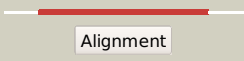

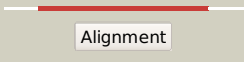

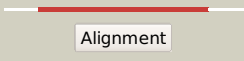

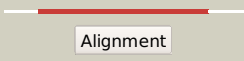

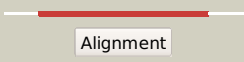

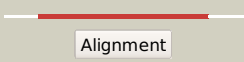

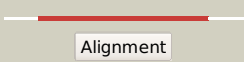

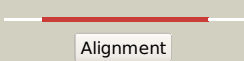

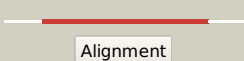

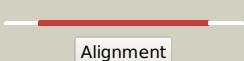

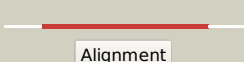












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1357c_(-)_1525299_1526222
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	42261a95480711aa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xgdA_	 Alignment		100.0	26	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
2	c4rnhA_	 Alignment		100.0	35	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
3	c5m3cB_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
4	c3pjwA_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
5	c3sy8C_	 Alignment		100.0	28	PDB header: transcription regulator Chain: C: PDB Molecule: rocr; PDBTitle: crystal structure of the response regulator rocr
6	c4fokA_	 Alignment		100.0	21	PDB header: protein binding Chain: A: PDB Molecule: fimx; PDBTitle: 1.8 a crystal structure of the fimx eal domain in complex with c-digmp
7	c3qfzB_	 Alignment		100.0	20	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
8	c3hvbB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
9	c4hjfA_	 Alignment		100.0	36	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++
10	c3hv9A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
11	c4rniA_	 Alignment		100.0	39	PDB header: hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora phosphodiesterase domain, apo form

12	c4lykB	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase yaha; PDBTitle: crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++
13	c3s83A	Alignment		100.0	36	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea
14	c4f48A	Alignment		100.0	22	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of fimxeal-c-di-gmp-pilz complexes from2 xanthomonas campestris
15	c4y8eA	Alignment		100.0	32	PDB header: metal binding protein Chain: A: PDB Molecule: pa3825 eal; PDBTitle: pa3825-eal ca-apo structure
16	c4q6jB	Alignment		100.0	31	PDB header: unknown function Chain: B: PDB Molecule: lmo0131 protein; PDBTitle: crystal structure of eal domain protein from listeria monocytogenes2 egd-e
17	c4hu4B	Alignment		100.0	32	PDB header: signaling protein,hydrolase Chain: B: PDB Molecule: oxygen sensor protein dosp; PDBTitle: crystal structure of eal domain of the e. coli dosp - dimeric form
18	c3pfaA	Alignment		100.0	25	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
19	c5m1tB	Alignment		100.0	37	PDB header: signaling protein Chain: B: PDB Molecule: muacr phosphodiesterase; PDBTitle: pamucr phosphodiesterase, c-di-gmp complex
20	c2w27A	Alignment		100.0	17	PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein, with an eal2 domain, in complex with substrate c-di-gmp and calcium
21	d2basa1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
22	c2r6oB	Alignment	not modelled	100.0	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative diguanylate cyclase/phosphodiesterase (ggdef & eal) PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
23	c5yrpB	Alignment	not modelled	100.0	34	PDB header: biosynthetic protein Chain: B: PDB Molecule: sensory box/response regulator; PDBTitle: crystal structure of the eal domain of mycobacterium smegmatis dcpa
24	c3tlqB	Alignment	not modelled	100.0	17	PDB header: transcription Chain: B: PDB Molecule: regulatory protein ydiv; PDBTitle: crystal structure of eal-like domain protein ydiv
25	c3kzpA	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative diguanylate cyclase/phosphodiesterase; PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listeria monocytigenes
26	c5hxgA	Alignment	not modelled	100.0	16	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein stm1697; PDBTitle: stm1697-flhd complex
27	c3hvwA	Alignment	not modelled	97.4	7	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
28	c4hb0B	Alignment	not modelled	96.0	13	PDB header: flavoprotein,signaling protein Chain: B: PDB Molecule: appa protein;

28	c9mrvB	Alignment	not modelled	90.0	13	PDBTitle: dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides PDB header: isomerase
29	c5zknA	Alignment	not modelled	94.6	15	Chain: A; PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
30	c3khtA	Alignment	not modelled	94.5	13	PDB header: signaling protein Chain: A; PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
31	c4r3uD	Alignment	not modelled	93.7	18	PDB header: isomerase Chain: D; PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
32	c3tvkA	Alignment	not modelled	93.6	8	PDB header: transferase Chain: A; PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
33	d1p6qa	Alignment	not modelled	93.3	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
34	d1zesa1	Alignment	not modelled	93.3	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
35	d1a53a	Alignment	not modelled	92.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
36	c2pz0B	Alignment	not modelled	92.7	13	PDB header: hydrolase Chain: B; PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
37	c3hebB	Alignment	not modelled	92.7	18	PDB header: transcription regulator Chain: B; PDB Molecule: response regulator receiver domain protein (chey); PDBTitle: crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
38	c3to5A	Alignment	not modelled	92.5	13	PDB header: signaling protein Chain: A; PDB Molecule: chey homolog; PDBTitle: high resolution structure of chey3 from vibrio cholerae
39	c6ekhY	Alignment	not modelled	92.3	15	PDB header: metal binding protein Chain: Y; PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis
40	c3b2nA	Alignment	not modelled	91.9	12	PDB header: transcription Chain: A; PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
41	d1mvoa	Alignment	not modelled	91.9	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
42	d1w25a1	Alignment	not modelled	91.8	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
43	c3q58A	Alignment	not modelled	91.6	16	PDB header: isomerase Chain: A; PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
44	c5wq0C	Alignment	not modelled	91.5	16	PDB header: signaling protein Chain: C; PDB Molecule: stage 0 sporulation protein; PDBTitle: receiver domain of spo0a from paenisporsarcina sp. tg-14
45	c2zayA	Alignment	not modelled	91.3	13	PDB header: signaling protein Chain: A; PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
46	c2p0aA	Alignment	not modelled	91.0	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
47	c3eulB	Alignment	not modelled	90.9	14	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
48	c5t3yA	Alignment	not modelled	90.7	13	PDB header: signaling protein Chain: A; PDB Molecule: two-component system response regulator; PDBTitle: solution structure of response regulator protein from burkholderia2 multivorans
49	c3gt7A	Alignment	not modelled	90.6	13	PDB header: hydrolase Chain: A; PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal transduction2 histidine kinase from syntrophus aciditrophicus
50	d1y0ea	Alignment	not modelled	90.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
51	c4h60A	Alignment	not modelled	90.4	13	PDB header: signaling protein Chain: A; PDB Molecule: chemotaxis protein chey; PDBTitle: high resolution structure of vibrio cholerae chemotaxis protein chey42 crystallized in low ph (4.0) condition
52	d1krwa	Alignment	not modelled	90.4	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						Fold: Flavodoxin-like

53	d1heya_	Alignment	not modelled	90.4	14	Superfamily: CheY-like Family: CheY-related
54	c3cg0A_	Alignment	not modelled	90.4	18	PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase PDBTitle: crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
55	c5uicA_	Alignment	not modelled	90.4	14	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
56	d1u0sy_	Alignment	not modelled	89.9	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
57	c3w9sB_	Alignment	not modelled	89.7	8	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
58	d2ayxa1	Alignment	not modelled	89.6	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c2c3zA_	Alignment	not modelled	89.3	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
60	d1jbea_	Alignment	not modelled	89.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
61	c4q7eA_	Alignment	not modelled	89.1	13	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
62	c2ayxA_	Alignment	not modelled	88.9	16	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
63	d1dz3a_	Alignment	not modelled	88.7	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c6ifhA_	Alignment	not modelled	88.5	12	PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spo0f from paenisporsarcina sp. tg-14
65	d1qkka_	Alignment	not modelled	88.4	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	c2yxba_	Alignment	not modelled	88.2	16	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
67	c3qjaA_	Alignment	not modelled	88.2	14	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
68	c1w25B_	Alignment	not modelled	88.0	15	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
69	c3nhzA_	Alignment	not modelled	87.7	17	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
70	c3t6kB_	Alignment	not modelled	87.4	13	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
71	c4e7pA_	Alignment	not modelled	87.3	12	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 berylliofluoride
72	d1i3ca_	Alignment	not modelled	87.2	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
73	c3igsB_	Alignment	not modelled	87.1	17	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
74	c3w9zA_	Alignment	not modelled	87.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
75	c4eukA_	Alignment	not modelled	86.8	14	PDB header: signaling protein Chain: A: PDB Molecule: histidine kinase 5; PDBTitle: crystal structure
76	d1eh9a3	Alignment	not modelled	86.3	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
77	c2jk1A_	Alignment	not modelled	86.0	8	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain

78	d2pl1a1	Alignment	not modelled	85.9	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
79	c3qvqB_	Alignment	not modelled	85.8	16	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase olei02445; PDBTitle: the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
80	c2zwmA_	Alignment	not modelled	85.7	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
81	c3tsmB_	Alignment	not modelled	85.7	14	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
82	d1dbwa_	Alignment	not modelled	85.6	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
83	c6bmaA_	Alignment	not modelled	85.6	14	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
84	d1m5wa_	Alignment	not modelled	85.2	12	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
85	d1k66a_	Alignment	not modelled	85.1	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
86	c4qpiC_	Alignment	not modelled	85.0	14	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
87	d1k68a_	Alignment	not modelled	84.8	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	c3wy3A_	Alignment	not modelled	84.5	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
89	d1vc4a_	Alignment	not modelled	84.3	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
90	d1yioa2	Alignment	not modelled	84.1	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
91	c1gcyA_	Alignment	not modelled	83.4	20	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
92	d2a9pa1	Alignment	not modelled	83.4	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
93	d2bhua3	Alignment	not modelled	83.3	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	d1zh2a1	Alignment	not modelled	83.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c4r7oE_	Alignment	not modelled	82.6	8	PDB header: hydrolase Chain: E: PDB Molecule: glycerophosphoryl diester phosphodiesterase, putative; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterasefrom bacillus anthraci
96	c3c3mA_	Alignment	not modelled	82.5	14	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
97	c2qr3A_	Alignment	not modelled	82.3	15	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
98	c2v82A_	Alignment	not modelled	82.2	15	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
99	c2qvqA_	Alignment	not modelled	82.2	13	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
100	d1ny5a1	Alignment	not modelled	82.0	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
101	c5iejA_	Alignment	not modelled	81.8	18	PDB header: protein Chain: A: PDB Molecule: sdrG; PDBTitle: solution structure of the bef3-activated conformation of sdrG from2 pseudomonas melonis fr1
102	d1a04a2	Alignment	not modelled	81.8	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
103	c3hdgE_	Alignment	not modelled	81.8	12	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

104	c3cnbC_	Alignment	not modelled	81.7	22	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
105	c5dlcC_	Alignment	not modelled	81.5	14	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
106	c4tvuA_	Alignment	not modelled	81.4	20	PDB header: isomerase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: crystal structure of trehalose synthase from deinococcus radiodurans2 reveals a closed conformation for catalysis of the intramolecular3 isomerization
107	c1zjaB_	Alignment	not modelled	81.3	11	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
108	c3dhuC_	Alignment	not modelled	80.9	16	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus plantarum
109	d1g5aa2	Alignment	not modelled	80.8	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
110	c5t91A_	Alignment	not modelled	80.8	14	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of b. subtilis 168 glpq in complex with bicine
111	c3gl9B_	Alignment	not modelled	80.7	12	PDB header: signaling protein Chain: B: PDB Molecule: response regulator; PDBTitle: the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
112	c5briaA_	Alignment	not modelled	80.7	16	PDB header: signaling protein Chain: A: PDB Molecule: candidate response regulator, chey; PDBTitle: bacteriophytochrome response regulator rtbrr
113	d1ps9a1	Alignment	not modelled	80.5	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
114	c5lwkB_	Alignment	not modelled	80.5	10	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
115	d1m7xa3	Alignment	not modelled	80.3	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
116	c3i42A_	Alignment	not modelled	80.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like); PDBTitle: structure of response regulator receiver domain (chey-like) from2 methylobacillus flagellatus
117	d1ys7a2	Alignment	not modelled	80.1	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	c3ch0A_	Alignment	not modelled	80.0	27	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
119	d1h5ya_	Alignment	not modelled	79.9	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
120	c3cu5B_	Alignment	not modelled	79.8	9	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