Phyre^2

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Description	RVBD2417c_(-)_2715482_2716324
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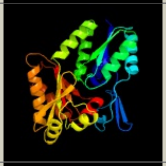
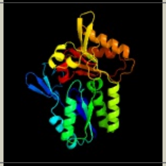
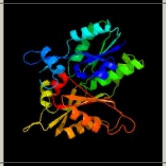
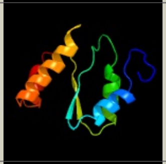
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dkeA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fatty acid kinase (fak) b1 protein; **PDBTitle:** the x-ray crystal structure of streptococcus pneumoniae fatty acid2 kinase (fak) b1 protein loaded with palmitic acid (c16:0) to 1.763 angstrom resolution
2	c2dt8A_	Alignment		100.0	31	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** fatty acid binding of a degv family protein from thermus thermophilus
3	c3fysA_	Alignment		100.0	28	**PDB header:**fatty acid-binding protein **Chain:** A: **PDB Molecule:**protein degv; **PDBTitle:** crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
4	c6cngA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fatty acid kinase (fak) b3 protein; **PDBTitle:** the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b3 protein loaded with linoleic acid to 1.47 angstrom3 resolution
5	c3lupA_	Alignment		100.0	23	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
6	d1pzxa_	Alignment		100.0	24	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
7	c5utoB_	Alignment		100.0	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**edd domain protein, degv family; **PDBTitle:** the crystal structure of the staphylococcus aureus fatty acid kinase2 (fak) b1 protein loaded with palmitic acid to 1.83 angstrom3 resolution
8	c3nyiA_	Alignment		100.0	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fat acid-binding protein; **PDBTitle:** the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
9	c6dj6B_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid kinase (fak) b2 protein (spr1019); **PDBTitle:** the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b2 protein loaded with cis-oleic acid to 1.9 angstrom3 resolution
10	c2g7zB_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
11	c3fdjA_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.

12	c4x9xA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**degv domain-containing protein mw1315; **PDBTitle:** biochemical roles for conserved residues in the bacterial fatty acid2 binding protein family
13	c3jr7A_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized egv family protein cog1307; **PDBTitle:** the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
14	c3pl5A_	Alignment		100.0	24	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** fatty acid binding protein
15	d1mgpa_	Alignment		100.0	22	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
16	c1mgpA_	Alignment		100.0	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
17	c3eglC_	Alignment		100.0	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
18	c3gx1A_	Alignment		95.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
19	d3ct6a1	Alignment		93.9	10	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
20	c3gdwA_	Alignment		79.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
21	d3beda1	Alignment	not modelled	67.7	15	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
22	c1un9B_	Alignment	not modelled	64.7	29	**PDB header:**kinase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
23	c3iprC_	Alignment	not modelled	56.6	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
24	d1oi2a_	Alignment	not modelled	56.5	17	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
25	d1un8a4	Alignment	not modelled	55.0	19	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
26	c3ostA_	Alignment	not modelled	54.6	9	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase kcc4; **PDBTitle:** structure of the kinase associated-1 (ka1) from kcc4p
27	c2qv5A_	Alignment	not modelled	54.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
28	c4ikgA_	Alignment	not modelled	52.3	12	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**cell death activator cide-3; **PDBTitle:** crystal structure of cell death-inducing dffa-like effector c
29	c4tkzA_	Alignment	not modelled	50.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein gbs1890;

29	c4tkzA_	Alignment	not modelled	50.0	11	**PDBTitle:** crystal structure of phosphotransferase system component eiia from2 streptococcus agalactiae
30	c2do6A_	Alignment	not modelled	49.8	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
31	c2d9sA_	Alignment	not modelled	49.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
32	c2jnhA_	Alignment	not modelled	48.5	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
33	d2fi9a1	Alignment	not modelled	47.2	12	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
34	c4u10B_	Alignment	not modelled	44.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; **PDBTitle:** probing the structure and mechanism of de-n-acetylase from2 aggregatibacter actinomycetemcomitans
35	c3orsD_	Alignment	not modelled	44.4	16	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
36	c2eelA_	Alignment	not modelled	44.1	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**cell death activator cide-a; **PDBTitle:** solution structure of the cide-n domain of human cell death2 activator cide-a
37	c4d2kB_	Alignment	not modelled	43.5	18	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**drep2; **PDBTitle:** crystal structure of drep2 cide domain
38	c1zowB_	Alignment	not modelled	42.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase iii; **PDBTitle:** crystal structure of s. aureus fabh, beta-ketoacyl carrier protein2 synthase iii
39	d1d4ba_	Alignment	not modelled	42.2	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
40	c1sjiA_	Alignment	not modelled	39.9	8	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calsequestrin, cardiac muscle isoform; **PDBTitle:** comparing skeletal and cardiac calsequestrin structures and their2 calcium binding: a proposed mechanism for coupled calcium binding and3 protein polymerization
41	c3iz5s_	Alignment	not modelled	37.5	14	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l18a (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
42	d1hnja1	Alignment	not modelled	35.2	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
43	c2iu6B_	Alignment	not modelled	34.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** regulation of the dha operon of lactococcus lactis
44	c5t3uA_	Alignment	not modelled	32.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
45	c3izcs_	Alignment	not modelled	32.0	13	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
46	c3jsyA_	Alignment	not modelled	31.2	17	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
47	c5xpcD_	Alignment	not modelled	30.7	16	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**dnaation factor-related protein 4; **PDBTitle:** crystal structure of drep4 cide domain
48	c1ibxB_	Alignment	not modelled	30.6	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**chimera of igg binding protein g and dna **PDBTitle:** nmr structure of dff40 and dff45 n-terminal domain complex
49	d1ibxb_	Alignment	not modelled	30.6	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
50	d1xnga1	Alignment	not modelled	27.9	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
51	c1a8yA_	Alignment	not modelled	27.2	6	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**calsequestrin; **PDBTitle:** crystal structure of calsequestrin from rabbit skeletal muscle2 sarcoplasmic reticulum at 2.4 a resolution
52	c6dq3B_	Alignment	not modelled	26.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** streptococcus pyogenes deacetylase pdi in complex with acetate
53	c5i1tA_	Alignment	not modelled	26.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stage ii sporulation protein d; **PDBTitle:** 2.6 angstrom resolution crystal structure of stage ii sporulation2 protein d (spoiid) from clostridium difficile in complex with3 triacetylchitotriose
54	c6cwxA_	Alignment	not modelled	26.4	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease p protein subunit p20;

54	c6cwxA_	Alignment	not modelled	26.4	8	**PDBTitle:** crystal structure of human ribonuclease p/mrp proteins rpp20/rpp25
55	c6fmgC_	Alignment	not modelled	26.3	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system mannose-specific transporter subunit iiab; **PDBTitle:** structure of the mannose transporter iia domain from streptococcus2 pneumoniae
56	c4rwrB_	Alignment	not modelled	25.6	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**stage ii sporulation protein d; **PDBTitle:** 2.1 angstrom crystal structure of stage ii sporulation protein d from2 bacillus anthracis
57	d1vz0a1	Alignment	not modelled	25.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
58	c5lwcA_	Alignment	not modelled	24.7	4	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**bacteriocin bacsp222; **PDBTitle:** nmr solution structure of bacteriocin bacsp222 from staphylococcus2 pseudintermedius 222
59	c2ov6A_	Alignment	not modelled	21.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit f; **PDBTitle:** the nmr structure of subunit f of the methanogenic a1ao atp synthase2 and its interaction with the nucleotide-binding subunit b
60	d2fvta1	Alignment	not modelled	21.8	8	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
61	c3j3bq_	Alignment	not modelled	20.6	11	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l18; **PDBTitle:** structure of the human 60s ribosomal proteins
62	c1r71B_	Alignment	not modelled	18.8	19	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in complex with2 the operator dna
63	d1c9fa_	Alignment	not modelled	18.7	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
64	d1r71a_	Alignment	not modelled	18.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
65	c1fvoB_	Alignment	not modelled	18.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
66	c5xceB_	Alignment	not modelled	17.8	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 29; **PDBTitle:** crystal structure of wild type vps29 from entamoeba histolytica
67	c5l7aA_	Alignment	not modelled	17.5	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin-dependent regulator **PDBTitle:** the crystal structure of the human snf5/ini1 domain
68	c1hyuA_	Alignment	not modelled	17.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
69	c2e18B_	Alignment	not modelled	16.9	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
70	c2qnxA_	Alignment	not modelled	16.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxycarbonyl)dithio]-undecanoic acid
71	c2wshC_	Alignment	not modelled	16.6	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
72	c2i6oA_	Alignment	not modelled	16.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfolobus solfataricus protein tyrosine **PDBTitle:** crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
73	d1f2ri_	Alignment	not modelled	16.1	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
74	c3lfhF_	Alignment	not modelled	16.0	9	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
75	c4xgjA_	Alignment	not modelled	15.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a domain of unknown function (duf1537) from2 pectobacterium atrosepticum (eca3761), target efi-511609, apo3 structure, domain swapped dimer
76	d1ewqa4	Alignment	not modelled	14.8	16	**Fold:**MutS N-terminal domain-like **Superfamily:**DNA repair protein MutS, domain I **Family:**DNA repair protein MutS, domain I
77	d1pj3a1	Alignment	not modelled	14.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
78	c2gm2A_	Alignment	not modelled	14.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
						Fold:PTS system fructose IIA component-like

79	d1pdoa_	Alignment	not modelled	14.5	16	**Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
80	d1mkza_	Alignment	not modelled	13.8	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
81	c5dxlA_	Alignment	not modelled	13.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-6-phosphate phosphatase; **PDBTitle:** structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
82	c3fiuD_	Alignment	not modelled	13.1	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
83	c4f78A_	Alignment	not modelled	13.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d,d-dipeptidase/d,d-carboxypeptidase; **PDBTitle:** crystal structure of vancomycin resistance d,d-dipeptidase vanxyg
84	d3efxd1	Alignment	not modelled	13.0	21	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
85	c1fokA_	Alignment	not modelled	12.9	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (foki restriction endonucleas); **PDBTitle:** structure of restriction endonuclease foki bound to dna
86	c3bxwB_	Alignment	not modelled	12.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chitinase domain-containing protein 1; **PDBTitle:** crystal structure of stabilin-1 interacting chitinase-like protein,2 si-clp
87	c4q6qA_	Alignment	not modelled	12.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**conserved hypothetical secreted protein; **PDBTitle:** structural analysis of the zn-form ii of helicobacter pylori csd4, a2 d,l-carboxypeptidase
88	d3b48a1	Alignment	not modelled	12.7	9	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
89	d1l5ja2	Alignment	not modelled	11.6	40	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
90	d1vlva1	Alignment	not modelled	11.5	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
91	c3zhiA_	Alignment	not modelled	11.5	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ci; **PDBTitle:** n-terminal domain of the ci repressor from bacteriophage tp901-1
92	c3ct4B_	Alignment	not modelled	11.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts-dependent dihydroxyacetone kinase, dihydroxyacetone- **PDBTitle:** structure of dha-kinase subunit dhak from l. lactis
93	c1ortD_	Alignment	not modelled	11.2	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
94	d1w7ab4	Alignment	not modelled	11.2	11	**Fold:**MutS N-terminal domain-like **Superfamily:**DNA repair protein MutS, domain I **Family:**DNA repair protein MutS, domain I
95	d1zpda1	Alignment	not modelled	11.1	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
96	d1xi8a3	Alignment	not modelled	11.1	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
97	d1qcza_	Alignment	not modelled	10.8	17	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
98	d1s3la_	Alignment	not modelled	10.2	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
99	c1s3mA_	Alignment	not modelled	10.2	23	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase