
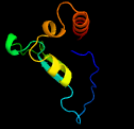


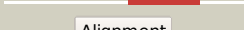




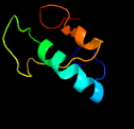











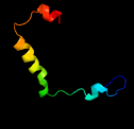






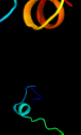

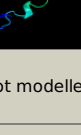


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2972c (-) _3327033_3327746
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	777423d939f00c40

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vgbA_	 Alignment		99.0	25	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of nmeacas9 hnh domain bound to anti-crispr acric1
2	c5axwA_	 Alignment		98.5	19	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
3	c4ogeA_	 Alignment		97.8	40	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease domain protein; PDBTitle: crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
4	c2qgpA_	 Alignment		97.5	22	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87.
5	c4cmqB_	 Alignment		96.8	30	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
6	d1ouoa_	 Alignment		94.1	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Endonuclease I
7	c5mkwA_	 Alignment		92.2	19	PDB header: hydrolase Chain: A: PDB Molecule: dna annealing helicase and endonuclease zranb3; PDBTitle: crystal structure of the human zranb3 hnh domain
8	c5h0mA_	 Alignment		85.2	28	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion
9	c5fhzF_	 Alignment		37.8	18	PDB header: oxidoreductase Chain: F: PDB Molecule: aldehyde dehydrogenase family 1 member a3; PDBTitle: human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid
10	d1jmx1	 Alignment		28.6	13	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
11	c2o2qA_	 Alignment		27.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp

12	c4qyjD	Alignment		27.5	20	PDB header: oxidoreductase Chain: D: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
13	c5b2oA	Alignment		26.4	50	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of francisella novicida cas9 in complex with sgrna2 and target dna (tgg pam)
14	c2m76A	Alignment		24.0	32	PDB header: signaling protein Chain: A: PDB Molecule: carnitine o-palmitoyltransferase 1, brain isoform; PDBTitle: structure of the regulatory domain of human brain carnitine2 palmitoyltransferase 1
15	d1pbya1	Alignment		23.9	4	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
16	c2hqhE	Alignment		23.4	64	PDB header: structural protein, protein binding Chain: E: PDB Molecule: restin; PDBTitle: crystal structure of p150glued and clip-170
17	c3e2uF	Alignment		23.4	64	PDB header: protein binding Chain: F: PDB Molecule: cap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued)
18	c3e2uE	Alignment		23.4	64	PDB header: protein binding Chain: E: PDB Molecule: cap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued)
19	d1bxsa	Alignment		23.1	22	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
20	c3vz0B	Alignment		22.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad-dependent aldehyde dehydrogenase; PDBTitle: structural insights into cofactor and substrate selection by gox0499
21	c2hg2A	Alignment	not modelled	21.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase a; PDBTitle: structure of lactaldehyde dehydrogenase
22	c2mnjA	Alignment	not modelled	21.7	26	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: nmr solution structure of the yeast pih1 and tah1 c-terminal domains2 complex
23	c4o5hD	Alignment	not modelled	21.2	22	PDB header: oxidoreductase Chain: D: PDB Molecule: phenylacetaldehyde dehydrogenase; PDBTitle: x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
24	c3b4wA	Alignment	not modelled	21.1	27	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
25	c3e2uH	Alignment	not modelled	20.7	64	PDB header: protein binding Chain: H: PDB Molecule: cap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued)
26	d1o9ja	Alignment	not modelled	20.4	18	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
27	c4pxlB	Alignment	not modelled	20.3	33	PDB header: oxidoreductase Chain: B: PDB Molecule: cytosolic aldehyde dehydrogenase rf2c; PDBTitle: structure of zm ald2-3 (rf2c) in complex with nad
						PDB header: oxidoreductase Chain: G: PDB Molecule: gamma-glutamyl-gamma-

28	c4lihG	Alignment	not modelled	19.9	16	aminobutyraldehyde dehydrogenase; PDBTitle: the crystal structure of gamma-glutamyl-gamma-aminobutyraldehyde2 dehydrogenase from burkholderia cenocepacia j2315
29	c5mz5A	Alignment	not modelled	19.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: aldh21); PDBTitle: crystal structure of aldehyde dehydrogenase 21 (aldh21) from2 physcomitrella patens in its apoform
30	c5iuuA	Alignment	not modelled	18.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase family protein; PDBTitle: crystal structure of indole-3-acetaldehyde dehydrogenase in apo form
31	c3efvC	Alignment	not modelled	16.8	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
32	c3rh9A	Alignment	not modelled	16.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase (nad(p(+))); PDBTitle: the crystal structure of oxidoreductase from marinobacter aquaeolei
33	c3r64A	Alignment	not modelled	15.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nad dependent benzaldehyde dehydrogenase; PDBTitle: crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
34	c4jz6A	Alignment	not modelled	15.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: salicylaldehyde dehydrogenase nahf; PDBTitle: crystal structure of a salicylaldehyde dehydrogenase from pseudomonas2 putida g7 complexed with salicylaldehyde
35	c5vbfH	Alignment	not modelled	14.7	16	PDB header: oxidoreductase Chain: H: PDB Molecule: nad-dependent succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of succinate semialdehyde dehydrogenase from2 burkholderia vietnamiensis
36	c2ve5H	Alignment	not modelled	14.1	11	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
37	d1pgl22	Alignment	not modelled	14.0	22	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
38	d2f2ha3	Alignment	not modelled	13.9	9	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Putative glucosidase YicI, domain 3
39	c4h7nA	Alignment	not modelled	13.9	9	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: the structure of putative aldehyde dehydrogenase puta from anaena2 variabilis.
40	c5f7sA	Alignment	not modelled	13.8	26	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 31; PDBTitle: cycloalternan-degrading enzyme from trueperella pyogenes
41	c1xsiF	Alignment	not modelled	13.6	11	PDB header: hydrolase Chain: F: PDB Molecule: putative family 31 glucosidase yici; PDBTitle: structure of a family 31 alpha glucosidase
42	d1ny722	Alignment	not modelled	13.5	17	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
43	c3ifgH	Alignment	not modelled	13.1	16	PDB header: oxidoreductase Chain: H: PDB Molecule: succinate-semialdehyde dehydrogenase (nadp+); PDBTitle: crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
44	d1wnda	Alignment	not modelled	13.0	16	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
45	d2fnoa1	Alignment	not modelled	12.7	23	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
46	c3pqaA	Alignment	not modelled	12.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: lactaldehyde dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
47	c4pt3C	Alignment	not modelled	12.4	24	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase; PDBTitle: nadph complex structure of aldehyde dehydrogenase from bacillus cereus
48	c3rkoE	Alignment	not modelled	12.1	31	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
49	c3rkoA	Alignment	not modelled	12.1	31	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
50	c4go4E	Alignment	not modelled	12.1	16	PDB header: oxidoreductase Chain: E: PDB Molecule: putative gamma-hydroxyuconic semialdehyde dehydrogenase; PDBTitle: crystal structure of pnpe in complex with nicotinamide adenine2 dinucleotide
51	c5u0mB	Alignment	not modelled	12.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: n-succinylglutamate 5-semialdehyde dehydrogenase; PDBTitle: fatty aldehyde dehydrogenase from marinobacter aquaeolei vt8 and2 cofactor complex PDB header: oxidoreductase

52	c5tjrE	Alignment	not modelled	11.7	13	Chain: E; PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: x-ray crystal structure of a methylmalonate semialdehyde dehydrogenase2 from pseudomonas sp. aac
53	c4dngB	Alignment	not modelled	11.4	13	PDB header: oxidoreductase Chain: B; PDB Molecule: uncharacterized aldehyde dehydrogenase aldy; PDBTitle: crystal structure of putative aldehyde dehydrogenase from bacillus2 subtilis subsp. subtilis str. 168
54	c3prlD	Alignment	not modelled	11.3	9	PDB header: oxidoreductase Chain: D; PDB Molecule: nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125
55	c4pxnB	Alignment	not modelled	11.2	11	PDB header: oxidoreductase Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: structure of zm ald7 in complex with nad
56	c3vdoB	Alignment	not modelled	11.2	18	PDB header: dna binding protein/protein binding Chain: B; PDB Molecule: anti-sigma-k factor rska; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
57	c3rosA	Alignment	not modelled	10.9	27	PDB header: oxidoreductase Chain: A; PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
58	c3ek1C	Alignment	not modelled	10.8	13	PDB header: oxidoreductase Chain: C; PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
59	c5j6bB	Alignment	not modelled	10.4	18	PDB header: oxidoreductase Chain: B; PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from burkholderia2 thailandensis in covalent complex with nadph
60	c4e4gF	Alignment	not modelled	10.3	13	PDB header: oxidoreductase Chain: F; PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
61	c4itaA	Alignment	not modelled	10.2	18	PDB header: oxidoreductase Chain: A; PDB Molecule: succinate-semialdehyde dehydrogenase; PDBTitle: structure of bacterial enzyme in complex with cofactor
62	c2w8qA	Alignment	not modelled	10.2	13	PDB header: oxidoreductase Chain: A; PDB Molecule: succinate-semialdehyde dehydrogenase, PDBTitle: the crystal structure of human ssadh in complex with ssa.
63	d1w7ca3	Alignment	not modelled	10.2	26	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
64	c5j4aA	Alignment	not modelled	9.6	25	PDB header: toxin Chain: A; PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct toxin from burkholderia pseudomallei e479 in complex with2 cognate cdii immunity protein
65	c4yweE	Alignment	not modelled	9.3	22	PDB header: oxidoreductase Chain: E; PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of a putative aldehyde dehydrogenase from2 burkholderia cenocepacia
66	c1t90B	Alignment	not modelled	9.3	16	PDB header: oxidoreductase Chain: B; PDB Molecule: probable methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate semialdehyde dehydrogenase from2 bacillus subtilis
67	d1o04a	Alignment	not modelled	9.3	27	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
68	c2jg7G	Alignment	not modelled	9.2	18	PDB header: oxidoreductase Chain: G; PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
69	d1ag8a	Alignment	not modelled	9.1	24	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
70	c4xsjA	Alignment	not modelled	9.0	53	PDB header: transport protein Chain: A; PDB Molecule: lysozyme, calcium uniporter protein, mitochondrial; PDBTitle: crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter fused with t4 lysozyme
71	d1euha	Alignment	not modelled	8.9	9	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
72	c3ed6B	Alignment	not modelled	8.7	16	PDB header: oxidoreductase Chain: B; PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
73	c4h73E	Alignment	not modelled	8.7	9	PDB header: oxidoreductase Chain: E; PDB Molecule: aldehyde dehydrogenase; PDBTitle: thermostable aldehyde dehydrogenase from pyrobaculum sp. complexed2 with nadp+
74	c5x5uB	Alignment	not modelled	8.6	15	PDB header: oxidoreductase Chain: B; PDB Molecule: alpha-ketoglutaric semialdehyde dehydrogenase; PDBTitle: crystal structure of alpha-ketoglutarate-semialdehyde dehydrogenase2 (kgsadh) complexed with nad
75	c3k2wD	Alignment	not modelled	8.5	11	PDB header: oxidoreductase Chain: D; PDB Molecule: betaine-aldehyde dehydrogenase; PDBTitle: crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
						PDB header: oxidoreductase Chain: A; PDB Molecule: n-succinylglutamate 5-semialdehyde

76	c4knaA	Alignment	not modelled	8.4	16	dehydrogenase; PDBTitle: crystal structure of an n-succinylglutamate 5-semialdehyde2 dehydrogenase from burkholderia thailandensis
77	c6g72A	Alignment	not modelled	8.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-ubiquinone oxidoreductase chain 3; PDBTitle: mouse mitochondrial complex i in the deactive state
78	d1ky8a	Alignment	not modelled	8.2	18	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
79	c5v89A	Alignment	not modelled	8.2	15	PDB header: ligase / protein binding Chain: A: PDB Molecule: dcn1-like protein 4; PDBTitle: structure of dcn4 pony domain bound to cul1 whb
80	c6ghcA	Alignment	not modelled	8.2	29	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eocmkra restriction endonuclease
81	c5omtA	Alignment	not modelled	7.8	7	PDB header: hydrolase Chain: A: PDB Molecule: nucb; PDBTitle: endonuclease nucb
82	c3topA	Alignment	not modelled	7.7	29	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: maltase-glucoamylase, intestinal; PDBTitle: crystal structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
83	c5dkyA	Alignment	not modelled	7.6	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha glucosidase-like protein; PDBTitle: crystal structure of glucosidase ii alpha subunit (dnj-bound from)
84	c4xpsA	Alignment	not modelled	7.6	26	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of the mutant d365a of pedobacter saltans gh312 alpha-galactosidase complexed with p-nitrophenyl-alpha-3 galactopyranoside
85	c5izdE	Alignment	not modelled	7.3	13	PDB header: oxidoreductase Chain: E: PDB Molecule: d-glyceraldehyde dehydrogenase (nadp(+)); PDBTitle: wild-type glyceraldehyde dehydrogenase from thermoplasma acidophilum2 in complex with nadp
86	c4gaoA	Alignment	not modelled	7.3	19	PDB header: ligase/peptide Chain: A: PDB Molecule: dcn1-like protein 2; PDBTitle: dcn1 complex with n-terminally acetylated nedd8 e2 peptide
87	c3i44A	Alignment	not modelled	7.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
88	d1a4sa	Alignment	not modelled	7.1	18	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
89	c2bpbB	Alignment	not modelled	7.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
90	c5m73D	Alignment	not modelled	7.0	43	PDB header: rna binding protein Chain: D: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
91	c5kzxA	Alignment	not modelled	7.0	28	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-glucosidase; PDBTitle: crystal structure of human gaa
92	c4innA	Alignment	not modelled	7.0	11	PDB header: transport protein Chain: A: PDB Molecule: hp1028; PDBTitle: protein hp1028 from the human pathogen helicobacter pylori belongs to2 the lipocalin family
93	c6feyH	Alignment	not modelled	6.8	33	PDB header: peptide binding protein Chain: H: PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
94	c6feyF	Alignment	not modelled	6.6	33	PDB header: peptide binding protein Chain: F: PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
95	c2wfuB	Alignment	not modelled	6.5	33	PDB header: signaling protein Chain: B: PDB Molecule: probable insulin-like peptide 5 b chain; PDBTitle: crystal structure of dilp5 variant db
96	c2wfvB	Alignment	not modelled	6.5	33	PDB header: signaling protein Chain: B: PDB Molecule: probable insulin-like peptide 5 b chain; PDBTitle: crystal structure of dilp5 variant c4
97	c3lppA	Alignment	not modelled	6.4	18	PDB header: hydrolase Chain: A: PDB Molecule: sucrase-isomaltase; PDBTitle: crystal complex of n-terminal sucrase-isomaltase with kotalanol
98	d1miwa2	Alignment	not modelled	6.3	22	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
99	c3rlcA	Alignment	not modelled	6.2	20	PDB header: structural protein Chain: A: PDB Molecule: a1 protein; PDBTitle: crystal structure of the read-through domain from bacteriophage qbeta2 a1 protein, hexagonal crystal form