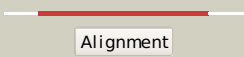


| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3c3wB_ |  Alignment |  | 100.0 | 26 | PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr |
| 2 | c1zn2A_ |  Alignment |  | 100.0 | 22 | PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr |
| 3 | c1rnlA_ |  Alignment |  | 100.0 | 26 | PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl |
| 4 | c3klnC_ |  Alignment |  | 100.0 | 17 | PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst |
| 5 | c1kgsA_ |  Alignment |  | 100.0 | 15 | PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima |
| 6 | c3r0jA_ |  Alignment |  | 99.9 | 21 | PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis |
| 7 | c1ys7B_ |  Alignment |  | 99.9 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+ |
| 8 | c2qwrA_ |  Alignment |  | 99.9 | 21 | PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis |
| 9 | c2oqrA_ |  Alignment |  | 99.9 | 24 | PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis |
| 10 | c2hqrA_ |  Alignment |  | 99.9 | 9 | PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism |
| 11 | d1s8na_ |  Alignment |  | 99.9 | 21 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c1p2fA_ | Alignment | | 99.9 | 16 | PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog |
| 13 | c2ayxA_ | Alignment | | 99.8 | 20 | PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain |
| 14 | c3eq2A_ | Alignment | | 99.8 | 20 | PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb |
| 15 | c1ny5A_ | Alignment | | 99.7 | 20 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state |
| 16 | d1ny5a1 | Alignment | | 99.7 | 20 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 17 | d1u0sy_ | Alignment | | 99.7 | 28 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 18 | d1jbea_ | Alignment | | 99.7 | 21 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 19 | c3b2nA_ | Alignment | | 99.7 | 27 | PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus |
| 20 | c3cz5B_ | Alignment | | 99.7 | 27 | PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1 |
| 21 | c3f6cB_ | Alignment | not modelled | 99.7 | 99 | PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli |
| 22 | c1w25B_ | Alignment | not modelled | 99.7 | 19 | PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp |
| 23 | c3breA_ | Alignment | not modelled | 99.7 | 22 | PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702 |
| 24 | c3sztB_ | Alignment | not modelled | 99.7 | 14 | PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone |
| 25 | c3eulB_ | Alignment | not modelled | 99.7 | 24 | PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis |
| 26 | d1dz3a_ | Alignment | not modelled | 99.7 | 23 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 27 | d1kgsa2 | Alignment | not modelled | 99.7 | 19 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 28 | c3cu5B_ | Alignment | not modelled | 99.7 | 20 | PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional |

| | | | | | |
|----|-------------------------|-----------|--------------|------|---|
| | | | | | regulator arac2 from clostridium phytofermentans isdg |
| 29 | c1h0mD_ | Alignment | not modelled | 99.7 | 21 PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna |
| 30 | c2q0aA_ | Alignment | not modelled | 99.7 | 22 PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing |
| 31 | d1ys7a2 | Alignment | not modelled | 99.7 | 21 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 32 | c1a2oB_ | Alignment | not modelled | 99.7 | 15 PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain |
| 33 | c3rqia_ | Alignment | not modelled | 99.7 | 12 PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate |
| 34 | d1a04a2 | Alignment | not modelled | 99.7 | 27 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 35 | d1peva_ | Alignment | not modelled | 99.7 | 21 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 36 | d2pl1a1 | Alignment | not modelled | 99.7 | 18 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 37 | d2ayxa1 | Alignment | not modelled | 99.7 | 20 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 38 | d2a9pa1 | Alignment | not modelled | 99.7 | 28 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 39 | c3dzdA_ | Alignment | not modelled | 99.7 | 13 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state |
| 40 | c3hdgE_ | Alignment | not modelled | 99.7 | 17 PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes |
| 41 | d1mvoa_ | Alignment | not modelled | 99.7 | 23 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 42 | d1dbwa_ | Alignment | not modelled | 99.7 | 19 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 43 | c2zwmA_ | Alignment | not modelled | 99.7 | 26 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis |
| 44 | c3i5aA_ | Alignment | not modelled | 99.7 | 22 PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae |
| 45 | c3qp5C_ | Alignment | not modelled | 99.7 | 23 PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl) |
| 46 | c2rjnA_ | Alignment | not modelled | 99.7 | 17 PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis |
| 47 | d1qkka_ | Alignment | not modelled | 99.7 | 18 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 48 | c2qr3A_ | Alignment | not modelled | 99.7 | 19 PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis |
| 49 | c2jrlA_ | Alignment | not modelled | 99.7 | 14 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer |
| 50 | c3cfyA_ | Alignment | not modelled | 99.7 | 18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus |
| 51 | d1krwa_ | Alignment | not modelled | 99.7 | 19 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 52 | c3h1gA_ | Alignment | not modelled | 99.7 | 20 PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori |
| 53 | d1p6qa_ | Alignment | not modelled | 99.7 | 22 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |

| | | | | | | |
|----|--------------------------|-----------|--------------|------|----|---|
| 54 | c2qv0A | Alignment | not modelled | 99.7 | 19 | PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae |
| 55 | c3nhzA | Alignment | not modelled | 99.7 | 25 | PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra |
| 56 | dlw25a1 | Alignment | not modelled | 99.7 | 19 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 57 | dlvioa2 | Alignment | not modelled | 99.7 | 21 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 58 | dlzh2a1 | Alignment | not modelled | 99.7 | 25 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 59 | dlheya | Alignment | not modelled | 99.7 | 19 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 60 | c3hv2B | Alignment | not modelled | 99.7 | 16 | PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5 |
| 61 | c2qzjC | Alignment | not modelled | 99.7 | 14 | PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile |
| 62 | c3jteA | Alignment | not modelled | 99.7 | 22 | PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum |
| 63 | c3hzhA | Alignment | not modelled | 99.7 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (cheY-3); PDBTitle: crystal structure of the cheX-cheY-bef3-mg+2 complex from2 borrelia burgdorferi |
| 64 | c3gt7A | Alignment | not modelled | 99.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus |
| 65 | dlzgza1 | Alignment | not modelled | 99.6 | 18 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 66 | c3t6kB | Alignment | not modelled | 99.6 | 21 | PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution |
| 67 | dlzesa1 | Alignment | not modelled | 99.6 | 20 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 68 | c3t8yA | Alignment | not modelled | 99.6 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheB |
| 69 | d2r25b1 | Alignment | not modelled | 99.6 | 23 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 70 | c3crnA | Alignment | not modelled | 99.6 | 16 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, cheY-like; PDBTitle: crystal structure of response regulator receiver domain protein (cheY-2 like) from methanospirillum hungatei jf-1 |
| 71 | c2zayA | Alignment | not modelled | 99.6 | 18 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans |
| 72 | c3lteH | Alignment | not modelled | 99.6 | 22 | PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri |
| 73 | dlxfha1 | Alignment | not modelled | 99.6 | 16 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 74 | c3cnbC | Alignment | not modelled | 99.6 | 17 | PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding response regulator, merr family; PDBTitle: crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h |
| 75 | dl1a2oa1 | Alignment | not modelled | 99.6 | 17 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 76 | c3cloC | Alignment | not modelled | 99.6 | 24 | PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution |
| 77 | c3a0rB | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360) |
| 78 | c3c0A | Alignment | not modelled | 99.6 | 21 | PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| 78 | c3cg4A_ | Alignment | not modelled | 99.6 | 21 | PDBTitle: crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding |
| 79 | c3cg4A_ | Alignment | not modelled | 99.6 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like); PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1 |
| 80 | d1p4wa_ | Alignment | not modelled | 99.6 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 81 | c3c3mA_ | Alignment | not modelled | 99.6 | 15 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1 |
| 82 | c2qxyB_ | Alignment | not modelled | 99.6 | 17 | PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima |
| 83 | c2jk1A_ | Alignment | not modelled | 99.6 | 23 | PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain |
| 84 | c3hebB_ | Alignment | not modelled | 99.6 | 21 | PDB header: transcription regulator Chain: B: PDB Molecule: response regulator receiver domain protein (chey); PDBTitle: crystal structure of response regulator receiver domain from2 rhodospirillum rubrum |
| 85 | c3c97A_ | Alignment | not modelled | 99.6 | 18 | PDB header: signaling protein, transferase Chain: A: PDB Molecule: signal transduction histidine kinase; PDBTitle: crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae |
| 86 | c2krfB_ | Alignment | not modelled | 99.6 | 21 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a |
| 87 | d1k66a_ | Alignment | not modelled | 99.6 | 13 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 88 | c3khtA_ | Alignment | not modelled | 99.6 | 29 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis |
| 89 | c1zljE_ | Alignment | not modelled | 99.6 | 32 | PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain |
| 90 | c3n0rA_ | Alignment | not modelled | 99.6 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution |
| 91 | d1mb3a_ | Alignment | not modelled | 99.6 | 22 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 92 | d1l3la1 | Alignment | not modelled | 99.6 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 93 | c3i42A_ | Alignment | not modelled | 99.6 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus |
| 94 | c3kcnA_ | Alignment | not modelled | 99.6 | 20 | PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica |
| 95 | c3mmnA_ | Alignment | not modelled | 99.6 | 22 | PDB header: transferase Chain: A: PDB Molecule: histidine kinase homolog; PDBTitle: crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+ |
| 96 | d1a04a1 | Alignment | not modelled | 99.6 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 97 | d1fsea_ | Alignment | not modelled | 99.6 | 30 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 98 | c3snkA_ | Alignment | not modelled | 99.6 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution |
| 99 | c3m6mF_ | Alignment | not modelled | 99.6 | 25 | PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpff complexed with rec domain of rpfc |
| 100 | c2rdmB_ | Alignment | not modelled | 99.6 | 16 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419 |
| 101 | c3grcD_ | Alignment | not modelled | 99.6 | 15 | PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666 |
| 102 | c2qvga_ | Alignment | not modelled | 99.6 | 19 | PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 103 | c1x3uA | Alignment | not modelled | 99.6 | 33 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot |
| 104 | c2rnjA | Alignment | not modelled | 99.6 | 26 | PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain |
| 105 | c3gl9B | Alignment | not modelled | 99.6 | 21 | PDB header: signaling protein Chain: B: PDB Molecule: response regulator; PDBTitle: the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism |
| 106 | c2hqaA | Alignment | not modelled | 99.5 | 15 | PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism |
| 107 | c3hdvB | Alignment | not modelled | 99.5 | 16 | PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida |
| 108 | d1p2fa2 | Alignment | not modelled | 99.5 | 15 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 109 | d1i3ca | Alignment | not modelled | 99.5 | 13 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 110 | c3nhmA | Alignment | not modelled | 99.5 | 20 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus |
| 111 | d2b4aa1 | Alignment | not modelled | 99.5 | 15 | Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related |
| 112 | c3ilhA | Alignment | not modelled | 99.5 | 20 | PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii |
| 113 | d1yioa1 | Alignment | not modelled | 99.5 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 114 | c3h5iA | Alignment | not modelled | 99.5 | 18 | PDB header: transcription Chain: A: PDB Molecule: response regulator/sensory box protein/ggdef PDBTitle: crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydotherrhus hydrogenoformans |
| 115 | d1dcfa | Alignment | not modelled | 99.5 | 17 | Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor |
| 116 | c3eodA | Alignment | not modelled | 99.5 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb |
| 117 | c2jpcA | Alignment | not modelled | 99.5 | 35 | PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein |
| 118 | c3eqzB | Alignment | not modelled | 99.5 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from colwellia2 psychrerythraea |
| 119 | c3luaA | Alignment | not modelled | 99.5 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum |
| 120 | c2j48A | Alignment | not modelled | 99.5 | 15 | PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein. |