Phyre2

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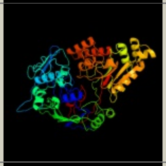
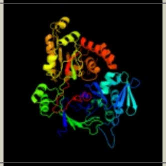
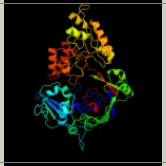
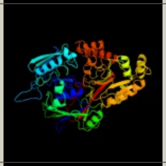
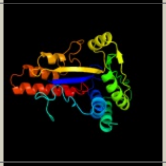
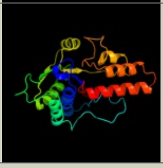
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dpea_	Alignment		100.0	100	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
2	c3tpaA_	Alignment		100.0	51	**PDB header:**heme binding protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** structure of hbpa2 from haemophilus parasuis
3	c3m8uA_	Alignment		100.0	52	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
4	d1jeta_	Alignment		100.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
5	d1zlqa1	Alignment		100.0	26	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
6	c3o9pA_	Alignment		100.0	21	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**periplasmic murein peptide-binding protein; **PDBTitle:** the structure of the escherichia coli murein tripeptide binding2 protein mppa
7	c2wokA_	Alignment		100.0	22	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**clavulanic acid biosynthesis oligopeptide **PDBTitle:** clavulanic acid biosynthesis oligopeptide2 binding protein 2 complexed with bradykinin
8	d1uqwa_	Alignment		100.0	26	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
9	d1xoca1	Alignment		100.0	26	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	c3t66A_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
11	c1ztyA_	Alignment		100.0	21	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein

12	c2o7jA_	Alignment		100.0	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
13	c3rqtA_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
14	d1vr5a1	Alignment		100.0	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
15	c2grvC_	Alignment		100.0	18	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
16	c3ftoA_	Alignment		100.0	19	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**oligopeptide-binding protein oppa; **PDBTitle:** crystal structure of oppa in a open conformation
17	c3ry3B_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
18	c2d5wA_	Alignment		100.0	21	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**peptide abc transporter, peptide-binding protein; **PDBTitle:** the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
19	c3lvuB_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
20	c3pamB_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transmembrane protein; **PDBTitle:** crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
21	c3o6pA_	Alignment	not modelled	100.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**peptide abc transporter, peptide-binding protein; **PDBTitle:** crystal structure of peptide abc transporter, peptide-binding protein
22	c3tmgA_	Alignment	not modelled	96.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
23	c3l6gA_	Alignment	not modelled	95.8	7	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
24	c3chgB_	Alignment	not modelled	95.2	8	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
25	c2rejA_	Alignment	not modelled	94.6	5	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
26	c3r6uA_	Alignment	not modelled	92.9	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
27	d1r9la_	Alignment	not modelled	92.6	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						PDB header:peptide binding protein

28	c3nohA_	Alignment	not modelled	91.5	20	**Chain:** A: **PDB Molecule:**putative peptide binding protein; **PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
29	d1sw5a_	Alignment	not modelled	88.6	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
30	c3pppA_	Alignment	not modelled	86.2	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
31	d1e5da1	Alignment	not modelled	85.0	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
32	d1ycga1	Alignment	not modelled	83.0	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
33	c3f6sI_	Alignment	not modelled	70.0	12	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
34	c3hlyA_	Alignment	not modelled	63.9	11	**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.
35	c3kzgB_	Alignment	not modelled	62.9	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**arginine 3rd transport system periplasmic binding **PDBTitle:** crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
36	d1f4pa_	Alignment	not modelled	62.6	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
37	c3ir1F_	Alignment	not modelled	60.1	16	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
38	c3kn3C_	Alignment	not modelled	52.2	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
39	c2o1mB_	Alignment	not modelled	49.6	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable amino-acid abc transporter **PDBTitle:** crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
40	c3gxaA_	Alignment	not modelled	47.9	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
41	c2ek8A_	Alignment	not modelled	46.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
42	d1vmea1	Alignment	not modelled	45.4	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
43	c2rc9A_	Alignment	not modelled	44.0	5	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate [nmda] receptor subunit 3a; **PDBTitle:** crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
44	c3o66A_	Alignment	not modelled	39.6	5	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
45	c3d7nA_	Alignment	not modelled	38.2	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
46	d1ykga1	Alignment	not modelled	37.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
47	c3un6A_	Alignment	not modelled	34.4	5	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein saouhsc_00137; **PDBTitle:** 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
48	d1tlla2	Alignment	not modelled	33.7	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
49	c3r39A_	Alignment	not modelled	33.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative periplasmic binding protein; **PDBTitle:** crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
50	d1s8na_	Alignment	not modelled	32.8	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	c2q9uB_	Alignment	not modelled	32.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
52	d2vv5a2	Alignment	not modelled	32.3	18	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain

						Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
53	c2y7iB_	Alignment	not modelled	31.2	7	**PDB header:**arginine-binding protein **Chain:** B: **PDB Molecule:**stm4351; **PDBTitle:** structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
54	c3lr1A_	Alignment	not modelled	30.1	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tungstate abc transporter, periplasmic tungstate- **PDBTitle:** the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
55	d2a5sa1	Alignment	not modelled	30.0	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
56	c3muqB_	Alignment	not modelled	29.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
57	c3k2dA_	Alignment	not modelled	28.9	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**abc-type metal ion transport system, periplasmic component; **PDBTitle:** crystal structure of immunogenic lipoprotein a from vibrio vulnificus
58	d1wdna_	Alignment	not modelled	28.9	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
59	d1xhfa1	Alignment	not modelled	28.6	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	d2a9pa1	Alignment	not modelled	28.1	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c3k4uA_	Alignment	not modelled	27.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding component of abc transporter; **PDBTitle:** crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
62	d1xs5a_	Alignment	not modelled	27.0	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
63	d5nula_	Alignment	not modelled	26.7	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
64	c2q2aD_	Alignment	not modelled	26.6	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**artj; **PDBTitle:** crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
65	d2fz5a1	Alignment	not modelled	26.6	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
66	d1mvoa_	Alignment	not modelled	26.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c2j48A_	Alignment	not modelled	25.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
68	c2ylnA_	Alignment	not modelled	25.4	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter, periplasmic binding protein, **PDBTitle:** crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
69	c3hn0A_	Alignment	not modelled	25.1	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
70	d1mb3a_	Alignment	not modelled	25.0	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	d1zgza1	Alignment	not modelled	24.0	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c3g41A_	Alignment	not modelled	23.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amino acid abc transporter, periplasmic amino acid-binding **PDBTitle:** the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
73	c1ychD_	Alignment	not modelled	23.1	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
74	c3n5lA_	Alignment	not modelled	23.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding protein component of abc phosphonate transporter; **PDBTitle:** crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
75	c3i6vA_	Alignment	not modelled	23.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic his/glu/gln/arg/opine family-binding protein; **PDBTitle:** crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
						Fold: Flavodoxin-like

76	d1ys7a2	Alignment	not modelled	22.7	11	**Superfamily:**CheY-like **Family:**CheY-related
77	c3fniA_	Alignment	not modelled	22.6	17	**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
78	d1kjna_	Alignment	not modelled	22.6	13	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
79	d1hsla_	Alignment	not modelled	22.2	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
80	d2arka1	Alignment	not modelled	21.9	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
81	d1bvyf_	Alignment	not modelled	21.9	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
82	c1bvyF_	Alignment	not modelled	21.9	11	**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)
83	c2f06B_	Alignment	not modelled	21.8	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
84	c1twyG_	Alignment	not modelled	21.4	6	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
85	d1twya_	Alignment	not modelled	21.4	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
86	c2yjpB_	Alignment	not modelled	20.8	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative abc transporter, periplasmic binding protein, **PDBTitle:** crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
87	c3ix1B_	Alignment	not modelled	20.6	6	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
88	c3ix1A_	Alignment	not modelled	20.6	6	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
89	c3nbmA_	Alignment	not modelled	20.4	12	**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.
90	c3t6kB_	Alignment	not modelled	19.9	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
91	c3kbrA_	Alignment	not modelled	19.9	5	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
92	d1p99a_	Alignment	not modelled	19.5	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
93	c1p99A_	Alignment	not modelled	19.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
94	d1lsta_	Alignment	not modelled	18.3	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
95	c3delC_	Alignment	not modelled	18.2	9	**PDB header:**protein binding, transport protein **Chain:** C: **PDB Molecule:**arginine binding protein; **PDBTitle:** the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
96	c2hnbA_	Alignment	not modelled	17.8	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
97	d1g7da_	Alignment	not modelled	17.7	19	**Fold:**ERP29 C domain-like **Superfamily:**ERP29 C domain-like **Family:**ERP29 C domain-like
98	d2a5la1	Alignment	not modelled	17.6	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
99	d2p0la1	Alignment	not modelled	17.6	12	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like