
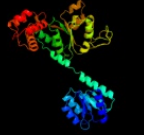


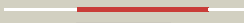




























Phyre2

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Description	P14375
Date	Thu Jan 5 11:33:59 GMT 2012
Unique Job ID	f96fd4137ff0b0e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	 Alignment		100.0	43	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	 Alignment		100.0	42	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
3	c2c99A_	 Alignment		100.0	45	PDB header: transcription regulation Chain: A: PDB Molecule: psp operon transcriptional activator; PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
4	d1ny5a2	 Alignment		100.0	50	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	c1ojlF_	 Alignment		100.0	92	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
6	c3co5B_	 Alignment		99.9	25	PDB header: transcription regulator Chain: B: PDB Molecule: putative two-component system transcriptional response PDBTitle: crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
7	c2ayxA_	 Alignment		99.9	31	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
8	c1w25B_	 Alignment		99.9	30	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
9	c3eq2A_	 Alignment		99.9	31	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
10	d2ayxa1	 Alignment		99.9	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
11	d1ny5a1	 Alignment		99.9	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

12	c2rjnA	Alignment		99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
13	c3breA	Alignment		99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
14	dlys7a2	Alignment		99.9	35	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
15	d1dbwa	Alignment		99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
16	dljbea	Alignment		99.9	33	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	d1kgsa2	Alignment		99.9	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
18	d1mvoa	Alignment		99.9	34	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
19	d1qkka	Alignment		99.9	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
20	d1peya	Alignment		99.9	37	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
21	d2a9pa1	Alignment	not modelled	99.9	34	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
22	c3cfyA	Alignment	not modelled	99.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
23	c3i5aA	Alignment	not modelled	99.9	23	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
24	c2zwmA	Alignment	not modelled	99.9	34	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus subtilis
25	d1w25a1	Alignment	not modelled	99.9	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
26	c3r0jA	Alignment	not modelled	99.9	31	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
27	d2pl1a1	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	d1yioa2	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						PDB header: transcription Chain: A: PDB Molecule: two-component system response

29	c2qr3A_	Alignment	not modelled	99.9	32	regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
30	d1krwa_	Alignment	not modelled	99.9	40	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
31	c3cu5B_	Alignment	not modelled	99.9	29	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
32	c3hv2B_	Alignment	not modelled	99.9	30	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
33	c2jrlA_	Alignment	not modelled	99.9	34	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
34	c3gt7A_	Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
35	c3jteA_	Alignment	not modelled	99.9	30	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
36	c3nhzA_	Alignment	not modelled	99.9	38	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
37	c3eulB_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
38	c1a2oB_	Alignment	not modelled	99.9	24	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
39	d1zesal	Alignment	not modelled	99.8	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	c3hdgE_	Alignment	not modelled	99.8	23	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 wolinetella3 succinogenes
41	c2qzjC_	Alignment	not modelled	99.8	27	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
42	c3t6kB_	Alignment	not modelled	99.8	33	PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
43	d1a04a2	Alignment	not modelled	99.8	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
44	d1u0sy_	Alignment	not modelled	99.8	33	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	d1p6qa_	Alignment	not modelled	99.8	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
46	d1s8na_	Alignment	not modelled	99.8	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
47	d1zh2a1	Alignment	not modelled	99.8	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
48	d1heya_	Alignment	not modelled	99.8	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	d1zgza1	Alignment	not modelled	99.8	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
50	c3crnA_	Alignment	not modelled	99.8	26	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
51	c3rqia_	Alignment	not modelled	99.8	27	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
52	c3kcnA_	Alignment	not modelled	99.8	23	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodospirillum baltica
53	c3b2nA_	Alignment	not modelled	99.8	21	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
						PDB header: transcription regulator

54	c3cz5B	Alignment	not modelled	99.8	26	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
55	c2zayA	Alignment	not modelled	99.8	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas acetoxidans
56	d1dz3a	Alignment	not modelled	99.8	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
57	d1xhfa1	Alignment	not modelled	99.8	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
58	c1ys7B	Alignment	not modelled	99.8	33	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
59	c3lteH	Alignment	not modelled	99.8	23	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
60	c3c3mA	Alignment	not modelled	99.8	33	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
61	c3hdvB	Alignment	not modelled	99.8	25	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
62	c3cnbC	Alignment	not modelled	99.8	24	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
63	d1k66a	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c2gwrA	Alignment	not modelled	99.8	34	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
65	c1kgsA	Alignment	not modelled	99.8	26	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
66	c3h1gA	Alignment	not modelled	99.8	30	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
67	c2jk1A	Alignment	not modelled	99.8	22	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
68	c3cg4A	Alignment	not modelled	99.8	23	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
69	c2qv0A	Alignment	not modelled	99.8	22	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
70	d2r25b1	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
71	c2qxyB	Alignment	not modelled	99.8	26	PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
72	c3a0rB	Alignment	not modelled	99.8	29	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein tra (tm1360)
73	c3pfiB	Alignment		99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
74	d1p2fa2	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	c3cg0A	Alignment	not modelled	99.8	26	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
76	d1r6bx3	Alignment	not modelled	99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
77	c3khtA	Alignment	not modelled	99.8	20	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis

78	c2rdmB_	Alignment	not modelled	99.8	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
79	c1zn2A_	Alignment	not modelled	99.8	25	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styrr
80	c3hzhA_	Alignment	not modelled	99.8	22	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (chey-3); PDBTitle: crystal structure of the cheX-cheY-bef3-mg+2 complex from2 borrelia burgdorferi
81	c3grcD_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
82	c3gl9B_	Alignment	not modelled	99.8	31	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
83	c3f6cB_	Alignment	not modelled	99.8	19	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
84	c3t8yA_	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
85	c3hebB_	Alignment	not modelled	99.8	27	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
86	d1mb3a_	Alignment	not modelled	99.8	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	c1p2fA_	Alignment	not modelled	99.8	27	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompR/phob homolog
88	c2qvqA_	Alignment	not modelled	99.8	26	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
89	c2hqoA_	Alignment	not modelled	99.8	22	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
90	d1i3ca_	Alignment	not modelled	99.8	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
91	c2oqrA_	Alignment	not modelled	99.8	28	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
92	d1w25a2	Alignment	not modelled	99.8	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
93	c3q9sA_	Alignment	not modelled	99.8	34	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
94	d2b4aa1	Alignment	not modelled	99.8	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c2j48A_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
96	d1a2oa1	Alignment	not modelled	99.8	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
97	d1dcfa_	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
98	c3m6mF_	Alignment	not modelled	99.8	30	PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpff complexed with rec domain of rpfc
99	c3eodA_	Alignment	not modelled	99.8	29	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
100	c3mmnA_	Alignment	not modelled	99.8	31	PDB header: transferase Chain: A: PDB Molecule: histidine kinase homolog; PDBTitle: crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
101	c3n0rA_	Alignment	not modelled	99.8	26	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
102	c3h5iA_	Alignment	not modelled	99.8	29	PDB header: transcription Chain: A: PDB Molecule: response regulator/sensory box protein/ggdef PDBTitle: crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3

						carboxydotherrus hydrogeniformans
103	c3nhmA_	Alignment	not modelled	99.8	26	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
104	c1qvrB_	Alignment	not modelled	99.8	20	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
105	c3luaA_	Alignment	not modelled	99.8	20	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
106	c3c97A_	Alignment	not modelled	99.8	21	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
107	c2hqrA_	Alignment	not modelled	99.8	18	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
108	c3snkA_	Alignment	not modelled	99.8	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
109	c3ktoA_	Alignment	not modelled	99.8	18	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
110	c3ilhA_	Alignment	not modelled	99.8	18	PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
111	c1r6bX_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
112	c3eqzB_	Alignment	not modelled	99.7	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from colwellia2 psychrerythraea
113	c3i42A_	Alignment	not modelled	99.7	22	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 methylobacillus flagellatus
114	c3nbxX_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
115	c1in8A_	Alignment	not modelled	99.7	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
116	c3pxiB_	Alignment	not modelled	99.7	18	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
117	d1um8a_	Alignment	not modelled	99.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
118	c3lufB_	Alignment	not modelled	99.7	26	PDB header: signaling protein Chain: B: PDB Molecule: two-component system response regulator/ggdef PDBTitle: structure of probable two-component system response2 regulator/ggdef domain protein
119	d1qvra3	Alignment	not modelled	99.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
120	d1k68a_	Alignment	not modelled	99.7	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related