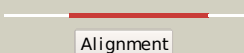
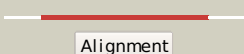
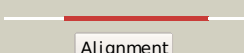
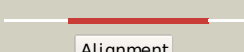
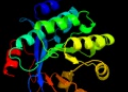
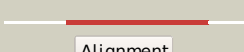
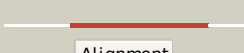
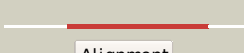
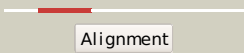
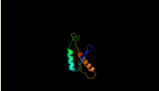


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
2	c3hvbB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
3	c3gfbB_	 Alignment		100.0	19	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-di-gmp complex
4	c3hvv9A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	 Alignment		100.0	30	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: crystal structure of eal domain from caulobacter crescentus cb15
6	c3pfmA_	 Alignment		100.0	21	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
7	c2w27A_	 Alignment		100.0	21	PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium
8	c2r6oB_	 Alignment		100.0	30	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
9	d2basa1	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
10	c3kzpA_	 Alignment		100.0	20	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
11	c1w25B_	 Alignment		99.0	10	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-di-gmp

12	c3ezuA	Alignment		98.9	14	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
13	c3breA	Alignment		98.5	16	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
14	c3i5aA	Alignment		98.4	14	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
15	c3mtkA	Alignment		97.9	13	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
16	c3icIA	Alignment		97.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
17	c3hvwA	Alignment		97.8	7	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
18	c3hvaA	Alignment		97.8	11	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
19	c3ignA	Alignment		97.8	10	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
20	c3i5cA	Alignment		97.7	16	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wpsr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wpsr from pseudomonas aeruginosa
21	d1w25a3	Alignment	not modelled	97.7	12	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
22	c3i5bA	Alignment	not modelled	97.6	16	PDB header: signaling protein Chain: A: PDB Molecule: wpsr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
23	c3qyyB	Alignment	not modelled	97.6	19	PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
24	d1y0ea	Alignment	not modelled	96.1	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
25	c3khtA	Alignment	not modelled	96.0	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
26	c2ayxA	Alignment	not modelled	95.8	15	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
27	d1mvoa	Alignment	not modelled	95.0	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	d1w25a1	Alignment	not modelled	94.6	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						Fold: Flavodoxin-like

29	d1p6qa_	Alignment	not modelled	94.5	10	Superfamily: CheY-like Family: CheY-related
30	c2zayA_	Alignment	not modelled	94.4	12	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
31	c3nhzA_	Alignment	not modelled	94.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
32	c3hebB_	Alignment	not modelled	94.0	17	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
33	c3q58A_	Alignment	not modelled	94.0	15	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
34	d2pl1a1	Alignment	not modelled	93.9	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
35	c3eulB_	Alignment	not modelled	93.7	9	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narI from mycobacterium tuberculosis
36	c2yxbA_	Alignment	not modelled	93.4	12	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
37	d1heya_	Alignment	not modelled	93.2	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
38	d1jbea_	Alignment	not modelled	93.0	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
39	c3gt7A_	Alignment	not modelled	92.7	11	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
40	c3gr7A_	Alignment	not modelled	92.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
41	d1krwa_	Alignment	not modelled	92.3	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
42	c2p0oA_	Alignment	not modelled	92.0	14	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
43	d1ys7a2	Alignment	not modelled	92.0	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
44	d1zesal	Alignment	not modelled	91.7	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	d1qkka_	Alignment	not modelled	91.5	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
46	d2a9pa1	Alignment	not modelled	91.5	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
47	d1dz3a_	Alignment	not modelled	91.3	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
48	d1k66a_	Alignment	not modelled	91.3	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	c3b2nA_	Alignment	not modelled	91.1	10	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
50	c2jk1A_	Alignment	not modelled	91.0	12	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
51	d1ua7a2	Alignment	not modelled	90.8	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
52	d1a53a_	Alignment	not modelled	90.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
53	d1i3ca_	Alignment	not modelled	90.7	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
54	c3igsB_	Alignment	not modelled	90.6	16	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

55	c2c3zA	Alignment	not modelled	90.5	13	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 <i>sulfolobus solfataricus</i>
56	c3edeB	Alignment	not modelled	90.3	19	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
57	c1cygA	Alignment	not modelled	90.3	15	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
58	d1ny5a1	Alignment	not modelled	90.3	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c3i42A	Alignment	not modelled	90.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from <i>methylobacillus flagellatus</i>
60	d1zh2a1	Alignment	not modelled	90.1	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
61	d1yioa2	Alignment	not modelled	89.9	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	d1kgsa2	Alignment	not modelled	89.4	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
63	c3czkA	Alignment	not modelled	89.2	14	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
64	d1kkoa1	Alignment	not modelled	88.9	12	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
65	d1xhfa1	Alignment	not modelled	88.4	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	c2gjlA	Alignment	not modelled	88.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
67	d1u0sy	Alignment	not modelled	88.3	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	d1a04a2	Alignment	not modelled	87.9	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
69	c2iswB	Alignment	not modelled	87.9	16	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
70	d2bhua3	Alignment	not modelled	87.8	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
71	d2ayxa1	Alignment	not modelled	87.4	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
72	d1g5aa2	Alignment	not modelled	87.3	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
73	c2rjnA	Alignment	not modelled	87.3	9	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
74	c2zwmA	Alignment	not modelled	86.8	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
75	c3cnbC	Alignment	not modelled	86.8	12	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
76	d1eh9a3	Alignment	not modelled	86.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
77	c3cg4A	Alignment	not modelled	86.6	11	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
78	c3lteH	Alignment	not modelled	86.5	13	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
79	d1xm3a	Alignment	not modelled	86.4	15	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
						PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver;

80	c3t6kB	Alignment	not modelled	86.0	10	PDBTitle: crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
81	c1tcmB	Alignment	not modelled	85.8	14	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
82	c1qhoA	Alignment	not modelled	85.7	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
83	c3nhmA	Alignment	not modelled	85.6	11	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
84	c2j48A	Alignment	not modelled	85.5	11	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
85	c3ffsC	Alignment	not modelled	85.3	14	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
86	d1fmfa	Alignment	not modelled	85.2	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
87	c3bw2A	Alignment	not modelled	85.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
88	d2guya2	Alignment	not modelled	85.1	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c2yw3E	Alignment	not modelled	85.1	16	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
90	c2qr3A	Alignment	not modelled	85.1	13	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
91	c2htmB	Alignment	not modelled	85.0	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
92	c1bagA	Alignment	not modelled	84.8	10	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
93	c1zjaB	Alignment	not modelled	84.8	12	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
94	d1rd5a	Alignment	not modelled	84.5	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
95	c3hv2B	Alignment	not modelled	84.4	8	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
96	d2r25b1	Alignment	not modelled	84.2	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
97	c3luaA	Alignment	not modelled	84.2	10	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
98	c3grcD	Alignment	not modelled	84.1	14	PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
99	c2by0A	Alignment	not modelled	84.0	14	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
100	c3gl9B	Alignment	not modelled	83.7	14	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
101	c3t8yA	Alignment	not modelled	83.7	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
102	c2pz0B	Alignment	not modelled	83.5	15	PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
103	d1zgza1	Alignment	not modelled	83.2	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

104	d1h3ga3	Alignment	not modelled	82.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	c3c3mA	Alignment	not modelled	82.5	9	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
106	c3f6cB	Alignment	not modelled	82.5	15	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
107	c1jibA	Alignment	not modelled	82.5	18	PDB header: hydrolase Chain: A: PDB Molecule: neopullulanase; PDBTitle: complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
108	c3k8kB	Alignment	not modelled	82.3	15	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
109	c3c97A	Alignment	not modelled	82.2	16	PDB header: signaling protein, transferase Chain: A: PDB Molecule: signal transduction histidine kinase; PDBTitle: crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
110	c3crnA	Alignment	not modelled	82.2	12	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
111	c2qvqA	Alignment	not modelled	82.1	9	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
112	d1ccwa	Alignment	not modelled	82.0	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
113	c3khjE	Alignment	not modelled	82.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
114	c2jrlA	Alignment	not modelled	81.9	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
115	d1lwha2	Alignment	not modelled	81.8	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
116	d1mb3a	Alignment	not modelled	81.7	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
117	d1dbwa	Alignment	not modelled	81.6	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	c1jgiA	Alignment	not modelled	81.6	9	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of the active site mutant glu328gln of2 amylsucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
119	c3kruC	Alignment	not modelled	81.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
120	c3dhuC	Alignment	not modelled	81.0	11	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum