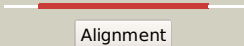

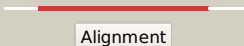

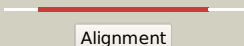







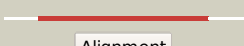




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3409c_choD_3827171_3828907
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	8580746c6ec1c199

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5hsaG_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: G: PDB Molecule: alcohol oxidase 1; PDBTitle: alcohol oxidase aox1 from pichia pastoris
2	c6h3gC_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol oxidase; PDBTitle: alcohol oxidase from phanerochaete chrysosporium
3	c4yntA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose oxidase, putative; PDBTitle: crystal structure of aspergillus flavus fad glucose dehydrogenase
4	c1cf3A_	 Alignment		100.0	15	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from aspergillus niger
5	c1gpeA_	 Alignment		100.0	13	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense
6	c3fimB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
7	c3q9tB_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase
8	c4qi7A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdh
9	c4h7uA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose dehydrogenase; PDBTitle: crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype
10	c5nccB_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and 2 palmitic acid
11	c4qi6A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcum thermophilum, mtc dh

12	c4qi4A_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcus thermophilum cellobiose2 dehydrogenase, mtdh
13	c1naaB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B; PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
14	c6a2uD_	Alignment		100.0	19	PDB header: signaling protein/oxidoreductase Chain: D; PDB Molecule: glucose dehydrogenase; PDBTitle: crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
15	c2jbvA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into the2 catalytic mechanism
16	c3t37A_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of pyridoxine 4-oxidase from mesorhizobium loti
17	c4udpA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: glucose-methanol-choline oxidoreductase; PDBTitle: crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
18	c1ju2A_	Alignment		100.0	16	PDB header: lyase Chain: A; PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
19	c1coyA_	Alignment		100.0	21	PDB header: oxidoreductase(oxygen receptor) Chain: A; PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase complexed with a steroid2 substrate. implications for fad dependent alcohol oxidases
20	c2gewA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
21	c4z24A_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702)
22	c4migC_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: C; PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
23	c2igoG_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: G; PDB Molecule: pyranose oxidase; PDBTitle: crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose
24	c2f5vA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: pyranose 2-oxidase; PDBTitle: reaction geometry and thermostability mutant of pyranose 2-oxidase2 from the white-rot fungus peniophora sp.
25	d1cf3a1	Alignment	not modelled	100.0	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
26	d1kdga1	Alignment	not modelled	100.0	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
27	d1gpea1	Alignment	not modelled	100.0	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
28	d1n4wa1	Alignment	not modelled	100.0	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
						Fold: FAD/NAD(P)-binding domain

29	d3coxa1	Alignment	not modelled	100.0	30	Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
30	d2f5va1	Alignment	not modelled	100.0	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
31	d1ju2a1	Alignment	not modelled	100.0	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
32	c4repA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
33	c5glgA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase 2; PDBTitle: the novel function of osm1 under anaerobic condition in the er was2 revealed by crystal structure of osm1, a soluble fumarate reductase3 in yeast
34	c4at2A	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketosteroid-delta4-5alpha-dehydrogenase; PDBTitle: the crystal structure of 3-ketosteroid-delta4-(5alpha)-2 dehydrogenase from rhodococcus jostii rha1 in complex3 with 4-androstene-3,17- dione
35	d2bcgg1	Alignment	not modelled	99.6	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
36	d1d5ta1	Alignment	not modelled	99.6	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
37	c1yq4A	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
38	c3vr8E	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquoinol-fumarate reductase from the parasitic2 nematode ascaris suum
39	c1qo8A	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
40	c1jrxA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
41	c1d4cB	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the flavocytochrome c2 fumarate reductase of shewanella putrefaciens strain mr-1
42	c2aczA	Alignment	not modelled	99.5	14	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
43	c4c3yF	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-ketosteroid dehydrogenase; PDBTitle: crystal structure of 3-ketosteroid delta1-dehydrogenase from2 rhodococcus erythropolis sq1 in complex with 1,4-androstadiene-3,17-3 dione
44	d1y0pa2	Alignment	not modelled	99.5	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
45	c5xmjE	Alignment	not modelled	99.5	14	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
46	c1gndA	Alignment	not modelled	99.5	12	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
47	c2rghA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
48	c6c87A	Alignment	not modelled	99.5	14	PDB header: protein transport Chain: A: PDB Molecule: rab gdp dissociation inhibitor alpha; PDBTitle: crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri
49	d1ryia1	Alignment	not modelled	99.5	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
50	c3p4rM	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
51	d2gf3a1	Alignment	not modelled	99.5	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
52	c2bs3A	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolfinella succinogenes
53	d1qo8a2	Alignment	not modelled	99.5	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

53	d1q00z	Alignment	not modelled	99.3	10	Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain PDB header: oxidoreductase
54	c3axbA	Alignment	not modelled	99.4	20	Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix
55	c1kf6A	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
56	c2rgoA	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
57	c2r4jA	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted glycerol-3-2 phosphate dehydrogenase in complex with dhap
58	c3dmeB	Alignment	not modelled	99.4	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from bordetella2 pertussis. northeast structural genomics target ber141
59	d1kf6a2	Alignment	not modelled	99.4	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
60	d2bs2a2	Alignment	not modelled	99.4	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
61	d1d4ca2	Alignment	not modelled	99.4	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
62	c3cpiH	Alignment	not modelled	99.4	12	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
63	c4p9sA	Alignment	not modelled	99.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
64	c1ltxR	Alignment	not modelled	99.4	11	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
65	c6n56A	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavo protein subunit; PDBTitle: crystal structure of fumarate reductase, flavo protein subunit, from2 helicobacter pylori g27
66	d1pj5a2	Alignment	not modelled	99.4	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
67	c5hxwF	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
68	d2gqfa1	Alignment	not modelled	99.4	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
69	d1neka2	Alignment	not modelled	99.4	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
70	c3da1A	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
71	c3cirM	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
72	c3dqzA	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
73	c1zkqA	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
74	c5mogB	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
75	c1pj6A	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
76	c4x9mA	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
77	c2c3dB	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxopropyl-com reductase; PDBTitle: 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
78	c5fjnB	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: B: PDB Molecule: l-amino acid deaminase; PDBTitle: structure of l-amino acid deaminase from proteus

					myxofaciens2 in complex with anthranilate
79	d2i0za1	Alignment	not modelled	99.3	19 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
80	d1vg0a1	Alignment	not modelled	99.3	11 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
81	c2nvkX	Alignment	not modelled	99.3	16 PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
82	c6gg2A	Alignment	not modelled	99.3	14 PDB header: oxidoreductase Chain: A: PDB Molecule: amino acid oxidase fmpa; PDBTitle: the structure of fsqb from aspergillus fumigatus, a flavoenzyme of the2 amine oxidase family
83	c2fjaC	Alignment	not modelled	99.3	14 PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
84	c4cnjD	Alignment	not modelled	99.3	18 PDB header: oxidoreductase Chain: D: PDB Molecule: l-amino acid oxidase; PDBTitle: l-aminoacetone oxidase from streptococcus oligofermentans2 belongs to a new 3-domain family of bacterial flavoproteins
85	c2gqfA	Alignment	not modelled	99.2	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
86	c4ap3A	Alignment	not modelled	99.2	31 PDB header: oxidoreductase Chain: A: PDB Molecule: steroid monooxygenase; PDBTitle: oxidized steroid monooxygenase bound to nadp
87	c2zxiC	Alignment	not modelled	99.2	19 PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
88	c4xwzA	Alignment	not modelled	99.2	19 PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
89	c4dgaA	Alignment	not modelled	99.2	16 PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis
90	d1w4xa1	Alignment	not modelled	99.2	32 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
91	c1zmcG	Alignment	not modelled	99.2	24 PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
92	c2hqmB	Alignment	not modelled	99.2	18 PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
93	c3g05B	Alignment	not modelled	99.2	19 PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
94	c2gahB	Alignment	not modelled	99.2	20 PDB header: oxidoreductase Chain: B: PDB Molecule: heterotetrameric sarcosine oxidase beta-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
95	c1v59B	Alignment	not modelled	99.2	13 PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
96	d1chua2	Alignment	not modelled	99.2	28 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
97	c2olnA	Alignment	not modelled	99.2	21 PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
98	c3gyxA	Alignment	not modelled	99.2	14 PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
99	c5mq6A	Alignment	not modelled	99.2	25 PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase-like protein; PDBTitle: polycyclic ketone monooxygenase from the thermophilic fungus2 thermothelomyces thermophila
100	c2a8xA	Alignment	not modelled	99.2	16 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
101	c6jdkA	Alignment	not modelled	99.2	25 PDB header: oxidoreductase Chain: A: PDB Molecule: baeyer-villiger monooxygenase; PDBTitle: crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
102	c3djeA	Alignment	not modelled	99.2	15 PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine: oxygen oxidoreductase; PDBTitle: crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
					PDB header: oxidoreductase

103	c3urhB_	Alignment	not modelled	99.2	18	Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from <i>Sinorhizobium meliloti</i> 1021
104	c3ka7A_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from <i>Methanosarcina mazei</i> . northeast structural genomics consortium target id3 mar208
105	c2eq8E_	Alignment	not modelled	99.2	26	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from <i>Thermus thermophilus</i> 2 hb8 with psbdp
106	c3jskN_	Alignment	not modelled	99.2	27	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from <i>Neurospora crassa</i>
107	c5ttkB_	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from <i>Pseudomonas putida</i>
108	c1hyuA_	Alignment	not modelled	99.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
109	d2gmha1	Alignment	not modelled	99.1	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
110	c1bwcA_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
111	c3cesB_	Alignment	not modelled	99.1	20	PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of e.coli mmng (gida), a highly-conserved trna2 modifying enzyme
112	c3v76A_	Alignment	not modelled	99.1	24	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from <i>Sinorhizobium meliloti</i>
113	c2cfyB_	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
114	c3bhkA_	Alignment	not modelled	99.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: monomeric sarcosine oxidase; PDBTitle: crystal structure of r49k mutant of monomeric sarcosine oxidase2 crystallized in phosphate as precipitant
115	c5w4cA_	Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from <i>Cryptococcus neoformans</i> in complex with fad (fo conformation)
116	c1y56B_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from <i>P. horikoshii</i>
117	c3nlcA_	Alignment	not modelled	99.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956; PDBTitle: crystal structure of the vp0956 protein from <i>Vibrio parahaemolyticus</i> .2 northeast structural genomics consortium target vpr147
118	d1jnra2	Alignment	not modelled	99.1	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
119	c1onfA_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of <i>Plasmodium falciparum</i> glutathione reductase
120	c1chuA_	Alignment	not modelled	99.1	29	PDB header: flavoenzyme Chain: A: PDB Molecule: protein (l-aspartate oxidase); PDBTitle: structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family