

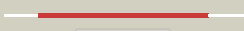





















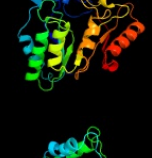
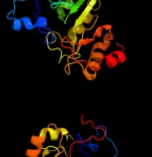

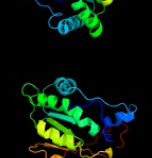
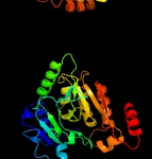

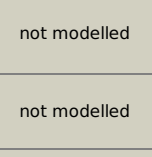


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0213c (-) _254637_255950
Date	Tue Jul 23 14:50:27 BST 2019
Unique Job ID	7933c838537b4ee4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ul4A_	 Alignment		100.0	25	PDB header: metal binding protein Chain: A: PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
2	c6fd2B_	 Alignment		100.0	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative apramycin biosynthetic oxidoreductase 4; PDBTitle: radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
3	c4jc0B_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
4	c5l7jA_	 Alignment		100.0	19	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
5	c2qgqF_	 Alignment		100.0	9	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
6	c3cixA_	 Alignment		100.0	18	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
7	d1olta_	 Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
8	c6qk7C_	 Alignment		99.9	18	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
9	d1r30a_	 Alignment		99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
10	c1r30A_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
11	c3t7vA_	 Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)

12	c5exkG	Alignment		99.9	15	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
13	c6iazA	Alignment		99.9	15	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
14	c4u0pB	Alignment		99.8	13	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
15	c3rfaA	Alignment		99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
16	c4wxcC	Alignment		99.8	13	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
17	c4rtbA	Alignment		99.7	16	PDB header: lyase Chain: A: PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
18	c3rfaB	Alignment		99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
19	c4fheA	Alignment		99.6	7	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
20	c6fz6B	Alignment		99.6	15	PDB header: transferase Chain: B: PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
21	c4r33A	Alignment	not modelled	99.6	15	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
22	d1tv8a	Alignment	not modelled	99.5	10	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
23	c5vslB	Alignment	not modelled	99.5	8	PDB header: antiviral protein Chain: B: PDB Molecule: radical s-adenosyl methionine domain-containing protein 2; PDBTitle: crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
24	c5v1tA	Alignment	not modelled	99.5	10	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
25	c2yx0A	Alignment	not modelled	99.5	10	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
26	c3c8fA	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
27	c2a5hC	Alignment	not modelled	99.3	13	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
						PDB header: antiviral protein

28	c6b4cH_	Alignment	not modelled	99.2	8	Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
29	c6efnA_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
30	c4k39A_	Alignment	not modelled	99.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmecepe with bound adomet and cp18cys peptide
31	c5th5C_	Alignment	not modelled	99.0	12	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
32	c4m7tA_	Alignment	not modelled	99.0	11	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
33	d3bula2	Alignment	not modelled	98.6	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
34	c5wggA_	Alignment	not modelled	98.5	8	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
35	c1bmtB_	Alignment	not modelled	98.4	16	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of 2 the b12-binding domains of methionine synthase
36	c1y80A_	Alignment	not modelled	98.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
37	c4jgiB_	Alignment	not modelled	98.0	14	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
38	c6nhbB_	Alignment	not modelled	97.8	16	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
39	c4hh3C_	Alignment	not modelled	97.8	13	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
40	c2i2xD_	Alignment	not modelled	97.8	18	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
41	d1ccwa_	Alignment	not modelled	97.8	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
42	d7reqa2	Alignment	not modelled	97.7	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
43	d1xrsb1	Alignment	not modelled	97.7	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
44	c1k98A_	Alignment	not modelled	97.7	16	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
45	c2z2uA_	Alignment	not modelled	97.6	10	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
46	c2yxbA_	Alignment	not modelled	97.6	14	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
47	c3ezxA_	Alignment	not modelled	97.5	15	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
48	c4njka_	Alignment	not modelled	97.5	13	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
49	c4r3uD_	Alignment	not modelled	97.5	13	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
50	c1xrsB_	Alignment	not modelled	97.3	16	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
51	c3canA_	Alignment	not modelled	97.2	8	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
52	d1fmfa_	Alignment	not modelled	97.2	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
53	c4hh0B_	Alignment	not modelled	97.1	15	PDB header: flavoprotein,signaling protein Chain: B: PDB Molecule: appa protein; PDBTitle: dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides
54	c3ubnA_	Alignment	not modelled	96.2	10	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator;

54	c5wmpA	Alignment	not modelled	95.3	19	PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
55	c1e1cA	Alignment	not modelled	95.6	16	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
56	c6ifhA	Alignment	not modelled	95.4	12	PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spo0f from paenisporsarcina sp. tg-14
57	d1mvoa	Alignment	not modelled	95.2	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
58	d1kgsa2	Alignment	not modelled	94.8	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c1ys7B	Alignment	not modelled	94.7	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
60	c3dzdA	Alignment	not modelled	94.7	6	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
61	c3rmjB	Alignment	not modelled	94.6	11	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
62	d1ny5a1	Alignment	not modelled	94.6	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
63	d1ys7a2	Alignment	not modelled	94.5	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c2jr1A	Alignment	not modelled	94.4	6	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
65	c6c8vA	Alignment	not modelled	94.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
66	c3bleA	Alignment	not modelled	94.4	10	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
67	c2rjnA	Alignment	not modelled	94.2	11	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
68	c5uicA	Alignment	not modelled	94.0	16	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
69	c5ep0A	Alignment	not modelled	93.8	15	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
70	c3cfyA	Alignment	not modelled	93.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo repressor2 protein from vibrio parahaemolyticus
71	c3hdqE	Alignment	not modelled	93.6	8	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinnella3 succinogenes
72	d2pl1a1	Alignment	not modelled	93.5	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
73	c4q7eA	Alignment	not modelled	93.4	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator of a two component regulatory system; PDBTitle: non-phosphorylated hemr receiver domain from leptospira biflexa
74	d1yioa2	Alignment	not modelled	93.4	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	d1xhfa1	Alignment	not modelled	93.3	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	d1peya	Alignment	not modelled	93.3	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
77	c1ny5A	Alignment	not modelled	93.2	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
78	d2a9pa1	Alignment	not modelled	93.2	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
79	c4qpiC	Alignment	not modelled	93.1	13	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain PDB header: dna binding protein

80	c3f6cB_	Alignment	not modelled	93.0	13	Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
81	c3w9sB_	Alignment	not modelled	93.0	16	PDB header: signaling protein/antimicrobial protein Chain: B: PDB Molecule: ompr family response regulator in two-component regulatory PDBTitle: crystal structure analysis of the n-terminal receiver domain of2 response regulator pmra
82	c2zwmA_	Alignment	not modelled	93.0	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
83	d1dbwa_	Alignment	not modelled	93.0	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	d1krwa_	Alignment	not modelled	92.7	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
85	c2ayxA_	Alignment	not modelled	92.5	12	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
86	d2ayxa1	Alignment	not modelled	92.5	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	c2ftpA_	Alignment	not modelled	92.5	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
88	c5c8eC_	Alignment	not modelled	92.5	16	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
89	c5u8mA_	Alignment	not modelled	92.1	13	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
90	c3nhzA_	Alignment	not modelled	92.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
91	c3bicA_	Alignment	not modelled	91.9	15	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
92	c4lzlA_	Alignment	not modelled	91.8	12	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
93	d1qkka_	Alignment	not modelled	91.5	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
94	d1zesa1	Alignment	not modelled	91.5	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c3crnA_	Alignment	not modelled	91.2	14	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
96	c1zn2A_	Alignment	not modelled	91.2	11	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styf
97	c3rqia_	Alignment	not modelled	91.0	12	PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
98	c3hv2B_	Alignment	not modelled	90.9	8	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
99	c2oqrA_	Alignment	not modelled	90.9	13	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
100	d1h4pa_	Alignment	not modelled	90.7	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
101	c2qr3A_	Alignment	not modelled	90.7	17	PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
102	c4s05B_	Alignment	not modelled	90.7	17	PDB header: transcription/dna Chain: B: PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
103	c4ldaF_	Alignment	not modelled	90.4	13	PDB header: transcription Chain: F: PDB Molecule: tadz; PDBTitle: crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
104	c4z87B_	Alignment	not modelled	90.3	10	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii

						bound to gdp
105	c5m7nA_	Alignment	not modelled	89.9	13	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
106	c3c3mA_	Alignment	not modelled	89.9	11	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
107	d1zgza1	Alignment	not modelled	89.8	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
108	c3jteA_	Alignment	not modelled	89.7	11	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
109	c2gwrA_	Alignment	not modelled	89.6	12	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
110	c3a0rB_	Alignment	not modelled	89.6	16	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
111	c3eq2A_	Alignment	not modelled	89.6	20	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas aeruginosa rssb
112	d1jbea_	Alignment	not modelled	89.2	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
113	c1w25B_	Alignment	not modelled	88.9	8	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
114	d1yx1a1	Alignment	not modelled	88.9	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
115	c3ivuB_	Alignment	not modelled	88.6	16	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
116	c4fxsA_	Alignment	not modelled	88.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
117	c3cu5B_	Alignment	not modelled	88.4	8	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
118	c3r0jA_	Alignment	not modelled	88.2	15	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
119	c3fd0B_	Alignment	not modelled	87.9	12	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
120	c6ekhY_	Alignment	not modelled	87.9	13	PDB header: metal binding protein Chain: Y: PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis