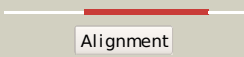

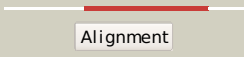

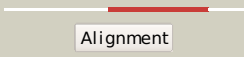



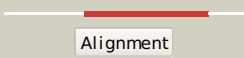

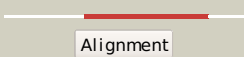



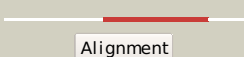

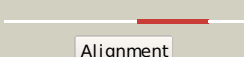
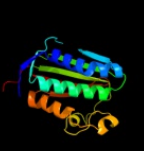
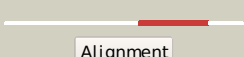
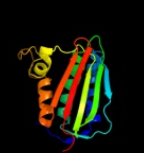
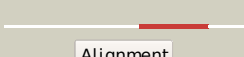












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3d2rB_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; <b>PDBTitle:</b> crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
2	<a href="#">c2q8fA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; <b>PDBTitle:</b> structure of pyruvate dehydrogenase kinase isoform 1
3	<a href="#">c3d36B_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> sporulation kinase b; <b>PDBTitle:</b> how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
4	<a href="#">c2c2aA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
5	<a href="#">c2bu8A_</a>	 Alignment		100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase kinase isoenzyme 2; <b>PDBTitle:</b> crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
6	<a href="#">c1y8oA_</a>	 Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; <b>PDBTitle:</b> crystal structure of the pdk3-l2 complex
7	<a href="#">c1g1vA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase <b>PDBTitle:</b> branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complexed with atp-gamma-s
8	<a href="#">c3a0rA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
9	<a href="#">c3a0tA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> catalytic domain of histidine kinase thka (tm1359) in2 complex with adp and mg ion (trigonal)
10	<a href="#">d2c2aa2</a>	 Alignment		100.0	32	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
11	<a href="#">d1id0a_</a>	 Alignment		100.0	25	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase

12	<a href="#">d1gkza2</a>	Alignment		100.0	15	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
13	<a href="#">d1jm6a2</a>	Alignment		100.0	17	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
14	<a href="#">c1b3qa</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (chemotaxis protein chea); <b>PDBTitle:</b> crystal structure of chea-289, a signal transducing histidine kinase
15	<a href="#">d1bxda</a>	Alignment		100.0	29	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
16	<a href="#">d1i58a</a>	Alignment		100.0	21	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
17	<a href="#">c2ch4A</a>	Alignment		100.0	21	<b>PDB header:</b> transferase/chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chea; <b>PDBTitle:</b> complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
18	<a href="#">d1ysra1</a>	Alignment		99.9	26	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
19	<a href="#">c3jz3B</a>	Alignment		99.9	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein qsec; <b>PDBTitle:</b> structure of the cytoplasmic segment of histidine kinase qsec
20	<a href="#">d1r62a</a>	Alignment		99.9	24	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
21	<a href="#">c3gieA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase desk; <b>PDBTitle:</b> crystal structure of desk_h188e in complex with amp-pcp
22	<a href="#">d2hkja3</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
23	<a href="#">c3ehgA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase (yocf protein); <b>PDBTitle:</b> crystal structure of the atp-binding domain of desk in complex with2 atp
24	<a href="#">c1mx0D</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> type ii dna topoisomerase vi subunit b; <b>PDBTitle:</b> structure of topoisomerase subunit
25	<a href="#">c2zbkB</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
26	<a href="#">c3zxqa</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxia sensor histidine kinase response regulator dost; <b>PDBTitle:</b> crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
27	<a href="#">c2q2eB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
28	<a href="#">c3zxoB</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> redox sensor histidine kinase response regulator devs; <b>PDBTitle:</b> crystal structure of the mutant atp-binding domain of2

					mycobacterium tuberculosis doss
29	<a href="#">d1h7sa2</a>	Alignment	not modelled	99.5	13 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
30	<a href="#">d1th8a_</a>	Alignment	not modelled	99.5	22 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
31	<a href="#">d1bkna2</a>	Alignment	not modelled	99.5	17 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
32	<a href="#">dlixma_</a>	Alignment	not modelled	99.5	14 <b>Fold:</b> Sporulation response regulatory protein Spo0B <b>Superfamily:</b> Sporulation response regulatory protein Spo0B <b>Family:</b> Sporulation response regulatory protein Spo0B
33	<a href="#">d1y8oa2</a>	Alignment	not modelled	99.4	13 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
34	<a href="#">d1b63a2</a>	Alignment	not modelled	99.4	18 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
35	<a href="#">c3zrwB_</a>	Alignment	not modelled	99.1	24 <b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> af1503 protein, osmolarity sensor protein envz; <b>PDBTitle:</b> the structure of the dimeric hamp-dhp fusion a291v mutant
36	<a href="#">c3na3A_</a>	Alignment	not modelled	99.0	20 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein mlh1; <b>PDBTitle:</b> mutl protein homolog 1 isoform 1 from homo sapiens
37	<a href="#">c3lnrA_</a>	Alignment	not modelled	98.8	9 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
38	<a href="#">c3h4lB_</a>	Alignment	not modelled	98.7	16 <b>PDB header:</b> dna binding protein, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein pms1; <b>PDBTitle:</b> crystal structure of n terminal domain of a dna repair protein
39	<a href="#">d1kija2</a>	Alignment	not modelled	98.5	18 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
40	<a href="#">c1bkna_</a>	Alignment	not modelled	98.4	20 <b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> mutl; <b>PDBTitle:</b> crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
41	<a href="#">d1s16a2</a>	Alignment	not modelled	98.4	15 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
42	<a href="#">d1pvga2</a>	Alignment	not modelled	98.3	14 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
43	<a href="#">d1ei1a2</a>	Alignment	not modelled	98.3	11 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
44	<a href="#">c1y4sA_</a>	Alignment	not modelled	98.2	19 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein htpg; <b>PDBTitle:</b> conformation rearrangement of heat shock protein 90 upon2 adp binding
45	<a href="#">c3iedA_</a>	Alignment	not modelled	98.2	16 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn
46	<a href="#">c1ei1B_</a>	Alignment	not modelled	98.2	11 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase b; <b>PDBTitle:</b> dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center
47	<a href="#">c1kijB_</a>	Alignment	not modelled	98.2	19 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
48	<a href="#">c1zxnb_</a>	Alignment	not modelled	98.2	11 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase ii, alpha isozyme; <b>PDBTitle:</b> human dna topoisomerase iia atpase/adp
49	<a href="#">d1uy1a_</a>	Alignment	not modelled	98.2	21 <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
50	<a href="#">c2fwyA_</a>	Alignment	not modelled	98.1	21 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp 90-alpha; <b>PDBTitle:</b> structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
51	<a href="#">c1s16B_</a>	Alignment	not modelled	98.1	13 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> topoisomerase iv subunit b; <b>PDBTitle:</b> crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp

52	<a href="#">d2asxa1</a>	Alignment	not modelled	98.0	25	<b>Fold:</b> HAMP domain-like <b>Superfamily:</b> HAMP domain-like <b>Family:</b> HAMP domain
53	<a href="#">c2cg9A</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent molecular chaperone hsp82; <b>PDBTitle:</b> crystal structure of an hsp90-sba1 closed chaperone complex
54	<a href="#">clea6A</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> pms1 protein homolog 2; <b>PDBTitle:</b> n-terminal 40kda fragment of nhpms2 complexed with adp
55	<a href="#">c1qzrA</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase ii; <b>PDBTitle:</b> crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
56	<a href="#">c3ke6A</a>	Alignment	not modelled	97.9	30	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein rv1364c/mtl1410; <b>PDBTitle:</b> the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
57	<a href="#">c2akpA</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent molecular chaperone hsp82; <b>PDBTitle:</b> hsp90 delta24-n210 mutant
58	<a href="#">c3pehB</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> endoplasmic homolog; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative
59	<a href="#">dluyma</a>	Alignment	not modelled	97.9	20	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
60	<a href="#">d2iwxal</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
61	<a href="#">c1zwhA</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent molecular chaperone hsp82; <b>PDBTitle:</b> yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
62	<a href="#">dls14a</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
63	<a href="#">c3g7bB</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> staphylococcus aureus gyrase b co-complex with inhibitor
64	<a href="#">c2iorA</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein htpg; <b>PDBTitle:</b> crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp
65	<a href="#">c2iopD</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> chaperone protein htpg; <b>PDBTitle:</b> crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
66	<a href="#">d2gqpa1</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
67	<a href="#">dljoya</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> ROP-like <b>Superfamily:</b> Homodimeric domain of signal transducing histidine kinase <b>Family:</b> Homodimeric domain of signal transducing histidine kinase
68	<a href="#">dlqy5a</a>	Alignment	not modelled	97.5	20	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
69	<a href="#">c3lnuA</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit b; <b>PDBTitle:</b> crystal structure of pare subunit
70	<a href="#">c2o1wB</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> endoplasmic; <b>PDBTitle:</b> structure of n-terminal plus middle domains (n+m) of grp94
71	<a href="#">d2c2aa1</a>	Alignment	not modelled	97.1	28	<b>Fold:</b> ROP-like <b>Superfamily:</b> Homodimeric domain of signal transducing histidine kinase <b>Family:</b> Homodimeric domain of signal transducing histidine kinase
72	<a href="#">c2o1uA</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic; <b>PDBTitle:</b> structure of full length grp94 with amp-pnp bound
73	<a href="#">c2rm8A</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory rhodopsin ii transducer; <b>PDBTitle:</b> the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
74	<a href="#">c3cwvB</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase, b subunit, truncated; <b>PDBTitle:</b> crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
75	<a href="#">c3lmmA</a>	Alignment	not modelled	79.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3

					consortium target cdr35
76	<a href="#">d1g0oa_</a>	Alignment	not modelled	59.7	16 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
77	<a href="#">c3n0rA_</a>	Alignment	not modelled	59.3	13 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr stress response regulator at 1.25 angstrom2 resolution
78	<a href="#">c3s8mA_</a>	Alignment	not modelled	51.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acp reductase; <b>PDBTitle:</b> the crystal structure of fabv
79	<a href="#">d1oaaa_</a>	Alignment	not modelled	44.9	11 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
80	<a href="#">c2z1nA_</a>	Alignment	not modelled	44.4	31 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of ape0912 from aeropyrum pernix k1
81	<a href="#">c3ctmH_</a>	Alignment	not modelled	43.2	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
82	<a href="#">d1y5ma1</a>	Alignment	not modelled	41.3	8 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">c3o38D_</a>	Alignment	not modelled	38.6	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
84	<a href="#">c3rd5A_</a>	Alignment	not modelled	38.6	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mypaa.01249.c; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
85	<a href="#">d1gz6a_</a>	Alignment	not modelled	38.0	28 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
86	<a href="#">d2h7ma1</a>	Alignment	not modelled	37.9	12 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
87	<a href="#">c3gdfA_</a>	Alignment	not modelled	37.4	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nadp-dependent mannitol dehydrogenase; <b>PDBTitle:</b> crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladospirum herbarum.
88	<a href="#">c2p68A_</a>	Alignment	not modelled	37.1	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of aq_1716 from aquifex aeolicus vf5
89	<a href="#">c3i1jB_</a>	Alignment	not modelled	37.0	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain <b>PDBTitle:</b> structure of a putative short chain dehydrogenase from2 pseudomonas syringae
90	<a href="#">d1h5qa_</a>	Alignment	not modelled	35.3	24 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
91	<a href="#">c3gaff_</a>	Alignment	not modelled	35.2	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 7-alpha-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
92	<a href="#">d2bela_</a>	Alignment	not modelled	34.8	9 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
93	<a href="#">c2o2sA_</a>	Alignment	not modelled	34.4	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
94	<a href="#">d1yxma1</a>	Alignment	not modelled	34.3	24 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
95	<a href="#">c3sx2F_</a>	Alignment	not modelled	34.1	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative 3-ketoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
96	<a href="#">c3uf0A_</a>	Alignment	not modelled	33.7	28 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
97	<a href="#">c2kseA_</a>	Alignment	not modelled	33.5	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein qsec; <b>PDBTitle:</b> backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmg) target 4311c
98	<a href="#">c2ntnB_</a>	Alignment	not modelled	31.5	32 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of maba-c60v/g139a/s144l
99	<a href="#">c2zpaB_</a>	Alignment	not modelled	31.2	23 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ypfi; <b>PDBTitle:</b> crystal structure of trna(met) cytidine acetyltransferase
100	<a href="#">c3r1iB_</a>	Alignment	not modelled	31.2	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase;



						<b>PDBTitle:</b> crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
101	<a href="#">d1zbqa1</a>	Alignment	not modelled	31.1	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
102	<a href="#">c1zbqB</a>	Alignment	not modelled	31.1	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase 4; <b>PDBTitle:</b> crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
103	<a href="#">c3ai3A</a>	Alignment	not modelled	30.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-sorbose reductase; <b>PDBTitle:</b> the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
104	<a href="#">c3t6oA</a>	Alignment	not modelled	30.6	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter/antisigma-factor antagonist stas; <b>PDBTitle:</b> the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
105	<a href="#">d1xsea</a>	Alignment	not modelled	30.0	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
106	<a href="#">c3tjrA</a>	Alignment	not modelled	29.9	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
107	<a href="#">c3ak4C</a>	Alignment	not modelled	29.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-dependent quinuclidinone reductase; <b>PDBTitle:</b> crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
108	<a href="#">c3kvoB</a>	Alignment	not modelled	28.9	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxysteroid dehydrogenase-like protein 2; <b>PDBTitle:</b> crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdl2)
109	<a href="#">c3ek2D</a>	Alignment	not modelled	28.6	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of enoyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
110	<a href="#">c3ksuA</a>	Alignment	not modelled	28.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-acyl carrier protein reductase; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase from2 oenococcus oeni psu-1
111	<a href="#">d1q8ka2</a>	Alignment	not modelled	28.1	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eIF-2-alpha, C-terminal domain <b>Family:</b> eIF-2-alpha, C-terminal domain
112	<a href="#">c3ftpD</a>	Alignment	not modelled	28.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein)2 reductase from burkholderia pseudomallei at 2.05 a3 resolution
113	<a href="#">c2b4qB</a>	Alignment	not modelled	27.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rhannolipids biosynthesis 3-oxoacyl-[acyl- <b>PDBTitle:</b> pseudomonas aeruginosa rhlg/nadp active-site complex
114	<a href="#">c3pxxE</a>	Alignment	not modelled	27.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
115	<a href="#">c1yb1B</a>	Alignment	not modelled	27.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase type xi; <b>PDBTitle:</b> crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
116	<a href="#">d1yb1a</a>	Alignment	not modelled	27.0	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
117	<a href="#">c3emkA</a>	Alignment	not modelled	26.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose/ribitol dehydrogenase; <b>PDBTitle:</b> 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
118	<a href="#">d1uzma1</a>	Alignment	not modelled	26.3	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
119	<a href="#">d1w6ua</a>	Alignment	not modelled	26.2	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
120	<a href="#">d1xg5a</a>	Alignment	not modelled	25.1	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases