






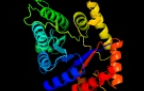














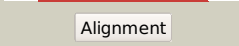

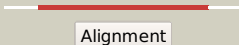

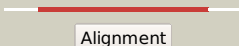



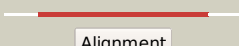

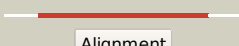

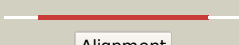






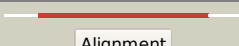

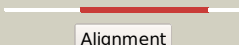


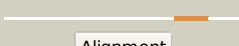
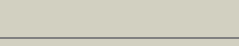


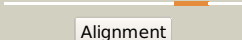
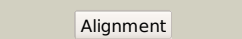

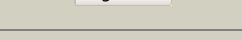
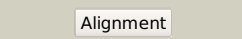
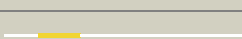
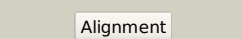

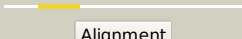

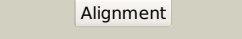

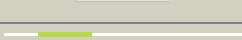

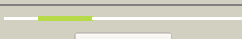
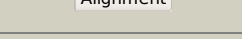

Phyre2

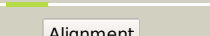
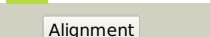
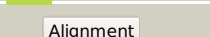
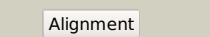
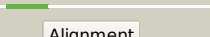
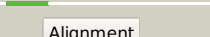
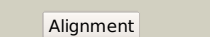
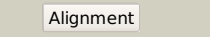
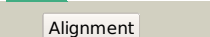

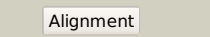
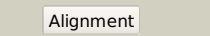
| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2893 (-) _3202430_3203407 |
| Date | Thu Aug 8 16:20:04 BST 2019 |
| Unique Job ID | df5d88f3f21791e0 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | d1ezwa_ |  Alignment |  | 100.0 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases |
| 2 | d1luca_ |  Alignment |  | 100.0 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase) |
| 3 | c3raoB_ |  Alignment |  | 100.0 | 21 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987. |
| 4 | c3sdoB_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei |
| 5 | d1tvla_ |  Alignment |  | 100.0 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases |
| 6 | c1tvIA_ |  Alignment |  | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis |
| 7 | c1z69D_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420 |
| 8 | c5tlcA_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b |
| 9 | c3c8nB_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis |
| 10 | d1rhca_ |  Alignment |  | 100.0 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases |
| 11 | d1nqka_ |  Alignment |  | 100.0 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases |

| | | | | | | |
|----|-------------------------|---|---|-------|----|---|
| 12 | c5dqpA_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1 |
| 13 | d1f07a_ |  Alignment |  | 100.0 | 22 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases |
| 14 | c5wanA_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway |
| 15 | c2wgkA_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida |
| 16 | c5w4zA_ |  Alignment |  | 100.0 | 24 | PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified frm and2 substrate riboflavin |
| 17 | d1lucb_ |  Alignment |  | 100.0 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase) |
| 18 | c2i7gA_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens |
| 19 | c3b9nB_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada) |
| 20 | c2b81D_ |  Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus |
| 21 | c6friD_ |  Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi |
| 22 | c6ak1B_ |  Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans |
| 23 | d1nfpa_ |  Alignment | not modelled | 99.9 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390) |
| 24 | d1fvpa_ |  Alignment | not modelled | 98.7 | 11 | Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390) |
| 25 | c5zmyF_ |  Alignment | not modelled | 89.0 | 23 | PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids |
| 26 | d1o5ka_ |  Alignment | not modelled | 85.7 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 27 | c3c6cA_ |  Alignment | not modelled | 85.4 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution |
| 28 | c3no5C_ |  Alignment | not modelled | 83.7 | 18 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a |

| | | | | | | |
|----|-------------------------|---|--------------|------|----|---|
| | | | | | | resolution |
| 29 | c3chvA |  Alignment | not modelled | 83.0 | 14 | PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution |
| 30 | c2y7eA |  Alignment | not modelled | 82.2 | 18 | PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form) |
| 31 | c3e49A |  Alignment | not modelled | 80.2 | 14 | PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution |
| 32 | c3lotC |  Alignment | not modelled | 80.2 | 9 | PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution |
| 33 | c3d0cB |  Alignment | not modelled | 79.1 | 12 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution |
| 34 | d1jpdx1 |  Alignment | not modelled | 77.6 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 35 | c2r8wB |  Alignment | not modelled | 76.5 | 18 | PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58 |
| 36 | c3pueA |  Alignment | not modelled | 76.2 | 8 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution |
| 37 | c3e02A |  Alignment | not modelled | 75.8 | 11 | PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution |
| 38 | c3e96B |  Alignment | not modelled | 75.1 | 18 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii |
| 39 | c3qy6A |  Alignment | not modelled | 73.2 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases |
| 40 | c3lerA |  Alignment | not modelled | 72.0 | 14 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168 |
| 41 | c2ehhE |  Alignment | not modelled | 70.9 | 9 | PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus |
| 42 | d2a6na1 |  Alignment | not modelled | 70.8 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 43 | c4nncA |  Alignment | not modelled | 69.6 | 14 | PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate |
| 44 | c4ur7B |  Alignment | not modelled | 69.3 | 17 | PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate |
| 45 | d1xxxa1 |  Alignment | not modelled | 69.0 | 11 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 46 | d1jpmal | Alignment | not modelled | 68.7 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 47 | c2yxgD | Alignment | not modelled | 68.6 | 9 | PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa) |
| 48 | c4n4qD | Alignment | not modelled | 67.4 | 8 | PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii |
| 49 | c6mqhA | Alignment | not modelled | 66.4 | 10 | PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei |
| 50 | c3si9B | Alignment | not modelled | 65.2 | 10 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae |
| 51 | d1f74a | Alignment | not modelled | 63.9 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 52 | c5ud6B | Alignment | not modelled | 63.6 | 6 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound |

| | | | | | | |
|----|-------------------------|---|--------------|------|----|---|
| 53 | c4uxdC |  Alignment | not modelled | 61.9 | 8 | PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus |
| 54 | c2vc6A |  Alignment | not modelled | 61.5 | 13 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. melloti with pyruvate bound |
| 55 | c4ah7C |  Alignment | not modelled | 61.4 | 6 | PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate |
| 56 | c3eb2A |  Alignment | not modelled | 61.1 | 11 | PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution |
| 57 | c4icnB |  Alignment | not modelled | 61.0 | 10 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica |
| 58 | c3cprB |  Alignment | not modelled | 60.0 | 13 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution |
| 59 | c3na8A |  Alignment | not modelled | 59.6 | 10 | PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa |
| 60 | c4xkyC |  Alignment | not modelled | 59.2 | 10 | PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution |
| 61 | c4i7vD |  Alignment | not modelled | 58.6 | 11 | PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhds with pyruvate |
| 62 | c3noeA |  Alignment | not modelled | 58.3 | 10 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa |
| 63 | c6daoB |  Alignment | not modelled | 57.4 | 3 | PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine |
| 64 | c3cqkB |  Alignment | not modelled | 55.0 | 22 | PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate |
| 65 | d1j93a |  Alignment | not modelled | 54.4 | 15 | Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD |
| 66 | c3daqB |  Alignment | not modelled | 54.1 | 8 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus |
| 67 | c3bi8A |  Alignment | not modelled | 53.2 | 13 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum |
| 68 | c6daqA |  Alignment | not modelled | 53.1 | 11 | PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate |
| 69 | c6k0aC |  Alignment | not modelled | 49.1 | 8 | PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p |
| 70 | d1xp3a1 |  Alignment | not modelled | 48.6 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV |
| 71 | c2v9dB |  Alignment | not modelled | 48.4 | 13 | PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12 |
| 72 | c5ktIA |  Alignment | not modelled | 47.9 | 14 | PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis. |
| 73 | c3lmzA |  Alignment | not modelled | 47.5 | 11 | PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distazonis atcc 8503 at 1.44 a resolution |
| 74 | d1w3ja |  Alignment | not modelled | 47.2 | 8 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 75 | d2gl5a1 |  Alignment | not modelled | 47.0 | 28 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 76 | c3fkKA |  Alignment | not modelled | 47.0 | 11 | PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase |
| 77 | c6ahuJ |  Alignment | not modelled | 46.3 | 16 | PDB header: hydrolase/rna Chain: J: PDB Molecule: ribonuclease p protein subunit p30; PDBTitle: cryo-em structure of human ribonuclease p with mature trna |
| 78 | c2wjeA |  Alignment | not modelled | 44.6 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | streptococcus pneumoniae tigr4. |
| 79 | d2noca1 | Alignment | not modelled | 43.5 | 13 | Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like |
| 80 | c5c54D | Alignment | not modelled | 42.7 | 8 | PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminate lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from <i>2 corynebacterium glutamicum</i> |
| 81 | c5ikyA | Alignment | not modelled | 42.0 | 16 | PDB header: hydrolase,lyase Chain: A: PDB Molecule: oxalate biosynthetic component 1; PDBTitle: apo structure of obc1, a bifunctional enzyme for quorum sensing-2 dependent oxalogenesis |
| 82 | c3h5dD | Alignment | not modelled | 41.4 | 13 | PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae |
| 83 | c3n2xB | Alignment | not modelled | 39.5 | 13 | PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate |
| 84 | c2m2jA | Alignment | not modelled | 39.0 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: solution nmr structure of the n-terminal domain of stm1478 from <i>2 salmonella typhimurium lt2</i> : target str147a of the northeast3 structural genomics consortium (nesg), and apc101565 of the midwest4 center for structural genomics (mcsng). |
| 85 | c2r94B | Alignment | not modelled | 38.7 | 16 | PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax |
| 86 | c4nq1B | Alignment | not modelled | 37.8 | 13 | PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site |
| 87 | c4b5nA | Alignment | not modelled | 37.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4) |
| 88 | c2rfgB | Alignment | not modelled | 36.4 | 16 | PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution |
| 89 | c3ewbX | Alignment | not modelled | 35.4 | 16 | PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes |
| 90 | c3g0sA | Alignment | not modelled | 34.8 | 13 | PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2 |
| 91 | d1bqga1 | Alignment | not modelled | 34.6 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 92 | d1tzza1 | Alignment | not modelled | 34.0 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 93 | d1xkya1 | Alignment | not modelled | 33.5 | 8 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 94 | c3lciA | Alignment | not modelled | 32.8 | 13 | PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w |
| 95 | c5gquA | Alignment | not modelled | 32.6 | 15 | PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan branching enzyme glgb; PDBTitle: crystal structure of branching enzyme from cyanothecce sp. atcc 51142 |
| 96 | c3vniC | Alignment | not modelled | 31.9 | 13 | PDB header: isomerase Chain: C: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars |
| 97 | c1ydoC | Alignment | not modelled | 31.8 | 14 | PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181. |
| 98 | d1hl2a | Alignment | not modelled | 31.7 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 99 | d1oyaa | Alignment | not modelled | 31.2 | 19 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 100 | c5zfsA | Alignment | not modelled | 30.4 | 16 | PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose |
| 101 | c4rtbA | Alignment | not modelled | 30.4 | 11 | PDB header: lyase Chain: A: PDB Molecule: hydG protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydG from <i>2 carboxydotherrmus hydrogenoformans</i> |
| 102 | d1jdfa1 | Alignment | not modelled | 30.3 | 9 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 103 | c4wvc | Alignment | not modelled | 30.0 | 16 | PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 103 | c4wca_ | Alignment | not modelled | 30.0 | 10 | PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase PDB header: oxidoreductase |
| 104 | c4a3uB_ | Alignment | not modelled | 29.9 | 19 | Chain: B; PDB Molecule: nadh\;flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr) |
| 105 | d1e2ka_ | Alignment | not modelled | 28.5 | 12 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 106 | c2gg8A_ | Alignment | not modelled | 28.4 | 23 | PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone |
| 107 | c3s5oA_ | Alignment | not modelled | 28.0 | 10 | PDB header: lyase Chain: A; PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate |
| 108 | d1uoka2 | Alignment | not modelled | 28.0 | 11 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain |
| 109 | c2oztA_ | Alignment | not modelled | 28.0 | 18 | PDB header: lyase Chain: A; PDB Molecule: tlr1174 protein; PDBTitle: crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1 |
| 110 | c2x7vA_ | Alignment | not modelled | 27.9 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc |
| 111 | c3b4uB_ | Alignment | not modelled | 27.7 | 17 | PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58 |
| 112 | c3bh1A_ | Alignment | not modelled | 27.7 | 45 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0371 protein dip2346; PDBTitle: crystal structure of protein dip2346 from corynebacterium diphtheriae |
| 113 | d1vyra_ | Alignment | not modelled | 27.2 | 19 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 114 | c4tmcB_ | Alignment | not modelled | 27.2 | 15 | PDB header: flavoprotein Chain: B; PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde |
| 115 | c5tchG_ | Alignment | not modelled | 27.0 | 23 | PDB header: lyase Chain: G; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant |
| 116 | c5uurA_ | Alignment | not modelled | 26.4 | 18 | PDB header: transferase Chain: A; PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid |
| 117 | c1ydnA_ | Alignment | not modelled | 26.2 | 9 | PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35. |
| 118 | c1bf2A_ | Alignment | not modelled | 26.0 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase |
| 119 | c3dcpB_ | Alignment | not modelled | 25.5 | 16 | PDB header: hydrolase Chain: B; PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141. |
| 120 | d1m53a2 | Alignment | not modelled | 25.4 | 14 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain |