Phyre^2

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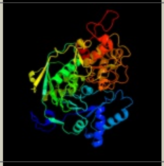
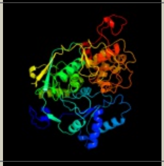
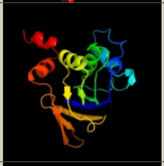
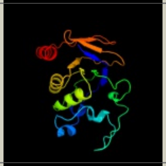
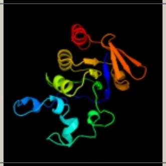
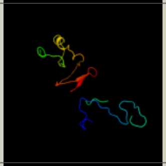
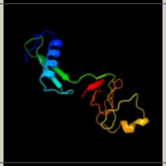
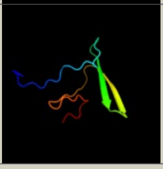
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1l5jB_	Alignment		100.0	100	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aconitate hydratase 2; **PDBTitle:** crystal structure of e. coli aconitase b.
2	d1l5ja3	Alignment		100.0	100	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
3	d1acoa2	Alignment		100.0	22	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
4	c5acnA_	Alignment		100.0	22	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
5	d2b3ya2	Alignment		100.0	22	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
6	c2b3yB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
7	d1l5ja1	Alignment		100.0	100	**Fold:**alpha-alpha superhelix **Superfamily:**Aconitase B, N-terminal domain **Family:**Aconitase B, N-terminal domain
8	d1l5ja2	Alignment		100.0	100	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
9	d1v7la_	Alignment		99.9	28	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
10	c2pkpA_	Alignment		99.9	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
11	d2b3ya1	Alignment		99.7	25	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like

12	d1acoa1	Alignment		99.7	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
13	c2hcuA_	Alignment		99.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
14	c3q3wB_	Alignment		99.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
15	c3h5jA_	Alignment		99.5	20	**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
16	c3t07D_	Alignment		87.8	20	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
17	c2e28A_	Alignment		72.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
18	d1kbla2	Alignment		54.6	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
19	d1vbga2	Alignment		53.4	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
20	d1h6za2	Alignment		45.4	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
21	d1xdpa3	Alignment	not modelled	42.0	11	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
22	d2fe0a1	Alignment	not modelled	37.9	30	**Fold:**Smp-1-like **Superfamily:**Smp-1-like **Family:**Smp-1-like
23	d2hi6a1	Alignment	not modelled	35.7	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
24	d2gp4a1	Alignment	not modelled	35.6	32	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
25	c2gp4A_	Alignment	not modelled	34.3	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
26	d2z1ca1	Alignment	not modelled	31.5	11	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
27	d2ot2a1	Alignment	not modelled	27.0	17	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
28	c2gefA_	Alignment	not modelled	24.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease vp4; **PDBTitle:** crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism
29	d1zyma2	Alignment	not modelled	23.0	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain

29	d1zyma2	Alignment	not modelled	23.0	14	**Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
30	c2fsdB_	Alignment	not modelled	22.8	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**putative baseplate protein; **PDBTitle:** a common fold for the receptor binding domains of2 lactococcal phages? the crystal structure of the head3 domain of phage bil170
31	d1kjna_	Alignment	not modelled	22.3	16	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
32	c3d0fA_	Alignment	not modelled	21.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
33	d1uw4a_	Alignment	not modelled	21.2	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Smg-4/UPF3
34	c3pcoC_	Alignment	not modelled	20.7	23	**PDB header:**ligase **Chain:** C: **PDB Molecule:**phenylalanyl-trna synthetase, alpha subunit; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
35	c3r74B_	Alignment	not modelled	19.5	21	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
36	c3d3rA_	Alignment	not modelled	19.5	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
37	c1dgsB_	Alignment	not modelled	19.3	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
38	d2ivda2	Alignment	not modelled	19.2	29	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
39	c1ni5A_	Alignment	not modelled	18.9	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
40	d3d3ra1	Alignment	not modelled	18.9	18	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
41	d1obra_	Alignment	not modelled	18.9	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Carboxypeptidase T
42	c2ebbA_	Alignment	not modelled	18.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
43	c3k2gA_	Alignment	not modelled	18.2	14	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
44	d1r5ta_	Alignment	not modelled	17.8	22	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
45	c2fgxA_	Alignment	not modelled	17.7	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
46	c3l4gI_	Alignment	not modelled	17.5	21	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
47	d2pjua1	Alignment	not modelled	17.3	19	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
48	c2xecD_	Alignment	not modelled	17.1	9	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
49	c3b8fB_	Alignment	not modelled	17.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative blasticidin s deaminase; **PDBTitle:** crystal structure of the cytidine deaminase from bacillus anthracis
50	d1elka_	Alignment	not modelled	17.0	21	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
51	d1uwza_	Alignment	not modelled	16.5	9	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
52	d2d30a1	Alignment	not modelled	16.5	17	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
53	c3r2nC_	Alignment	not modelled	16.3	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from

						mycobacterium leprae
54	c2yb1A_	Alignment	not modelled	16.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
55	c2kenA_	Alignment	not modelled	15.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
56	c2duwA_	Alignment	not modelled	15.8	21	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
57	c2q5cA_	Alignment	not modelled	15.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
58	c3dcpB_	Alignment	not modelled	15.5	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol-phosphatase; **PDBTitle:** crystal structure of the putative histidinol phosphatase2 hisk from listeria monocytogenes. northeast structural3 genomics consortium target lmr141.
59	c3bolB_	Alignment	not modelled	15.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
60	d2jnaa1	Alignment	not modelled	15.3	13	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
61	c3h8aF_	Alignment	not modelled	15.0	27	**PDB header:**lyase/protein binding **Chain:** F: **PDB Molecule:**rnase e; **PDBTitle:** crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
62	c2jz2A_	Alignment	not modelled	14.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
63	c1pt1B_	Alignment	not modelled	14.7	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
64	c2e21A_	Alignment	not modelled	14.7	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
65	d1gg2g_	Alignment	not modelled	14.6	30	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
66	d2gysa1	Alignment	not modelled	14.6	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
67	d1w44a_	Alignment	not modelled	14.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
68	c3h8aE_	Alignment	not modelled	14.3	27	**PDB header:**lyase/protein binding **Chain:** E: **PDB Molecule:**rnase e; **PDBTitle:** crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
69	c2owoA_	Alignment	not modelled	14.1	23	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
70	d1seza2	Alignment	not modelled	13.9	24	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
71	d2fr5a1	Alignment	not modelled	13.8	9	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
72	d2cb5a_	Alignment	not modelled	13.7	23	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
73	c1ytzI_	Alignment	not modelled	13.6	25	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 activated state
74	d2ga5a1	Alignment	not modelled	13.6	29	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
75	c2fhdA_	Alignment	not modelled	13.5	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
76	c3dmoD_	Alignment	not modelled	13.5	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytidine deaminase; **PDBTitle:** 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei
77	d1iuka_	Alignment	not modelled	13.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
78	d1ppya_	Alignment	not modelled	13.4	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
						PDB header:transcription regulator

79	c2l33A_	Alignment	not modelled	13.4	27	**Chain:** A: **PDB Molecule:**interleukin enhancer-binding factor 3; **PDBTitle:** solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast structural genomics3 consortium target hr4527e
80	d1jjca_	Alignment	not modelled	13.3	20	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
81	c3imoC_	Alignment	not modelled	13.3	26	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14
82	d2fz5a1	Alignment	not modelled	13.3	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
83	c6r1rD_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** D: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441d mutant r1 protein from2 escherichia coli
84	c5r1rD_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** D: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441a mutant r1 protein from2 escherichia coli
85	c7r1rE_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** E: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441q mutant r1 protein from2 escherichia coli
86	c7r1rD_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** D: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441q mutant r1 protein from2 escherichia coli
87	c6r1rE_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** E: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441d mutant r1 protein from2 escherichia coli
88	c5r1rE_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** E: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441a mutant r1 protein from2 escherichia coli
89	c5r1rF_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** F: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441a mutant r1 protein from2 escherichia coli
90	c7r1rF_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** F: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441q mutant r1 protein from2 escherichia coli
91	c6r1rF_	Alignment	not modelled	13.2	55	**PDB header:**complex (oxidoreductase/peptide) **Chain:** F: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase e441d mutant r1 protein from2 escherichia coli
92	c2xaxD_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y730no2y and y731a modified r12 subunit of e. coli
93	c2xakD_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y730no2y modified r1 subunit of e.2 coli
94	c2x1yF_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y731no2y modified r1 subunit of e.2 coli to 2.1 a resolution
95	c2x3sE_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y730no2y and c439a modified r12 subunit of e. coli
96	c2x33F_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y731no2y and y730f modified r12 subunit of e. coli
97	c2x3sF_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y730no2y and c439a modified r12 subunit of e. coli
98	c1r1rF_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**ribonucleotide reductase r2 protein; **PDBTitle:** ribonucleotide reductase r1 protein mutant y730f with a2 reduced active site from escherichia coli
99	c2x0zF_	Alignment	not modelled	13.0	55	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 subunit **PDBTitle:** ribonucleotide reductase y730no2y modified r1 subunit of e.2 coli