Phyre^2

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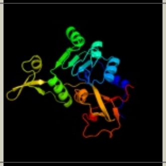
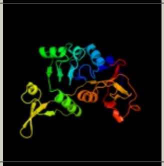
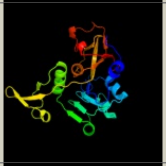
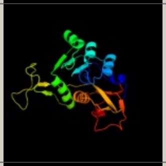
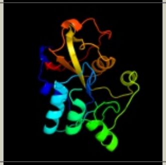
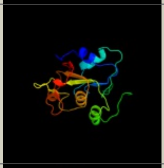
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cdkA_	Alignment		100.0	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
2	d1k6da_	Alignment		100.0	100	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
3	d1ooya2	Alignment		100.0	39	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
4	d2ahua2	Alignment		100.0	26	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
5	c3rrlC_	Alignment		100.0	42	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
6	d1poia_	Alignment		100.0	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
7	c2ahvC_	Alignment		100.0	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative enzyme ydif; **PDBTitle:** crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
8	c1ooyA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase, **PDBTitle:** succinyl-coa:3-ketoacid coa transferase from pig heart
9	c2g39A_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
10	c2nvvF_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
11	c3gk7A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum

12	c2hj0A_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative citrate lyase, alfa subunit; **PDBTitle:** crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 (casp target).
13	c2oasA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
14	d2g39a1	Alignment		100.0	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
15	c1xr4B_	Alignment		100.0	26	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**putative citrate lyase alpha chain/citrate-acp transferase; **PDBTitle:** x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium]
16	c3eh7A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
17	c3d3uA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
18	d1xr4a1	Alignment		99.9	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
19	c1m0sA_	Alignment		98.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
20	c3l7oB_	Alignment		98.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
21	c1uj6A_	Alignment	not modelled	97.8	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
22	c2f8mB_	Alignment	not modelled	97.8	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
23	d2g39a2	Alignment	not modelled	97.7	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
24	c3kwmC_	Alignment	not modelled	97.7	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
25	c1lk5C_	Alignment	not modelled	97.7	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
26	d1m0sa1	Alignment	not modelled	97.7	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
27	c3hheA_	Alignment	not modelled	97.7	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
28	c3cdkD_	Alignment	not modelled	97.6	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
						PDB header:isomerase

29	c1lkzB_	Alignment	not modelled	97.6	19	**Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
30	c2pjmA_	Alignment	not modelled	97.6	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
31	d1xr4a2	Alignment	not modelled	97.5	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
32	c3u7jA_	Alignment	not modelled	97.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
33	d1uj4a1	Alignment	not modelled	97.1	23	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
34	c1xtzA_	Alignment	not modelled	97.1	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
35	d1lk5a1	Alignment	not modelled	96.5	28	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
36	d1ooya1	Alignment	not modelled	96.4	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
37	d1poib_	Alignment	not modelled	96.2	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
38	d2ahua1	Alignment	not modelled	95.8	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
39	c3ecsD_	Alignment	not modelled	92.3	21	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
40	d1vb5a_	Alignment	not modelled	87.6	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
41	d1o8bb1	Alignment	not modelled	85.0	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
42	c1ydmC_	Alignment	not modelled	83.7	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein yqgn; **PDBTitle:** x-ray structure of northeast structural genomics target sr44
43	c2jcbA_	Alignment	not modelled	81.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase family protein; **PDBTitle:** the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)
44	d1t9ka_	Alignment	not modelled	80.7	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
45	c3a11D_	Alignment	not modelled	72.6	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
46	d1soua_	Alignment	not modelled	71.7	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
47	d1sbqa_	Alignment	not modelled	68.3	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
48	c1u3fA_	Alignment	not modelled	68.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydrofolate synthetase; **PDBTitle:** structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
49	c3nzeB_	Alignment	not modelled	54.8	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
50	d2gnpa1	Alignment	not modelled	54.2	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
51	d1wkca_	Alignment	not modelled	53.7	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
52	d1t5oa_	Alignment	not modelled	52.9	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
53	c2yvkA_	Alignment	not modelled	45.2	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
54	c3hy4A_	Alignment	not modelled	45.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase; **PDBTitle:** structure of human mthfs with n5-iminium phosphate

55	d1o8ba1	Alignment	not modelled	42.4	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
56	d3efba1	Alignment	not modelled	39.3	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
57	c2w48D_	Alignment	not modelled	37.9	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
58	c1dbgA_	Alignment	not modelled	32.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
59	d1ofla_	Alignment	not modelled	27.9	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
60	d2nyga1	Alignment	not modelled	23.0	20	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
61	c3kv1A_	Alignment	not modelled	18.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
62	d2grea1	Alignment	not modelled	17.3	6	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
63	c3smaD_	Alignment	not modelled	17.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
64	d1ru4a_	Alignment	not modelled	16.7	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate transeliminase
65	d2okga1	Alignment	not modelled	16.6	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
66	c3bo9B_	Alignment	not modelled	16.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nitroalkan dioxygenase; **PDBTitle:** crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
67	d2r5fa1	Alignment	not modelled	16.0	6	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
68	d1gwma_	Alignment	not modelled	15.3	10	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 29 carbohydrate binding module, CBM29
69	d1t3ka_	Alignment	not modelled	14.5	10	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
70	c2ri0B_	Alignment	not modelled	13.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
71	c3myrE_	Alignment	not modelled	13.5	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
72	d1vlfm1	Alignment	not modelled	12.6	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
73	d1kqfa1	Alignment	not modelled	12.6	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
74	d2jioa1	Alignment	not modelled	11.5	21	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
75	d1gmxa_	Alignment	not modelled	10.3	14	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
76	d1y5ia1	Alignment	not modelled	9.3	28	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
77	c1wcuA_	Alignment	not modelled	9.3	12	**PDB header:**carbohydrate binding **Chain:** A: **PDB Molecule:**non-catalytic protein 1; **PDBTitle:** cbm29_1, a family 29 carbohydrate binding module from2 piromyces equi
78	d1h0ha1	Alignment	not modelled	9.2	21	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
79	d1g8ka1	Alignment	not modelled	8.4	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
80	c3rgwS_	Alignment	not modelled	8.4	8	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster

81	d1vqod1	Alignment	not modelled	8.2	33	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**Ribosomal protein L5
82	d1frfs_	Alignment	not modelled	8.1	10	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
83	d1ogya1	Alignment	not modelled	7.8	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
84	c4a1cD_	Alignment	not modelled	7.8	14	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l11; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
85	d1eu1a1	Alignment	not modelled	7.5	32	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
86	d1wv2a_	Alignment	not modelled	7.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
87	d1xpna_	Alignment	not modelled	7.3	17	**Fold:**Prealbumin-like **Superfamily:**Hypothetical protein PA1324 **Family:**Hypothetical protein PA1324
88	d1tmoa1	Alignment	not modelled	7.2	28	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
89	c2r47C_	Alignment	not modelled	6.9	26	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
90	d1l7da2	Alignment	not modelled	6.7	19	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
91	c2ki8A_	Alignment	not modelled	6.6	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
92	d1htwa_	Alignment	not modelled	6.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
93	c2zfnA_	Alignment	not modelled	6.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
94	c3tdqB_	Alignment	not modelled	6.2	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
95	c2wpnA_	Alignment	not modelled	6.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
96	c3e4fB_	Alignment	not modelled	6.1	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
97	c3d35A_	Alignment	not modelled	5.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** crystal structure of rtt109-ac-coa complex
98	d2o0ma1	Alignment	not modelled	5.8	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
99	c2o0mA_	Alignment	not modelled	5.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis