





















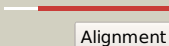

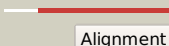







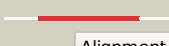







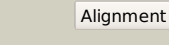
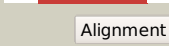

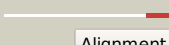

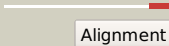
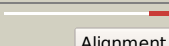



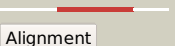
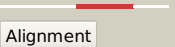
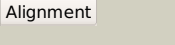
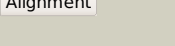

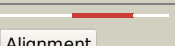

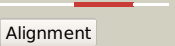
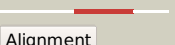
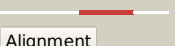
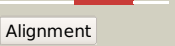
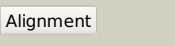
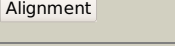

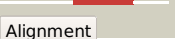

Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3116_(moeB2)_3482773_3483942
 Date Thu Aug 8 16:20:29 BST 2019
 Unique Job ID 27e4ddc4975c7eda

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h77B_	 Alignment		100.0	25	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: e1 enzyme for ubiquitin like protein activation in complex with ubl
2	d1jw9b_	 Alignment		100.0	41	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
3	c1zfnA_	 Alignment		100.0	38	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
4	d1yovb1	 Alignment		100.0	33	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
5	c3h9gA_	 Alignment		100.0	25	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
6	c3gznb_	 Alignment		100.0	31	PDB header: protein binding/ligase Chain: B: PDB Molecule: nedd8-activating enzyme e1 catalytic subunit; PDBTitle: structure of nedd8-activating enzyme in complex with nedd8 and mln4924
7	c5ff5A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: paaa; PDBTitle: crystal structure of semet paaa
8	c2nvuB_	 Alignment		100.0	34	PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
9	c3vh3A_	 Alignment		100.0	21	PDB header: metal binding protein/protein transport Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of atg7ctd-atg8 complex
10	c3vh1A_	 Alignment		100.0	24	PDB header: metal binding protein Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of saccharomyces cerevisiae atg7 (1-595)
11	c4d7aA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: trna threonylcarbamoyladenosine dehydratase; PDBTitle: crystal structure of e. coli trna n6-threonylcarbamoyladenosine2 dehydratase, tcda, in complex with amp at 1.801 angstrom3 resolution

12	c3kydB_	 Alignment		100.0	28	PDB header: ligase Chain: B; PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1~sumo1-amp tetrahedral intermediate mimic
13	c3kycB_	 Alignment		100.0	31	PDB header: ligase Chain: B; PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1 complex with a sumo1-amp mimic
14	c1y8qD_	 Alignment		100.0	30	PDB header: ligase Chain: D; PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
15	c1y8qA_	 Alignment		100.0	21	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-like 1 activating enzyme e1a; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
16	c6dc6A_	 Alignment		100.0	30	PDB header: signaling protein/ligase Chain: A; PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of human ubiquitin activating enzyme e1 (uba1) in2 complex with ubiquitin
17	c3cmmA_	 Alignment		100.0	27	PDB header: ligase/protein binding Chain: A; PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of the uba1-ubiquitin complex
18	c4ii3A_	 Alignment		100.0	30	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of s. pombe ubiquitin activating enzyme 1 (uba1) in2 complex with ubiquitin and atp/mg
19	c3gucB_	 Alignment		100.0	25	PDB header: transferase Chain: B; PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
20	d1yova1	 Alignment		100.0	24	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
21	c4p22A_	 Alignment	not modelled	100.0	27	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of n-terminal fragments of e1
22	c3wv9D_	 Alignment	not modelled	100.0	22	PDB header: transferase Chain: D; PDB Molecule: hmd co-occurring protein hcge; PDBTitle: guanylylpyridinol (gp)- and atp-bound hcge from methanothermobacter2 marburgensis
23	c3i2vA_	 Alignment	not modelled	99.9	27	PDB header: transferase Chain: A; PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
24	c3tp9B_	 Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase and rhodanese domain protein; PDBTitle: crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
25	c1yt8A_	 Alignment	not modelled	99.9	21	PDB header: transferase Chain: A; PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
26	d1yt8a4	 Alignment	not modelled	99.8	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
27	d1yt8a1	 Alignment	not modelled	99.8	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
28	c3ilmD_	 Alignment	not modelled	99.8	26	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h

29	c5ve5C	 Alignment	not modelled	99.8	34	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bbprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytofirmans in complex with glutathione
30	c4f67A	 Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nsg) target lgr82
31	c3d1pA	 Alignment	not modelled	99.8	30	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
32	c3icrA	 Alignment	not modelled	99.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
33	c6mxvA	 Alignment	not modelled	99.8	34	PDB header: unknown function Chain: A: PDB Molecule: rhodanese-like family protein; PDBTitle: the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
34	c2hhgA	 Alignment	not modelled	99.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa3614; PDBTitle: structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
35	c3fojA	 Alignment	not modelled	99.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
36	d1yt8a2	 Alignment	not modelled	99.8	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
37	c3emeA	 Alignment	not modelled	99.8	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rhodanese-like domain protein; PDBTitle: crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
38	c1e0cA	 Alignment	not modelled	99.8	22	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
39	c6bevB	 Alignment	not modelled	99.8	33	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
40	c3hzuA	 Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
41	c6h98A	 Alignment	not modelled	99.8	25	PDB header: transferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
42	d1yt8a3	 Alignment	not modelled	99.8	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
43	d1qxnA	 Alignment	not modelled	99.8	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
44	c3gk5A	 Alignment	not modelled	99.8	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein tvg0868615; PDBTitle: crystal structure of rhodanese-related protein (tvg0868615) from2 thermoplasma volcanium, northeast structural genomics consortium3 target tvr109a
45	c3aaxB	 Alignment	not modelled	99.8	23	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
46	c3ntaA	 Alignment	not modelled	99.8	30	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
47	c1uarA	 Alignment	not modelled	99.8	25	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
48	c1urhA	 Alignment	not modelled	99.8	27	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
49	d1e0ca1	 Alignment	not modelled	99.8	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
50	c1boiA	 Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
51	d1gmxa	Alignment	not modelled	99.8	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
52	d1c25a	Alignment	not modelled	99.8	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase

						Family: Cell cycle control phosphatase, catalytic domain
53	c3nhvE_	Alignment	not modelled	99.8	27	PDB header: structural genomics, unknown function Chain: E; PDB Molecule: bh2092 protein; PDBTitle: crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
54	d1tq1a_	Alignment	not modelled	99.8	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
55	c3k9rA_	Alignment	not modelled	99.8	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: alr3790 protein; PDBTitle: x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anaebaena sp. northeast structural genomics consortium target3 nsr437c.
56	d1ymka1	Alignment	not modelled	99.7	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
57	c3olhA_	Alignment	not modelled	99.7	27	PDB header: transferase Chain: A; PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
58	c3f4aA_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
59	c3g5jA_	Alignment	not modelled	99.7	30	PDB header: nucleotide binding protein Chain: A; PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
60	c2moiA_	Alignment	not modelled	99.7	24	PDB header: membrane protein Chain: A; PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
61	c2dcqA_	Alignment	not modelled	99.7	24	PDB header: unknown function Chain: A; PDB Molecule: putative protein at4g01050; PDBTitle: fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
62	c2uzqE_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: E; PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
63	c2j6pF_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: F; PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
64	d1rha1	Alignment	not modelled	99.7	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
65	c2fsxA_	Alignment	not modelled	99.7	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
66	c3ippA_	Alignment	not modelled	99.7	23	PDB header: transferase Chain: A; PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
67	d1uara2	Alignment	not modelled	99.7	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
68	c2jtqA_	Alignment	not modelled	99.7	28	PDB header: transferase Chain: A; PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
69	d1e0ca2	Alignment	not modelled	99.7	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
70	c3utnX_	Alignment	not modelled	99.7	26	PDB header: transferase Chain: X; PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae
71	c3op3A_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A; PDB Molecule: m-phase inducer phosphatase 3; PDBTitle: crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens
72	d1rha2	Alignment	not modelled	99.7	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
73	d1urha1	Alignment	not modelled	99.7	26	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
74	c2k0zA_	Alignment	not modelled	99.7	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
75	d1t3ka_	Alignment	not modelled	99.7	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
76	d1uara1	Alignment	not modelled	99.6	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
77	d1okqa1	Alignment	not modelled	99.6	12	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
						Fold: Rhodanese/Cell cycle control phosphatase

78	d1okga2	Alignment	not modelled	99.6	19	Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
79	c1okgA	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
80	c2vswB	Alignment	not modelled	99.6	27	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 16; PDBTitle: the structure of the rhodanese domain of the human dual specificity2 phosphatase 16
81	c1wv9B	Alignment	not modelled	99.5	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
82	c2eg4B	Alignment	not modelled	99.5	29	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
83	d2gwfa1	Alignment	not modelled	99.5	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
84	c4bs9A	Alignment	not modelled	99.5	22	PDB header: isomerase Chain: A: PDB Molecule: trud; PDBTitle: structure of the heterocyclase trud
85	d1whba	Alignment	not modelled	99.5	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
86	d1urha2	Alignment	not modelled	99.5	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
87	c2oucB	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mkp5
88	d1hzma	Alignment	not modelled	99.4	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
89	c3r2uC	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
90	c4rl6A	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04l03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
91	c2axqA	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
92	c1e5IA	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
93	d1pjqa1	Alignment	not modelled	98.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
94	c5l78A	Alignment	not modelled	98.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
95	d1vi2a1	Alignment	not modelled	98.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
96	c3ic5A	Alignment	not modelled	98.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroiy.
97	c2z2vA	Alignment	not modelled	98.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
98	c4inaA	Alignment	not modelled	97.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolfinella2 succinogenes. northeast structural genomics consortium target wsr35
99	c2nloA	Alignment	not modelled	97.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
100	c3tozA	Alignment	not modelled	97.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
101	c1vi2B	Alignment	not modelled	97.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
102	c1gpjA	Alignment	not modelled	97.8	22	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
103	c1nitB	Alignment	not modelled	97.7	21	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of

103	c1pjb_	Alignment	not modelled	97.7	41	cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
104	c4n7rB_	Alignment	not modelled	97.7	27	PDB header: oxidoreductase/protein binding Chain: B: PDB Molecule: glutamyl-trna reductase 1, chloroplastic; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
105	c4pjpB_	Alignment	not modelled	97.6	22	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
106	d1pzqa1	Alignment	not modelled	97.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
107	d1e5qa1	Alignment	not modelled	97.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
108	d1np3a2	Alignment	not modelled	97.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
109	c3pgjB_	Alignment	not modelled	97.6	31	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
110	c4tskA_	Alignment	not modelled	97.6	21	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
111	c3pvzD_	Alignment	not modelled	97.6	15	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
112	c3tumA_	Alignment	not modelled	97.6	34	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
113	c5yeqB_	Alignment	not modelled	97.5	19	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: the structure of sac-kari protein
114	c4bgvB_	Alignment	not modelled	97.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: 1.8 a resolution structure of the malate dehydrogenase from2 picrophilus torridus in its apo form
115	c4xcvA_	Alignment	not modelled	97.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent 2-hydroxyacid dehydrogenase; PDBTitle: probable 2-hydroxyacid dehydrogenase from rhizobium etli cfn 42 in2 complex with nadph
116	c2eggA_	Alignment	not modelled	97.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
117	c1bg6A_	Alignment	not modelled	97.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
118	c4kqxB_	Alignment	not modelled	97.5	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: mutant slackia exigua kari ddv in complex with nad and an inhibitor
119	d2pgda2	Alignment	not modelled	97.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	d1gpja2	Alignment	not modelled	97.4	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain