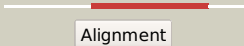

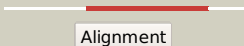

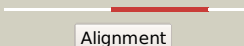







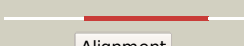











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1032c_(trcS)_1156430_1157959
Date	Wed Jul 31 22:05:10 BST 2019
Unique Job ID	2c457962159dc651

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4i5sA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
2	c3d2rB_	 Alignment		100.0	15	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
3	c4ew8A_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: sensor protein divl; PDBTitle: crystal structure of a c-terminal part of tyrosine kinase (divl) from2 caulobacter crescentus cb15 at 2.50 a resolution (psi community3 target, shapiro l.)
4	c3d36B_	 Alignment		100.0	20	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
5	c2q8fA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
6	c3criB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex.
7	c2bu8A_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
8	c1y8oA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
9	c4biuB_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
10	c5idjA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: cell cycle histidine kinase ccka; PDBTitle: bifunctional histidine kinase ccka (domains dhp-ca) in complex with2 adp/mg2+
11	c4kp4B_	 Alignment		100.0	26	PDB header: transferase/signaling protein Chain: B: PDB Molecule: osmolarity sensor protein envz, histidine kinase; PDBTitle: deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.

12	c6dk8B_	Alignment		100.0	28	PDB header: signaling protein Chain: B: PDB Molecule: rets (regulator of exopolysaccharide and type iii PDBTitle: rets kinase region without cobalt
13	c2c2aA_	Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
14	c1qjvA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s
15	c4u7nA_	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: histidine protein kinase sensor protein; PDBTitle: inactive structure of histidine kinase
16	c3tz5A_	Alignment		100.0	17	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, PDBTitle: crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
17	c5idmA_	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: cell cycle histidine kinase ccka; PDBTitle: bifunctional histidine kinase ccka (domain, ca) in complex with c-di-2 gmp and amppnp/mg2+
18	c4gczB_	Alignment		100.0	27	PDB header: signaling protein, de novo protein Chain: B: PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor
19	c4biyD_	Alignment		100.0	29	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
20	c3a0tA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: catalytic domain of histidine kinase thka (tm1359) in complex with adp2 and mg ion (trigonal)
21	c3a0rA_	Alignment	not modelled	100.0	23	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)
22	c6blkB_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine-protein kinase/phosphatase PDBTitle: mycobacterial sensor histidine kinase mprb
23	d1jm6a2	Alignment	not modelled	100.0	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
24	c3sl2A_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase yycg; PDBTitle: atp forms a stable complex with the essential histidine kinase walk2 (yycg) domain Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase
25	d2c2aa2	Alignment	not modelled	100.0	32	Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
26	d1gkza2	Alignment	not modelled	100.0	21	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
27	d1bxda_	Alignment	not modelled	100.0	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

28	d1id0a_	Alignment	not modelled	100.0	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
29	c1b3qA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
30	c4pl9A_	Alignment	not modelled	99.9	31	PDB header: transferase Chain: A: PDB Molecule: ethylene receptor 1; PDBTitle: structure of the catalytic domain of etr1 from arabidopsis thaliana
31	c2ch4A_	Alignment	not modelled	99.9	27	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
32	d1i58a_	Alignment	not modelled	99.9	29	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
33	d1ysra1	Alignment	not modelled	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
34	c4r39A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: histidine kinase domain from erythrobacter litoralis el346 blue-light2 activated histidine kinase
35	c4fmtB_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: chpt protein; PDBTitle: crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
36	c4ctiA_	Alignment	not modelled	99.9	26	PDB header: signaling protein Chain: A: PDB Molecule: osmolarity sensor protein envz, af1503; PDBTitle: escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
37	c6nb0A_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: histidine kinase; PDBTitle: crystal structure of histidine kinase from burkholderia phymatum2 stm815
38	c3jz3B_	Alignment	not modelled	99.9	34	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
39	d1r62a_	Alignment	not modelled	99.9	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
40	c4r3aA_	Alignment	not modelled	99.9	19	PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis el346 blue-light activated histidine kinase
41	c6e95A_	Alignment	not modelled	99.9	13	PDB header: signaling protein Chain: A: PDB Molecule: staphylococcus aureus agrc histidine kinase module fused to PDBTitle: chimeric structure of saccharomyces cerevisiae gcn4 leucine zipper2 fused to staphylococcus aureus agrc cytoplasmic histidine kinase3 module (dataset isotropically truncated by hkl2000)
42	c4qpkA_	Alignment	not modelled	99.9	13	PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
43	d2hkja3	Alignment	not modelled	99.9	21	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	c5epvB_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: B: PDB Molecule: blue-light-activated histidine kinase; PDBTitle: histidine kinase domain from the lov-hk blue-light receptor from2 brucella abortus
45	c4gt8A_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein vras; PDBTitle: crystal structure of the catalytic and atp-binding domain from vras in2 complex with adp
46	c3gieA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of deskc_h188e in complex with amp- pcp
47	c1mx0D_	Alignment	not modelled	99.8	22	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
48	c2zkbB_	Alignment	not modelled	99.8	23	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
49	c3ehgA_	Alignment	not modelled	99.7	23	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
50	c4bxiA_	Alignment	not modelled	99.7	18	PDB header: atp-binding protein Chain: A: PDB Molecule: accessory gene regulator protein c; PDBTitle: crystal structure of atp binding domain of agrc from2 staphylococcus aureus
51	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

52	c2q2eB_	Alignment	not modelled	99.7	17	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from 2 methanosarcina mazei
53	d1h7sa2	Alignment	not modelled	99.6	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
54	d1bkna2	Alignment	not modelled	99.5	19	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
55	c3zxoB_	Alignment	not modelled	99.5	23	PDB header: transferase Chain: B: PDB Molecule: redox sensor histidine kinase response regulator devs; PDBTitle: crystal structure of the mutant atp-binding domain of 2 mycobacterium tuberculosis doss
56	d1b63a2	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: DNA gyrase/MutL, N-terminal domain
57	d1ixma_	Alignment	not modelled	99.4	14	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
58	d1th8a_	Alignment	not modelled	99.4	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
59	d1y8oa2	Alignment	not modelled	99.4	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
60	c5jefA_	Alignment	not modelled	99.4	14	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in 2 asymmetric holo state
61	c3na3A_	Alignment	not modelled	99.1	18	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
62	c4geeA_	Alignment	not modelled	99.0	21	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna gyrase subunit b; PDBTitle: pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.
63	c4gn0D_	Alignment	not modelled	98.9	17	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
64	c4b6cB_	Alignment	not modelled	98.9	17	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b,dna gyrase subunit b,dna gyrase PDBTitle: structure of the m. smegmatis gyrb atpase domain in complex with an2 aminopyrazinamide
65	c4emvA_	Alignment	not modelled	98.7	23	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna topoisomerase iv, b subunit; PDBTitle: crystal structure of a topoisomerase atp inhibitor
66	c5j5pB_	Alignment	not modelled	98.6	26	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase 4 subunit b; PDBTitle: amp-pnp-stabilized atpase domain of topoisomerase iv from 2 streptococcus pneumoniae, complex type i
67	c3h4lB_	Alignment	not modelled	98.6	15	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
68	d1kija2	Alignment	not modelled	98.6	22	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	c1bkna_	Alignment	not modelled	98.6	19	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
70	d1s16a2	Alignment	not modelled	98.5	21	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
71	c5ix1A_	Alignment	not modelled	98.5	19	PDB header: transcription Chain: A: PDB Molecule: morc family cw-type zinc finger protein 3; PDBTitle: crystal structure of mouse morc3 atpase-cw cassette in complex with 2 amppnp and h3k4me3 peptide
72	c1kijB_	Alignment	not modelled	98.5	20	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
73	c5ofbB_	Alignment	not modelled	98.5	20	PDB header: nuclear protein Chain: B: PDB Molecule: morc family cw-type zinc finger protein 2; PDBTitle: crystal structure of human morc2 (residues 1-603) with spinal muscular2 atrophy mutation s87l
74	d1ei1a2	Alignment	not modelled	98.5	24	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

75	c3zrwB_	Alignment	not modelled	98.4	21	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
76	c1ej1B_	Alignment	not modelled	98.4	24	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
77	d1pvgq2	Alignment	not modelled	98.3	17	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
78	c3lnrA_	Alignment	not modelled	98.3	10	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
79	c3iedA_	Alignment	not modelled	98.3	17	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
80	c1s16B_	Alignment	not modelled	98.2	23	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
81	c4hymA_	Alignment	not modelled	98.2	21	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: topoisomerase iv, subunit b; PDBTitle: pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.
82	c1zxnB_	Alignment	not modelled	98.2	19	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
83	c3zm7E_	Alignment	not modelled	98.2	17	PDB header: isomerase Chain: E: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
84	c1ea6A_	Alignment	not modelled	98.2	15	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
85	c5x9yC_	Alignment	not modelled	98.2	25	PDB header: dna binding protein Chain: C: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the atpase domain from bacterial mismatch repair2 endonuclease aquifex aeolicus mutl.
86	c1qzrA_	Alignment	not modelled	98.1	18	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)
87	d1uy1a_	Alignment	not modelled	98.1	19	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
88	c3ke6A_	Alignment	not modelled	98.1	27	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
89	c1y4sA_	Alignment	not modelled	98.0	16	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
90	c3omuB_	Alignment	not modelled	98.0	23	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein 83; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from2 trypanosoma brucei, tb10.26.1080 in the presence of a3 thienopyrimidine derivative
91	c2fwyA_	Alignment	not modelled	98.0	19	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
92	c4j0bB_	Alignment	not modelled	98.0	20	PDB header: chaperone Chain: B: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: structure of mitochondrial hsp90 (trap1) with adp-bef3
93	c4ipeA_	Alignment	not modelled	98.0	24	PDB header: chaperone Chain: A: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: crystal structure of mitochondrial hsp90 (trap1) with amppnp
94	c3g7bB_	Alignment	not modelled	98.0	23	PDB header: isomerase/isomerase inhibitor Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with methyl ({5-[4-(4-2 hydroxypiperidin-1-yl)-2-phenyl-1,3-thiazol-5-yl]-1h-pyrazol-3-3-yl}methyl)carbamate inhibitor
95	c2cg9A_	Alignment	not modelled	97.9	24	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
96	d2asxa1	Alignment	not modelled	97.9	23	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
97	c2iopD_	Alignment	not modelled	97.9	15	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
98	c4qfha_	Alignment	not modelled	97.8	18	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-amppnp complex

99	c5fwkA	Alignment	not modelled	97.8	28	PDB header: signaling protein Chain: A: PDB Molecule: heat shock protein hsp 90 beta; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
100	d1s14a	Alignment	not modelled	97.8	21	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
101	d2iwx1	Alignment	not modelled	97.8	19	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
102	c5ulsA	Alignment	not modelled	97.8	22	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of grp94 in the active conformation
103	c1zwhA	Alignment	not modelled	97.8	19	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
104	d1uyma	Alignment	not modelled	97.7	22	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
105	c3pehB	Alignment	not modelled	97.7	22	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
106	c2akpA	Alignment	not modelled	97.7	25	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
107	c2iorA	Alignment	not modelled	97.7	13	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp
108	c5thA	Alignment	not modelled	97.7	24	PDB header: chaperone Chain: A: PDB Molecule: c-terminal spycatcher fusion of wildtype zebrafish trf PDBTitle: heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
109	c3lnuA	Alignment	not modelled	97.7	22	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
110	c3zx6A	Alignment	not modelled	97.6	18	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
111	d1qy5a	Alignment	not modelled	97.4	23	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
112	c2o1wB	Alignment	not modelled	97.3	23	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
113	d2gqpa1	Alignment	not modelled	97.2	29	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
114	c2o1uA	Alignment	not modelled	97.2	32	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
115	c6gauB	Alignment	not modelled	97.0	27	PDB header: dna binding protein Chain: B: PDB Molecule: dna gyrase subunit b,dna gyrase subunit a; PDBTitle: extremely 'open' clamp structure of dna gyrase: role of the2 corynebacteriales gyrb specific insert
116	d1joya	Alignment	not modelled	94.9	19	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
117	c4mt8A	Alignment	not modelled	94.5	23	PDB header: transferase Chain: A: PDB Molecule: ethylene response sensor 1; PDBTitle: structure of the ers1 dimerization and histidine phosphotransfer2 domain from arabidopsis thaliana
118	c3cwwB	Alignment	not modelled	94.5	19	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
119	c5ukvA	Alignment	not modelled	93.0	59	PDB header: transferase Chain: A: PDB Molecule: atp-binding protein; PDBTitle: dhp domain of phor of m. tuberculosis - semet
120	d2c2aa1	Alignment	not modelled	92.7	33	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase