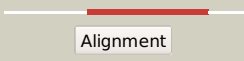
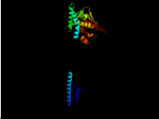
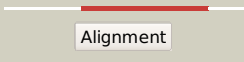

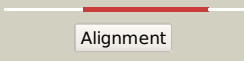

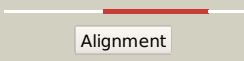

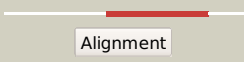

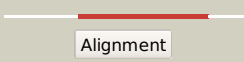

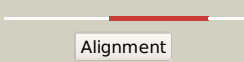

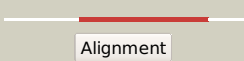

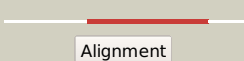

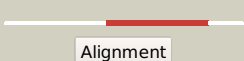

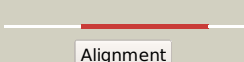












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0982_(mprB)_1097512_1099026
Date	Wed Jul 31 22:05:05 BST 2019
Unique Job ID	4ff41c10bdf95a91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4i5sA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative histidine kinase covs; vick-like protein; <b>PDBTitle:</b> structure and function of sensor histidine kinase
2	<a href="#">c3d2rB_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; <b>PDBTitle:</b> crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
3	<a href="#">c2q8fA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; <b>PDBTitle:</b> structure of pyruvate dehydrogenase kinase isoform 1
4	<a href="#">c4ew8A_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein divl; <b>PDBTitle:</b> 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.)
5	<a href="#">c3d36B_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> sporulation kinase b; <b>PDBTitle:</b> how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
6	<a href="#">c3criB_</a>	 Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase [lipoamide] kinase isozyme 2, <b>PDBTitle:</b> crystal structure of the pdhk2-l2 complex.
7	<a href="#">c4kp4B_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> osmolarity sensor protein envz, histidine kinase; <b>PDBTitle:</b> deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.
8	<a href="#">c2bu8A_</a>	 Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase kinase isoenzyme 2; <b>PDBTitle:</b> crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
9	<a href="#">c4biuB_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein cpax; <b>PDBTitle:</b> crystal structure of cpaxhdc (orthorhombic form 1)
10	<a href="#">c5idjA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle histidine kinase ccka; <b>PDBTitle:</b> bifunctional histidine kinase ccka (domains dhp-ca) in complex with2 adp/mg2+
11	<a href="#">c1y8oA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; <b>PDBTitle:</b> crystal structure of the pdk3-l2 complex

12	<a href="#">c2c2aA_</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
13	<a href="#">c1qjvA_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; <b>PDBTitle:</b> branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s
14	<a href="#">c6dk8B_</a>	Alignment		100.0	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> rets (regulator of exopolysaccharide and type iii <b>PDBTitle:</b> rets kinase region without cobalt
15	<a href="#">c3tz5A_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, <b>PDBTitle:</b> crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
16	<a href="#">c4u7nA_</a>	Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine protein kinase sensor protein; <b>PDBTitle:</b> inactive structure of histidine kinase
17	<a href="#">c4gczB_</a>	Alignment		100.0	18	<b>PDB header:</b> signaling protein, de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> blue-light photoreceptor, sensor protein fixl; <b>PDBTitle:</b> structure of a blue-light photoreceptor
18	<a href="#">c6blkB_</a>	Alignment		100.0	72	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> signal transduction histidine-protein kinase/phosphatase <b>PDBTitle:</b> mycobacterial sensor histidine kinase mprb
19	<a href="#">c4biyD_</a>	Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (monoclinic form 2)
20	<a href="#">c3a0rA_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
21	<a href="#">c5idmA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle histidine kinase ccka; <b>PDBTitle:</b> bifunctional histidine kinase ccka (domain, ca) in complex with c-di-2 gmp and amppnp/mg2+
22	<a href="#">d1jm6a2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
23	<a href="#">c3a0tA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> catalytic domain of histidine kinase thka (tm1359) in complex with adp2 and mg ion (trigonal)
24	<a href="#">d1bxda_</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
25	<a href="#">c1b3qA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (chemotaxis protein chea); <b>PDBTitle:</b> crystal structure of chea-289, a signal transducing histidine kinase
26	<a href="#">c3sl2A_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase yycg; <b>PDBTitle:</b> atp forms a stable complex with the essential histidine kinase walk2 (yycg) domain
27	<a href="#">d2c2aa2</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase <b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase

28	<a href="#">d1gkza2</a>	Alignment	not modelled	99.9	21	II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
29	<a href="#">d1id0a_</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
30	<a href="#">c4ctiA_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> osmolarity sensor protein envz, af1503; <b>PDBTitle:</b> escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
31	<a href="#">c2ch4A_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> transferase/chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chea; <b>PDBTitle:</b> complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
32	<a href="#">d1i58a_</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
33	<a href="#">c4fmtB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> chpt protein; <b>PDBTitle:</b> crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
34	<a href="#">c4pl9A_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ethylene receptor 1; <b>PDBTitle:</b> structure of the catalytic domain of etr1 from arabidopsis thaliana
35	<a href="#">d1ysra1</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
36	<a href="#">c6nb0A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase; <b>PDBTitle:</b> crystal structure of histidine kinase from burkholderia phymatum2 stm815
37	<a href="#">c4r39A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> blue-light-activated histidine kinase 2; <b>PDBTitle:</b> histidine kinase domain from erythrobacter litoralis el346 blue-light2 activated histidine kinase
38	<a href="#">c3jz3B_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein qsec; <b>PDBTitle:</b> structure of the cytoplasmic segment of histidine kinase qsec
39	<a href="#">c4qpkA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotransferase; <b>PDBTitle:</b> 1.7 angstrom structure of a bacterial phosphotransferase
40	<a href="#">c4r3aA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> blue-light-activated histidine kinase 2; <b>PDBTitle:</b> erythrobacter litoralis el346 blue-light activated histidine kinase
41	<a href="#">d2hkja3</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
42	<a href="#">c6e95A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus agrc histidine kinase module fused to <b>PDBTitle:</b> chimeric structure of saccharomyces cerevisiae gcn4 leucine zipper2 fused to staphylococcus aureus agrc cytoplasmic histidine kinase3 module (dataset isotropically truncated by hkl2000)
43	<a href="#">d1r62a_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
44	<a href="#">c4gt8A_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein vras; <b>PDBTitle:</b> crystal structure of the catalytic and atp-binding domain from vras in2 complex with adp
45	<a href="#">c5epvB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> blue-light-activated histidine kinase; <b>PDBTitle:</b> histidine kinase domain from the lov-hk blue-light receptor from2 brucella abortus
46	<a href="#">c3gieA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase desk; <b>PDBTitle:</b> crystal structure of desk_h188e in complex with amp-pcp
47	<a href="#">c2zkbB_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
48	<a href="#">c1mx0D_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> type ii dna topoisomerase vi subunit b; <b>PDBTitle:</b> structure of topoisomerase subunit
49	<a href="#">c2q2eB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
50	<a href="#">c3ehgA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase (yocf protein); <b>PDBTitle:</b> crystal structure of the atp-binding domain of desk in complex with2 atp
51	<a href="#">c4bxiA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> accessory gene regulator protein c; <b>PDBTitle:</b> crystal structure of atp binding domain of agrc from2 staphylococcus aureus
						<b>PDB header:</b> transferase

52	<a href="#">c3zxqA_</a>	Alignment	not modelled	99.6	18	<b>Chain:</b> A: <b>PDB Molecule:</b> hypoxia sensor histidine kinase response regulator dost; <b>PDBTitle:</b> crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
53	<a href="#">d1h7sa2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
54	<a href="#">c3zxoB_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> redox sensor histidine kinase response regulator devs; <b>PDBTitle:</b> crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
55	<a href="#">d1bkna2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
56	<a href="#">d1b63a2</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
57	<a href="#">d1ixma_</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> Sporulation response regulatory protein Spo0B <b>Superfamily:</b> Sporulation response regulatory protein Spo0B <b>Family:</b> Sporulation response regulatory protein Spo0B
58	<a href="#">d1th8a_</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
59	<a href="#">d1y8oa2</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
60	<a href="#">c3na3A_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein mlh1; <b>PDBTitle:</b> mutl protein homolog 1 isoform 1 from homo sapiens
61	<a href="#">c5jefA_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite sensor protein narq; <b>PDBTitle:</b> fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
62	<a href="#">c4geeA_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> 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	<a href="#">c3h4lB_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> dna binding protein, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein pms1; <b>PDBTitle:</b> crystal structure of n terminal domain of a dna repair protein
64	<a href="#">c4b6cB_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b,dna gyrase subunit b,dna gyrase <b>PDBTitle:</b> structure of the m. smegmatis gyrb atpase domain in complex with an2 aminopyrazinamide
65	<a href="#">c4gn0D_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
66	<a href="#">c3zrwB_</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> af1503 protein, osmolarity sensor protein envz; <b>PDBTitle:</b> the structure of the dimeric hamp-dhp fusion a291v mutant
67	<a href="#">c4emvA_</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase iv, b subunit; <b>PDBTitle:</b> crystal structure of a topoisomerase atp inhibitor
68	<a href="#">c5j5pB_</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> isomerase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase 4 subunit b; <b>PDBTitle:</b> amp-pnp-stabilized atpase domain of topoisomerase iv from2 streptococcus pneumoniae, complex type i
69	<a href="#">c1bknA_</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> mutl; <b>PDBTitle:</b> crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
70	<a href="#">c3omuB_</a>	Alignment	not modelled	98.4	25	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock protein 83; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an hsp90 from2 trypanosoma brucei, tb10.26.1080 in the presence of a3 thienopyrimidine derivative
71	<a href="#">d1kija2</a>	Alignment	not modelled	98.4	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
72	<a href="#">c5ix1A_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> morc family cw-type zinc finger protein 3; <b>PDBTitle:</b> crystal structure of mouse morc3 atpase-cw cassette in complex with2 amppnp and h3k4me3 peptide
73	<a href="#">c2cg9A_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent molecular chaperone hsp82; <b>PDBTitle:</b> crystal structure of an hsp90-sba1 closed chaperone complex
74	<a href="#">d1pvga2</a>	Alignment	not modelled	98.3	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA

						topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
75	<a href="#">c5ofbB</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> smorc family cw-type zinc finger protein 2; <b>PDBTitle:</b> crystal structure of human morc2 (residues 1-603) with spinal muscular2 atrophy mutation s871
76	<a href="#">d1s16a2</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
77	<a href="#">c1y4sA</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein htpg; <b>PDBTitle:</b> conformation rearrangement of heat shock protein 90 upon2 adp binding
78	<a href="#">c1ea6A</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> pms1 protein homolog 2; <b>PDBTitle:</b> n-terminal 40kda fragment of nhpms2 complexed with adp
79	<a href="#">d1uy1a</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
80	<a href="#">d1ei1a2</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
81	<a href="#">c3iedA</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn
82	<a href="#">c5x9yC</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein mutl; <b>PDBTitle:</b> crystal structure of the atpase domain from bacterial mismatch repair2 endonuclease aquifex aeolicus mutl.
83	<a href="#">c3lnrA</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
84	<a href="#">c4ipeA</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated protein 1; <b>PDBTitle:</b> crystal structure of mitochondrial hsp90 (trap1) with amppnp
85	<a href="#">c1kijB</a>	Alignment	not modelled	98.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
86	<a href="#">c5fwkA</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp 90 beta; <b>PDBTitle:</b> atomic cryoem structure of hsp90-cdc37-cdk4 complex
87	<a href="#">c2fwyA</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp 90-alpha; <b>PDBTitle:</b> structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
88	<a href="#">c1zxnB</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase ii, alpha isozyme; <b>PDBTitle:</b> human dna topoisomerase iia atpase/adp
89	<a href="#">c1ei1B</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase b; <b>PDBTitle:</b> dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center
90	<a href="#">c5ulsA</a>	Alignment	not modelled	98.1	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic; <b>PDBTitle:</b> structure of grp94 in the active conformation
91	<a href="#">c2akpA</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent molecular chaperone hsp82; <b>PDBTitle:</b> hsp90 delta24-n210 mutant
92	<a href="#">c4hymA</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv, subunit b; <b>PDBTitle:</b> 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.
93	<a href="#">c4j0bB</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> tnf receptor-associated protein 1; <b>PDBTitle:</b> structure of mitochondrial hsp90 (trap1) with adp-bef3
94	<a href="#">d2iwxa1</a>	Alignment	not modelled	98.0	23	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
95	<a href="#">c5tthA</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal spycatcher fusion of wildtype zebrafish tnfr <b>PDBTitle:</b> heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
96	<a href="#">c2iopD</a>	Alignment	not modelled	98.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> chaperone protein htpg; <b>PDBTitle:</b> crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
97	<a href="#">c3pehB</a>	Alignment	not modelled	98.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> endoplasmic homolog; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pf1070c in the presence of a thienopyrimidine derivative
98	<a href="#">c1s16B</a>	Alignment	not modelled	98.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> topoisomerase iv subunit b;

98	<a href="#">c1310b_</a>	Alignment	not modelled	98.0	23	<b>PDBTitle:</b> crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp <b>PDB header:</b> chaperone
99	<a href="#">c2lorA_</a>	Alignment	not modelled	98.0	27	<b>Chain:</b> A; <b>PDB Molecule:</b> chaperone protein htpg; <b>PDBTitle:</b> crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp
100	<a href="#">d1uyma_</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
101	<a href="#">c3ke6A_</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> protein rv1364c/mt1410; <b>PDBTitle:</b> the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
102	<a href="#">c1zwhA_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent molecular chaperone hsp82; <b>PDBTitle:</b> yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
103	<a href="#">c4gfhA_</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> dna topoisomerase 2; <b>PDBTitle:</b> topoisomerase ii-dna-amppnp complex
104	<a href="#">c3zm7E_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> isomerase <b>Chain:</b> E; <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
105	<a href="#">c1qzrA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> dna topoisomerase ii; <b>PDBTitle:</b> crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
106	<a href="#">c2o1wB_</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> endoplasmic; <b>PDBTitle:</b> structure of n-terminal plus middle domains (n+m) of grp94
107	<a href="#">c2o1uA_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> endoplasmic; <b>PDBTitle:</b> structure of full length grp94 with amp-pnp bound
108	<a href="#">c3g7bB_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> B; <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> 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
109	<a href="#">d2gqpa1</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
110	<a href="#">d1s14a_</a>	Alignment	not modelled	97.3	24	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
111	<a href="#">d2asxa1</a>	Alignment	not modelled	97.3	21	<b>Fold:</b> HAMP domain-like <b>Superfamily:</b> HAMP domain-like <b>Family:</b> HAMP domain
112	<a href="#">c3zx6A_</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> signaling <b>Chain:</b> A; <b>PDB Molecule:</b> hamp, methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
113	<a href="#">d1qy5a_</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Heat shock protein 90, HSP90, N-terminal domain
114	<a href="#">c3lnuA_</a>	Alignment	not modelled	96.9	35	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> topoisomerase iv subunit b; <b>PDBTitle:</b> crystal structure of pare subunit
115	<a href="#">d1joya_</a>	Alignment	not modelled	96.8	28	<b>Fold:</b> ROP-like <b>Superfamily:</b> Homodimeric domain of signal transducing histidine kinase <b>Family:</b> Homodimeric domain of signal transducing histidine kinase
116	<a href="#">c6gauB_</a>	Alignment	not modelled	96.7	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> dna gyrase subunit b,dna gyrase subunit a; <b>PDBTitle:</b> extremely 'open' clamp structure of dna gyrase: role of the2 corynebacteriales gyrb specific insert
117	<a href="#">c4mt8A_</a>	Alignment	not modelled	96.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ethylene response sensor 1; <b>PDBTitle:</b> structure of the ers1 dimerization and histidine phosphotransfer2 domain from arabidopsis thaliana
118	<a href="#">c4g97A_</a>	Alignment	not modelled	95.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of the response regulator phyrr from brucella abortus
119	<a href="#">c5ukvA_</a>	Alignment	not modelled	95.7	32	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-binding protein; <b>PDBTitle:</b> dhp domain of phor of m. tuberculosis - semet
120	<a href="#">c4qicC_</a>	Alignment	not modelled	95.1	13	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> sensory transduction regulatory protein, anti-anti-sigma <b>PDBTitle:</b> co-crystal structure of anti-anti-sigma factor phyrr complexed with2 anti-sigma factor nepr from bartonella quintana