







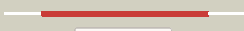












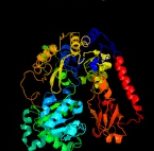


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2900c_(fdhF)_3209416_3211755
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	2257afbbde220186

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1h0hA_	 Alignment		100.0	25	PDB header: electron transport Chain: A: PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
2	c1kqgA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
3	c2v45A_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
4	c2e7zA_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahj; PDBTitle: acetylene hydratase from pelobacter acetylenicus
5	c2nyaF_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
6	c1h5nC_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
7	c5ch7E_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: E: PDB Molecule: dmsO reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
8	c1tmoA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
9	c1ogyA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
10	c2vpyE_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
11	c2iv2X_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli

12	c6cz7C_	Alignment		100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: arra; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
13	c1eu1A_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethyl sulfoxide reductase; PDBTitle: the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
14	c2ivfA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
15	c1y5iA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
16	c4aayE_	Alignment		100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: araoa; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
17	c1g8jC_	Alignment		100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
18	c1vlfO_	Alignment		100.0	17	PDB header: oxidoreductase Chain: Q: PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
19	d1kqfa2	Alignment		100.0	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
20	d2jioa2	Alignment		100.0	24	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
21	d1h0ha2	Alignment	not modelled	100.0	27	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
22	d2iv2x2	Alignment	not modelled	100.0	28	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
23	d1ogya2	Alignment	not modelled	100.0	23	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
24	d1dmra2	Alignment	not modelled	100.0	17	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
25	d1tmoa2	Alignment	not modelled	100.0	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
26	d1y5ia2	Alignment	not modelled	100.0	24	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
27	d1g8ka2	Alignment	not modelled	100.0	22	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
28	d1eu1a2	Alignment	not modelled	100.0	17	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3

29	d1vlfm2	Alignment	not modelled	100.0	17	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
30	c6f0kB	Alignment	not modelled	100.0	14	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
31	c6btmB	Alignment	not modelled	100.0	17	PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
32	c2fugC	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
33	c5t5mB	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdb; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, trigonal form at 2.5 a.
34	c6gcsA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
35	c5lnk3	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
36	d2fug32	Alignment	not modelled	100.0	18	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
37	d1kqfa1	Alignment	not modelled	99.9	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d2jioa1	Alignment	not modelled	99.9	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d1h0ha1	Alignment	not modelled	99.9	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
40	d1ogya1	Alignment	not modelled	99.9	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
41	d1dmra1	Alignment	not modelled	99.9	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
42	d1eu1a1	Alignment	not modelled	99.8	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
43	d1g8ka1	Alignment	not modelled	99.8	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
44	d1vlfm1	Alignment	not modelled	99.8	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
45	d1tmoa1	Alignment	not modelled	99.8	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
46	c5t5iL	Alignment	not modelled	99.8	26	PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdc; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
47	c2ki8A	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
48	d2iv2x1	Alignment	not modelled	99.7	18	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
49	d1y5ia1	Alignment	not modelled	99.6	10	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
50	d1tk9a	Alignment	not modelled	97.6	19	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
51	d1x92a	Alignment	not modelled	97.4	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
52	c5by2A	Alignment	not modelled	97.3	13	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
53	c3etnD	Alignment	not modelled	97.1	19	PDB header: isomerase Chain: D: PDB Molecule: putative phosphosugar isomerase involved in capsule PDBTitle: crystal structure of putative phosphosugar isomerase

						involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
54	c2x3yA_	Alignment	not modelled	97.1	12	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
55	c3g68A_	Alignment	not modelled	97.0	12	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
56	c2yvaB_	Alignment	not modelled	97.0	15	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
57	c3euaD_	Alignment	not modelled	97.0	17	PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
58	c3knzA_	Alignment	not modelled	97.0	14	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
59	c3fkjA_	Alignment	not modelled	96.9	18	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
60	d1x94a_	Alignment	not modelled	96.8	19	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
61	c2a3nA_	Alignment	not modelled	96.8	12	PDB header: sugar binding protein Chain: A: PDB Molecule: putative glucosamine-fructose-6-phosphate aminotransferase; PDBTitle: crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
62	c3fj1A_	Alignment	not modelled	96.5	15	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
63	c3trjC_	Alignment	not modelled	96.5	14	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
64	c2zj3A_	Alignment	not modelled	96.5	14	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
65	d1jeoa_	Alignment	not modelled	96.3	18	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
66	d1vima_	Alignment	not modelled	96.1	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
67	c3fxaA_	Alignment	not modelled	96.0	20	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
68	d1ozha1	Alignment	not modelled	96.0	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
69	c5cupB_	Alignment	not modelled	95.9	25	PDB header: transferase Chain: B: PDB Molecule: phosphate propanoyltransferase; PDBTitle: structure of rhodopseudomonas palustris pdul - phosphate bound form
70	c4s1wA_	Alignment	not modelled	95.8	15	PDB header: transferase Chain: A: PDB Molecule: glutamine--fructose-6-phosphate aminotransferase PDBTitle: structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus subsp. aureus mu50
71	d2ez9a1	Alignment	not modelled	95.6	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
72	c3pkiF_	Alignment	not modelled	95.6	23	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
73	d1m3sa_	Alignment	not modelled	95.6	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
74	c3k35D_	Alignment	not modelled	95.5	23	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
75	c3cvjB_	Alignment	not modelled	95.4	19	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
76	c5i01B_	Alignment	not modelled	95.2	13	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
77	d2ji7a1	Alignment	not modelled	95.1	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
78	d2djia1	Alignment	not modelled	95.1	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain

79	d2ihta1	Alignment	not modelled	95.1	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
80	c3hbaA	Alignment	not modelled	95.0	15	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
81	d1m2ka	Alignment	not modelled	94.8	31	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
82	c5oj7A	Alignment	not modelled	94.8	22	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacylase; PDBTitle: sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
83	d1ybha1	Alignment	not modelled	94.8	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
84	c2amIB	Alignment	not modelled	94.6	14	PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
85	c3shoA	Alignment	not modelled	94.5	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
86	c3jwpA	Alignment	not modelled	94.4	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein sir2 homologue; PDBTitle: crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
87	d1ma3a	Alignment	not modelled	94.4	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
88	d2b4ya1	Alignment	not modelled	94.3	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
89	c2xhzC	Alignment	not modelled	94.1	14	PDB header: isomerase Chain: C: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
90	c3zg6A	Alignment	not modelled	94.0	24	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-6; PDBTitle: the novel de-long chain fatty acid function of human sirt6
91	c1nriA	Alignment	not modelled	93.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
92	d1nria	Alignment	not modelled	93.9	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
93	d1s5pa	Alignment	not modelled	93.9	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
94	d1q6za1	Alignment	not modelled	93.7	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
95	c2pjhB	Alignment	not modelled	93.6	14	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
96	d1moqa	Alignment	not modelled	93.6	15	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
97	c4s12C	Alignment	not modelled	93.4	16	PDB header: lyase Chain: C: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
98	c4lzjD	Alignment	not modelled	93.4	17	PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: crystal structure of murq from h.influenzae with bound inhibitor
99	c2puwA	Alignment	not modelled	93.3	16	PDB header: transferase Chain: A: PDB Molecule: isomerase domain of glutamine-fructose-6-phosphate PDBTitle: the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
100	d1yc5a1	Alignment	not modelled	93.3	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
101	c5uqiA	Alignment	not modelled	92.9	17	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
102	d1ovma1	Alignment	not modelled	92.6	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
103	c4ga5H	Alignment	not modelled	92.4	22	PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
						Fold: DHS-like NAD/FAD-binding domain

104	d1zpdA1	Alignment	not modelled	92.2	14	Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
105	c5e7pA_	Alignment	not modelled	91.9	13	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
106	d2fug31	Alignment	not modelled	91.7	13	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
107	c4rjB_	Alignment	not modelled	91.6	16	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
108	d1j5xa_	Alignment	not modelled	90.7	16	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
109	c1cz5A_	Alignment	not modelled	90.4	16	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
110	d1pvdA1	Alignment	not modelled	89.9	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
111	d1e32a1	Alignment	not modelled	89.8	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
112	d1cz5a1	Alignment	not modelled	89.0	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
113	c3tbfA_	Alignment	not modelled	89.0	13	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate aminotransferase PDBTitle: c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
114	c4ivnB_	Alignment	not modelled	88.5	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
115	d1x9ja_	Alignment	not modelled	87.4	13	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
116	c2decA_	Alignment	not modelled	87.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 325aa long hypothetical protein; PDBTitle: crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
117	c4i5iA_	Alignment	not modelled	86.9	21	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog
118	c2ji6B_	Alignment	not modelled	86.8	14	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with 3-deaza-2 thdp and oxalyl-coa
119	c3lq1A_	Alignment	not modelled	86.1	13	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
120	c4ffnA_	Alignment	not modelled	85.5	21	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp