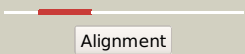

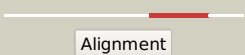

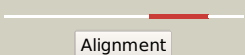

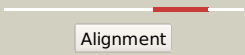

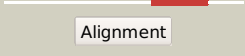



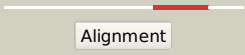

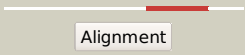

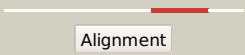

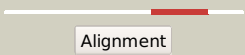
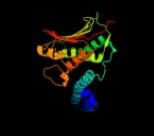
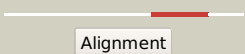



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1028c_(kdpD)_1149108_1151690
Date	Wed Jul 31 22:05:10 BST 2019
Unique Job ID	5a2457f0a364ee56

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r8rB_	 Alignment		100.0	54	PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
2	c4ew8A_	 Alignment		100.0	27	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.)
3	c2c2aA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
4	c4kp4B_	 Alignment		100.0	24	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	c3d36B_	 Alignment		100.0	22	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
6	c5idjA_	 Alignment		100.0	27	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+
7	c4u7nA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: histidine protein kinase sensor protein; PDBTitle: inactive structure of histidine kinase
8	c3d2rB_	 Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
9	c2q8fA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
10	c6dk8B_	 Alignment		100.0	23	PDB header: signaling protein Chain: B: PDB Molecule: rets (regulator of exopolysaccharide and type iii PDBTitle: rets kinase region without cobalt
11	c3cr1B_	 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.

12	c2bu8A_	Alignment		100.0	17	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
13	c1y8oA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
14	c1qjvA_	Alignment		100.0	14	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	c3tz5A_	Alignment		100.0	14	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	c4i5sA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
17	c4biyD_	Alignment		100.0	28	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
18	c4gczB_	Alignment		100.0	24	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	c4biuB_	Alignment		100.0	29	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
20	c3a0rA_	Alignment		100.0	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)
21	c5idmA_	Alignment	not modelled	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+
22	c1b3qA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
23	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
24	d1bxda_	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
25	c3a0tA_	Alignment	not modelled	99.9	21	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)
26	c6blkB_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine-protein kinase/phosphatase PDBTitle: mycobacterial sensor histidine kinase mprb
27	d2c2aa2	Alignment	not modelled	99.9	25	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	d1gkza2	Alignment	not modelled	99.9	17	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 PDB header: transferase
29	c4fmtB_	Alignment	not modelled	99.9	17	Chain: B: PDB Molecule: chpt protein; PDBTitle: crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
30	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
31	d1jm6a2	Alignment	not modelled	99.9	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase
32	d1ld0a_	Alignment	not modelled	99.9	23	Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase
33	c3sl2A_	Alignment	not modelled	99.9	28	Family: Histidine kinase 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
34	c4pl9A_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: ethylene receptor 1; PDBTitle: structure of the catalytic domain of etr1 from arabidopsis thaliana
35	d1ysra1	Alignment	not modelled	99.9	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase
36	c3jz3B_	Alignment	not modelled	99.9	30	Family: Histidine kinase PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
37	d1i58a_	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
38	c2ch4A_	Alignment	not modelled	99.9	21	Family: Histidine kinase 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
39	c4qpka_	Alignment	not modelled	99.9	14	PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
40	c5epvB_	Alignment	not modelled	99.9	14	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
41	c6e95A_	Alignment	not modelled	99.9	10	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	c3gieA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of deskc_h188e in complex with amp-pcp
43	c4r3aA_	Alignment	not modelled	99.8	19	PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis el346 blue-light activated histidine kinase
44	c4gt8A_	Alignment	not modelled	99.8	18	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
45	c4ctiA_	Alignment	not modelled	99.8	27	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
46	d1r62a_	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
47	d2hkja3	Alignment	not modelled	99.7	21	Family: Histidine kinase Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase
48	c3ehgA_	Alignment	not modelled	99.7	17	Family: DNA gyrase/MutL, N-terminal domain 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
49	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
50	c3zxoB_	Alignment	not modelled	99.6	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
51	d1ixma_	Alignment	not modelled	99.6	13	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
						PDB header: isomerase

52	c2zkbB	Alignment	not modelled	99.5	22	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	c1mx0D	Alignment	not modelled	99.5	21	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
54	c4bxiA	Alignment	not modelled	99.5	14	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
55	c2q2eB	Alignment	not modelled	99.4	19	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
56	d1th8a	Alignment	not modelled	99.4	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
57	c2ksfA	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein kdpd; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor kdpd, center for structures of membrane proteins (csm)3 target 4312c
58	d1h7sa2	Alignment	not modelled	99.3	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
59	d1y8oa2	Alignment	not modelled	99.3	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
60	d1b63a2	Alignment	not modelled	99.2	13	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
61	d2c2aa1	Alignment	not modelled	99.2	28	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
62	d1bkna2	Alignment	not modelled	99.2	13	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
63	c4mt8A	Alignment	not modelled	99.0	24	PDB header: transferase Chain: A: PDB Molecule: ethylene response sensor 1; PDBTitle: structure of the ers1 dimerization and histidine phosphotransfer2 domain from arabidopsis thaliana
64	c3dloC	Alignment	not modelled	99.0	26	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
65	c5ukvA	Alignment	not modelled	98.9	29	PDB header: transferase Chain: A: PDB Molecule: atp-binding protein; PDBTitle: dhp domain of phor of m. tuberculosis - semet
66	c3hgmD	Alignment	not modelled	98.9	20	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
67	c3loqA	Alignment	not modelled	98.9	15	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
68	d1tq8a	Alignment	not modelled	98.9	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
69	c5ahwC	Alignment	not modelled	98.8	27	PDB header: signaling protein Chain: C: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein msMeg_3811 in2 complex with camp
70	c3s3tD	Alignment	not modelled	98.8	16	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
71	c3fh0A	Alignment	not modelled	98.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
72	d1mjha	Alignment	not modelled	98.8	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
73	d2z3va1	Alignment	not modelled	98.8	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
74	c3mt0A	Alignment	not modelled	98.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
75	c3na3A	Alignment	not modelled	98.7	17	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
76	c4wnyA	Alignment	not modelled	98.7	25	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress

						protein2 family from burkholderia pseudomallei
77	c4geeA	Alignment	not modelled	98.6	22	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.
78	d1joya	Alignment	not modelled	98.6	31	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
79	c2pfsA	Alignment	not modelled	98.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
80	c4r2jA	Alignment	not modelled	98.6	9	PDB header: metal binding protein, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
81	c4r2lB	Alignment	not modelled	98.6	14	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
82	d1jmva	Alignment	not modelled	98.5	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
83	c3fg9B	Alignment	not modelled	98.4	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
84	c4b6cB	Alignment	not modelled	98.4	20	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
85	c3h4lB	Alignment	not modelled	98.4	18	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
86	d2gm3a1	Alignment	not modelled	98.3	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
87	c3olqA	Alignment	not modelled	98.3	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
88	c4emvA	Alignment	not modelled	98.3	18	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna topoisomerase iv, b subunit; PDBTitle: crystal structure of a topoisomerase atp inhibitor
89	d1q77a	Alignment	not modelled	98.2	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
90	d1kja2	Alignment	not modelled	98.2	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
91	c3zrwB	Alignment	not modelled	98.2	27	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
92	c5j5pB	Alignment	not modelled	98.2	28	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
93	d1pvga2	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: DNA gyrase/MutL, N-terminal domain
94	c5ix1A	Alignment	not modelled	98.1	16	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
95	d1s16a2	Alignment	not modelled	98.0	19	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
96	d1ei1a2	Alignment	not modelled	98.0	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
97	c2dumD	Alignment	not modelled	98.0	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
98	c1bkna	Alignment	not modelled	98.0	14	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
99	c5ofbB	Alignment	not modelled	98.0	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
						PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: topoisomerase iv, subunit b;

100	c4hymA_	Alignment	not modelled	97.9	20	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.
101	c3zm7E_	Alignment	not modelled	97.9	28	PDB header: isomerase Chain: E: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
102	c1ei1B_	Alignment	not modelled	97.9	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
103	c5x9yC_	Alignment	not modelled	97.9	29	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.
104	c3ab8B_	Alignment	not modelled	97.8	18	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein ttha0350; PDBTitle: crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
105	c1kijB_	Alignment	not modelled	97.8	22	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
106	c1s16B_	Alignment	not modelled	97.8	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
107	c1zxnB_	Alignment	not modelled	97.8	23	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
108	c1ea6A_	Alignment	not modelled	97.7	18	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
109	c3idfA_	Alignment	not modelled	97.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: usp-like protein; PDBTitle: the crystal structure of a usp-like protein from wolinnella2 succinogenes to 2.0a
110	c3g7bB_	Alignment	not modelled	97.7	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
111	c2jaxA_	Alignment	not modelled	97.7	21	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein tb31.7; PDBTitle: universal stress protein rv2623 from mycobacterium2 tuberculosis
112	c1qzrA_	Alignment	not modelled	97.6	23	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)
113	c3vrhA_	Alignment	not modelled	97.6	19	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
114	c1y4sA_	Alignment	not modelled	97.5	24	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
115	c3ke6A_	Alignment	not modelled	97.5	28	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
116	c2e21A_	Alignment	not modelled	97.5	17	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of til5 in a complex with amppnp from aquifex2 aeolicus.
117	d1uyla_	Alignment	not modelled	97.5	13	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
118	c3omuB_	Alignment	not modelled	97.5	19	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
119	c2fwyA_	Alignment	not modelled	97.4	13	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
120	c3iedA_	Alignment	not modelled	97.4	18	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