















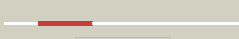


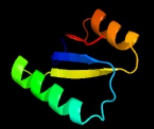


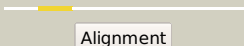

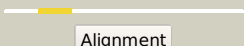


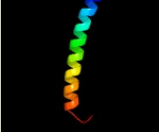
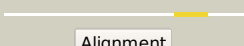

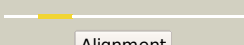

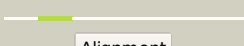








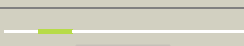


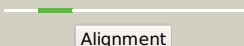
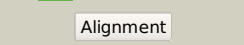
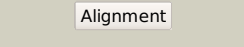
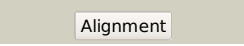


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0180c_(-)_210890_212248
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	fd33bea773768fd4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cniA_	 Alignment		99.4	17	PDB header: transport protein Chain: A: PDB Molecule: putative abc type-2 transporter; PDBTitle: crystal structure of a domain of a putative abc type-2 transporter2 from thermotoga maritima msb8
2	c6an7D_	 Alignment		99.4	8	PDB header: transport protein Chain: D: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
3	c6an7C_	 Alignment		99.4	9	PDB header: transport protein Chain: C: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
4	c5do7B_	 Alignment		99.2	10	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
5	c5do7A_	 Alignment		99.2	9	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
6	c5nj3B_	 Alignment		99.1	13	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
7	c5njgB_	 Alignment		98.9	13	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: part of the structure that could be2 built de novo
8	c5xjyA_	 Alignment		98.4	11	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
9	d2p0sa1	 Alignment		91.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: PG0945 N-terminal domain-like
10	c6esvA_	 Alignment		76.8	10	PDB header: signaling protein Chain: A: PDB Molecule: putative periplasmic phosphite-binding-like protein (pbl) PDBTitle: structure of the phosphate-bound form of aixox from rhizobium sp. str.2 nt-26
11	c3fkqA_	 Alignment		74.5	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution

12	c3eulB_		Alignment		74.4	13	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative response2 regulator narI from mycobacterium tuberculosis
13	c1a2oB_		Alignment		73.7	16	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheB regulation by a2 phosphorylation-activated domain
14	c2l9uA_		Alignment		72.1	29	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
15	c2l9uB_		Alignment		72.1	29	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
16	d1a2oa1		Alignment		70.3	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	c5lq8A_		Alignment		68.9	11	PDB header: periplasmic binding protein Chain: A: PDB Molecule: putative phosphonate binding protein for abc transporter; PDBTitle: 1.52 a resolution structure of phnd1 from prochlorococcus marinus (mit2 9301) in complex with methylphosphonate
18	d1heya_		Alignment		66.1	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
19	c5wq0C_		Alignment		65.0	7	PDB header: signaling protein Chain: C: PDB Molecule: stage 0 sporulation protein; PDBTitle: receiver domain of spo0a from paenisporsarcina sp. tg-14
20	c5i4cA_		Alignment		64.3	6	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: crystal structure of non-phosphorylated receiver domain of the stress2 response regulator rcsb from escherichia coli
21	c3k2dA_		Alignment	not modelled	63.6	4	PDB header: immune system Chain: A: PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from vibrio vulnificus
22	c4e7pA_		Alignment	not modelled	63.1	17	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of receiver domain of putative narI family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog beryllifluoride
23	c1rnlA_		Alignment	not modelled	62.0	15	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narI; PDBTitle: the nitrate/nitrite response regulator protein narI from narI
24	c5o8yG_		Alignment	not modelled	61.0	4	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
25	c2lpmA_		Alignment	not modelled	59.8	8	PDB header: transcription regulator Chain: A: PDB Molecule: two-component response regulator; PDBTitle: chemical shift and structure assignments for sma0114
26	c6ekhY_		Alignment	not modelled	58.9	10	PDB header: metal binding protein Chain: Y: PDB Molecule: chemotaxis protein cheY; PDBTitle: crystal structure of activated cheY from methanococcus maripaludis
27	d1jbea_		Alignment	not modelled	58.5	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	c5uicA_		Alignment	not modelled	58.5	18	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver

						domain, qseb
29	d1dbwa_	Alignment	not modelled	58.4	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
30	c4hycB_	Alignment	not modelled	58.2	15	PDB header: transcription activator Chain: B; PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
31	c5ub6B_	Alignment	not modelled	57.9	11	PDB header: metal binding protein Chain: B; PDB Molecule: phosphate-binding protein; PDBTitle: xac2383 from xanthomonas citri bound to pyrophosphate
32	d1dz3a_	Alignment	not modelled	56.8	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
33	c4de8A_	Alignment	not modelled	54.9	13	PDB header: membrane protein Chain: A; PDB Molecule: cps2a; PDBTitle: lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
34	c1kgsA_	Alignment	not modelled	54.8	14	PDB header: dna binding protein Chain: A; PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an omp/prphob homolog from thermotoga2 maritima
35	c2ixaA_	Alignment	not modelled	54.1	18	PDB header: hydrolase Chain: A; PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
36	c2h9bB_	Alignment	not modelled	53.3	7	PDB header: transcription Chain: B; PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
37	c4z9nB_	Alignment	not modelled	53.1	14	PDB header: transport protein Chain: B; PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
38	d2ayxa1	Alignment	not modelled	52.9	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
39	c3c3wB_	Alignment	not modelled	52.2	15	PDB header: transcription Chain: B; PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
40	c5z6vA_	Alignment	not modelled	51.9	10	PDB header: protein transport Chain: A; PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
41	c3ir1F_	Alignment	not modelled	51.1	4	PDB header: protein binding Chain: F; PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria meningitidis
42	d2ghra1	Alignment	not modelled	50.9	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
43	c3gxaA_	Alignment	not modelled	50.0	5	PDB header: protein binding Chain: A; PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
44	c5lwkB_	Alignment	not modelled	49.8	19	PDB header: transcription Chain: B; PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
45	c5b70B_	Alignment	not modelled	49.7	10	PDB header: transcription Chain: B; PDB Molecule: lysr family transcriptional regulator; PDBTitle: oxyr2 e204g regulatory domain from vibrio vulnificus
46	d1wd5a_	Alignment	not modelled	49.1	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
47	c3cu5B_	Alignment	not modelled	48.6	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
48	d1s8na_	Alignment	not modelled	47.4	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	c3t6kB_	Alignment	not modelled	47.0	15	PDB header: signaling protein Chain: B; PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a putative response regulator (caur_3799) from2 chloroflexus aurantiacus j-10-fl at 1.86 a resolution
50	c2rjnA_	Alignment	not modelled	47.0	24	PDB header: hydrolase Chain: A; PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
51	c3ho7A_	Alignment	not modelled	46.1	8	PDB header: transcription Chain: A; PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
52	c4if4A_	Alignment	not modelled	45.8	10	PDB header: transcription Chain: A; PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus
53	c3to5A_	Alignment	not modelled	45.6	19	PDB header: signaling protein Chain: A; PDB Molecule: chey homolog;

						PDBTitle: high resolution structure of chey3 from vibrio cholerae
54	c2ql3G_	Alignment	not modelled	45.5	5	PDB header: transcription Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
55	c5kxbB_	Alignment	not modelled	44.6	11	PDB header: signaling protein Chain: B: PDB Molecule: osmolarity two-component system protein ssk1; PDBTitle: co-crystal structure of the saccharomyces cerevisiae histidine2 phosphotransfer signaling protein ypd1 and the receiver domain of its3 downstream response regulator ssk1
56	c6m8oA_	Alignment	not modelled	44.3	12	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
57	d2esna2	Alignment	not modelled	43.8	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
58	c5f64C_	Alignment	not modelled	43.7	12	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
59	c2qv0A_	Alignment	not modelled	43.5	15	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
60	c3r0jA_	Alignment	not modelled	42.9	9	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
61	c3chgB_	Alignment	not modelled	42.8	13	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
62	c2h9qC_	Alignment	not modelled	42.4	7	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
63	c6jf1A_	Alignment	not modelled	42.2	13	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
64	c3cz5B_	Alignment	not modelled	42.2	19	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
65	c3t8yA_	Alignment	not modelled	42.1	11	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
66	c5z72B_	Alignment	not modelled	41.7	10	PDB header: transcription Chain: B: PDB Molecule: ccpc; PDBTitle: crystal structure of ccpc regulatory domain in complex with citrate2 from bacillus amyloliquefaciens
67	c2gwrA_	Alignment	not modelled	40.3	13	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
68	c3up9A_	Alignment	not modelled	40.3	7	PDB header: methionine-binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative lipoprotein (actodo_00931) from2 actinomyces odontolyticus atcc 17982 at 2.35 a resolution
69	c3cg4A_	Alignment	not modelled	40.1	17	PDB header: structural genomics, unknown function 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
70	c3n6uA_	Alignment	not modelled	39.8	10	PDB header: transcription regulator Chain: A: PDB Molecule: lysyr type regulator of tsambcd; PDBTitle: effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
71	c3cnbC_	Alignment	not modelled	39.7	19	PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding response regulator, merr family; PDBTitle: crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
72	d1i6aa_	Alignment	not modelled	39.6	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	c3sokB_	Alignment	not modelled	39.4	13	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
74	c2f7cA_	Alignment	not modelled	38.4	7	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
75	d8abpa_	Alignment	not modelled	37.7	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
76	d1p6qa_	Alignment	not modelled	37.7	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
77	c1ztoA_	Alignment	not modelled	36.7	40	PDB header: potassium channel Chain: A: PDB Molecule: potassium channel protein rck4; PDBTitle: inactivation gate of potassium channel rck4, nmr, 82

						structures
78	c3p7iA_	Alignment	not modelled	36.6	4	PDB header: transport protein Chain: A: PDB Molecule: phnd, subunit of alkylphosphonate abc transporter; PDBTitle: crystal structure of escherichia coli phnd in complex with 2-2 aminoethyl phosphonate
79	c5me4A_	Alignment	not modelled	36.3	16	PDB header: transport protein Chain: A: PDB Molecule: probable phosphite transport system-binding protein htxb; PDBTitle: the structure of htxb from pseudomonas stutzeri in complex with 2 hypophosphite to 1.52 a resolution
80	c3breA_	Alignment	not modelled	36.3	16	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
81	c2zayA_	Alignment	not modelled	36.0	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
82	d1zgza1	Alignment	not modelled	35.8	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
83	d1a04a2	Alignment	not modelled	35.6	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	c2hxrA_	Alignment	not modelled	35.5	11	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
85	c3hv2B_	Alignment	not modelled	34.7	25	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
86	c2oqrA_	Alignment	not modelled	34.2	18	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
87	c4q5tA_	Alignment	not modelled	34.2	5	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of an atmb (putative membrane lipoprotein) from2 streptococcus mutans ua159 at 1.91 a resolution
88	d1ys7a2	Alignment	not modelled	33.6	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	c4qpiC_	Alignment	not modelled	33.5	20	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
90	c5tpiA_	Alignment	not modelled	33.2	8	PDB header: hydrolase Chain: A: PDB Molecule: putative transcriptional regulator (lysr family); PDBTitle: 1.47 angstrom crystal structure of the c-terminal substrate binding2 domain of lysr family transcriptional regulator from klebsiella3 pneumoniae.
91	c3a0rB_	Alignment	not modelled	33.1	14	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)
92	c3n5iA_	Alignment	not modelled	33.1	2	PDB header: transport protein Chain: A: PDB Molecule: binding protein component of abc phosphonate transporter; PDBTitle: crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
93	c3nhzA_	Alignment	not modelled	32.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
94	c3f6cB_	Alignment	not modelled	32.3	12	PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
95	d1kgsa2	Alignment	not modelled	32.2	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c4b09F_	Alignment	not modelled	32.1	19	PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
97	c2f78A_	Alignment	not modelled	32.0	7	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate
98	c3lufB_	Alignment	not modelled	31.7	14	PDB header: signaling protein Chain: B: PDB Molecule: two-component system response regulator/ggdef domain PDBTitle: structure of probable two-component system response regulator/ggdef2 domain protein
99	c2rejA_	Alignment	not modelled	31.6	13	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
100	c5x5jA_	Alignment	not modelled	31.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader receiver domain
101	c4qhqA_	Alignment	not modelled	31.5	11	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: the structure of a nutrient binding protein from burkholderia2 cenocepacia bound to methionine

102	c3b2nA_	Alignment	not modelled	31.4	12	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
103	d1r9la_	Alignment	not modelled	31.2	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
104	c4oz9A_	Alignment	not modelled	31.1	10	PDB header: lyase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
105	c2mswA_	Alignment	not modelled	30.9	11	PDB header: transferase Chain: A: PDB Molecule: response regulator/sensor histidine kinase; PDBTitle: ligand-induced folding of a receiver domain
106	d1xfal_	Alignment	not modelled	30.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
107	c3oxnD_	Alignment	not modelled	30.2	13	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
108	d1mb3a_	Alignment	not modelled	30.0	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c2hqrA_	Alignment	not modelled	30.0	20	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
110	d1peya_	Alignment	not modelled	30.0	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
111	d1fmfa_	Alignment	not modelled	29.6	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
112	c4s05B_	Alignment	not modelled	29.5	20	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
113	c1kn7A_	Alignment	not modelled	29.5	38	PDB header: membrane protein Chain: A: PDB Molecule: voltage-gated potassium channel protein kv1.4; PDBTitle: solution structure of the tandem inactivation domain2 (residues 1-75) of potassium channel rck4 (kv1.4)
114	c4rnsA_	Alignment	not modelled	29.4	15	PDB header: transcription Chain: A: PDB Molecule: pcp degradation transcriptional activation protein; PDBTitle: pcpr inducer binding domain (apo-form)
115	c1ny5A_	Alignment	not modelled	29.3	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
116	d1b7go1	Alignment	not modelled	29.2	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
117	c3jv9B_	Alignment	not modelled	29.1	14	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
118	c5xt2C_	Alignment	not modelled	29.0	10	PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
119	c4q7eA_	Alignment	not modelled	28.5	24	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
120	d2pl1a1	Alignment	not modelled	28.5	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related