
28	c3qqmD_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: D: PDB Molecule: mlr3007 protein; PDBTitle: crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a resolution
						PDB header: lyase

29	c4k6nA_	Alignment	not modelled	100.0	15	Chain: A: PDB Molecule: aminodeoxychorismate lyase; PDBTitle: crystal structure of yeast 4-amino-4-deoxychorismate lyase
30	c3cebA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: d-aminoacid aminotransferase-like plp-dependent enzyme; PDBTitle: crystal structure of a putative 4-amino-4-deoxychorismate lyase2 (hs_0128) from haemophilus somnus 129pt at 2.40 a resolution
31	c4h5fB_	Alignment	not modelled	66.6	17	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc superfamily atp binding cassette PDBTitle: crystal structure of an amino acid abc transporter substrate-binding2 protein from streptococcus pneumoniae canada mdr_19a bound to l-3 arginine, form 1
32	c4q0cA_	Alignment	not modelled	65.9	19	PDB header: transferase Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: 3.1 a resolution crystal structure of the b. pertussis bvgs2 periplasmic domain
33	c2ylnA_	Alignment	not modelled	60.6	19	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
34	c5t0wA_	Alignment	not modelled	60.3	22	PDB header: transport protein Chain: A: PDB Molecule: anccdt-1; PDBTitle: crystal structure of the ancestral amino acid-binding protein anccdt-2 1, a precursor of cyclohexadienyl dehydratase
35	c5gzsA_	Alignment	not modelled	60.3	14	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: structure of vc protein
36	d1wdna_	Alignment	not modelled	58.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
37	c4pshA_	Alignment	not modelled	55.9	14	PDB header: protein transport Chain: A: PDB Molecule: abc-type transporter, periplasmic subunit family 3; PDBTitle: structure of holo argbp from t. maritima
38	c3k4uA_	Alignment	not modelled	55.8	12	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
39	c4ymxB_	Alignment	not modelled	54.8	22	PDB header: transport protein Chain: B: PDB Molecule: abc-type amino acid transport system, periplasmic PDBTitle: crystal structure of the substrate binding protein of an amino acid2 abc transporter
40	c3r39A_	Alignment	not modelled	54.5	17	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
41	c3kzgB_	Alignment	not modelled	54.1	16	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
42	c4f3pB_	Alignment	not modelled	53.9	17	PDB header: transport protein Chain: B: PDB Molecule: glutamine-binding periplasmic protein; PDBTitle: crystal structure of a glutamine-binding periplasmic protein from2 burkholderia pseudomallei in complex with glutamine
43	c3g41A_	Alignment	not modelled	51.4	16	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
44	c3vvfA_	Alignment	not modelled	49.1	18	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, binding protein; PDBTitle: crystal structure of ttc0807 complexed with arginine
45	c4pp0B_	Alignment	not modelled	48.4	18	PDB header: transport protein Chain: B: PDB Molecule: nopaline-binding periplasmic protein; PDBTitle: structure of the bbp noct-m117n in complex with pyronopaline
46	d1hsla_	Alignment	not modelled	45.8	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
47	c6dnmA_	Alignment	not modelled	45.7	11	PDB header: chaperone Chain: A: PDB Molecule: export chaperone sats; PDBTitle: the crystal structure of sats c-terminal domain
48	c4hubl_	Alignment	not modelled	43.9	24	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l11p; PDBTitle: the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the l7/l12 and l1 stalk, l5 and lx proteins
49	c4eq9A_	Alignment	not modelled	43.8	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein-amino acid PDBTitle: 1.4 angstrom crystal structure of abc transporter glutathione-binding2 protein gsht from streptococcus pneumoniae strain canada mdr_19a in3 complex with glutathione
50	d1lsta_	Alignment	not modelled	43.6	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
51	c4i62A_	Alignment	not modelled	42.2	11	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: 1.05 angstrom crystal structure of an amino acid abc transporter2 substrate-binding protein abpa from streptococcus pneumoniae canada3 mdr_19a bound to l-arginine

52	c4oenA	 Alignment	not modelled	41.1	24	PDB header: transport protein Chain: A: PDB Molecule: second substrate binding domain of putative amino acid abc PDBTitle: crystal structure of the second substrate binding domain of a putative2 amino acid abc transporter from streptococcus pneumoniae canada3 mdr_19a
53	c2ieeB	 Alignment	not modelled	40.9	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable abc transporter extracellular-binding protein PDBTitle: crystal structure of yckb_bacsu from bacillus subtilis. northeast2 structural genomics consortium target sr574.
54	c2y7iB	 Alignment	not modelled	39.1	10	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
55	c5colB	 Alignment	not modelled	38.1	32	PDB header: translation Chain: B: PDB Molecule: 50s ribosomal protein l11; PDBTitle: ribosomal protein l11 from methanococcus jannaschii
56	c3h7mA	 Alignment	not modelled	36.5	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with similarity2 to periplasmic binding proteins
57	c4kptA	 Alignment	not modelled	35.7	20	PDB header: transport protein Chain: A: PDB Molecule: glutamine abc transporter permease and substrate binding PDBTitle: crystal structure of substrate binding domain 1 (sbd1) of abc2 transporter glnpq from lactococcus lactis
58	c5orgA	 Alignment	not modelled	35.5	14	PDB header: octopine-binding protein Chain: A: PDB Molecule: octopine-binding periplasmic protein; PDBTitle: structure of the periplasmic binding protein (pbp) occj from a.2 tumefaciens b6 in complex with octopine.
59	c4kr5B	 Alignment	not modelled	34.9	18	PDB header: transport protein Chain: B: PDB Molecule: glutamine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcus lactis glnp substrate binding domain2 2 (sbd2) in open conformation
60	c6detA	 Alignment	not modelled	34.7	14	PDB header: transport protein Chain: A: PDB Molecule: tv2483; PDBTitle: the crystal structure of tv2483 bound to l-arginine
61	c6h2tA	 Alignment	not modelled	34.5	18	PDB header: signaling protein Chain: A: PDB Molecule: probable glutamine-binding lipoprotein glnh (glnbp); PDBTitle: glnh bound to glu, mycobacterium tuberculosis
62	c2q2aD	 Alignment	not modelled	32.3	20	PDB header: transport protein Chain: D: PDB Molecule: artj; PDBTitle: crystal structures of the arginine-, lysine-, histidine-binding2 protein artj from the thermophilic bacterium geobacillus3 stearothermophilus
63	c4oz9A	 Alignment	not modelled	30.9	14	PDB header: lyase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
64	c5hmtA	 Alignment	not modelled	30.5	15	PDB header: transport protein Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: crystal structure of the cyclohexadienyl dehydratase-like solute-2 binding protein sar11_1068 from candidatus pelagibacter ubique.
65	c5josA	 Alignment	not modelled	29.4	16	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: crystal structure of an ancestral cyclohexadienyl dehydratase, anccdt-2 3(p188l).
66	c4g4pA	 Alignment	not modelled	28.9	23	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, amino acid-binding/permease PDBTitle: crystal structure of glutamine-binding protein from enterococcus2 faecalis at 1.5 a
67	d2f34a1	 Alignment	not modelled	28.9	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
68	c3hv1A	 Alignment	not modelled	28.6	20	PDB header: transport protein Chain: A: PDB Molecule: polar amino acid abc uptake transporter substrate PDBTitle: crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
69	c6a80B	 Alignment	not modelled	28.4	12	PDB header: transport protein Chain: B: PDB Molecule: putative amino acid-binding periplasmic abc transporter PDBTitle: crystal structure of putative amino acid binding periplasmic abc2 transporter protein from candidatus liberibacter asiaticus in complex3 with cystine
70	c5dtbB	 Alignment	not modelled	28.2	15	PDB header: membrane protein Chain: B: PDB Molecule: cg3822; PDBTitle: crystal structure of the drosophila cg3822 kair1d ligand binding2 domain complex with glutamate
71	c2hi1A	 Alignment	not modelled	27.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 2; PDBTitle: the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
72	c4ohnA	 Alignment	not modelled	27.1	19	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: crystal structure of an abc uptake transporter substrate binding2 protein from streptococcus pneumoniae with bound histidine
73	c5ikbA	 Alignment	not modelled	26.9	19	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor ionotropic, kainate 4, glutamate receptor PDBTitle: crystal structure of the kainate receptor gluk4 ligand binding domain2 in complex with kainate

74	c3delC_		Alignment	not modelled	26.7	14	PDB header: protein binding, transport protein Chain: C: PDB Molecule: arginine binding protein; PDBTitle: the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
75	c3chgB_		Alignment	not modelled	25.9	14	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
76	c2kngA_		Alignment	not modelled	25.7	12	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
77	c2ppyB_		Alignment	not modelled	24.4	17	PDB header: transport protein Chain: B: PDB Molecule: ionotropic glutamate receptor bacterial homologue; PDBTitle: crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
78	d1vqon1		Alignment	not modelled	24.3	21	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
79	c2o1mB_		Alignment	not modelled	23.4	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable amino-acid abc transporter extracellular-binding PDBTitle: crystal structure of the probable amino-acid abc transporter2 extracellular-binding protein ytmk from bacillus subtilis. northeast3 structural genomics consortium target sr572
80	d2ic1a1		Alignment	not modelled	23.3	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Cysteine dioxygenase type I
81	c6f37B_		Alignment	not modelled	22.9	14	PDB header: sugar binding protein Chain: B: PDB Molecule: nano3, fucose-binding lectin protein; PDBTitle: fusion protein of rsl and trimeric coiled coil
82	c4zv2A_		Alignment	not modelled	22.5	27	PDB header: solute-binding protein Chain: A: PDB Molecule: ancqr; PDBTitle: an ancestral arginine-binding protein bound to glutamine
83	c1vcnA_		Alignment	not modelled	22.1	34	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
84	c3i6vA_		Alignment	not modelled	22.1	20	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
85	c2xx7B_		Alignment	not modelled	21.6	20	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution.
86	c2rejA_		Alignment	not modelled	21.5	8	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
87	c4z9nB_		Alignment	not modelled	21.2	16	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
88	c3kbrA_		Alignment	not modelled	20.7	11	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
89	c4qicB_		Alignment	not modelled	20.7	23	PDB header: signaling protein/dna binding protein Chain: B: PDB Molecule: anti-sigma factor nepr; PDBTitle: co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
90	d1mqia_		Alignment	not modelled	20.4	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
91	d1dzfa1		Alignment	not modelled	20.0	7	Fold: Restriction endonuclease-like Superfamily: Eukaryotic RPB5 N-terminal domain Family: Eukaryotic RPB5 N-terminal domain
92	c5uh0A_		Alignment	not modelled	19.6	12	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: 1.95 angstrom resolution crystal structure of fragment (35-274) of2 membrane-bound lytic murein transglycosylase f from yersinia pestis.
93	d1mxsa_		Alignment	not modelled	19.4	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
94	d3elna1		Alignment	not modelled	18.9	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Cysteine dioxygenase type I
95	c4alzA_		Alignment	not modelled	18.9	16	PDB header: membrane protein Chain: A: PDB Molecule: yop proteins translocation protein d; PDBTitle: the yersinia t3ss basal body component yscd reveals a different2 structural periplasmatic domain organization to known homologue prgh
96	c4c0rB_		Alignment	not modelled	18.3	6	PDB header: transport protein Chain: B: PDB Molecule: putative amino acid binding protein; PDBTitle: molecular and structural basis of glutathione import in2 gram-positive bacteria via gsht and the cystine abc3 importer tcybc of streptococcus mutans.

97	c4zdmA_	Alignment	not modelled	18.3	10	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor kainate-like protein; PDBTitle: pleurobrachia bachei iglur3 lbd glycine complex
98	c6gpcB_	Alignment	not modelled	18.0	14	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: crystal structure of the arginine-bound form of domain 1 from tmargbp
99	dluxca_	Alignment	not modelled	17.6	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator