Phyre2

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Description	RVBD3351c_(-)_3767517_3768311
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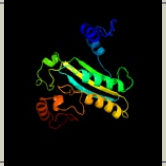
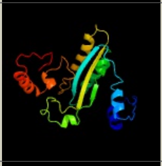
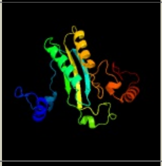
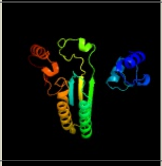
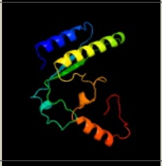
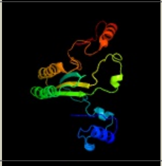
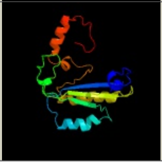
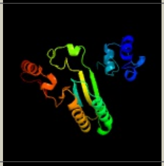
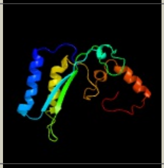
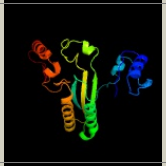
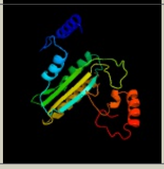
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6f74B_	Alignment		99.9	17	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**alcohol oxidase; **PDBTitle:** crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
2	c6f73B_	Alignment		99.9	16	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**mtvao615; **PDBTitle:** crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1
3	c3popD_	Alignment		99.9	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gilr oxidase; **PDBTitle:** the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
4	c2wdwB_	Alignment		99.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative hexose oxidase; **PDBTitle:** the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
5	c5i1wD_	Alignment		99.8	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**crmk; **PDBTitle:** crystal structure of crmk, a flavoenzyme involved in the shunt product2 recycling mechanism in caerulomycin biosynthesis
6	c2y3rC_	Alignment		99.8	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group
7	c2ipiD_	Alignment		99.8	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox); **PDBTitle:** crystal structure of aclacinomycin oxidoreductase
8	c4ud8B_	Alignment		99.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fad-binding and bbe domain-containing protein; **PDBTitle:** atbbe15
9	c6eo5A_	Alignment		99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ppbbe-like 1 d396n; **PDBTitle:** physcomitrella patens bbe-like 1 variant d396n
10	c3vteA_	Alignment		99.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tetrahydrocannabinolic acid synthase; **PDBTitle:** crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
11	c3tsjA_	Alignment		99.8	19	**PDB header:**allergen, oxidoreductase **Chain:** A: **PDB Molecule:**pollen allergen phl p 4; **PDBTitle:** crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity

12	c3w8wA_	Alignment		99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative fad-dependent oxygenase encm; **PDBTitle:** the crystal structure of encm
13	c3d2hA_	Alignment		99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
14	c5d79B_	Alignment		99.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**berberine bridge enzyme-like protein; **PDBTitle:** structure of bbe-like #28 from arabidopsis thaliana
15	c3fwaA_	Alignment		99.7	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
16	c5l6fA_	Alignment		99.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad linked oxidase-like protein; **PDBTitle:** xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
17	c1zr6A_	Alignment		99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
18	c3rjaA_	Alignment		99.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbohydrate oxidase; **PDBTitle:** crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
19	c4ml8C_	Alignment		99.5	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytokinin oxidase 2; **PDBTitle:** structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
20	c2bvfA_	Alignment		99.5	12	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase; **PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
21	c4oalB_	Alignment	not modelled	99.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytokinin dehydrogenase 4; **PDBTitle:** crystal structure of maize cytokinin oxidase/dehydrogenase 4 (zmcko4)2 in complex with phenylurea inhibitor cppu in alternative spacegroup
22	c6c80B_	Alignment	not modelled	99.4	13	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cytokinin oxidase luckx1.1; **PDBTitle:** crystal structure of a flax cytokinin oxidase
23	c3bw7A_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1; **PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
24	c2exrA_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7; **PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
25	c1wveB_	Alignment	not modelled	99.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
26	c3pm9A_	Alignment	not modelled	99.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
27	c4fdoA_	Alignment	not modelled	99.0	19	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**oxidoreductase dpre1; **PDBTitle:** mycobacterium tuberculosis dpre1 in complex with ct319
28	c2vfvA_	Alignment	not modelled	99.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xylitol oxidase; **PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2):

						complex2 with sulphite
29	c4bc9C_	Alignment	not modelled	98.9	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase, peroxisomal; **PDBTitle:** mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
30	c5fxpA_	Alignment	not modelled	98.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol oxidase; **PDBTitle:** crystal structure of eugenol oxidase in complex with2 vanillin
31	c3js8A_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** solvent-stable cholesterol oxidase
32	c1i19B_	Alignment	not modelled	98.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase from b.sterolicum
33	c1ahuB_	Alignment	not modelled	98.2	15	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
34	d1w1oa1	Alignment	not modelled	96.5	18	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cytokinin dehydrogenase 1
35	d1wvfa1	Alignment	not modelled	95.9	12	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
36	c2uuvC_	Alignment	not modelled	95.7	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
37	d1e8ga1	Alignment	not modelled	94.6	13	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
38	c1f0xA_	Alignment	not modelled	81.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
39	d1f0xa1	Alignment	not modelled	73.6	36	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**D-lactate dehydrogenase
40	d2i0ka1	Alignment	not modelled	68.3	27	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cholesterol oxidase
41	d1kx9b_	Alignment	not modelled	38.9	29	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
42	c2gvsA_	Alignment	not modelled	36.3	36	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**chemosensory protein csp-sg4; **PDBTitle:** nmr solution structure of cspsg4
43	c5cwsE_	Alignment	not modelled	34.3	14	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**nucleoporin nup57; **PDBTitle:** crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
44	d1n8va_	Alignment	not modelled	32.5	29	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
45	c4yh5B_	Alignment	not modelled	31.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**levoglucosan kinase; **PDBTitle:** lipomyces starkeyi levoglucosan kinase bound to adp and manganese
46	c4guzA_	Alignment	not modelled	30.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable arylamine n-acetyl transferase; **PDBTitle:** structure of the arylamine n-acetyltransferase from mycobacterium2 abscessus
47	d1w4ta1	Alignment	not modelled	26.1	32	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
48	c3lnbA_	Alignment	not modelled	25.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase family protein; **PDBTitle:** crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
49	d1w5ra1	Alignment	not modelled	24.1	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
50	c2vfbA_	Alignment	not modelled	24.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylamine n-acetyltransferase; **PDBTitle:** the structure of mycobacterium marinum arylamine n-2 acetyltransferase
51	d1e2ta_	Alignment	not modelled	24.0	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
52	d1g7sa2	Alignment	not modelled	23.7	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
53	d2bsza1	Alignment	not modelled	22.4	29	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
54	c4dmoB_	Alignment	not modelled	21.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-hydroxyarylamine o-acetyltransferase; **PDBTitle:** crystal structure of the (baccr)nat3 arylamine n-acetyltransferase2 from bacillus cereus reveals a unique cys-his-glu catalytic triad

55	c2pfrB_	Alignment	not modelled	21.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylamine n-acetyltransferase 2; **PDBTitle:** human n-acetyltransferase 2
56	c2dt7A_	Alignment	not modelled	19.9	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
57	c3cwyA_	Alignment	not modelled	19.3	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein cagd; **PDBTitle:** structure of cagd from h. pylori pathogenicity island crystallized in2 the presence of cu(ii) ions
58	c3d9wA_	Alignment	not modelled	18.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine n-2 acetyltransferase
59	d1e89a_	Alignment	not modelled	16.6	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
60	c2hcuA_	Alignment	not modelled	16.4	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus mutans
61	c3h5jA_	Alignment	not modelled	16.3	36	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
62	c3q3wB_	Alignment	not modelled	15.2	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
63	c5a4aA_	Alignment	not modelled	14.7	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**maternal effect protein oskar; **PDBTitle:** crystal structure of the osk domain of drosophila oskar
64	c3wwoA_	Alignment	not modelled	14.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(s)-hydroxynitrile lyase; **PDBTitle:** s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
65	c5g1mA_	Alignment	not modelled	13.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase; **PDBTitle:** crystal structure of nagz from pseudomonas aeruginosa
66	c3dqzB_	Alignment	not modelled	13.4	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis thaliana
67	c6nvoA_	Alignment	not modelled	11.9	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nuclease mpe; **PDBTitle:** crystal structure of pseudomonas putida nuclease mpe
68	c2luyA_	Alignment	not modelled	11.7	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**meiotic chromosome segregation protein p8b7.28c; **PDBTitle:** solution structure of the tandem zinc finger domain of fission yeast2 stc1
69	c6fsiA_	Alignment	not modelled	11.7	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** crystal structure of semiquinone flavodoxin 1 from bacillus cereus2 (1.32 a resolution)
70	c3p2mA_	Alignment	not modelled	11.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible hydrolase; **PDBTitle:** crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
71	c5iobC_	Alignment	not modelled	11.7	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-glucosidase-related glycosidases; **PDBTitle:** crystal structure of beta-n-acetylglucosaminidase-like protein from2 corynebacterium glutamicum
72	c4gvgB_	Alignment	not modelled	11.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-hexosaminidase; **PDBTitle:** crystal structure of salmonella typhimurium family 3 glycoside2 hydrolase (nagz)
73	d1vfsa2	Alignment	not modelled	10.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
74	c3stxB_	Alignment	not modelled	9.8	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methylketone synthase 1; **PDBTitle:** crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate
75	c6gwjK_	Alignment	not modelled	9.8	9	**PDB header:**rna binding protein **Chain:** K: **PDB Molecule:**probable trna n6-adenosine threonylcarbamoyltransferase; **PDBTitle:** protein complex
76	c4em8A_	Alignment	not modelled	9.5	67	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase b; **PDBTitle:** the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
77	c3qd5B_	Alignment	not modelled	9.5	44	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
78	d1e5da1	Alignment	not modelled	9.4	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
79	c4lfnD_	Alignment	not modelled	9.4	56	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**galactose-6-phosphate isomerase subunit b;

						PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-ribulose
80	d1nn4a_	Alignment	not modelled	9.4	33	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
81	c6ahuK_	Alignment	not modelled	9.2	38	**PDB header:**hydrolase/rna **Chain:** K: **PDB Molecule:**ribonuclease p protein subunit p21; **PDBTitle:** cryo-em structure of human ribonuclease p with mature trna
82	d1g8ka2	Alignment	not modelled	9.2	12	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
83	d1dmra2	Alignment	not modelled	9.0	15	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
84	c4uuzC_	Alignment	not modelled	9.0	29	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna replication licensing factor mcm2; **PDBTitle:** mcm2-histone complex
85	c6mu0A_	Alignment	not modelled	8.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable ribose-5-phosphate isomerase b; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
86	c1jjoB_	Alignment	not modelled	8.8	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**neuroserpin; **PDBTitle:** crystal structure of mouse neuroserpin (cleaved form)
87	c4lfmA_	Alignment	not modelled	8.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**galactose-6-phosphate isomerase subunit a; **PDBTitle:** crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-psicose
88	d3c70a1	Alignment	not modelled	8.4	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
89	c2pkpA_	Alignment	not modelled	8.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
90	c3m1pA_	Alignment	not modelled	8.2	56	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
91	c3k7pA_	Alignment	not modelled	8.2	56	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
92	c6ah3K_	Alignment	not modelled	8.1	10	**PDB header:**hydrolase/rna **Chain:** K: **PDB Molecule:**ribonuclease p protein subunit rpr2; **PDBTitle:** cryo-em structure of yeast ribonuclease p with pre-trna substrate
93	c6fxwA_	Alignment	not modelled	8.1	67	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ribose 5-phosphate isomerase; **PDBTitle:** structure of leishmania infantum type b ribose 5-phosphate isomerase
94	c1g8jC_	Alignment	not modelled	8.1	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
95	c3he8A_	Alignment	not modelled	8.0	56	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
96	c3vbaE_	Alignment	not modelled	8.0	31	**PDB header:**lyase **Chain:** E: **PDB Molecule:**isopropylmalate/citramalate isomerase small subunit; **PDBTitle:** crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
97	c3s5pA_	Alignment	not modelled	7.9	67	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
98	c4lidA_	Alignment	not modelled	7.8	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**a-100; **PDBTitle:** a100, a dna binding scaffold from sulfolobus spindle-shape virus 1
99	c3j20F_	Alignment	not modelled	7.8	26	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**30s ribosomal protein s5p; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)