
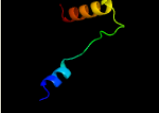



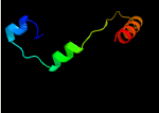

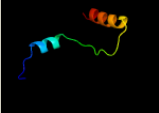

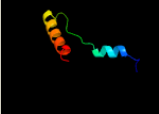

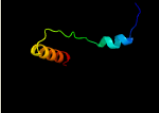

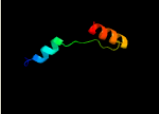

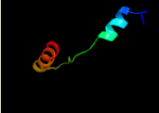

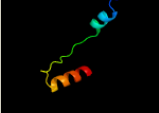

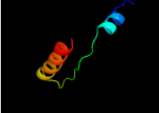




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1519_(- )_1710739_1711008
Date	Fri Aug 2 13:30:10 BST 2019
Unique Job ID	9a4d61919902e23f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bcxA_</a>	 Alignment		92.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; <b>PDBTitle:</b> e1 dehydrase
2	<a href="#">c4k2bA_</a>	 Alignment		90.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
3	<a href="#">d2fnuA1</a>	 Alignment		90.2	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
4	<a href="#">c5w70B_</a>	 Alignment		87.7	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> l-glutamine:2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> x-ray structure of rbmb from streptomyces ribosidificus
5	<a href="#">c2po3B_</a>	 Alignment		87.5	30	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-dehydrase; <b>PDBTitle:</b> crystal structure analysis of desi in the presence of its2 tdp-sugar product
6	<a href="#">c5k8bA_</a>	 Alignment		86.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate <b>PDBTitle:</b> 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
7	<a href="#">c3ju7B_</a>	 Alignment		86.1	39	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative plp-dependent aminotransferase; <b>PDBTitle:</b> crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
8	<a href="#">c3frkB_</a>	 Alignment		81.1	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> qdtb; <b>PDBTitle:</b> x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
9	<a href="#">c3uwcA_</a>	 Alignment		77.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleotide-sugar aminotransferase; <b>PDBTitle:</b> structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
10	<a href="#">d1o69a_</a>	 Alignment		71.5	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
11	<a href="#">c5u20C_</a>	 Alignment		69.3	26	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine

12	<a href="#">c4ytjC_</a>	Alignment		68.3	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cals13; <b>PDBTitle:</b> crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
13	<a href="#">c6ewqA_</a>	Alignment		67.9	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative capsular polysaccharide biosynthesis protein; <b>PDBTitle:</b> putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form
14	<a href="#">c3dr4B_</a>	Alignment		60.7	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative perosamine synthetase; <b>PDBTitle:</b> gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
15	<a href="#">c2c7tA_</a>	Alignment		59.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
16	<a href="#">c4qgrA_</a>	Alignment		57.5	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> degt/dnrj/eryc1/strs aminotransferase; <b>PDBTitle:</b> crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
17	<a href="#">d1b9ha_</a>	Alignment		54.7	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
18	<a href="#">c3nysA_</a>	Alignment		48.9	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase wbpe; <b>PDBTitle:</b> x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
19	<a href="#">c2r0tA_</a>	Alignment		46.8	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5-phosphate-dependent dehydrase; <b>PDBTitle:</b> crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine
20	<a href="#">d1mdoa_</a>	Alignment		46.2	27	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
21	<a href="#">c5uidC_</a>	Alignment	not modelled	45.8	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase tlmj; <b>PDBTitle:</b> the crystal structure of an aminotransferase tlmj from2 streptoaloteichus hindustanus
22	<a href="#">c2ogeC_</a>	Alignment	not modelled	44.4	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transaminase; <b>PDBTitle:</b> x-ray structure of s. venezuelae desv in its internal2 aldimine form
23	<a href="#">c4xauG_</a>	Alignment	not modelled	41.5	32	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of ats13 from actinomadura melliura
24	<a href="#">c4lc3B_</a>	Alignment	not modelled	37.3	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative udp-4-amino-4-deoxy-l-arabinose-2-oxoglutarate <b>PDBTitle:</b> x-ray crystal structure of a putative udp-4-amino-4-deoxy-l-arabinose-2-oxoglutarate aminotransferase from burkholderia cenocepacia
25	<a href="#">c5dotA_</a>	Alignment	not modelled	13.4	67	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
26	<a href="#">c5douC_</a>	Alignment	not modelled	13.3	67	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
27	<a href="#">c2qlcC_</a>	Alignment	not modelled	13.0	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein radc homolog; <b>PDBTitle:</b> the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s

28	<a href="#">d1a9xb2</a>	Alignment	not modelled	11.9	50	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
29	<a href="#">c3lx4B_</a>	Alignment	not modelled	11.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fe-hydrogenase; <b>PDBTitle:</b> stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
30	<a href="#">d1e5ba_</a>	Alignment	not modelled	10.9	28	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family II
31	<a href="#">d2csfa1</a>	Alignment	not modelled	9.7	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> CUT domain
32	<a href="#">c1keeH_</a>	Alignment	not modelled	9.7	50	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> carbamoyl-phosphate synthetase small chain; <b>PDBTitle:</b> inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
33	<a href="#">c5lutG_</a>	Alignment	not modelled	9.1	44	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> blm helicase; <b>PDBTitle:</b> structures of dhbn domain of gallus gallus blm helicase
34	<a href="#">c1h8bB_</a>	Alignment	not modelled	9.0	43	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> titin; <b>PDBTitle:</b> ef-hands 3,4 from alpha-actinin / z-repeat 7 from titin
35	<a href="#">c2mf3A_</a>	Alignment	not modelled	8.0	60	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> u2-segestritoxin-sf1a; <b>PDBTitle:</b> sgtx-sf1a
36	<a href="#">d3c8ya1</a>	Alignment	not modelled	7.1	50	<b>Fold:</b> Fe-only hydrogenase <b>Superfamily:</b> Fe-only hydrogenase <b>Family:</b> Fe-only hydrogenase
37	<a href="#">c4iaoD_</a>	Alignment	not modelled	7.0	47	<b>PDB header:</b> hydrolase/transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein sir4; <b>PDBTitle:</b> crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4
38	<a href="#">d1hehc_</a>	Alignment	not modelled	6.9	22	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family II
39	<a href="#">c3femB_</a>	Alignment	not modelled	6.8	39	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxine biosynthesis protein snz1; <b>PDBTitle:</b> structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
40	<a href="#">c1jy2O_</a>	Alignment	not modelled	6.7	77	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of the central region of bovine fibrinogen (e52 fragment) at 1.4 angstroms resolution
41	<a href="#">c2zbtB_</a>	Alignment	not modelled	6.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
42	<a href="#">c3c6cA_</a>	Alignment	not modelled	5.7	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminohexanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
43	<a href="#">c2a45H_</a>	Alignment	not modelled	5.4	77	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of the complex between thrombin and the central "e"2 region of fibrin
44	<a href="#">c3bbpD_</a>	Alignment	not modelled	5.3	58	<b>PDB header:</b> protein transport/splicing <b>Chain:</b> D: <b>PDB Molecule:</b> grip and coiled-coil domain-containing protein 2; <b>PDBTitle:</b> rab6-gtp:gcc185 rab binding domain complex