

Email spiwokv@vscht.cz

Description tbn1\_\_\_

Date Sun Oct 7 15:47:42
BST 2018

Unique Job ID 888c645d580a078d

Detailed template information

info	information						
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information	
1	c3sngA_	Alignment		100.0	100	PDB header:hydrolase Chain: A: PDB Molecule:nuclease; PDBTitle: x-ray structure of fully glycosylated bifunctional nuclease tbn1 from2 solanum lycopersicum (tomato)	
2	<u>c3w52A_</u>	Alignment		100.0	54	PDB header:hydrolase Chain: A: PDB Molecule:endonuclease 2; PDBTitle: zinc-dependent bifunctional nuclease	
3	<u>d1ak0a</u> _	Alignment		100.0	29	Fold:Phospholipase C/P1 nuclease Superfamily:Phospholipase C/P1 nuclease Family:P1 nuclease	
4	<u>c5fbfA</u>	Alignment		100.0	29	PDB header:hydrolase Chain: A: PDB Molecule:nuclease s1; PDBTitle: s1 nuclease from aspergillus oryzae in complex with two molecules of2 2'-deoxycytidine-5'-monophosphate	
5	<u>dlah7a</u> _	Alignment		100.0	15	Fold:Phospholipase C/P1 nuclease Superfamily:Phospholipase C/P1 nuclease Family:Phospholipase C	
6	<u>dlkhoal</u>	Alignment		98.5	17	Fold:Phospholipase C/P1 nuclease Superfamily:Phospholipase C/P1 nuclease Family:Phospholipase C	
7	dlolpal	Alignment		98.4	19	Fold:Phospholipase C/P1 nuclease Superfamily:Phospholipase C/P1 nuclease Family:Phospholipase C	
8	c1olpB_	Alignment		97.4	18	PDB header:hydrolase Chain: B: PDB Molecule:alpha-toxin; PDBTitle: alpha toxin from clostridium absonum	
9	clgygA_	Alignment	The state of the s	97.3	21	PDB header:hydrolase Chain: A: PDB Molecule:phospholipase c; PDBTitle: r32 closed form of alpha-toxin from clostridium perfringens2 strain cer89l43	
10	<u>dlcalal</u>	Alignment		97.0	18	Fold:Phospholipase C/P1 nuclease Superfamily:Phospholipase C/P1 nuclease Family:Phospholipase C	
11	c4xpmA_	Alignment	***	40.4	30	PDB header:protein binding Chain: A: PDB Molecule:protein meh1; PDBTitle: crystal structure of ego-tc	

13 Catesta. Alignment.  14 Catesta. Alignment.  15 Catesta. Alignment.  16 Catesta. Alignment.  17 Catesta. Alignment.  18 Catesta. Alignment.  19 Catesta. Alignment.  19 Catesta. Alignment.  10 Catesta. Alignment.  11 Catesta. Alignment.  12 Catesta. Alignment.  13 Catesta. Alignment.  14 Catesta. Alignment.  15 Catesta. Alignment.  16 Catesta. Alignment.  17 Catesta. Alignment.  18 Catesta. Alignment.  19 Catesta. Alignment.  10 Catesta. Alignment.  11 Catesta. Alignment.  12 Catesta. Alignment.  13 Catesta. Alignment.  14 Catesta. Alignment.  15 Catesta. Alignment.  16 Catesta. Alignment.  17 Catesta. Alignment.  18 Catesta. Alignment.  19 Catesta. Alignment.  10 Catesta. Alignment.  10 Catesta. Alignment.  10 Catesta. Alignment.  11 Catesta. Alignment.  12 Catesta. Alignment.  13 Catesta. Alignment.  14 Catesta. Alignment.  15 Catesta. Alignment.  16 Catesta. Alignment.  17 Catesta. Catesta. Alignment.  18 Catesta. Alignment.  19 Catesta. Alignment				4		
15 Clipul. Algument   16 Child. Algument   17 Clipul. Algument   18 Clipul. Algument   18 Clipul. Algument   18 Clipul. Algument   18 Clipul. Algument   19 De Bederritus binding protein growth of felie particular skills.   19 De Bederritus could promite, unknown function   19 Clipul. Algument   19 Clipul. Clipul. Clipul. Algument   19 Clipul.	12	c2gq1A_	Alignment	5	16.9	8 Chain: A: PDB Molecule:fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-
14.2 21. Chain. 2: PDB Moleculery Its problem.  15. CLIDIA. Alignment  10.4 17. PDB Meader visus and of the problem from bacillac substitic polarisation of the problem from bacillac substitic polarisation of the panieukopenia wirus (strain b) wiral popularisation of foliare panieukopenia wirus empty 2 particles of popularisation of foliare panieukopenia wirus empty 2 particles of popularisation of popular	13	c2rhsB_	Alignment	2000	15.3	21 <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein
15 clipul. Alignment 10.4 17 PDB Moleculerione panieutopenia virus dermination of faline panieutopenia virus empty particles  16 cstud. Alignment 9.6 25 PDB Moleculerione determination of faline panieutopenia virus empty particles  17 d2ccqual. Alignment 9.6 15 Pold: Record and protein conting associated protein pold Moleculerione conting associated protein pold: PDB Moleculerione continue con	14	c3d0wD_	Alignment		14.2	12 Chain: D: PDB Molecule:yflh protein; PDBTitle: crystal structure of yflh protein from bacillus subtilis.
16 záfugl. Alignment  9.6 16 Schigl. Alignment  9.6 17 dzagal Alignment  9.6 18 Superfamily TaxXiv place protein sorting-associated protein rot modelled  9.6 18 Superfamily TaxXiv place protein 473: PDBT Moleculeura finger fregion 370: 2 400: of human zinc finger protein 473: PDBT Moleculeura finger fregion 370: 2 400: of human zinc finger protein 473: PDBT Moleculeura finger fregion 370: 2 400: of human zinc finger protein 473: PDBT Moleculeura finger protein 473: PDBTMT in zinc finger fregion 370: 2 400: of human zinc finger protein 473: PDBTMT in zinc finger fregion 370: 2 400: of human zinc finger protein 473: PDBTMT in zinc finger fregion 370: 2 400: of human zinc finger protein 473: PDBTMT in zinc finger fregion 370: 2 400: of human zinc finger protein 473: PDBTMT in zinc finger fregion 2 400: of human zinc finger protein 473: PDBTMT in zinc finger fregion 2 400: of human zinc finger protein 473: PDBTMT in z	15	clfpvA_	Alignment	ي الم	10.4	17 <b>Chain:</b> A: <b>PDB Molecule:</b> feline panleukopenia virus (strain b) viral <b>PDBTitle:</b> structure determination of feline panleukopenia virus
18 c2eouA. Alignment  9.6 18 Superfamily: 7a0600-like Family: 7a06	16	c5fugl_	Alignment	4	9.6	Chain: I: PDB Molecule: vacuolar protein sorting-associated protein 72 homolog;
18 \$260UA Alignment  9.6 36 Chain: A: PDB Molecule; an Engine protein 473; PDBTHEs solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473  PDB header: Virus Chain: A: PDB Molecule; capsid; PDBTHEs solution structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4  20 \$\frac{4971B}{2}\$ Alignment  9.0 PDB header: Virus Chain: A: PDB Molecule; capsid; PDBTHEs: structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4  21 \$\frac{4100}{2}\$ Alignment  22 \$\frac{4971B}{2}\$ Alignment  23 \$\frac{4019}{2}\$ Alignment  24 \$\frac{4019}{2}\$ Alignment  25 \$\frac{4383B}{2}\$ Alignment  26 \$\frac{4019}{2}\$ Alignment  27 \$\frac{4019}{2}\$ Alignment  28 \$\frac{4019}{2}\$ Alignment  29 \$\frac{4019}{2}\$ Alignment  20 \$\frac{4019}{2}\$ Alignment  21 \$\frac{4019}{2}\$ Alignment  22 \$\frac{4019}{2}\$ Alignment  23 \$\frac{4028A}{2}\$ Alignment  24 \$\frac{4019}{2}\$ Alignment  25 \$\frac{4028A}{2}\$ Alignment  26 \$\frac{4019}{2}\$ Alignment  27 \$\frac{40100}{2}\$ Alignment  28 \$\frac{4019}{2}\$ Alignment  29 \$\frac{401000}{2}\$ Alignment  20 \$\frac{401000}{2}\$ Alignment  21 \$\frac{401000}{2}\$ Alignment  22 \$\frac{4010000}{2}\$ Alignment  23 \$40100000000000000000000000000000000000	17	d2qzga1	Alignment		9.6	18 Superfamily:Ta0600-like
9.5 22 Cahara Alignment  9.5 22 Chain: B: PDB Moleculescapsid; PDBTitle: structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4  20 Cap71B Alignment  9.0 24 Chain: B: PDB Moleculesphenylalanine—trna ligase beta subunit; PDBTitle: apo phers from p. aeuriginosa  21 d1jicb6 Alignment  22 c3h3gB Alignment  23 d2qsba1 Alignment  10 modelled  7.9 45 PDBTitle: crystal structure of the extracellular domain of PheRS, PheT  PDB header:membrane protein Chain: B: PDB Moleculesphenylalanine—trna ligase beta subunit; PDBTitle: apo phers from p. aeuriginosa  PDB header:membrane protein Chain: B: PDB Moleculesphenylalanine—trna ligase beta subunit; PDBTitle: crystal structure of the extracellular domain of the human parathyroid hormone-related protein; PDBTitle: crystal structure of the extracellular domain of the human parathyroid? hormone receiped (pthrp) in complex with parathyroid hormone-related3 protein (pthrp)  Politie: crystal structure of the extracellular domain of the human parathyroid? hormone-related3 protein (pthrp)  Politie: crystal structure of the heterotrimeric sectl3-nup145c-nup842 ungental protein, protein transport Chain: C. PDB Moleculesupcin protein protein transport Chain: C. PDB Moleculesupcin complex  PDB header: virus  25 c4qc8A Alignment not modelled  7.4 15 PDBTitle: crystal structure of the heterotrimeric sectl3-nup145c-nup842 ungental protein, protein transport Chain: C. PDB Moleculesupcin protein	18	c2eouA_	Alignment		9.6	36 Chain: A: PDB Molecule:zinc finger protein 473; PDBTitle: solution structure of the c2h2 type zinc finger (region
20 c4p71B Alignment  9.0  24 Chain: B: PDB Molecule:phenylalaninetrna ligase beta subunit: PDBTitle: apo phers from p. aeuriginosa  Fold:PheT/TilS domain Superfamily:PheT/TilS domain Family:B3/B4 domain of PheRS, PheT  PDB header:membrane protein Chain: B: PDB Molecule:parathyroid hormone-related protein; PDBTitle: crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pthr) in complex with parathyroid hormone-related3 protein (pthrp)  23 d2qsba1 Alignment not modelled 7.9  24 c3ikoC Alignment not modelled 7.9  25 c4qcBA Alignment not modelled 7.4  26 d1m5ha1 Alignment not modelled 7.3  27 d1mvma Alignment not modelled 7.3  28 d1spia Alignment not modelled 7.3  29 Fold:PerT/TilS domain Superfamily:PheT/TilS domain Family:PerT/TilS domain Family:Pab Molecule:parathyroid hormone-related protein; PDBTitle: crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pthr) in complex with parathyroid hormone-related 3 protein (pthrp)  Fold:Bromodomain-like Superfamily:Ta0600-like PDB header:structural protein, protein transport Chain: C: PDB Molecule:pucleoprin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoprin complex PDB header:virus Chain: C: PDB Molecule:pucleoprin complex PDBTitle: crystal structural annotation of pathogenic bovine parvovirus-1  Fold:Iterredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Farvoviridae-like VP Fold:Carbohydrate phosphatase  Fold:Carbohydrate phosphatase	19	<u>c2g8gA</u>	Alignment		9.5	22 Chain: A: PDB Molecule:capsid; PDBTitle: structurally mapping the diverse phenotype of adeno-2
21 dl.jicb6 Alignment not modelled 8.0 35 Superfamily:PheT/TilS domain Family:Ba/B4 domain of PheRS, PheT  PDB header:membrane protein Chain: 8: PDB Molecule:parathyroid hormone-related protein; Chain: 8: PDB Molecule:parathyroid hormone-related protein; Chain: 8: PDB Molecule:parathyroid hormone-related protein; PDB Title: crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pth1r) in complex with parathyroid hormone-related3 protein (pthrp)  23 d2qsbal Alignment not modelled 7.9 22 Superfamily:Ta0600-like Family:Ta0600-like  PDB header:structural protein, protein transport Chain: C: PDB Molecule:nucleoporin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex  PDB header:structural protein, protein transport Chain: C: PDB Molecule:nucleoporin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex  PDB header:structural annotation of pathogenic bovine parvovirus-1  5 c4qc8A Alignment not modelled 7.4 15 Chain: A: PDB Molecule:vp2; PDBTitle: structural annotation of pathogenic bovine parvovirus-1  Fold:Ferredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase  Fold:Terredoxin-like/VP (viral coat and capsid proteins)  Superfamily:sparvoviridae-like VP  Fold:Terredoxin-like VP  Fold:Terredoxin-like VP  Fold:Terredoxin-like VP  Fold:Terredoxin-like VP  Fold:Terredoxin-like/VP (viral coat and capsid proteins)  Superfamily:SpNA viruses  Family:Porvoviridae-like VP  Fold:Carbohydrate phosphatase	20	<u>c4p71B</u> _	Alignment		9.0	24 Chain: B: PDB Molecule:phenylalaninetrna ligase beta subunit;
Alignment not modelled 7.9 45 PDB Title: crystal structure of the extracellular domain of the human parathyroid2 hormone-related protein; protein (pthr) in complex with parathyroid hormone-related3 protein (pthrp)  23 d2qsba1 Alignment not modelled 7.9 25 Fold:Bromodomain-like Superfamily:Ta0600-like Family:Ta0600-like  PDB header:structural protein, protein transport Chain: C: PDB Molecule:nucleoporin nup84; PDBTtle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex  PDB header:virus  25 c4qc8A Alignment not modelled 7.4 15 Chain: A: PDB Molecule:vp2; PDBTtle: structural annotation of pathogenic bovine parvovirus-1  Fold:Ferredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase  Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins)  Alignment not modelled 7.3 11 Superfamily:ssDNA viruses Family:Parvoviridae-like VP  Fold:Carbohydrate phosphatase  Fold:Carbohydrate phosphatase	21	d1jjcb6	Alignment	not modelled	8.0	35 Superfamily:PheT/TilS domain
Alignment not modelled 7.9 22 Superfamily:Ta0600-like Family:Ta0600-like  24 C3ikoC Alignment not modelled 7.5 9 PDB header:structural protein, protein transport Chain: C: PDB Molecule:nucleoporin nup84; PDBTItle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex  25 C4qc8A Alignment not modelled 7.4 15 Chain: A: PDB Molecule:vp2; PDBTitle: structural annotation of pathogenic bovine parvovirus-1  26 d1m5ha1 Alignment not modelled 7.3 29 Fold:Ferredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase  27 d1mvma Alignment not modelled 7.3 11 Superfamily:ssDNA viruses Family:Parvoviridae-like VP  Fold:Carbohydrate phosphatase  28 d1spia Alignment not modelled 6.9 17 Superfamily:Carbohydrate phosphatase	22	<u>c3h3gB</u> _	Alignment	not modelled	7.9	Chain: B: PDB Molecule:parathyroid hormone-related protein; 45 PDBTitle: crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pth1r) in complex with parathyroid
24 c3ikoC Alignment not modelled 7.5 9 Chain: C: PDB Molecule:nucleoporin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex  25 c4qc8A Alignment not modelled 7.4 15 Chain: A: PDB Molecule:vp2; PDBTitle: structural annotation of pathogenic bovine parvovirus-1  26 d1m5ha1 Alignment not modelled 7.3 29 formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase  27 d1mvma Alignment not modelled 7.3 11 Superfamily:ssDNA viruses Family:Parvoviridae-like VP  28 d1spia Alignment not modelled 6.9 17 Superfamily:Carbohydrate phosphatase	23	d2qsba1	Alignment	not modelled	7.9	Fold:Bromodomain-like 22 Superfamily:Ta0600-like
25 c4qc8A Alignment not modelled 7.4 15 Chain: A: PDB Molecule:vp2; PDBTitle: structural annotation of pathogenic bovine parvovirus-1  26 d1m5ha1 Alignment not modelled 7.3 29 Fold:Ferredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase  27 d1mvma Alignment not modelled 7.3 11 Superfamily:ssDNA viruses Family:Parvoviridae-like VP  28 d1spia Alignment not modelled 6.9 17 Superfamily:Carbohydrate phosphatase  Superfamily:SsDNA viruses Family:Parvoviridae-like VP	24	c3ikoC_	Alignment	not modelled	7.5	9 Chain: C: PDB Molecule:nucleoporin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-
26 d1m5ha1 Alignment not modelled 7.3 Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase  27 d1mvma Alignment not modelled 7.3 11 Superfamily:spDNA viruses Family:Parvoviridae-like VP  28 d1spia Alignment not modelled 6.9 17 Superfamily:Carbohydrate phosphatase  Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase  Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins)  Superfamily:SpDNA viruses Family:Parvoviridae-like VP  Fold:Carbohydrate phosphatase	25	<u>c4qc8A_</u>	Alignment	not modelled	7.4	PDB header:virus 15 Chain: A: PDB Molecule:vp2;
27 dlmvma Alignment not modelled 7.3 Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins) 11 Superfamily:ssDNA viruses Family:Parvoviridae-like VP  Fold:Carbohydrate phosphatase 28 dlspia Alignment not modelled 6.9 17 Superfamily:Carbohydrate phosphatase	26	d1m5ha1	Alignment	not modelled	7.3	Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin
28 dlspia_ Alignment not modelled 6.9 17 Superfamily:Carbohydrate phosphatase	27	d1mvma_	Alignment	not modelled	7.3	Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins)  11 Superfamily:ssDNA viruses
	28	d1spia_	Alignment	not modelled	6.9	17 Superfamily:Carbohydrate phosphatase

	_	_	_			PDB header:hydrolase
29	c1zgxA_	Alignment	not modelled	6.8	12	Chain: A: PDB Molecule:guanyl-specific ribonuclease sa; PDBTitle: crystal structure of ribonuclease mutant
30	c5chlA_	Alignment	not modelled	6.8	45	PDB header:chaperone Chain: A: PDB Molecule:vacuolar protein sorting-associated protein 72 homolog; PDBTitle: structural basis of h2a.z recognition by yl1 histone chaperone2 component of srcap/swr1 chromatin remodeling complex
31	d1bk4a_	Alignment	not modelled	6.6	14	Fold:Carbohydrate phosphatase Superfamily:Carbohydrate phosphatase Family:Inositol monophosphatase/fructose-1,6-bisphosphatase-like
32	d1c8da_	Alignment	not modelled	6.4	17	Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily:ssDNA viruses Family:Parvoviridae-like VP
33	d1bh9a_	Alignment	not modelled	6.4	25	Fold:Histone-fold Superfamily:Histone-fold Family:TBP-associated factors, TAFs
34	c4g0rA_	Alignment	not modelled	6.3	17	PDB header:virus/dna Chain: A: PDB Molecule:capsid protein vp1; PDBTitle: structural characterization of h-1 parvovirus: comparison of2 infectious virions to replication defective particles
35	<u>c3kieF_</u>	Alignment	not modelled	6.3	22	PDB header:virus Chain: F: PDB Molecule:capsid protein vp1; PDBTitle: crystal structure of adeno-associated virus serotype 3b
36	<u>d1lp3a</u> _	Alignment	not modelled	6.2	22	Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily:ssDNA viruses Family:Parvoviridae-like VP
37	d2b0la1	Alignment	not modelled	6.0	13	Fold:DNA/RNA-binding 3-helical bundle Superfamily:"Winged helix" DNA-binding domain Family:CodY HTH domain
38	d2ebfx2	Alignment	not modelled	5.9	30	Fold:EreA/ChaN-like Superfamily:EreA/ChaN-like Family:PMT domain-like
39	c2fhyL_	Alignment	not modelled	5.8	11	PDB header:hydrolase Chain: L: PDB Molecule:fructose-1,6-bisphosphatase 1; PDBTitle: structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor
40	d1ftaa_	Alignment	not modelled	5.8	11	Fold:Carbohydrate phosphatase Superfamily:Carbohydrate phosphatase Family:Inositol monophosphatase/fructose-1,6-bisphosphatase-like
41	<u>c2l1iA_</u>	Alignment	not modelled	5.7	17	PDB header:transcription Chain: A: PDB Molecule:hltf protein; PDBTitle: nmr structure of the hltf hiran domain
42	<u>d1d9qa_</u>	Alignment	not modelled	5.7	11	Fold:Carbohydrate phosphatase Superfamily:Carbohydrate phosphatase Family:Inositol monophosphatase/fructose-1,6-bisphosphatase-like
43	<u>c3nttA_</u>	Alignment	not modelled	5.6	11	PDB header:virus Chain: A: PDB Molecule:capsid protein; PDBTitle: structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis
44	c1k3vA_	Alignment	not modelled	5.5	22	PDB header:virus Chain: A: PDB Molecule:capsid protein vp2; PDBTitle: porcine parvovirus capsid
45	d1k3va_	Alignment	not modelled	5.5	22	Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily:ssDNA viruses Family:Parvoviridae-like VP
46	d1s58a_	Alignment	not modelled	5.5	12	Fold:Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily:ssDNA viruses Family:Parvoviridae-like VP
47	d1nuwa_	Alignment	not modelled	5.3	14	Fold:Carbohydrate phosphatase Superfamily:Carbohydrate phosphatase Family:Inositol monophosphatase/fructose-1,6-bisphosphatase-like
48	c3pcoD_	Alignment	not modelled	5.1	31	PDB header:ligase Chain: D: PDB Molecule:phenylalanyl-trna synthetase, beta chain; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp