Phyre^2

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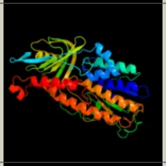
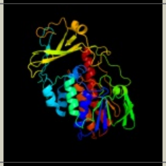
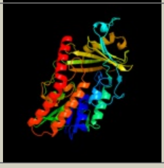
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qa2A_	Alignment		100.0	20	**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
2	c3fmwC_	Alignment		100.0	20	**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.
3	c1pn0A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenol 2-monooxygenase; **PDBTitle:** phenol hydroxylase from trichosporon cutaneum
4	c2dkhA_	Alignment		100.0	20	**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	c1phhA_	Alignment		100.0	20	**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
6	c3ihgA_	Alignment		100.0	18	**PDB header:**flavoprotein, oxidoreductase **Chain:** A: **PDB Molecule:**rdme; **PDBTitle:** crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
7	c2r0gB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rebc; **PDBTitle:** chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
8	c3i3lA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
9	c3e1tA_	Alignment		100.0	16	**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
10	c2x3nA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-dependent monooxygenase; **PDBTitle:** crystal structure of pqsl, a probable fad-dependent2 monooxygenase from pseudomonas aeruginosa
11	c3allA_	Alignment		100.0	17	**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	c3nixF_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**flavoprotein/dehydrogenase; **PDBTitle:** crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
13	c3gmbB_	Alignment		100.0	17	**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	c3c4aA_	Alignment		100.0	16	**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
15	c2rgjA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** crystal structure of flavin-containing monooxygenase phzs
16	d1k0ia1	Alignment		100.0	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
17	c2xdoC_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
18	c3atrA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
19	c2vouA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,6-dihydroxypyridine hydroxylase; **PDBTitle:** structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
20	c3cgvA_	Alignment		100.0	15	**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
21	d1pn0a1	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
22	d3c96a1	Alignment	not modelled	100.0	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
23	c2bryA_	Alignment	not modelled	100.0	14	**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
24	c3ihmB_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**styrene monooxygenase a; **PDBTitle:** structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
25	c2ardA_	Alignment	not modelled	100.0	14	**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
26	d2voua1	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	c2weuD_	Alignment	not modelled	100.0	16	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
28	c2pyxA_	Alignment	not modelled	100.0	16	**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
						PDB header:biosynthetic protein, flavoprotein

29	c2e4gB_	Alignment	not modelled	100.0	15	**Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
30	c2gmhA_	Alignment	not modelled	100.0	15	**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
31	d2gmha1	Alignment	not modelled	100.0	14	**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	13	**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	c1yvvB_	Alignment	not modelled	99.8	16	**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.
34	c3qj4A_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
35	c3da1A_	Alignment	not modelled	99.6	10	**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.
36	c1y56B_	Alignment	not modelled	99.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sarcosine oxidase; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
37	c2olnA_	Alignment	not modelled	99.5	18	**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
38	c3ka7A_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
39	c3i6dA_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of ppo from bacillus subtilis with af
40	c3bhkA_	Alignment	not modelled	99.5	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
41	c3nyeA_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
42	c2ivdA_	Alignment	not modelled	99.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
43	d2ivda1	Alignment	not modelled	99.5	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
44	c3ab1B_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
45	c2vvlD_	Alignment	not modelled	99.4	12	**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.
46	c3ps9A_	Alignment	not modelled	99.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
47	c3dmeB_	Alignment	not modelled	99.4	14	**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
48	c1pj6A_	Alignment	not modelled	99.4	13	**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
49	d1b5qa1	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
50	c1s3bB_	Alignment	not modelled	99.4	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
51	c3k7tB_	Alignment	not modelled	99.4	19	**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
52	c2gahB_	Alignment	not modelled	99.4	14	**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
53	c3f8rD_	Alignment	not modelled	99.4	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**thioredoxin reductase (trxb-3); **PDBTitle:** crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
54	c2zxiC_	Alignment	not modelled	99.3	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
55	c2r4jA_	Alignment	not modelled	99.3	15	**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
56	d2gqfa1	Alignment	not modelled	99.3	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
57	c3pvcA_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
58	c3cesB_	Alignment	not modelled	99.3	17	**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
59	c3cp8C_	Alignment	not modelled	99.3	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
60	c1c0iA_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** crystal structure of d-amino acid oxidase in complex with2 two anthranylate molecules
61	c2yg4B_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
62	c1ryiB_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycine oxidase; **PDBTitle:** structure of glycine oxidase with bound inhibitor glycolate
63	c3lovA_	Alignment	not modelled	99.3	15	**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
64	d1kf6a2	Alignment	not modelled	99.2	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
65	d1jnra2	Alignment	not modelled	99.2	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
66	c2q7vA_	Alignment	not modelled	99.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of deinococcus radiodurans thioredoxin2 reductase
67	d1neka2	Alignment	not modelled	99.2	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
68	c3g05B_	Alignment	not modelled	99.2	17	**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
69	d2bs2a2	Alignment	not modelled	99.2	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
70	c1ltxR_	Alignment	not modelled	99.2	14	**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
71	c3jskN_	Alignment	not modelled	99.2	20	**PDB header:**biosynthetic protein **Chain:** N: **PDB Molecule:**cypbp37 protein; **PDBTitle:** thiazole synthase from neurospora crassa
72	c1sezA_	Alignment	not modelled	99.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase, mitochondrial; **PDBTitle:** crystal structure of protoporphyrinogen ix oxidase
73	c1f8sA_	Alignment	not modelled	99.2	15	**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.
74	c3h8lA_	Alignment	not modelled	99.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidase; **PDBTitle:** the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism
75	c3rhaA_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
76	c2rgoA_	Alignment	not modelled	99.2	11	**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
77	c3djeA_	Alignment	not modelled	99.2	11	**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
78	c2rghA_	Alignment	not modelled	99.1	11	**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
79	d1reoa1	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
80	d2i0za1	Alignment	not modelled	99.1	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
81	c2zbwA_	Alignment	not modelled	99.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
82	c3fbsB_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
83	c3nksA_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of human protoporphyrinogen ix oxidase
84	d1qo8a2	Alignment	not modelled	99.1	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
85	c3lzxB_	Alignment	not modelled	99.1	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase 2; **PDBTitle:** crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
86	d1w4xa1	Alignment	not modelled	99.1	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
87	d1rp0a1	Alignment	not modelled	99.1	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
88	d1pj5a2	Alignment	not modelled	99.1	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
89	c2a87A_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
90	c3d8xB_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
91	c2uzzD_	Alignment	not modelled	99.0	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-methyl-l-tryptophan oxidase; **PDBTitle:** x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
92	d2cula1	Alignment	not modelled	99.0	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GidA-like
93	c3gwdA_	Alignment	not modelled	99.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase
94	d2gf3a1	Alignment	not modelled	99.0	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
95	d1d4ca2	Alignment	not modelled	98.9	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
96	c1kifE_	Alignment	not modelled	98.9	13	**PDB header:**flavoprotein **Chain:** E: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** d-amino acid oxidase from pig kidney
97	d2gjca1	Alignment	not modelled	98.9	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
98	d1ryia1	Alignment	not modelled	98.9	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
99	c1h83A_	Alignment	not modelled	98.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase; **PDBTitle:** structure of polyamine oxidase in complex with2 1,8-diaminooctane
100	d1o5wa1	Alignment	not modelled	98.9	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
101	c3p4rM_	Alignment	not modelled	98.9	19	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**fumarate reductase flavoprotein subunit; **PDBTitle:** crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
102	c2aczA_	Alignment	not modelled	98.9	18	**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
103	c2cduB_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
104	c1kf6A_	Alignment	not modelled	98.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase flavoprotein; **PDBTitle:** e. coli quinol-fumarate reductase with bound inhibitor hqno

105	c1yq4A_	Alignment	not modelled	98.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
106	c1w4xA_	Alignment	not modelled	98.8	19	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
107	c3hyxC_	Alignment	not modelled	98.8	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfide-quinone reductase; **PDBTitle:** 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
108	c1xdiA_	Alignment	not modelled	98.8	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
109	c1hyuA_	Alignment	not modelled	98.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
110	d1y0pa2	Alignment	not modelled	98.8	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
111	c3nlcA_	Alignment	not modelled	98.8	16	**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
112	c2e5vA_	Alignment	not modelled	98.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate oxidase; **PDBTitle:** crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
113	c1qo8A_	Alignment	not modelled	98.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
114	c1jrxA_	Alignment	not modelled	98.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
115	c3v76A_	Alignment	not modelled	98.7	25	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavoprotein; **PDBTitle:** the crystal structure of a flavoprotein from sinorhizobium meliloti
116	d2gv8a1	Alignment	not modelled	98.7	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
117	d2iida1	Alignment	not modelled	98.7	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
118	c1vqwB_	Alignment	not modelled	98.7	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein with similarity to flavin-containing **PDBTitle:** crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
119	d2v5za1	Alignment	not modelled	98.7	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
120	c3r9uA_	Alignment	not modelled	98.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** thioredoxin-disulfide reductase from campylobacter jejuni.