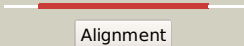
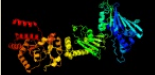
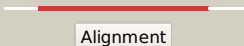

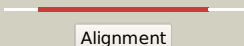







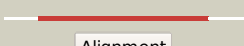




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2299c_(htpG)_2570069_2572012
Date	Mon Aug 5 13:25:44 BST 2019
Unique Job ID	ab77bad1db90337d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fwkA_	 Alignment		100.0	41	PDB header: signaling protein Chain: A: PDB Molecule: heat shock protein hsp 90 beta; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
2	c5ulsA_	 Alignment		100.0	42	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of grp94 in the active conformation
3	c2cg9A_	 Alignment		100.0	41	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
4	c5tthA_	 Alignment		100.0	35	PDB header: chaperone Chain: A: PDB Molecule: c-terminal spycatcher fusion of wildtype zebrafish tnf PDBTitle: heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
5	c2iopD_	 Alignment		100.0	47	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
6	c4ipeA_	 Alignment		100.0	35	PDB header: chaperone Chain: A: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: crystal structure of mitochondrial hsp90 (trap1) with amppnp
7	c4j0bB_	 Alignment		100.0	34	PDB header: chaperone Chain: B: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: structure of mitochondrial hsp90 (trap1) with adp-bef3
8	c2o1uA_	 Alignment		100.0	41	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
9	c2o1wB_	 Alignment		100.0	45	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
10	c1y4sA_	 Alignment		100.0	50	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
11	c2cgeD_	 Alignment		100.0	38	PDB header: chaperone Chain: D: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex

12	c2o1tB	Alignment		100.0	41	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of middle plus c-terminal domains (m+c) of grp94
13	c3hjcA	Alignment		100.0	39	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 83-1; PDBTitle: crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
14	c3q6nF	Alignment		100.0	39	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein hsp 90-alpha; PDBTitle: crystal structure of human mc-hsp90 in p21 space group
15	c2gq0B	Alignment		100.0	48	PDB header: chaperone, hydrolase Chain: B: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of the middle domain of htpg, the e. coli hsp90
16	c3pryA	Alignment		100.0	43	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp 90-beta; PDBTitle: crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution
17	d1usua	Alignment		100.0	42	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Hsp90 middle domain
18	c1hk7A	Alignment		100.0	42	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp82; PDBTitle: middle domain of hsp90
19	c1y6zA	Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: heat shock protein, putative; PDBTitle: middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
20	c3pehB	Alignment		100.0	35	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
21	d1qy5a	Alignment	not modelled	100.0	44	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
22	d2iwxal	Alignment	not modelled	100.0	44	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
23	c1zwhA	Alignment	not modelled	100.0	44	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
24	c2iorA	Alignment	not modelled	100.0	52	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
25	d1uyma	Alignment	not modelled	100.0	45	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
26	c2fwyA	Alignment	not modelled	100.0	46	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
27	d1uyla	Alignment	not modelled	100.0	46	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
28	c3iedA	Alignment	not modelled	100.0	46	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
29	d2gqa1	Alignment	not modelled	100.0	46	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
30	c3omuB	Alignment	not modelled	100.0	45	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein 83; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from <i>Trypanosoma brucei</i> , tb10.26.1080 in the presence of a 3-thienopyrimidine derivative
31	c2akpA	Alignment	not modelled	100.0	44	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
32	c5ix1A	Alignment	not modelled	100.0	17	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
33	d1sf8a	Alignment	not modelled	100.0	42	Fold: HSP90 C-terminal domain Superfamily: HSP90 C-terminal domain Family: HSP90 C-terminal domain
34	c2q2eB	Alignment	not modelled	99.9	24	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from <i>Methanosarcina mazei</i>
35	c5ofbB	Alignment	not modelled	99.8	21	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 muscular atrophy mutation s871
36	d1b63a2	Alignment	not modelled	99.8	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
37	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
38	c3na3A	Alignment	not modelled	99.7	18	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
39	c2zkbB	Alignment	not modelled	99.7	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
40	c1bknA	Alignment	not modelled	99.7	19	PDB header: dna repair Chain: A: PDB Molecule: mutl; PDBTitle: crystal structure of an n-terminal 40kd fragment of e. coli 2 dna mismatch repair protein mutl
41	c3h4lB	Alignment	not modelled	99.7	16	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
42	d1bkn2	Alignment	not modelled	99.7	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
43	d2hkja3	Alignment	not modelled	99.6	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
44	d1h7sa2	Alignment	not modelled	99.6	25	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
45	d1kja2	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
46	d1pvga2	Alignment	not modelled	99.5	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	c5j5pB	Alignment	not modelled	99.5	16	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase 4 subunit b; PDBTitle: amp-pnp-stabilized atpase domain of topoisomerase iv from <i>Streptococcus pneumoniae</i> , complex type i
48	c1ea6A	Alignment	not modelled	99.5	29	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
49	c1ei1B	Alignment	not modelled	99.4	15	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
50	d1s16a2	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: DNA gyrase/MutL, N-terminal domain
51	c1kiiB	Alignment	not modelled	99.4	16	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b;

51	c1kjb_	Alignment	not modelled	99.4	10	PDBTitle: crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
52	d1e1a2	Alignment	not modelled	99.3	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
53	c4hymA_	Alignment	not modelled	99.2	13	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.
54	c4geeA_	Alignment	not modelled	99.2	17	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.
55	c1s16B_	Alignment	not modelled	99.2	18	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
56	c5x9yC_	Alignment	not modelled	99.2	27	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.
57	c4emvA_	Alignment	not modelled	99.2	20	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna topoisomerase iv, b subunit; PDBTitle: crystal structure of a topoisomerase atp inhibitor
58	c5v44A_	Alignment	not modelled	99.1	21	PDB header: chaperone Chain: A: PDB Molecule: saccin; PDBTitle: crystal structure of the sr1 domain of human saccin
59	c3zm7E_	Alignment	not modelled	99.1	8	PDB header: isomerase Chain: E: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
60	c4b6cB_	Alignment	not modelled	99.1	14	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
61	d1s14a_	Alignment	not modelled	98.7	20	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
62	c3g7bB_	Alignment	not modelled	98.6	12	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
63	c1qzrA_	Alignment	not modelled	98.5	20	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)
64	c1y8oA_	Alignment	not modelled	98.5	24	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
65	c2q8fA_	Alignment	not modelled	98.5	19	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
66	c1zxnB_	Alignment	not modelled	98.5	15	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
67	c3d2rB_	Alignment	not modelled	98.4	22	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
68	c3crlB_	Alignment	not modelled	98.4	23	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhK2-l2 complex.
69	c4gfhA_	Alignment	not modelled	98.3	19	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-amppnp complex
70	c1gfvA_	Alignment	not modelled	98.3	37	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
71	c3d36B_	Alignment	not modelled	98.2	26	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
72	c2bu8A_	Alignment	not modelled	98.2	22	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
73	c4ew8A_	Alignment	not modelled	98.2	26	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.)
						PDB header: transferase/signaling protein Chain: B: PDB Molecule: osmolarity sensor protein envz, histidine

74	c4kp4B_	Alignment	not modelled	98.1	23	kinase; PDBTitle: deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.
75	d1gkza2	Alignment	not modelled	98.1	28	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
76	d1jm6a2	Alignment	not modelled	98.1	20	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
77	c3lnuA_	Alignment	not modelled	98.0	18	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
78	c3tz5A_	Alignment	not modelled	97.9	24	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipamide]] kinase, PDBTitle: crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
79	c4u7nA_	Alignment	not modelled	97.9	21	PDB header: transferase Chain: A: PDB Molecule: histidine protein kinase sensor protein; PDBTitle: inactive structure of histidine kinase
80	c5idjA_	Alignment	not modelled	97.9	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+
81	c2c2aA_	Alignment	not modelled	97.8	19	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
82	c1b3qA_	Alignment	not modelled	97.6	21	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
83	c2ch4A_	Alignment	not modelled	97.6	30	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
84	c5idmA_	Alignment	not modelled	97.5	26	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+
85	d1y8oa2	Alignment	not modelled	97.4	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
86	d2c2aa2	Alignment	not modelled	97.4	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
87	c3a0tA_	Alignment	not modelled	97.4	17	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)
88	c6gauB_	Alignment	not modelled	97.3	13	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
89	c4i5sA_	Alignment	not modelled	97.3	16	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
90	c4biuB_	Alignment	not modelled	97.2	22	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
91	c4gczB_	Alignment	not modelled	97.2	21	PDB header: signaling protein, de novo protein Chain: B: PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor
92	c6blkB_	Alignment	not modelled	97.1	24	PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine-protein kinase/phosphatase PDBTitle: mycobacterial sensor histidine kinase mprb
93	d1th8a_	Alignment	not modelled	97.1	22	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
94	c4i3hA_	Alignment	not modelled	97.0	21	PDB header: isomerase/dna Chain: A: PDB Molecule: topoisomerase iv subunit b, dna topoisomerase 4 subunit a PDBTitle: a three-gate structure of topoisomerase iv from streptococcus2 pneumoniae
95	c4gt8A_	Alignment	not modelled	97.0	21	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
96	c6dk8B_	Alignment	not modelled	96.9	19	PDB header: signaling protein Chain: B: PDB Molecule: rets (regulator of exopolysaccharide and type iii PDBTitle: rets kinase region without cobalt
97	d1i58a_	Alignment	not modelled	96.9	23	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

98	d1ysra1	Alignment	not modelled	96.8	24	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
99	c4r39A	Alignment	not modelled	96.7	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
100	c3sl2A	Alignment	not modelled	96.7	23	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
101	d1id0a	Alignment	not modelled	96.7	16	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
102	c3cwwB	Alignment	not modelled	96.3	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
103	c4biyD	Alignment	not modelled	95.9	25	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
104	c3gieA	Alignment	not modelled	95.8	28	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of desk_c_h188e in complex with amp-pcp
105	d1bxda	Alignment	not modelled	95.7	24	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
106	c3a0rA	Alignment	not modelled	95.4	20	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)
107	c6e95A	Alignment	not modelled	95.3	23	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)
108	c4gpkA	Alignment	not modelled	95.3	19	PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
109	c4ctiA	Alignment	not modelled	95.1	22	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
110	c4pl9A	Alignment	not modelled	95.1	16	PDB header: transferase Chain: A: PDB Molecule: ethylene receptor 1; PDBTitle: structure of the catalytic domain of etr1 from arabidopsis thaliana
111	c3jz3B	Alignment	not modelled	94.8	18	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
112	d1ixma	Alignment	not modelled	94.4	17	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
113	c3ehgA	Alignment	not modelled	94.2	24	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
114	c4r3aA	Alignment	not modelled	92.9	16	PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis el346 blue-light activated histidine kinase
115	c4fmtB	Alignment	not modelled	91.5	14	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
116	c3zxqA	Alignment	not modelled	90.4	23	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
117	c4bxiA	Alignment	not modelled	90.1	24	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
118	c3zxoB	Alignment	not modelled	79.2	23	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
119	c5epvB	Alignment	not modelled	77.1	16	PDB header: transferase Chain: B: PDB Molecule: blue-light-activated histidine kinase; PDBTitle: histidine kinase domain from the low-hk blue-light receptor from2 brucella abortus
120	c3j9aA	Alignment	not modelled	67.2	25	PDB header: viral protein Chain: A: PDB Molecule: capsid protein vp26 homolog; PDBTitle: backbone model of the smallest capsid protein (scp) of kaposi's2 sarcoma-associated herpesvirus (kshv)