Phyre²

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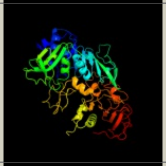
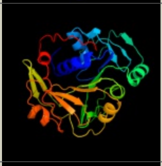
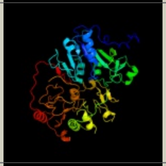
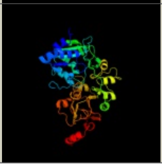
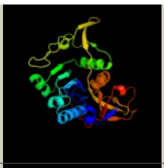
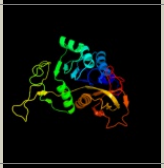
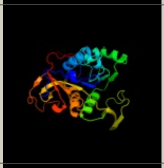
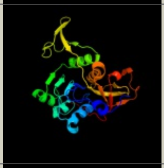
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ahvC_	Alignment		100.0	100	**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
2	c1ooyA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase, **PDBTitle:** succinyl-coa:3-ketoacid coa transferase from pig heart
3	d2ahua2	Alignment		100.0	98	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
4	d2ahua1	Alignment		100.0	97	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
5	c3gk7A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
6	c2g39A_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
7	c2oasA_	Alignment		100.0	21	**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.
8	c2hj0A_	Alignment		100.0	20	**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).
9	c2nvvF_	Alignment		100.0	16	**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.
10	c1xr4B_	Alignment		100.0	20	**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]
11	c3eh7A_	Alignment		100.0	23	**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

12	d1ooya2	Alignment		100.0	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
13	d1poia_	Alignment		100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
14	c3d3uA_	Alignment		100.0	20	**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
15	c3cdkA_	Alignment		100.0	26	**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
16	c3rrlC_	Alignment		100.0	26	**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
17	d1poib_	Alignment		100.0	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
18	d1k6da_	Alignment		100.0	28	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
19	d1ooya1	Alignment		100.0	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
20	c3cdkD_	Alignment		100.0	24	**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
21	d2g39a1	Alignment	not modelled	100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
22	d2g39a2	Alignment	not modelled	100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
23	d1xr4a2	Alignment	not modelled	100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
24	d1xr4a1	Alignment	not modelled	99.9	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
25	c3l7oB_	Alignment	not modelled	98.1	21	**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
26	c3hheA_	Alignment	not modelled	98.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
27	c1lk5C_	Alignment	not modelled	98.0	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
28	c3kwmC_	Alignment	not modelled	97.9	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
						Fold: NagB/RpiA/CoA transferase-like

29	d1m0sa1	Alignment	not modelled	97.9	19	**Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
30	c1m0sA_	Alignment	not modelled	97.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
31	c2f8mB_	Alignment	not modelled	97.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
32	c1lkzB_	Alignment	not modelled	97.6	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
33	c2pjmA_	Alignment	not modelled	97.5	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
34	d1lk5a1	Alignment	not modelled	97.4	23	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
35	c1uj6A_	Alignment	not modelled	97.3	20	**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
36	d1uj4a1	Alignment	not modelled	97.1	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
37	c1xtzA_	Alignment	not modelled	96.3	24	**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
38	c3u7jA_	Alignment	not modelled	96.2	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
39	d1o8bb1	Alignment	not modelled	93.9	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
40	c2yvkA_	Alignment	not modelled	93.1	11	**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
41	d1t5oa_	Alignment	not modelled	92.8	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
42	c1pt9B_	Alignment	not modelled	83.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
43	c3ecsD_	Alignment	not modelled	81.5	15	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
44	d1vb5a_	Alignment	not modelled	81.1	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
45	d1pnoa_	Alignment	not modelled	80.9	28	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
46	d1t9ka_	Alignment	not modelled	72.4	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
47	d1d4oa_	Alignment	not modelled	71.2	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
48	d1o8ba1	Alignment	not modelled	66.1	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
49	c3a11D_	Alignment	not modelled	61.8	13	**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
50	c3mvnA_	Alignment	not modelled	33.7	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
51	c3nzeB_	Alignment	not modelled	30.6	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.
52	c2gezF_	Alignment	not modelled	26.1	36	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-asparaginase beta subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
53	c2gacD_	Alignment	not modelled	25.8	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
54	c2a8lB_	Alignment	not modelled	19.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**threonine aspartase 1; **PDBTitle:** crystal structure of human taspase1 (t234a mutant)

55	d2gnpa1	Alignment	not modelled	18.5	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
56	c1k2xB_	Alignment	not modelled	18.2	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
57	c1k2xD_	Alignment	not modelled	18.2	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
58	c1jn9D_	Alignment	not modelled	18.2	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene
59	c1t3mB_	Alignment	not modelled	17.8	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
60	c1t3mD_	Alignment	not modelled	17.8	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
61	c1jn9B_	Alignment	not modelled	17.8	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene
62	c1dbgA_	Alignment	not modelled	17.4	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
63	d2r5fa1	Alignment	not modelled	15.7	4	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
64	d3efba1	Alignment	not modelled	14.7	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
65	d1gmxa_	Alignment	not modelled	14.5	9	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
66	c2zalD_	Alignment	not modelled	14.1	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
67	d2fvga1	Alignment	not modelled	14.0	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
68	d1ofla_	Alignment	not modelled	13.1	6	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
69	d1t3ka_	Alignment	not modelled	13.0	0	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
70	d1gwma_	Alignment	not modelled	12.0	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 29 carbohydrate binding module, CBM29
71	c2zalB_	Alignment	not modelled	11.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
72	c2w48D_	Alignment	not modelled	10.4	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
73	d1kqfa1	Alignment	not modelled	10.2	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
74	c3kv1A_	Alignment	not modelled	9.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
75	d1vlfm1	Alignment	not modelled	9.6	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
76	c3hy4A_	Alignment	not modelled	9.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase; **PDBTitle:** structure of human mthfs with n5-iminium phosphate
77	d2grea1	Alignment	not modelled	9.2	24	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
78	d2nyga1	Alignment	not modelled	8.9	18	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
79	d2jioa1	Alignment	not modelled	8.7	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
80	c2bruC_	Alignment	not modelled	8.2	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
81	d1h0ha1	Alignment	not modelled	8.2	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal

						domain
82	c2zfnA_	Alignment	not modelled	8.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
83	c3d35A_	Alignment	not modelled	7.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** crystal structure of rtt109-ac-coa complex
84	d1vhea1	Alignment	not modelled	7.7	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
85	c1p4vA_	Alignment	not modelled	7.4	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(4)-(beta-n-acetylglucosaminyl)-l-asparaginase **PDBTitle:** crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
86	d1ogya1	Alignment	not modelled	7.2	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
87	d1y5ia1	Alignment	not modelled	7.2	33	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
88	d1u0fa_	Alignment	not modelled	7.1	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
89	d1l7da2	Alignment	not modelled	7.0	31	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
90	d1yloa1	Alignment	not modelled	7.0	13	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
91	d1eu1a1	Alignment	not modelled	6.9	28	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
92	c2o0mA_	Alignment	not modelled	6.8	15	**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
93	d2o0ma1	Alignment	not modelled	6.8	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
94	d1pjca2	Alignment	not modelled	6.5	18	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
95	d1y0ya1	Alignment	not modelled	6.4	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
96	d1ru4a_	Alignment	not modelled	6.4	10	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate transeliminase
97	c3pe3D_	Alignment	not modelled	6.1	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
98	c3cz7A_	Alignment	not modelled	6.1	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** molecular basis for the autoregulation of the protein acetyl2 transferase rtt109
99	c2ri0B_	Alignment	not modelled	5.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans