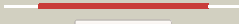



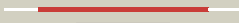





















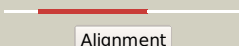

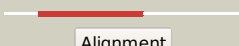

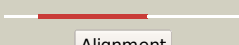

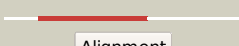

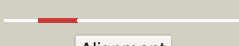
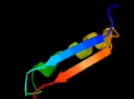














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0323c_(-)_390580_391251
Date	Tue Jul 23 14:50:39 BST 2019
Unique Job ID	ca99bfeffd5efc6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3we7A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph0499; PDBTitle: crystal structure of diacetylchitobiose deacetylase from pyrococcus2 horikoshii
2	c5cgzA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: 4-oxalmesaconate hydratase; PDBTitle: crystal structure of galb, the 4-carboxy-2-hydroxymuconate hydratase,2 from pseudomonas putida kt2440
3	c2ixdB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
4	d1uana_	 Alignment		100.0	26	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
5	c5bmoB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein lnmX; PDBTitle: lnmX protein, a putative glcnaC-pi de-n-acetylase from streptomyces2 atroolivaceus
6	c3dfiA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
7	c3dfmA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
8	c1q7tA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
9	d1q74a_	 Alignment		100.0	27	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
10	d1efva1	 Alignment		96.4	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
11	c1t9gR_	 Alignment		96.1	13	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: electron transfer flavoprotein alpha-subunit, PDBTitle: structure of the human mcd:etf complex

12	c1efvA_	 Alignment		96.1	13	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein; PDBTitle: three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
13	c3ih5A_	 Alignment		95.7	16	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
14	c6fahE_	 Alignment		95.0	19	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
15	c3dzcA_	 Alignment		94.2	14	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
16	c4i2iA_	 Alignment		94.1	18	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
17	c5ol2D_	 Alignment		93.6	21	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
18	d1qrda_	 Alignment		93.4	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
19	c3clrD_	 Alignment		93.2	16	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus
20	d1dxqa_	 Alignment		92.3	24	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
21	c3ot5D_	 Alignment	not modelled	92.2	11	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
22	c1o94D_	 Alignment	not modelled	91.7	12	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
23	c4hwgA_	 Alignment	not modelled	91.6	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
24	d1d4aa_	 Alignment	not modelled	91.4	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
25	c4gi5B_	 Alignment	not modelled	91.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: quinone reductase; PDBTitle: crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
26	d1efpb_	 Alignment	not modelled	91.1	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
27	d3clsd1	 Alignment	not modelled	91.1	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
28	c3beoA_	 Alignment	not modelled	90.1	11	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnac 2-epimerases

29	d3clsc1	Alignment	not modelled	88.5	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
30	d2qwxal	Alignment	not modelled	88.1	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
31	c5ol2E	Alignment	not modelled	87.0	20	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
32	d1efpa1	Alignment	not modelled	83.9	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
33	c4nesA	Alignment	not modelled	80.4	10	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glcnaC 2-2 epimerase in complex with udp-glcnaC and udp
34	c2jimH	Alignment	not modelled	79.9	6	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
35	c2r60A	Alignment	not modelled	79.0	24	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
36	d1o94c	Alignment	not modelled	78.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
37	c3okaA	Alignment	not modelled	78.1	10	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimB' in complex with2 gdp-man (triclinic crystal form)
38	c5dldA	Alignment	not modelled	75.7	13	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcnaC and udp
39	c5enzA	Alignment	not modelled	74.7	11	PDB header: isomerase Chain: A: PDB Molecule: udp-glcnaC 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
40	c3ha2B	Alignment	not modelled	72.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-quinone reductase; PDBTitle: crystal structure of protein (nadh-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
41	d1f0ka	Alignment	not modelled	71.6	20	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
42	c3eywA	Alignment	not modelled	69.7	9	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
43	c5tukC	Alignment	not modelled	68.0	12	PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51)
44	c6fahB	Alignment	not modelled	67.3	17	PDB header: flavoprotein Chain: B: PDB Molecule: caffeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
45	c5lvaA	Alignment	not modelled	66.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(p)h-fmn oxidoreductase; PDBTitle: crystal structure of thermophilic tryptophan halogenase (th-hal)2 enzyme from streptomycin violaceusniger.
46	d1efvb	Alignment	not modelled	66.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
47	c1efpC	Alignment	not modelled	66.5	14	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
48	c3f2vA	Alignment	not modelled	66.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 14; PDBTitle: crystal structure of the general stress protein 14 (tde0354) in2 complex with fmn from treponema denticola, northeast structural3 genomics consortium target tdr58.
49	c5w8sA	Alignment	not modelled	65.9	14	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
50	d1v4va	Alignment	not modelled	65.2	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
51	d1xlma	Alignment	not modelled	63.9	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
52	d1fpza	Alignment	not modelled	58.1	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
53	c5ahkB	Alignment	not modelled	56.1	9	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetoxyhydroxy acid synthase pf5 from2

						pseudomonas protegens
54	d1f6da	Alignment	not modelled	53.4	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
55	c4kpuB	Alignment	not modelled	52.6	15	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
56	d2d1pb1	Alignment	not modelled	52.6	13	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
57	c1ltxR	Alignment	not modelled	51.4	21	PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
58	d2iida1	Alignment	not modelled	50.2	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
59	d1seza1	Alignment	not modelled	50.0	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
60	c3khtA	Alignment	not modelled	48.9	20	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
61	c2jb1B	Alignment	not modelled	48.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: l-amino acid oxidase; PDBTitle: the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
62	c1sezA	Alignment	not modelled	48.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase
63	c4p5pA	Alignment	not modelled	46.7	17	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi family protein; PDBTitle: x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
64	c1f8sA	Alignment	not modelled	46.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
65	c5xvsA	Alignment	not modelled	45.2	10	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetyl bacillosamine 2-epimerase PDBTitle: crystal structure of udp-glcna2 2-epimerase neuc complexed with udp
66	c1fpzF	Alignment	not modelled	44.1	17	PDB header: hydrolase Chain: F: PDB Molecule: cyclin-dependent kinase inhibitor 3; PDBTitle: crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
67	d1bxca	Alignment	not modelled	43.7	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
68	d1muwa	Alignment	not modelled	42.5	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
69	c4dgaA	Alignment	not modelled	41.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crt1 from pantoea ananatis
70	d1u9ca	Alignment	not modelled	41.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
71	d1a9xa4	Alignment	not modelled	40.8	9	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
72	c3kkIA	Alignment	not modelled	40.3	10	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
73	c3eooL	Alignment	not modelled	40.0	19	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
74	d1dkua1	Alignment	not modelled	38.6	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
75	c2gejA	Alignment	not modelled	38.4	12	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
76	d1bxba	Alignment	not modelled	38.1	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
77	c2vouA	Alignment	not modelled	37.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
						PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin

78	c5zesA	Alignment	not modelled	37.2	20	glucosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from 2 synechococcus species pcc 7942 - udp complex
79	c3rpeA	Alignment	not modelled	36.9	13	PDB header: oxidoreductase Chain: A; PDB Molecule: modulator of drug activity b; PDBTitle: 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
80	c5tulA	Alignment	not modelled	36.7	13	PDB header: oxidoreductase Chain: A; PDB Molecule: tetracycline destructase tet(55); PDBTitle: crystal structure of tetracycline destructase tet(55)
81	c5ji5A	Alignment	not modelled	36.2	8	PDB header: hydrolase Chain: A; PDB Molecule: bupha.10154.a.b1; PDBTitle: crystal structure of a histone deacetylase superfamily protein from 2 burkholderia phymatum phymatum
82	c5zmpA	Alignment	not modelled	35.9	11	PDB header: hydrolase Chain: A; PDB Molecule: lysine deacetylase; PDBTitle: the structure of a lysine deacetylase
83	d1c3pa	Alignment	not modelled	35.7	10	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
84	c3s2uA	Alignment	not modelled	35.4	22	PDB header: transferase Chain: A; PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
85	d2qlka1	Alignment	not modelled	34.8	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
86	c4repA	Alignment	not modelled	34.7	18	PDB header: oxidoreductase, flavoprotein Chain: A; PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
87	c5w4cA	Alignment	not modelled	34.6	12	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
88	d2hy5b1	Alignment	not modelled	34.1	11	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
89	c4j33B	Alignment	not modelled	33.9	25	PDB header: oxidoreductase Chain: B; PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of kynurenine 3-monooxygenase (kmo-394)
90	d1vb3a1	Alignment	not modelled	33.6	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
91	c4bz7A	Alignment	not modelled	33.4	10	PDB header: hydrolase Chain: A; PDB Molecule: histone deacetylase 8; PDBTitle: crystal structure of schistosoma mansoni hdac8 complexed with m344
92	c3ia7A	Alignment	not modelled	33.1	8	PDB header: transferase Chain: A; PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
93	c5fn0C	Alignment	not modelled	32.3	25	PDB header: oxidoreductase Chain: C; PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of pseudomonas fluorescens kynurenine-3-2 monooxygenase (kmo) in complex with gsk180
94	d2afwa1	Alignment	not modelled	31.9	29	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent cytopeptidases Family: Glutaminyl-peptide cyclotransferase-like
95	c4a69A	Alignment	not modelled	31.7	8	PDB header: transcription Chain: A; PDB Molecule: histone deacetylase 3;; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate
96	d1t64a	Alignment	not modelled	31.4	8	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
97	c5li3A	Alignment	not modelled	31.2	14	PDB header: signaling protein Chain: A; PDB Molecule: acetoin utilization protein; PDBTitle: crystal structure of hdac-like protein from p. aeruginosa in complex2 with a photo-switchable inhibitor.
98	c2bi8A	Alignment	not modelled	30.6	18	PDB header: isomerase Chain: A; PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
99	c3maxB	Alignment	not modelled	30.5	8	PDB header: hydrolase Chain: B; PDB Molecule: histone deacetylase 2; PDBTitle: crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
100	c2c4kD	Alignment	not modelled	30.1	6	PDB header: regulatory protein Chain: D; PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
101	c3ew8A	Alignment	not modelled	29.9	8	PDB header: hydrolase Chain: A; PDB Molecule: histone deacetylase 8; PDBTitle: crystal structure analysis of human hdac8 d101l variant
102	d2c4ka1	Alignment	not modelled	29.8	9	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
103	c5du2B	Alignment	not modelled	29.8	12	PDB header: transferase Chain: B; PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase

104	c5eowA_	Alignment	not modelled	28.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monoxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monoxygenase from2 pseudomonas putida kt2440
105	c3p2oA_	Alignment	not modelled	28.4	14	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
106	d7reqb2	Alignment	not modelled	27.3	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
107	c2f46A_	Alignment	not modelled	27.1	10	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
108	c2cmgA_	Alignment	not modelled	27.0	23	PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of spermidine synthase from helicobacter2 pylori
109	c4xkmB_	Alignment	not modelled	26.9	13	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of xylose isomerase from an human intestinal tract2 microbe bacteroides thetaiotaomicron
110	c6aioA_	Alignment	not modelled	26.7	23	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monoxygenase pnpa from2 pseudomonas putida dll-e4
111	c5brjA_	Alignment	not modelled	26.6	18	PDB header: signaling protein Chain: A: PDB Molecule: two component response regulator; PDBTitle: structure of the bacteriophytochrome response regulator atbr
112	c3c4vB_	Alignment	not modelled	25.7	15	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
113	d3c10a1	Alignment	not modelled	25.6	16	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
114	c2c2xB_	Alignment	not modelled	25.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
115	c3p2oB_	Alignment	not modelled	25.3	14	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
116	c3qi7A_	Alignment	not modelled	25.1	8	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
117	c1zz0C_	Alignment	not modelled	25.0	18	PDB header: hydrolase Chain: C: PDB Molecule: histone deacetylase-like amidohydrolase; PDBTitle: crystal structure of a hdac-like protein with acetate bound
118	d1p5fa_	Alignment	not modelled	24.8	3	Fold: Flavodoxin-like Superfamily: Class 1 glutamine amidotransferase-like Family: DJ-1/Pfpl
119	c5eefA_	Alignment	not modelled	24.7	13	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: hdac6; PDBTitle: crystal structure of danio rerio histone deacetylase 6 catalytic2 domain 1 in complex with trichostatin a
120	c4fzrA_	Alignment	not modelled	24.0	11	PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase