Phyre2

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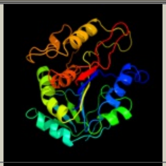
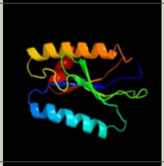
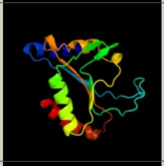
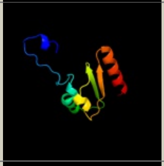
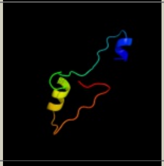
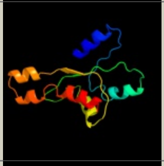
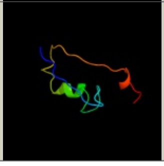
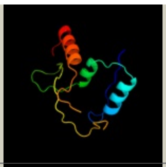
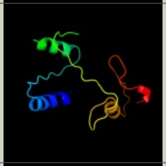
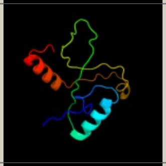
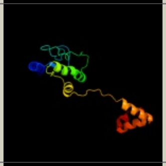
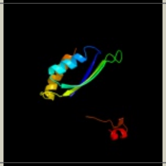
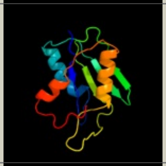
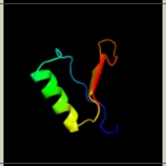
Description	P24197
Date	Thu Jan 5 11:41:08 GMT 2012
Unique Job ID	c618af4b35299999

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pw6a1	Alignment		100.0	95	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
2	d1b4ub_	Alignment		100.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
3	c3bd0D_	Alignment		99.4	12	**PDB header:**peptide binding protein **Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii
4	c3lp5A_	Alignment		78.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell surface hydrolase; **PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
5	d1ja1a2	Alignment		77.4	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
6	d2q7sa1	Alignment		73.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FGase-like
7	d2pjua1	Alignment		68.1	14	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
8	c2pjuD_	Alignment		67.8	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
9	d1bvyf_	Alignment		61.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
10	c1bvyF_	Alignment		61.7	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
11	c3bmaC_	Alignment		60.6	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase; **PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6

12	c3ozbF_	Alignment		58.0	23	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
13	c2q5cA_	Alignment		57.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
14	d2ac7a1	Alignment		54.3	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
15	c3exaD_	Alignment		52.9	14	**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.
16	c3n0vD_	Alignment		45.4	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
17	c3fleB_	Alignment		40.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
18	d1b1ca_	Alignment		37.5	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
19	d1ojra_	Alignment		35.6	24	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
20	d1f4pa_	Alignment		35.4	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
21	c3tl6B_	Alignment	not modelled	31.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
22	d1odma_	Alignment	not modelled	31.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
23	c3qpbB_	Alignment	not modelled	30.8	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
24	d2gv8a2	Alignment	not modelled	27.3	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
25	d1vhwa_	Alignment	not modelled	26.6	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
26	c2gfqC_	Alignment	not modelled	26.3	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
27	d2odfa1	Alignment	not modelled	24.2	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FGase-like
28	c3jrnA_	Alignment	not modelled	22.9	13	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**at1g72930 protein; **PDBTitle:** crystal structure of tir domain from arabidopsis thaliana
						Fold: AraD/HMP-PK domain-like

29	d1pvta_	Alignment	not modelled	22.3	29	**Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
30	d1w4xa2	Alignment	not modelled	22.2	6	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
31	c3eufC_	Alignment	not modelled	22.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
32	d1jw9b_	Alignment	not modelled	22.0	26	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
33	c3i0pA_	Alignment	not modelled	21.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica
34	d1odka_	Alignment	not modelled	20.8	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
35	d1rxya_	Alignment	not modelled	20.1	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
36	c1tjnA_	Alignment	not modelled	19.7	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
37	d1tjna_	Alignment	not modelled	19.7	26	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
38	d1cqxa3	Alignment	not modelled	19.3	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
39	d1npya1	Alignment	not modelled	18.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
40	d2h1ia1	Alignment	not modelled	18.4	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
41	c2cdh1_	Alignment	not modelled	18.4	13	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
42	c1zfnA_	Alignment	not modelled	18.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase thif; **PDBTitle:** structural analysis of escherichia coli thif
43	d2i9ca1	Alignment	not modelled	18.2	16	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**RPA1889-like
44	d1np3a2	Alignment	not modelled	17.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
45	c1y8qD_	Alignment	not modelled	17.4	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
46	d1p77a1	Alignment	not modelled	17.4	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
47	d1wyza1	Alignment	not modelled	17.2	16	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
48	c3d3qB_	Alignment	not modelled	17.1	13	**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
49	d1t8sa_	Alignment	not modelled	16.7	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
50	d1vkza2	Alignment	not modelled	16.6	25	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
51	d2fuea1	Alignment	not modelled	16.3	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
52	c3k35D_	Alignment	not modelled	16.3	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
53	c3pkiF_	Alignment	not modelled	16.3	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
54	d1uala_	Alignment	not modelled	16.2	9	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
55	d1iiba_	Alignment	not modelled	16.2	23	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit

56	d1a9xa3	Alignment	not modelled	16.1	25	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
57	c3cmmA_	Alignment	not modelled	14.8	24	**PDB header:**ligase/protein binding **Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1 1; **PDBTitle:** crystal structure of the uba1-ubiquitin complex
58	d1q1ra2	Alignment	not modelled	14.6	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
59	d1nvta1	Alignment	not modelled	14.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
60	c3h9gA_	Alignment	not modelled	14.3	11	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
61	c3kydB_	Alignment	not modelled	14.2	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sumo-activating enzyme subunit 2; **PDBTitle:** human sumo e1~sumo1-amp tetrahedral intermediate mimic
62	d1nxua_	Alignment	not modelled	14.1	28	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
63	c1wb4A_	Alignment	not modelled	14.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-xylanase y; **PDBTitle:** s954a mutant of the feruloyl esterase module from2 clostridium thermocellum complexed with sinapinate
64	c1z2iA_	Alignment	not modelled	14.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
65	d2csua2	Alignment	not modelled	13.9	13	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
66	d1ykga1	Alignment	not modelled	13.8	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
67	d2bida_	Alignment	not modelled	13.6	18	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
68	d1gsoa2	Alignment	not modelled	13.6	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
69	c2rgwD_	Alignment	not modelled	13.5	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
70	d1wb4a1	Alignment	not modelled	13.5	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
71	d1nhpa2	Alignment	not modelled	13.0	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
72	d1vi2a1	Alignment	not modelled	12.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
73	c3louB_	Alignment	not modelled	12.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
74	c3vh1A_	Alignment	not modelled	12.7	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
75	d1vdca2	Alignment	not modelled	12.6	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
76	c3gucB_	Alignment	not modelled	12.2	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
77	c3nbmA_	Alignment	not modelled	12.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
78	d1a9xa4	Alignment	not modelled	11.9	36	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
79	c3h16A_	Alignment	not modelled	11.8	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tir protein; **PDBTitle:** crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
80	c2l2qA_	Alignment	not modelled	11.8	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi

81	c3vh3A_	Alignment	not modelled	11.7	18	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
82	d1pv1a_	Alignment	not modelled	11.6	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
83	d5pnta_	Alignment	not modelled	11.5	25	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
84	d1dg9a_	Alignment	not modelled	11.3	25	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
85	d1k9sa_	Alignment	not modelled	11.2	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
86	c2wmyH_	Alignment	not modelled	11.1	27	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
87	d1yqea1	Alignment	not modelled	11.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
88	d1gpja2	Alignment	not modelled	10.9	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
89	c2rduA_	Alignment	not modelled	10.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1; **PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
90	c1w4xA_	Alignment	not modelled	10.7	7	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
91	c2g8yB_	Alignment	not modelled	10.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
92	c2gi4A_	Alignment	not modelled	10.6	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
93	c3nvbA_	Alignment	not modelled	10.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
94	c3hbaA_	Alignment	not modelled	10.4	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
95	d2gfqa1	Alignment	not modelled	10.4	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
96	d1trba2	Alignment	not modelled	10.3	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
97	c3t38B_	Alignment	not modelled	10.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
98	d1fl2a2	Alignment	not modelled	9.9	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
99	c1np3B_	Alignment	not modelled	9.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa