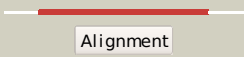

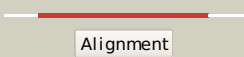

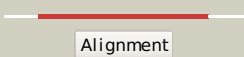

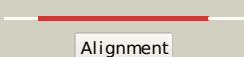

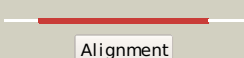

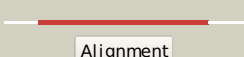

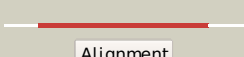

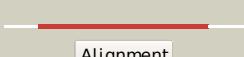

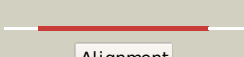

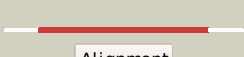














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qa2A_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase cab; PDBTitle: crystal structure of cab, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
2	c3i3lA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
3	c3fmwC_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: oxygenase; PDBTitle: the crystal structure of mtmoiv, a baeyer-villiger2 monooxygenase from the mithramycin biosynthetic pathway in3 streptomyces argillaceus.
4	c2dkhA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
5	c3e1tA_	 Alignment		100.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: halogenase; PDBTitle: structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
6	c1phhA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: p-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
7	c3nixF_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
8	c3atrA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
9	c1pn0A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
10	c3ihgA_	 Alignment		100.0	14	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
11	c3allA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a

12	c2r0gB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
13	c3gmbB_	Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic2 acid oxygenase
14	c3cgvA_	Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: geranylgeranyl reductase related protein; PDBTitle: crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
15	c2rgjA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
16	c2x3nA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-dependent monooxygenase; PDBTitle: crystal structure of pqsl, a probable fad-dependent2 monooxygenase from pseudomonas aeruginosa
17	c3c4aA_	Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: probable tryptophan hydroxylase viod; PDBTitle: crystal structure of viod hydroxylase in complex with fad2 from chromobacterium violaceum. northeast structural3 genomics consortium target cvr158
18	c2xdoC_	Alignment		100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
19	c2pyxA_	Alignment		100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase; PDBTitle: crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
20	c2ardA_	Alignment		100.0	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase prna; PDBTitle: the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
21	c2e4gB_	Alignment	not modelled	100.0	15	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
22	c2gmhA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
23	c2weuD_	Alignment	not modelled	100.0	12	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
24	c2vouA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorus
25	d1k0ia1	Alignment	not modelled	100.0	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
26	d2gmha1	Alignment	not modelled	100.0	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
27	c2bryA_	Alignment	not modelled	100.0	12	PDB header: transport Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
28	d3c96a1	Alignment	not modelled	100.0	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain

29	c3ihmB_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
30	d1pn0a1	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
31	d2voua1	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	c3nrnA_	Alignment	not modelled	99.9	10	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
33	c3dmeB_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
34	c3da1A_	Alignment	not modelled	99.8	11	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.
35	c2oInA_	Alignment	not modelled	99.8	11	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
36	c1yvvB_	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
37	c3bhkA_	Alignment	not modelled	99.7	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
38	c2r4iA_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
39	c1y56B_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
40	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
41	d2gqfa1	Alignment	not modelled	99.7	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
42	c1pj6A_	Alignment	not modelled	99.7	14	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
43	c2gahB_	Alignment	not modelled	99.7	14	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
44	c3pvcA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmC from yersinia pestis
45	c3djeA_	Alignment	not modelled	99.7	12	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
46	c3nyeA_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
47	c1ltxR_	Alignment	not modelled	99.6	19	PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
48	c3qj4A_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
49	c3ka7A_	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
50	c2zxiC_	Alignment	not modelled	99.6	14	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
51	d1neka2	Alignment	not modelled	99.6	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
52	d1qo8a2	Alignment	not modelled	99.6	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
53	c2uzzD_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase;

					PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
54	c1ryiB_	Alignment	not modelled	99.6	14 PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
55	d2bs2a2	Alignment	not modelled	99.6	17 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
56	c3f8rD_	Alignment	not modelled	99.6	13 PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfobolus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
57	d1kf6a2	Alignment	not modelled	99.6	14 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
58	d2gf3a1	Alignment	not modelled	99.6	16 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
59	c2rgoA_	Alignment	not modelled	99.6	15 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
60	c3fbsB_	Alignment	not modelled	99.6	14 PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
61	c3k7tB_	Alignment	not modelled	99.6	14 PDB header: oxidoreductase Chain: B: PDB Molecule: 6-hydroxy-l-nicotine oxidase; PDBTitle: crystal structure of apo-form 6-hydroxy-l-nicotine oxidase,2 crystal form p3121
62	c3g05B_	Alignment	not modelled	99.6	15 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
63	d1d4ca2	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
64	c2vv1D_	Alignment	not modelled	99.5	16 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.
65	c3dgzA_	Alignment	not modelled	99.5	19 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
66	d1jnra2	Alignment	not modelled	99.5	14 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
67	c3cesB_	Alignment	not modelled	99.5	15 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
68	c2rghA_	Alignment	not modelled	99.5	17 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
69	c3cp8C_	Alignment	not modelled	99.5	16 PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
70	c1zkqA_	Alignment	not modelled	99.5	19 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
71	c1s3bB_	Alignment	not modelled	99.5	14 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
72	c2zbwA_	Alignment	not modelled	99.5	16 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hbb8
73	d2ivda1	Alignment	not modelled	99.5	15 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
74	d1rp0a1	Alignment	not modelled	99.5	17 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
75	c2ivdA_	Alignment	not modelled	99.5	13 PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
76	c3i6dA_	Alignment	not modelled	99.5	12 PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
77	d1y0pa2	Alignment	not modelled	99.5	14 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
78	c3jskN_	Alignment	not modelled	99.5	12 PDB header: biosynthetic protein Chain: N: PDB Molecule: cybbp37 protein; PDBTitle: thiazole synthase from neurospora crassa

79	c2eq8E_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
80	c1bwcA_	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
81	c2gqfA_	Alignment	not modelled	99.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
82	c3ab1B_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
83	c1c0iA_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-amino acid oxidase; PDBTitle: crystal structure of d-amino acid oxidase in complex with2 two anthranilate molecules
84	c1yq4A_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
85	c2a8xA_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
86	d1w4xa1	Alignment	not modelled	99.4	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
87	c3ic9D_	Alignment	not modelled	99.4	24	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
88	c3ctyA_	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
89	c2q7vA_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase
90	d1ryia1	Alignment	not modelled	99.4	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
91	d2i0za1	Alignment	not modelled	99.4	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
92	d1reoa1	Alignment	not modelled	99.4	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
93	c2aczA_	Alignment	not modelled	99.4	17	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
94	c1lpfB_	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
95	c2eq7B_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
96	c2yg4B_	Alignment	not modelled	99.4	11	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
97	c2hqmB_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
98	c2nvkX_	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
99	d1pj5a2	Alignment	not modelled	99.4	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
100	c1geuA_	Alignment	not modelled	99.4	15	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
101	c3urhB_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
102	c1jrxA_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
103	d2iida1	Alignment	not modelled	99.4	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain

104	c1qo8A_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
105	d1b5qa1	Alignment	not modelled	99.4	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
106	c3v76A_	Alignment	not modelled	99.4	16	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
107	c1v59B_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
108	c3o0hA_	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
109	c3gwdA_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase
110	c1ebdB_	Alignment	not modelled	99.4	18	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
111	c1ojtA_	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
112	c1f6mF_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
113	c3rhaA_	Alignment	not modelled	99.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
114	c2c3dB_	Alignment	not modelled	99.3	16	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
115	c3p4rM_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
116	c1f8sA_	Alignment	not modelled	99.3	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.
117	c3r9uA_	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
118	c3lzxB_	Alignment	not modelled	99.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
119	c2cfyB_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
120	c1d4cB_	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1