






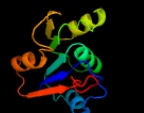
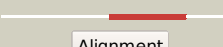
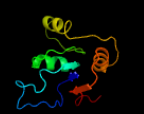























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1697_(-)_1921549_1922730
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	635f6fce54c77ccb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mu5A_</a>	 Alignment		99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of maf glycosyltransferase from magnetospirillum magneticum2 amb-1
2	<a href="#">c3lm8D_</a>	 Alignment		99.3	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thiamine pyrophosphokinase; <b>PDBTitle:</b> crystal structure of thiamine pyrophosphokinase from bacillus2 subtilis, northeast structural genomics consortium target sr677
3	<a href="#">c3ihkC_</a>	 Alignment		99.2	27	<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
4	<a href="#">c3melC_</a>	 Alignment		99.1	26	<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
5	<a href="#">c3l8mA_</a>	 Alignment		99.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiamine pyrophosphokinase; <b>PDBTitle:</b> crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86
6	<a href="#">c3cq9C_</a>	 Alignment		99.0	22	<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
7	<a href="#">c3k94A_</a>	 Alignment		99.0	31	<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
8	<a href="#">c2f17A_</a>	 Alignment		98.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase 1; <b>PDBTitle:</b> mouse thiamin pyrophosphokinase in a ternary complex with2 pyrithiamin pyrophosphate and amp at 2.5 angstrom
9	<a href="#">c1ig0A_</a>	 Alignment		98.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of yeast thiamin pyrophosphokinase
10	<a href="#">c2hh9A_</a>	 Alignment		98.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> thiamin pyrophosphokinase from candida albicans
11	<a href="#">d1ig0a2</a>	 Alignment		98.6	22	<b>Fold:</b> Thiamin pyrophosphokinase, catalytic domain <b>Superfamily:</b> Thiamin pyrophosphokinase, catalytic domain <b>Family:</b> Thiamin pyrophosphokinase, catalytic domain

12	<a href="#">d1ig3a2</a>	Alignment		98.6	23	<b>Fold:</b> Thiamin pyrophosphokinase, catalytic domain <b>Superfamily:</b> Thiamin pyrophosphokinase, catalytic domain <b>Family:</b> Thiamin pyrophosphokinase, catalytic domain
13	<a href="#">c2omkB</a>	Alignment		98.3	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
14	<a href="#">c2e28A</a>	Alignment		95.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure analysis of pyruvate kinase from bacillus2 stearrowthermophilus
15	<a href="#">c4j0nA</a>	Alignment		93.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isatin hydrolase b; <b>PDBTitle:</b> crystal structure of a manganese dependent isatin hydrolase
16	<a href="#">c5ibzD</a>	Alignment		93.1	30	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a novel cyclase (pfam04199).
17	<a href="#">c5fbtA</a>	Alignment		92.7	21	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate synthase; <b>PDBTitle:</b> crystal structure of rifampin phosphotransferase rph-lm from listeria2 monocytogenes in complex with rifampin
18	<a href="#">d1kbla2</a>	Alignment		92.4	18	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
19	<a href="#">d1ytlA1</a>	Alignment		91.0	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> ACDE2-like
20	<a href="#">d1zyna2</a>	Alignment		90.4	17	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
21	<a href="#">d1vbgA2</a>	Alignment	not modelled	90.4	13	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
22	<a href="#">c3t07D</a>	Alignment	not modelled	90.3	12	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
23	<a href="#">c5nnaB</a>	Alignment	not modelled	89.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> isatin hydrolase a; <b>PDBTitle:</b> isatin hydrolase a (iha) from labrenzia aggregata bound to benzyl2 benzoate
24	<a href="#">d1h6za2</a>	Alignment	not modelled	89.4	16	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
25	<a href="#">c4coaA</a>	Alignment	not modelled	87.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase from bacillus2 anthracis complexed with 2-aminoacetophenone.
26	<a href="#">d1r61a</a>	Alignment	not modelled	86.1	22	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Putative cyclase <b>Family:</b> Putative cyclase
27	<a href="#">c6ar9A</a>	Alignment	not modelled	83.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase, putative; <b>PDBTitle:</b> crystal structure of hypoxanthine-guanine-xanthine2 phosphorybosyltransferase in complex with [(2-{{[2-(2-amino-6-oxo-1,6-3 dihydro-9h-purin-9-yl)ethyl]](e)-2-phosphonoethenyl]amino}ethoxy)4 methyl]phosphonic acid
						<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor

28	<a href="#">c2vt2A</a>	Alignment	not modelled	83.1	24	rex; <b>PDBTitle:</b> structure and functional properties of the bacillus subtilis2 transcriptional repressor rex
29	<a href="#">c4cobA</a>	Alignment	not modelled	82.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure kynurenine formamidase from pseudomonas aeruginosa
30	<a href="#">d2hi6a1</a>	Alignment	not modelled	82.2	28	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> AF0055-like
31	<a href="#">c4cogB</a>	Alignment	not modelled	81.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase from burkholderia2 cenocepacia
32	<a href="#">c5nmpF</a>	Alignment	not modelled	80.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> isatin hydrolase; <b>PDBTitle:</b> isatin hydrolase a (iha) from ralstonia solanacearum
33	<a href="#">d1pjqa1</a>	Alignment	not modelled	78.9	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
34	<a href="#">d2b0aa1</a>	Alignment	not modelled	78.1	17	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Putative cyclase <b>Family:</b> Putative cyclase
35	<a href="#">c5j9wB</a>	Alignment	not modelled	78.1	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
36	<a href="#">c4cxA</a>	Alignment	not modelled	76.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c-1-tetrahydrofolate synthase, cytoplasmic, putative; <b>PDBTitle:</b> the crystal structure of trypanosoma brucei n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor and inhibitor
37	<a href="#">d1kyqa1</a>	Alignment	not modelled	76.1	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
38	<a href="#">c4ldaF</a>	Alignment	not modelled	75.8	16	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> tadz; <b>PDBTitle:</b> crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
39	<a href="#">c4b4uB</a>	Alignment	not modelled	75.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii n5,2 n10-methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor
40	<a href="#">d2jfga1</a>	Alignment	not modelled	74.8	14	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
41	<a href="#">c1kyqC</a>	Alignment	not modelled	74.7	15	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
42	<a href="#">c3i07B</a>	Alignment	not modelled	73.5	19	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
43	<a href="#">c5xoeA</a>	Alignment	not modelled	70.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent 6-phosphofructokinase; <b>PDBTitle:</b> crystal structure of the apo staphylococcus aureus phosphofructokinase
44	<a href="#">c2c2xB</a>	Alignment	not modelled	69.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase- <b>PDBTitle:</b> three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
45	<a href="#">c3nglA</a>	Alignment	not modelled	69.6	19	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
46	<a href="#">c3opyG</a>	Alignment	not modelled	69.4	19	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> 6-phosphofructo-1-kinase alpha-subunit; <b>PDBTitle:</b> crystal structure of pichia pastoris phosphofructokinase in the t-2 state
47	<a href="#">c1a4iB</a>	Alignment	not modelled	69.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
48	<a href="#">c3o8nA</a>	Alignment	not modelled	68.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructokinase, muscle type; <b>PDBTitle:</b> structure of phosphofructokinase from rabbit skeletal muscle
49	<a href="#">c5zf1A</a>	Alignment	not modelled	68.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methylenetetrahydrofolate dehydrogenase; <b>PDBTitle:</b> molecular structure of a novel 5,10-methylenetetrahydrofolate2 dehydrogenase from the silkworm, bombyx mori
50	<a href="#">c1edzA</a>	Alignment	not modelled	68.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methylenetetrahydrofolate dehydrogenase; <b>PDBTitle:</b> structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
51	<a href="#">d1b0aa1</a>	Alignment	not modelled	66.8	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain

52	<a href="#">c3p2oA</a>	Alignment	not modelled	66.2	19	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
53	<a href="#">c3opyE</a>	Alignment	not modelled	65.9	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> 6-phosphofructo-1-kinase alpha-subunit; <b>PDBTitle:</b> crystal structure of pichia pastoris phosphofructokinase in the t-2 state
54	<a href="#">c2dt5A</a>	Alignment	not modelled	65.3	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> at-rich dna-binding protein; <b>PDBTitle:</b> crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
55	<a href="#">c4ehiB</a>	Alignment	not modelled	64.7	14	<b>PDB header:</b> hydrolase,transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
56	<a href="#">c5x5jA</a>	Alignment	not modelled	64.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ader; <b>PDBTitle:</b> crystal structure of response regulator ader receiver domain
57	<a href="#">c6nkoA</a>	Alignment	not modelled	64.3	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> forh; <b>PDBTitle:</b> crystal structure of forh
58	<a href="#">d4pfka</a>	Alignment	not modelled	63.4	20	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
59	<a href="#">c6apeA</a>	Alignment	not modelled	62.8	23	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of bifunctional protein fold from helicobacter2 pylori
60	<a href="#">c3opyB</a>	Alignment	not modelled	62.5	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-1-kinase beta-subunit; <b>PDBTitle:</b> crystal structure of pichia pastoris phosphofructokinase in the t-2 state
61	<a href="#">c3opyH</a>	Alignment	not modelled	62.5	11	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> 6-phosphofructo-1-kinase beta-subunit; <b>PDBTitle:</b> crystal structure of pichia pastoris phosphofructokinase in the t-2 state
62	<a href="#">c6d73C</a>	Alignment	not modelled	61.9	31	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel, subfamily m; <b>PDBTitle:</b> cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
63	<a href="#">c3zpgA</a>	Alignment	not modelled	61.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribd; <b>PDBTitle:</b> acinetobacter baumannii ribd, form 2
64	<a href="#">d1a4ia1</a>	Alignment	not modelled	61.3	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
65	<a href="#">c4a5oB</a>	Alignment	not modelled	61.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
66	<a href="#">c6bpqC</a>	Alignment	not modelled	60.7	32	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> structure of the cold- and menthol-sensing ion channel trpm8
67	<a href="#">c6bpqD</a>	Alignment	not modelled	60.7	32	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> structure of the cold- and menthol-sensing ion channel trpm8
68	<a href="#">c6bpqA</a>	Alignment	not modelled	60.7	32	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> structure of the cold- and menthol-sensing ion channel trpm8
69	<a href="#">c6bpqB</a>	Alignment	not modelled	60.7	32	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> structure of the cold- and menthol-sensing ion channel trpm8
70	<a href="#">c3p2oB</a>	Alignment	not modelled	60.1	17	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
71	<a href="#">c4a26B</a>	Alignment	not modelled	59.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase, cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
72	<a href="#">c5nhsB</a>	Alignment	not modelled	59.2	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
73	<a href="#">d1a9xa4</a>	Alignment	not modelled	58.8	18	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
74	<a href="#">d1lssa</a>	Alignment	not modelled	58.8	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
75	<a href="#">d1dbwa</a>	Alignment	not modelled	58.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related <b>PDB header:</b> lyase

76	<a href="#">c3nzoB_</a>	Alignment	not modelled	58.3	14	<b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
77	<a href="#">d1pfka_</a>	Alignment	not modelled	57.4	18	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
78	<a href="#">d2gv8a2</a>	Alignment	not modelled	57.3	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
79	<a href="#">c2yvqA_</a>	Alignment	not modelled	56.8	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
80	<a href="#">c5zz5D_</a>	Alignment	not modelled	55.9	26	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> redox-sensing transcriptional repressor rex
81	<a href="#">d1mvoa_</a>	Alignment	not modelled	55.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
82	<a href="#">c1b0aA_</a>	Alignment	not modelled	55.0	20	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fold bifunctional protein); <b>PDBTitle:</b> 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
83	<a href="#">c5kojD_</a>	Alignment	not modelled	54.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase femo beta subunit protein nifk; <b>PDBTitle:</b> nitrogenase mofep protein in the ids oxidized state
84	<a href="#">c5l9wb_</a>	Alignment	not modelled	54.3	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
85	<a href="#">c3dfzB_</a>	Alignment	not modelled	54.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
86	<a href="#">d1v6sa_</a>	Alignment	not modelled	54.2	21	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
87	<a href="#">c1fcdB_</a>	Alignment	not modelled	53.9	24	<b>PDB header:</b> electron transport(flavocytochrome) <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c sulfide dehydrogenase (flavin- <b>PDBTitle:</b> the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
88	<a href="#">c4p1pB_</a>	Alignment	not modelled	53.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
89	<a href="#">c3snkA_</a>	Alignment	not modelled	52.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator chey-like protein; <b>PDBTitle:</b> crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
90	<a href="#">d1fcdA1</a>	Alignment	not modelled	52.6	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
91	<a href="#">c1pjtB_</a>	Alignment	not modelled	51.2	16	<b>PDB header:</b> transferase/oxidoreductase/lyase <b>Chain:</b> B: <b>PDB Molecule:</b> siroheme synthase; <b>PDBTitle:</b> the structure of the ser128bala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
92	<a href="#">d1dcfa_</a>	Alignment	not modelled	51.0	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
93	<a href="#">c3trjC_</a>	Alignment	not modelled	50.9	13	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
94	<a href="#">c6od1A_</a>	Alignment	not modelled	50.6	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of rpos; <b>PDBTitle:</b> irad-bound to rssb d58p variant
95	<a href="#">c3vbaE_</a>	Alignment	not modelled	50.2	22	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> isopropylmalate/citramalate isomerase small subunit; <b>PDBTitle:</b> crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
96	<a href="#">c5m45K_</a>	Alignment	not modelled	48.7	14	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> acetone carboxylase beta subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
97	<a href="#">d1c1jba_</a>	Alignment	not modelled	48.7	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
98	<a href="#">c5u8mA_</a>	Alignment	not modelled	48.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
99	<a href="#">d2f48a1</a>	Alignment	not modelled	48.0	15	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
100	<a href="#">c2xdqA_</a>	Alignment	not modelled	47.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chlnc-hlb)2 complex <b>Fold:</b> Ribonuclease H-like motif

101	<a href="#">d3bzka5</a>	Alignment	not modelled	47.3	23	<b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
102	<a href="#">c4a1oB</a>	Alignment	not modelled	47.2	19	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
103	<a href="#">c4lzlA</a>	Alignment	not modelled	46.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
104	<a href="#">d1u0sy</a>	Alignment	not modelled	46.6	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
105	<a href="#">c3wg9D</a>	Alignment	not modelled	46.6	31	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of rsp, a rex-family repressor
106	<a href="#">c2dwcB</a>	Alignment	not modelled	45.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl <b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
107	<a href="#">d1fsga</a>	Alignment	not modelled	45.5	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
108	<a href="#">c4dadA</a>	Alignment	not modelled	44.6	16	<b>PDB header:</b> signaling protein, signal transduction <b>Chain:</b> A: <b>PDB Molecule:</b> putative pilus assembly-related protein; <b>PDBTitle:</b> crystal structure of a putative pilus assembly-related protein2 (bps2195) from burkholderia pseudomallei k96243 at 2.50 a resolution3 (psi community target, shapiro I.)
109	<a href="#">c2higA</a>	Alignment	not modelled	44.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-1-fructokinase; <b>PDBTitle:</b> crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
110	<a href="#">c3elbA</a>	Alignment	not modelled	44.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ethanolamine-phosphate cytidyltransferase; <b>PDBTitle:</b> human ctp: phosphoethanolamine cytidyltransferase in complex with2 cmp
111	<a href="#">d1zcza1</a>	Alignment	not modelled	43.6	15	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
112	<a href="#">c3ketA</a>	Alignment	not modelled	43.4	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
113	<a href="#">d1fw8a</a>	Alignment	not modelled	43.2	13	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
114	<a href="#">c1thzA</a>	Alignment	not modelled	43.1	20	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
115	<a href="#">c2r8zC</a>	Alignment	not modelled	42.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
116	<a href="#">d1jb9a1</a>	Alignment	not modelled	42.1	25	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
117	<a href="#">d1g8ma1</a>	Alignment	not modelled	41.1	20	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
118	<a href="#">d2b3za2</a>	Alignment	not modelled	41.0	17	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
119	<a href="#">c4tlmC</a>	Alignment	not modelled	40.2	13	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> receptor subunit glun1; <b>PDBTitle:</b> crystal structure of glun1/glun2b nmda receptor, structure 2
120	<a href="#">c3g8gA</a>	Alignment	not modelled	40.2	43	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rna-binding protein, contains thump <b>PDBTitle:</b> a cytidine deaminase edits c-to-u in transfer rnas in2 archaea