Phyre2

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Description	RVBD0449c_(-)_537232_538551
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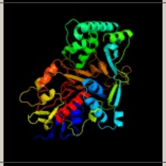
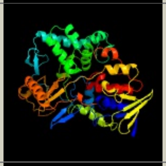
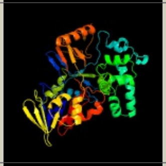
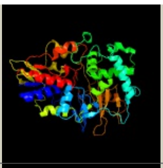
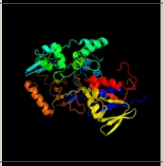
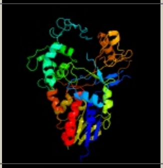
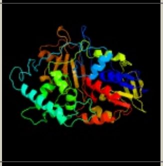
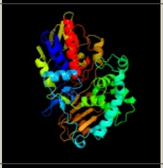
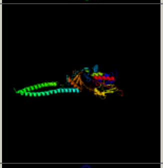
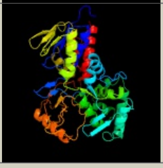
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fjhB_	Alignment		100.0	26	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**lkce; **PDBTitle:** crystal structure of the seleniated lkce from streptomyces rochei
2	c4gutA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1b; **PDBTitle:** crystal structure of lsd2-npac
3	c1s3bB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase [flavin-containing] b; **PDBTitle:** crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
4	c2ivdA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
5	c5ttkB_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase; **PDBTitle:** crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida
6	c3uteB_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
7	c2yg4B_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
8	c3k7tB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-hydroxy-l-nicotine oxidase; **PDBTitle:** crystal structure of apo-form 6-hydroxy-l-nicotine oxidase, crystal2 form p3121
9	c4dshB_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of reduced udp-galactopyranose mutase
10	c1f8sA_	Alignment		100.0	17	**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.
11	c3nksA_	Alignment		100.0	20	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of human protoporphyrinogen ix oxidase

12	c2vvlD_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**monoamine oxidase n; **PDBTitle:** the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
13	c4iv9B_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**tryptophan 2-monooxygenase; **PDBTitle:** structure of the flavoprotein tryptophan-2-monooxygenase
14	c3x0vA_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lysine oxidase; **PDBTitle:** structure of l-lysine oxidase
15	c3rhaA_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
16	c2b9yA_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
17	c6cr0A_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**(s)-6-hydroxynicotine oxidase; **PDBTitle:** 1.55 a resolution structure of (s)-6-hydroxynicotine oxidase from2 shinella hzn7
18	c5mbxA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal n(1)-acetyl-spermine/spermidine oxidase; **PDBTitle:** crystal structure of reduced murine n1-acetylpolyamine oxidase in2 complex with n1-acetylspermine
19	c2v1dA_	Alignment		100.0	15	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
20	c5mogB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phytoene dehydrogenase, chloroplastic/chromoplastic; **PDBTitle:** oryza sativa phytoene desaturase inhibited by norflurazon
21	c2xagA_	Alignment	not modelled	100.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
22	c3we0A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase/monooxygenase; **PDBTitle:** l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
23	c2hkoA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
24	c3i6dA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of ppo from bacillus subtilis with af
25	c4i58A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexylamine oxidase; **PDBTitle:** cyclohexylamine oxidase from brevibacterium oxydans ih-35a
26	c3lovA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
27	c2jb1B_	Alignment	not modelled	100.0	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
28	c1h83A_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase; **PDBTitle:** structure of polyamine oxidase in complex with2 1,8-diaminooctane

29	c1sezA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase, mitochondrial; **PDBTitle:** crystal structure of protoporphyrinogen ix oxidase
30	c1i8tB_	Alignment	not modelled	100.0	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
31	d1o5wa1	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
32	c3bnuA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase fms1; **PDBTitle:** crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
33	c5g3sB_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-tryptophan oxidase vioa; **PDBTitle:** the structure of the l-tryptophan oxidase vioa from chromobacterium2 violaceum - samarium derivative
34	c3ka7A_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
35	c4mo2A_	Alignment	not modelled	100.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of udp-n-acetylgalactopyranose mutase from2 campylobacter jejuni
36	c2bi8A_	Alignment	not modelled	100.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
37	d2v5za1	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
38	c4repA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase, flavoprotein **Chain:** A: **PDB Molecule:**gamma-carotene desaturase; **PDBTitle:** crystal structure of gamma-carotenoid desaturase
39	c3hdqI_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
40	c1v0jB_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from mycobacterium tuberculosis
41	c1ltxR_	Alignment	not modelled	100.0	14	**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
42	c2yr6A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pro-enzyme of l-phenylalanine oxidase; **PDBTitle:** crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501
43	d2dw4a2	Alignment	not modelled	100.0	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
44	d2iida1	Alignment	not modelled	100.0	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
45	d1b5qa1	Alignment	not modelled	100.0	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
46	d1reoa1	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
47	c4dgkA_	Alignment	not modelled	99.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phytoene dehydrogenase; **PDBTitle:** crystal structure of phytoene desaturase crti from pantoea ananatis
48	c6c87A_	Alignment	not modelled	99.9	11	**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	c3nrnA_	Alignment	not modelled	99.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf1083; **PDBTitle:** crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
50	c3cpiH_	Alignment	not modelled	99.9	9	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**rab gdp-dissociation inhibitor; **PDBTitle:** crystal structure of yeast rab-gdi
51	d2ivda1	Alignment	not modelled	99.9	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
52	d1d5ta1	Alignment	not modelled	99.9	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
53	c1gndA_	Alignment	not modelled	99.9	11	**PDB header:**gtpase activation **Chain:** A: **PDB Molecule:**guanine nucleotide dissociation inhibitor; **PDBTitle:** guanine nucleotide dissociation inhibitor, alpha-isoform
54	c3p1wA_	Alignment	not modelled	99.9	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**rabgdi protein; **PDBTitle:** crystal structure of rab gdi from plasmodium falciparum, pfl2060c
						PDB header:oxidoreductase

55	c2e1mA_	Alignment	not modelled	99.9	17	**Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
56	c3qj4A_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
57	d2bcgg1	Alignment	not modelled	99.9	9	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
58	d1i8ta1	Alignment	not modelled	99.9	16	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
59	d1vg0a1	Alignment	not modelled	99.8	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
60	d1seza1	Alignment	not modelled	99.8	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
61	d2bi7a1	Alignment	not modelled	99.8	15	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
62	c1yvvB_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase, flavin-containing; **PDBTitle:** x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
63	c4ia6B_	Alignment	not modelled	99.8	16	**PDB header:**immune system **Chain:** B: **PDB Molecule:**myosin-crossreactive antigen; **PDBTitle:** hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah)
64	c3nlcA_	Alignment	not modelled	99.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vp0956; **PDBTitle:** crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
65	c4rslA_	Alignment	not modelled	99.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl peptide oxidase; **PDBTitle:** structure of fructosyl peptide oxidase from e. terrenum
66	c3ps9A_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
67	c3k30B_	Alignment	not modelled	99.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
68	c6de6B_	Alignment	not modelled	99.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9
69	c6qkgB_	Alignment	not modelled	99.7	19	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**ncr a; **PDBTitle:** 2-naphthoyl-coa reductase(ncr)
70	c4xwzA_	Alignment	not modelled	99.6	12	**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
71	c4x9mA_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-alpha-glycerophosphate oxidase; **PDBTitle:** oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
72	c1pj6A_	Alignment	not modelled	99.6	11	**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
73	c3pvcA_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
74	c3djeA_	Alignment	not modelled	99.6	14	**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
75	c5fjnB_	Alignment	not modelled	99.6	17	**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
76	c4p9sA_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethylglycine dehydrogenase; **PDBTitle:** crystal structure of the mature form of rat dmgdh
77	c3dmeB_	Alignment	not modelled	99.6	15	**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
78	c5hxwF_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**l-amino acid deaminase; **PDBTitle:** l-amino acid deaminase from proteus vulgaris
79	c1ps9A_	Alignment	not modelled	99.6	12	**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
80	c2cduB_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase

						from2 lactobacillus sanfranciscensis
81	c6du7C_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutathione reductase; **PDBTitle:** glutathione reductase from streptococcus pneumoniae
82	c2gahB_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**heterotetrameric sarcosine oxidase beta-subunit; **PDBTitle:** heterotetrameric sarcosine: structure of a diflavin2 metaloenzyme at 1.85 a resolution
83	c2olnA_	Alignment	not modelled	99.5	17	**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
84	c2eq7B_	Alignment	not modelled	99.5	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
85	c6gg2A_	Alignment	not modelled	99.5	16	**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
86	c3urhB_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
87	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
88	c3axbA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix
89	c3bhkA_	Alignment	not modelled	99.5	14	**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
90	c3cp8C_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
91	c3i3lA_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
92	c3o0hA_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase from bartonella henselae
93	c1xdiA_	Alignment	not modelled	99.4	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
94	c6j39A_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase/inhibitor **Chain:** A: **PDB Molecule:**fad-dependent glycine oxydase; **PDBTitle:** crystal structure of cmis2 with inhibitor
95	c3cp2A_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from e. coli
96	c2bcpA_	Alignment	not modelled	99.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidase; **PDBTitle:** structural analysis of streptococcus pyogenes nadh oxidase: c44s nox2 with azide
97	c3nyeA_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
98	c4yshA_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine oxidase; **PDBTitle:** crystal structure of glycine oxidase from geobacillus kaustophilus
99	c4j56A_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2; **PDBTitle:** structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
100	c4b1bB_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom
101	c1y56B_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sarcosine oxidase; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
102	d1pj5a2	Alignment	not modelled	99.4	10	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
103	c1geuA_	Alignment	not modelled	99.4	12	**PDB header:**oxidoreductase(flavoenzyme) **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** anatomy of an engineered nad-binding site
104	d1w4xa1	Alignment	not modelled	99.4	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
105	c3cesB_	Alignment	not modelled	99.4	18	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
						Fold:FAD/NAD(P)-binding domain

106	d1ryia1	Alignment	not modelled	99.3	20	**Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
107	c1m6iA_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programmed cell death protein 8; **PDBTitle:** crystal structure of apoptosis inducing factor (aif)
108	c3g05B_	Alignment	not modelled	99.3	22	**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
109	c1tytA_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase, oxidized form; **PDBTitle:** crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
110	c6jdkA_	Alignment	not modelled	99.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**baeyer-villiger monooxygenase; **PDBTitle:** crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
111	c5v36A_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase,oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** 1.88 angstrom resolution crystal structure of glutathione reductase2 from streptococcus mutans ua159 in complex with fad
112	c4ap3A_	Alignment	not modelled	99.3	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**steroid monooxygenase; **PDBTitle:** oxidized steroid monooxygenase bound to nadp
113	c2v3aA_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin reductase; **PDBTitle:** crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
114	d2voua1	Alignment	not modelled	99.3	31	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
115	c1nhqA_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase (h2o2(a)) **Chain:** A: **PDB Molecule:**nadh peroxidase; **PDBTitle:** crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
116	d2gqfa1	Alignment	not modelled	99.3	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
117	c5xgvB_	Alignment	not modelled	99.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyre3; **PDBTitle:** the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
118	c2w0hA_	Alignment	not modelled	99.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase; **PDBTitle:** x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
119	c2qa2A_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyketide oxygenase cabe; **PDBTitle:** crystal structure of cabe, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
120	c2eq8E_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp