
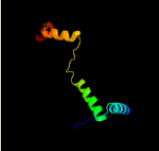
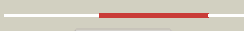


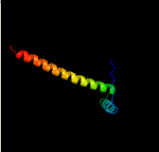



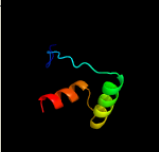



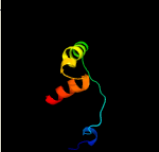



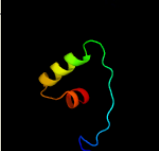

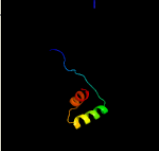

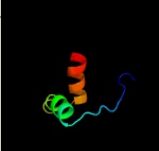
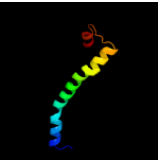
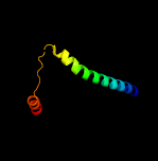

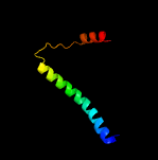
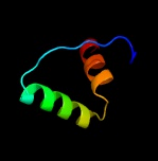
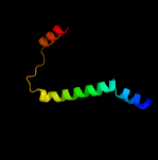

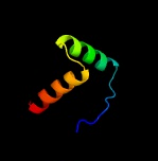
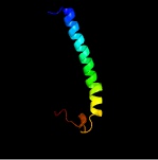


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0918 (-) _1024215_1024691
Date	Fri Jul 26 01:50:51 BST 2019
Unique Job ID	0daa54cc4a11afa9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gtsC_	 Alignment		99.9	26	PDB header: transcription Chain: C; PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
2	d1y9ba1	 Alignment		99.9	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
3	c6ajnF_	 Alignment		99.8	27	PDB header: toxin Chain: F; PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
4	c6gtrD_	 Alignment		97.2	26	PDB header: transcription Chain: D; PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat y144f mutant toxin bound to the c-terminus of2 the antitoxin atar and acetyl-coa
5	c6qeqD_	 Alignment		96.3	21	PDB header: dna binding protein Chain: D; PDB Molecule: pcff; PDBTitle: pcff from enterococcus faecalis pcf10
6	c6g1nB_	 Alignment		94.2	18	PDB header: antitoxin Chain: B; PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
7	c4p7dA_	 Alignment		93.4	14	PDB header: toxin Chain: A; PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
8	c2an7A_	 Alignment		87.6	19	PDB header: dna binding protein Chain: A; PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
9	c3qoqC_	 Alignment		82.6	15	PDB header: transcription/dna Chain: C; PDB Molecule: alginate and motility regulator z; PDBTitle: crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
10	c2ba3A_	 Alignment		81.9	31	PDB header: dna binding protein Chain: A; PDB Molecule: nika; PDBTitle: nmr structure of nika n-terminal fragment
11	d1mnta_	 Alignment		81.8	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors

12	c4napD	Alignment		75.5	11	PDB header: transport protein Chain: D: PDB Molecule: extracellular solute-binding protein, family 7; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Desulfovibrio alaskensis</i> g20 (dde_0634), target efi-510102, with 3 bound d-tryptophan
13	c4mx6A	Alignment		73.4	13	PDB header: transport protein Chain: A: PDB Molecule: trap-type c4-dicarboxylate:h+ symport system substrate- PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Shewanella oneidensis</i> (so_3134), target efi-510275, with bound 3 succinate
14	d2bj7a1	Alignment		71.7	8	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
15	c4pfiA	Alignment		68.4	12	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Marinobacter aquaeolei</i> vt8 (maqu_2829, target efi-510133), apo open 3 structure
16	d1b28a	Alignment		66.2	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
17	c4p56C	Alignment		65.4	21	PDB header: solute-binding protein Chain: C: PDB Molecule: putative extracellular solute-binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Bordetella bronchiseptica</i> , target efi-510038 (bb2442), with bound 3 (r)-mandelate and (s)-mandelate
18	c1u9pA	Alignment		65.1	13	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
19	d1myla	Alignment		61.4	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
20	c2hpgB	Alignment		60.7	9	PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding PDBTitle: the crystal structure of a thermophilic trap periplasmic 2 binding protein
21	d2hzaa1	Alignment	not modelled	60.6	11	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
22	c5yrzC	Alignment	not modelled	60.4	8	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from <i>Streptococcus pneumoniae</i>
23	c1q5vB	Alignment	not modelled	58.0	8	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
24	c2k5jB	Alignment	not modelled	57.6	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from <i>Shigella flexneri</i> 2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
25	c4mncA	Alignment	not modelled	57.6	18	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>Polaromonas</i> sp. js666 (bpro_4736), target efi-510156, with bound 3 benzoyl formate, space group p21
26	d1p94a	Alignment	not modelled	57.1	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
27	c2k29A	Alignment	not modelled	55.8	18	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of <i>E. coli</i> antitoxin relb
28	c4p91B	Alignment	not modelled	55.0	9	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter dctp subunit;

28	c3094B	Alignment	not modelled	53.0	9	PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> rhodospirillum rubrum palustris haa2 (rpb_3329), target efi-510223, with 3 bound succinate
29	d1myIb	Alignment	not modelled	54.1	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
30	c3gyyC	Alignment	not modelled	53.0	18	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the 2 apo-state
31	c2ca9B	Alignment	not modelled	52.7	8	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
32	c3fxbB	Alignment	not modelled	51.4	26	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
33	c2hzkB	Alignment	not modelled	50.4	17	PDB header: ligand binding, transport protein Chain: B: PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding subunit from a 2 trap transporter in its open form
34	c2vpnB	Alignment	not modelled	48.4	18	PDB header: transport Chain: B: PDB Molecule: periplasmic substrate binding protein; PDBTitle: high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
35	c4ovpB	Alignment	not modelled	47.7	14	PDB header: solute-binding protein Chain: B: PDB Molecule: c4-dicarboxylate transport system substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> sulfatobacter sp. nas-14.1, target efi-510292, with bound alpha-d-3 manuronate
36	c3d3jA	Alignment	not modelled	47.0	16	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
37	c4me7E	Alignment	not modelled	45.3	14	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with 2 cognate antitoxin maze
38	c3d3kD	Alignment	not modelled	45.0	16	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
39	c2bj3D	Alignment	not modelled	44.5	8	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
40	c4x8rB	Alignment	not modelled	43.9	20	PDB header: solute-binding protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> rhodobacter sphaeroides (rsph17029_2138, target efi-510205) with 3 bound glucuronate
41	c4n4uA	Alignment	not modelled	42.7	18	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter periplasmic solute-binding PDBTitle: crystal structure of abc transporter solute binding protein bb07192 from bordetella bronchiseptica rb50, target efi-510049
42	c4pbqC	Alignment	not modelled	41.6	16	PDB header: solute-binding protein Chain: C: PDB Molecule: putative trap periplasmic solute binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> haemophilus influenzae rdaw (hicg_00826, target efi-510123) with 3 bound l-gulonate
43	c5i7iB	Alignment	not modelled	41.0	22	PDB header: transport protein Chain: B: PDB Molecule: trap solute binding protein; PDBTitle: crystal structure of a marine metagenome trap solute binding protein 2 specific for aromatic acid ligands (sorcerer ii global ocean sampling 3 expedition, unidentified microbe, locus tag gos_1523157) in complex 4 with co-crystallized 3-hydroxybenzoate
44	d2hzab1	Alignment	not modelled	38.7	8	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
45	c4q2uM	Alignment	not modelled	37.5	12	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
46	c4pe3A	Alignment	not modelled	36.3	19	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> rhodobacter sphaeroides (rsph17029_3620, target efi-510199), apo open 3 structure
47	c4mcoC	Alignment	not modelled	34.6	9	PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> rhodospirillum rubrum ferrereducens (rfer_1840), target efi-510211, with bound 3 malonate
48	c4pddA	Alignment	not modelled	34.3	14	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from <i>2</i> polaromonas sp js666 (bpro_0088, target efi-510167) bound to d-3 erythronate
49	c2zzxD	Alignment	not modelled	33.9	11	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in 2 complex with lactate PDB header: toxin/toxin inhibitor

50	c4fxeB	Alignment	not modelled	33.3	18	Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
51	c4p8bA	Alignment	not modelled	31.7	19	PDB header: transport protein Chain: A: PDB Molecule: trap-type transporter, periplasmic component; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ralstonia eutropha h16 (h16_a1328), target efi-510189, with bound3 (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-acetolactate)
52	c5mnwA	Alignment	not modelled	29.8	13	PDB header: lyase Chain: A: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: solution structure of the cinaciguat bound human beta1 h-nox.
53	c2pfyA	Alignment	not modelled	29.6	18	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
54	c4pf8A	Alignment	not modelled	29.0	22	PDB header: transport protein Chain: A: PDB Molecule: trap-t family transporter, dctp (periplasmic binding) PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfitobacter sp. nas-14.1 (target efi-510299) with bound beta-d-3 galacturonate
55	c3u65B	Alignment	not modelled	28.4	14	PDB header: transport protein Chain: B: PDB Molecule: tp33 protein; PDBTitle: the crystal structure of tat-p(t) (tp0957)
56	c4petA	Alignment	not modelled	27.9	11	PDB header: solute-binding protein Chain: A: PDB Molecule: extracellular solute-binding protein, family 7; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 colwellia psychrerythraea (cps_0129, target efi-510097) with bound3 calcium and pyruvate
57	c2kila	Alignment	not modelled	27.8	7	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
58	c5zh6B	Alignment	not modelled	27.6	20	PDB header: allergen Chain: B: PDB Molecule: parvalbumin spv-ii; PDBTitle: crystal structure of parvalbumin spv-ii of mustelus griseus
59	c4pakA	Alignment	not modelled	27.5	18	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 verminephrobacter eiseniae ef01-2 (veis_3954, target efi-510324) a3 nephridial symbiont of the earthworm eisenia foetida, bound to (r)-4 pantoic acid
60	c4pfrA	Alignment	not modelled	27.4	7	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered
61	c4yicA	Alignment	not modelled	27.1	13	PDB header: transport protein Chain: A: PDB Molecule: trap transporter solute binding protein; PDBTitle: crystal structure of a trap transporter solute binding protein2 (ipr025997) from bordetella bronchiseptica rb50 (bb0280, target efi-3 500035) with bound picolinic acid
62	c2kycA	Alignment	not modelled	25.2	20	PDB header: calcium binding protein Chain: A: PDB Molecule: parvalbumin, thymic cpv3; PDBTitle: solution structure of ca-free chicken parvalbumin 3 (cpv3)
63	c2cpmA	Alignment	not modelled	24.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sperm-associated antigen 7; PDBTitle: solution structure of the r3h domain of human sperm-2 associated antigen 7
64	c4p1IA	Alignment	not modelled	24.7	16	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_2479), target efi-510085,3 with bound d-glucuronate, spg i213
65	c3fs7D	Alignment	not modelled	22.8	17	PDB header: metal binding protein Chain: D: PDB Molecule: parvalbumin, thymic; PDBTitle: crystal structure of gallus gallus beta-parvalbumin (avian thymic2 hormone)
66	c4n6dA	Alignment	not modelled	22.3	5	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter-dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens dsm2638 (desal_3247), target efi-510112,3 phased with i3c, open complex, c-terminus of symmetry mate bound in4 ligand binding site
67	c2pfzA	Alignment	not modelled	22.3	7	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
68	c4xeqC	Alignment	not modelled	21.5	11	PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio vulgaris (deval_0042, target efi-510114) bound to3 copurified (r)-pantoic acid
69	c6a6xC	Alignment	not modelled	20.4	13	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
70	c6hfoA	Alignment	not modelled	20.4	24	PDB header: chaperone Chain: A: PDB Molecule: tetratricopeptide repeat protein 4; PDBTitle: human hsp90 co-chaperone ttc4 c-domain
						PDB header: transport protein Chain: A: PDB Molecule: twin-arginine translocation pathwav signal:

71	c5im2A_	Alignment	not modelled	20.3	14	PDBTitle: crystal structure of a trap solute binding protein from rhodofera2 ferrereducens t118 (rfer_2570, target efi-510210) in complex with3 copurified benzoate PDB header: transport protein Chain: C: PDB Molecule: trap dicarboxylate transporter, dctp subunit;
72	c4n8gC_	Alignment	not modelled	20.3	18	PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_0660), target efi-501075,3 with bound d-alanine-d-alanine PDB header: transport protein
73	c4pf6A_	Alignment	not modelled	20.3	18	Chain: A: PDB Molecule: c4-dicarboxylate-binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans (rd1_0742, target efi-510239) with bound 3-3 deoxy-d-manno-oct-2-ulosonic acid (kdo) PDB header: transport protein
74	c4n5wB_	Alignment	not modelled	20.2	18	Chain: B: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 chromohalobacter salexigens dsm 3043 (csal_0678), target efi-501078,3 with bound 1,2-ethanediol PDB header: transport protein
75	c4nguA_	Alignment	not modelled	19.7	16	Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio alaskensis g20 (dde_1548), target efi-510103, with3 bound d-ala-d-ala
76	d1bu3a_	Alignment	not modelled	19.7	17	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
77	c4ovqA_	Alignment	not modelled	19.6	20	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate abc transporter, substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans, target efi-510230, with bound beta-d-3 glucuronate
78	c5lp2B_	Alignment	not modelled	17.5	18	PDB header: cell adhesion Chain: B: PDB Molecule: hopq; PDBTitle: adhesin domain of the type 1 hopq of helicobacter pylori strain g27
79	d1rjva_	Alignment	not modelled	17.5	13	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
80	c2kz2A_	Alignment	not modelled	17.1	17	PDB header: metal binding protein Chain: A: PDB Molecule: calmodulin; PDBTitle: calmodulin, c-terminal domain, f92e mutant
81	d1rwyA_	Alignment	not modelled	16.8	17	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
82	d1a75a_	Alignment	not modelled	16.7	17	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
83	c2o0cB_	Alignment	not modelled	16.5	16	PDB header: signaling protein Chain: B: PDB Molecule: alr2278 protein; PDBTitle: crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
84	d2pvba_	Alignment	not modelled	16.2	20	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
85	c4n8yA_	Alignment	not modelled	16.2	25	PDB header: transport protein Chain: A: PDB Molecule: putative trap-type c4-dicarboxylate transport system, PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 bradyrhizobium sp. btai1 b (bbta_0128), target efi-5100563 (bbta_0128), complex with alpha/beta-d-galacturonate
86	c3h87D_	Alignment	not modelled	15.7	15	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
87	c4ln5A_	Alignment	not modelled	15.6	20	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 burkholderia ambifaria (bamb_6123), target efi-510059, with bound3 glycerol and chloride ion
88	c2otoD_	Alignment	not modelled	15.5	28	PDB header: surface active protein, toxin Chain: D: PDB Molecule: m protein; PDBTitle: n-terminal fragment of streptococcus pyogenes m1 protein
89	d1pvaa_	Alignment	not modelled	14.8	17	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
90	c2ph5A_	Alignment	not modelled	14.4	17	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
91	c4ovsB_	Alignment	not modelled	13.9	11	PDB header: solute-binding protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfurospirillum deleyianum dsm 6946 (sdel_0447), target efi-510309,3 with bound succinate
92	d1bdta_	Alignment	not modelled	13.8	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
93	d3e9va1	Alignment	not modelled	13.7	24	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like

94	d1b8la_	Alignment	not modelled	13.0	23	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
95	c4b6aC_	Alignment	not modelled	12.8	27	PDB header: ribosome Chain: C: PDB Molecule: 60s ribosomal protein l4-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
96	d1bazb_	Alignment	not modelled	12.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
97	d1rroa_	Alignment	not modelled	12.7	13	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
98	c5td3B_	Alignment	not modelled	11.9	25	PDB header: oxidoreductase Chain: B: PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure of catechol 1,2-dioxygenase from burkholderia2 vietnamiensis
99	d5pala_	Alignment	not modelled	11.8	13	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin