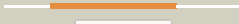

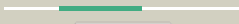

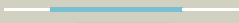




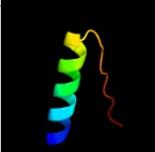







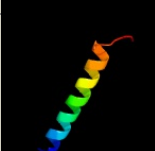



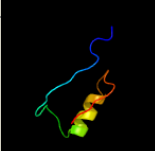
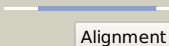

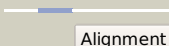
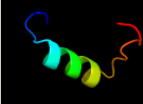
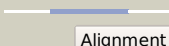
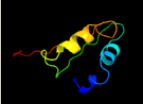
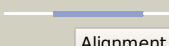

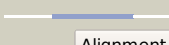
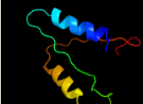
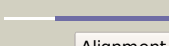


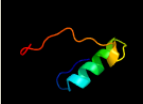

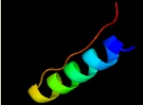

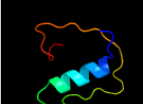
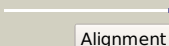
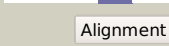

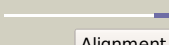
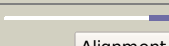
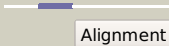
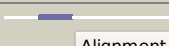
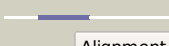


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1476_(-)_1666210_1666770
Date	Fri Aug 2 13:30:05 BST 2019
Unique Job ID	9407236113326cb0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kptA_	 Alignment		82.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative secreted protein; PDBTitle: solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a
2	c5dboA_	 Alignment		47.7	16	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
3	c6hwhT_	 Alignment		39.9	14	PDB header: electron transport Chain: T: PDB Molecule: uncharacterized protein msmeg_4692/msmei_4575; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
4	c2kw7A_	 Alignment		38.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
5	c4zquA_	 Alignment		37.9	8	PDB header: toxin Chain: A: PDB Molecule: cdia-ct toxin, conserved domain protein; PDBTitle: cdia-ct/cdii toxin and immunity complex from yersinia2 pseudotuberculosis
6	c5anpB_	 Alignment		35.6	9	PDB header: unknown function Chain: B: PDB Molecule: ba41; PDBTitle: crystal structure of the ba41 protein from bizonia argentinensis
7	c3wrpB_	 Alignment		33.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
8	c2jx5A_	 Alignment		25.2	21	PDB header: ribosomal protein Chain: A: PDB Molecule: glub(s27a); PDBTitle: solution structure of the ubiquitin domain n-terminal to2 the s27a ribosomal subunit of giardia lamblia
9	c2rmzA_	 Alignment		23.9	26	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
10	c4wpgA_	 Alignment		23.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
11	c2x3dC_	 Alignment		23.1	21	PDB header: unknown function Chain: C: PDB Molecule: sso6206; PDBTitle: crystal structure of sso6206 from sulfolobus solfataricus p2

12	c5vxsF_		Alignment		22.0	13	PDB header: lyase Chain: F: PDB Molecule: citrate lyase subunit beta-like protein, mitochondrial; PDBTitle: crystal structure analysis of human clybl in apo form
13	d1gjja1		Alignment		21.8	25	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
14	c5k9xA_		Alignment		21.7	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
15	c5lvaA_		Alignment		21.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(p)h-fmn oxidoreductase; PDBTitle: crystal structure of thermophilic tryptophan halogenase (th-hal)2 enzyme from streptomycin violaceusniger.
16	d1rtta_		Alignment		20.3	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
17	c5d88A_		Alignment		19.4	23	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
18	d1ni9a_		Alignment		18.8	32	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: GlpX-like bacterial fructose-1,6-bisphosphatase
19	c4g6uA_		Alignment		18.2	4	PDB header: toxin Chain: A: PDB Molecule: ec869 cdia-ct; PDBTitle: cdia-ct/cdii toxin and immunity complex from escherichia coli
20	c4ar0A_		Alignment		18.1	17	PDB header: transport Chain: A: PDB Molecule: type iv pilus biogenesis and competence protein pilq; PDBTitle: n0 domain of neisseria meningitidis pilus assembly protein pilq
21	c5ohdB_		Alignment	not modelled	17.8	22	PDB header: membrane protein Chain: B: PDB Molecule: growth hormone receptor; PDBTitle: putative inactive (dormant) dimeric state of ghr transmembrane domain
22	c6jdkA_		Alignment	not modelled	17.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: baeyer-villiger monooxygenase; PDBTitle: crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
23	c4mozC_		Alignment	not modelled	17.2	21	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
24	c2advB_		Alignment	not modelled	16.9	33	PDB header: hydrolase Chain: B: PDB Molecule: glutaryl 7- aminocephalosporanic acid acylase; PDBTitle: crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
25	c6an7D_		Alignment	not modelled	16.3	16	PDB header: transport protein Chain: D: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
26	d1h9ea_		Alignment	not modelled	16.3	25	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
27	c5ltwK_		Alignment	not modelled	16.1	35	PDB header: protein binding Chain: K: PDB Molecule: heat shock protein beta-6; PDBTitle: complex of human 14-3-3 sigma clu1 mutant with phosphorylated heat2 shock protein b6
28	c2outA_		Alignment	not modelled	15.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mu-like prophage flumu protein gp35, protein PDBTitle: solution structure of hi1506, a novel two domain protein2

						from haemophilus influenzae
29	c3f2vA_	Alignment	not modelled	14.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 14; PDBTitle: crystal structure of the general stress protein 14 (tde0354) in2 complex with fmn from treponema denticola, northeast structural3 genomics consortium target tdr58.
30	c5b04G_	Alignment	not modelled	14.4	19	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
31	c6cfwL_	Alignment	not modelled	13.8	23	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
32	c3u7rB_	Alignment	not modelled	13.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent fmn reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
33	c3q9qB_	Alignment	not modelled	13.2	30	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
34	c2kncA_	Alignment	not modelled	13.2	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
35	c6f2rT_	Alignment	not modelled	13.0	20	PDB header: chaperone Chain: T: PDB Molecule: heat shock protein beta-3,heat shock protein beta-3,heat PDBTitle: a hetrotetramer of human hspb2 and hspb3
36	c5b04B_	Alignment	not modelled	12.8	13	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
37	c3ha2B_	Alignment	not modelled	12.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-quinone reductase; PDBTitle: crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
38	c2wj7D_	Alignment	not modelled	12.3	35	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alphab crystallin
39	c5j7xA_	Alignment	not modelled	12.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylaniline monooxygenase, putative; PDBTitle: baeyer-villiger monooxygenase bvmoaf1838 from aspergillus flavus
40	c5mq6A_	Alignment	not modelled	11.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase-like protein; PDBTitle: polycyclic ketone monooxygenase from the thermophilic fungus2 thermothelomyces thermophila
41	c2bolA_	Alignment	not modelled	11.0	26	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small heat shock2 protein
42	c3a11D_	Alignment	not modelled	10.8	22	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
43	c5m0zA_	Alignment	not modelled	10.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase from thermocrisum municipale.; PDBTitle: cyclohexanone monooxygenase from t. municipale: reduced enzyme bound2 to nadp+
44	c6daqA_	Alignment	not modelled	10.3	22	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
45	c1u0kA_	Alignment	not modelled	10.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gene product pa4716; PDBTitle: the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa
46	c6c14A_	Alignment	not modelled	10.2	7	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
47	c1qjjA_	Alignment	not modelled	9.9	25	PDB header: membrane protein Chain: A: PDB Molecule: lap2; PDBTitle: n-terminal constant region of the nuclear envelope protein2 lap2
48	c2lt2A_	Alignment	not modelled	9.8	12	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of ba42 protein from the psychrophilic bacteria bizionia2 argentinensis sp. nov.
49	c2y9kG_	Alignment	not modelled	9.7	11	PDB header: protein transport Chain: G: PDB Molecule: protein invg; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution
50	c4n6hA_	Alignment	not modelled	9.7	10	PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562, delta-type opioid receptor PDBTitle: 1.8 a structure of the human delta opioid 7tm receptor (psi community2 target)
51	c5tchG_	Alignment	not modelled	9.6	11	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
52	c4b9zA_	Alignment	not modelled	9.5	23	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase, putative, adg31b; PDBTitle: crystal structure of agd31b, alpha-transglucosylase,2

						complexed with acarbose PDB header: transferase
53	c2ks1B_	Alignment	not modelled	9.4	21	Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
54	d1xuba1	Alignment	not modelled	9.2	22	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: PhzC/PhzF-like
55	d3bpdA1	Alignment	not modelled	9.2	17	Fold: Ferredoxin-like Superfamily: MTH889-like Family: MTH889-like
56	c1spfA_	Alignment	not modelled	9.2	35	PDB header: lipoprotein(surface film) Chain: A: PDB Molecule: pulmonary surfactant-associated polypeptide c; PDBTitle: the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix
57	c3vsjA_	Alignment	not modelled	9.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-amino-5-chlorophenol 1,6-dioxygenase alpha subunit; PDBTitle: crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products
58	c1w4xA_	Alignment	not modelled	9.1	9	PDB header: oxygenase Chain: A: PDB Molecule: phenylacetone monooxygenase; PDBTitle: phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
59	d1w4xa2	Alignment	not modelled	9.0	9	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
60	c3uclA_	Alignment	not modelled	8.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: cyclohexanone-bound crystal structure of cyclohexanone monooxygenase2 in the rotated conformation
61	c6an7C_	Alignment	not modelled	8.7	14	PDB header: transport protein Chain: C: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
62	c2kncB_	Alignment	not modelled	8.5	26	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
63	d2raqa1	Alignment	not modelled	8.5	17	Fold: Ferredoxin-like Superfamily: MTH889-like Family: MTH889-like
64	c2e7zA_	Alignment	not modelled	8.4	18	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
65	c6dv5T_	Alignment	not modelled	8.3	30	PDB header: chaperone Chain: T: PDB Molecule: heat shock protein beta-1; PDBTitle: oligomeric complex of a hsp27 24-mer at 3.6 a resolution
66	c5zazA_	Alignment	not modelled	8.3	26	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
67	c4zeoH_	Alignment	not modelled	8.1	17	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
68	c2n2aA_	Alignment	not modelled	8.1	17	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains
69	c3uoqB_	Alignment	not modelled	8.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: otemo; PDBTitle: crystal structure of otemo complex with fad and nadp (form 1)
70	c3gwdA_	Alignment	not modelled	8.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase
71	c6f2rA_	Alignment	not modelled	7.9	37	PDB header: chaperone Chain: A: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
72	c2d0gA_	Alignment	not modelled	7.9	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase i; PDBTitle: crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tvai) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide
73	d1pdoa_	Alignment	not modelled	7.9	14	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
74	c6ezoH_	Alignment	not modelled	7.8	21	PDB header: membrane protein Chain: H: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
75	c2k74A_	Alignment	not modelled	7.7	14	PDB header: membrane protein, oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
76	c3fpvC_	Alignment	not modelled	7.7	22	PDB header: heme binding protein Chain: C: PDB Molecule: extracellular haem-binding protein; PDBTitle: crystal structure of hbps
77	c2bbjB_	Alignment	not modelled	7.7	15	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter

78	c6bwsA	Alignment	not modelled	7.6	17	PDB header: unknown function Chain: A: PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
79	d2gm3a1	Alignment	not modelled	7.3	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
80	c3gxxB	Alignment	not modelled	7.3	8	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt6; PDBTitle: structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
81	c2kluA	Alignment	not modelled	7.3	13	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
82	c4ap3A	Alignment	not modelled	7.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: steroid monooxygenase; PDBTitle: oxidized steroid monooxygenase bound to nadp
83	c2klrA	Alignment	not modelled	7.1	37	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin b chain; PDBTitle: solid-state nmr structure of the alpha-crystallin domain in alphas-2 crystallin oligomers
84	d1ydgA	Alignment	not modelled	7.1	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
85	c2k9yA	Alignment	not modelled	7.0	17	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
86	c2k9yB	Alignment	not modelled	7.0	17	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
87	c2z2uA	Alignment	not modelled	7.0	21	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
88	c5ey5A	Alignment	not modelled	6.9	18	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
89	c2fpgA	Alignment	not modelled	6.9	18	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [gdp-forming] alpha-chain, PDBTitle: crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
90	c3ju7B	Alignment	not modelled	6.7	10	PDB header: transferase Chain: B: PDB Molecule: putative plp-dependent aminotransferase; PDBTitle: crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
91	c6f2rE	Alignment	not modelled	6.7	37	PDB header: chaperone Chain: E: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
92	c6f2rI	Alignment	not modelled	6.7	37	PDB header: chaperone Chain: I: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
93	c3ptjA	Alignment	not modelled	6.6	10	PDB header: hydrolase Chain: A: PDB Molecule: upf0603 protein at1g54780, chloroplastic; PDBTitle: structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein atpl18.3
94	d1f61a	Alignment	not modelled	6.6	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
95	c3qphA	Alignment	not modelled	6.4	11	PDB header: transcription Chain: A: PDB Molecule: trmb, a global transcription regulator; PDBTitle: the three-dimensional structure of trmb, a global transcriptional2 regulator of the hyperthermophilic archaeon pyrococcus furiosus in3 complex with sucrose
96	c5d6aA	Alignment	not modelled	6.4	20	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase of the abc class; PDBTitle: 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
97	c2l8sA	Alignment	not modelled	6.4	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
98	c3e96B	Alignment	not modelled	6.1	9	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
99	d2j8xa1	Alignment	not modelled	6.0	31	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase