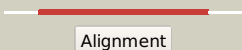







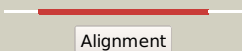

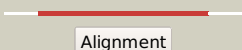



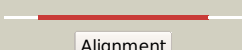

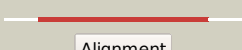

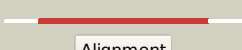









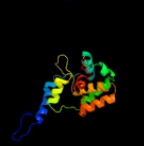




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3051c_nrdE_3412096_3414177
Date	Thu Aug 8 16:20:22 BST 2019
Unique Job ID	eb88bc9a0624d2b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1pemA_</a>	 Alignment		100.0	72	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase 2 alpha <b>PDBTitle:</b> ribonucleotide reductase protein r1e from salmonella2 typhimurium
2	<a href="#">c6cgmA_</a>	 Alignment		100.0	48	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> x-ray crystal structure of bacillus subtilis ribonucleotide reductase2 nrde alpha subunit (nucleotide free)
3	<a href="#">c3r1rB_</a>	 Alignment		100.0	24	<b>PDB header:</b> complex (oxidoreductase/peptide) <b>Chain:</b> B; <b>PDB Molecule:</b> ribonucleotide reductase r1 protein; <b>PDBTitle:</b> ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
4	<a href="#">c1zyzA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large chain 1; <b>PDBTitle:</b> structures of yeast ribonucleotide reductase i
5	<a href="#">c2wghA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large <b>PDBTitle:</b> human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
6	<a href="#">c2cvuA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large chain <b>PDBTitle:</b> structures of yeast ribonucleotide reductase i
7	<a href="#">c5im3A_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> crystal structure of the class i ribonucleotide reductase from2 pseudomonas aeruginosa in complex with datp
8	<a href="#">c3hnfA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large subunit; <b>PDBTitle:</b> crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
9	<a href="#">c3rsrA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large chain 1; <b>PDBTitle:</b> crystal structure of 5-nitp inhibition of yeast ribonucleotide2 reductase
10	<a href="#">c3pawD_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large chain 1; <b>PDBTitle:</b> low resolution x-ray crystal structure of yeast rnr1p with datp bound2 in the a-site
11	<a href="#">c1xjeA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleotide reductase, b12-dependent; <b>PDBTitle:</b> structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex

12	<a href="#">d1r1ra2</a>	Alignment		100.0	27	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> R1 subunit of ribonucleotide reductase, C-terminal domain
13	<a href="#">d1peqa2</a>	Alignment		100.0	74	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> R1 subunit of ribonucleotide reductase, C-terminal domain
14	<a href="#">c6dqxA</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase, alpha chain; <b>PDBTitle:</b> actinobacillus ureae class id ribonucleotide reductase alpha subunit
15	<a href="#">c6dqWB</a>	Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase, alpha chain; <b>PDBTitle:</b> flavobacterium johnsoniae class id ribonucleotide reductase alpha2 subunit
16	<a href="#">c6dqWD</a>	Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase, alpha chain; <b>PDBTitle:</b> flavobacterium johnsoniae class id ribonucleotide reductase alpha2 subunit
17	<a href="#">d1l1la</a>	Alignment		100.0	19	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> B12-dependent (class II) ribonucleotide reductase
18	<a href="#">d1peqa1</a>	Alignment		100.0	64	<b>Fold:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Superfamily:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Family:</b> R1 subunit of ribonucleotide reductase, N-terminal domain
19	<a href="#">d1r1ra1</a>	Alignment		100.0	11	<b>Fold:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Superfamily:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Family:</b> R1 subunit of ribonucleotide reductase, N-terminal domain
20	<a href="#">c4u3eA</a>	Alignment		98.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase
21	<a href="#">c1hk8A</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase; <b>PDBTitle:</b> structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp
22	<a href="#">d1hk8a</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit
23	<a href="#">c1h7bA</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase large <b>PDBTitle:</b> structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases, native nrdd
24	<a href="#">c3pg6D</a>	Alignment	not modelled	59.7	22	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase dtx3l; <b>PDBTitle:</b> the carboxyl terminal domain of human deltex 3-like
25	<a href="#">d1h16a</a>	Alignment	not modelled	57.7	15	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> PFL-like
26	<a href="#">d2okqa1</a>	Alignment	not modelled	51.4	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> YbaA-like
27	<a href="#">c3vndD</a>	Alignment	not modelled	47.1	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
28	<a href="#">c4ov9A</a>	Alignment	not modelled	41.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isopropylmalate synthase; <b>PDBTitle:</b> structure of isopropylmalate synthase binding with alpha-

						2 isopropylmalate
29	<a href="#">c2okqB_</a>	Alignment	not modelled	41.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ybaa; <b>PDBTitle:</b> crystal structure of unknown conserved ybaa protein from shigella2 flexneri
30	<a href="#">c5ey5A_</a>	Alignment	not modelled	39.7	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
31	<a href="#">d1h3ob_</a>	Alignment	not modelled	36.3	9	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
32	<a href="#">c3p9a_</a>	Alignment	not modelled	35.9	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> dna-packaging protein gp3; <b>PDBTitle:</b> an atomic view of the nonameric small terminase subunit of2 bacteriophage p22
33	<a href="#">d2ccqa1</a>	Alignment	not modelled	31.9	12	<b>Fold:</b> PUG domain-like <b>Superfamily:</b> PUG domain-like <b>Family:</b> PUG domain
34	<a href="#">c5udbB_</a>	Alignment	not modelled	29.5	11	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
35	<a href="#">c4juyB_</a>	Alignment	not modelled	27.4	8	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf31; <b>PDBTitle:</b> crystal structure of the pub domain of e3 ubiquitin ligase rnf31
36	<a href="#">d1ic8a2</a>	Alignment	not modelled	27.1	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
37	<a href="#">d1geqa_</a>	Alignment	not modelled	26.3	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
38	<a href="#">c6hqaK_</a>	Alignment	not modelled	25.8	10	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> subunit (61/68 kda) of tfiid and saga complexes; <b>PDBTitle:</b> molecular structure of promoter-bound yeast tfiid
39	<a href="#">d1qhma_</a>	Alignment	not modelled	25.8	15	<b>Fold:</b> PFL-like glycol radical enzymes <b>Superfamily:</b> PFL-like glycol radical enzymes <b>Family:</b> PFL-like
40	<a href="#">c5kzmA_</a>	Alignment	not modelled	24.3	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
41	<a href="#">c3u3iA_</a>	Alignment	not modelled	23.9	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid protein; <b>PDBTitle:</b> a rna binding protein from crimean-congo hemorrhagic fever virus
42	<a href="#">d1v93a_</a>	Alignment	not modelled	21.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FAD-linked oxidoreductase <b>Family:</b> Methylenetetrahydrofolate reductase
43	<a href="#">c5tchG_</a>	Alignment	not modelled	21.4	14	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
44	<a href="#">c4xgcB_</a>	Alignment	not modelled	18.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
45	<a href="#">c6fosO_</a>	Alignment	not modelled	17.5	10	<b>PDB header:</b> photosynthesis <b>Chain:</b> O: <b>PDB Molecule:</b> psam; <b>PDBTitle:</b> cyanidioschyzon merolae photosystem i
46	<a href="#">c5vodD_</a>	Alignment	not modelled	17.3	19	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> D: <b>PDB Molecule:</b> envelope glycoprotein ul130; <b>PDBTitle:</b> crystal structure of hcmv pentamer in complex with neutralizing2 antibody 9i6
47	<a href="#">c3navB_</a>	Alignment	not modelled	15.8	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
48	<a href="#">c5ze4A_</a>	Alignment	not modelled	15.6	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
49	<a href="#">d1msza_</a>	Alignment	not modelled	15.6	14	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
50	<a href="#">c1msza_</a>	Alignment	not modelled	15.6	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein smubp-2; <b>PDBTitle:</b> solution structure of the r3h domain from human smubp-2
51	<a href="#">d2d5ua1</a>	Alignment	not modelled	15.1	12	<b>Fold:</b> PUG domain-like <b>Superfamily:</b> PUG domain-like <b>Family:</b> PUG domain
52	<a href="#">c2xrgA_</a>	Alignment	not modelled	14.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
53	<a href="#">d1vmha_</a>	Alignment	not modelled	14.7	13	<b>Fold:</b> YjbQ-like <b>Superfamily:</b> YjbQ-like <b>Family:</b> YjbQ-like
54	<a href="#">d1vmfa_</a>	Alignment	not modelled	14.4	6	<b>Fold:</b> YjbQ-like <b>Superfamily:</b> YjbQ-like <b>Family:</b> YjbQ-like

55	<a href="#">d1vmja_</a>	Alignment	not modelled	14.1	23	<b>Fold:</b> YjbQ-like <b>Superfamily:</b> YjbQ-like <b>Family:</b> YjbQ-like
56	<a href="#">c3kowH_</a>	Alignment	not modelled	13.8	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> d-ornithine aminomutase s component; <b>PDBTitle:</b> crystal structure of ornithine 4,5 aminomutase backsoaked complex
57	<a href="#">d1td6a_</a>	Alignment	not modelled	13.7	23	<b>Fold:</b> Hypothetical protein MPN330 <b>Superfamily:</b> Hypothetical protein MPN330 <b>Family:</b> Hypothetical protein MPN330
58	<a href="#">c4pfxA_</a>	Alignment	not modelled	13.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase (galt1); <b>PDBTitle:</b> the highly conserved domain of unknown function 1792 has a distinct2 glycosyltransferase fold
59	<a href="#">d1vkna2</a>	Alignment	not modelled	13.4	14	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
60	<a href="#">c2i3eA_</a>	Alignment	not modelled	13.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> g-rich; <b>PDBTitle:</b> solution structure of catalytic domain of goldfish rich2 protein
61	<a href="#">c5v4aB_</a>	Alignment	not modelled	12.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase (duf1792); <b>PDBTitle:</b> a new glycosyltransferase (duf1792) from streptococcus sanguinis
62	<a href="#">d1v74b_</a>	Alignment	not modelled	12.4	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Colicin D immunity protein <b>Family:</b> Colicin D immunity protein
63	<a href="#">c3rcqA_</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl/asparaginyl beta-hydroxylase; <b>PDBTitle:</b> crystal structure of human aspartate beta-hydroxylase isoform a
64	<a href="#">c2p6hB_</a>	Alignment	not modelled	11.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
65	<a href="#">c2v1nA_</a>	Alignment	not modelled	11.7	19	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein kin homolog; <b>PDBTitle:</b> solution structure of the region 51-160 of human kin172 reveals a winged helix fold
66	<a href="#">c2xr9A_</a>	Alignment	not modelled	11.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> crystal structure of autotaxin (enpp2)
67	<a href="#">c5c8hA_</a>	Alignment	not modelled	11.4	30	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 2; <b>PDBTitle:</b> crystal structure of orc2 c-terminal domain
68	<a href="#">c4b56A_</a>	Alignment	not modelled	11.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
69	<a href="#">c5jqvA_</a>	Alignment	not modelled	11.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl/asparaginyl beta-hydroxylase; <b>PDBTitle:</b> aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
70	<a href="#">c5ym0A_</a>	Alignment	not modelled	10.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the crystal structure of dhad
71	<a href="#">c3oiyB_</a>	Alignment	not modelled	10.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase helicase domain; <b>PDBTitle:</b> helicase domain of reverse gyrase from thermotoga maritima
72	<a href="#">d1vpha_</a>	Alignment	not modelled	10.4	11	<b>Fold:</b> YjbQ-like <b>Superfamily:</b> YjbQ-like <b>Family:</b> YjbQ-like
73	<a href="#">c5ujmB_</a>	Alignment	not modelled	10.2	30	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2; <b>PDBTitle:</b> structure of the active form of human origin recognition complex and2 its atpase motor module
74	<a href="#">c5v89A_</a>	Alignment	not modelled	10.0	21	<b>PDB header:</b> ligase / protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dcn1-like protein 4; <b>PDBTitle:</b> structure of dcn4 pony domain bound to cul1 whb
75	<a href="#">c3ty3A_</a>	Alignment	not modelled	10.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable homoisocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of homoisocitrate dehydrogenase from2 schizosaccharomyces pombe bound to glycyL-glycyl-glycine
76	<a href="#">c3pe0B_</a>	Alignment	not modelled	9.9	36	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the central region of the plakin domain of plectin
77	<a href="#">c5i2gB_</a>	Alignment	not modelled	9.9	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diol dehydratase; <b>PDBTitle:</b> 1,2-propanediol dehydration in roseburia inulinivorans; structural2 basis for substrate and enantiomer selectivity
78	<a href="#">c2p6cB_</a>	Alignment	not modelled	9.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> aq_2013 protein; <b>PDBTitle:</b> crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
79	<a href="#">c5j84A_</a>	Alignment	not modelled	9.8	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form
80	<a href="#">c2i09A_</a>	Alignment	not modelled	9.6	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> asr4154 protein; <b>PDBTitle:</b> solution nmr structure of protein asr4154 from nostoc sp.

				pcc71202 northeast structural genomics consortium target id nsr143	
81	<a href="#">d2d0ob1</a>	Alignment	not modelled	9.4	19 <b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> B12-dependent dehydratase associated subunit <b>Family:</b> Dehydratase-reactivating factor beta subunit
82	<a href="#">c3h1yA</a>	Alignment	not modelled	9.3	9 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
83	<a href="#">c5xgqB</a>	Alignment	not modelled	9.0	10 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine-trna ligase; <b>PDBTitle:</b> crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase
84	<a href="#">c3q7cA</a>	Alignment	not modelled	8.9	15 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> exonuclease domain of lassa virus nucleoprotein bound to manganese
85	<a href="#">d2b4va2</a>	Alignment	not modelled	8.9	33 <b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> RNA editing terminal uridylyl transferase 2, RET2, catalytic domain
86	<a href="#">c5wqIC</a>	Alignment	not modelled	8.8	15 <b>PDB header:</b> protein binding/signaling protein/hydrol <b>Chain:</b> C: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> structure of a pdz-protease bound to a substrate-binding adaptor
87	<a href="#">c4cx8B</a>	Alignment	not modelled	8.7	50 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> pseudorabies virus protease; <b>PDBTitle:</b> monomeric pseudorabies virus protease pul26n at 2.5 a resolution
88	<a href="#">d1vkia</a>	Alignment	not modelled	8.6	7 <b>Fold:</b> YbaK/ProRS associated domain <b>Superfamily:</b> YbaK/ProRS associated domain <b>Family:</b> YbaK/ProRS associated domain
89	<a href="#">c2c1fA</a>	Alignment	not modelled	8.5	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional endo-1,4-beta-xylanase a; <b>PDBTitle:</b> the structure of the family 11 xylanase from neocallimastix2 patriciarum
90	<a href="#">c4djzH</a>	Alignment	not modelled	8.5	31 <b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> protease inhibitor sgpi-2; <b>PDBTitle:</b> catalytic fragment of masp-1 in complex with its specific inhibitor2 developed by directed evolution on sgci scaffold
91	<a href="#">c5d9aD</a>	Alignment	not modelled	8.2	13 <b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> polymerase acidic protein; <b>PDBTitle:</b> influenza c virus rna-dependent rna polymerase - space group p212121
92	<a href="#">c3w53A</a>	Alignment	not modelled	8.1	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of psychrophilic beta-glucosidase bglu from2 micrococcus antarcticus
93	<a href="#">d1j09a2</a>	Alignment	not modelled	8.1	17 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
94	<a href="#">c5dmuA</a>	Alignment	not modelled	8.0	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nhej polymerase; <b>PDBTitle:</b> structure of the nhej polymerase from methanocella paludicola
95	<a href="#">d1at3a</a>	Alignment	not modelled	8.0	40 <b>Fold:</b> Herpes virus serine proteinase, assemblin <b>Superfamily:</b> Herpes virus serine proteinase, assemblin <b>Family:</b> Herpes virus serine proteinase, assemblin
96	<a href="#">c3ig3A</a>	Alignment	not modelled	7.9	22 <b>PDB header:</b> signaling protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> plxna3 protein; <b>PDBTitle:</b> crystal structure of mouse plexin a3 intracellular domain
97	<a href="#">c1eu1A</a>	Alignment	not modelled	7.9	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
98	<a href="#">d1wiga2</a>	Alignment	not modelled	7.8	33 <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
99	<a href="#">c2v3sB</a>	Alignment	not modelled	7.8	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase osr1; <b>PDBTitle:</b> structural insights into the recognition of substrates and2 activators by the osr1 kinase