Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77374
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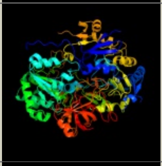
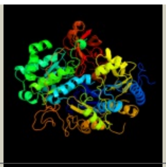
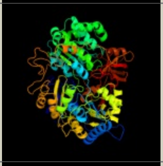
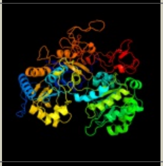
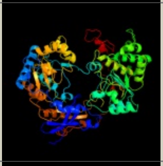
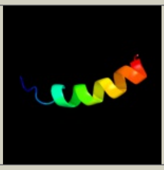
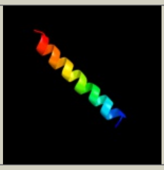
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y5iA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
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	c1tmoA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
4	c1h5nC_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
5	c1h0hA_	Alignment		100.0	24	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
6	c2e7zA_	Alignment		100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
7	c1eu1A_	Alignment		100.0	29	**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.
8	c1vlfQ_	Alignment		100.0	25	**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
9	c2vpyE_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**thiosulfate reductase; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
10	c2ivfA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
11	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

12	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
13	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
14	c2iv2X_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
15	c1g8jC_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
16	d1kqfa2	Alignment		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
17	d1y5ia2	Alignment		100.0	30	**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	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
19	d2jioa2	Alignment		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
20	d1dmra2	Alignment		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
21	d1vlfm2	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
22	d1eu1a2	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	d1h0ha2	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
24	d2iv2x2	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
25	d1ogya2	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
26	d1g8ka2	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
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	d1kqfa1	Alignment	not modelled	100.0	26	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d1tmoa1	Alignment	not modelled	100.0	34	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
31	d1dmra1	Alignment	not modelled	100.0	34	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1eu1a1	Alignment	not modelled	100.0	36	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
33	d1vlfm1	Alignment	not modelled	100.0	35	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
34	d1h0ha1	Alignment	not modelled	99.9	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d2jioa1	Alignment	not modelled	99.9	26	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
36	d1ogya1	Alignment	not modelled	99.9	26	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
37	d1g8ka1	Alignment	not modelled	99.9	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d1y5ia1	Alignment	not modelled	99.9	27	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d2iv2x1	Alignment	not modelled	99.9	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c2ki8A_	Alignment	not modelled	99.8	17	**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
41	d2fug31	Alignment	not modelled	96.9	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
42	d2ihta1	Alignment	not modelled	96.4	16	**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	96.2	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
44	d1ozha1	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	d1q6za1	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
46	d1e32a1	Alignment	not modelled	95.3	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
47	d2ji7a1	Alignment	not modelled	95.2	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
48	d2ez9a1	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
49	c2pq4B_	Alignment		95.1	41	**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
50	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)
51	d1ybha1	Alignment	not modelled	94.6	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
52	c3k35D_	Alignment	not modelled	94.4	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
53	d2djia1	Alignment	not modelled	94.3	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain

54	d1zpda1	Alignment	not modelled	94.0	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
55	d1x92a_	Alignment	not modelled	94.0	12	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
56	c2x3yA_	Alignment	not modelled	93.9	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
57	c3pkiF_	Alignment	not modelled	93.7	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
58	d1cz5a1	Alignment	not modelled	93.7	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
59	d1tk9a_	Alignment	not modelled	93.2	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
60	d1x94a_	Alignment	not modelled	93.2	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
61	d1ovma1	Alignment	not modelled	93.0	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
62	d1t9ba1	Alignment	not modelled	92.7	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
63	d1ma3a_	Alignment	not modelled	92.5	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
64	c3jwpA_	Alignment	not modelled	92.5	13	**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
65	c3hu2C_	Alignment	not modelled	91.8	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
66	c1s3sA_	Alignment	not modelled	91.6	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
67	d2b4ya1	Alignment	not modelled	91.6	7	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
68	c2e76D_	Alignment		91.3	27	**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
69	c3etnD_	Alignment	not modelled	90.8	13	**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
70	c3knzA_	Alignment	not modelled	90.8	16	**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
71	c3fxaA_	Alignment	not modelled	90.4	17	**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
72	c1p84E_	Alignment	not modelled	89.6	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
73	d1yc5a1	Alignment	not modelled	89.4	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
74	c2dwcB_	Alignment	not modelled	89.3	10	**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
75	c2yvaB_	Alignment	not modelled	89.3	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
76	c3cf1C_	Alignment	not modelled	89.2	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
77	c3euaD_	Alignment	not modelled	88.3	16	**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
78	d1pvda1	Alignment	not modelled	87.6	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
79	d1m2ka_	Alignment	not modelled	87.4	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
80	d1kjqa2	Alignment	not modelled	86.6	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
81	d1s5pa_	Alignment	not modelled	85.4	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
82	c2fynO_	Alignment	not modelled	84.5	29	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
83	c1kjjA_	Alignment	not modelled	84.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
84	d1ylea1	Alignment	not modelled	81.5	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
85	c2fyuE_	Alignment		80.9	10	**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
86	d1vima_	Alignment	not modelled	80.8	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
87	c2ji6B_	Alignment	not modelled	80.7	15	**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
88	c1wlfA_	Alignment	not modelled	80.7	33	**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
89	c2a3nA_	Alignment	not modelled	79.9	11	**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
90	d1m3sa_	Alignment	not modelled	78.5	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
91	d1qcsa1	Alignment	not modelled	74.9	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
92	d1jeoa_	Alignment	not modelled	74.9	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
93	c1jscA_	Alignment	not modelled	74.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
94	c3g68A_	Alignment	not modelled	74.0	15	**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
95	d1wlfa2	Alignment	not modelled	73.4	32	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
96	c2x7jA_	Alignment	not modelled	73.1	16	**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
97	c3q2oB_	Alignment	not modelled	71.2	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
98	c3trjC_	Alignment	not modelled	70.6	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
99	c3fkjA_	Alignment	not modelled	70.4	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
100	c3orqA_	Alignment	not modelled	68.0	17	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
						PDB header:structural genomics, unknown function

101	c3m7aA_	Alignment	not modelled	65.2	38	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution
102	c3lq1A_	Alignment	not modelled	65.0	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
103	c3glsC_	Alignment	not modelled	64.8	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
104	d1cr5a1	Alignment	not modelled	64.4	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
105	c2amlB_	Alignment	not modelled	63.2	18	**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
106	c2l66B_	Alignment	not modelled	62.9	27	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
107	c3iwfA_	Alignment	not modelled	62.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
108	c1qdnA_	Alignment	not modelled	59.8	15	**PDB header:**fusion protein **Chain:** A: **PDB Molecule:**protein (n-ethylmaleimide sensitive fusion **PDBTitle:** amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
109	d1nria_	Alignment	not modelled	58.7	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
110	c1nriA_	Alignment	not modelled	58.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
111	d1b25a1	Alignment	not modelled	56.3	17	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
112	c3pjyB_	Alignment	not modelled	55.4	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
113	d2vbua1	Alignment	not modelled	54.7	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
114	c3cvjB_	Alignment	not modelled	53.8	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
115	c2zj3A_	Alignment	not modelled	53.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
116	c3uvzB_	Alignment	not modelled	52.4	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
117	d1moqa_	Alignment	not modelled	49.5	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
118	c2xhzC_	Alignment	not modelled	49.0	15	**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
119	c2ev2B_	Alignment	not modelled	49.0	21	**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
120	d1d4oa_	Alignment	not modelled	48.4	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)