

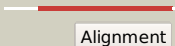



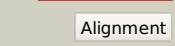





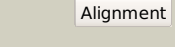

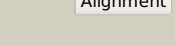
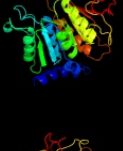
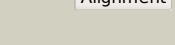




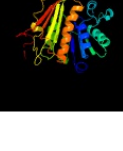


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3206c_(moeB1)_3582528_3583706
Date	Thu Aug 8 16:20:40 BST 2019
Unique Job ID	447bfaff2a80b58e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h77B_	 Alignment		100.0	22	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	c1zfnA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
3	d1jw9B_	 Alignment		100.0	38	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
4	c3h9gA_	 Alignment		100.0	23	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
5	d1yovb1	 Alignment		100.0	30	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
6	c5ff5A_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: paaa; PDBTitle: crystal structure of semet paaa
7	c3gznb_	 Alignment		100.0	29	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
8	c3vh3A_	 Alignment		100.0	20	PDB header: metal binding protein/protein transport Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of atg7ctd-atg8 complex
9	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)
10	c4d7aA_	 Alignment		100.0	21	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
11	c2nvuB_	 Alignment		100.0	31	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

12	c3kydB_	Alignment		100.0	25	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	28	PDB header: ligase Chain: B; PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1 complex with a sumo1-amp mimic
14	c1y8qA_	Alignment		100.0	23	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-like 1 activating enzyme e1a; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
15	c1y8qD_	Alignment		100.0	26	PDB header: ligase Chain: D; PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
16	c3gucB_	Alignment		100.0	19	PDB header: transferase Chain: B; PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
17	d1yova1	Alignment		100.0	30	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
18	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
19	c4p22A_	Alignment		100.0	26	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of n-terminal fragments of e1
20	c4ii3A_	Alignment		100.0	27	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
21	c3cmmA_	Alignment	not modelled	100.0	28	PDB header: ligase/protein binding Chain: A; PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of the uba1-ubiquitin complex
22	c3wv9D_	Alignment	not modelled	100.0	21	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	28	PDB header: transferase Chain: A; PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
24	c4f67A_	Alignment	not modelled	99.9	16	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 (nesg) target lgr82
25	c3tp9B_	Alignment	not modelled	99.9	32	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
26	c1yt8A_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A; PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
27	d1yt8a4	Alignment	not modelled	99.8	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
						Fold: Rhodanese/Cell cycle control phosphatase

28	d1yt8a1	Alignment	not modelled	99.8	16	Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
29	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
30	c3fojA_	Alignment	not modelled	99.8	28	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.
31	c3d1pA_	Alignment	not modelled	99.8	22	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	25	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
33	c2hhgA_	Alignment	not modelled	99.8	26	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
34	c5ve5C_	Alignment	not modelled	99.8	29	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytotfirmans in complex with glutathione
35	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
36	d1yt8a2	Alignment	not modelled	99.8	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
37	c6mxvA_	Alignment	not modelled	99.8	26	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
38	c6bevB_	Alignment	not modelled	99.8	31	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
39	d1qxna_	Alignment	not modelled	99.8	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
40	d1yt8a3	Alignment	not modelled	99.8	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
41	d1c25a_	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
42	c3gk5A_	Alignment	not modelled	99.8	27	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
43	d1tq1a_	Alignment	not modelled	99.8	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
44	c3ntaA_	Alignment	not modelled	99.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
45	c3nhvE_	Alignment	not modelled	99.8	26	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
46	c6h98A_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
47	c3f4aA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
48	c3k9rA_	Alignment	not modelled	99.8	24	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 anabaena sp. northeast structural genomics consortium target3 nsr437c.
49	d1gmxa_	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
50	d1ymka1	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
51	c2moiA_	Alignment	not modelled	99.8	27	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
52	c2fcvA_	Alignment	not modelled	99.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related

52	c21bxA	Alignment	not modelled	99.8	20	PDB header: sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
53	c2dcqA	Alignment	not modelled	99.7	20	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
54	c2j6pF	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: F; PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
55	c3g5jA	Alignment	not modelled	99.7	29	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
56	c1e0cA	Alignment	not modelled	99.7	24	PDB header: sulfurtransferase Chain: A; PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
57	c2uzqE	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: E; PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
58	c3aaxB	Alignment	not modelled	99.7	21	PDB header: transferase Chain: B; PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
59	c1boiA	Alignment	not modelled	99.7	21	PDB header: transferase Chain: A; PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
60	c3hzuA	Alignment	not modelled	99.7	24	PDB header: transferase Chain: A; PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
61	c1urhA	Alignment	not modelled	99.7	21	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
62	c1uarA	Alignment	not modelled	99.7	24	PDB header: transferase Chain: A; PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
63	d1e0ca1	Alignment	not modelled	99.7	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
64	c2jtqA	Alignment	not modelled	99.7	25	PDB header: transferase Chain: A; PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
65	c3olhA	Alignment	not modelled	99.7	22	PDB header: transferase Chain: A; PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
66	d1uara2	Alignment	not modelled	99.7	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
67	c3op3A	Alignment	not modelled	99.7	20	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
68	d1t3ka	Alignment	not modelled	99.7	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
69	c2k0zA	Alignment	not modelled	99.7	21	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
70	d1rha1	Alignment	not modelled	99.7	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
71	c3utnX	Alignment	not modelled	99.7	27	PDB header: transferase Chain: X; PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae
72	c3ippA	Alignment	not modelled	99.6	23	PDB header: transferase Chain: A; PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
73	d1rha2	Alignment	not modelled	99.6	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
74	c1wv9B	Alignment	not modelled	99.6	27	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
75	d1e0ca2	Alignment	not modelled	99.6	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
76	d1urha1	Alignment	not modelled	99.6	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
77	c2vswB	Alignment	not modelled	99.6	26	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

78	d1okga2	Alignment	not modelled	99.6	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
79	d1whba_	Alignment	not modelled	99.5	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
80	d1uara1	Alignment	not modelled	99.5	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
81	d1okga1	Alignment	not modelled	99.5	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
82	d2gwfa1	Alignment	not modelled	99.5	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
83	c2eg4B_	Alignment	not modelled	99.5	30	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
84	c2oucB_	Alignment	not modelled	99.5	22	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mkp5
85	c3r2uC_	Alignment	not modelled	99.5	17	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
86	c1okgA_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
87	d1hzma_	Alignment	not modelled	99.4	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
88	d1urha2	Alignment	not modelled	99.4	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
89	c4bs9A_	Alignment	not modelled	99.3	21	PDB header: isomerase Chain: A: PDB Molecule: trud; PDBTitle: structure of the heterocyclase trud
90	c4rl6A_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04103_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	c1e51A_	Alignment	not modelled	98.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
93	c5178A_	Alignment	not modelled	98.3	21	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)
94	d1pjqa1	Alignment	not modelled	98.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
95	d1vi2a1	Alignment	not modelled	98.2	18	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	98.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
97	c2z2vA_	Alignment	not modelled	98.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
98	c1vi2B_	Alignment	not modelled	98.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
99	c4inaA_	Alignment	not modelled	98.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinella2 succinogenes. northeast structural genomics consortium target wsr35
100	c2nloA_	Alignment	not modelled	97.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
101	c3tozA_	Alignment	not modelled	97.9	16	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.
102	c1gpiA_	Alignment	not modelled	97.9	22	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
103	d1pzga1	Alianment	not modelled	97.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: LDH N-terminal domain-like
104	d1e5qa1	Alignment	not modelled	97.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
105	c1pjtB_	Alignment	not modelled	97.7	20	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
106	c3pgjB_	Alignment	not modelled	97.7	28	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
107	c4pjpB_	Alignment	not modelled	97.7	18	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
108	c3tumA_	Alignment	not modelled	97.7	29	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+
109	c4n7rB_	Alignment	not modelled	97.7	28	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
110	c2eggA_	Alignment	not modelled	97.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
111	c4bgvB_	Alignment	not modelled	97.6	25	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
112	c3u62A_	Alignment	not modelled	97.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from thermotoga maritima
113	c2hjrK_	Alignment	not modelled	97.6	19	PDB header: oxidoreductase Chain: K: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of cryptosporidium parvum malate2 dehydrogenase
114	d1gpja2	Alignment	not modelled	97.6	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
115	d9ldta1	Alignment	not modelled	97.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
116	d1i0za1	Alignment	not modelled	97.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
117	c1bg6A_	Alignment	not modelled	97.5	25	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	c4tskA_	Alignment	not modelled	97.5	18	PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
119	d1np3a2	Alignment	not modelled	97.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	c3o8qB_	Alignment	not modelled	97.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae