

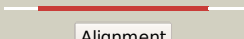

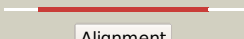



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1718 (-)_1944816_1945634
Date	Fri Aug 2 13:30:32 BST 2019
Unique Job ID	2ede24f73da63e25

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3chvA_	 Alignment		100.0	35	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
2	c2y7eA_	 Alignment		100.0	37	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)
3	c3e49A_	 Alignment		100.0	34	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
4	c3no5C_	 Alignment		100.0	33	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
5	c3lotC_	 Alignment		100.0	34	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
6	c3e02A_	 Alignment		100.0	36	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
7	c3c6cA_	 Alignment		100.0	34	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
8	c5zmyF_	 Alignment		100.0	25	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
9	c4nncA_	 Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate
10	c5ikyA_	 Alignment		100.0	25	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
11	d1m5wa_	 Alignment		97.1	24	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase

12	c2h90A_	Alignment		96.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
13	d1mxsa_	Alignment		96.9	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
14	d1r30a_	Alignment		96.7	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
15	c1r30A_	Alignment		96.7	16	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
16	c3cixA_	Alignment		96.5	18	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
17	d1h1ya_	Alignment		96.4	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
18	c5dlcC_	Alignment		96.4	19	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
19	d1z41a1	Alignment		96.4	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
20	c3kruC_	Alignment		96.4	16	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
21	d1rd5a_	Alignment	not modelled	96.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
22	c4e38A_	Alignment	not modelled	96.2	17	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
23	c1djinB_	Alignment	not modelled	96.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
24	d1wbha1	Alignment	not modelled	96.1	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
25	c1ps9A_	Alignment	not modelled	96.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
26	c3gk0H_	Alignment	not modelled	95.9	26	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
27	c5ocsB_	Alignment	not modelled	95.9	19	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depentdent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
28	c3giaA_	Alignment	not modelled	95.9	14	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase;

28	c3qjaA	Alignment	not modelled	95.9	14	PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
29	d1yxa1	Alignment	not modelled	95.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
30	c6oviA	Alignment	not modelled	95.8	17	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
31	c1tx2A	Alignment	not modelled	95.7	12	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
32	d1tx2a	Alignment	not modelled	95.7	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
33	c5exkG	Alignment	not modelled	95.7	11	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
34	c6bmaA	Alignment	not modelled	95.7	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
35	c3tsmB	Alignment	not modelled	95.6	12	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
36	d1vhca	Alignment	not modelled	95.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
37	c3igsB	Alignment	not modelled	95.4	20	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
38	c3gr7A	Alignment	not modelled	95.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
39	c5zjnB	Alignment	not modelled	95.2	14	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
40	c3q58A	Alignment	not modelled	95.0	18	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
41	c2v82A	Alignment	not modelled	94.8	16	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
42	c2c3zA	Alignment	not modelled	94.8	17	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
43	c3noyA	Alignment	not modelled	94.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
44	c3o6cA	Alignment	not modelled	94.6	19	PDB header: transferase Chain: A: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
45	d1ajza	Alignment	not modelled	94.6	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
46	d1ps9a1	Alignment	not modelled	94.4	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
47	c4jicB	Alignment	not modelled	94.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
48	d1a53a	Alignment	not modelled	94.3	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
49	d1rpxa	Alignment	not modelled	94.2	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
50	c6mywA	Alignment	not modelled	94.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
51	c3k30B	Alignment	not modelled	94.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioes simplex
52	c3labA	Alignment	not modelled	94.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
						PDB header: oxidoreductase

53	c3hf3A	Alignment	not modelled	94.0	17	Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
54	c2yw3E	Alignment	not modelled	93.9	21	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
55	c3t7vA	Alignment	not modelled	93.8	14	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
56	c3w9zA	Alignment	not modelled	93.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
57	c4qnwA	Alignment	not modelled	93.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
58	c3tr9A	Alignment	not modelled	93.5	17	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroiC2 acid from coxiella burnetii
59	d1vc4a	Alignment	not modelled	93.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
60	c4rtbA	Alignment	not modelled	93.2	15	PDB header: lyase Chain: A: PDB Molecule: hydG protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydG from2 carboxydotherrnus hydrogenoformans
61	d2flja1	Alignment	not modelled	92.9	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
62	d1oyaa	Alignment	not modelled	92.8	27	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
63	d1vyra	Alignment	not modelled	92.8	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	c4qccA	Alignment	not modelled	92.6	18	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
65	c3bg3B	Alignment	not modelled	92.4	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
66	d1djqa1	Alignment	not modelled	92.2	11	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	c4rnxA	Alignment	not modelled	91.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme
68	c3k13A	Alignment	not modelled	91.3	12	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
69	c3tdnB	Alignment	not modelled	91.0	11	PDB header: de novo protein Chain: B: PDB Molecule: flr symmetric alpha-beta tim barrel; PDBTitle: computationally designed two-fold symmetric tim-barrel protein, flr
70	d1tqja	Alignment	not modelled	91.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
71	d1vjja	Alignment	not modelled	90.2	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	d1ad1a	Alignment	not modelled	90.2	13	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
73	c4bk9B	Alignment	not modelled	90.0	13	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
74	c2yx0A	Alignment	not modelled	89.9	14	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
75	c5n2pA	Alignment	not modelled	89.9	9	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfobolus solfataricus tryptophan synthase a
76	c2vp8A	Alignment	not modelled	89.7	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
77	c6qkgB	Alignment	not modelled	89.6	11	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
78	c4jn6C	Alignment	not modelled	89.6	11	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37

79	d1j5ta_	Alignment	not modelled	89.6	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
80	d1icpa_	Alignment	not modelled	89.4	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	c5dxxA_	Alignment	not modelled	89.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2
82	c4xp7A_	Alignment	not modelled	89.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
83	c6agzA_	Alignment	not modelled	88.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from pichia sp. aku4542
84	c5visB_	Alignment	not modelled	88.6	13	PDB header: hydrolase,oxidoreductase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: 1.73 angstrom resolution crystal structure of dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
85	c4tmcB_	Alignment	not modelled	88.5	22	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
86	c5umfB_	Alignment	not modelled	88.3	15	PDB header: isomerase Chain: B: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
87	c3gkaB_	Alignment	not modelled	88.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
88	d1gwja_	Alignment	not modelled	88.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
89	c4u0pB_	Alignment	not modelled	87.8	17	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
90	c4cczA_	Alignment	not modelled	87.8	10	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
91	d1xcfa_	Alignment	not modelled	87.6	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
92	c4df2A_	Alignment	not modelled	87.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: p. stiptis oye2.6 complexed with p-chlorophenol
93	c4a3uB_	Alignment	not modelled	86.9	16	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)
94	c3atyA_	Alignment	not modelled	86.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye
95	d2zdra2	Alignment	not modelled	86.6	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
96	c3dz1A_	Alignment	not modelled	86.6	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
97	c1ydnA_	Alignment	not modelled	86.1	12	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.
98	c2gq8A_	Alignment	not modelled	86.1	14	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
99	c5aheA_	Alignment	not modelled	86.1	13	PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa
100	c4mwaA_	Alignment	not modelled	85.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
101	c4b5nA_	Alignment	not modelled	85.3	33	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
102	c3vmmA_	Alignment	not modelled	85.1	23	PDB header: ligase Chain: A: PDB Molecule: alanine-anticapsin ligase bacd; PDBTitle: crystal structure of bacd, an l-amino acid dipeptide ligase from2 bacillus subtilis
103	d1q45a_	Alignment	not modelled	84.7	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
104	c2bdqA_	Alignment	not modelled	84.7	9	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis

						protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
105	c6cluC_	Alignment	not modelled	84.7	14	PDB header: antimicrobial protein Chain: C; PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
106	c2vefB_	Alignment	not modelled	84.6	14	PDB header: transferase Chain: B; PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
107	d1i4na_	Alignment	not modelled	84.6	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
108	d1wa3a1	Alignment	not modelled	84.3	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
109	c4jc0B_	Alignment	not modelled	84.0	16	PDB header: transferase Chain: B; PDB Molecule: ribosomal protein s12 methyltransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
110	c1nvmG_	Alignment	not modelled	83.3	9	PDB header: lyase/oxidoreductase Chain: G; PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
111	c4rmvD_	Alignment	not modelled	83.3	25	PDB header: oxidoreductase/inhibitor Chain: D; PDB Molecule: nadh dehydrogenase 1; PDBTitle: g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde
112	c2pcqA_	Alignment	not modelled	83.0	13	PDB header: lyase Chain: A; PDB Molecule: putative dihydrodipicolinate synthase; PDBTitle: crystal structure of putative dihydrodipicolinate synthase (ttha0737)2 from thermus thermophilus hb8
113	c3si9B_	Alignment	not modelled	82.5	15	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
114	c5epdA_	Alignment	not modelled	82.1	10	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol trinitrate reductase; PDBTitle: crystal structure of glycerol trinitrate reductase xdpb from2 agrobacterium sp. r89-1 (apo form)
115	c6ei9A_	Alignment	not modelled	81.9	18	PDB header: flavoprotein Chain: A; PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
116	c3inpA_	Alignment	not modelled	81.8	13	PDB header: isomerase Chain: A; PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
117	c3bg3A_	Alignment	not modelled	81.5	14	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
118	c2yciX_	Alignment	not modelled	81.5	12	PDB header: transferase Chain: X; PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
119	c6daqA_	Alignment	not modelled	81.4	15	PDB header: lyase Chain: A; PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
120	c3qc3B_	Alignment	not modelled	81.4	14	PDB header: isomerase Chain: B; PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution