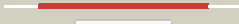



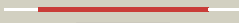




























Phyre2

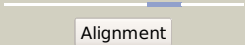
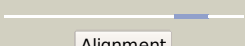
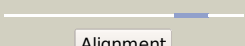
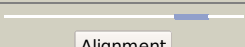
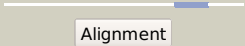


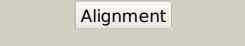
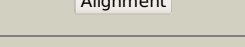
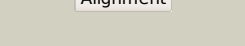
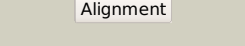



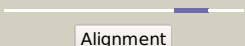
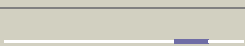

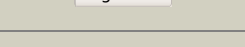
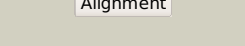
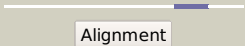
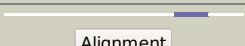

Email	mdejesus@rockefeller.edu
Description	RVBD0570_(nrdZ)_661298_663376
Date	Fri Jul 26 01:50:12 BST 2019
Unique Job ID	ed0e4a88b47e40a1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5im3A_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: crystal structure of the class i ribonucleotide reductase from2 pseudomonas aeruginosa in complex with datp
2	c1zyzA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain 1; PDBTitle: structures of yeast ribonucleotide reductase i
3	c3hnfA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large subunit; PDBTitle: crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
4	c3r1rB_	 Alignment		100.0	24	PDB header: complex (oxidoreductase/peptide) Chain: B: PDB Molecule: ribonucleotide reductase r1 protein; PDBTitle: ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
5	c2cvuA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain PDBTitle: structures of yeast ribonucleotide reductase i
6	c2wghA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large PDBTitle: human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
7	c3pawD_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase large chain 1; PDBTitle: low resolution x-ray crystal structure of yeast rnr1p with datp bound2 in the a-site
8	c1pemA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase 2 alpha PDBTitle: ribonucleotide reductase protein r1e from salmonella2 typhimurium
9	c3rsrA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain 1; PDBTitle: crystal structure of 5-nitp inhibition of yeast ribonucleotide2 reductase
10	c1xjeA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase, b12-dependent; PDBTitle: structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex
11	c6cgmA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: x-ray crystal structure of bacillus subtilis ribonucleotide reductase2 nrde alpha subunit (nucleotide free)

12	c6dqxA_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside-diphosphate reductase, alpha chain; PDBTitle: actinobacillus ureae class id ribonucleotide reductase alpha subunit
13	c6dqwB_	Alignment		100.0	29	PDB header: oxidoreductase Chain: B; PDB Molecule: ribonucleoside-diphosphate reductase, alpha chain; PDBTitle: flavobacterium johnsoniae class id ribonucleotide reductase alpha2 subunit
14	d1r1ra2	Alignment		100.0	27	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
15	d1peqa2	Alignment		100.0	33	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
16	d1l1la_	Alignment		100.0	20	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: B12-dependent (class II) ribonucleotide reductase
17	c6dqwD_	Alignment		100.0	31	PDB header: oxidoreductase Chain: D; PDB Molecule: ribonucleoside-diphosphate reductase, alpha chain; PDBTitle: flavobacterium johnsoniae class id ribonucleotide reductase alpha2 subunit
18	d1r1ra1	Alignment		100.0	18	Fold: R1 subunit of ribonucleotide reductase, N-terminal domain Superfamily: R1 subunit of ribonucleotide reductase, N-terminal domain Family: R1 subunit of ribonucleotide reductase, N-terminal domain
19	d1peqa1	Alignment		99.9	16	Fold: R1 subunit of ribonucleotide reductase, N-terminal domain Superfamily: R1 subunit of ribonucleotide reductase, N-terminal domain Family: R1 subunit of ribonucleotide reductase, N-terminal domain
20	c5olkD_	Alignment		99.7	31	PDB header: oxidoreductase Chain: D; PDB Molecule: ribonucleoside-diphosphate reductase, beta subunit 1; PDBTitle: crystal structure of the atp-cone-containing nrdb from2 leeuwenhoekiella blandensis
21	d1hk8a_	Alignment	not modelled	98.4	17	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
22	c1hk8A_	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: A; PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dntp
23	c1h7bA_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: A; PDB Molecule: anaerobic ribonucleotide-triphosphate reductase large PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases, native nrdd
24	c4u3eA_	Alignment	not modelled	98.3	17	PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
25	d1h16a_	Alignment	not modelled	83.8	18	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
26	c5i2gB_	Alignment	not modelled	71.0	19	PDB header: lyase Chain: B; PDB Molecule: diol dehydratase; PDBTitle: 1,2-propanediol dehydration in roseburia inulinivorans; structural2 basis for substrate and enantiomer selectivity
27	d1qhma_	Alignment	not modelled	64.9	17	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
28	c2f3oB_	Alignment	not modelled	56.3	20	PDB header: unknown function Chain: B; PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycy radical enzyme from archaeoglobus2 fulgidus

29	c5k9xA	Alignment	not modelled	51.3	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
30	c5fayA	Alignment	not modelled	49.3	19	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine-lyase; PDBTitle: y208f mutant of choline tma-lyase
31	d1r9da	Alignment	not modelled	48.3	20	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
32	c5ey5A	Alignment	not modelled	47.6	17	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
33	c3pg6D	Alignment	not modelled	46.3	21	PDB header: ligase Chain: D: PDB Molecule: e3 ubiquitin-protein ligase dtx3l; PDBTitle: the carboxyl terminal domain of human deltex 3-like
34	c1obfO	Alignment	not modelled	39.3	31	PDB header: glycolytic pathway Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylooxidans at 1.7 a3 resolution.
35	c2ekcA	Alignment	not modelled	33.8	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
36	d1h3ob	Alignment	not modelled	32.9	19	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
37	c3vndD	Alignment	not modelled	32.1	17	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
38	c5kzmA	Alignment	not modelled	30.7	14	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
39	c5a0uA	Alignment	not modelled	29.7	20	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine lyase; PDBTitle: structure of cutc choline lyase choline bound form from klebsiella2 pneumoniae.
40	c2x5kO	Alignment	not modelled	29.1	19	PDB header: oxidoreductase Chain: O: PDB Molecule: d-erythrose-4-phosphate dehydrogenase; PDBTitle: structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
41	d1hdgo2	Alignment	not modelled	27.8	31	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
42	c3ng3A	Alignment	not modelled	26.6	28	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
43	d1geqa	Alignment	not modelled	25.4	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	c5tchG	Alignment	not modelled	24.7	20	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
45	c2d2iO	Alignment	not modelled	24.5	22	PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
46	c1hdgO	Alignment	not modelled	24.3	31	PDB header: oxidoreductase (aldehy(d)-nad(a)) Chain: O: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution
47	c5dbul	Alignment	not modelled	24.3	16	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
48	c2i3eA	Alignment	not modelled	23.9	33	PDB header: hydrolase Chain: A: PDB Molecule: g-rich; PDBTitle: solution structure of catalytic domain of goldfish rich2 protein
49	c1cerC	Alignment	not modelled	23.7	31	PDB header: oxidoreductase (aldehy(d)-nad(a)) Chain: C: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
50	c6fosO	Alignment	not modelled	23.5	17	PDB header: photosynthesis Chain: O: PDB Molecule: psam; PDBTitle: cyanidioschyzon merolae photosystem i
51	c3navB	Alignment	not modelled	23.1	16	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
52	d1zeta1	Alignment	not modelled	23.0	11	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain

53	c6hqaK	 Alignment	not modelled	22.9	19	PDB header: transcription Chain: K; PDB Molecule: subunit (61/68 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
54	c3b20R	 Alignment	not modelled	22.6	22	PDB header: oxidoreductase Chain: R; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadfrom synechococcus elongatus"
55	c1ihxD	 Alignment	not modelled	22.2	28	PDB header: oxidoreductase Chain: D; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
56	c3ngjC	 Alignment	not modelled	22.0	23	PDB header: lyase Chain: C; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
57	d1ub3a	 Alignment	not modelled	21.9	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	c3sthA	 Alignment	not modelled	21.7	31	PDB header: oxidoreductase Chain: A; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
59	d1o0ya	 Alignment	not modelled	21.3	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
60	d2ccqa1	 Alignment	not modelled	21.0	16	Fold: PUG domain-like Superfamily: PUG domain-like Family: PUG domain
61	c4xbsA	 Alignment	not modelled	20.9	23	PDB header: lyase Chain: A; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
62	c5ur0B	 Alignment	not modelled	20.7	28	PDB header: oxidoreductase Chain: B; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
63	c4dibF	 Alignment	not modelled	20.1	19	PDB header: oxidoreductase Chain: F; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 bacillus anthracis str. Sterne
64	c3docD	 Alignment	not modelled	20.0	28	PDB header: oxidoreductase Chain: D; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of trka glyceraldehyde-3-phosphate dehydrogenase2 from brucella melitensis
65	c3hjaB	 Alignment	not modelled	19.4	28	PDB header: oxidoreductase Chain: B; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 borrelia burgdorferi
66	c5ymrB	 Alignment	not modelled	19.3	16	PDB header: lyase Chain: B; PDB Molecule: formate acetyltransferase; PDBTitle: the crystal structure of iseg
67	c6ok4A	 Alignment	not modelled	18.9	25	PDB header: oxidoreductase Chain: A; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase (gapdh)2 from chlamydia trachomatis with bound nad
68	c2pkrl	 Alignment	not modelled	18.5	19	PDB header: oxidoreductase Chain: I; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase aor; PDBTitle: crystal structure of (a+cte)4 chimeric form of photosynthetic2 glyceraldehyde-3-phosphate dehydrogenase, complexed with nadp
69	d1k3ta2	 Alignment	not modelled	17.7	25	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
70	c3h9eO	 Alignment	not modelled	17.7	28	PDB header: oxidoreductase Chain: O; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase, testis-specific; PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
71	c1rm4O	 Alignment	not modelled	17.4	19	PDB header: oxidoreductase Chain: O; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
72	d1ic8a2	 Alignment	not modelled	17.3	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
73	c1s7cA	 Alignment	not modelled	17.2	33	PDB header: structural genomics, oxidoreductase Chain: A; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
74	d1i32a2	 Alignment	not modelled	17.1	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like

75	c2v3sB	 Alignment	not modelled	16.8	21	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase osr1; PDBTitle: structural insights into the recognition of substrates and2 activators by the osr1 kinase
76	c3cieC	 Alignment	not modelled	16.8	25	PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
77	d1obfo2	 Alignment	not modelled	16.6	31	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
78	c5udbB	 Alignment	not modelled	16.4	3	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
79	d1ulra	 Alignment	not modelled	16.4	11	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
80	c2b4rQ	 Alignment	not modelled	16.3	25	PDB header: oxidoreductase Chain: Q: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
81	d1n7ka	 Alignment	not modelled	16.3	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
82	c2i5pO	 Alignment	not modelled	16.1	31	PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
83	c5hc7A	 Alignment	not modelled	15.7	23	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: prenyltransferase for protein; PDBTitle: crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolo-isopentenylidiphosphate
84	c2dchX	 Alignment	not modelled	15.6	14	PDB header: hydrolase Chain: X: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
85	c2vg2C	 Alignment	not modelled	15.5	23	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
86	c4n7bA	 Alignment	not modelled	15.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: lytb; PDBTitle: structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
87	c5knnG	 Alignment	not modelled	15.1	33	PDB header: ligase Chain: G: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: evolutionary gain of alanine mischarging to non-cognate trnas with a2 g4:u69 base pair
88	c3oa3A	 Alignment	not modelled	15.0	13	PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
89	d1rm4a2	 Alignment	not modelled	14.9	19	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
90	d1vkna2	 Alignment	not modelled	14.8	10	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
91	d1ueha	 Alignment	not modelled	14.5	23	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
92	c4ynhA	 Alignment	not modelled	14.1	33	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 5; PDBTitle: structure of the c. elegans sas-5 implico dimerization domain
93	c2i09A	 Alignment	not modelled	14.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
94	d2g82a2	 Alignment	not modelled	14.0	31	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
95	c3br8A	 Alignment	not modelled	14.0	18	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: crystal structure of acylphosphatase from bacillus subtilis
96	c6az1X	 Alignment	not modelled	13.9	21	PDB header: ribosome/antibiotic Chain: X: PDB Molecule: ribosomal protein s19e; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
97	d1avca2	 Alignment	not modelled	13.8	13	Fold: Annexin Superfamily: Annexin Family: Annexin
98	d1m1ha1	 Alignment	not modelled	13.6	19	Fold: N-utilization substance G protein NusG, insert domain Superfamily: N-utilization substance G protein NusG, insert domain Family: N-utilization substance G protein NusG, insert domain
99	c5jqyA	 Alignment	not modelled	12.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and

