











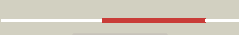
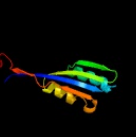





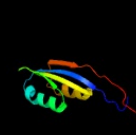




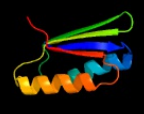



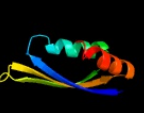




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3002c_(ilvH)_3360634_3361140
 Date Thu Aug 8 16:20:17 BST 2019
 Unique Job ID c55825e1debfeaf3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pc6C_	 Alignment		100.0	46	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
2	c2f1fA_	 Alignment		100.0	43	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
3	c2fgcA_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
4	d2fgca2	 Alignment		100.0	48	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
5	d2pc6a2	 Alignment		100.0	53	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
6	c2lvwA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
7	d2pc6a1	 Alignment		100.0	42	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
8	d2f1fa2	 Alignment		100.0	39	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
9	d2f1fa1	 Alignment		100.0	49	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
10	d2fgca1	 Alignment		99.9	40	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
11	d2f06a2	 Alignment		99.4	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like

12	d1sc6a3	Alignment		99.3	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
13	d1ygya3	Alignment		99.1	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
14	c3ibwA_	Alignment		98.7	19	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
15	c2f06B_	Alignment		98.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
16	c1ygyA_	Alignment		98.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
17	c2nyiB_	Alignment		97.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
18	d1u8sa1	Alignment		97.6	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
19	d1u8sa2	Alignment		97.6	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
20	c3n0vD_	Alignment		97.5	11	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
21	c1u8sB_	Alignment	not modelled	97.4	13	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
22	d1zpa1	Alignment	not modelled	97.3	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
23	c6dzsD_	Alignment	not modelled	97.3	30	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
24	c3nrbd_	Alignment	not modelled	97.3	16	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
25	c3obiC_	Alignment	not modelled	97.2	19	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
26	c5uscB_	Alignment	not modelled	97.2	24	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
27	c3louB_	Alignment	not modelled	97.1	13	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
						PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron

28	c1y7pB_	Alignment	not modelled	97.1	20	Chain: B; PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
29	c3o1lB_	Alignment	not modelled	97.0	10	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
30	d2qmwa2	Alignment	not modelled	97.0	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
31	c1ybaC_	Alignment	not modelled	97.0	19	PDB header: oxidoreductase Chain: C; PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
32	c3mwbA_	Alignment	not modelled	96.9	21	PDB header: lyase Chain: A; PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
33	c4lubA_	Alignment	not modelled	96.9	15	PDB header: lyase Chain: A; PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
34	c3luyA_	Alignment	not modelled	96.8	16	PDB header: isomerase Chain: A; PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
35	c3k5pA_	Alignment	not modelled	96.8	15	PDB header: oxidoreductase Chain: A; PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
36	c2qmxB_	Alignment	not modelled	96.7	15	PDB header: ligase Chain: B; PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
37	c3mtjA_	Alignment	not modelled	96.6	14	PDB header: oxidoreductase Chain: A; PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
38	c2qmwA_	Alignment	not modelled	96.4	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
39	d2f06a1	Alignment	not modelled	96.1	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
40	c3w7bB_	Alignment	not modelled	96.1	16	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
41	c3s1tB_	Alignment	not modelled	96.0	17	PDB header: transferase Chain: B; PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
42	d1phza1	Alignment	not modelled	95.9	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
43	c2dtjA_	Alignment	not modelled	95.7	21	PDB header: transferase Chain: A; PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
44	c2re1A_	Alignment	not modelled	95.6	18	PDB header: transferase Chain: A; PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
45	c5yeiF_	Alignment	not modelled	95.2	20	PDB header: transferase Chain: F; PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
46	c2zhoB_	Alignment	not modelled	94.9	20	PDB header: transferase Chain: B; PDB Molecule: aspartokinase; PDBTitle: crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
47	d2nzca1	Alignment	not modelled	94.7	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
48	d2hmfa3	Alignment	not modelled	94.2	28	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
49	c2mdaB_	Alignment	not modelled	93.7	13	PDB header: oxidoreductase Chain: B; PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
50	d2cdqa2	Alignment	not modelled	92.5	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
51	c3mahA_	Alignment	not modelled	92.5	15	PDB header: transferase Chain: A; PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
52	d2hmfa2	Alignment	not modelled	91.3	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
53	c3l76B_	Alignment	not modelled	91.1	15	PDB header: transferase Chain: B; PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis

54	c1tdjA	Alignment	not modelled	90.6	13	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
55	c6mx1A	Alignment	not modelled	88.0	16	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional aspartokinase/homoserine dehydrogenase 1; PDBTitle: the crystal structure of the regulatory domain of aspartokinase in the2 bifunctional aspartokinase/homoserine dehydrogenase 1 from3 escherichia coli str. k-12 substr. mg1655
56	c3ab4K	Alignment	not modelled	87.5	22	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
57	c2pnmA	Alignment	not modelled	87.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
58	d2j0wa2	Alignment	not modelled	83.4	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
59	d2cdqa3	Alignment	not modelled	82.9	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
60	c3c1nA	Alignment	not modelled	82.4	20	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
61	c2rjzA	Alignment	not modelled	81.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
62	c5denA	Alignment	not modelled	81.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
63	d3dhxa1	Alignment	not modelled	80.3	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
64	d2qswa1	Alignment	not modelled	78.6	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
65	c2dgbA	Alignment	not modelled	74.7	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein purs; PDBTitle: structure of thermus thermophilus purs in the p21 form
66	c3mgjA	Alignment	not modelled	74.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1480; PDBTitle: crystal structure of the saccharop_dh_n domain of mj1480 protein from2 methanococcus jannaschii. northeast structural genomics consortium3 target mjr83a.
67	c3p96A	Alignment	not modelled	72.6	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
68	d1gtda	Alignment	not modelled	71.9	18	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
69	d1rwua	Alignment	not modelled	70.2	18	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
70	c1rwuA	Alignment	not modelled	70.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
71	d2qrra1	Alignment	not modelled	69.8	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
72	c2gv1A	Alignment	not modelled	69.8	22	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: nmr solution structure of the acylphosphatase from2 eschaerichia coli
73	d1lapsa	Alignment	not modelled	69.2	18	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
74	d1tdja2	Alignment	not modelled	69.1	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
75	c2jsxA	Alignment	not modelled	66.2	18	PDB header: chaperone Chain: A: PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
76	d1urra	Alignment	not modelled	64.9	11	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
77	d2j0wa3	Alignment	not modelled	60.9	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
78	c3tviD	Alignment	not modelled	57.8	18	PDB header: transferase Chain: D: PDB Molecule: aspartokinase; PDBTitle: crystal structure of clostridium acetobutylicum aspartate kinase2 (caak): an important allosteric enzyme for industrial amino acids3 production PDB header: transferase

79	c2j0wA_	Alignment	not modelled	56.5	17	Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
80	c4hi2B_	Alignment	not modelled	55.1	16	PDB header: hydrolase Chain: B: PDB Molecule: acylphosphatase; PDBTitle: crystal structure of an acylphosphatase protein cage
81	d2acya_	Alignment	not modelled	55.0	16	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
82	c5yeiG_	Alignment	not modelled	53.1	23	PDB header: transferase Chain: G: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
83	d1w2ia_	Alignment	not modelled	52.8	19	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
84	c2zw2B_	Alignment	not modelled	51.2	13	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpsurs)
85	d1vq3a_	Alignment	not modelled	49.1	16	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
86	d1o51a_	Alignment	not modelled	46.1	16	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
87	c2kxfA_	Alignment	not modelled	41.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target gilaa.01396.a
88	c3br8A_	Alignment	not modelled	41.1	14	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: crystal structure of acylphosphatase from bacillus subtilis
89	d1t4aa_	Alignment	not modelled	39.9	18	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
90	c5t86A_	Alignment	not modelled	39.2	29	PDB header: toxin Chain: A: PDB Molecule: cdia toxin; PDBTitle: crystal structure of cdi complex from e. coli a0 34/86
91	c2bjeA_	Alignment	not modelled	38.2	21	PDB header: hydrolase Chain: A: PDB Molecule: acylphosphatase; PDBTitle: acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
92	c2lqjA_	Alignment	not modelled	37.5	13	PDB header: hydrolase Chain: A: PDB Molecule: mg2+ transport protein; PDBTitle: solution structure of the c-terminal domain of the mgtc protein from2 mycobacterium tuberculosis
93	c2dcIB_	Alignment	not modelled	36.1	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
94	d1ulra_	Alignment	not modelled	35.0	21	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
95	c3hdvB_	Alignment	not modelled	33.9	14	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
96	d1zj8a1	Alignment	not modelled	31.5	15	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
97	d1aopa2	Alignment	not modelled	30.9	6	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
98	c3eodA_	Alignment	not modelled	29.8	22	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
99	d1xjca_	Alignment	not modelled	28.9	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	c3cg4A_	Alignment	not modelled	28.7	35	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
101	c2yx5A_	Alignment	not modelled	27.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
102	c5jk5A_	Alignment	not modelled	26.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
103	c3wdoA_	Alignment	not modelled	25.7	21	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
104	d1qkka_	Alignment	not modelled	25.5	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						Fold: Ferredoxin-like

105	d1n0ua5	Alignment	not modelled	25.5	16	Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
106	c2cdqB	Alignment	not modelled	23.5	19	PDB header: transferase Chain: B; PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
107	c2n8IA	Alignment	not modelled	23.2	19	PDB header: rna binding protein/rna Chain: A; PDB Molecule: insulin-like growth factor 2 mrna-binding protein 1; PDBTitle: zipcode-binding-protein-1 kh3kh4(dd) domains in complex with the kh32 rna target
108	d2a9pa1	Alignment	not modelled	23.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c2cveA	Alignment	not modelled	22.6	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein ttha1053; PDBTitle: crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
110	c1jqcC	Alignment	not modelled	22.5	15	PDB header: ribosome Chain: C; PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
111	d1dcfa	Alignment	not modelled	22.2	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
112	d2ayxa1	Alignment	not modelled	21.7	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
113	c5fv8B	Alignment	not modelled	20.5	46	PDB header: structural protein Chain: B; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
114	c5fv8A	Alignment	not modelled	20.5	46	PDB header: structural protein Chain: A; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
115	d1ixra2	Alignment	not modelled	20.4	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain