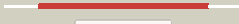



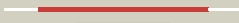




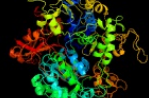









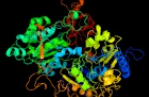




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1161_(narG)_1287333_1291031
Date	Wed Jul 31 22:05:24 BST 2019
Unique Job ID	82eac6824880aca3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y5iA_	 Alignment		100.0	46	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
2	d1y5ia2	 Alignment		100.0	46	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
3	c2ivfA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
4	c5ch7E_	 Alignment		100.0	38	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
5	c1kqgA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
6	c1h0hA_	 Alignment		100.0	18	PDB header: electron transport Chain: A: PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
7	c6cz7C_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: arra; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
8	c2nyaF_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
9	c1vifQ_	 Alignment		100.0	21	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
10	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
11	c1tmoA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia

12	c1h5nC_	Alignment		100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
13	c2e7zA_	Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
14	c1eu1A_	Alignment		100.0	27	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.
15	c2vpyE_	Alignment		100.0	27	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
16	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
17	c2iv2X_	Alignment		100.0	26	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
18	d1h0ha2	Alignment		100.0	19	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
19	d1kqfa2	Alignment		100.0	19	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	c4aayE_	Alignment		100.0	22	PDB header: oxidoreductase Chain: E: PDB Molecule: arOa; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
21	c1g8jC_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
22	d2jioa2	Alignment	not modelled	100.0	25	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	d1vlfm2	Alignment	not modelled	100.0	25	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	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
25	d1tmoa2	Alignment	not modelled	100.0	25	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	d1dmra2	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
27	d2iv2x2	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
28	d1eu1a2	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

29	d1g8ka2	Alignment	not modelled	100.0	25	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	c6btmB_	Alignment	not modelled	100.0	19	PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
31	c6f0kB_	Alignment	not modelled	100.0	22	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
32	c2fugC_	Alignment	not modelled	100.0	25	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	c6gcsA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
34	c5lnk3_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
35	c5t5mB_	Alignment	not modelled	100.0	21	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
36	d2fug32	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
37	d1y5ia1	Alignment	not modelled	100.0	46	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d1eu1a1	Alignment	not modelled	99.9	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d1vlfm1	Alignment	not modelled	99.9	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
40	d1tmoa1	Alignment	not modelled	99.9	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
41	d1kqfa1	Alignment	not modelled	99.9	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
42	d1h0ha1	Alignment	not modelled	99.9	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
43	d1dmra1	Alignment	not modelled	99.9	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
44	d2jioa1	Alignment	not modelled	99.9	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
45	d1g8ka1	Alignment	not modelled	99.9	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
46	d1ogya1	Alignment	not modelled	99.9	23	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
47	d2iv2x1	Alignment	not modelled	99.9	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
48	c2ki8A_	Alignment	not modelled	99.7	19	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
49	c5t5il_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdd; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
50	d2ihta1	Alignment	not modelled	96.9	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
51	d1ozha1	Alignment	not modelled	96.8	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
52	c3etnD_	Alignment	not modelled	96.7	11	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
						PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate

53	c3euaD_	Alignment	not modelled	96.5	17	deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
54	c2pjhB_	Alignment	not modelled	96.2	11	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
55	d1tk9a_	Alignment	not modelled	96.2	8	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
56	c4ga5H_	Alignment	not modelled	96.2	18	PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
57	d1zpd1	Alignment	not modelled	96.1	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
58	c5e7pA_	Alignment	not modelled	96.1	14	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
59	c2a3nA_	Alignment	not modelled	96.1	16	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
60	d2ez9a1	Alignment	not modelled	96.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	d1ybha1	Alignment	not modelled	96.0	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
62	d1q6za1	Alignment	not modelled	96.0	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
63	d2fug31	Alignment	not modelled	95.9	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
64	c2yvaB_	Alignment	not modelled	95.9	9	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
65	d2djia1	Alignment	not modelled	95.9	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
66	c5ifwB_	Alignment	not modelled	95.8	11	PDB header: signaling protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
67	d1vima_	Alignment	not modelled	95.7	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
68	d1x92a_	Alignment	not modelled	95.6	10	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
69	d1lovma1	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
70	d2ji7a1	Alignment	not modelled	95.5	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
71	c5cupB_	Alignment	not modelled	95.3	35	PDB header: transferase Chain: B: PDB Molecule: phosphate propanoyltransferase; PDBTitle: structure of rhodospseudomonas palustris pdul - phosphate bound form
72	c5by2A_	Alignment	not modelled	95.1	8	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
73	c3fkjA_	Alignment	not modelled	95.1	17	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
74	c3cf2B_	Alignment	not modelled	94.8	11	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
75	c1cz5A_	Alignment	not modelled	94.8	12	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)
76	d1jeoa_	Alignment	not modelled	94.6	10	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
77	d1m3sa_	Alignment	not modelled	94.5	11	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
78	d1e32a1	Alignment	not modelled	94.3	11	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
						PDB header: hydrolase

79	c3k35D_	Alignment	not modelled	94.3	16	Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
80	d1m2ka_	Alignment	not modelled	94.2	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
81	d1nrria_	Alignment	not modelled	94.2	11	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
82	c1nrria_	Alignment	not modelled	94.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from <i>Haemophilus influenzae</i>
83	c2x3ya_	Alignment	not modelled	94.0	11	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from <i>Burkholderia pseudomallei</i>
84	c6opcF_	Alignment	not modelled	93.9	10	PDB header: motor protein Chain: F: PDB Molecule: cell division control protein 48; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
85	d1cz5a1	Alignment	not modelled	93.6	12	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
86	c3pkiF_	Alignment	not modelled	93.6	19	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
87	d1pvda1	Alignment	not modelled	93.4	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
88	c3fxaA_	Alignment	not modelled	93.4	12	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (Imof2365_0531) from <i>Listeria monocytogenes</i> str. 4b f2365 at 1.60 a3 resolution
89	d2b4ya1	Alignment	not modelled	93.1	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
90	d1t9ba1	Alignment	not modelled	93.0	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
91	c3hu2C_	Alignment	not modelled	93.0	11	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
92	c4s12C_	Alignment	not modelled	92.9	13	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 <i>Yersinia enterocolitica</i> .
93	c5oj7A_	Alignment	not modelled	92.5	11	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase; PDBTitle: sirtuin 4 orthologue from <i>Xenopus tropicalis</i> in complex with adp-2 ribose
94	c4rjB_	Alignment	not modelled	92.5	13	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from <i>Bacillus subtilis</i> bound to thdp - crystal2 form ii
95	c4lzjD_	Alignment	not modelled	92.5	11	PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: crystal structure of murq from <i>H. influenzae</i> with bound inhibitor
96	c3shoA_	Alignment	not modelled	92.4	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from <i>Sphaerobacter2 thermophilus</i> (sugar isomerase domain)
97	c3zg6A_	Alignment	not modelled	92.4	19	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
98	d1ma3a_	Alignment	not modelled	92.4	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
99	c3knzA_	Alignment	not modelled	92.2	23	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from <i>Salmonella typhimurium</i> lt2 at 2.50 a resolution
100	d1x94a_	Alignment	not modelled	92.1	11	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
101	c1s3sA_	Alignment	not modelled	91.7	11	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter) PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
102	d1yc5a1	Alignment	not modelled	91.3	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
103	c3jwpA_	Alignment	not modelled	91.2	16	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
104	c3cviB_	Alignment	not modelled	91.1	15	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
105	c1ozhD_	Alignment	not modelled	91.0	15	PDB header: lyase Chain: D: PDB Molecule: acetolactate synthase, catabolic; PDBTitle: the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
106	c3cf1C_	Alignment	not modelled	90.4	11	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
107	c3fj1A_	Alignment	not modelled	90.3	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
108	c3g68A_	Alignment	not modelled	90.2	16	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
109	c5i01B_	Alignment	not modelled	88.7	10	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
110	c2dwcB_	Alignment	not modelled	88.5	18	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
111	c2vbiF_	Alignment	not modelled	87.7	13	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
112	d1s5pa_	Alignment	not modelled	87.2	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
113	c2pgnA_	Alignment	not modelled	87.0	16	PDB header: hydrolase Chain: A: PDB Molecule: cyclohexane-1,2-dione hydrolase (cdh); PDBTitle: the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
114	c2vbgB_	Alignment	not modelled	86.9	11	PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
115	c2djiA_	Alignment	not modelled	86.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
116	c4ivnB_	Alignment	not modelled	86.3	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannan-6p
117	c3hbaA_	Alignment	not modelled	85.0	14	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
118	c5g4gF_	Alignment	not modelled	84.9	12	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
119	c2ji6B_	Alignment	not modelled	84.9	13	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
120	c2panF_	Alignment	not modelled	84.6	14	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase