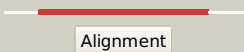

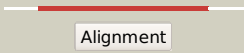



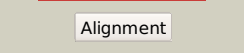



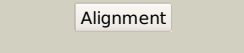

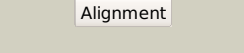

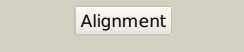

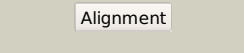



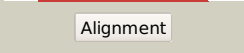












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0600c_(-)_697907_698413
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	12f28d9d070cccad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d2rB_	 Alignment		100.0	18	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
2	c3cr1B_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex.
3	d1bxda_	 Alignment		100.0	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
4	c4kp4B_	 Alignment		100.0	31	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.
5	c4i5sA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
6	c2bu8A_	 Alignment		100.0	21	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
7	c2q8fA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
8	c4ew8A_	 Alignment		100.0	30	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.)
9	d1ld0a_	 Alignment		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
10	c1y8oA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
11	c5idmA_	 Alignment		100.0	30	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+

12	c6blkB	Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine-protein kinase/phosphatase PDBTitle: mycobacterial sensor histidine kinase mprb
13	c1qjvA	Alignment		100.0	19	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
14	c3d36B	Alignment		100.0	24	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
15	c3tz5A	Alignment		100.0	20	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
16	c2c2aA	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
17	d2c2aa2	Alignment		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
18	c5idjA	Alignment		100.0	30	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+
19	c3a0tA	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: catalytic domain of histidine kinase thka (tm1359) in complex with2 adp2 and mg ion (trigonal)
20	d1jm6a2	Alignment		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
21	c3sl2A	Alignment	not modelled	100.0	28	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
22	c4u7nA	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: histidine protein kinase sensor protein; PDBTitle: inactive structure of histidine kinase
23	c4gczB	Alignment	not modelled	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
24	d1gkza2	Alignment	not modelled	100.0	19	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
25	d1ysrA1	Alignment	not modelled	100.0	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
26	c4biuB	Alignment	not modelled	100.0	28	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
27	c3a0rA	Alignment	not modelled	100.0	21	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)
28	c6dk8B	Alignment	not modelled	100.0	24	PDB header: signaling protein Chain: B: PDB Molecule: rets (regulator of exopolysaccharide and type iii

					PDBTitle: rets kinase region without cobalt
29	c4pl9A_	Alignment	not modelled	100.0	28 PDB header: transferase Chain: A: PDB Molecule: ethylene receptor 1; PDBTitle: structure of the catalytic domain of etr1 from arabidopsis thaliana
30	c4biyD_	Alignment	not modelled	100.0	29 PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
31	d1i58a_	Alignment	not modelled	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: Histidine kinase
32	c2ch4A_	Alignment	not modelled	99.9	24 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
33	c1b3qA_	Alignment	not modelled	99.9	22 PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
34	d1r62a_	Alignment	not modelled	99.9	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
35	c3jz3B_	Alignment	not modelled	99.9	31 PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
36	c4gt8A_	Alignment	not modelled	99.9	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
37	c4r3aA_	Alignment	not modelled	99.9	17 PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis el346 blue-light activated histidine kinase
38	c4r39A_	Alignment	not modelled	99.9	21 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
39	c6nb0A_	Alignment	not modelled	99.9	18 PDB header: transferase Chain: A: PDB Molecule: histidine kinase; PDBTitle: crystal structure of histidine kinase from burkholderia phymatum2 stm815
40	c3ehgA_	Alignment	not modelled	99.8	17 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
41	c3zxqA_	Alignment	not modelled	99.8	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
42	c4fmtB_	Alignment	not modelled	99.8	19 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
43	c6e95A_	Alignment	not modelled	99.8	20 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)
44	c4ctiA_	Alignment	not modelled	99.8	33 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
45	c3zxoB_	Alignment	not modelled	99.8	25 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
46	c4bxiA_	Alignment	not modelled	99.8	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
47	c5epvB_	Alignment	not modelled	99.8	15 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
48	d2hkja3	Alignment	not modelled	99.8	16 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
49	c3gieA_	Alignment	not modelled	99.7	21 PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of deskc_h188e in complex with amp-ppc
50	c4qpkA_	Alignment	not modelled	99.7	12 PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
51	c1mx0D_	Alignment	not modelled	99.6	18 PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
52	c2zkbB_	Alignment	not modelled	99.6	17 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

53	c2q2eB	Alignment	not modelled	99.5	20	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
54	d1h7sa2	Alignment	not modelled	99.5	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
55	d1th8a	Alignment	not modelled	99.4	23	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
56	d1bkna2	Alignment	not modelled	99.4	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
57	d1y8oa2	Alignment	not modelled	99.3	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
58	d1b63a2	Alignment	not modelled	99.2	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
59	c4geeA	Alignment	not modelled	98.8	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.
60	d1ixma	Alignment	not modelled	98.8	10	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
61	c3na3A	Alignment	not modelled	98.7	21	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
62	c4b6cB	Alignment	not modelled	98.4	24	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
63	c3h4lB	Alignment	not modelled	98.4	14	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
64	c4emvA	Alignment	not modelled	98.2	21	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna topoisomerase iv, b subunit; PDBTitle: crystal structure of a topoisomerase atp inhibitor
65	c5ix1A	Alignment	not modelled	98.0	14	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 with2 amppnp and h3k4me3 peptide
66	c3ke6A	Alignment	not modelled	97.9	36	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
67	c5ofbB	Alignment	not modelled	97.8	19	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
68	c5j5pB	Alignment	not modelled	97.8	26	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase 4 subunit b; PDBTitle: amp-pnp-stabilized atpase domain of topoisomerase iv from2 streptococcus pneumoniae, complex type i
69	d1kija2	Alignment	not modelled	97.8	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
70	c1bkna	Alignment	not modelled	97.8	21	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
71	c5x9yC	Alignment	not modelled	97.7	15	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.
72	d1pvga2	Alignment	not modelled	97.7	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
73	c1ea6A	Alignment	not modelled	97.6	18	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
74	c3iedA	Alignment	not modelled	97.6	11	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
75	d1ei1a2	Alignment	not modelled	97.6	29	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 PDB header: isomerase

76	c3zm7E_	Alignment	not modelled	97.6	21	Chain: E; PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
77	d1uyla_	Alignment	not modelled	97.6	10	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
78	d1s16a2	Alignment	not modelled	97.6	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
79	c3omuB_	Alignment	not modelled	97.5	13	PDB header: chaperone Chain: B; PDB Molecule: heat shock protein 83; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from 2 trypanosoma Brucei, tb10.26.1080 in the presence of a3 thienopyrimidine derivative
80	c1y4sA_	Alignment	not modelled	97.5	22	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon 2 adp binding
81	c2fwyA_	Alignment	not modelled	97.5	10	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
82	c4ipeA_	Alignment	not modelled	97.5	16	PDB header: chaperone Chain: A; PDB Molecule: tnf receptor-associated protein 1; PDBTitle: crystal structure of mitochondrial hsp90 (trap1) with amppnp
83	c1ei1B_	Alignment	not modelled	97.5	28	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
84	c2akpA_	Alignment	not modelled	97.5	11	PDB header: chaperone Chain: A; PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
85	c1kijB_	Alignment	not modelled	97.4	22	PDB header: isomerase Chain: B; PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the 43k atpase domain of thermophilus2 gyrase b in complex with novobiocin
86	c4hymA_	Alignment	not modelled	97.4	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.
87	d2iwxa1	Alignment	not modelled	97.4	15	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	c1zwhA_	Alignment	not modelled	97.4	15	PDB header: chaperone Chain: A; PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
89	d1uyma_	Alignment	not modelled	97.4	12	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
90	c1s16B_	Alignment	not modelled	97.2	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
91	c3pehB_	Alignment	not modelled	97.1	18	PDB header: chaperone Chain: B; PDB Molecule: endoplasmic homolog; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pf1070c in the presence of a thienopyrimidine derivative
92	c5fwkA_	Alignment	not modelled	97.1	22	PDB header: signaling protein Chain: A; PDB Molecule: heat shock protein hsp 90 beta; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
93	c2iorA_	Alignment	not modelled	97.1	17	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
94	c5ulsA_	Alignment	not modelled	97.1	22	PDB header: chaperone Chain: A; PDB Molecule: endoplasmic; PDBTitle: structure of grp94 in the active conformation
95	c5tthA_	Alignment	not modelled	97.1	15	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
96	c1zxnB_	Alignment	not modelled	97.0	15	PDB header: isomerase Chain: B; PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
97	c3g7bB_	Alignment	not modelled	96.9	16	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
98	c1qzrA_	Alignment	not modelled	96.8	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)
						PDB header: chaperone

99	c4j0bB_	Alignment	not modelled	96.8	12	Chain: B: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: structure of mitochondrial hsp90 (trap1) with adp-bef3
100	d1qy5a_	Alignment	not modelled	96.7	17	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
101	d2gqpa1	Alignment	not modelled	96.7	17	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	c2cg9A_	Alignment	not modelled	96.6	12	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
103	c2iopD_	Alignment	not modelled	96.6	17	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
104	d1s14a_	Alignment	not modelled	96.5	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
105	c4gfhA_	Alignment	not modelled	96.4	17	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-ampnpn complex
106	c3lnuA_	Alignment	not modelled	96.1	24	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
107	c2o1wB_	Alignment	not modelled	95.6	24	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
108	c2o1uA_	Alignment	not modelled	94.0	24	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
109	c6gauB_	Alignment	not modelled	88.0	22	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
110	c3cwwB_	Alignment	not modelled	80.9	14	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
111	d1wmaa1	Alignment	not modelled	59.2	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c4i3hA_	Alignment	not modelled	56.2	25	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
113	c4ldnA_	Alignment	not modelled	35.7	18	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of a putative purine nucleoside phosphorylase from2 vibrio fischeri es114 (target nysgrc-029521)
114	c4ggoA_	Alignment	not modelled	35.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
115	c4fd3D_	Alignment	not modelled	23.6	25	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of apo-formed ymtoar1
116	c3tfoD_	Alignment	not modelled	23.5	21	PDB header: oxidoreductase Chain: D: PDB Molecule: putative 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
117	d2o23a1	Alignment	not modelled	21.9	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	c3nywD_	Alignment	not modelled	21.6	30	PDB header: oxidoreductase Chain: D: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a betaketoacyl-[acp] reductase (fabg) from2 bacteroides thetaiotaomicron
119	d1spxa_	Alignment	not modelled	21.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	d1odka_	Alignment	not modelled	20.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases