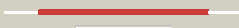









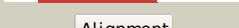

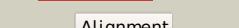

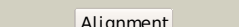

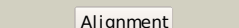

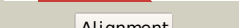

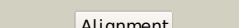



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P31574
Date	Thu Jan 5 11:48:20 GMT 2012
Unique Job ID	93024fd1f3927cac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1efpC_	 Alignment		100.0	31	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
2	d1efva2	 Alignment		100.0	45	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
3	d1efpa2	 Alignment		100.0	48	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
4	d3clsd2	 Alignment		100.0	42	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
5	c3ih5A_	 Alignment		100.0	16	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
6	d1efva1	 Alignment		100.0	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
7	d3clsd1	 Alignment		100.0	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
8	c1t9gR_	 Alignment		100.0	14	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: electron transfer flavoprotein alpha-subunit, PDBTitle: structure of the human mcad:etf complex
9	c1o94D_	 Alignment		100.0	17	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
10	d1efpa1	 Alignment		100.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
11	c3fetA_	 Alignment		100.0	18	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein subunit alpha related PDBTitle: crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum

12	d1efvb_	Alignment		99.8	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
13	d3clsc1	Alignment		99.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
14	d1efpb_	Alignment		99.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
15	d1o94c_	Alignment		99.7	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
16	d1t9ba1	Alignment		98.9	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
17	d1ozha1	Alignment		98.8	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
18	d2ez9a1	Alignment		98.5	23	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
19	d2ji7a1	Alignment		98.4	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
20	d2ihta1	Alignment		98.3	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
21	d1q6za1	Alignment	not modelled	98.0	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
22	c1ozhD_	Alignment	not modelled	98.0	16	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.
23	d1ybha1	Alignment	not modelled	97.8	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
24	c2q27B_	Alignment	not modelled	97.7	13	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
25	d2djia1	Alignment	not modelled	97.6	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
26	c1powA_	Alignment	not modelled	97.6	22	PDB header: oxidoreductase(oxygen as acceptor) Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
27	c2pgnA_	Alignment	not modelled	97.5	14	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
28	c2djia_	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2

						viridans containing fad
29	c3lq1A_	Alignment	not modelled	97.4	15	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
30	c2ji6B_	Alignment	not modelled	97.4	17	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
31	c1t9dB_	Alignment	not modelled	97.3	17	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
32	c1upaC_	Alignment	not modelled	97.1	14	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
33	c1yi1A_	Alignment	not modelled	97.0	16	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
34	c2ag1A_	Alignment	not modelled	97.0	20	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
35	c3eyaE_	Alignment	not modelled	96.9	16	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
36	c2panF_	Alignment	not modelled	96.7	20	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
37	c2v3wC_	Alignment	not modelled	96.6	15	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
38	c2x7jA_	Alignment	not modelled	96.6	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
39	d1zpdA1	Alignment	not modelled	96.5	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
40	d1pvdA1	Alignment	not modelled	96.2	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
41	d1m2ka_	Alignment	not modelled	96.1	23	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
42	d1yc5a1	Alignment	not modelled	96.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
43	c1jscA_	Alignment	not modelled	95.9	14	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
44	d2b4ya1	Alignment	not modelled	95.4	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
45	c3glsC_	Alignment	not modelled	95.2	27	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
46	c3k35D_	Alignment	not modelled	95.1	22	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
47	c1zpdA_	Alignment	not modelled	94.9	14	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
48	d1ma3a_	Alignment	not modelled	94.9	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
49	c3pkiF_	Alignment	not modelled	94.5	20	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
50	c2vbiF_	Alignment	not modelled	94.4	11	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
51	c2jlaD_	Alignment	not modelled	94.3	11	PDB header: transferase Chain: D: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
52	d1q1aa_	Alignment	not modelled	94.3	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
53	c1q14A_	Alignment	not modelled	93.5	13	PDB header: hydrolase Chain: A: PDB Molecule: hst2 protein; PDBTitle: structure and autoregulation of the yeast hst2 homolog of

						sir2
54	d1ovma1	Alignment	not modelled	93.2	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
55	c2w93A	Alignment	not modelled	92.7	17	PDB header: lyase Chain: A: PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
56	d1s5pa	Alignment	not modelled	92.5	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
57	d1j8fa	Alignment	not modelled	91.7	32	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
58	c3jwpA	Alignment	not modelled	90.7	22	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
59	c2hjhB	Alignment	not modelled	90.0	16	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
60	c1ovmC	Alignment	not modelled	89.6	13	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
61	c2vbgB	Alignment	not modelled	88.9	13	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
62	c2nxwB	Alignment	not modelled	87.5	13	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
63	c3cf4G	Alignment	not modelled	84.7	21	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
64	d1uana	Alignment	not modelled	83.4	13	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
65	d1tq8a	Alignment	not modelled	82.7	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
66	d1x94a	Alignment	not modelled	78.7	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
67	c2x3yA	Alignment	not modelled	77.3	15	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
68	c2ixdB	Alignment	not modelled	70.3	11	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from2 bacillus cereus
69	c2pn1A	Alignment	not modelled	67.2	16	PDB header: ligase Chain: A: PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
70	c3fxaA	Alignment	not modelled	59.9	14	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
71	c2ze5A	Alignment	not modelled	53.9	19	PDB header: transferase Chain: A: PDB Molecule: isopentenyl transferase; PDBTitle: crystal structure of adenosine phosphate-isopentenyltransferase
72	c1nvmG	Alignment	not modelled	52.7	12	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
73	c3shoA	Alignment	not modelled	52.0	21	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)
74	d1tk9a	Alignment	not modelled	51.7	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
75	c2xhzC	Alignment	not modelled	49.5	13	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
76	c1nriA	Alignment	not modelled	46.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
77	d1nria	Alignment	not modelled	46.1	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain

78	c3d3qB_	Alignment	not modelled	45.1	16	PDB header: transferase Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
79	c3dahB_	Alignment	not modelled	44.4	10	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
80	d1moqa_	Alignment	not modelled	44.1	13	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
81	c2dwcB_	Alignment	not modelled	44.0	20	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
82	c3uvzB_	Alignment	not modelled	42.5	16	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
83	d2iyva1	Alignment	not modelled	42.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
84	c2amlB_	Alignment	not modelled	41.3	20	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	d1kjqaz	Alignment	not modelled	40.9	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
86	c3crqA_	Alignment	not modelled	40.1	27	PDB header: transferase Chain: A: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: structure of trna dimethylallyltransferase: rna2 modification through a channel
87	c3exaD_	Alignment	not modelled	40.0	23	PDB header: transferase Chain: D: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
88	c1u9yD_	Alignment	not modelled	38.1	13	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
89	c3ga2A_	Alignment	not modelled	36.3	14	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
90	c3a8tA_	Alignment	not modelled	35.1	31	PDB header: transferase Chain: A: PDB Molecule: adenylate isopentenyltransferase; PDBTitle: plant adenylate isopentenyltransferase in complex with atp
91	c1dkrB_	Alignment	not modelled	33.6	19	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
92	c3euaD_	Alignment	not modelled	32.9	29	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
93	d1jmva_	Alignment	not modelled	32.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
94	c3bo9B_	Alignment	not modelled	30.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkane dioxygenase; PDBTitle: crystal structure of putative nitroalkane dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
95	c3t61A_	Alignment	not modelled	30.8	9	PDB header: transferase Chain: A: PDB Molecule: gluconokinase; PDBTitle: crystal structure of a gluconokinase from sinorhizobium meliloti 1021
96	d1q77a_	Alignment	not modelled	30.5	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
97	d1kaga_	Alignment	not modelled	30.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
98	c3trjC_	Alignment	not modelled	29.7	12	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
99	c3fozB_	Alignment	not modelled	28.9	27	PDB header: transferase/rna Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
100	c3m0zD_	Alignment	not modelled	28.7	22	PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from klebsiella2 pneumoniae.

101	d1a9xa4	Alignment	not modelled	28.5	9	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
102	d1nvma2	Alignment	not modelled	27.4	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
103	c3tbfa_	Alignment	not modelled	27.3	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.
104	c2p3wB_	Alignment	not modelled	25.8	21	PDB header: protein binding Chain: B: PDB Molecule: probable serine protease htra3; PDBTitle: crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
105	d1pama3	Alignment	not modelled	25.5	31	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
106	d1nt2a_	Alignment	not modelled	25.4	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue
107	c3eplA_	Alignment	not modelled	24.8	26	PDB header: transferase/rna Chain: A: PDB Molecule: trna isopentenyltransferase; PDBTitle: crystallographic snapshots of eukaryoti c2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
108	c1rr2A_	Alignment	not modelled	24.8	10	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
109	d1rkba_	Alignment	not modelled	24.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
110	c3be4A_	Alignment	not modelled	23.5	16	PDB header: transferase Chain: A: PDB Molecule: adenylate kinase; PDBTitle: crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360
111	c3lpnB_	Alignment	not modelled	23.5	8	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
112	d1csla3	Alignment	not modelled	22.1	38	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
113	c3muxB_	Alignment	not modelled	21.8	23	PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
114	c3m6yA_	Alignment	not modelled	21.4	23	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
115	c2k1ha_	Alignment	not modelled	21.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ser13; PDBTitle: solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
116	d1g8sa_	Alignment	not modelled	20.7	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue