

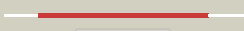










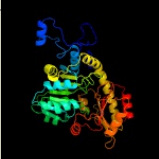










Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0391_(metZ)_470013_471233
 Date Tue Jul 23 14:50:46 BST 2019
 Unique Job ID 0e6adb9f5d770b46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ndnC_	 Alignment		100.0	100	PDB header: lyase Chain: C; PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
2	d2ctza1	 Alignment		100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
3	d1qgna_	 Alignment		100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
4	d1e5ea_	 Alignment		100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
5	c2cb1A_	 Alignment		100.0	39	PDB header: lyase Chain: A; PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
6	d1y4ia1	 Alignment		100.0	39	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
7	c5dx5B_	 Alignment		100.0	37	PDB header: lyase Chain: B; PDB Molecule: methionine gamma-lyase; PDBTitle: crystal structure of methionine gamma-lyase from clostridium2 sporogenes
8	c2nmpC_	 Alignment		100.0	32	PDB header: lyase Chain: C; PDB Molecule: cystathionine gamma-lyase; PDBTitle: crystal structure of human cystathionine gamma lyase
9	c1i41J_	 Alignment		100.0	35	PDB header: lyase Chain: J; PDB Molecule: cystathionine gamma-synthase; PDBTitle: cystathionine gamma-synthase in complex with the inhibitor2 appa
10	c3aemD_	 Alignment		100.0	31	PDB header: lyase Chain: D; PDB Molecule: methionine gamma-lyase; PDBTitle: reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
11	d1n8pa_	 Alignment		100.0	33	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like

12	c5igB_	Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: cys/met metabolism pyridoxal-phosphate-dependent enzyme; PDBTitle: crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution
13	c6cjbA_	Alignment		100.0	34	PDB header: lyase Chain: A: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from legionella2 pneumophila philadelphia 1 covalently bound to pyridoxal phosphate
14	c2gqnB_	Alignment		100.0	25	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-lyase; PDBTitle: cystathionine beta-lyase (cbl) from escherichia coli in complex with 2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
15	d1cl1a_	Alignment		100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
16	c5x5hA_	Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: cystathionine beta-lyases/cystathionine gamma-synthases; PDBTitle: crystal structure of metb from corynebacterium glutamicum
17	c1ibjC_	Alignment		100.0	34	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
18	d1ibja_	Alignment		100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
19	c4oc9N_	Alignment		100.0	34	PDB header: lyase Chain: N: PDB Molecule: putative o-acetylhomoserine (thiol)-lyase; PDBTitle: 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at 4 position 205
20	d1cs1a_	Alignment		100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
21	c3e6gA_	Alignment	not modelled	100.0	39	PDB header: lyase Chain: A: PDB Molecule: cystathionine gamma-lyase-like protein; PDBTitle: crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
22	c4q31A_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: A: PDB Molecule: cystathione gamma lyase cale6; PDBTitle: the crystal structure of cystathione gamma lyase (cale6) from2 micromonospora echinospora
23	c3qi6B_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: B: PDB Molecule: cystathionine gamma-synthase metb (cgs); PDBTitle: crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99
24	c4l0oA_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: A: PDB Molecule: cystathionine gamma-synthase; PDBTitle: structure determination of cystathionine gamma-synthase from2 helicobacter pylori
25	d1gc0a_	Alignment	not modelled	100.0	36	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
26	c4kamC_	Alignment	not modelled	100.0	37	PDB header: transferase Chain: C: PDB Molecule: o-acetylhomoserine sulfhydrylase metc; PDBTitle: x-ray crystal structure of o-acetylhomoserine sulfhydrylase metc from2 mycobacterium marinum atcc baa-535 / m
27	c5tt2D_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: D: PDB Molecule: cystathionine gamma-lyase; PDBTitle: inactive conformation of engineered human cystathionine gamma lyase2 (e59n, r119l, e339v) to depleting methionine
28	c3ri6A_	Alignment	not modelled	100.0	36	PDB header: transferase Chain: A: PDB Molecule: o-acetylhomoserine sulfhydrylase; PDBTitle: a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway

						of wolinella3 succinogenes PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yhfs; PDBTitle: crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli
29	c4j8IA_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
30	d1pffa_	Alignment	not modelled	100.0	36	PDB header: lyase Chain: B: PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus cereus.2 northeast structural genomics consortium target bcr213
31	c3ht4B_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase family protein, ynbB b.subtilis PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
32	c3hvyC_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: putative cystathionine beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
33	c3fd0B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
34	c5w70B_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: carbon-sulfur lyase involved in aluminum resistance; PDBTitle: crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
35	c3gwpA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
36	c2po3B_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
37	c3bcxA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate PDBTitle: x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate
38	c5k8bA_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
39	d1b9ha_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylo-inosose aminotransferase; PDBTitle: crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
40	c2c7tA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
41	c4k2bA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: pyridoxamine 5-phosphate-dependent dehydrase; PDBTitle: crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine
42	c2r0tA_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
43	d1mdoa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
44	d1o69a_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
45	c5z0yA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: degtd/dnrj/eryc1/strs aminotransferase; PDBTitle: crystal structure of a degtd dnrj eryc1 strs aminotransferase from2 brucella abortus
46	c4qgrA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
47	c3caiA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
48	c2ogeC_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
49	c5uidC_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
50	c3dr4B_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: cals13; PDBTitle: crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
51	c4vtjC_	Alignment	not modelled	100.0	18	

52	c3ju7B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: putative plp-dependent aminotransferase; PDBTitle: crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
53	c4xauG_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: G: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of ats13 from actinomadura melliura
54	c3frkB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: qdtb; PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
55	c3hqtB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
56	c4bhel_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: I: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp
57	c3uwcA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: nucleotide-sugar aminotransferase; PDBTitle: structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
58	c5utsC_	Alignment	not modelled	100.0	9	PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
59	c3wy7D_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
60	c2w8wA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
61	c3nysA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase wbpe; PDBTitle: x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
62	c3lwsF_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: F: PDB Molecule: aromatic amino acid beta-eliminating lyase/threonine PDBTitle: crystal structure of putative aromatic amino acid beta-eliminating2 lyase/threonine aldolase. (yp_001813866.1) from exiguobacterium sp.3 255-15 at 2.00 a resolution
63	c6hrhA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
64	d1bs0a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
65	c3vaxA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein dnda; PDBTitle: crystal structure of dnda from streptomyces lividans
66	c4j5uB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
67	d1vjoa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
68	c4wxfC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
69	c3wgcB_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
70	c3a2bA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
71	c3hbxB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
72	c3n0lA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
73	d2bwna1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
74	d1jf9a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
75	c5u20C_	Alignment	not modelled	100.0	10	PDB header: transferase Chain: C: PDB Molecule: putative aminotransferase; PDBTitle: x-ray structure of the wlrg aminotransferase from campylobacter2 jejuni, internal plp-aldimine
76	c4lnjA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form

77	c4lc3B_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: putative udp-4-amino-4-deoxy-l-arabinose- -oxoglutarate PDBTitle: x-ray crystal structure of a putative udp-4-amino-4-deoxy- l-arabinose-2 -oxoglutarate aminotransferase from burkholderia cenocepacia
78	c3ecdC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
79	d1kl1a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
80	d2fnua1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
81	c3mafB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
82	c5xtaA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinat synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
83	c3pj0D_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: D: PDB Molecule: lmo0305 protein; PDBTitle: crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
84	c5vc2A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
85	c3nnkC_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: ureidoglycine-glyoxylate aminotransferase; PDBTitle: biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
86	c4n0wA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase from2 burkholderia cenocepacia with covalently attached pyridoxal phosphate
87	d1c4ka2	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
88	c6hnuA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
89	c6ewqA_	Alignment	not modelled	100.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative capsular polysaccharide biosynthesis protein; PDBTitle: putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form
90	d1qz9a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
91	c2dkjB_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
92	c3w1hB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) selenium transferase; PDBTitle: crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
93	c3e9kA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3- hydroxyhippuric acid2 inhibitor complex
94	d2v1pa1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
95	c4je5C_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: aromatic/aminoadipate aminotransferase 1; PDBTitle: crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
96	c5jayB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxonanoate synthase from2 burkholderia xenovorans
97	c3tqxA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 2-amino-3-ketobutyrate coenzyme a ligase; PDBTitle: structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
98	c4q6rB_	Alignment	not modelled	99.9	14	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: sphingosine-1-phosphate lyase 1; PDBTitle: crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1- yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
99	c4iw7A_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of 8-amino-7-oxonanoate synthase (biof) from2 francisella tularensis.
						PDB header: structural genomics, unknown function

100	c2hdyA_	Alignment	not modelled	99.9	14	Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
101	d1dfoa_	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
102	d1fc4a_	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
103	c3kaxB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
104	d1m6sa_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
105	c4q76B_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
106	c6c9eB_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
107	d1tpla_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
108	d1w7la_	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
109	d1t3ia_	Alignment	not modelled	99.9	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
110	d1bw0a_	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
111	c5zsqA_	Alignment	not modelled	99.9	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
112	c3islA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
113	c3l8aB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
114	c3b46B_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
115	c3lvmB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
116	c5kz5M_	Alignment	not modelled	99.9	14	PDB header: transferase/oxidoreductase Chain: M: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
117	d2hoxa1	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
118	c6c3aB_	Alignment	not modelled	99.9	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
119	d1svva_	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
120	c4w91C_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp