
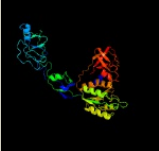
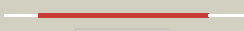






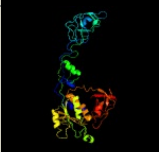

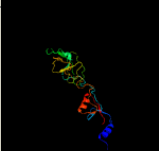

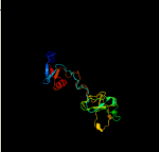

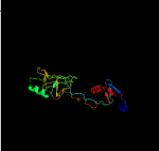

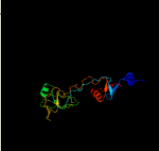















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0438c_(moeA2)_526146_527363
Date	Tue Jul 23 14:50:51 BST 2019
Unique Job ID	85fe181ec5d87b59

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nqqA_</a>	 Alignment		100.0	34	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
2	<a href="#">c5g2rA_</a>	 Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein cnx1; <b>PDBTitle:</b> crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
3	<a href="#">c1uz5A_</a>	 Alignment		100.0	29	<b>PDB header:</b> molybdopterin biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> 402aa long hypothetical molybdopterin <b>PDBTitle:</b> the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
4	<a href="#">c2fu3A_</a>	 Alignment		100.0	35	<b>PDB header:</b> biosynthetic protein/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> gephyrin; <b>PDBTitle:</b> crystal structure of gephyrin e-domain
5	<a href="#">c1wu2B_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics,biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin biosynthesis moea protein; <b>PDBTitle:</b> crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
6	<a href="#">d1uz5a2</a>	 Alignment		100.0	29	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
7	<a href="#">d1wu2a2</a>	 Alignment		100.0	34	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
8	<a href="#">d2nqra2</a>	 Alignment		100.0	41	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
9	<a href="#">d2ftsa2</a>	 Alignment		100.0	38	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
10	<a href="#">d2nqra3</a>	 Alignment		100.0	34	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
11	<a href="#">d2ftsa3</a>	 Alignment		100.0	36	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like

12	<a href="#">d1uz5a3</a>	Alignment		100.0	34	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
13	<a href="#">d1wu2a3</a>	Alignment		100.0	26	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
14	<a href="#">c2pjkA</a>	Alignment		100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 178aa long hypothetical molybdenum cofactor <b>PDBTitle:</b> structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
15	<a href="#">d1y5ea1</a>	Alignment		100.0	15	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
16	<a href="#">c2is8A</a>	Alignment		100.0	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis enzyme, moab2; <b>PDBTitle:</b> crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
17	<a href="#">d1mkza</a>	Alignment		100.0	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
18	<a href="#">d1xi8a3</a>	Alignment		100.0	27	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
19	<a href="#">d1jlja</a>	Alignment		100.0	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
20	<a href="#">c2qq1A</a>	Alignment		100.0	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis mog; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
21	<a href="#">d2g2ca1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
22	<a href="#">c3rfqC</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
23	<a href="#">c3kbqA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ta0487; <b>PDBTitle:</b> the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
24	<a href="#">c2g4rB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin biosynthesis mog protein; <b>PDBTitle:</b> anomalous substructure of moga
25	<a href="#">d1uuya</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
26	<a href="#">c4lhbC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> molybdopterin adenylyltransferase; <b>PDBTitle:</b> crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
27	<a href="#">d2f7wa1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
28	<a href="#">c4xcwF</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> molybdopterin adenylyltransferase; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99

29	<a href="#">c4uuwA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> cina-like protein; <b>PDBTitle:</b> competence or damage-inducible protein cina from thermus thermophilus
30	<a href="#">d1di6a</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
31	<a href="#">d1xi8a2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
32	<a href="#">d2nqra1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
33	<a href="#">d1wu2a1</a>	Alignment	not modelled	99.3	22	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
34	<a href="#">d1xi8a1</a>	Alignment	not modelled	99.2	25	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
35	<a href="#">d2ftsai</a>	Alignment	not modelled	99.1	26	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
36	<a href="#">d1uz5a1</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
37	<a href="#">c2rirA</a>	Alignment	not modelled	93.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
38	<a href="#">c2yxbA</a>	Alignment	not modelled	92.5	24	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
39	<a href="#">c3d4oA</a>	Alignment	not modelled	92.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
40	<a href="#">c1l9xA</a>	Alignment	not modelled	91.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
41	<a href="#">d1l9xa</a>	Alignment	not modelled	91.4	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
42	<a href="#">c3d54D</a>	Alignment	not modelled	91.2	28	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 1; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
43	<a href="#">d1gpma2</a>	Alignment	not modelled	90.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
44	<a href="#">c4gudA</a>	Alignment	not modelled	89.2	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit hish; <b>PDBTitle:</b> crystal structure of amidotransferase hish from vibrio cholerae
45	<a href="#">d1i7qb</a>	Alignment	not modelled	89.0	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
46	<a href="#">c3l4eA</a>	Alignment	not modelled	88.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized peptidase lmo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
47	<a href="#">c6a4tB</a>	Alignment	not modelled	88.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidase e; <b>PDBTitle:</b> crystal structure of peptidase e from deinococcus radiodurans r1
48	<a href="#">c3louB</a>	Alignment	not modelled	87.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
49	<a href="#">d1fmfa</a>	Alignment	not modelled	87.5	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
50	<a href="#">c3c7cB</a>	Alignment	not modelled	87.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> octopine dehydrogenase; <b>PDBTitle:</b> a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
51	<a href="#">d1t3ta2</a>	Alignment	not modelled	87.1	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
52	<a href="#">d1l7da1</a>	Alignment	not modelled	86.8	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
53	<a href="#">c3w7bB</a>	Alignment	not modelled	86.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
54	<a href="#">d1wl8a1</a>	Alignment	not modelled	85.8	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
						<b>Fold:</b> Flavodoxin-like

55	<a href="#">d1ka9h_</a>	Alignment	not modelled	85.5	45	<b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
56	<a href="#">c3n0vD_</a>	Alignment	not modelled	85.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
57	<a href="#">d1pjca1</a>	Alignment	not modelled	85.2	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
58	<a href="#">d7reqa2</a>	Alignment	not modelled	84.4	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
59	<a href="#">c3o1lB_</a>	Alignment	not modelled	84.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
60	<a href="#">c6qurA_</a>	Alignment	not modelled	84.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> mapping the allosteric communication network of aminodeoxychorismate2 synthase
61	<a href="#">d1qdlb_</a>	Alignment	not modelled	83.9	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
62	<a href="#">c2y0dB_</a>	Alignment	not modelled	83.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
63	<a href="#">c4ycsC_</a>	Alignment	not modelled	83.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
64	<a href="#">c5mvrA_</a>	Alignment	not modelled	83.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsae; <b>PDBTitle:</b> crystal structure of bacillus subtilus ydib
65	<a href="#">c3melC_</a>	Alignment	not modelled	83.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> thiamin pyrophosphokinase family protein; <b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
66	<a href="#">c3en0A_</a>	Alignment	not modelled	82.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
67	<a href="#">d2a9va1</a>	Alignment	not modelled	82.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
68	<a href="#">d1l1qb_</a>	Alignment	not modelled	82.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
69	<a href="#">d1q7ra_</a>	Alignment	not modelled	82.6	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
70	<a href="#">d1jvna2</a>	Alignment	not modelled	82.6	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
71	<a href="#">c3cq9C_</a>	Alignment	not modelled	82.6	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein lp_1622; <b>PDBTitle:</b> crystal structure of the lp_1622 protein from lactobacillus plantarum.2 northeast structural genomics consortium target lpr114
72	<a href="#">c3fijD_</a>	Alignment	not modelled	82.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> lin1909 protein; <b>PDBTitle:</b> crystal structure of a uncharacterized protein lin1909
73	<a href="#">c3rgwS_</a>	Alignment	not modelled	81.0	18	<b>PDB header:</b> oxidoreductase/oxidoreductase <b>Chain:</b> S: <b>PDB Molecule:</b> membrane-bound hydrogenase (nife) small subunit hoxk; <b>PDBTitle:</b> crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
74	<a href="#">c4l8fA_</a>	Alignment	not modelled	80.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
75	<a href="#">c3k94A_</a>	Alignment	not modelled	80.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase from geobacillus2 thermodenitrificans, northeast structural genomics consortium target3 gtr2
76	<a href="#">d9ldta1</a>	Alignment	not modelled	80.6	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
77	<a href="#">d1yq9a1</a>	Alignment	not modelled	80.1	15	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nickel-iron hydrogenase, small subunit
78	<a href="#">c3ihkC_</a>	Alignment	not modelled	80.1	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase from s.mutans,2 northeast structural genomics consortium target smr83
79	<a href="#">c3r74B_</a>	Alignment	not modelled	79.5	17	<b>PDB header:</b> lyase, biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate/para-aminobenzoate synthases component i; <b>PDBTitle:</b> crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha

80	<a href="#">c4dioB_</a>	Alignment	not modelled	79.2	26	part 1; <b>PDBTitle:</b> the crystal structure of transhydrogenase from sinorhizobium meliloti
81	<a href="#">c1u4sA_</a>	Alignment	not modelled	78.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
82	<a href="#">c3myrE_</a>	Alignment	not modelled	77.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> hydrogenase (nife) small subunit hyda; <b>PDBTitle:</b> crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
83	<a href="#">d1agxa_</a>	Alignment	not modelled	76.2	13	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
84	<a href="#">c2issF_</a>	Alignment	not modelled	75.7	19	<b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
85	<a href="#">d1ccwa_</a>	Alignment	not modelled	74.1	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
86	<a href="#">d2nv0a1_</a>	Alignment	not modelled	73.8	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
87	<a href="#">c4ypoB_</a>	Alignment	not modelled	73.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
88	<a href="#">c1jvnB_</a>	Alignment	not modelled	73.1	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
89	<a href="#">c2p2dA_</a>	Alignment	not modelled	72.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase i; <b>PDBTitle:</b> crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i
90	<a href="#">d1bg6a2_</a>	Alignment	not modelled	72.7	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	<a href="#">d1k9vf_</a>	Alignment	not modelled	72.5	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
92	<a href="#">c2eezG_</a>	Alignment	not modelled	72.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
93	<a href="#">c2an1D_</a>	Alignment	not modelled	72.4	29	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
94	<a href="#">c4hh3C_</a>	Alignment	not modelled	71.7	18	<b>PDB header:</b> flavoprotein/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> structure of the appa-ppsr2 core complex from rb. sphaeroides
95	<a href="#">c1np3B_</a>	Alignment	not modelled	71.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetoxy acid isomeroeductase from2 pseudomonas aeruginosa
96	<a href="#">c2ppwA_</a>	Alignment	not modelled	71.2	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
97	<a href="#">c3p2yA_</a>	Alignment	not modelled	70.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
98	<a href="#">c4egjD_</a>	Alignment	not modelled	70.4	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
99	<a href="#">d1dja3_</a>	Alignment	not modelled	70.3	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
100	<a href="#">c3he8A_</a>	Alignment	not modelled	69.9	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
101	<a href="#">d1vcoa1_</a>	Alignment	not modelled	69.7	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
102	<a href="#">c4wb1B_</a>	Alignment	not modelled	69.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cals8; <b>PDBTitle:</b> crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
103	<a href="#">c1w19E_</a>	Alignment	not modelled	68.8	20	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> 6,7-dimethyl-8-ribityllumazine synthase; <b>PDBTitle:</b> lumazine synthase from mycobacterium tuberculosis bound to 3-(1,3,7-2 trihydro-9-d-ribityl-2,6,8-purinetrione-7-yl)propane 1-phosphate
104	<a href="#">c3onoA_</a>	Alignment	not modelled	68.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose/galactose isomerase; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase lacab rpib from2 vibrio parahaemolyticus

105	<a href="#">c2vpiA_</a>	Alignment	not modelled	68.6	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase; <b>PDBTitle:</b> human gmp synthetase - glutaminase domain
106	<a href="#">c5dmxC_</a>	Alignment	not modelled	68.6	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
107	<a href="#">c6hcyA_</a>	Alignment	not modelled	68.3	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> metalloreductase steap4; <b>PDBTitle:</b> human steap4 bound to nadp, fad, heme and fe(iii)-nta.
108	<a href="#">c3k13A_</a>	Alignment	not modelled	67.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydrofolate-homocysteine methyltransferase; <b>PDBTitle:</b> structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
109	<a href="#">c4oqyA_</a>	Alignment	not modelled	67.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-imine reductase; <b>PDBTitle:</b> streptomyces sp. gf3546 imine reductase
110	<a href="#">d1uxja1</a>	Alignment	not modelled	67.4	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
111	<a href="#">c4j07E_</a>	Alignment	not modelled	67.3	20	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> 6,7-dimethyl-8-ribityllumazine synthase; <b>PDBTitle:</b> crystal structure of a probable riboflavin synthase, beta chain ribh2 (6,7-dimethyl-8-ribityllumazine synthase, dmrl synthase, lumazine3 synthase) from mycobacterium leprae
112	<a href="#">c5ocmA_</a>	Alignment	not modelled	67.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad_gly3p_dh, nad-dependent glycerol-3-phosphate <b>PDBTitle:</b> imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate
113	<a href="#">c4r3uD_</a>	Alignment	not modelled	66.6	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase small subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
114	<a href="#">c3whpA_</a>	Alignment	not modelled	66.4	23	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
115	<a href="#">d1o7ja_</a>	Alignment	not modelled	66.3	15	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
116	<a href="#">d1zq1a2</a>	Alignment	not modelled	66.2	17	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
117	<a href="#">c4eggD_</a>	Alignment	not modelled	65.5	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
118	<a href="#">c3dfuB_</a>	Alignment	not modelled	65.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein from 6-phosphogluconate <b>PDBTitle:</b> crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
119	<a href="#">d2naca2</a>	Alignment	not modelled	65.2	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
120	<a href="#">c3e7hA_</a>	Alignment	not modelled	65.1	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> the crystal structure of the beta subunit of the dna-directed rna2 polymerase from vibrio cholerae o1 biovar eltor