
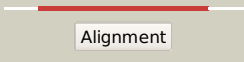
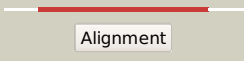
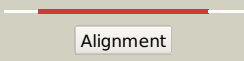
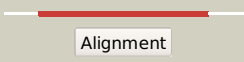
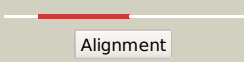
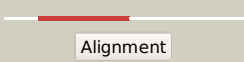
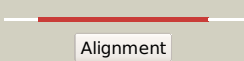
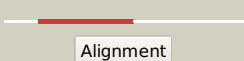
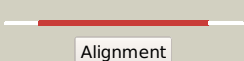
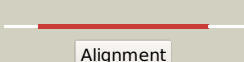
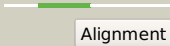

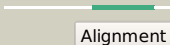

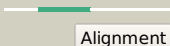
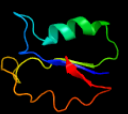
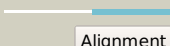

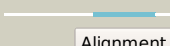

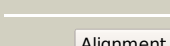
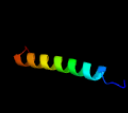
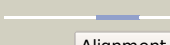

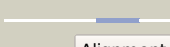



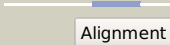


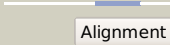
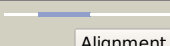
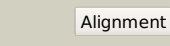
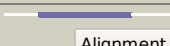



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0259c_(-)_310774_311517
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	f3f1e37a651f42c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5zt7A_</a>	 Alignment		100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> sirohhydrochlorin ferrochelatae; <b>PDBTitle:</b> sirb from bacillus subtilis with co2+
2	<a href="#">c2jh3C_</a>	 Alignment		100.0	24	<b>PDB header:</b> ribosomal protein <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal protein s2-related protein; <b>PDBTitle:</b> the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelataes but also4 with two additional novel domains
3	<a href="#">c2xvzA_</a>	 Alignment		100.0	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chelatae, putative; <b>PDBTitle:</b> cobalt chelatae cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
4	<a href="#">d1qgoa_</a>	 Alignment		100.0	18	<b>Fold:</b> Chelatae-like <b>Superfamily:</b> Chelatae <b>Family:</b> Cobalt chelatae CbiK
5	<a href="#">c4ccsA_</a>	 Alignment		100.0	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cbix; <b>PDBTitle:</b> the structure of cbix, the terminal enzyme for biosynthesis2 of siroheme in denitrifying bacteria
6	<a href="#">c1tjnA_</a>	 Alignment		99.9	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sirohhydrochlorin cobaltochelatae; <b>PDBTitle:</b> crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
7	<a href="#">d1tjna_</a>	 Alignment		99.9	22	<b>Fold:</b> Chelatae-like <b>Superfamily:</b> Chelatae <b>Family:</b> CbiX-like
8	<a href="#">d2hk6a1</a>	 Alignment		99.9	16	<b>Fold:</b> Chelatae-like <b>Superfamily:</b> Chelatae <b>Family:</b> Ferrochelatae
9	<a href="#">c3lyhB_</a>	 Alignment		99.9	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cobalamin (vitamin b12) biosynthesis cbix protein; <b>PDBTitle:</b> crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
10	<a href="#">d2hrca1</a>	 Alignment		99.8	14	<b>Fold:</b> Chelatae-like <b>Superfamily:</b> Chelatae <b>Family:</b> Ferrochelatae
11	<a href="#">d1lbqa_</a>	 Alignment		99.5	12	<b>Fold:</b> Chelatae-like <b>Superfamily:</b> Chelatae <b>Family:</b> Ferrochelatae

12	<a href="#">d3ct6a1</a>	 Alignment		54.1	9	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> DhaM-like
13	<a href="#">d2dja1</a>	 Alignment		44.0	14	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
14	<a href="#">d3b48a1</a>	 Alignment		42.2	14	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> DhaM-like
15	<a href="#">c2eh6A_</a>	 Alignment		35.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
16	<a href="#">d1ybha1</a>	 Alignment		34.0	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
17	<a href="#">c2uwjE_</a>	 Alignment		30.1	19	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> type iii export protein psce; <b>PDBTitle:</b> structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
18	<a href="#">d2ji7a1</a>	 Alignment		29.4	12	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
19	<a href="#">d1pvda1</a>	 Alignment		29.3	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
20	<a href="#">d1q6za1</a>	 Alignment		27.0	14	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
21	<a href="#">d1ovma1</a>	 Alignment	not modelled	26.2	8	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
22	<a href="#">d3clsc1</a>	 Alignment	not modelled	26.2	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
23	<a href="#">d2ez9a1</a>	 Alignment	not modelled	25.6	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
24	<a href="#">d1ozha1</a>	 Alignment	not modelled	22.4	11	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
25	<a href="#">c2e85B_</a>	 Alignment	not modelled	21.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase 3 maturation protease; <b>PDBTitle:</b> crystal structure of the hydrogenase 3 maturation protease
26	<a href="#">c5ow0B_</a>	 Alignment	not modelled	19.4	20	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein, beta subunit; <b>PDBTitle:</b> crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
27	<a href="#">d1vhna_</a>	 Alignment	not modelled	18.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
28	<a href="#">d2a5la1</a>	 Alignment	not modelled	17.2	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
						<b>PDB header:</b> flavoprotein

29	<a href="#">c5ol2E_</a>	Alignment	not modelled	16.9	19	<b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
30	<a href="#">d1zpd1</a>	Alignment	not modelled	16.8	4	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
31	<a href="#">c5ganD_</a>	Alignment	not modelled	16.5	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> spliceosomal protein dib1; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
32	<a href="#">c2gruB_</a>	Alignment	not modelled	16.2	6	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-deoxy-scylo-inosose synthase; <b>PDBTitle:</b> crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
33	<a href="#">c6nkeA_</a>	Alignment	not modelled	16.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate synthase; <b>PDBTitle:</b> wild-type gggps from thermoplasma volcanium
34	<a href="#">c4gijC_</a>	Alignment	not modelled	14.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pseudouridine-5'-phosphate glycosidase; <b>PDBTitle:</b> crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
35	<a href="#">c5mx2r_</a>	Alignment	not modelled	13.8	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
36	<a href="#">d2iht1</a>	Alignment	not modelled	13.4	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
37	<a href="#">c4kpuB_</a>	Alignment	not modelled	13.3	22	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
38	<a href="#">c4ub6R_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
39	<a href="#">c5tistr_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
40	<a href="#">c5gthR_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> native xfel structure of photosystem ii (dark dataset)
41	<a href="#">c5ws6R_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> native xfel structure of photosystem ii (preflash two-flash dataset)
42	<a href="#">c5tisR_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
43	<a href="#">c5kaiR_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
44	<a href="#">c5ws5R_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> native xfel structure of photosystem ii (preflash dark dataset)
45	<a href="#">c5gtiR_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> native xfel structure of photosystem ii (two flash dataset)
46	<a href="#">c4pj0R_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
47	<a href="#">c3i4jC_</a>	Alignment	not modelled	13.3	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
48	<a href="#">c5mx2R_</a>	Alignment	not modelled	13.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
49	<a href="#">d1s0aa_</a>	Alignment	not modelled	12.4	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
50	<a href="#">c3iwpK_</a>	Alignment	not modelled	12.2	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> copper homeostasis protein cutc homolog; <b>PDBTitle:</b> crystal structure of human copper homeostasis protein cutc
51	<a href="#">c5kair_</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
52	<a href="#">c4ub8R_</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
53	<a href="#">c4il6R_</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> structure of sr-substituted photosystem ii
54	<a href="#">c5kafr_</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 3.0

						a2 resolution
55	<a href="#">c5kafR_</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 3.0 a2 resolution
56	<a href="#">c4pj0r_</a>	Alignment	not modelled	12.0	33	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> photosystem ii protein y; <b>PDBTitle:</b> structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
57	<a href="#">c3iprC_</a>	Alignment	not modelled	11.6	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the enterococcus faecalis gluconate2 specific eiaa phosphotransferase system component
58	<a href="#">c5ti8A_</a>	Alignment	not modelled	11.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate aminotransferase from pseudomonas
59	<a href="#">d3beda1</a>	Alignment	not modelled	10.6	23	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> EIIA-man component-like
60	<a href="#">d2gsaa_</a>	Alignment	not modelled	10.1	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
61	<a href="#">c6d6zA_</a>	Alignment	not modelled	9.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nickel-dependent lactate racemase; <b>PDBTitle:</b> structure of the 2nd lactate racemase homolog apoprotein from2 thermoanaerobacterium thermosaccharolyticum
62	<a href="#">c3ckvA_</a>	Alignment	not modelled	9.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a mycobacterial protein
63	<a href="#">c3lv2A_</a>	Alignment	not modelled	9.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
64	<a href="#">d1pdoa_</a>	Alignment	not modelled	9.2	11	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> EIIA-man component-like
65	<a href="#">c3wqtB_</a>	Alignment	not modelled	9.0	19	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> staphylococcus aureus ftsa complexed with amppnp
66	<a href="#">d1vkma_</a>	Alignment	not modelled	8.9	8	<b>Fold:</b> Indigoidine synthase A-like <b>Superfamily:</b> Indigoidine synthase A-like <b>Family:</b> Indigoidine synthase A-like
67	<a href="#">d1nh8a2</a>	Alignment	not modelled	8.8	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
68	<a href="#">d1qgva_</a>	Alignment	not modelled	8.7	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> spliceosomal protein U5-15Kd
69	<a href="#">c5vyeA_</a>	Alignment	not modelled	8.5	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine aldolase; <b>PDBTitle:</b> crystal structure of l-threonine aldolase from pseudomonas putida
70	<a href="#">c2vbgB_</a>	Alignment	not modelled	8.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain alpha-ketoacid decarboxylase; <b>PDBTitle:</b> the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
71	<a href="#">d1u7na_</a>	Alignment	not modelled	7.9	14	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> PlsX-like
72	<a href="#">c2h90A_</a>	Alignment	not modelled	7.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
73	<a href="#">c3mtqA_</a>	Alignment	not modelled	7.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphoenolpyruvate-dependent sugar <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
74	<a href="#">d1qopa_</a>	Alignment	not modelled	7.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
75	<a href="#">c3dodA_</a>	Alignment	not modelled	7.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
76	<a href="#">c3gr7A_</a>	Alignment	not modelled	7.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal crystal form
77	<a href="#">c4jicB_</a>	Alignment	not modelled	7.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gtn reductase; <b>PDBTitle:</b> glycerol trinitrate reductase nera from agrobacterium radiobacter
78	<a href="#">d2nly1</a>	Alignment	not modelled	7.0	10	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> Divergent polysaccharide deacetylase
						<b>Fold:</b> Phosphoglycerate kinase

79	<a href="#">d1vpea_</a>	Alignment	not modelled	6.9	16	<b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
80	<a href="#">c6fmgC_</a>	Alignment	not modelled	6.9	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system mannose-specific transporter subunit iiab; <b>PDBTitle:</b> structure of the mannose transporter iia domain from streptococcus2 pneumoniae
81	<a href="#">c4tkzA_</a>	Alignment	not modelled	6.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein gbs1890; <b>PDBTitle:</b> crystal structure of phosphotransferase system component eiaa from2 streptococcus agalactiae
82	<a href="#">d1z41a1</a>	Alignment	not modelled	6.7	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
83	<a href="#">c5zbyA_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protease hyci; <b>PDBTitle:</b> crystal structure of a [nife] hydrogenase maturation protease hyci2 from thermococcus kodakarensis kod1
84	<a href="#">c4rf1B_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-1-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii
85	<a href="#">c4xfrB_</a>	Alignment	not modelled	6.2	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a domain of unknown function (duf1537) from2 bordetella bronchiseptica (bb3215), target efi-511620, with bound3 citrate, domain swapped dimer, space group p6522
86	<a href="#">c5m99A_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
87	<a href="#">c3h75A_</a>	Alignment	not modelled	6.1	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic sugar-binding domain protein; <b>PDBTitle:</b> crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
88	<a href="#">d1v6sa_</a>	Alignment	not modelled	5.9	13	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
89	<a href="#">d1djqa1</a>	Alignment	not modelled	5.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
90	<a href="#">c3s99A_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> basic membrane lipoprotein; <b>PDBTitle:</b> crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
91	<a href="#">c5kinC_</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
92	<a href="#">c5t3uA_</a>	Alignment	not modelled	5.4	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
93	<a href="#">c3vndD_</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
94	<a href="#">c4r9nA_</a>	Alignment	not modelled	5.2	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0547 protein; <b>PDBTitle:</b> deor family transcriptional regulator from listeria monocytogenes.
95	<a href="#">d1ydha_</a>	Alignment	not modelled	5.2	11	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
96	<a href="#">c2kc8B_</a>	Alignment	not modelled	5.1	48	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
97	<a href="#">c6erkB_</a>	Alignment	not modelled	5.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis
98	<a href="#">c3cf4G_</a>	Alignment	not modelled	5.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
99	<a href="#">c2kvcA_</a>	Alignment	not modelled	5.1	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a