Email	l.a.kelley@imperial.ac.uk
Description	P46923
Date	Thu Jan 5 12:04:40 GMT 2012
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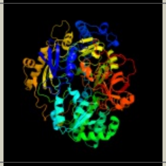
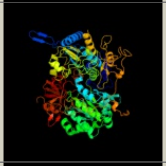
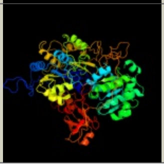
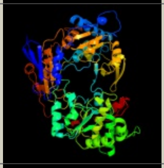
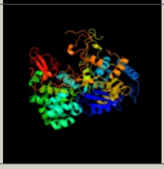
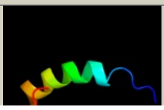
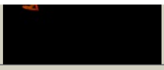
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1h5nC_	Alignment		100.0	50	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
2	c1tmoA_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
3	c1eu1A_	Alignment		100.0	49	**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.
4	c1vlfQ_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
5	c2e7zA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
6	c1kqgA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
7	c1h0hA_	Alignment		100.0	20	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
8	c1y5iA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
9	c2vpyE_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**thiosulfate reductase; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
10	c2ivfA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
11	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

12	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
13	c2v45A_	Alignment		100.0	19	**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
14	d1dmra2	Alignment		100.0	49	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
15	c2iv2X_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
16	c1g8jC_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
17	d1eu1a2	Alignment		100.0	50	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
18	d1tmoa2	Alignment		100.0	37	**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	d1vlfm2	Alignment		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
20	d1kqfa2	Alignment		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
21	d2jioa2	Alignment	not modelled	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
22	d1h0ha2	Alignment	not modelled	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
23	d1y5ia2	Alignment	not modelled	100.0	26	**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	d2iv2x2	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
25	d1ogya2	Alignment	not modelled	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
26	d1g8ka2	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
27	c2fugC_	Alignment	not modelled	100.0	17	**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
28	d2fug32	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

29	d1tmoa1	Alignment	not modelled	100.0	44	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d1eu1a1	Alignment	not modelled	100.0	45	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
31	d1dmra1	Alignment	not modelled	100.0	50	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1vlfm1	Alignment	not modelled	100.0	32	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
33	d1kqfa1	Alignment	not modelled	100.0	26	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
34	d1h0ha1	Alignment	not modelled	99.9	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d2jioa1	Alignment	not modelled	99.9	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
36	d1g8ka1	Alignment	not modelled	99.9	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
37	d1ogya1	Alignment	not modelled	99.9	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d1y5ia1	Alignment	not modelled	99.9	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
39	c2ki8A_	Alignment	not modelled	99.9	15	**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
40	d2iv2x1	Alignment	not modelled	99.8	30	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
41	d2fug31	Alignment	not modelled	96.9	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
42	d1ozha1	Alignment	not modelled	96.7	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
43	c2pjhB_	Alignment	not modelled	96.3	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
44	d2ez9a1	Alignment	not modelled	96.1	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
45	d2ihta1	Alignment	not modelled	95.9	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
46	d2djia1	Alignment	not modelled	95.9	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
47	c3knzA_	Alignment	not modelled	95.7	12	**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
48	d2ji7a1	Alignment	not modelled	95.6	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
49	c3euaD_	Alignment	not modelled	95.5	13	**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
50	d1zpda1	Alignment	not modelled	95.2	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
51	d1e32a1	Alignment	not modelled	95.1	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
52	c3k35D_	Alignment	not modelled	95.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
53	c2pq4B_	Alignment		94.8	38	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-

						352 signal peptide
54	c1cz5A_	Alignment	not modelled	94.7	14	**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)
55	d1q6za1	Alignment	not modelled	94.7	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
56	c3pkiF_	Alignment	not modelled	94.6	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
57	d1tk9a_	Alignment	not modelled	94.5	11	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
58	d1ybha1	Alignment	not modelled	94.4	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
59	d1ovma1	Alignment	not modelled	94.3	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
60	d1x94a_	Alignment	not modelled	94.2	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
61	d1cz5a1	Alignment	not modelled	93.8	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
62	d1ma3a_	Alignment	not modelled	93.8	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
63	d2b4ya1	Alignment	not modelled	93.7	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
64	c1s3sA_	Alignment	not modelled	93.1	12	**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
65	c2a3nA_	Alignment	not modelled	93.0	15	**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
66	c3fxaA_	Alignment	not modelled	93.0	18	**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
67	c3fkjA_	Alignment	not modelled	92.9	14	**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
68	c3etnD_	Alignment	not modelled	92.8	16	**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
69	c3hu2C_	Alignment	not modelled	92.7	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
70	d1m2ka_	Alignment	not modelled	92.6	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
71	c3cvjB_	Alignment	not modelled	91.7	18	**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
72	c3jwpA_	Alignment	not modelled	91.7	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
73	d1s5pa_	Alignment	not modelled	91.5	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
74	d1t9ba1	Alignment	not modelled	91.1	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
75	d1yc5a1	Alignment	not modelled	90.8	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
76	c2x7jA_	Alignment	not modelled	90.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
77	c3fj1A_	Alignment	not modelled	89.5	17	**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
78	c2yvaB_	Alignment	not modelled	89.4	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
79	c2e76D_	Alignment	not modelled	89.2	22	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
80	c3hbaA_	Alignment	not modelled	89.2	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	c3cf1C_	Alignment	not modelled	88.8	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
82	d1x92a_	Alignment	not modelled	88.3	10	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
83	d1vima_	Alignment	not modelled	87.4	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
84	c3g68A_	Alignment	not modelled	87.2	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
85	d1m3sa_	Alignment	not modelled	87.1	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
86	d1pvda1	Alignment	not modelled	85.9	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
87	c2x3yA_	Alignment	not modelled	84.5	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
88	d1jeoa_	Alignment	not modelled	83.7	22	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
89	d1qcsa1	Alignment	not modelled	83.4	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
90	c2vbiF_	Alignment	not modelled	83.4	11	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
91	c2zj3A_	Alignment	not modelled	82.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
92	c2djiA_	Alignment	not modelled	82.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
93	c1ozhD_	Alignment	not modelled	82.5	11	**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.
94	c1wlfA_	Alignment	not modelled	81.8	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1; **PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
95	c3shoA_	Alignment	not modelled	81.4	14	**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)
96	d1moqa_	Alignment	not modelled	81.3	24	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
97	c2amlB_	Alignment	not modelled	81.2	19	**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
98	c2ev2B_	Alignment	not modelled	81.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
99	c1p84E_	Alignment	not modelled	80.9	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
100	c1zpdA_	Alignment	not modelled	80.7	9	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
101	c1jxaA_	Alignment	not modelled	80.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
102	d1ylea1	Alignment	not modelled	80.2	26	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
						PDB header:oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-

103	c2fynO_	Alignment	not modelled	79.8	35	sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
104	c2decA_	Alignment	not modelled	78.0	15	**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
105	c3lq1A_	Alignment	not modelled	77.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
106	d1wlfa2	Alignment	not modelled	76.9	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
107	c2vbgB_	Alignment	not modelled	75.7	12	**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
108	c1nriA_	Alignment	not modelled	72.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
109	d1nria_	Alignment	not modelled	72.3	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
110	c1ovmC_	Alignment	not modelled	72.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
111	c2xhzC_	Alignment	not modelled	71.8	21	**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
112	c2ji6B_	Alignment	not modelled	70.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
113	c2fyuE_	Alignment	not modelled	70.0	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
114	c1t9dB_	Alignment	not modelled	69.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetolactate synthase, mitochondrial; **PDBTitle:** crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
115	c2panF_	Alignment	not modelled	66.8	17	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
116	c2yujA_	Alignment	not modelled	65.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
117	d1cr5a1	Alignment	not modelled	65.6	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
118	c1y6uA_	Alignment	not modelled	64.8	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
119	c3trjC_	Alignment	not modelled	64.7	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
120	c3fqmA_	Alignment	not modelled	64.1	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural protein 5a; **PDBTitle:** crystal structure of a novel dimeric form of hcv ns5a domain i protein