Phyre^2

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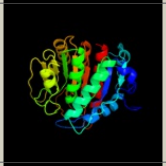
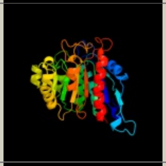
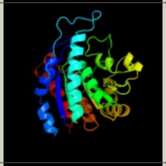
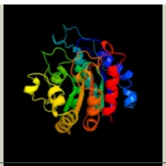
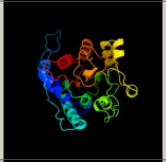
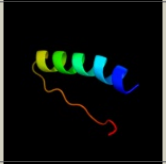
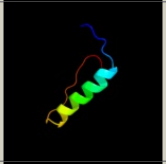
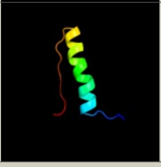
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nipB_	Alignment		100.0	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-guanidinopropionase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
2	d1gq6a_	Alignment		100.0	40	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
3	c3nioF_	Alignment		100.0	40	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**guanidinobutyrase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinobutyrase
4	c3m1rF_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**formimidoylglutamase; **PDBTitle:** the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
5	c3lhlA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative agmatinase; **PDBTitle:** crystal structure of a putative agmatinase from clostridium difficile
6	d1woha_	Alignment		100.0	29	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
7	d1xfka_	Alignment		100.0	23	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
8	d2a0ma1	Alignment		100.0	24	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
9	c3pzlA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**agmatine ureohydrolase; **PDBTitle:** the crystal structure of agmatine ureohydrolase of thermoplasma2 volcanium
10	d1pq3a_	Alignment		100.0	25	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
11	d1d3va_	Alignment		100.0	27	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases

12	d2ceva_	Alignment		100.0	30	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
13	c3mmrA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arginase; **PDBTitle:** structure of plasmodium falciparum arginase in complex with abh
14	d2aeba1	Alignment		100.0	29	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
15	c2eivH_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**arginase; **PDBTitle:** crystal structure of the arginase from thermus thermophilus
16	c3a8tA_	Alignment		80.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
17	c3d3qB_	Alignment		71.7	20	**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
18	c3eplA_	Alignment		67.9	17	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
19	c3fozB_	Alignment		67.5	25	**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)
20	c3exaD_	Alignment		65.1	9	**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.
21	c3crqA_	Alignment	not modelled	64.5	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
22	d1umya_	Alignment	not modelled	59.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
23	c3godA_	Alignment	not modelled	50.1	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cas1; **PDBTitle:** structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense
24	d1lt7a_	Alignment	not modelled	43.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
25	d2fiqa1	Alignment	not modelled	39.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
26	d1tifa_	Alignment	not modelled	32.6	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Translation initiation factor IF3, N-terminal domain **Family:**Translation initiation factor IF3, N-terminal domain
27	d1hi9a_	Alignment	not modelled	31.3	15	**Fold:**Dipeptide transport protein **Superfamily:**Dipeptide transport protein **Family:**Dipeptide transport protein
28	c2oh2B_	Alignment	not modelled	30.4	20	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
29	c2ze5A	Alignment	not modelled	28.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl transferase;

29	c2ze5A_	Alignment	not modelled	28.5	14	**PDBTitle:** crystal structure of adenosine phosphate-isopentenyltransferase
30	c3nkdB_	Alignment	not modelled	27.5	17	**PDB header:**immune system **Chain:** B: **PDB Molecule:**crispr-associated protein cas1; **PDBTitle:** structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
31	c1t94B_	Alignment	not modelled	24.3	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa
32	d1kyqa1	Alignment	not modelled	23.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
33	c2c2xB_	Alignment	not modelled	22.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
34	c1k98A_	Alignment	not modelled	22.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
35	c3pv9D_	Alignment	not modelled	22.2	17	**PDB header:**immune system **Chain:** D: **PDB Molecule:**putative uncharacterized protein ph1245; **PDBTitle:** structure of ph1245, a cas1 from pyrococcus horikoshii
36	c3lfxE_	Alignment	not modelled	19.0	10	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of tm1797, a cas1 protein from thermotoga maritima
37	c2z84A_	Alignment	not modelled	17.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ufm1-specific protease 1; **PDBTitle:** insights from crystal and solution structures of mouse ufsp1
38	d3bofa2	Alignment	not modelled	15.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
39	c3ecsD_	Alignment	not modelled	14.9	14	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
40	c2yzsB_	Alignment	not modelled	14.4	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 aquifex aeolicus
41	c1a4iB_	Alignment	not modelled	13.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
42	d2bona1	Alignment	not modelled	12.9	14	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
43	c1vbwA_	Alignment	not modelled	12.9	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**trypsin inhibitor bgit; **PDBTitle:** crystal structure of bitter gourd trypsin inhibitor
44	c3mr2A_	Alignment	not modelled	12.7	36	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
45	d1t94a2	Alignment	not modelled	12.1	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
46	d1b74a1	Alignment	not modelled	11.6	12	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
47	c3pu6A_	Alignment	not modelled	11.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
48	d2hkja1	Alignment	not modelled	11.2	22	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Topoisomerase VI-B subunit middle domain
49	d1w85b1	Alignment	not modelled	11.2	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
50	d1b0aa1	Alignment	not modelled	10.6	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
51	c3h7aC_	Alignment	not modelled	10.4	6	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of short-chain dehydrogenase from2 rhodopseudomonas palustris
52	c3l07B_	Alignment	not modelled	10.2	24	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
53	c1b0aA_	Alignment	not modelled	10.0	27	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
54	c3nglA_	Alignment	not modelled	9.8	24	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum

55	c3dfzB_	Alignment	not modelled	9.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
56	c3s40C_	Alignment	not modelled	9.5	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
57	c2bp7F_	Alignment	not modelled	9.5	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
58	d1ccra_	Alignment	not modelled	9.3	34	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
59	d1dwma_	Alignment	not modelled	9.3	23	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
60	d1k1sa2	Alignment	not modelled	9.3	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
61	c3gqcB_	Alignment	not modelled	9.1	17	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
62	c1tinA_	Alignment	not modelled	8.8	20	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**trypsin inhibitor v; **PDBTitle:** three-dimensional structure in solution of cucurbita maxima2 trypsin inhibitor-v determined by nmr spectroscopy
63	c2w9kA_	Alignment	not modelled	8.8	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crithidia fasciculata cytochrome c
64	d1k8kg_	Alignment	not modelled	8.7	13	**Fold:**alpha-alpha superhelix **Superfamily:**Arp2/3 complex 16 kDa subunit ARPC5 **Family:**Arp2/3 complex 16 kDa subunit ARPC5
65	d1ebfa2	Alignment	not modelled	8.6	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Homoserine dehydrogenase-like
66	c3auzA_	Alignment	not modelled	8.6	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
67	c3bolB_	Alignment	not modelled	8.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
68	d2d5ra1	Alignment	not modelled	8.2	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
69	c1k1qA_	Alignment	not modelled	8.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
70	d1ytca_	Alignment	not modelled	8.1	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
71	c2fllA_	Alignment	not modelled	8.0	24	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
72	d1im4a_	Alignment	not modelled	7.9	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
73	c3fwaA_	Alignment	not modelled	7.9	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
74	c3av0A_	Alignment	not modelled	7.9	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
75	c1t3nB_	Alignment	not modelled	7.8	36	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
76	c1sseA_	Alignment	not modelled	7.7	38	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**ap-1 like transcription factor yap1; **PDBTitle:** solution structure of the oxidized form of the yap1 redox2 domain
77	c4a26B_	Alignment	not modelled	7.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
78	d1t5oa_	Alignment	not modelled	7.6	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
79	c2ri0B_	Alignment	not modelled	7.5	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
80	d1ii7a_	Alignment	not modelled	7.4	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
						Fold: Flavodoxin-like

81	d3bula2	Alignment	not modelled	7.3	23	**Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
82	d2ozlb1	Alignment	not modelled	7.2	10	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
83	c3outC_	Alignment	not modelled	7.0	10	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
84	c1fcdB_	Alignment	not modelled	7.0	15	**PDB header:**electron transport(flavocytochrome) **Chain:** B: **PDB Molecule:**flavocytochrome c sulfide dehydrogenase (flavin- **PDBTitle:** the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
85	d1qs0b1	Alignment	not modelled	6.9	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
86	c3p2oB_	Alignment	not modelled	6.9	32	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
87	c2aq4A_	Alignment	not modelled	6.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
88	c3p2oA_	Alignment	not modelled	6.8	24	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
89	d1j20a2	Alignment	not modelled	6.7	33	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
90	d1a4ia1	Alignment	not modelled	6.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
91	c2r8kB_	Alignment	not modelled	6.6	9	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
92	d1vyra_	Alignment	not modelled	6.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
93	d1zeta2	Alignment	not modelled	6.6	27	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
94	d1poia_	Alignment	not modelled	6.4	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
95	d1ju2a1	Alignment	not modelled	6.3	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
96	d2qapa1	Alignment	not modelled	6.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
97	d2bfdb1	Alignment	not modelled	6.0	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
98	c1cirA_	Alignment	not modelled	6.0	28	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** complex of two fragments of ci2 [(1-40)(dot)(41-64)]
99	d1fcda1	Alignment	not modelled	6.0	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains