Phyre^{2}

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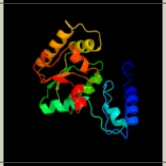
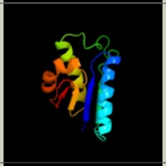
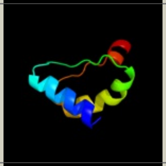
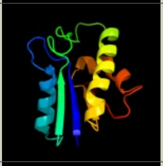
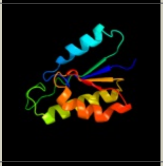
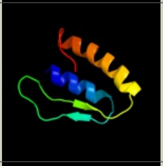
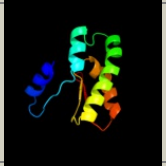
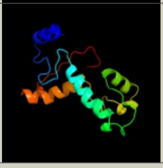
Description	P77252
Date	Thu Jan 5 12:26:51 GMT 2012
Unique Job ID	f3812b2a9db4a239

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kwlA_	Alignment		99.9	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
2	c3ojcD_	Alignment		92.0	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative aspartate/glutamate racemase; **PDBTitle:** crystal structure of a putative asp/glu racemase from yersinia pestis
3	c3s81A_	Alignment		91.0	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
4	c2dx7B_	Alignment		90.1	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
5	c3outC_	Alignment		89.9	12	**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.
6	c2zskA_	Alignment		87.1	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
7	c3hfrA_	Alignment		78.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
8	c1b74A_	Alignment		78.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
9	c2jfoB_	Alignment		77.9	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
10	d1jfla1	Alignment		77.1	10	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
11	c2dwuA_	Alignment		76.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis

12	c2jfqA_	Alignment		73.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
13	c2jfzB_	Alignment		73.7	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
14	c2gzmB_	Alignment		70.1	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
15	c2ohoA_	Alignment		69.3	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
16	c1zuwA_	Alignment		66.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
17	d1vk8a_	Alignment		64.4	13	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
18	d1b74a1	Alignment		53.6	15	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
19	c2eq5D_	Alignment		50.4	6	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
20	d3c8ya1	Alignment		50.2	15	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
21	c2epiA_	Alignment	not modelled	49.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0045 protein mj1052; **PDBTitle:** crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannascii (form 2)
22	c1c4cA_	Alignment	not modelled	46.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
23	c3lx4B_	Alignment	not modelled	45.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fe-hydrogenase; **PDBTitle:** stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
24	d1lxja_	Alignment	not modelled	44.1	7	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
25	c3hlyA_	Alignment	not modelled	42.3	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
26	d1hfel1	Alignment	not modelled	40.9	11	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
27	d2a9va1	Alignment	not modelled	39.1	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
28	c3qvjB_	Alignment	not modelled	38.8	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae

29	d2iboa1	Alignment	not modelled	38.7	9	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
30	d1jfla2	Alignment	not modelled	37.8	17	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
31	c3cf4A_	Alignment	not modelled	37.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
32	c2jfnA_	Alignment	not modelled	35.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
33	c1hfeL_	Alignment	not modelled	34.3	11	**PDB header:**hydrogenase **Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
34	d1yqha1	Alignment	not modelled	32.3	11	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
35	d2fzva1	Alignment	not modelled	31.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
36	c1gx7A_	Alignment	not modelled	29.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [fe] hydrogenase large subunit; **PDBTitle:** best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
37	c1x0lB_	Alignment	not modelled	25.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
38	d3pmga1	Alignment	not modelled	24.9	16	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
39	c3fniA_	Alignment	not modelled	22.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
40	d2dx7a1	Alignment	not modelled	21.3	17	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
41	d1xaca_	Alignment	not modelled	20.9	24	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
42	c2ct6A_	Alignment	not modelled	20.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
43	c1u6tA_	Alignment	not modelled	20.2	12	**PDB header:**protein binding, signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like
44	d1lxna_	Alignment	not modelled	19.8	16	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
45	d1kfia1	Alignment	not modelled	19.1	16	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
46	c2fb6A_	Alignment	not modelled	17.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of conserved protein of unknown function bt1422 from2 bacteroides thetaiotaomicron
47	c3blxL_	Alignment	not modelled	17.2	13	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 2; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
48	d1z2wa1	Alignment	not modelled	16.2	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
49	c3blxM_	Alignment	not modelled	15.5	13	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
50	c3rh0A_	Alignment	not modelled	15.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
51	d1rtta_	Alignment	not modelled	15.3	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
52	d2auna2	Alignment	not modelled	15.3	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
						PDB header:biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein;

53	c3l3bA_	Alignment	not modelled	14.0	20	**PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
54	c3ijfX_	Alignment	not modelled	13.5	11	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
55	c3h75A_	Alignment	not modelled	13.1	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
56	c3onoA_	Alignment	not modelled	12.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
57	d1j09a2	Alignment	not modelled	11.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
58	c3gjzB_	Alignment	not modelled	11.7	18	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
59	d2bisa1	Alignment	not modelled	11.7	20	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
60	c3c8nB_	Alignment	not modelled	11.3	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable f420-dependent glucose-6-phosphate dehydrogenase **PDBTitle:** crystal structure of apo-fgd1 from mycobacterium tuberculosis
61	c2jr7A_	Alignment	not modelled	11.0	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
62	d1w0da_	Alignment	not modelled	11.0	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
63	c1c4gB_	Alignment	not modelled	10.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
64	c2dgdD_	Alignment	not modelled	10.0	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
65	d1wgea1	Alignment	not modelled	9.9	19	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
66	c3o1hB_	Alignment	not modelled	9.9	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
67	d1fjha_	Alignment	not modelled	9.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
68	c2vlbC_	Alignment	not modelled	9.6	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
69	c1zrsB_	Alignment	not modelled	9.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
70	c2fzvC_	Alignment	not modelled	9.5	8	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
71	d1h75a_	Alignment	not modelled	9.3	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
72	c3afhA_	Alignment	not modelled	9.1	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 2; **PDBTitle:** crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
73	c3u1hA_	Alignment	not modelled	9.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
74	d1rbli_	Alignment	not modelled	9.1	7	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
75	c2wlbB_	Alignment	not modelled	8.3	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
76	c3lcmB_	Alignment	not modelled	8.2	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
77	c2z0fA_	Alignment	not modelled	8.2	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphoglucomutase; **PDBTitle:** crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
						Fold:UDP-Glycosyltransferase/glycogen phosphorylase

78	d1pn3a_	Alignment	not modelled	8.2	15	**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
79	c2x49A_	Alignment	not modelled	8.2	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**invasion protein inva; **PDBTitle:** crystal structure of the c-terminal domain of inva
80	c3na7A_	Alignment	not modelled	8.2	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
81	c2gejA_	Alignment	not modelled	8.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
82	c2ppwA_	Alignment	not modelled	7.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
83	c3h7hA_	Alignment	not modelled	7.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
84	d1r7ha_	Alignment	not modelled	7.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
85	c3c4vB_	Alignment	not modelled	7.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
86	c3he8A_	Alignment	not modelled	7.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
87	c3ikzA_	Alignment	not modelled	7.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
88	d1b43a2	Alignment	not modelled	7.0	20	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
89	d1g2ua_	Alignment	not modelled	7.0	21	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
90	c2fuvB_	Alignment	not modelled	6.9	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
91	c3c5yD_	Alignment	not modelled	6.9	11	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
92	d2d30a1	Alignment	not modelled	6.9	11	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
93	d1coza_	Alignment	not modelled	6.9	7	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Cytidylyltransferase
94	c2jadA_	Alignment	not modelled	6.9	7	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**yellow fluorescent protein glutaredoxin fusion **PDBTitle:** yellow fluorescent protein - glutaredoxin fusion protein
95	c3nbmA_	Alignment	not modelled	6.7	18	**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.
96	c3dmoD_	Alignment	not modelled	6.7	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytidine deaminase; **PDBTitle:** 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei
97	c3orsD_	Alignment	not modelled	6.6	13	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
98	d8abpa_	Alignment	not modelled	6.5	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
99	c3fmfA_	Alignment	not modelled	6.5	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate