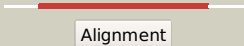

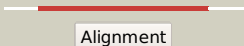

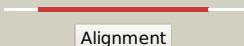







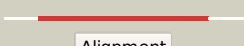











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0940c_(-)_1050597_1051463
Date	Fri Jul 26 01:50:53 BST 2019
Unique Job ID	d272b3ba188f9f58

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b81D_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
2	d1luca_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
3	d1tvla_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
4	c1tvIA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
5	c3raoB_	 Alignment		100.0	29	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.
6	c1z69D_	 Alignment		100.0	21	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
7	c3sdoB_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
8	d1ezwa_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
9	c5tlcA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
10	d1lucb_	 Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
11	c2wgkA_	 Alignment		100.0	22	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

12	c3c8nB_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
13	c5wanA_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
14	c6friD_	Alignment		100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
15	d1nqka_	Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
16	d1rhca_	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
17	c5w4zA_	Alignment		100.0	21	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
18	c3b9nB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
19	d1f07a_	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
20	c6ak1B_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
21	c2i7qA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
22	c5dqpA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
23	d1nfpa_	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	Alignment	not modelled	97.3	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c3qy6A_	Alignment	not modelled	89.7	18	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
26	c3wqoB_	Alignment	not modelled	82.9	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
27	c2wjeA_	Alignment	not modelled	76.2	9	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
28	d1o5ka_	Alignment	not modelled	68.0	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
29	d1xp3a1	Alignment	not modelled	67.3	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like

						Family: Endonuclease IV
30	c3b0vD	Alignment	not modelled	66.7	25	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with 2 trna
31	c6ej9A	Alignment	not modelled	65.9	14	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
32	c3fkA	Alignment	not modelled	64.7	8	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
33	c3aamA	Alignment	not modelled	63.1	14	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease iv; PDBTitle: crystal structure of endonuclease iv from thermus thermophilus hb8
34	c3d0cB	Alignment	not modelled	62.0	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
35	c3w9zA	Alignment	not modelled	60.1	10	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
36	d2a6na1	Alignment	not modelled	56.9	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
37	c2zvrA	Alignment	not modelled	56.3	20	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from thermotoga maritima
38	c3na8A	Alignment	not modelled	55.7	10	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from pseudomonas aeruginosa
39	c3qfeB	Alignment	not modelled	54.6	9	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family 2 protein from coccidioides immitis
40	d1xxa1	Alignment	not modelled	54.5	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
41	d2fiqa1	Alignment	not modelled	54.4	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
42	c2r8wB	Alignment	not modelled	53.7	19	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from agrobacterium tumefaciens str. c58
43	c3e96B	Alignment	not modelled	53.7	24	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
44	c3fa4D	Alignment	not modelled	51.7	10	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate 2 lyase superfamily member, triclinic crystal form
45	d1xcfa	Alignment	not modelled	50.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
46	c5n2pA	Alignment	not modelled	49.1	7	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfobolus solfataricus tryptophan synthase a
47	c4n4qD	Alignment	not modelled	49.0	13	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
48	c3dcpB	Alignment	not modelled	48.8	13	PDB header: hydrolase Chain: B: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
49	c1ydnA	Alignment	not modelled	47.6	10	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.
50	c3pueA	Alignment	not modelled	46.6	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dihydrodipicolinate synthase from acinetobacter baumannii with lysine at 2.6a resolution
51	c6mqhA	Alignment	not modelled	46.4	15	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
52	c4xkyC	Alignment	not modelled	42.1	15	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
53	d1z41a1	Alignment	not modelled	41.6	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
54	c3daqB	Alignment	not modelled	40.1	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus

55	c5dxxA	Alignment	not modelled	40.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2
56	d1oyaa	Alignment	not modelled	39.9	33	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
57	c2r94B	Alignment	not modelled	39.8	29	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
58	d1vjia	Alignment	not modelled	39.4	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	c2hmcA	Alignment	not modelled	39.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
60	c3kwsB	Alignment	not modelled	39.0	10	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distazonis atcc 8503 at 1.68 a resolution
61	c3cprB	Alignment	not modelled	38.2	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
62	c3b4uB	Alignment	not modelled	37.6	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
63	c3gr7A	Alignment	not modelled	36.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
64	c3eb2A	Alignment	not modelled	36.8	14	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
65	c4gx9A	Alignment	not modelled	36.8	27	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit epsilon,dna polymerase iii PDBTitle: crystal structure of a dna polymerase iii alpha-epsilon chimera
66	c1ydoC	Alignment	not modelled	36.0	20	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.
67	c2yz5B	Alignment	not modelled	35.7	21	PDB header: hydrolase Chain: B: PDB Molecule: histidinol phosphatase; PDBTitle: histidinol phosphate phosphatase complexed with phosphate
68	c4i7vD	Alignment	not modelled	34.4	18	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhdp5 with pyruvate
69	c2nuxB	Alignment	not modelled	34.2	7	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
70	c6arhA	Alignment	not modelled	33.6	14	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: crystal structure of human nal at a resolution of 1.6 angstrom
71	c3noeA	Alignment	not modelled	33.3	8	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
72	c2yb1A	Alignment	not modelled	33.2	21	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
73	d1oy0a	Alignment	not modelled	33.1	29	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
74	d2q02a1	Alignment	not modelled	33.1	7	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
75	c3bi8A	Alignment	not modelled	33.0	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
76	c2ekcA	Alignment	not modelled	32.8	27	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
77	d1q45a	Alignment	not modelled	32.6	29	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	c4jicB	Alignment	not modelled	32.6	32	PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
79	c4uxdC	Alignment	not modelled	32.4	6	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

80	d1gwja_	Alignment	not modelled	32.3	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	c3l5aA_	Alignment	not modelled	32.2	24	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
82	c2ze3A_	Alignment	not modelled	32.1	31	PDB header: isomerase Chain: A; PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
83	d1lcpa_	Alignment	not modelled	31.6	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
84	c3navB_	Alignment	not modelled	31.6	20	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
85	c4lsbA_	Alignment	not modelled	31.1	18	PDB header: lyase Chain: A; PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
86	c2h90A_	Alignment	not modelled	31.0	19	PDB header: oxidoreductase Chain: A; PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
87	c4a3uB_	Alignment	not modelled	30.8	26	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh\flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
88	c4b5nA_	Alignment	not modelled	30.8	22	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sy4)
89	c4df2A_	Alignment	not modelled	30.7	25	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh dehydrogenase; PDBTitle: p. stiptitis oye2.6 complexed with p-chlorophenol
90	c3g0sA_	Alignment	not modelled	30.6	10	PDB header: lyase Chain: A; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
91	d1djqal	Alignment	not modelled	30.4	29	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	c3lyeA_	Alignment	not modelled	30.4	27	PDB header: hydrolase Chain: A; PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
93	c6e1jB_	Alignment	not modelled	29.8	18	PDB header: plant protein Chain: B; PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
94	c4icnB_	Alignment	not modelled	29.7	18	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
95	c2cw6B_	Alignment	not modelled	29.6	11	PDB header: lyase Chain: B; PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
96	c2x7vA_	Alignment	not modelled	29.4	7	PDB header: hydrolase Chain: A; PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
97	c4tmcB_	Alignment	not modelled	29.0	20	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
98	c4qnwA_	Alignment	not modelled	29.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
99	d1f74a_	Alignment	not modelled	28.7	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
100	c3e38A_	Alignment	not modelled	28.7	11	PDB header: hydrolase Chain: A; PDB Molecule: two-domain protein containing predicted php-like metal- PDBTitle: crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bv_u_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
101	d1s2wa_	Alignment	not modelled	28.6	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
102	c4lrc_	Alignment	not modelled	28.5	13	PDB header: lyase/oxidoreductase Chain: C; PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
103	c4rnxA_	Alignment	not modelled	28.4	33	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme PDB header: oxidoreductase

104	c3noyA_	Alignment	not modelled	28.2	18	Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
105	d1aora1	Alignment	not modelled	27.7	11	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
106	d1ujqa_	Alignment	not modelled	27.6	33	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
107	c3ivuB_	Alignment	not modelled	27.4	22	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
108	d1uoua2	Alignment	not modelled	27.2	15	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
109	c2gq8A_	Alignment	not modelled	27.2	22	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
110	d1vyra_	Alignment	not modelled	26.5	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
111	c4ovxA_	Alignment	not modelled	26.3	17	PDB header: isomerase Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
112	c2qiWA_	Alignment	not modelled	26.0	44	PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
113	c3rmjB_	Alignment	not modelled	25.8	29	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
114	d1b25a1	Alignment	not modelled	25.6	11	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
115	c3kruC_	Alignment	not modelled	25.5	33	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
116	d1muma_	Alignment	not modelled	24.8	33	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
117	c3gkaB_	Alignment	not modelled	24.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
118	c1b4nD_	Alignment	not modelled	24.5	11	PDB header: oxidoreductase Chain: D: PDB Molecule: formaldehyde ferredoxin oxidoreductase; PDBTitle: formaldehyde ferredoxin oxidoreductase from pyrococcus furiosus,2 complexed with glutarate
119	d1w3ia_	Alignment	not modelled	24.2	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
120	c3n2xB_	Alignment	not modelled	24.1	15	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