


















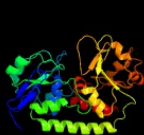


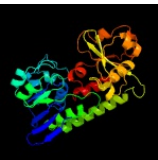
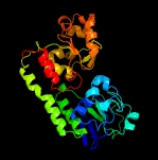
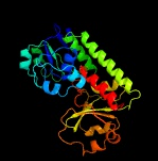

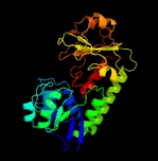

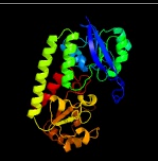
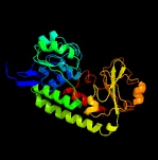


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0265c_(-)_316511_317503
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	ea9855285d4cb94f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4pm4B_	 Alignment		100.0	100	PDB header: solute-binding protein Chain: B: PDB Molecule: iron complex transporter substrate-binding protein; PDBTitle: structure of a putative periplasmic iron siderophore binding protein2 (rv0265c) from mycobacterium tuberculosis h37rv
2	c4mdyA_	 Alignment		100.0	64	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic solute binding protein from2 mycobacterium smegmatis str. mc2 155
3	c4h59A_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: iron-compound abc transporter, iron compound-binding PDBTitle: crystal structure of iron uptake abc transporter substrate-binding2 protein p1aa from streptococcus pneumoniae canada mdr_19a bound to3 bis-tris propane
4	c3eiwA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: htsa protein; PDBTitle: crystal structure of staphylococcus aureus lipoprotein, htsa
5	c3tnyA_	 Alignment		100.0	20	PDB header: metal transport Chain: A: PDB Molecule: yfyi (abc transport system substrate-binding protein); PDBTitle: structure of yfyi from bacillus cereus bound to the siderophore iron2 (iii) schizokinen
6	c5az3A_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: abc-type transporter, periplasmic component; PDBTitle: crystal structure of heme binding protein hmut
7	c4hn9B_	 Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: iron complex transport system substrate-binding protein; PDBTitle: crystal structure of iron abc transporter solute-binding protein from2 eubacterium eligens
8	c3tlkB_	 Alignment		100.0	19	PDB header: metal transport Chain: B: PDB Molecule: ferrienterobactin-binding periplasmic protein; PDBTitle: crystal structure of holo fepb
9	c3gfvA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized abc transporter solute-binding protein PDBTitle: crystal structure of petrobactin-binding protein yclq from bacillu2 subtilis
10	c3r5tA_	 Alignment		100.0	20	PDB header: metal transport Chain: A: PDB Molecule: ferric vibriobactin abc transporter, periplasmic ferric PDBTitle: crystal structure of holo-viup
11	c3tefA_	 Alignment		100.0	20	PDB header: transport protein Chain: A: PDB Molecule: iron(iii) abc transporter, periplasmic iron-compound- PDBTitle: crystal structure of the periplasmic catecholate-siderophore binding2 protein vctp from vibrio cholerae

12	d2chua1	Alignment		100.0	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like
13	c3pshA	Alignment		100.0	16	PDB header: metal transport Chain: A: PDB Molecule: protein hi_1472; PDBTitle: classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
14	c6allB	Alignment		100.0	18	PDB header: metal transport Chain: B: PDB Molecule: fe(3+)-citrate-binding protein yfmc; PDBTitle: crystal structure of a predicted ferric/iron (iii) hydroxamate2 siderophore substrate binding protein from bacillus anthracis
15	c5cr9A	Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: abc-type fe3+-hydroxamate transport system, periplasmic PDBTitle: crystal structure of abc-type fe3+-hydroxamate transport system from2 saccharomonospora viridis dsm 43017
16	c6mfIA	Alignment		100.0	22	PDB header: metal transport Chain: A: PDB Molecule: baub; PDBTitle: structure of siderophore binding protein baub bound to a complex2 between two molecules of acinetobactin and ferric iron.
17	c4ovkA	Alignment		100.0	14	PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic solute binding protein from2 veillonella parvula dsm 2008
18	c5dh0B	Alignment		100.0	17	PDB header: protein binding Chain: B: PDB Molecule: siderophore periplasmic binding protein; PDBTitle: structure of the siderophore periplasmic binding protein from the2 fuscachelin gene cluster of thermobifida fusca in p41
19	c4mx8C	Alignment		100.0	14	PDB header: solute-binding protein Chain: C: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of troa-like periplasmic binding protein2 peripla_bp_2 from xylanimonas cellulolytica
20	c4jccA	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: iron-compound abc transporter, iron-compound-binding PDBTitle: crystal structure of iron uptake abc transporter substrate-binding2 protein piva from streptococcus pneumoniae canada mdr_19a
21	c5gj3A	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: periplasmic heme-binding protein rhut from roseiflexus sp. rs-1 in2 two-heme bound form (holo-2)
22	c4mlzB	Alignment	not modelled	100.0	16	PDB header: solute binding protein Chain: B: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic binding protein from jonesia2 denitrificans
23	c4ljsA	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: the crystal structure of a periplasmic binding protein from2 veillonella parvula dsm 2008
24	c4pagA	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: abc transporter solute binding protein from sulfurospirillum2 deleyianum dsm 6946
25	c4b8yA	Alignment	not modelled	100.0	13	PDB header: transport protein/siderophore Chain: A: PDB Molecule: fhud2; PDBTitle: ferrichrome-bound fhud2
26	c4inpA	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: iron (iii) abc transporter, periplasmic iron-binding PDBTitle: the crystal structure of helicobacter pylori ceue (hp1561) with ni(ii)2 bound
27	c6b2xB	Alignment	not modelled	100.0	14	PDB header: metal transport Chain: B: PDB Molecule: solute-binding periplasmic protein of iron/siderophore abc PDBTitle: apo yiuA crystal form 1
28	c3be5D	Alignment	not modelled	100.0	19	PDB header: metal transport Chain: D: PDB Molecule: putative iron compound-binding protein of abc transporter PDBTitle: crystal structure of fite (crystal form 1), a group iii periplasmic2 siderophore binding protein
29	c4n01B	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding protein;

29	c1lv1B_	Alignment	not modelled	100.0	13	PDBTitle: the crystal structure of a periplasmic binding protein from2 veillonella parvula dsm 2008 PDB header: transport protein
30	c2phzA_	Alignment	not modelled	100.0	14	Chain: A; PDB Molecule: iron-uptake system-binding protein; PDBTitle: crystal structure of iron-uptake system-binding protein feua from2 bacillus subtilis. northeast structural genomics target sr580.
31	d2phza1	Alignment	not modelled	100.0	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like
32	c2x4IA_	Alignment	not modelled	100.0	13	PDB header: transport Chain: A; PDB Molecule: ferric-siderophore receptor protein; PDBTitle: crystal structure of dese, a ferric-siderophore receptor protein from2 streptomyces coelicolor
33	c5ggxD_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: D; PDB Molecule: iron(iii) abc transporter, periplasmic iron-compound- PDBTitle: crystal structure of fe3+ - desferal bound siderophore binding protein2 fhud from vibrio cholerae
34	c5flyB_	Alignment	not modelled	100.0	17	PDB header: metal transport Chain: B; PDB Molecule: ferrichrome-binding periplasmic protein; PDBTitle: the fhud protein from s.pseudintermedius
35	c4mo9A_	Alignment	not modelled	100.0	15	PDB header: solute-binding protein Chain: A; PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of troa-like periplasmic binding protein fepb from2 veillonella parvula
36	c5b58T_	Alignment	not modelled	100.0	18	PDB header: metal binding protein Chain: T; PDB Molecule: putative heme transport system, substrate-binding protein; PDBTitle: inward-facing conformation of abc heme importer bhuuv in complex with2 periplasmic heme binding protein bhut from burkholderia cenocepacia
37	c4m7oA_	Alignment	not modelled	100.0	13	PDB header: iron binding protein Chain: A; PDB Molecule: iron-binding protein; PDBTitle: the crystal structure of a possible an iron-binding (periplasmic2 solute-binding) protein from staphylococcus epidermidis atcc 12228.
38	c5jqoA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A; PDB Molecule: lmo2184 protein; PDBTitle: crystal structure of an abc transporter substrate-binding protein from2 listeria monocytogenes egd-e
39	c2r79A_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A; PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa
40	d1esza_	Alignment	not modelled	100.0	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Periplasmic ferric siderophore binding protein FhuD
41	c5yscA_	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A; PDB Molecule: vitamin b12-binding protein; PDBTitle: crystal structure of periplasmic vitamin b12 binding protein btuf of2 vibrio cholerae
42	c2r7aC_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: C; PDB Molecule: bacterial heme binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein from shigella2 dysenteriae
43	c5khlB_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: B; PDB Molecule: hemin abc transporter, periplasmic hemin-binding protein PDBTitle: crystal structure of periplasmic heme binding protein hutb of vibrio2 cholerae
44	c3md9A_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A; PDB Molecule: hemin-binding periplasmic protein hmut; PDBTitle: structure of apo form of a periplasmic heme binding protein
45	c2q8pA_	Alignment	not modelled	100.0	9	PDB header: metal transport Chain: A; PDB Molecule: iron-regulated surface determinant e; PDBTitle: crystal structure of selenomethionine labelled s. aureus isde2 complexed with heme
46	c3g9qA_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A; PDB Molecule: ferrichrome-binding protein; PDBTitle: crystal structure of the fhud fold-family bsu3320, a periplasmic2 binding protein component of a fep/fec-like ferrichrome abc3 transporter from bacillus subtilis. northeast structural genomics4 consortium target sr577a
47	c3mwgA_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: A; PDB Molecule: iron-regulated abc transporter siderophore-binding protein PDBTitle: crystal structure of staphylococcus aureus sira
48	d1n2za_	Alignment	not modelled	100.0	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
49	d2etva1	Alignment	not modelled	100.0	9	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like
50	c5n6yD_	Alignment	not modelled	93.6	12	PDB header: oxidoreductase Chain: D; PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
51	c2ynmC_	Alignment	not modelled	92.4	11	PDB header: oxidoreductase Chain: C; PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
52	c3aerC_	Alignment	not modelled	90.6	11	PDB header: oxidoreductase Chain: C; PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the light-independent protochlorophyllide

						reductase2 catalyzing a key reduction for greening in the dark
53	d1qh8a_	Alignment	not modelled	87.3	13	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
54	c5n6yE_	Alignment	not modelled	86.7	12	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrogenase vanadium-iron protein beta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
55	c3pdiG_	Alignment	not modelled	86.5	15	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
56	c5vytD_	Alignment	not modelled	85.4	16	PDB header: transferase Chain: D: PDB Molecule: gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- PDBTitle: crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis
57	c3pdiB_	Alignment	not modelled	81.0	8	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
58	c2ov3A_	Alignment	not modelled	78.7	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein component of an abc type zinc PDBTitle: crystal structure of 138-173 znua deletion mutant plus zinc bound
59	d1mioa_	Alignment	not modelled	77.2	9	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
60	d1m1na_	Alignment	not modelled	75.5	11	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
61	c3aoeC_	Alignment	not modelled	66.3	17	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
62	c2xdqA_	Alignment	not modelled	59.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
63	c3aerB_	Alignment	not modelled	59.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
64	c5kojD_	Alignment	not modelled	56.9	10	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase femo beta subunit protein nifk; PDBTitle: nitrogenase mofep protein in the ids oxidized state
65	c4rvqA_	Alignment	not modelled	55.2	12	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
66	d1pq4a_	Alignment	not modelled	53.2	17	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
67	d1a9xb2	Alignment	not modelled	52.5	27	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
68	d1qh8b_	Alignment	not modelled	52.3	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
69	c2ynmD_	Alignment	not modelled	52.2	14	PDB header: oxidoreductase Chain: D: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
70	d1miob_	Alignment	not modelled	51.1	6	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
71	c2e76D_	Alignment	not modelled	48.2	25	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
72	c1z7eC_	Alignment	not modelled	38.3	25	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
73	c5uyvA_	Alignment	not modelled	37.4	15	PDB header: metal transport Chain: A: PDB Molecule: periplasmic chelated iron-binding protein yfea; PDBTitle: yfea ancillary sites that do not co-load with site 2
74	c2yxbA_	Alignment	not modelled	36.3	17	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
75	c1keeH_	Alignment	not modelled	36.3	28	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
76	d1fmta2	Alignment	not modelled	35.1	16	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase

77	c2fynO_	Alignment	not modelled	32.6	35	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
78	d1zgha2	Alignment	not modelled	29.9	5	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
79	c4cl2A_	Alignment	not modelled	25.8	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
80	c2z4dA_	Alignment	not modelled	25.5	7	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: nmr structures of yeast proteasome component rpn13
81	c2g04B_	Alignment	not modelled	24.5	21	PDB header: isomerase Chain: B: PDB Molecule: probable fatty-acid-coa racemase far; PDBTitle: crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
82	d1xk7a1	Alignment	not modelled	23.9	22	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
83	d1q3qa2	Alignment	not modelled	22.6	16	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
84	c1p84E_	Alignment	not modelled	22.3	16	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
85	d2blna2	Alignment	not modelled	21.7	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
86	c2fyuE_	Alignment	not modelled	21.3	24	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
87	c4b4tX_	Alignment	not modelled	21.2	7	PDB header: hydrolase Chain: X: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
88	d1x74a1	Alignment	not modelled	21.2	22	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
89	d1gm1a_	Alignment	not modelled	20.8	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
90	c2z59A_	Alignment	not modelled	20.3	7	PDB header: protein transport Chain: A: PDB Molecule: protein adrm1; PDBTitle: complex structures of mouse rpn13 (22-130aa) and ubiquitin
91	c2r2yA_	Alignment	not modelled	20.1	7	PDB header: protein binding Chain: A: PDB Molecule: protein adrm1; PDBTitle: crystal structure of the proteasomal rpn13 pru-domain
92	c2xdqB_	Alignment	not modelled	19.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
93	c3cq9C_	Alignment	not modelled	19.6	15	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein lp_1622; PDBTitle: crystal structure of the lp_1622 protein from lactobacillus plantarum.2 northeast structural genomics consortium target lpr114
94	c3dc7B_	Alignment	not modelled	18.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein lp_3323; PDBTitle: crystal structure of the protein q88s8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109.
95	c3rfoA_	Alignment	not modelled	18.4	23	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
96	d1assa_	Alignment	not modelled	18.3	13	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
97	c2kr0A_	Alignment	not modelled	18.2	7	PDB header: protein binding Chain: A: PDB Molecule: proteasomal ubiquitin receptor adrm1; PDBTitle: solution structure of the proteasome ubiquitin receptor rpn13
98	c2r8rB_	Alignment	not modelled	18.0	23	PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
99	c5yx6D_	Alignment	not modelled	17.3	18	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein rv3272; PDBTitle: crystal structure of rv3272 from m. tuberculosis orthorhombic form