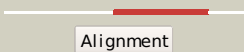
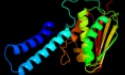
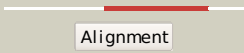


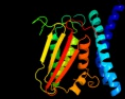



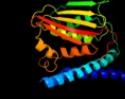
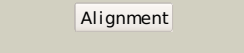
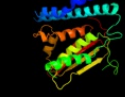


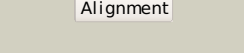



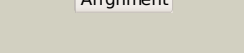

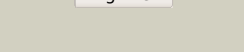









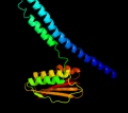
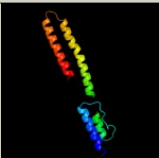


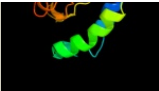


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d36B_	 Alignment		100.0	32	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: sporulation kinase b; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
2	c2c2aA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
3	c2q8fA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
4	c3d2rB_	 Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
5	c2bu8A_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
6	c1y8oA_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
7	c1qjvA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complexed with atp-gamma-s
8	c3a0rA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
9	c3a0tA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: catalytic domain of histidine kinase thka (tm1359) in2 complex with adp and mg ion (trigonal)
10	c1b3qA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
11	d2c2aa2	 Alignment		100.0	37	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase

12	d1ld0a_	Alignment		99.9	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
13	d1gkza2	Alignment		99.9	24	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
14	d1bxda_	Alignment		99.9	28	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
15	d1jm6a2	Alignment		99.9	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
16	d1i58a_	Alignment		99.9	35	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
17	c3jz3B_	Alignment		99.9	27	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
18	c2ch4A_	Alignment		99.9	33	PDB header: transferase/chemotaxis Chain: A: PDB Molecule: chemotaxis protein chea; PDBTitle: complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
19	d1ysra1	Alignment		99.9	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
20	c3gieA_	Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of desck_h188e in complex with amp-pcp
21	d1r62a_	Alignment	not modelled	99.8	27	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
22	c3ehgA_	Alignment	not modelled	99.7	18	PDB header: transferase Chain: A: PDB Molecule: sensor kinase (yocf protein); PDBTitle: crystal structure of the atp-binding domain of desk in complex with2 atp
23	d2hkja3	Alignment	not modelled	99.7	23	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
24	d1ixma_	Alignment	not modelled	99.7	15	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
25	c3zxqA_	Alignment	not modelled	99.7	21	PDB header: transferase Chain: A: PDB Molecule: hypoxia sensor histidine kinase response regulator dost; PDBTitle: crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
26	c3zxoB_	Alignment	not modelled	99.6	22	PDB header: transferase Chain: B: PDB Molecule: redox sensor histidine kinase response regulator devs; PDBTitle: crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
27	c1mx0D_	Alignment	not modelled	99.6	20	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
28	c2zhkP	Alignment	not modelled	99.6	21	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b;

28	c220kB	Alignment	not modelled	99.0	21	PDBTitle: crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
29	c2q2eB	Alignment	not modelled	99.5	21	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
30	d1th8a	Alignment	not modelled	99.4	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
31	d1h7sa2	Alignment	not modelled	99.4	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
32	d1y8oa2	Alignment	not modelled	99.3	14	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
33	d1bkna2	Alignment	not modelled	99.3	23	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
34	d1b63a2	Alignment	not modelled	99.2	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
35	d2c2aa1	Alignment	not modelled	99.0	20	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
36	c3na3A	Alignment	not modelled	98.8	23	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
37	d1joya	Alignment	not modelled	98.8	23	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
38	c3zrwB	Alignment		98.6	19	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
39	c3h4lB	Alignment	not modelled	98.5	24	PDB header: dna binding protein, protein binding Chain: B: PDB Molecule: dna mismatch repair protein pms1; PDBTitle: crystal structure of n terminal domain of a dna repair protein
40	c1kijB	Alignment	not modelled	98.3	21	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
41	d1kija2	Alignment	not modelled	98.2	27	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
42	d1pvga2	Alignment	not modelled	98.1	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
43	d1ei1a2	Alignment	not modelled	98.1	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
44	c1bkna	Alignment	not modelled	98.1	26	PDB header: dna repair Chain: A: PDB Molecule: mutl; PDBTitle: crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
45	c1ei1B	Alignment	not modelled	98.0	21	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase b; PDBTitle: dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center
46	d1s16a2	Alignment	not modelled	98.0	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
47	c1s16B	Alignment	not modelled	97.9	20	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp
48	c1zxnB	Alignment	not modelled	97.8	24	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
49	c1ea6A	Alignment	not modelled	97.8	18	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
50	c1y4sA	Alignment	not modelled	97.8	27	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htgp; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding PDB header: chaperone

51	c2iorA_	Alignment	not modelled	97.7	23	Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp
52	c1qzrA_	Alignment	not modelled	97.7	21	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase ii; PDBTitle: crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
53	c3ke6A_	Alignment	not modelled	97.7	26	PDB header: unknown function Chain: A: PDB Molecule: protein rv1364c/mt1410; PDBTitle: the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
54	d2gqa1	Alignment	not modelled	97.6	28	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
55	c3g7bB_	Alignment	not modelled	97.6	17	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with inhibitor
56	d1uyla_	Alignment	not modelled	97.5	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
57	c3iedA_	Alignment	not modelled	97.4	23	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein; PDBTitle: crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn
58	c2fwyA_	Alignment	not modelled	97.4	16	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp 90-alpha; PDBTitle: structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
59	c2o1wB_	Alignment	not modelled	97.3	26	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
60	c2iopD_	Alignment	not modelled	97.2	26	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
61	c2cg9A_	Alignment	not modelled	97.2	28	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
62	c3pehB_	Alignment	not modelled	97.2	24	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic homolog; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative
63	d1uyma_	Alignment	not modelled	97.1	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
64	d2iwxal	Alignment	not modelled	97.1	21	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
65	c3lnuA_	Alignment	not modelled	97.1	23	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
66	c2akpA_	Alignment	not modelled	97.1	25	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
67	c1zwhA_	Alignment	not modelled	97.0	21	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
68	d1s14a_	Alignment	not modelled	96.9	15	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
69	d1qy5a_	Alignment	not modelled	96.8	25	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
70	c2o1uA_	Alignment	not modelled	96.1	30	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
71	d3by8a1	Alignment		93.3	26	Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
72	c3cwvB_	Alignment	not modelled	92.5	15	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase, b subunit, truncated; PDBTitle: crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
						Fold: Profilin-like

73	d1p0za_	Alignment		92.4	17	Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
74	d1g0oa_	Alignment	not modelled	61.7	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c3rd5A_	Alignment	not modelled	61.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: mypaa.01249.c; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
76	c3o38D_	Alignment	not modelled	57.3	25	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
77	c3s8mA_	Alignment	not modelled	53.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acp reductase; PDBTitle: the crystal structure of fabv
78	d1oaaa_	Alignment	not modelled	52.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	d1y5ma1	Alignment	not modelled	48.4	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
80	c2p68A_	Alignment	not modelled	47.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
81	c2z1nA_	Alignment	not modelled	47.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
82	c3lmmA_	Alignment	not modelled	45.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
83	c3f5sA_	Alignment	not modelled	43.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of putative short chain dehydrogenase from shigella2 flexneri 2a str. 301
84	c3ftpD_	Alignment	not modelled	42.7	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein)2 reductase from burkholderia pseudomallei at 2.05 a3 resolution
85	c3i1jB_	Alignment	not modelled	42.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain PDBTitle: structure of a putative short chain dehydrogenase from2 pseudomonas syringae
86	d1qsga_	Alignment	not modelled	41.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	d1gz6a_	Alignment	not modelled	41.7	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	d2h7ma1	Alignment	not modelled	41.6	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
89	c3ctmH_	Alignment	not modelled	41.5	17	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
90	c3pxxE_	Alignment	not modelled	40.9	17	PDB header: oxidoreductase Chain: E: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
91	d1h5qa_	Alignment	not modelled	40.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c3r1iB_	Alignment	not modelled	40.5	31	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
93	c3sx2F_	Alignment	not modelled	40.5	17	PDB header: oxidoreductase Chain: F: PDB Molecule: putative 3-ketoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
94	d2bela_	Alignment	not modelled	39.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	c3uf0A_	Alignment	not modelled	39.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
96	c3afnC_	Alignment	not modelled	39.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
97	c2o2sA_	Alignment	not modelled	38.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acyl carrier reductase; PDBTitle: the structure of t. gondii enoyl acyl carrier protein

						reductase in2 complex with nad and triclosan
98	c3gaffF_	Alignment	not modelled	38.2	19	PDB header: oxidoreductase Chain: F: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
99	c3kvoB_	Alignment	not modelled	37.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxysteroid dehydrogenase-like protein 2; PDBTitle: crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdl2)
100	c3ak4C_	Alignment	not modelled	37.1	23	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
101	c3ek2D_	Alignment	not modelled	37.1	4	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of eonyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
102	c3tjrA_	Alignment	not modelled	37.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
103	d1yxma1	Alignment	not modelled	36.9	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
104	c3ai3A_	Alignment	not modelled	36.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
105	c3f9iB_	Alignment	not modelled	35.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
106	d1xg5a_	Alignment	not modelled	35.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	d1xsea_	Alignment	not modelled	35.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	d1w6ua_	Alignment	not modelled	34.8	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	c2ntnB_	Alignment	not modelled	34.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of maba-c60v/g139a/s144l
110	c2v1bA_	Alignment	not modelled	34.4	9	PDB header: transferase Chain: A: PDB Molecule: nph1-1; PDBTitle: n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
111	c3emkA_	Alignment	not modelled	34.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
112	d1nffa_	Alignment	not modelled	33.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
113	c3lf2B_	Alignment	not modelled	33.9	27	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain oxidoreductase q9hya2; PDBTitle: nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
114	c1yb1B_	Alignment	not modelled	33.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase type xi; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
115	c3ksuA_	Alignment	not modelled	33.2	7	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-acyl carrier protein reductase; PDBTitle: crystal structure of short-chain dehydrogenase from2 oenococcus oeni psu-1
116	c1zbqB_	Alignment	not modelled	32.1	31	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase 4; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
117	d1zbqa1	Alignment	not modelled	32.1	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	c3k31B_	Alignment	not modelled	32.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
119	d1j0ga_	Alignment	not modelled	32.0	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
120	c2vz8B_	Alignment	not modelled	31.6	21	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase