Phyre^2

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Description	P77223
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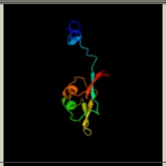
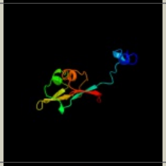
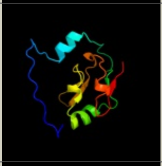
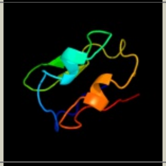
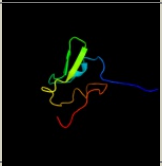
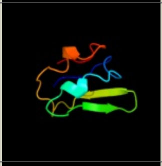
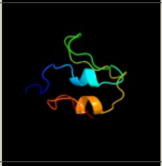
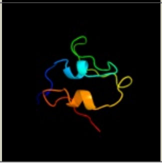
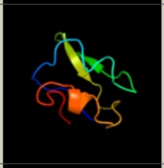
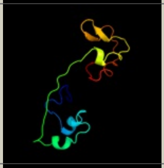
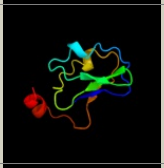
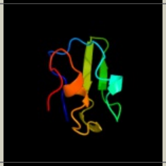
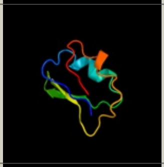
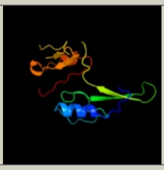
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gthD_	Alignment		99.8	33	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
2	d1gtea5	Alignment		99.6	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
3	c2c3yA_	Alignment		99.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
4	c2gmhA_	Alignment		99.6	13	**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
5	c3gyxJ_	Alignment		99.5	29	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
6	d1hfel2	Alignment		99.5	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
7	d1jnrb_	Alignment		99.5	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	c2ivfB_	Alignment		99.5	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
9	d7fd1a_	Alignment		99.5	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
10	c2fugG_	Alignment		99.5	35	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase chain 9; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
11	d2fug91	Alignment		99.5	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins

12	d2c42a5	Alignment		99.5	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
13	d1bc6a_	Alignment		99.5	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
14	d1y5ib1	Alignment		99.4	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
15	d2fdna_	Alignment		99.4	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
16	c2zvsB_	Alignment		99.4	29	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**uncharacterized ferredoxin-like protein yfhl; **PDBTitle:** crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
17	d1xera_	Alignment		99.4	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
18	d1dura_	Alignment		99.4	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
19	d1h98a_	Alignment		99.4	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
20	d1fcaa_	Alignment		99.4	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
21	d1blua_	Alignment	not modelled	99.4	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
22	d1rgva_	Alignment	not modelled	99.4	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
23	c1kqfB_	Alignment		99.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
24	d1jb0c_	Alignment	not modelled	99.3	37	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
25	d1vlfn2	Alignment	not modelled	99.3	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
26	c1gx7A_	Alignment	not modelled	99.3	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [fe] hydrogenase large subunit; **PDBTitle:** best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
27	c2vpyB_	Alignment	not modelled	99.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)

28	d1clfa_	Alignment	not modelled	99.3	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
29	c1hfeL_	Alignment	not modelled	99.3	25	**PDB header:**hydrogenase **Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
30	d2fug34	Alignment	not modelled	99.3	13	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
31	d1kqfb1	Alignment	not modelled	99.3	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
32	c1ti2F_	Alignment	not modelled	99.2	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
33	c2v2kB_	Alignment	not modelled	99.2	29	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
34	c2fgoA_	Alignment	not modelled	99.2	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
35	d1iqza_	Alignment	not modelled	99.2	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
36	d2gmha3	Alignment	not modelled	99.2	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
37	c1c4cA_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
38	d3c8ya3	Alignment	not modelled	99.2	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
39	c3bk7A_	Alignment	not modelled	99.1	34	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
40	d1vjwa_	Alignment	not modelled	99.1	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
41	d1h0hb_	Alignment	not modelled	99.1	13	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
42	c2fugC_	Alignment	not modelled	99.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
43	d3c7bb1	Alignment	not modelled	99.0	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
44	c3c7bE_	Alignment	not modelled	99.0	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
45	c1dwlA_	Alignment	not modelled	98.9	29	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
46	d1sj1a_	Alignment	not modelled	98.9	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
47	c2v4jE_	Alignment	not modelled	98.9	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
48	d1fxra_	Alignment	not modelled	98.8	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
49	c2v4jA_	Alignment	not modelled	98.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
50	c3c7bA_	Alignment	not modelled	98.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	d2bs2b1	Alignment	not modelled	97.8	30	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
52	d1kf6b1	Alignment	not modelled	97.8	29	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin

						Family: Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	d1nekb1	Alignment	not modelled	97.7	29	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
54	c1nekB_	Alignment	not modelled	97.6	34	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
55	c2h89B_	Alignment	not modelled	97.5	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
56	c2bs2E_	Alignment	not modelled	97.5	35	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
57	c2b76N_	Alignment	not modelled	97.4	30	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
58	c3cf4A_	Alignment	not modelled	97.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
59	d2v4jb1	Alignment	not modelled	96.4	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
60	d2v4ja1	Alignment	not modelled	93.3	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
61	d3c7ba1	Alignment	not modelled	93.2	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
62	c2vdcl_	Alignment	not modelled	87.7	30	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
63	d1fxda_	Alignment	not modelled	76.5	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
64	c1f8sA_	Alignment	not modelled	32.4	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.
65	c2pmzS_	Alignment	not modelled	27.7	23	**PDB header:**translation, transferase **Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
66	c2yg4B_	Alignment	not modelled	27.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
67	c3nlcA_	Alignment	not modelled	27.0	25	**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
68	c1ltxR_	Alignment	not modelled	26.7	16	**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
69	c1h83A_	Alignment	not modelled	26.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase; **PDBTitle:** structure of polyamine oxidase in complex with2 1,8-diaminooctane
70	c3rhaA_	Alignment	not modelled	26.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
71	d1vg0a1	Alignment	not modelled	24.9	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
72	c3bnuA_	Alignment	not modelled	24.8	15	**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
73	c1gndA_	Alignment	not modelled	24.7	13	**PDB header:**gtpase activation **Chain:** A: **PDB Molecule:**guanine nucleotide dissociation inhibitor; **PDBTitle:** guanine nucleotide dissociation inhibitor, alpha-isoform
74	c1sezA_	Alignment	not modelled	24.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase, mitochondrial; **PDBTitle:** crystal structure of protoporphyrinogen ix oxidase
75	c2jb1B_	Alignment	not modelled	23.5	18	**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
76	c1s3bB_	Alignment	not modelled	21.6	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
						Fold:FAD/NAD(P)-binding domain

77	d1seza1	Alignment	not modelled	21.2	21	**Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
78	c3p1wA_	Alignment	not modelled	21.0	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**rabgdi protein; **PDBTitle:** crystal structure of rab gdi from plasmodium falciparum, pfl2060c
79	d2dw4a2	Alignment	not modelled	20.8	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
80	c3cpiH_	Alignment	not modelled	20.7	6	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**rab gdp-dissociation inhibitor; **PDBTitle:** crystal structure of yeast rab-gdi
81	d2bcgg1	Alignment	not modelled	19.5	6	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
82	d1d5ta1	Alignment	not modelled	19.5	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
83	d1reoa1	Alignment	not modelled	19.4	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
84	c3hdqI_	Alignment	not modelled	19.1	16	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
85	d1b5qa1	Alignment	not modelled	18.7	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
86	d1gtea1	Alignment	not modelled	18.5	44	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
87	c2vvlD_	Alignment	not modelled	18.5	19	**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.
88	c2xdoC_	Alignment	not modelled	18.5	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
89	c2ivdA_	Alignment	not modelled	18.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
90	c2e1mA_	Alignment	not modelled	18.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
91	c2bi8A_	Alignment	not modelled	17.7	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad
92	c3qj4A_	Alignment	not modelled	17.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
93	c1i8tB_	Alignment	not modelled	17.0	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
94	c3ka7A_	Alignment	not modelled	16.8	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
95	c3nksA_	Alignment	not modelled	16.7	24	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of human protoporphyrinogen ix oxidase
96	c2b9yA_	Alignment	not modelled	16.6	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
97	d2iida1	Alignment	not modelled	16.5	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
98	c2xagA_	Alignment	not modelled	16.0	18	**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
99	c2v1dA_	Alignment	not modelled	16.0	18	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition