Phyre^2

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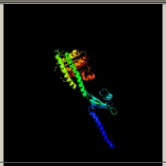
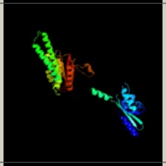
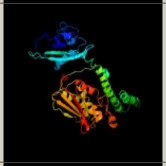
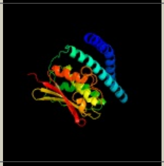
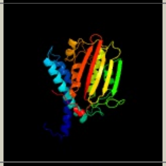
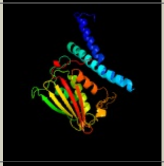
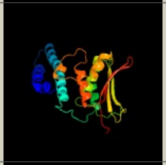
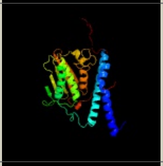
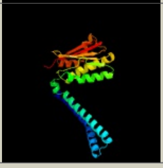
Description	RVBD0490_(senX3)_579352_580584
Date	Fri Jul 26 01:50:03 BST 2019
Unique Job ID	c565b56d7c66bc94

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4i5sA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative histidine kinase covs; vick-like protein; **PDBTitle:** structure and function of sensor histidine kinase
2	c4gczB_	Alignment		100.0	19	**PDB header:**signaling protein, de novo protein **Chain:** B: **PDB Molecule:**blue-light photoreceptor, sensor protein fixl; **PDBTitle:** structure of a blue-light photoreceptor
3	c3a0rA_	Alignment		100.0	19	**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)
4	c4ew8A_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein divl; **PDBTitle:** crystal structure of a c-terminal part of tyrosine kinase (divl) from2 caulobacter crescentus cb15 at 2.50 a resolution (psi community3 target, shapiro l.)
5	c2c2aA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
6	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
7	c3d2rB_	Alignment		100.0	16	**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
8	c2q8fA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
9	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
10	c2bu8A_	Alignment		100.0	16	**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
11	c3crlB_	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	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+
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	c4kp4B_	Alignment		100.0	29	**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.
15	c4u7nA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine protein kinase sensor protein; **PDBTitle:** inactive structure of histidine kinase
16	c1gjvA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; **PDBTitle:** branched-chain alpha-ketoacid dehydrogenase kinase (bck) complxed with2 atp-gamma-s
17	c3tz5A_	Alignment		100.0	21	**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
18	c4r3aA_	Alignment		100.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**blue-light-activated histidine kinase 2; **PDBTitle:** erythrobacter litoralis el346 blue-light activated histidine kinase
19	c4biuB_	Alignment		99.9	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein cpxa; **PDBTitle:** crystal structure of cpxahdc (orthorhombic form 1)
20	c4biyD_	Alignment		99.9	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein cpxa; **PDBTitle:** crystal structure of cpxahdc (monoclinic form 2)
21	c5idmA_	Alignment	not modelled	99.9	32	**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	c3a0tA_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** catalytic domain of histidine kinase thka (tm1359) in complex with adp2 and mg ion (trigonal)
23	d1jm6a2	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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
24	d1gkza2	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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
25	c6blkB_	Alignment	not modelled	99.9	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**signal transduction histidine-protein kinase/phosphatase **PDBTitle:** mycobacterial sensor histidine kinase mprb
26	d2c2aa2	Alignment	not modelled	99.9	32	**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
27	d1id0a_	Alignment	not modelled	99.9	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase

28	c1b3qA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
29	d1bxda_	Alignment	not modelled	99.9	27	**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
30	c3sl2A_	Alignment	not modelled	99.9	36	**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
31	c4fmtB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**chpt protein; **PDBTitle:** crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
32	c2ch4A_	Alignment	not modelled	99.9	27	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
33	d1i58a_	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
34	c4pl9A_	Alignment	not modelled	99.9	28	**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	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
36	c6nb0A_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase; **PDBTitle:** crystal structure of histidine kinase from burkholderia phymatum2 stm815
37	c3jz3B_	Alignment	not modelled	99.8	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
38	c4r39A_	Alignment	not modelled	99.8	15	**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	c4qpkA_	Alignment	not modelled	99.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**phosphotransferase; **PDBTitle:** 1.7 angstrom structure of a bacterial phosphotransferase
40	d1r62a_	Alignment	not modelled	99.7	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
41	c4gt8A_	Alignment	not modelled	99.7	15	**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
42	c5epvB_	Alignment	not modelled	99.7	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
43	d2hkja3	Alignment	not modelled	99.7	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
44	c4ctiA_	Alignment	not modelled	99.6	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**osmolarity sensor protein envz, af1503; **PDBTitle:** escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
45	c6e95A_	Alignment	not modelled	99.6	11	**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)
46	c2zbkB_	Alignment	not modelled	99.5	24	**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
47	c3gieA_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
48	c1mx0D_	Alignment	not modelled	99.5	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
49	c3ehgA_	Alignment	not modelled	99.5	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
50	c3zxqA_	Alignment	not modelled	99.5	20	**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
51	c2q2eB_	Alignment	not modelled	99.4	22	**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

52	c4bxiA_	Alignment	not modelled	99.4	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
53	c3zxoB_	Alignment	not modelled	99.4	21	**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
54	d1th8a_	Alignment	not modelled	99.2	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
55	d1bkna2	Alignment	not modelled	99.2	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
56	d1h7sa2	Alignment	not modelled	99.2	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
57	d1b63a2	Alignment	not modelled	99.1	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
58	c3volA_	Alignment	not modelled	99.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**aerotaxis transducer aer2; **PDBTitle:** x-ray crystal structure of pas-hamp aer2 in the cn-bound form
59	c4ehoD_	Alignment	not modelled	99.0	10	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**bacteriophytochrome, pas/pac sensor; **PDBTitle:** crystal structure of the bacteriophytochrome rpbphp1
60	c4lrzG_	Alignment	not modelled	99.0	9	**PDB header:**transferase/transcription regulator **Chain:** G: **PDB Molecule:**pts-dependent dihydroxyacetone kinase operon regulatory **PDBTitle:** crystal structure of the e.coli dhar(n)-dhal complex
61	d1y8oa2	Alignment	not modelled	98.9	18	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
62	d1ixma_	Alignment	not modelled	98.9	14	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
63	c4hj6A_	Alignment	not modelled	98.9	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lov protein; **PDBTitle:** crystal structure of rhodobacter sphaeroides lov protein
64	c3sw1B_	Alignment	not modelled	98.9	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**sensory box protein; **PDBTitle:** structure of a full-length bacterial lov protein
65	c2pr6A_	Alignment	not modelled	98.8	12	**PDB header:**flavoprotein, signaling protein **Chain:** A: **PDB Molecule:**blue-light photoreceptor; **PDBTitle:** structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure)
66	c2gj3A_	Alignment	not modelled	98.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nitrogen fixation regulatory protein; **PDBTitle:** crystal structure of the fad-containing pas domain of the protein nifl2 from azotobacter vinelandii.
67	c3mxqC_	Alignment	not modelled	98.8	6	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
68	c2v1bA_	Alignment	not modelled	98.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nph1-1; **PDBTitle:** n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
69	d1ew0a_	Alignment	not modelled	98.8	16	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
70	c3bwlA_	Alignment	not modelled	98.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
71	c6i20A_	Alignment	not modelled	98.8	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**aureochrome1-like protein; **PDBTitle:** flavin analogue sheds light on light-oxygen-voltage domain mechanism
72	c4mn5A_	Alignment	not modelled	98.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kinase walk; **PDBTitle:** crystal structure of pas domain of s. aureus yycg
73	c3mqoB_	Alignment	not modelled	98.7	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
74	c3mfxA_	Alignment	not modelled	98.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef family protein; **PDBTitle:** crystal structure of the sensory box domain of the sensory-box/ggdef2 protein so_1695 from shewanella oneidensis, northeast structural3 genomics consortium target sor288b
75	c3caxA_	Alignment	not modelled	98.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695

76	c5xgdA_	Alignment	not modelled	98.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein pa0861; **PDBTitle:** crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
77	c2ykfA_	Alignment	not modelled	98.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sensor histidine kinase pdtas; **PDBTitle:** sensor region of a sensor histidine kinase
78	c4hh2D_	Alignment	not modelled	98.7	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, ppsr; **PDBTitle:** structure of ppsr without the hth motif from rb. sphaeroides
79	c3lyxA_	Alignment	not modelled	98.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef domain protein; **PDBTitle:** crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
80	d1y28a_	Alignment	not modelled	98.7	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
81	c3k3dA_	Alignment	not modelled	98.7	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410; **PDBTitle:** the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
82	c2mwgB_	Alignment	not modelled	98.7	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**blue-light photoreceptor; **PDBTitle:** full-length solution structure of ytva, a lov-photoreceptor protein2 and regulator of bacterial stress response
83	c3luqC_	Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of a pas domain from a sensory box histidine2 kinase regulator from geobacter sulfurreducens to 2.5a
84	c1v9yA_	Alignment	not modelled	98.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heme pas sensor protein; **PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
85	d1v9ya_	Alignment	not modelled	98.7	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
86	c2jheB_	Alignment	not modelled	98.6	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 - 190)
87	c3mr0B_	Alignment	not modelled	98.6	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sensory box histidine kinase/response regulator; **PDBTitle:** crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264
88	c3kx0X_	Alignment	not modelled	98.6	12	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
89	c3b33A_	Alignment	not modelled	98.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
90	c3oloB_	Alignment	not modelled	98.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**two-component sensor histidine kinase; **PDBTitle:** crystal structure of a pas domain from two-component sensor histidine2 kinase
91	c3na3A_	Alignment	not modelled	98.5	28	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
92	c2w0nA_	Alignment	not modelled	98.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein dcus; **PDBTitle:** plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
93	c5hwvA_	Alignment	not modelled	98.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase tods; **PDBTitle:** crystal structure of pas1 complexed with toluene
94	c2qkpD_	Alignment	not modelled	98.5	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
95	c5fq1A_	Alignment	not modelled	98.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase; **PDBTitle:** structure of the cytoplasmic pas domain of the geobacillus2 thermodenitrificans histidine kinase cita
96	c2r78D_	Alignment	not modelled	98.5	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
97	c4geeA_	Alignment	not modelled	98.4	19	**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.
98	c3fg8B_	Alignment	not modelled	98.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
99	c5svuD_	Alignment	not modelled	98.4	11	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**adagio protein 1; **PDBTitle:** structure and kinetics of the lov domain of zeitlupe determine its2 circadian function in arabidopsis
100	c3ue6C_	Alignment	not modelled	98.3	10	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**aureochrome1; **PDBTitle:** the dark structure of the blue-light photoreceptor aureochrome1 lov
						PDB header:structural genomics, unknown function

101	c3mjqB_	Alignment	not modelled	98.3	7	**Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
102	d1xj3a1	Alignment	not modelled	98.3	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
103	c5iu1A_	Alignment	not modelled	98.3	11	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**ctr1-like protein; **PDBTitle:** n-terminal pas domain homodimer of ppanr map3k from physcomitrella2 patens.
104	c4hp4A_	Alignment	not modelled	98.2	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**eag-like k[+] channel; **PDBTitle:** crystal structure of pas domain from the fruit-fly elk potassium2 channel
105	c6ceqC_	Alignment	not modelled	98.2	18	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** the aer2 receptor from vibrio cholerae is a dual pas-heme oxygen2 sensor
106	d1nwza_	Alignment	not modelled	98.2	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
107	c2l4rA_	Alignment	not modelled	98.2	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h member 2; **PDBTitle:** nmr solution structure of the n-terminal pas domain of herg
108	c2wkqA_	Alignment	not modelled	98.2	9	**PDB header:**transferase, cell adhesion **Chain:** A: **PDB Molecule:**nph1-1, ras-related c3 botulinum toxin substrate 1; **PDBTitle:** structure of a photoactivatable rac1 containing the lov2 c450a mutant
109	c3p7nB_	Alignment	not modelled	98.2	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
110	c3fc7B_	Alignment	not modelled	98.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**htr-like protein; **PDBTitle:** the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
111	c3t50B_	Alignment	not modelled	98.1	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**blue-light-activated histidine kinase; **PDBTitle:** x-ray structure of the lov domain from the lov-hk sensory protein from2 brucella abortus (dark state).
112	c4b6cB_	Alignment	not modelled	98.1	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b,dna gyrase subunit b,dna gyrase **PDBTitle:** structure of the m. smegmatis gyrb atpase domain in complex with an2 aminopyrazinamide
113	d1n9la_	Alignment	not modelled	98.1	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
114	c3h4lB_	Alignment	not modelled	98.1	22	**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
115	c3eehA_	Alignment	not modelled	98.1	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative light and redox sensing histidine kinase; **PDBTitle:** the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
116	c6dgjA_	Alignment	not modelled	98.1	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rpfr; **PDBTitle:** cronobacter turicensis rpfr quorum-sensing receptor pas domain in2 complex with bdsf
117	c2vlgD_	Alignment	not modelled	98.0	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
118	d1bywa_	Alignment	not modelled	98.0	8	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
119	d1ll8a_	Alignment	not modelled	98.0	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
120	d1otda_	Alignment	not modelled	98.0	7	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like