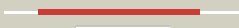
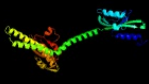































Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1364c_(-)_1535689_1537650 |
| Date | Wed Jul 31 22:05:46 BST 2019 |
| Unique Job ID | d2e3e669e39ab64e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c4gczB_ |  Alignment |  | 100.0 | 21 | PDB header: signaling protein, de novo protein Chain: B: PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor |
| 2 | c4i5sA_ |  Alignment |  | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase |
| 3 | c4r3aA_ |  Alignment |  | 100.0 | 20 | PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis ei346 blue-light activated histidine kinase |
| 4 | c3a0rA_ |  Alignment |  | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360) |
| 5 | c3ke6A_ |  Alignment |  | 100.0 | 98 | 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 |
| 6 | c2c2aA_ |  Alignment |  | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein |
| 7 | c4ew8A_ |  Alignment |  | 99.9 | 20 | 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.) |
| 8 | c2q8fA_ |  Alignment |  | 99.9 | 18 | PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1 |
| 9 | c2bu8A_ |  Alignment |  | 99.9 | 14 | 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 |
| 10 | c3crlB_ |  Alignment |  | 99.9 | 15 | PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex. |
| 11 | c3d2rB_ |  Alignment |  | 99.9 | 12 | 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 |

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|----|------------------------|-----------|---|------|----|--|
| 12 | c5tdjA | Alignment |  | 99.8 | 13 | 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 | c1qjvA | Alignment |  | 99.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s |
| 14 | c1y8oA | Alignment |  | 99.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex |
| 15 | c3d36B | Alignment |  | 99.8 | 17 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: sporulation kinase b; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearotherophilus kinb with the inhibitor sda |
| 16 | c4u7nA | Alignment |  | 99.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: histidine protein kinase sensor protein; PDBTitle: inactive structure of histidine kinase |
| 17 | c4kp4B | Alignment |  | 99.8 | 15 | 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. |
| 18 | c4biyD | Alignment |  | 99.8 | 13 | PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2) |
| 19 | c3k3dA | Alignment |  | 99.8 | 90 | 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 |
| 20 | c3tz5A | Alignment |  | 99.8 | 15 | 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 |
| 21 | c4hj6A | Alignment | not modelled | 99.8 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: lov protein; PDBTitle: crystal structure of rhodobacter sphaeroides lov protein |
| 22 | c6dk8B | Alignment | not modelled | 99.8 | 18 | PDB header: signaling protein Chain: B: PDB Molecule: rets (regulator of exopolysaccharide and type iii PDBTitle: rets kinase region without cobalt |
| 23 | c4r39A | Alignment | not modelled | 99.8 | 16 | 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 |
| 24 | c6i20A | Alignment | not modelled | 99.8 | 11 | PDB header: transcription Chain: A: PDB Molecule: aureochrome1-like protein; PDBTitle: flavin analogue sheds light on light-oxygen-voltage domain mechanism |
| 25 | c3kx0X | Alignment | not modelled | 99.8 | 92 | PDB header: signaling protein Chain: X: PDB Molecule: uncharacterized protein rv1364c/mt1410; PDBTitle: crystal structure of the pas domain of rv1364c |
| 26 | c3sw1B | Alignment | not modelled | 99.8 | 17 | PDB header: signaling protein Chain: B: PDB Molecule: sensory box protein; PDBTitle: structure of a full-length bacterial lov protein |
| 27 | c2wkqA | Alignment | not modelled | 99.8 | 15 | 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 |
| 28 | c3caxA | Alignment | not modelled | 99.8 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pf0695; PDBTitle: crystal structure of uncharacterized protein pf0695 |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c4biuB_ | Alignment | not modelled | 99.7 | 13 | PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1) |
| 30 | c4ehoD_ | Alignment | not modelled | 99.7 | 16 | PDB header: signaling protein Chain: D: PDB Molecule: bacteriophytochrome, pas/pac sensor; PDBTitle: crystal structure of the bacteriophytochrome rpbphp1 |
| 31 | c2v1bA_ | Alignment | not modelled | 99.7 | 14 | 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)) |
| 32 | c5idmA_ | Alignment | not modelled | 99.7 | 17 | 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+ |
| 33 | c1b3qA_ | Alignment | not modelled | 99.7 | 16 | PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase |
| 34 | c2gj3A_ | Alignment | not modelled | 99.7 | 14 | 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. |
| 35 | c5hwwA_ | Alignment | not modelled | 99.7 | 14 | PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase tods; PDBTitle: crystal structure of pas1 complexed with toluene |
| 36 | c3ue6C_ | Alignment | not modelled | 99.7 | 14 | PDB header: signaling protein Chain: C: PDB Molecule: aureochrome1; PDBTitle: the dark structure of the blue-light photoreceptor aureochrome1 lov |
| 37 | c2pr6A_ | Alignment | not modelled | 99.7 | 15 | 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) |
| 38 | c2mwgB_ | Alignment | not modelled | 99.7 | 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 |
| 39 | c4hh2D_ | Alignment | not modelled | 99.7 | 16 | PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, ppsr; PDBTitle: structure of ppsr without the hth motif from rb. sphaerooides |
| 40 | c3lyxA_ | Alignment | not modelled | 99.7 | 13 | 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 |
| 41 | c3mqoB_ | Alignment | not modelled | 99.7 | 18 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: the crystal structure of the pas domain in complex with isopropanol of 2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a |
| 42 | c3mr0B_ | Alignment | not modelled | 99.7 | 13 | 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 |
| 43 | c5va1A_ | Alignment | not modelled | 99.7 | 12 | PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel |
| 44 | c5svuD_ | Alignment | not modelled | 99.7 | 14 | 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 |
| 45 | c2l4rA_ | Alignment | not modelled | 99.7 | 11 | 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 |
| 46 | c3a0tA_ | Alignment | not modelled | 99.7 | 16 | 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) |
| 47 | c2ch4A_ | Alignment | not modelled | 99.7 | 24 | PDB header: transferase/chemotaxis Chain: A: PDB Molecule: chemotaxis protein chea; PDBTitle: complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew |
| 48 | c5epvB_ | Alignment | not modelled | 99.7 | 11 | 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 |
| 49 | c3luqC_ | Alignment | not modelled | 99.6 | 23 | 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 |
| 50 | c3mxqC_ | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae |
| 51 | c4lrzG_ | Alignment | not modelled | 99.6 | 12 | 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 |
| 52 | d2c2aa2 | Alignment | not modelled | 99.6 | 19 | 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 PDB header: plant protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c5iu1A_ | Alignment | not modelled | 99.6 | 12 | Chain: A: PDB Molecule: ctr1-like protein; PDBTitle: n-terminal pas domain homodimer of ppanr map3k from physcomitrella2 patens. |
| 54 | d1n9la_ | Alignment | not modelled | 99.6 | 17 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain |
| 55 | c3t50B_ | Alignment | not modelled | 99.6 | 14 | 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). |
| 56 | d1bywa_ | Alignment | not modelled | 99.6 | 10 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain |
| 57 | d1y28a_ | Alignment | not modelled | 99.6 | 13 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain |
| 58 | d1ew0a_ | Alignment | not modelled | 99.6 | 20 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain |
| 59 | d1jm6a2 | Alignment | not modelled | 99.6 | 22 | Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 60 | c2z6dB_ | Alignment | not modelled | 99.6 | 12 | PDB header: transferase Chain: B: PDB Molecule: phototropin-2; PDBTitle: crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana |
| 61 | d1gkza2 | Alignment | not modelled | 99.6 | 19 | Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 62 | d1p97a_ | Alignment | not modelled | 99.6 | 11 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Hypoxia-inducible factor Hif2a, C-terminal domain |
| 63 | c4kuoA_ | Alignment | not modelled | 99.6 | 11 | PDB header: signaling protein Chain: A: PDB Molecule: blue-light photoreceptor; PDBTitle: a superfast recovering full-length lov protein from the marine2 phototrophic bacterium dinoroseobacter shibae (photoexcited state) |
| 64 | c4hoiB_ | Alignment | not modelled | 99.6 | 14 | PDB header: transport protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: crystal structure of pas domain from the mouse eag1 potassium channel |
| 65 | d1jnua_ | Alignment | not modelled | 99.6 | 10 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain |
| 66 | c6blkB_ | Alignment | not modelled | 99.6 | 19 | PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine-protein kinase/phosphatase PDBTitle: mycobacterial sensor histidine kinase mprb |
| 67 | c6rhgB_ | Alignment | not modelled | 99.6 | 16 | PDB header: fluorescent protein Chain: B: PDB Molecule: multi-sensor hybrid histidine kinase; PDBTitle: structure of chloroflexus aggregans cagg_3753 lov domain |
| 68 | c4fmtB_ | Alignment | not modelled | 99.6 | 11 | 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 |
| 69 | d1i58a_ | Alignment | not modelled | 99.6 | 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 |
| 70 | d1bxda_ | Alignment | not modelled | 99.6 | 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 |
| 71 | c3mfxA_ | Alignment | not modelled | 99.6 | 12 | 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 |
| 72 | c3f1oB_ | Alignment | not modelled | 99.6 | 10 | PDB header: transcription Chain: B: PDB Molecule: aryl hydrocarbon receptor nuclear translocator; PDBTitle: crystal structure of the high affinity heterodimer of hif2 alpha and2 arnt c-terminal pas domains, with an internally-bound artificial3 ligand |
| 73 | c6nb0A_ | Alignment | not modelled | 99.6 | 15 | PDB header: transferase Chain: A: PDB Molecule: histidine kinase; PDBTitle: crystal structure of histidine kinase from burkholderia phymatum2 stm815 |
| 74 | c2qkpD_ | Alignment | not modelled | 99.6 | 16 | 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 |
| 75 | c3rtyA_ | Alignment | not modelled | 99.6 | 11 | PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: structure of an enclosed dimer formed by the drosophila period protein |
| 76 | c3vola_ | Alignment | not modelled | 99.6 | 15 | 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 PDB header: signaling protein |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 77 | c1v9yA_ | Alignment | not modelled | 99.5 | 12 | Chain: A: PDB Molecule: heme pas sensor protein; PDBTitle: crystal structure of the heme pas sensor domain of ec dos (ferric2 form) |
| 78 | d1v9ya_ | Alignment | not modelled | 99.5 | 12 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain |
| 79 | c3b33A_ | Alignment | not modelled | 99.5 | 11 | 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 |
| 80 | c5xgdA_ | Alignment | not modelled | 99.5 | 14 | 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 |
| 81 | c4wn5A_ | Alignment | not modelled | 99.5 | 12 | PDB header: transcription Chain: A: PDB Molecule: hypoxia-inducible factor 3-alpha; PDBTitle: crystal structure of the c-terminal per-arnt-sim (pasb) of human hif-2 3alpha9 bound to 18:1-1-monoacylglycerol |
| 82 | c3mjgB_ | Alignment | not modelled | 99.5 | 9 | PDB header: structural genomics, unknown function 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. |
| 83 | c4f3lA_ | Alignment | not modelled | 99.5 | 9 | PDB header: transcription/activator Chain: A: PDB Molecule: circadian locomoter output cycles protein kaput; PDBTitle: crystal structure of the heterodimeric clock:bmal1 transcriptional2 activator complex |
| 84 | c3sl2A_ | Alignment | not modelled | 99.5 | 24 | 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 |
| 85 | c2ykfA_ | Alignment | not modelled | 99.5 | 12 | PDB header: transferase Chain: A: PDB Molecule: probable sensor histidine kinase pdtas; PDBTitle: sensor region of a sensor histidine kinase |
| 86 | c2r78D_ | Alignment | not modelled | 99.5 | 13 | 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 |
| 87 | c3bw1A_ | Alignment | not modelled | 99.5 | 13 | PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of pas domain of htr-like protein from haloarcula2 marismortui |
| 88 | d1th8a_ | Alignment | not modelled | 99.5 | 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 |
| 89 | c3fg8B_ | Alignment | not modelled | 99.5 | 21 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rha05790; PDBTitle: crystal structure of pas domain of rha05790 |
| 90 | c4f3lB_ | Alignment | not modelled | 99.5 | 11 | PDB header: transcription/activator Chain: B: PDB Molecule: bmal1b; PDBTitle: crystal structure of the heterodimeric clock:bmal1 transcriptional2 activator complex |
| 91 | d1id0a_ | Alignment | not modelled | 99.5 | 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 |
| 92 | c4pl9A_ | Alignment | not modelled | 99.5 | 21 | PDB header: transferase Chain: A: PDB Molecule: ethylene receptor 1; PDBTitle: structure of the catalytic domain of etr1 from arabidopsis thaliana |
| 93 | c4wujB_ | Alignment | not modelled | 99.5 | 9 | PDB header: circadian clock protein Chain: B: PDB Molecule: glycoside hydrolase family 15, cellulose signaling PDBTitle: structural biochemistry of a fungal lov domain photoreceptor reveals2 an evolutionarily conserved pathway integrating blue-light and3 oxidative stress |
| 94 | d1ysra1 | Alignment | not modelled | 99.5 | 18 | Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase |
| 95 | c2kdkA_ | Alignment | not modelled | 99.5 | 10 | PDB header: transcription regulator Chain: A: PDB Molecule: aryl hydrocarbon receptor nuclear translocator-like protein PDBTitle: structure of human circadian clock protein bmal2 c-terminal pas domain |
| 96 | c3h9wA_ | Alignment | not modelled | 99.5 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diguanylate cyclase with pas/pac sensor; PDBTitle: crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mgr66c |
| 97 | c4hp4A_ | Alignment | not modelled | 99.5 | 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 |
| 98 | c4qpkA_ | Alignment | not modelled | 99.5 | 9 | PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase |
| 99 | c5akpA_ | Alignment | not modelled | 99.5 | 15 | PDB header: signaling protein Chain: A: PDB Molecule: phytochrome-like protein; PDBTitle: crystal structure of the dark-adapted full-length2 bacteriophytochrome xccbph from xanthomonas campestris3 bound to bv chromophore |
| 100 | d1xj3a1 | Alignment | not modelled | 99.4 | 12 | Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | Family: Heme-binding PAS domain |
| 101 | c3gieA_ | Alignment | not modelled | 99.4 | 12 | PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of deskc_h188e in complex with amp-pcp |
| 102 | c3fc7B_ | Alignment | not modelled | 99.4 | 21 | 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 |
| 103 | c3oloB_ | Alignment | not modelled | 99.4 | 11 | 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 |
| 104 | c3p7nB_ | Alignment | not modelled | 99.4 | 15 | PDB header: dna binding protein Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis |
| 105 | c3eehA_ | Alignment | not modelled | 99.4 | 14 | 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 |
| 106 | c2vlgD_ | Alignment | not modelled | 99.4 | 11 | PDB header: transferase Chain: D: PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer |
| 107 | c4zp4D_ | Alignment | not modelled | 99.4 | 10 | PDB header: protein transport/transcription Chain: D: PDB Molecule: endothelial pas domain-containing protein 1; PDBTitle: crystal structure of the heterodimeric hif-2a:arnt complex |
| 108 | c3jz3B_ | Alignment | not modelled | 99.4 | 14 | PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec |
| 109 | c3icyB_ | Alignment | not modelled | 99.4 | 13 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: sensor protein; PDBTitle: the crystal structure of sensory box histidine kinase/response2 regulator domain from chlorobium tepidum t1s |
| 110 | c6e95A_ | Alignment | not modelled | 99.4 | 12 | 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) |
| 111 | c3gecA_ | Alignment | not modelled | 99.4 | 12 | PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: crystal structure of a tandem pas domain fragment of2 drosophila period |
| 112 | c3gdiB_ | Alignment | not modelled | 99.4 | 11 | PDB header: transcription Chain: B: PDB Molecule: period circadian protein homolog 2; PDBTitle: mammalian clock protein mper2 - crystal structure of a pas domain2 fragment |
| 113 | c4mn5A_ | Alignment | not modelled | 99.4 | 14 | PDB header: transferase Chain: A: PDB Molecule: sensor protein kinase walk; PDBTitle: crystal structure of pas domain of s. aureus yycg |
| 114 | c3ewkA_ | Alignment | not modelled | 99.4 | 13 | PDB header: flavoprotein Chain: A: PDB Molecule: sensor protein; PDBTitle: structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos |
| 115 | c5sy5B_ | Alignment | not modelled | 99.4 | 10 | PDB header: transcription Chain: B: PDB Molecule: neuronal pas domain-containing protein 1; PDBTitle: crystal structure of the heterodimeric npas1-arnt complex |
| 116 | c4dj3B_ | Alignment | not modelled | 99.4 | 10 | PDB header: protein binding Chain: B: PDB Molecule: period circadian protein homolog 3; PDBTitle: unwinding the differences of the mammalian period clock proteins from2 crystal structure to cellular function |
| 117 | c4ctiA_ | Alignment | not modelled | 99.4 | 15 | 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 |
| 118 | c4gt8A_ | Alignment | not modelled | 99.4 | 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 |
| 119 | c4dj2C_ | Alignment | not modelled | 99.3 | 11 | PDB header: protein binding Chain: C: PDB Molecule: period circadian protein homolog 1; PDBTitle: unwinding the differences of the mammalian period clock proteins from2 crystal structure to cellular function |
| 120 | d2hkja3 | Alignment | not modelled | 99.3 | 11 | 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 |